UNIVERSITY OF DELHI

MASTER OF SCIENCE
(TWO-YEAR PROGRAMME)
IN
PLANT MOLECULAR BIOLOGY AND BIOTECHNOLOGY
(Effective from the Academic Year 2025-2026)

BROCHURE

Department of Plant Molecular Biology
Faculty of Interdisciplinary and Applied Sciences
University of Delhi, South Campus
New Delhi – 110 021, India

NEP 2020 based syllabus as approved in the meeting of 'Committee of Courses' held on 04.12.2025*, in the meeting of 'Faculty of Interdisciplinary and Applied Sciences' held on* 23.02.2026*, and meeting of 'Standing Committee' held on*_____________

Revised Syllabus as approved by Academic Council on _____, 2026
and
Executive Council on _____, 2026

Contents

I. About the Department

The **Department of Plant Molecular Biology,** established in 1988 under the Faculty of Interdisciplinary and Applied Sciences (FIAS), advances research and education in frontier areas of plant molecular biology and biotechnology. It was enriched by the merger of the **Unit for Plant Cell and Molecular Biology** in 1988 (originally established by the DST) and the award of 'Committee on Strengthening of Infrastructure for Science and Technology (COSIST)' grant by the UGC (1990–1995). The Department was recognized under UGC's Special Assistance Programme (DRS Phase I-III, 2002-2018) to strengthen research and teaching in Functional Genomics. Since its inception, the Department has been led by eminent scientists, including Prof. S.C. Maheshwari (1988–1992), Prof. Akhilesh K. Tyagi (1988, 1992–95, 1998–2001), Prof. Jitendra P. Khurana (1995–1998, 2001–2004, 2014–2016), Prof. Paramjit Khurana (2004–2007, 2016–19), Prof. Anil Grover (2007–2010, 2019–2022), Prof. Indranil Dasgupta (2010–2013), Prof. Madan Mohan (2013–2014), Prof. Sanjay Kapoor (2022-2025), and Prof. Girdhar K. Pandey (2025–present).

We are one of the India's top-ranking institutions for Plant Science Education and Research, nestled within the secure and picturesque South Campus of the University of Delhi. With Delhi University's rich legacy of academic and research excellence, the Department of Plant Molecular Biology is committed to upholding and advancing this tradition through its innovative teaching and cutting-edge research programmes. Since its establishment, DPMB has been at the forefront of numerous multinational research initiatives, fostering a dynamic, globally connected research community, notably through the Rockefeller Rice Biotechnology Program (1990-2000), which bolstered expertise in transgenics and gene analysis. With the turn of the millennium, the Department played a pivotal role in large-scale genome sequencing, contributing to the complete sequencing of the rice genome (2005), tomato genome (2012), and wheat genome (2019) as part of several international consortia. Our faculty maintains strong collaborations with leading international researchers through bilateral research programmes, providing young scientists with unparalleled opportunities to engage in world-class research and turn their aspirations into reality.

Faculty members have undertaken several research initiatives supported by major grants from DBT, DST, UGC, CSIR, DAE-BRNS, the European Commission, and the Rockefeller Foundation (in the area of the Centre for Plant Molecular Biology, Genome Sequencing Initiatives, and Functional Genomics). Faculty members actively participate in multi-institutional and international collaborations, producing 900+ publications in high-impact journals such as *Nature*, *Genome Research*, *Nucleic Acids Research*, *Trends in Biotechnology*, *Trends in Plant Science*, *Plant Journal*, *Plant Physiology*, *Plant Biotechnology Journal*, *New Phytologist*, *Journal of Experimental Botany*, *Plant Cell & Environment*, *and Bioessays*, and others, along with several patents. Their contributions have been recognized through national and international fellowships and awards.

While emphasizing fundamental research and training, the Department is committed to translational applications for human welfare. Its alumni hold key positions in academia and research institutions in the country and worldwide, including Washington State University;

University of Nebraska, Lincoln; Texas Tech University Health Sciences Centre Rothamsted Research Station), Guru Jambheshwar University (Hisar), Bioseed Research (Hyderabad), ICAR-IARI, ICGEB, BRIC-NIPGR, JNU, IIT Delhi, BRIC-NII, Indraprastha University, IISER (Bhopal), TERI University, CIMAP (Lucknow), Birsa Agricultural University (Ranchi), Assam Agricultural University (Jorhat), BITS (Hyderabad), NABI (Mohali), University of Hyderabad, among others. Many lead research groups in both academia and industry, making significant contributions to the advancement of plant molecular biology.

II. Introduction to NEP Programme

a. Scope

The National Education Policy (NEP) 2020 aims to transform post-graduate education by introducing flexibility, interdisciplinary, and skill-oriented learning. The program is structured to equip students with advanced knowledge and specialized skills, preparing them for research and innovation. The key features of this program include a flexible program structure, interdisciplinary learning, multiple entry and exit points, credit mobility, a focus on emerging fields, skill-based learning, continuous assessment, and an emphasis on research and skill development. NEP2020 modernizes post-graduate education by making it flexible, industry-aligned, and student-centric, empowering learners to shape their academic journey in line with their interests and career aspirations.

b. Definition of Keywords

i. **"Discipline Specific Core (DSC)"** means a course that a student admitted to a particular programme must successfully complete to receive the degree, and which cannot be substituted by any other course. DSCs shall be the core credit courses of that particular discipline, appropriately graded and arranged across the semesters of study undertaken by the student, with multiple exit options as per NEP 2020.

ii. **"Discipline Specific Elective (DSE)"** shall be a pool of credit courses of that particular discipline (single discipline programme of study) or those disciplines (multidisciplinary programme of study), as the case may be, which a student chooses to study from his/her particular discipline(s). This course is to be selected by a student out of such courses offered in the same or any other Department/Centre of FIAS.

iii. **"Generic Electives (GEs)"** are a pool of courses designed to provide students with multidisciplinary or interdisciplinary education. Various disciplines of study (excluding the GEs offered by the parent discipline), in groups of odd and even semesters, from which a student can choose. The concerned Department would identify the GEs specified in the framework as GEs to be taught in a Programme.

iv. **"Skill Enhancement Courses (SEC)"** are skill-based courses across all disciplines aimed at providing students with hands-on training, competencies, and proficiency. SEC courses may be chosen from a pool of courses designed to provide skill-based instruction.

v. **"Dissertation"** means a research project completed and written as part of a postgraduate degree.

vi. **"Credit"** is a unit by which the coursework is measured. It determines the number of hours of instruction required per week. One credit is equivalent to one hour of teaching (lecture or tutorial) or two hours of practical work/field work per week.

vii. **"SGPA"** is the Semester Grade Point Average calculated for individual semesters.

viii. **"CGPA"** is the Cumulative Grade Point Average calculated for all courses completed by the students at any time. The CGPA is calculated each year for both semesters combined.

ix. **"Grand CGPA"** is calculated in the last year of the course by clubbing together the CGPAs of the two years, i.e., four semesters. Grand CGPA is given in the transcript form. To benefit the student, a formula for converting the Grand CGPA into percentage marks is provided in the transcript.

III. M.Sc. PMBB Programme Details

The **M.Sc. Programme in Plant Molecular Biology and Biotechnology (PMBB)** at the Department of Plant Molecular Biology (PMB), University of Delhi South Campus (UDSC), offers an enriching and dynamic learning experience at the forefront of modern plant sciences. Designed to keep pace with cutting-edge advancements, this program equips students with the expertise necessary for a potential career in Crop Biotechnology and allied fields. With a meticulously structured curriculum, the PMBB program nurtures future-ready researchers and skilled professionals, bridging the gap between academia and industry. Graduates of this program are well-positioned to contribute to leading research institutions and drive innovation in the rapidly growing Plant Biotechnology sector, both in India and abroad.

Our comprehensive curriculum encompasses Classroom Teaching, Laboratory Practical sessions, Tutorials in the form of Seminars, and an invigorating Dissertation component. Throughout this PG programme, students will explore courses in Discipline Specific Core, Discipline Specific Elective, Generic Elective, Advanced Research Methodology/Tools for Research, Techniques of Research Writing, and Skill-based papers, which are intelligently distributed across four Semesters. These courses will be taught within the PMB Department, while the students will have the opportunity to choose from a diverse array of topics offered by sister Departments within the Faculty of Interdisciplinary and Applied Sciences (FIAS) at UDSC for the remaining paper(s).

The journey begins in the **first semester** with three core Papers from the PMB Department, delving into the Basics of Genetics and Molecular Biology, Molecular Cell Biology, and Recombinant DNA technology. Additionally, the course also offers three elective courses focusing on advanced subjects: 'Model Organisms in Molecular Biology Research', 'Plants in Human Health and Nutrition', and 'Laboratory Instrumentation & Safety'. Students can choose any two of the three DSE papers offered, or select one DSE offered by PMB and one Generic Elective (GE) paper offered by other departments of FIAS. The DSEs and SEC papers provide an opportunity to delve deeper into specialized areas and expand the knowledge base. Notably, the paper on ‘Model Organisms in Molecular Biology Research’ is also open to students from other FIAS departments, as generic elective adding to the interdisciplinary learning experience.

In the **second semester**, students will dive into three captivating DSC papers viz. ‘Molecular Basis of Plant Development’, ‘Plant Biochemistry and Metabolism’, ‘Eukaryotic Gene expression and Regulation’ and any of the two DSE papers (‘Proteomics, Metabolomics, Cell Signaling’, ‘Plant-Environment Interaction’) or one DSE offered by PMB, and one GE offered by other departments of FIAS. Notably, the paper on ‘Proteomics, Metabolomics and Elementomics’ is also open as generic elective to students from other FIAS Departments.

In **third and fourth semester**, students may choose one of the three course structures offered: Structure 1 (PG with Course only), Structure 2 (PG with Course & Research), and Structure 3 (PG with Research only). In Structure 1, two core papers, four DSEs (of which one DSE is generic elective) along with one 2-credit course are offered in both semester 3 and 4. In Structure 2, two core, three DSEs (of which one DSE is generic elective) are offered along with dissertation work in semester 3 and two core, three DSEs (one DSE as generic elective) are offered along with dissertation work in semester 4. Structure 3 is research-intensive and offers one core, two DSEs and two 2-credit courses in semester 3 and two DSEs, one 2-credit course and dissertation work in semester 4. The details of papers are presented in the table below.

PMBB Programme Details

a. Programme Objectives:

The M.Sc. course in Plant Molecular Biology and Biotechnology at the Department of Plant Molecular Biology (PMB), UDSC, has been designed to provide students with comprehensive exposure to the latest advancements in the exciting and burgeoning areas of modern plant sciences. This program equips students with the necessary theoretical knowledge and practical skills to pursue cutting-edge research in plant molecular biology and related disciplines. Additionally, it aims to develop a skilled workforce capable of contributing to the rapidly growing Plant Biotechnology industry, opening avenues for careers in academia and industry.

b. Programme Specific Outcomes:

After successfully completing the program, students will have developed a comprehensive and in-depth understanding of plant systems at the molecular level. They will gain a clear and precise grasp of how plants respond at the molecular level to various environmental and developmental cues. In addition to building a strong theoretical foundation, students will acquire essential practical skills, encompassing both wet-lab techniques and computational analyses. This well-rounded training will equip them with the expertise necessary to undertake challenging research projects in their future careers. Furthermore, they will gain insights into the complexities of molecular engineering and its applications in developing improved crop varieties. The program is designed to equip students with the knowledge and skills required to meet the criteria for conducting research in line with the BioE3 (Biotechnology for Economy, Environment, and Employment) Policy of the Government of India. By integrating advanced biotechnological approaches with principles of environmental sustainability, students will be prepared to contribute to innovative solutions that address the growing global demand for food and agricultural resilience.

c. Programme Structure:

The M.Sc. in Plant Molecular Biology and Biotechnology (PMBB) is a two-year programme offering a comprehensive, structured curriculum that provides both fundamental knowledge and advanced expertise in the field. The program includes:

- **Discipline Specific Core (DSC): DSCs (4 credits each)** provide a strong foundation, ensuring students gain up-to-date concepts in plant molecular biology and biotechnology.
- **Discipline Specific Elective (DSE): DSEs discipline or internal elective papers (4 credits each)** offer an advanced and in-depth exploration of specific topics that build upon concepts introduced in the core papers. These electives also incorporate substantial hands-on training to enhance practical understanding and research skills.
- **Generic Elective (GE): Select DSEs are offered as Generic Electives (4 credits)** to provide specialized knowledge and practical insights in an emerging area of biological sciences, accessible to a broader cohort of life sciences students.
- **SECs (2 credits each)** are designed to provide practical, industry-relevant, and research-driven skills that prepare students for both academic and industry settings.
- **Three papers, each of 2 credits,** focus on advanced research methods in the core discipline, basic and advanced research tools, and research writing techniques.
- **A dissertation (12/26 credits)** is structured to engage students in independent research, develop problem-solving skills, and contribute to scientific advancements in the field.

The well-balanced curriculum ensures that graduates acquire both theoretical expertise and practical proficiency, equipping them for careers in academic research, biotechnology industries, and related scientific fields.

d. Course Credit Scheme:

The **M.Sc. program** in **Plant Molecular Biology and Biotechnology** is a two-year course divided into four semesters. A student is required to complete 88 credits to complete the course and be awarded a degree. A student has to accumulate 22 credits in each of the four semesters. The program structure is based on the Post Graduate Curricular Framework (PGCF) under NEP-2020.

Two-Year PG Course Credit Scheme

Structure-1 (Level 6.5): (PG with only coursework)

Semester	Core Courses		Elective courses		Skill-based course/ Hands on Learning		Research Methods/ Tools/ Writing		Dissertation/ Project		Total Credits
	No. of courses	Total credits	No. of courses	Total credits	No. of courses	Total credits	No. of courses	Total credits	No. of courses	Total credits	
I	3	12	2	8	1	2	-	-	-	-	22
II	3	12	2	8	1	2	-	-	-	-	22
III	2	8	3	12	1	2	-	-	-	-	22
IV	2	8	3	12	1	2	-	-	-	-	22
Total Credits	**40**		**40**		**8**		**-**		**-**		**88**

Structure-2 (Level 6.5): (PG with coursework and research)

Semester	Core Courses		Elective courses		Skill-based course/ Hands on Learning		Research Methods/ Tools/ Writing		Dissertation/ Project		Total Credits
	No. of courses	Total credits	No. of courses	Total credits	No. of courses	Total credits	No. of courses	Total credits	No. of courses	Total credits	
I	3	12	2	8	1	2	-	-	-	-	22
II	3	12	2	8	1	2	-	-	-	-	22
III	2	8	2	8	-	-	-	-	1	6	22
IV	2	8	2	8	-	-	-	-	1	6	22
Total Credits	**40**		**32**		**4**		**-**		**12**		**88**

Structure-3 (Level 6.5): (PG with research)

Semester	Core Courses		Elective courses		Skill-based course/ Hands on Learning		Research Methods/ Tools/ Writing		Dissertation/ Project		Total Credits
	No. of courses	Total credits	No. of courses	Total credits	No. of courses	Total credits	No. of courses	Total credits	No. of courses	Total credits	
I	3	12	2	8	1	2	-	-	-	-	22
II	3	12	2	8	1	2	-	-	-	-	22
III	1	4	1	4	-	-	2	4	1	10	22
IV	-	-	1	4	-	-	1	2	1	16	22
Total Credits	**28**		**24**		**4**		**6**		**26**		**88**

e. Semester-wise Programme Structure:

PMBB P.G. PROGRAMME STRUCTURE

First-Year Course Details (Common in Structures 1, 2, and 3)

PART- I	Semester 1			
Name of the Course	**Credit Distribution of the Course**			
	Theory/ Lecture	**Tutorial**	**Practical**	**Total Credits**
DISCIPLINE SPECIFIC CORE COURSES (DSC)				
PBSC101: Basic Molecular Biology and Genetics	3	0	1	4
PBSC102: Molecular Cell Biology	3	0	1	4
PBSC103: Recombinant DNA Technology- Concepts, Techniques, and Applications	3	0	1	4
DISCIPLINE SPECIFIC ELECTIVE COURSES (DSE)				
*PBSE104: Plants in Human Health and Nutrition	3	0	1	4
*PBSE105: Laboratory Instrumentation and Safety	3	0	1	4
$PBSE106: Model Organisms in Molecular Biology Research	3	1	0	4
SKILL ENHANCEMENT COURSE				
PBSEC107: Biological Data Analysis and Interpretation	1	0	1	2
TOTAL CREDITS IN SEMESTER 1				**22**

$PBSE106 is open to students from other departments as a generic elective.
Two DSEs OR one DSE* and one generic elective$ (courses offered by any FIAS departments, including DPMB) can be selected.*

PART-I	Semester 2			
Name of the Course	**Credit Distribution of the Course**			
	Theory/ Lecture	**Tutorial**	**Practical**	**Total Credits**
DISCIPLINE SPECIFIC CORE COURSES (DSC)				
PBSC201: Molecular Basis of Plant Development	3	0	1	4
PBSC202: Plant Biochemistry and Metabolism	3	0	1	4
PBSC203: Eukaryotic Gene expression and Regulation	3	0	1	4
DISCIPLINE SPECIFIC ELECTIVE COURSES (DSE)				
*PBSE204: Cell Signaling and Communication	3	0	1	4
*PBSE205: Plant-Environment Interaction	3	0	1	4
$PBSE206: Proteomics, Metabolomics, and Elementomics	3	1	0	4
SKILL ENHANCEMENT COURSE				
PBSEC207: Plant Tissue Culture and Transformation Methodologies	0	0	2	2
TOTAL CREDITS IN SEMESTER 2				**22**

$PBSE206 is open to students from other departments as a generic elective.
Two DSEs OR one DSE* and one generic elective$ (courses offered by any FIAS departments, including DPMB) can be selected.*

Second-Year Course Details (Structure 1 - PG with Coursework)

PART- II	Semester 3			
Name of the Course	**Credit Distribution of the Course**			
	Theory/ Lecture	**Tutorial**	**Practical**	**Total Credits**
DISCIPLINE SPECIFIC CORE COURSES (DSC)				
PBSC311: Plant Biotechnology	3	0	1	4
PBSC312: Molecular Plant Breeding	3	0	1	4
DISCIPLINE SPECIFIC ELECTIVE COURSES (DSE)				
*PBSE313: Metagenomics of Plant-associated Microbes	3	1	0	4
*PBSE314: Frontiers in Plant Molecular Biology	3	0	1	4
$PBSE315: Introduction to Bioinformatics	3	1	0	4
*PBSE316: Molecular Plant Evolution and Biodiversity	3	1	0	4
SKILL ENHANCEMENT COURSE				
PBSEC317: Emerging Techniques in Plant Biology	1	0	1	2
TOTAL CREDITS IN SEMESTER 3				**22**

$PBSE315 is open to students from other departments as a generic elective.
Three DSEs OR two DSEs* and one generic elective$ (courses offered by any FIAS departments, including DPMB) can be selected.*

PART- II	Semester 4			
Name of the Course	**Credit Distribution of the Course**			
	Theory/ Lecture	**Tutorial**	**Practical**	**Total Credits**
DISCIPLINE SPECIFIC CORE COURSES (DSC)				
PBSC411: Advances in Crop Biotechnology	3	0	1	4
PBSC412: Plant Secondary Metabolism and Applications	3	0	1	4
DISCIPLINE SPECIFIC ELECTIVE COURSES (DSE)				
*PBSE413: Epigenetics and Small RNA Biology	3	0	1	4
$PBSE414: Data Analytics and Biocuration	3	1	0	4
*PBSE415: Plant Phenomics	3	1	0	4
*PBSE416: Synthetic Biology	3	1	0	4
SKILL ENHANCEMENT COURSE				
PBSEC417: Advanced Research Methodology	1	0	1	2
TOTAL CREDITS IN SEMESTER 4				**22**

$PBSE414 is open to students from other departments as a generic elective.
Three DSEs OR two DSEs* and one generic elective$ (courses offered by any FIAS departments, including DPMB) can be selected.*

Second-Year Course Details (Structure 2 - PG with Coursework and Research)

PART- II	Semester 3			
Name of the Course	**Credit Distribution of the Course**			
	Theory/ Lecture	**Tutorial**	**Practical**	**Total Credits**
DISCIPLINE SPECIFIC CORE COURSES (DSC)				
PBSC321: Plant Biotechnology	3	0	1	4
PBSC322: Molecular Plant Breeding	3	0	1	4
DISCIPLINE SPECIFIC ELECTIVE COURSES (DSE)				
*PBSE323: Metagenomics of Plant-associated Microbes	3	1	0	4
*PBSE324: Frontiers in Plant Molecular Biology	3	0	1	4
$PBSE325: Introduction to Bioinformatics	3	1	0	4
DISSERTATION				
PBRE326: Dissertation-I	0	0	6	6
TOTAL CREDITS IN SEMESTER 3				**22**

$PBSE325 is open to students from other departments as a generic elective.
Two DSEs OR one DSEs* and one generic elective$ (courses offered by any FIAS departments, including DPMB) can be selected.*

PART- II	Semester 4			
Name of the Course	**Credit Distribution of the Course**			
	Theory/ Lecture	**Tutorial**	**Practical**	**Total Credits**
DISCIPLINE SPECIFIC CORE COURSES (DSC)				
PBSC421: Advances in Crop Biotechnology	3	0	1	4
PBSC422: Plant Secondary Metabolism and Applications	3	0	1	4
DISCIPLINE SPECIFIC ELECTIVE COURSES (DSE)				
*PBSE423: Epigenetics and Small RNA Biology	3	0	1	4
$PBSE424: Data Analytics and Biocuration	3	1	0	4
*PBSE425: Plant Phenomics	3	1	0	4
DISSERTATION				
PBRE426: Dissertation-II	0	0	6	6
TOTAL CREDITS IN SEMESTER 4				**22**

$PBSE424 is open to students from other departments as a generic elective.
Two DSEs OR one DSE* and one generic elective$ (courses offered by any FIAS departments, including DPMB) can be selected.*

Second-Year Course Details (Structure 3 - PG with Research)

PART- II	Semester 3			
Name of the Course	**Credit Distribution of the Course**			
	Theory/ Lecture	**Tutorial**	**Practical**	**Total Credits**
DISCIPLINE SPECIFIC CORE COURSES (DSC)				
PBSC331: Plant Biotechnology	3	0	1	4
DISCIPLINE SPECIFIC ELECTIVE COURSES (DSE)*				
PBSE334: Frontiers in Plant Molecular Biology	3	0	1	4
PBSE335: Introduction to Bioinformatics	3	1	0	4
RESEARCH METHODS/TOOLS/WRITING COURSES				
PBRM332: Advanced Research Methodology	1	0	1	2
PBRM333: Emerging Techniques in Plant Biology	1	0	1	2
DISSERTATION				
PBRE336: Dissertation-I	0	0	10	10
TOTAL CREDITS IN SEMESTER 3				**22**

**At least one elective course to be selected.*

PART- II	Semester 4			
Name of the Course	**Credit Distribution of the Course**			
	Theory/ Lecture	**Tutorial**	**Practical**	**Total Credits**
DISCIPLINE SPECIFIC ELECTIVE COURSES (DSE)*				
PBSE433: Epigenetics and Small RNA Biology	3	0	1	4
PBSE434: Data Analytics and Biocuration	3	1	0	4
RESEARCH METHODS/TOOLS/WRITING COURSES				
PBRM431: Research Presentation and Communication	1	0	1	2
DISSERTATION				
PBRE432: Dissertation-II	0	0	16	16
TOTAL CREDITS IN SEMESTER 4				**22**

**At least one elective course to be selected.*

Selection of Elective Courses

In each semester, students should opt for a specified number of Discipline Specific Elective (DSE) papers offered by the PMB department or open DSE/ generic elective (GE) papers offered by the sister departments of FIAS, UDSC. A minimum of **SIX** students must opt for the DSE/GE paper to be offered during the semester.

f. Eligibility for Admissions:

- A 3-year/6-semester bachelor's degree with a minimum of 120 credits for a 2-year/4-semester PG programme at level 6.5 on the National Higher Education Qualifications Framework (NHEQF).
- A student is eligible for admission in PMBB PG programs if the student qualifies the required papers of the Common University Entrance Test [CUET-(PG)] examination or the Graduate Aptitude Test-Biotechnology **(**GAT-B) examination (for DBT-supported postgraduate seats).
- All admissions are made in the order of merit in each category, which is based on the marks secured in the CUET(PG) or GAT-B examinations.
- An appropriate number of seats is reserved for the candidates belonging to reserved categories, and relaxation is applicable as per the university norms.

g. Assessment of Students' Performance:

The assessment of students in each semester under PGCF 2025 will be as per the University Notification No. Exam. VIII/Conduct/Misc./2025/12/19(i), dated: September 01, 2025 (Attached as Annexure- I) or any subsequent notifications. English shall be the medium of instruction and examination. The theory examination and internal assessment shall be a cumulative assessment of the teaching and learning in theory and tutorial classes. The end-term written examination for each course/paper shall be conducted at the end of the semester, as per the academic calendar notified by the University of Delhi. The distribution of marks for various courses is:

Total Credits	Lectures	Tutorials	Practical	End Term Theory Exam Marks	Duration of Theory Exam	Internal Assessment (IA) Marks	Tutorial	Practical Marks				Grand Total Marks
							CA	CA	End Term Practical	Viva - voce	Total	
4	3	1	0	90	3 hrs	30	40	0	0	0	0	160
4	3	0	1	90	3 hrs	30	0	10	20	10	40	160
4	0	0	4	0	NA	0	0	40	80	40	160	160
4	1	0	3	30	1 hr	10	0	30	60	30	120	160
4	2	0	2	60	2 hrs	20	0	20	40	20	80	160
2	1	0	1	30	1 hr	10	0	10	20**	10	40	80
2	0	0	2	0	NA	0	0	20	40**	20	80	80

(IA= Internal Assessment; CA= Continuous Assessment; NA= Not Applicable)

**In the case of two credit courses (Skill-Based Courses), which have practical components, there may be either an end-term practical examination or an end-term written examination, as per the nature of the course.

In any course where 1 credit is attributed to 'Tutorial', an objective assessment process must be developed to adequately assess and record the credit earned by a student in each course. Further, out of forty marks allocated for the Continuous Assessment of 01 credit tutorial, five marks shall be for attendance, which shall be distributed as follows:

- 67% attendance or more but less than 70% attendance – 1 mark
- 70% attendance or more but less than 75% attendance – 2 marks
- 75% attendance or more but less than 80% attendance – 3 marks
- 80% attendance or more but less than 85% attendance – 4 marks
- 85% attendance or more – 5 marks

h. Guidelines for the Award of Internal Assessment Marks:

The Internal Assessment (Assignments/Presentations and class tests) will be conducted in a continuous mode throughout the semester. Internal Assessment (IA) marks shall be 25% of the total marks of theory. For instance, if a course is of 4 credits having Lecture-Tutorial-Practical credits (3-1-0), the total marks of the course shall be 160 marks (4 credits x 40 marks), the total theory component shall be of 120 marks (3 credits x 40 marks), out of which 90 marks shall be for the end-term written exam and the IA component shall be of 30 marks (25% of 120 marks). Out of the 30 marks, 12 marks for class test and 12 marks for Assignments/Presentations, and 6 marks shall be for attendance. These six marks for attendance shall be distributed as follows:

- 67% attendance or more but less than 70% attendance – 1.2 marks
- 70% attendance or more but less than 75% attendance – 2.4 marks
- 75% attendance or more but less than 80% attendance – 3.6 marks
- 80% attendance or more but less than 85% attendance – 4.8 marks
- 85% attendance or more – 6.0 marks

i. Pass Percentage & Promotion Criteria:

- As per the UGC/University Examination Rules.

j. Conversion of Marks into Grades:

- As per the UGC/University Examination Rules.

k. Grade Points:

- As per the UGC/University Examination Rules.

l. CGPA Calculation:

- As per the UGC/University Examination Rules.

m. SGPA calculation:

- As per the UGC/University Examination Rules.

n. Grand SGPA calculation:

- As per the UGC/University Examination Rules.

o. Conversion of Grand CGPA into marks:

- As per the UGC/University Examination Rules.

p. Division of Degree into Classes:

- As per the UGC/University Examination Rules.

q. Attendance Requirement:

- As per the UGC/University Examination Rules.

r. Exit Point:

- Students who join a two-year postgraduate programme shall have only one exit point.

s. Span Period:

- As per the UGC/University Examination Rules.

IV. Course-wise Content Details for the PMBB Programme

SEMESTER 1

PBSC101: Basic Molecular Biology and Genetics

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSC101: Basic Molecular Biology and Genetics	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

The course aims to deliver in-depth knowledge of molecular biology with emphasis on genomic stability, DNA replication, transcription, translation, and gene regulation to the students using prokaryotic model systems. This course will also provide a deep understanding of genetic principles, from Mendelian inheritance to modern molecular genetics. Students will explore gene interactions, linkage, mapping techniques, and quantitative genetics. Through theoretical knowledge and analytical techniques, students will develop experimental and analytical skills in genetics and molecular biology.

Learning Outcomes

Upon completion, students will understand the processes of DNA replication, transcription, and translation, as well as the models of gene regulation. Students will have a strong foundation in classical and molecular genetics, enabling them to analyze genetic inheritance, gene mapping, and genome stability mechanisms. Students will develop skills in applying genetic analysis tools and interpreting experimental data. Students will learn methods to estimate point mutation, homologous recombination, and transposition. Further, students will acquire skills in cytogenetic techniques for chromosome analysis.

Course Content (45 hours)

Unit 1: Mechanism of Replication in Prokaryotes -- DNA polymerases and accessory proteins; Proteins at the origin of replication and replication fork; Concept of replicon; Fidelity of replication; Control of replication of chromosomes and extrachromosomal elements. 6 hours

Essential Readings: Weaver, R.F. (2012) Molecular Biology. McGraw Hill, UK, ISBN:9780073525327, Chapter 20 (DNA Replication); Griffiths, A., et al. (2020) Introduction to Genetic Analysis. 12th edition, W.H. Freeman, USA, ISBN:9781319114787, Chapter 7 (DNA: Structure and Replication); Krebs, J.E., et al. (2018) Lewin's Genes XII. Jones and Bartlett Publishers Inc., USA, ISBN:9781284104493, Chapter 1 (DNA Replication).

Unit 2: Prokaryotic Transcription, Translation, and its Regulation -- Discovery of RNA; Initiation of transcription: Promoters and other control elements; RNA polymerases and accessory factors; Sigma factors and their interactions with promoters; Transcriptional controls; Concept of operons; Transcription termination; Rho factor and polar mutations; Gene regulation in Bacteriophages: lysogenic and lytic cycles, regulation of gene expression; Initiation, elongation, and termination of translation and the accessory proteins; Structural and functional studies on ribosomes: ribosomal RNAs and proteins; Mapping the decoding and peptidyl transferase sites of ribosome; Transfer RNAs and genetic code; Translational fidelity.

16 hours

Essential Readings: Weaver, R.F. (2012) Molecular Biology. McGraw Hill, UK, ISBN:9780073525327, Chapter 6 (The mechanism of transcription in bacteria), Chapter 7 (Operons: fine control of bacterial transcription), Chapter 8 (Major shifts in bacterial transcription), Chapter 17 (The mechanism of translation I: Initiation), Chapter 18 (The mechanism of translation II: Elongation and termination).

Unit 3: Mendelian Principles, Gene Mapping, and Quantitative Genetics – Introduction to Mendelian Genetics; codominance, incomplete dominance, gene interactions (epistasis), pleiotropy, penetrance and expressivity, linkage and crossing over, sex linkage, genome imprinting; Genetic and physical maps; Molecular markers: RFLP, RAPD, AFLP, SSR, SNP; Mapping genes by interrupted mating, polygenic inheritance, QTL (Quantitative Trait Locus) mapping, LOD (Logarithm of Odds) score for linkage testing, pedigree analysis, karyotypes, tetrad analysis, Chi-square test in linkage analysis. 15 hours

Essential Readings: Griffiths, A., et al. (2020) Introduction to Genetic Analysis. 12th edition, W.H. Freeman, USA, ISBN:9781319114787, Chapter 2 (Single-gene inheritance), Chapter 3 (Independent assortment of genes), Chapter 4 (Mapping eukaryote chromosomes by recombination), Chapter 5 (Gene interaction), Chapter 18 (Population genetics), Chapter 19 (The inheritance of complex traits).

Unit 4: Maintenance of Genomic Flexibility and Integrity -- Spontaneous and induced mutations; Mutagens; Mechanisms of homologous and site-specific recombination (NHEJ, HR, MMEJ); Mechanism of meiotic crossing-over; DNA repair and retrieval systems; Transposons and retro-transposons. 8 hours

Essential Readings: Clarke, D. and Pazdernik, N. (2013) Molecular Biology. Academic Cell, USA, ISBN: 9780123785947, Chapter 13–15 (Mutations, recombination, and repair); Weaver, R.F. (2012) Molecular Biology. McGraw Hill, UK, ISBN:9780073525327, Chapter 20 (DNA replication, damage, and repair), Chapter 22 (Homologous recombination), Chapter 23 (Transposition).

Practicals (30 hours)

1. Extraction and analysis of genomic DNA from bacteria.
2. To perform bacteriophage plaque assay.
3. Study of frameshift mutation and homologous recombination by histochemical assays.
4. Visualization of chromatin structure using DAPI staining.
5. Analysis of cell ploidy by chromosomal counting at metaphase/flow cytometry.

Suggested Readings:

1. Clarke, D. and Pazdernik, N. (2013) Molecular Biology. Academic Cell, USA, ISBN:9780123785947.
2. Griffiths, A., et al. (2020) Introduction to Genetic Analysis. 12th edition, W.H. Freeman, USA, ISBN:9781319114787.
3. Tropp, B.E. (2014) Principles of Molecular Biology, Jones and Bartlett, USA, ISBN:9781449689179.
4. Weaver, R.F. (2012) Molecular Biology. McGraw Hill, UK, ISBN:9780073525327.
5. Krebs, J.E., et al. (2018) Lewin's genes XII. Jones & Bartlett Learning, ISBN:9781284104493.

PBSC102: Molecular Cell Biology

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSC102: Molecular Cell Biology	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

This paper is designed to provide an in-depth understanding of cell biology, focusing on the molecular and biochemical processes that regulate cellular functions. A key emphasis is placed on the molecular organization of biological macromolecules and their role in forming distinct subcellular structures, enabling the precise coordination of essential cellular processes.

Learning Outcomes

Students would learn about the structure-function relationship of cellular organelles from a molecular perspective, focusing on macromolecules at both cellular and subcellular levels. Students will explore key molecular, biochemical, and imaging techniques employed for studying cells and cellular processes. By integrating mechanistic insights, this course will equip students with the knowledge to design strategies for manipulating cellular processes to address challenges in managing nutrition and food security.

Course Content (45 hours)

Unit 1: Investigating the Cell and Cell wall -- Fundamentals of microscopy and imaging, techniques for analyzing the cell and its organelles; Cell wall composition and architecture, biogenesis and assembly, dynamic aspects of the cell wall during growth and differentiation.

9 hours

Essential Readings: Alberts, B., et al. (2022) Molecular Biology of the Cell. W.W. Norton & Company, ISBN: 9780393884821, Chapter 9 (Visualizing cells and their molecules); Buchanan, B.B, et al. (2015) Biochemistry and Molecular Biology of the Plants, American Society of Plant Physiologists, USA, ISBN:9780470714225, Chapter 2 (The Cell Wall).

Unit 2: Membrane and Endomembrane Systems -- Structural models, composition and dynamics; Transport of ions and macromolecules: transporters and channels; Sensory physiology; Endo- and exo-cytosis; Membrane proteins and carbohydrates and their significance in cellular processes; Structure and function of Golgi apparatus, lysosomes and endoplasmic reticulum and microbodies; Intracellular membrane trafficking and vesicular transport; Membrane maturation and specialization, extracellular vesicles, multivesicular bodies**,** Kajal bodies, dicing bodies, and cytoplasmic bodies. 20 hours

Essential Readings: Buchanan, B.B, et al. (2015) Biochemistry and Molecular Biology of the Plants. American Society of Plant Physiologists, USA, ISBN:9780470714225, Chapter 3 (Membrane transport); Alberts, B., et al. (2022) Molecular Biology of the Cell. W.W. Norton & Company, ISBN:9780393884821, Chapter 10 (Membrane structures), Chapter 11 (Small-molecule transport and electrical properties of membranes), Chapter 12 (Intracellular organizations and protein sorting), Chapter 13 (Intracellular membrane traffic).

Unit 3: Mitochondria, **Chloroplast, and Nucleus** – Structure; Organization; Structure-function relationship; Import and export of molecules; Biogenesis, origin and evolution;

Structure and function (architecture); Chromatin organization and packaging: heterochromatin, euchromatin, nucleosomes; Nuclear envelope and nuclear pore complex, Import and export of molecules. 12 hours

Essential Readings: Alberts, B., et al. (2022) Molecular Biology of the Cell. W.W. Norton & Company, ISBN: 9780393884821, Chapter 14 (Energy conversion and metabolic compartmentation: Mitochondria and Chloroplasts); Kleinsmith, L.J. and Kish, V.M. (1996) Principles of Cell & Molecular Biology, Harper Collins College Publishers, USA, ISBN:9780065004045, Chapter 10 (The nucleus and transcription of genetic information).

Unit 4: Cytoskeleton and Cellular Motility -- Organization and role of microtubules and microfilaments; Actin-binding proteins and their significance; Molecular motors; Intermediate filaments. 4 hours

Essential Readings: Alberts, B., et al. (2022) Molecular Biology of the Cell. W.W. Norton & Company, ISBN:9780393884821, Chapter 16 (The cytoskeleton); Buchanan, B.B, et al. (2015) Biochemistry and Molecular Biology of the Plants. American Society of Plant Physiologists, USA, ISBN:9780470714225, Chapter 5 (The cytoskeleton).

Practicals (30 hours)

1. High-resolution imaging of epidermal peel cells of *Arabidopsis thaliana*/ *Nicotiana benthamiana* under confocal microscope.
2. Transient expression of fluorescent-tagged protein via *Agrobacterium*-based infiltration of leaf epidermal cells.
3. Monitor the localization of fluorescent-tagged protein at the subcellular level under a confocal microscope.
4. Preparation and visualization of leaf protoplasts of *Arabidopsis thaliana*/*Nicotiana benthamiana*.
5. To study the pollen viability and the effect of calcium on pollen germination.

Suggested Readings:

1. Alberts, B., et al. (2022) Molecular biology of the cell. W.W. Norton & Company, ISBN:9780393884821.
2. Buchanan, B.B, et al. (2015) Biochemistry and molecular biology of the plants. American Society of Plant Physiologists, USA, ISBN:9780470714218.
3. Karp, J.G. (2019) Cell and Molecular Biology. John Wiley & Sons, USA, ISBN:9781119598169.
4. Kleinsmith, L.J. and Kish, V.M. (1996) Principles of cell & molecular biology. HarperCollins College Publishers, USA, ISBN:978-0065004045.
5. Lodish, H., et al. (2016) Molecular cell biology. Freeman & Co., USA, ISBN:9781464183393.
6. Ruzin, S.E. (1999) Plant microtechniques and microscopy. Oxford University Press, USA, ISBN:9780195089561.

PBSC103: Recombinant DNA Technology - Concepts, Techniques, and Applications

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSC103: Recombinant DNA Technology - Concepts, Techniques, and Applications	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

The course is designed to provide a comprehensive understanding of the principles, methodologies, and tools in recombinant DNA technology. This will familiarize students with advanced techniques in molecular biology and equip them with hands-on knowledge about genetic engineering tools. Furthermore, they will learn about the applications of recombinant DNA technology in agriculture, medicine, and industry, while addressing ethical, social and regulatory concerns. The course will prepare students for research and innovation in emerging fields such as synthetic biology, metabolic engineering, and genome editing. It will also provide a foundation for students to develop advanced knowledge for succeeding semesters.

Learning Outcomes

The candidate will develop an in-depth knowledge of the principles and applications of instrumentation, as well as basic and cutting-edge tools and techniques in recombinant DNA technology. Students will get acquainted with designing/conducting, and analyzing experiments and experimental data, respectively. The integration of theory and problem-solving exercises will motivate students to develop a keen research interest and enhance their understanding of the topics they are taught. They will be able to evaluate the impact of recombinant DNA technology in agriculture, healthcare, and industry. The course will enable students to develop innovative solutions in genetic engineering, synthetic biology, and protein engineering for real-world challenges.

Course Content (45 hours)

Unit 1: **Introduction to Recombinant DNA Technology** -- Historical perspectives and milestones; Basic principles and concepts; Methods of nucleic acids and protein analysis: Isolation and purification, electrophoresis techniques; Overview of genetic engineering tools.
6 hours

Essential Readings: Berg, P., et al. (2010) Personal reflections on the origins and emergence of recombinant DNA technology. Genetics, 184(1):9–17. DOI:10.1534/genetics; Primrose, S.B. and Twyman, R.M. (2006) Principles of Genetic Manipulation and Genomics. 7th edition. Blackwell Publishing, UK, ISBN:9781405135443, Chapter 1 (Gene manipulation: an all-embracing technique), Chapter 2 (Basic techniques), Chapter 3 (Cutting and joining DNA molecules).

Unit 2: DNA Cloning Methodologies and PCR -- Key enzymes: restriction endonucleases, nucleic acid modifying enzymes; Advanced cloning methods: TA cloning, topoisomerasebased cloning, ligation-independent cloning, Gateway technology, Gibson cloning; Vectors for gene cloning: plasmids, phages, phagemids, cosmids, and other advanced vectors for cloning large DNA fragments; Methods for selection and screening of recombinant clones; Host systems: bacteria, yeast, and plant cells; Isolation of gene of interest: Direct selection, construction and screening of genomic and cDNA libraries, labelling and detection of nucleic acids, enriching clones by subtractive cloning and differential screening, differential display; Polymerase Chain Reaction (PCR): concept and enzymes employed, optimization of PCR, types of PCR (touch-up, touch-down, hot-start, inverse, nested, gradient, Rapid Amplification of cDNA Ends (RACE), semi-quantitative and quantitative, Gene Splicing by Overlap Extension (gene SoEing), and applications of PCR; DNA sequencing methods. 15 hours

Essential Readings: Primrose, S.B. and Twyman, R.M. (2006) Principles of Genetic Manipulation and Genomics. 7th edition. Blackwell Publishing, UK, ISBN:9781405135443, Chapter 4 (Basic biology of plasmid and phage vectors), Chapter 5–9, 12 (Basic biology of plasmid and phage vectors, Cosmids, phasmids and other advanced vectors, Cloning strategies, Sequencing and mutagenesis, Cloning in bacteria other than *E. coli*, Cloning in *Saccharomyces cerevisiae* and other fungi, Gene transfer to plants); Brown, T.A. (2020) Gene Cloning and DNA Analysis: An Introduction. 8th edition. Wiley-Blackwell Publishing, UK, ISBN:9781119640783, Chapter 1–13 (Why Gene Cloning and DNA Analysis are important, Vectors for Gene Cloning: Plasmids and Bacteriophages, Purification of DNA from Living Cells, Manipulation of Purified DNA, Introduction of DNA into Living Cells, Cloning Vectors for *E. coli*, Cloning Vectors for Eukaryotes, How to Obtain a Clone of a Specific Gene, The Polymerase Chain Reaction, Sequencing Genes and Genomes, Studying Gene Expression and Function, Studying Genomes, Studying Transcriptomes and Proteomes, Production of Protein from Cloned Genes).

Unit 3: Methods to Study Gene Expression, Biomolecular Interactions and Protein Expression Systems -- Gene expression analyses at the transcriptional level (Northern blotting and its variants, real-time PCR, S1 nuclease mapping, *in situ* hybridization, RNase protection, nuclear run-on assays), translational level: Western blotting, Enzyme-Linked ImmunoSorbent Assay (ELISA) and immunofluorescence assays; DNA-protein: Electrophoretic Mobility Shift Assay (EMSA), DNase I footprinting, Chromatin ImmunoPrecipitation (ChIP), Yeast one-hybrid (Y1-H), RNA-protein: Y3-H, northwestern, RNA ImmunoPrecipitation (RIP); protein-protein interaction: Y2-H, pull down, Co-ImmunoPrecipitation (Co-IP), Fluorescence Resonance Energy Transfer (FRET), Bimolecular Fluorescence Complementation (BiFC); Protein Expression and Engineering: Tagging and overexpression of proteins in heterologous systems (*E. coli*, yeast, baculovirus, and mammals); Methods for mutagenesis of genes for obtaining altered proteins. 15 hours

Essential Readings: Primrose, S.B. and Twyman, R.M. (2006) Principles of Genetic Manipulation and Genomics. 7th edition. Blackwell Publishing, UK, ISBN:9781405135443, Chapter 11 (Studying Gene Expression and Function); Segundo-Val, A.S., et al. (2016) Introduction to gene expression analysis. Methods in Molecular Biology, 1434:29-43. DOI:10.1007/978-1-4939-3652-6_3; Ferraz, R.A.C., et al. (2021) DNA-protein interaction studies: a historical and comparative analysis. Plant Methods, 17:82, DOI:10.1186/s13007-021-00780-z; Ramanathan, M., et al. (2019) Methods to study RNA-protein interactions. Nature Methods, 16:225–234. DOI:10.1038/s41592-019-0330-1; Rao, V.S., et al. (2014) Protein-protein interaction detection: methods and analysis. International Journal of Proteomics, 2014:147648, DOI:10.1155/2014/147648; Baranowski, C., et al. (2025) Can protein expression be 'solved'? Trends in Biotechnology, 43(11):2724–2742. DOI:10.1016/j.tibtech.2025.04.021; Xia, Y., et al. (2015) New insights into the QuikChange™ process guide the use of Phusion DNA polymerase for site-directed mutagenesis. Nucleic Acids Research, 43(2):e12, DOI:10.1093/nar/gku1189.

Unit 4: Applications and Ethics of Recombinant DNA Technology -- Production of recombinant molecules for improving agronomic traits, diagnostic and therapeutic applications in human diseases; Impact and biosafety, moral, social, regulatory and ethical concerns; Future perspectives and emerging trends (introduction to gene editing, synthetic biology, and genome engineering, the role of artificial intelligence or AI, etc.) 9 hours

Essential Readings: Begna, T. and Okonkwo, J.C. (2020) Role of Recombinant DNA Technology in Agriculture. International Journal of Agriculture and Biosciences, 9(5):254–259; www.ijagbio.com; Khan, S., et al. (2016) Role of recombinant DNA technology to improve life. International Journal of Genomics, 2016:2405954. DOI:10.1155/2016/2405954; Bharathi, J.K., et al. (2024) Exploring recent progress of molecular farming for therapeutic and recombinant molecules in plant systems. Heliyon, 10(18):e37634. DOI:10.1016/j.heliyon.2024.e37634; Sharma, R., et al. (2022) Chapter on 'Ethical and Safety Concerns of Recombinant DNA Technology. In: A Complete Guide to Gene Cloning: From Basic to Advanced. Springer, ISBN:978-3-030-96850-2; Gholap, A.D., et al. (2025) Advances in artificial intelligence-envisioned technologies for protein and nucleic acid research. Drug Discovery Today, 30(5):10436, DOI:10.1016/j.drudis.2025.104362; Sun, S. (2025) Advancing Genetic Engineering through AI: Sequencing and Editing Innovations. Theoretical and Natural Science, 90(1):48–53, DOI:10.54254/2753-8818/2025.GU20450.

Practicals (30 hours)

1. Transformation of bacterial competent cells followed by blue-white screening for identification of recombinant plasmid.
2. Colony PCR for screening of recombinant plasmids.
3. Isolation of plasmid DNA from *E. coli* culture and quantitation of DNA.
4. Restriction digestion of plasmid DNA and resolution of the digested DNA by agarose gel electrophoresis.
5. Induction of protein expression in a heterologous bacterial system and analysis of the expressed protein using SDS-PAGE.

Suggested Readings:

1. Brown, T.A. (2020) Gene Cloning and DNA Analysis: An Introduction. 8th edition. Wiley-Blackwell Publishing, UK, ISBN:9781119640783.
2. Brown, T.A. (2024) Genomes 5. 5th edition. CRC Press, India, ISBN:9780367674076.
3. Dale J.W., et al. (2011) From Genes to Genomes: Concepts and Applications of DNA Technology. 3rd edition. John Wiley & Sons, UK, ISBN:9780470683859.
4. Glick B.R. and Patten C.L. (2022) Molecular Biotechnology: Principles and Applications of Recombinant DNA. 6th edition. ASM Press, USA, ISBN:9781683673668.
5. Watson, J.D, et al. (2006) Recombinant DNA: Genes and Genomes. 3rd edition. W.H. Freeman & Co, India, ISBN:9780716728665.
6. Green M.R. and Sambrook J. (2012) Molecular Cloning: A Laboratory Manual. 4th edition. CSHL Press, USA, ISBN:9781936113422.
7. Primrose, S.B. and Twyman, R.M. (2006) Principles of Genetic Manipulation and Genomics. 7th edition. Blackwell Publishing, UK, ISBN:9781405135443.

PBSE104: Plants in Human Health and Nutrition

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE104: Plants in Human Health and Nutrition	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

Plants play a crucial role in human health and nutrition by providing essential nutrients, bioactive compounds, and medicinal properties that support our well-being. The course aims to highlight the role of plants in human health and nutrition, and to explore the molecular basis of bioactive compounds found in plants. The students will gain knowledge of plant-derived pharmaceuticals, nutraceuticals, and functional food. Furthermore, strategies for improving plant nutrition and ethical issues will be taught.

Learning Outcomes

The students will be able to understand the role of plants in human life, analyse functional foods and nutraceuticals. They will be able to comprehend the molecular basis of phytochemical synthesis and explore the plants as pharmaceuticals. Utilizing this knowledge, the students will be able to design innovative and novel strategies for plant biofortification and metabolic engineering to develop novel plant-based foods and sustainable nutritional and drug resources.

Course Content (45 hours)

Unit 1: Role of Plants in Human Health and Nutrition -- Plants in human health from a biochemical perspective; History of plant-based nutrition and medicinal plants; Role of secondary metabolites in human health; Molecular basis of bioactive compounds and biosynthetic pathways. 10 hours

Essential Readings: Raskin, I., et al. (2002) Plants and human health in the twenty-first century. Trends in Biotechnology, 20(12):522–31, DOI:10.1016/s0167-7799(02)02080-2; El-Ramady, H., et al. (2022) Plant nutrition for human health: A pictorial review on plant bioactive compounds for sustainable agriculture. Sustainability, 14:8329, DOI:10.3390/su14148329; Xue, J., Yin, Y. (2024) Plant-based food: From nutritional value to health benefits. Foods, 13:3595, DOI:10.3390/foods13223595; Shahnawaz, M. and Sharma, P. (2026) Secondary metabolites for improvement of human health. Edited by: Srivastava A., and Mishra, A.K. In: Developments in applied microbiology and biotechnology, Secondary metabolites in stress and disease management, Academic Press, ISBN:9780443339592; Guo, M., et al. (2023) Strategies on biosynthesis and production of bioactive compounds in medicinal plants. Chinese Herbal Medicines, 16(1):13–26, DOI: 10.1016/j.chmed.2023.01.007.

Unit 2: Plant-based Nutraceuticals and Medicine Systems -- Phytochemicals, Traditional and non-traditional nutraceuticals; Plant-derived probiotics and prebiotics; Biotechnological approaches for biofortification for enhanced nutrition; Plant-based Medicine Systems: Traditional knowledge and ethnobotany; Ayurvedic, Yoga, Unani, Siddha, and Homeopathic (AYUSH), other traditional systems; Modern systems of plant-based medicine and their importance in human health. 15 hours

Essential Readings: Herbal Nutraceuticals: Products and Processes. (2024) Edited by: Upadhyay, S.K. and Singh, S.P., John Wiley & Sons Ltd., ISBN:9781394241545, Chapter 1 (Plants Based Nutraceuticals: An Overview), Chapter 2 (Herbal Nutraceutical as Alternative Medicine), Chapter 10 (The flavorful world: Exploring the applications of spices in nutraceuticals)]; Manisha, M., et al. (2025) Medicinal plants and traditional uses and modern applications. Journal of Neonatal Surgery, 14(3):162–175, DOI:10.52783/jns.v14.2210; https://ayushedu.bisag-n.gov.in/AYUSH_EDU/ayushknowledge.

Unit 3: Plants as Source of Pharmaceuticals -- Medicinal plants; Traditional plant-based formulations; Plant-derived molecules in drug development; Therapeutic use of poisonous plants; Pharmacogenomics; Ayurgenomics; Metabolic engineering for enhanced bioactive production; Good manufacturing practices (GMPs). 10 hours

Essential Readings: Wang, X., et al. (2025) Plant-based traditional remedies and their role in public health: ethnomedicinal perspectives for a growing population. Journal of Health Population and Nutrition, 44(1):300, DOI:10.1186/s41043-025-01036-5; Nasim, N., et al. (2022) Plant-derived natural products for drug discovery: current approaches and prospects. Nucleus (Calcutta), 65(3):399–411, DOI:10.1007/s13237-022-00405-3; Rajbongshi, B.L. and Mukherjee, A.K. (2025) Drugs from poisonous plants: Ethnopharmacological relevance to modern perspectives. Toxicon X, 25:100215, DOI:10.1016/j.toxcx.2025.100215; Aneesh, T.P., et al. (2009) Pharmacogenomics: the right drug to the right person. Journal of Clinical Medicine Research, 1(4):191–194, DOI: 10.4021/jocmr2009.08.1255; Wallace, R.K. (2020) Ayurgenomics and Modern Medicine. Medicina (Kaunas). 6(12):661, DOI:10.3390/medicina56120661; Martínez-Chávez, L.A. et al. (2024) Cutting-edge strategies to enhance bioactive compound production in plants: Potential value of integration of elicitation, metabolic engineering, and green nanotechnology. Agronomy, 14:2822, DOI:10.3390/agronomy14122822; https://www.csir.res.in/en/csir-success-stories/ayurgenomics-bringing-age-old-wisdom-healthcare-future; https://www.who.int/teams/health-product-policy-and-standards/standards-and-specifications/norms-and-standards/gmp; https://www.genome.gov/about-genomics/educational-resources/fact-sheets/pharmacogenomics.

Unit 4: Recent Advancements in Plant Science and Health – Plant vaccines; plant-focused biomanufacturing; DNA fingerprinting and barcoding of medicinal plants; Synthetic biology for producing plant-derived therapeutic agents; Plant-based meat alternatives and sustainable food sources; the role of microgreens and lower plants in nutrition; Climate change and its impact on beneficial plant compounds; Future perspectives and challenges; Ethical and regulatory guidelines. 10 hours

Essential Readings: Vo, D.K. and Trinh, K.T.L. (2025) Molecular farming for immunization: current advances and future prospects in plant-produced vaccines. Vaccines, 13:191, DOI:10.3390/vaccines13020191; Fujiyama, K., (2024) Recent advances in plant-based bioproduction. Journal of Bioscience and Bioengineering, 138(1):1–12, DOI:10.1016/j.jbiosc.2024.01.007; Chen, S., et al. (2023) DNA barcoding in herbal medicine: Retrospective and prospective. Journal of Pharmaceutical Analysis, 13(5):431–441, DOI:10.1016/j.jpha.2023.03.008; Selvakumari, E., et al. (2017) Application of DNA fingerprinting for plant identification. Journal of Academia and Industrial Research, 5(10):149–151, ISSN:2278-5213; Li, C-Q., et al. (2021) Recent advances in the synthetic biology of natural drugs. Frontiers in Bioengineering and Biotechnology, 9:691152, DOI:10.3389/fbioe.2021.691152; Andreani, G., et al. (2023) Plant-based meat alternatives: Technological, nutritional, environmental, market, and social challenges and opportunities. Nutrients, 15(2):452. DOI:10.3390/nu15020452; Rawat, D., et al. (2025) Microgreens: cultivation, nutrition, journey to space and market trends. International Journal of Plant & Soil Science, 37(10):22–32, DOI:10.9734/ijpss/2025/v37i105758; Alum, E.U. (2024) Climate change and its impact on the bioactive compound profile of medicinal plants: implications for global health. Plant Signalling and Behaviour, 19(1):2419683, DOI:10.1080/15592324.2024.2419683; Subramaniam, A. (2014) Present scenario, challenges and future perspectives in plant-based medicine development. Annals of Phytomedicine 3(1):31–36; Henkhaus, N., et al. (2020) Plant science decadal vision 2020–2030: Reimagining the potential of plants for a healthy and sustainable future. Plant Direct, 4(8):e00252, DOI:10.1002/pld3.252.

Practicals (30 hours)

1. Pharmacognostic evaluation (macroscopic and microscopic) of medicinal plants.
2. Qualitative analysis of secondary metabolites: Alkaloids, Flavonoids, Tannins, Glycosides, etc.

3. Quantitative analysis of secondary metabolites: Alkaloids, Flavonoids.
4. Perform chromatographic analysis of plant extracts.
5. Survey of medicinally important plants.

Suggested Readings:

1. Kumar, S., et al. (2022) Biofortification of staple crops. Springer Nature Singapore Pte Ltd., ISBN:9789811632792.
2. Crozier, A., et al. (2006) Plant secondary metabolites: occurrence, structure and role in the human diet. Blackwell Publishing Ltd., ISBN:9781405125093.
3. Simopoulos, A.P. and Gopalan, C. (2003) Plants in Human Health and Nutrition Policy, Volume 91, S. Karger AG, ISBN:9783805575546, DOI:10.1159/isbn.978-3-318-00954-5.
4. The Ayurvedic Pharmacopoeia of India, Part I, Part II, Vol I- Vol III. Council for Research in Ayurvedic Sciences (CCRAS).
5. Database on Medicinal Plants used in Ayurveda and Siddha, Vol I- Vol VIII, Central Council for Research in Ayurvedic Sciences (CCRAS).
6. Chowdhury, S.R. (2023) Textbook of food science and nutrition. Aarahan Publishers, ISBN:9789387270084.
7. Mudambi, R.S. and Rajagopal, M.V (1983) Foods and Nutrition. Wiley Eastern Ltd. 2nd edition, New Delhi, ISBN:9780852265833.
8. Keservani, R.K. (2024) Plant metabolites and vegetables as nutraceuticals. Academic Press, ISBN:9781774915448.
9. Usman, S. and Budhrani N. (2020) Textbook of medicinal plant biotechnology. S Vikas and Company.
10. Bharti, P.K. (2018) Nutraceuticals and pharmaceutical from medicinal plants, Discovery Publishing House Pvt. Ltd., ISBN:9789386841551.

PBSE105: Laboratory Instrumentation and Safety

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE105: Laboratory Instrumentation and Safety	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

The course aims to equip students with a comprehensive understanding of the essential laboratory instruments used in molecular biology, biotechnology, and related fields. It is designed to expose them to best practices and regulatory compliance necessary for maintaining a safe and efficient research environment.

Learning Outcomes

Students will understand the principles, operation, and applications of various laboratory instruments. They will develop proficiency in instrument calibration, maintenance, and troubleshooting to ensure accurate and reliable experimental outcomes. Students will gain hands-on experience with state-of-the-art laboratory equipment, preparing them for advanced research and industrial settings. They will also develop a strong understanding of laboratory best practices, including biosafety measures, waste disposal, and emergency response protocols.

Course Content (45 hours)

Unit 1: Introduction to Laboratory Safety and Waste Management -- Laboratory safety guidelines: safety rules, biosafety levels (BSL1–BSL4), handling biological specimens; Chemical, biological, and radiation safety: chemical and biological material labelling and inventory management; Chemical/non-chemical storage guidelines, transportation and usage precautions, chemical hazard and safety datasheets, safe handling of carcinogens, mutagens, and toxic chemicals, compressed gas cylinders and liquid cryogen containers; Biosafety cabinets and laminar airflow systems; Emergency preparedness and waste management: fire hazards, first-aid procedures for chemical spillage and exposure; Hazardous waste minimization and accumulation rules; Disposal of infectious or biological waste, including GMOs (modified microbes, transgenic plants). 15 hours

Essential Readings: Mourya, D.T., et al. (2014) Establishment of Biosafety Level-3 (BSL-3) laboratory: important criteria to consider while designing, constructing, commissioning & operating the facility in Indian setting. Indian Journal of Medical Research, 140(2):171–183, PMCID: PMC4216491; Regulations & Guidelines for Recombinant DNA Research and Biocontainment (2017), published by DBT, India. (https://dbtindia.gov.in/sites/default/files/uploadfiles/Regulations_%26_Guidelines_for_Reocminant_DNA_Research_and_Biocontainment%2C2017.pdf); Laboratory biosafety manual, 3rd edition, WHO (https://www.who.int/publications/i/item/9241546506); Meechan, P.J. and Potts, J. (2020) Biosafety in microbiological and biomedical laboratories, 6th edition, U.S. Department of Health and Human Services, CS308133-A.

Unit 2: Radiological Laboratories and Radiation Safety -- Nature of Radioactivity, biological effects of ionising radiation, operational radiation exposure limits, radiation hazard evaluation and control, planning of radioisotope laboratories, regulatory aspects of radioisotope laboratories, disposal of radioactive waste. 8 hours

Essential Readings: Wilson, K., et al. (Eds.). (2018). Wilson and Walker's principles and techniques of biochemistry and molecular biology. Cambridge University Press, ISBN:9781316677056, DOI: 10.1017/9781316677056, Chapter 9 (Radioisotope Techniques); The Atomic Energy (Safe disposal of radioactive wastes) Rules, 1987- for the safe disposal of radioactive wastes.

Unit 3: Essential Laboratory Instrumentation -- Operation, principles, calibrations, maintenance, and applications of general instruments: weighing balances, pH meter, autoclave, centrifuges, electrophoresis, spectrophotometers (UV-Vis and nanodrop), fluorometers, thermal cyclers (PCR, digital droplet PCR, and real-time PCR machines), incubators/shakers, chromatography, gel documentation system, phosphor imaging systems, Sanger sequencing instrumentation and techniques. 10 hours

Essential Readings: Tiwari, R., et al. (2025) An electronic analytical balance: a key instrument in the laboratory. Journal of Pharmaceutical and Biopharmaceutical Research, 7(1):25–534, DOI:10.25082/JPBR.2025.01.002; Ramstorp, M. (2003) Contamination control in practice: filtration and sterilisation. Wiley-VCH, ISBN:9783527612604, DOI:10.1002/9783527612604, Chapter 4 (Autoclaves and processes for the pharmaceutical industry); Beard, A., et al. (2023) Ullmann's encyclopedia of industrial chemistry, Wiley-VCH Verlag, Chapter (pH measurement and control, DOI:10.1002/14356007.e19_e01.pub2), Chapter (Centrifuges, Sedimenting, DOI: 10.1002/14356007.c05_c02.pub2); Green, M.R. and Sambrook, J. (2019) Analysis of DNA by agarose gel electrophoresis. Cold Spring Harbor Protocols, DOI:10.1101/pdb.top100388; Hou, Y., et al. (2023). Droplet-based digital PCR (ddPCR) and its applications. Trends in Analytical Chemistry, 158:116897, DOI:10.1016/j.trac.2022.116897; Bilkova, Z., et al. (2025) Fundamentals of protein affinity chromatography: How to prepare and properly use an affinity matrix. Journal of chromatography, 1756:466061. DOI:10.1016/j.chroma.2025.466061; Asad, N., et al. (2023) Sustainable and cost-effective gel documentation. Methods and Protocols, 6(2):21, DOI:10.3390/mps6020021; Upham, L.V. and Englert, D. (2003) Handbook of radioactivity analysis, 2nd edition, Chapter 13 (Radionuclide imaging), DOI:10.1016/B978-012436603-9/50018-1.

Unit 4: Advanced Instrumentation in Plant Molecular Biology Research -- Electroporators**,** Surface Plasmon Resonance (SPR) Systems, Isothermal Titration Calorimeter (ITC), BioLayer Interferometry (BLI), *in vivo* imaging system, phytotrons and greenhouses, photosynthesis measurement systems, Flow cytometry: fluidic system, optical system, signal detection and processing system, Fluorescent-Activated Cell Sorting (FACS); High-throughput plant phenomics systems, smart remote agriculture monitoring systems (Internet of Things or IoT-based monitoring, AI-based precision monitoring, data loggers). 12 hours

Essential Readings: Li, F., et. al. (2025) Current advances and future prospects of bulk and microfluidic-enabled electroporation systems. Biotechnology and Bioengineering, 122(6):1347–1365, DOI:10.1002/bit.28965; Butt, M.A. (2025) Surface Plasmon Resonance-based biodetection systems: Principles, progress and applications- a comprehensive review. Biosensors, 15(1):35, DOI:10.3390/bios15010035; Bastos, M., et al. (2023) Isothermal titration calorimetry, Nature Reviews Methods Primers, 3:17, DOI:10.1038/s43586-023-00199-x; Jug, A. et al. (2024) Biolayer interferometry and its applications in drug discovery and development. Trends in Analytical Chemistry, 176:117741, DOI:10.1016/j.trac.2024.117741.

Practicals (30 hours)

1. Precision measurement and liquid handling using micropipettes.
2. Preparation of molecular biology reagents and buffers.
3. Colorimetric analysis of different biomolecules using spectrophotometer.
4. Differential centrifugation for separation of cell organelles.
5. Demonstration of Sanger sequencing technology and flow cytometry instrument.

Suggested Readings:

1. Brown, T.A. (2023) Essential Molecular Biology: A Practical Approach, ISBN:9781383049282.
2. Robens, E., et al. (2014) Balances- instruments, manufacturers, history, Springer Berlin, Heidelberg, DOI:10.1007/978-3-642-36447-1.
3. Webster, J.G. and Eren, H. (2014). Measurement, Instrumentation, and Sensors Handbook, 2nd edition, CRC Press, ISBN:9781315217444, DOI:10.1201/b15664.
4. Westermeier, R. (2013) Chapter: Gel Electrophoresis *in book* Encyclopedia of life sciences, John Wiley & Sons, ISBN:9780470015902, DOI:10.1002/9780470015902.a0005335.pub2.
5. UV/Vis Spectrophotometry- Fundamentals and Applications (2025). Publisher: Mettler-Toledo Publication No. ME-30256131E.
6. The basics of UV-Vis spectrophotometry- a primer (2025), Agilent technologies. 5980-1397EN.
7. Instrumentation for Fluorescence Spectroscopy. In: Lakowicz, J.R. (eds) Principles of fluorescence spectroscopy (2006) Springer, Boston, MA, DOI:10.1007/978-0-387-46312-4_2.
8. Trouchet, A., et al. (2025) Digital PCR: from early developments to its future application in clinics. Lab on a chip, 25(16):3921–3961, DOI:10.1039/d5lc00055f.
9. Artika, I.M., et al. (2022). Real-time polymerase chain reaction: Current techniques, applications, and role in COVID-19 diagnosis. Genes, 13(12):2387, DOI:10.3390/genes13122387.
10. MicroPulser electroporator- Instruction manual and applications guide, 10000148532 Ver A (4006174) BIO-RAD.
11. Capelli, D. et al. (2023) Surface plasmon resonance technology: Recent advances, applications and experimental cases. TrAC Trends in Analytical Chemistry, 163:117079, DOI:10.1016/j.trac.2023.117079.
12. Wilson, K., et al. (2018) Wilson and Walker's principles and techniques of biochemistry and molecular biology. Cambridge University Press, ISBN:9781316677056, DOI:10.1017/9781316677056.
13. Green M.R. and Sambrook J. (2012) Molecular Cloning: A Laboratory Manual. 4th edition. CSHL Press, USA, ISBN:9781936113422.
14. McKinnon, K.M. (2018) Flow cytometry: an overview. Current Protocols in Immunology, 120(1):5–1, DOI:10.1002/cpim.40.
15. Doležel, J., et al. (2007) Estimation of nuclear DNA content in plants using flow cytometry. Nature Protocols, 2(9):2233–2244, DOI:10.1038/nprot.2007.310.

PBSE106: Model Organisms in Molecular Biology Research

<u>This course is open to students of other departments as a GE course.</u>

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE106: Model Organisms in Molecular Biology Research	4	3	1	0	B.Sc. in any branch of science	NA

Learning Objectives

Model organisms have a pivotal role in advancing our understanding of fundamental biological processes. The course aims to provide an in-depth understanding of the significance of model organisms in molecular biology research. It will familiarize students with the criteria for selecting model organisms and the diversity of models used across different biological kingdoms. It will provide an opportunity to examine the unique features, advantages, and limitations of various model systems. Information will be imparted on emerging model organisms and non-model organisms with unique features and cutting-edge advancements, such as artificial cell models. Ethical considerations will be discussed to ensure responsible research practices.

Learning Outcomes

Students will understand the importance of model organisms and their contributions to molecular biology research across different fields. They will be able to evaluate and select appropriate model systems for specific research objectives and explore the utility of emerging model systems and novel technologies in advancing molecular biology research. Students will be aware of ethical issues and guidelines for humane and sustainable research involving model organisms.

Course Content (45 hours)

Unit 1: Introduction to Model Organisms -- Fundamental concepts and importance of model organisms in molecular biology research, criteria for selecting model organisms, types of model organisms across different phyla, historical milestones, comparative overview between prokaryotic and eukaryotic model systems; Nobel prize-winning discoveries utilizing model organisms. 7 hours

Essential Readings: Müller, B. and Grossniklaus, U. (2010) Model organisms-a historical perspective. Journal of Proteomics, 73(11):2054–2063, DOI:10.1016/j.jprot.2010.08.002; Hedges, S.B. (2002) The origin and evolution of model organisms. Nature Reviews Genetics, 3(11):838–849, DOI:10.1038/nrg929; Davis R.H. (2004) The age of model organisms. Nature Reviews Genetics, 5(1):69–76, DOI:10.1038/nrg1250; Ambros, V. R., et al. (2025) From nematode to Nobel: How community-shared resources fueled the rise of *Caenorhabditis elegans* as a research organism. PNAS, 122(48):e2522808122, DOI:10.1073/pnas.2522808122.

Unit 2: Prokaryotic and Lower Eukaryotes Models -- Importance and utility of prokaryotic models and their genetic manipulation (e.g. *Escherichia coli*, *Bacillus subtilis*, etc.); Bacteriophages; Lower eukaryotes: Importance and utility of unicellular eukaryotes and their genetic manipulation; Yeast (*Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*); *Neurospora crassa*; *Dictyostelium discoideum.* 15 hours

Essential Readings: Davis, R.H. (2003) The microbial models of molecular biology: From genes to genome. Oxford Press, ISBN:9780195154368; Stülke, J., et al. (2023) *Bacillus subtilis*, a swiss army knife in science and biotechnology. Journal of Bacteriology, 205(5):e00102–23, DOI:10.1128/jb.00102-23; Akinsemolu, A.A., et al. (2024) Exploring *Bacillus subtilis*: Ecology, biotechnological applications and future prospects. Journal of Basic Microbiology, 64(6):2300614, DOI:10.1002/jobm.202300614; Nurse, P., et al. (1976) Genetic control of the cell division cycle in the fission yeast *Schizosaccharomyces pombe*. Molecular and General Genetics, 146(2):167–178, DOI:10.1007/BF00268085; Li, S.I. and Purugganan, M.D. (2011) The cooperative amoeba: Dictyostelium as a model for social evolution. Trends in Genetics, 27(2):48–54, DOI:10.1016/j.tig.2010.11.003.

Unit 3: **Animal and Plant Models** -- Importance and utility of animal models and their genetic manipulation, Invertebrates (*Drosophila melanogaster* and *Caenorhabditis elegans*), Vertebrates (*Mus musculus, Rattus norvegicus, Danio rerio, Xenopus laevis, Macaca* spp. and other primates); Cell lines as *in vitro* models; Human disease models; Plant models: Importance, utility and their genetic manipulation, single-celled green algae (*Chlamydomonas reinhardtii*, for biofuels-*Botryococcus braunii* and *Chlorella vulgaris*), lower plants (*Marchantia polymorpha* and *Physcomitrium patens*); Monocots (*Oryza sativa*, *Brachypodium distachyon*, *Panicum spp.*, other models); Dicots (*Arabidopsis thaliana*, *Medicago truncatula*, *Jatropha curcas*, and other models). 15 hours

Essential Readings: Irion, U. and Nüsslein-Volhard, C. (2022) Developmental genetics with model organisms. PNAS, 119(30):e2122148119, DOI:10.1073/pnas.2122148119; Kimble, J. and Nüsslein-Volhard, C. (2022) The great small organisms of developmental genetics: *Caenorhabditis elegans* and *Drosophila melanogaster*. Developmental Biology, 485:93–122, DOI:10.1016/j.ydbio.2022.02.013; Standley, A., et al. (2024) Working with miraculous mice: *Mus musculus* as a model organism. Current Protocols, 4(10):e70021, DOI:10.1002/cpz1.70021; Giansanti, M.G., et al. (2025) *Drosophila melanogaster*: How and why it became a model organism. International Journal of Molecular Sciences, 26(15):7485, DOI:10.3390/ijms26157485; Chang, C., et al. (2016) Field guide to plant model systems. Cell, 167(2):325–339, DOI:10.1016/j.cell.2016.08.031; Goodenough, U. (2023) The *Chlamydomonas* sourcebook Volume 1: Introduction to *Chlamydomonas* and its laboratory use. Academic Press, ISBN:9780128224571, DOI:10.1016/C2019-0-02739-2; Al-Hammadi, M., and Güngörmüşler, M. (2024) New insights into *Chlorella vulgaris* applications. Biotechnology and Bioengineering, 121(5):1486–1502, DOI:10.1002/bit.28666; Bowman, J.L., et al. (2022) The renaissance and enlightenment of *Marchantia* as a model system. The Plant Cell, 34(10):3512–3542, DOI:10.1093/plcell/koac219; Rensing, S.A., et al. (2020) The moss *Physcomitrium (Physcomitrella) patens*: A model organism for non-seed plants. The Plant Cell, 32(5):1361–1376, DOI:10.1105/tpc.19.00828; Scholthof, K.B.G., et al. (2018) *Brachypodium*: A monocot grass model genus for plant biology. The Plant Cell, 30(8):1673–1694, DOI:10.1105/tpc.18.00083; Goff, S.A. (1999) Rice as a model for cereal genomics. Current Opinion in Plant Biology, 2(2):86–89, DOI:10.1016/S1369-5266(99)80018-1; Woodward, A.W. and Bartel, B. (2018) Biology in bloom: a primer on the *Arabidopsis thaliana* model system. Genetics, 208(4):1337–1349, DOI:10.1534/genetics.118.300755; Nandety, R.S., et al. (2022) *Medicago truncatula* resources to study legume biology and symbiotic nitrogen fixation. Fundamental Research, 3(2):219–224, DOI:10.1016/j.fmre.2022.06.018.

Unit 4: Emerging Model Organisms and Ethics -- Non-model species with unique features, such as Tardigrades, Axolotls, *Octopus bimaculoides*; Advances in model research: development of artificial cell models, other pioneering studies for insights into untapped species and their potential applications; Ethical considerations: animal welfare, regulatory guidelines, ethical issues, alternatives to animal models (such as organoids, *in silico* simulations, and integration of AI and computational models). 8 hours

Essential Readings: Weronika, E. and Łukasz, K. (2017) Tardigrades in Space Research - Past and Future. Origins of Life and Evolution of Biospheres, 47(4):545–553, DOI:10.1007/s11084-016-9522-1; Møbjerg, N., et al. (2011) Survival in extreme environments-on the current knowledge of adaptations in tardigrades. Acta Physiol (Oxf). 202(3):409–420, DOI:10.1111/j.1748-1716.2011.02252.x; Hashimoto, T., et al. (2016) Extremotolerant tardigrade genome and improved radiotolerance of human cultured cells by tardigrade-unique protein. Nature Communications, 7:12808, DOI:10.1038/ncomms12808; Arce, H., et al. (2025) Modeling proximalisation in axolotl limb regeneration. Sci Rep., 15(1):1–17, DOI:10.1038/s41598-025-10527-8; Adamson, C.J. et al. (2022)

The amazing and anomalous axolotls as scientific models. Developmental Dynamics, 251(6):922–933. DOI:10.1002/dvdy.470; Nowoshilow, S., et al. (2018) The axolotl genome and the evolution of key tissue formation regulators. Nature, 554:50–55, DOI:10.1038/nature25458; Albertin, C.B., et al. (2015) The octopus genome and the evolution of cephalopod neural and morphological novelties. Nature, 524(7564):220–224, DOI:10.1038/nature14668; Kim, J. et al. (2020) Human organoids: model systems for human biology and medicine. Nature Reviews Molecular Cell Biology, 21(10):571–584, DOI:10.1038/s41580-020-0259-3; Lukyanenko, R., et al. (2022) Conceptual modelling for life sciences based on systemist foundations. BMC Bioinformatics, 23(11):1–28, DOI:10.1186/s12859-023-05287-z; Harline, K., et al. (2021) A life cycle for modeling biology at different scales. Frontiers in Plant Science, 12:710590, DOI:10.3389/fpls.2021.710590.

Tutorials (15 hours)

1. Exploration of online data resources and data analysis tools on model organisms:
   a. EcoCyc: Encyclopedia of *E. coli* genes and metabolism, and *Saccharomyces* Genome Database (SGD).
   b. WormBase (*Caenorhabditis elegans*), FlyBase (*Drosophila*), and Rat Genome Database (RGD).
   c. The *Arabidopsis* Information Resource (TAIR), Gramene and Rice Annotation Project Database (RAP-DB), Solanaceae Genomics Network (SGN), and LIS-Legume Information System.
2. Through role-play exercises, students will explore ethical considerations on the use of model organisms in research by debating from the perspective of a scientist, ethicist, and animal rights advocate.
3. Discussion on prospects of *in silico* simulation and computational models.

Suggested Readings:

1. Ankey, R.A. and Leonelli S. (2021) Model organisms. Cambridge University Press, ISBN: 9781108742320.
2. Grossman A.R. (2000) *Chlamydomonas reinhardtii* and photosynthesis: genetics to genomics. Current Opinion in Plant Biology, 3(2):132–137, DOI:10.1016/s1369-5266(99)00053-9.
3. Modlinska, K., and Pisula, W. (2020) The Norway rat, from an obnoxious pest to a laboratory pet. eLife, 9:e50651, DOI:10.7554/eLife.50651.
4. Boland, D.J., et al. (2024) Reclassification of *Botryococcus braunii* chemical races into separate species based on a comparative genomics analysis. PloS One, 19(7):e0304144, DOI: 10.1371/journal.pone.0304144.
5. Ishizaki, K., et al. (2016) Molecular genetic tools and techniques for *Marchantia polymorpha* research. Plant & Cell Physiology, 57(2):262–270, DOI:10.1093/pcp/pcv097.
6. Kohchi, T., et al. (2021) Development and Molecular Genetics of *Marchantia polymorpha*. Annual Review of Plant Biology, 72:677–702, DOI:10.1146/annurev-arplant-082520-094256.
7. Naramoto, S., et al. (2022) The bryophytes *Physcomitrium patens* and *Marchantia polymorpha* as model systems for studying evolutionary cell and developmental biology in plants. The Plant Cell, 34(1):228–246, DOI:10.1093/plcell/koab218.
8. Draper, J., et al. (2001) *Brachypodium distachyon*. A new model system for functional genomics in grasses. Plant Physiology, 127(4):1539–1555, DOI:10.1104/pp.010196.
9. Hasterok, R., et al. (2022) *Brachypodium*: 20 years as a grass biology model system; the way forward? Trends in Plant Science, *27*(10):1002–1016, DOI:10.1016/j.tplants.2022.04.008.
10. McLaughlin, S.B. and Kszos, L.A. (2005) Development of switchgrass (*Panicum virgatum*) as a bioenergy feedstock in the United States. Biomass and Bioenergy, 28(6):515-535, DOI: 10.1016/j.biombioe.2004.05.006.
11. Izawa, T. and Shimamoto, K. (1996) Becoming a model plant: The importance of rice to plant science. Trends in Plant Science, 1(3):95–99, DOI:10.1016/S1360-1385(96)80041-0.
12. Strader, L.C. et al. (2025). Core biological principles and tools stemming from basic *Arabidopsis* research. The Plant Cell, 37(7):koaf141, DOI:10.1093/plcell/koaf141.

13. Barker, D.G., et al. (1990) *Medicago truncatula*, a model plant for studying the molecular genetics of the Rhizobium-legume symbiosis. Plant Molecular Biology Reporter, 8:40–49, DOI:10.1007/BF02668879.
14. de Bruijn, F. (2020) The model legume *Medicago truncatula*. John Wiley & Sons, ISBN:9781119409144, DOI:10.1002/9781119409144.
15. Riayatsyah, T.M.I., et al. (2022) Current Progress of *Jatropha Curcas* commoditisation as biodiesel feedstock: A comprehensive review. Frontiers in Energy Research, 9:815416, DOI:10.3389/fenrg.2021.815416.
16. Emerging model organisms: A Laboratory Manual Vol 1 (2009) Cold Spring Harbor Laboratory Press, ISBN:9780879698720.
17. Jarret, R.L and McCluskey, K. (2020) Biological resources of model organisms. 1st edition, CRC Press, ISBN:9781138294615.
18. Davis, R H. (2003) The Microbial Models of Molecular Biology: From Genes to Genome. OUP Oxford Press, ISBN:9780195154368.
19. Tang B, Wang Y, Zhu J, Zhao W. (2015) Web resources for model organism studies. Genomics Proteomics Bioinformatics, 13(1):64–68, DOI:10.1016/j.gpb.2015.01.003.
20. Latest research and review articles from Scientific journals and book chapters.

PBSEC107: Biological Data Analysis and Interpretation

Course title & code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSEC107: Biological Data Analysis and Interpretation	2	1	0	1	B.Sc. in any branch of science	NA

Learning Objectives

This course provides an in-depth understanding of the fundamental and advanced research methodologies employed in plant molecular biology and biotechnology. It focuses on experimental design, data analysis, and scientific communication while integrating guest lectures of specialists (if required). Special emphasis will be given to high-throughput sequencing, genome editing, plant transformation techniques, and bioinformatics approaches relevant to molecular plant sciences.

Learning Outcomes

Upon completion of this course, students will be adept at designing robust biological experiments, performing comprehensive statistical analyses, and interpreting various data types with scientific rigor. They will gain proficiency in hypothesis testing, regression models, and survival analysis, while also understanding the ethical concerns in biostatistics. Learners will acquire knowledge to analyze transcriptomic data using tools like DESeq2 and DAVID. Additionally, they will develop the ability to create effective, publication-quality visualizations of complex biological datasets.

Course Content

(Lectures combined with problem-solving practical sessions; 15+30 = 45 hours)

Unit 1: Experimental Design and Biostatistics -- Principles of experimental design; Control groups, replication, and randomization; Types of biological data and measurement scales; descriptive statistics (mean, median, variance, standard deviation); Probability distributions (normal, binomial, Poisson); Hypothesis testing (t-tests, chi-square, ANOVA, non-parametric tests); Power analysis and sample size determination; Ethical considerations in biostatistics.

6 hours

Essential Readings: Triola, M., et al. (2018) Biostatistics for the Biological and Health Sciences, 3rd edition, Pearson, ISBN:9780137864102, Chapter 1 (Introduction to Statistics), Chapter 2 (Exploring Data with Tables and Graphs), Chapter 3 (Describing, Exploring, and Comparing Data), Chapter 4 (Probability), Chapter 5 (Discrete Probability Distributions), Chapter 6 (Normal Probability Distributions), Chapter 7 (Estimating Parameters and Determining Sample Sizes), Chapter 8 (Hypothesis Testing), Chapter 9 (Inferences from Two Samples), Chapter 10 (Correlation and Regression), Chapter 12 (Analysis of Variance); Maxwell, S.E., et al. (2008) Sample size planning for statistical power and accuracy in parameter estimation. Annual Review of Psychology, 59:537–563, DOI:10.1146/annurev.psych.59.103006.093735; Jackson, M. and Cox, D.R. (2013) The Principles of Experimental Design and Their Application in Sociology. Annual Review of Sociology, 39:27–49, DOI:10.1146/annurev-soc-071811-145443.

Unit 2: Gene Expression Analysis and Data Visualization -- Overview of transcriptomics; RNA sequencing (RNA-Seq), microarrays; Data preprocessing (quality control, normalization, transformation); Differential gene expression analysis; Functional enrichment, pathway analysis; Visualization techniques (heatmaps, volcano plots, expression profiles); Case studies; Hands-on analysis using tools like DESeq2, edgeR, STRING, DAVID; Principles of effective data visualization; Types of visualizations (bar plots, scatter plots, box plots, heatmaps); Visualization of complex biological data (networks, phylogenetic trees, multidimensional plots); Best practices for scientific presentations and publications. 9 hours

Essential Readings: Pevsner, J. (2015) Bioinformatics and Functional Genomics, 3rd edition, Wiley-Blackwell, ISBN:9781118581780, Chapter 9 (Analysis of Next-Generation Sequence Data), Chapter 10 (Bioinformatic Approaches to Ribonucleic Acid (RNA), Chapter 11 (Gene Expression: Microarray and RNA-seq Data Analysis); Van den Berge, K., et al. (2019) RNA Sequencing Data: A Hitchhiker's Guide to Expression Analysis. Annual Review of Biomedical Data Science, 2:139–173. DOI: 10.1146/annurev-biodatasci-072018-021255; O'Donoghue, S.I. et al. (2018) Visualization of Biomedical Data. Annual Review of Biomedical Data Science, 1:275–304, DOI:10.1146/annurev-biodatasci-080917-013424.

Practicals (30 hours)

1. Design an experiment (e.g., drug effect on bacteria) and identify variables, control groups, and the method of randomization.
2. Analyze sample datasets (e.g., plant development-based measurements during stress responses); Classify data and discuss implications for statistical tests.
3. Run t-tests, chi-square tests, and ANOVA on the provided datasets.
4. Identify genes differentially expressed across conditions (using microarray or NGS datasets) and interpret results (using log2 fold changes, p-values, adjusted p-values).

Suggested Readings:

1. Quinn, G.P. and Keough, M.J. (2002) Experimental design and data analysis for biologists. Cambridge University Press, ISBN:9780521009768.
2. Heath, D. (1995) An introduction to experimental design and statistics for biology. UCL Press, ISBN:9781857281323, DOI:10.1201/b12546.
3. Welham, S.J., et al. (2015) Statistical methods in biology: Design and analysis of experiments and regression. CRC Press, ISBN:9781032918327.
4. Daniel, W.W. and Cross, C.L. (2018) Biostatistics: A foundation for analysis in the health sciences.11th edition, Wiley, ISBN:9781118302798.
5. Barah, P., et al. (2021) Gene expression data analysis: A statistical and machine learning perspective. CRC Press, ISBN:9780367338893, DOI:10.1201/9780429322655.
6. Parmigiani, G., et al. (2003) The analysis of gene expression data: Methods and software. Springer New York, ISBN:9780387955773, DOI:10.1007/b97411.
7. Rangayyan, R.M. (2004) Biomedical image analysis. CRC Press, ISBN:9780849396953.
8. Hartvigsen, G. (2021) A primer in biological data analysis and visualization using R. 2nd edition, Columbia University Press, ISBN:9780231202138.

SEMESTER 2

PBSC201: Molecular Basis of Plant Development

Course title & code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSC201: Molecular Basis of Plant Development	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

The objective of this course is to provide an in-depth understanding of plant differentiation, development, and the regulatory mechanisms that govern these processes. Students will explore key concepts, including totipotency, organogenesis, and tissue differentiation, as well as light perception, plant growth, leaf and root development, floral induction, and reproductive processes. The course also covers the hormonal and molecular control of plant development, including seed development, dormancy, germination, senescence, and programmed cell death.

Learning Outcomes

Upon completion, students will have a comprehensive understanding of plant growth and developmental processes, from cellular differentiation to reproductive mechanisms. They will be able to analyze the molecular and genetic regulation of plant responses to environmental signals, particularly light. Students will gain expertise in the light- and hormonal-control of plant development. Students will develop the skills to analyze the developmental stages of microspores and embryos. The course will enhance their ability to conduct research in plant biology and to apply their knowledge to crop improvement.

Course Content (45 hours)

Unit 1: Plant Differentiation and Photomorphogenesis -- Totipotency, meristems, organogenesis, adventive somatic embryogenesis, apomixis, trichome and stomata; Phloem and xylem differentiation; Gametogenesis and embryogenesis; Skotomorphogenesis and photomorphogenesis; Molecular mechanisms of light perception, signal transduction and gene regulation; Biological clocks and their genetic and molecular determinants. 14 hours

Essential Readings: Turnbull, C.G. (2005) Plant architecture and its manipulation. Barcelona: Blackwell, Chapter 1 (Cellular architecture: Regulation of cell size, cell shape and organ initiation); Buchanan, B.B. et al. (2015) Biochemistry and Molecular Biology of Plants. 2nd edition, John Wiley & Sons Ltd., UK, ISBN:9780470714218, Chapter 18 (Signal Transduction); De Rybel, B., et al. (2016) Plant vascular development: from early specification to differentiation. Nature Reviews Molecular Cell Biology, 17(1):30–40, DOI:10.1038/nrm.2015.6; Jones, R., et al. (2012) The molecular life of plants. ASPB and Wiley-Blackwell, ISBN:9781118315989, Chapter 8 (Light perception and transduction); Cheng, M. C., et al. (2021) Phytochrome signaling networks. Annual Review of Plant Biology, 72:217–244, DOI:10.1146/annurev-arplant-080620-024221.

Unit 2: Leaf and Root Development -- Molecular basis of leaf development and polarity establishment; Venation patterns in leaves; Shoot branching and architecture; Hormonal control of leaf development; Stomatal development and movement; Phyllotaxy; Root apical meristem (RAM), primary and secondary root development, root hair and root system architecture (RSA); hormonal control of root development. 12 hours

Essential Readings: Wolpert, L., et al. (2015) Principles of Development. Oxford Publishers, UK, ISBN: 9780198709886, Chapter 13 (Plant Development); Taiz, L., et al. (2015) Plant Physiology and Development. Sinauer Associates Inc. Publishers, USA, ISBN:9781605352558, Chapter 19 (Vegetative Growth and Organogenesis).

Unit 3: Floral Induction and Regulation of Gametogenesis and Embryogenesis -- Photoperiodism and its significance; Vernalization and hormonal control; Inflorescence and floral determination; Molecular genetics of floral development and floral organ differentiation: floral development in *Arabidopsis* and *Antirrhinum*; Formation of male and female gametes, pollination and fertilization; Self incompatibility; Cytoplasmic inheritance; Epigenetic imprinting; Embryo formation and cell lineage development in *Arabidopsis* and Maize.

8 hours

Essential Readings: Buchanan, B.B. et al. (2015) Biochemistry and Molecular Biology of Plants. 2nd edition, John Wiley & Sons, Ltd, UK, ISBN:9780470714218, Chapter 19 (Molecular Regulation of Reproductive Development); Gilbert, S.F. (2000) Developmental Biology. INC Publishers, USA, ISBN:9780197699782, Chapter 20 (An overview of plant development); Wolpert, L. et al. (2015) Principles of Development. Oxford Publishers, UK, ISBN: 9780198709886, Chapter 13 (Plant Development).

Unit 4: Seed Development, Dormancy, Germination, and Programmed Cell Death (PCD) -- Seed maturation and dormancy; Hormonal control of seed germination, development, and seedling growth; Mobilization of food reserves during seed germination; Cell death, PCD, and apoptosis; Senescence in plants and its regulation; PCD during seed development, leaf development, and reproductive development; Energy and oxidative metabolism during senescence; Hormonal and environmental control of senescence. 11 hours

Essential Reading: Bentsink, L. and Koornneef, M. (2008) Seed dormancy and germination. The *Arabidopsis* Book, 6:e0119, American Society of Plant Biologists, DOI:10.1199/tab.0119; Sajeev, N., et al. (2024) A commitment for life: Decades of unraveling the molecular mechanisms behind seed dormancy and germination. The Plant Cell, 36(5):1358–1376, DOI:10.1093/plcell/koad328; Jones, R., et al. (2012) The molecular life of plants. ASPB and Wiley-Blackwell, ISBN:9781118315989, Chapter 6 (Seed to seedling: germination and mobilization of food reserves, Chapter 17 (Development and dormancy of resting structures); Buchanan, B.B. et al. (2015) Biochemistry and Molecular Biology of Plants. 2nd edition, John Wiley & Sons Ltd. UK, ISBN:9780470714218, Chapter 20 (Senescence and Cell Death); Domínguez, F. and Cejudo, F.J. (2014) Programmed cell death (PCD): an essential process of cereal seed development and germination. Frontiers in Plant Science, 5:366, DOI:10.3389/fpls.2014.00366.

Practicals (30 hours)

1. Study of photomorphogenesis and skotomorphogenesis (by using mutants).
2. Analysis of microspore development.
3. Study of root differentiation using cytokinin markers.
4. Estimation of chlorophyll degradation during leaf senescence.
5. Study of embryo development.

Suggested Readings:

1. Gilbert, S.F. (2000) Developmental Biology. INC Publishers, USA, ISBN:9780197699782.
2. Westhoff, P. (1998) Molecular Plant Development: from gene to plant. The Bath Press, UK, ISBN:9780198502043.
3. Wolpert, L., et al. (2015) Principles of Development. 5th edition, Oxford Publishers, UK, ISBN:9780198709886.
4. Buchanan, B.B., et al. (2015) Biochemistry & Molecular Biology of Plants. 2nd edition, John Wiley & Sons Ltd., UK, ISBN:9780470714218.

5. Taiz, L., et al. (2015) Plant Physiology and Development. 7th edition, Sinauer Associates Inc. Publishers, USA, ISBN:9781605352558.
6. Caño-Delgado, A., et al. (2010) Regulatory mechanisms for specification and patterning of plant vascular tissues. Annual Review of Cell and Developmental Biology, 26:605–637, DOI:10.1146/annurev-cellbio-100109-104107.
7. Schuetz, M., et al. (2013) Xylem tissue specification, patterning, and differentiation mechanisms. Journal of Experimental Botany, 64(1):11–31, DOI:10.1093/jxb/ers287.
8. Lehesranta, S.J., et al. (2010) Cell-to-cell communication in vascular morphogenesis. Current Opinion in Plant Biology, 13(1):59–65, DOI:10.1016/j.pbi.2009.09.004.

PBSC202: Plant Biochemistry and Metabolism

Course title & code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSC202: Plant Biochemistry and Metabolism	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

Plant biochemistry and metabolism is the study of biomolecules, biochemical processes, and the pathways of chemical energy flow. This course is designed to impart critical knowledge of plant-specific primary metabolism from a more mechanistic perspective, including photosynthesis, respiration, and the metabolism of carbohydrates, lipids, amino acids, and nucleotides. The course will also provide information on the uptake, transport, and assimilation of nutrients as well as long-distance transport mechanisms in plants. Furthermore, students will also learn to appreciate the importance of secondary metabolites produced by plants.

Learning Outcomes

This paper aims to provide a comprehensive understanding of the various metabolic processes that operate within a plant system. It would provide insights into the structural diversity of various biomolecules, their movement, synthesis and turnover. It would also aid in developing an understanding of the key components in metabolic pathways, with a focus on the genetic improvement of quality traits.

Course Content (45 hours)

Unit 1: Carbon Assimilation in Photosynthesis, and Uptake and Assimilation of Nutrients -- Light absorption and energy conversion; Calvin Cycle (C_3), Hatch-Slack pathway (C_4), Crassulacean Acid Metabolism (CAM), Reductive pentose phosphate pathway, Carbon dioxide uptake and assimilation, photorespiration, glycolate metabolism; Enhancing photosynthetic carbon assimilation by genetic engineering; Overview of essential mineral elements, molecular physiology of nutrient acquisition (Nitrogen, Potassium, Sulphur, and Phosphorus), role of essential mineral elements in plants; Nitrate uptake, assimilation and transport, nitrate reduction, pathways of ammonia assimilation, reductive amination, trans-amination; Regulation of transport and assimilation of essential nutrients. 17 Hours

Essential Readings: Buchanan, B.B. et al. (2015) Biochemistry and Molecular Biology of Plants. 2nd edition, John Wiley & Sons Ltd. UK, ISBN:9780470714218, Chapter 12 (Photosynthesis); Qin, K., et al. (2025) Engineering carbon assimilation in plants. Journal of Integrative Plant Biology, 67(4):926–948, DOI:10.1111/jipb.13825; Taiz, L. and Zeiger, E. (2002) Plant Physiology, 4th edition, ISBN:9780878938568, Unit II (Biochemistry and Metabolism); Taiz, L., et al. (2023) Plant physiology and development, 7th edition, Oxford University Press, ISBN:9780197614204, Unit III (Biochemistry and Metabolism).

Unit 2: Biological Oxidation and Release of Energy -- Glycolytic pathway, Kreb's cycle, high-energy compounds; Oxidative phosphorylation; Chemiosmotic hypothesis; Pentose phosphate shunt pathway; Regulation of citric acid cycle and cytochrome pathway; Interactions between mitochondria and other cellular compartments. 10 Hours

Essential Readings: Buchanan, B.B., et al. (2015) Biochemistry and Molecular Biology of Plants. 2nd edition, John Wiley & Sons Ltd. UK, ISBN:9780470714218, Chapter 14 (Respiration and Photorespiration); Nelson, L. et al. (2021) Lehninger Principles of Biochemistry, 8th edition. ISBN:9781319228002, Unit II (Bioenergetics and metabolism).

Unit 3: Metabolism of Biomolecules and Secondary Metabolites -- Composition, structure and function of biomolecules (carbohydrates, lipids, proteins, and nucleic acids), biosynthesis, inter-conversion and breakdown of carbohydrates and lipids, metabolism of nucleotides and amino acids; Biosynthesis of phenolic compounds, isoprenoids, alkaloids, glucosinolates and flavonoids, phenylpropanoid pathway, mevalonate (MVA) pathway, methylerythritol phosphate pathway; Importance of secondary metabolites; Metabolic engineering of secondary metabolite production; Biotechnological applications of secondary metabolites. 12 Hours

Essential Readings: Verpoorte, R. (2000) Secondary Metabolism. In: Verpoorte, R., Alfermann, A.W. (eds) Metabolic engineering of plant secondary metabolism. Springer Dordrecht, DOI:10.1007/978-94-015-9423-3_1; Crozier, A., et al. (2006) Plant secondary metabolites. Occurrence, Structure and Role in the Human Diet, Blackwell-Publishers, ISBN:9781405125093; Bhatla, S.C. and Lal, M.A. (2023) Secondary metabolites. In Plant physiology, development and metabolism, pp.765-808. Springer Nature Singapore, ISBN:9789819957354.

Unit 4: Long-distance Transport Mechanisms in Plants -- Transport of water: long-distance transport and short-distance transport events between xylem and nonvascular cells, transport modules, specific water channels, turgor and stomatal movements, translocation of ions and solutes from soil; Ion transport and solute movement; Passive and Active transport, Short-distance transport between phloem and nonvascular cells; Source-sink relationship, mechanisms of loading and unloading of photoassimilates. 6 hours

Essential Readings: Buchanan, B.B., et al. (2015) Biochemistry and Molecular Biology of Plants. 2nd edition, John Wiley & Sons Ltd. UK, ISBN:9780470714218; Taiz, L. and Zeiger, E. (2002) Plant physiology, 4th edition, ISBN:9780878938568, Unit II (Biochemistry and Metabolism); Taiz, L. et al. (2023) Plant Physiology and Development, 7th edition, Oxford University Press, ISBN:9780197614204.

Practicals (30 hours)

1. Substrate inducibility of nitrate reductase (NR) enzyme.
2. Determination of optimal pH for nitrate reductase activity.
3. Spectrophotometric assay of acid phosphatase.
4. Isolation of chloroplastic proteins and resolve them using SDS-PAGE.
5. Activity of mitochondrial marker enzyme, succinate dehydrogenase.

Suggested Readings:

1. Dey, P.M. and Harborne, J.B. (1997) Plant Biochemistry. Academic Press, USA, ISBN:9780122146749.
2. Metzler, D.E. (2007) Biochemistry. Academic Press, USA, ISBN:9780122146749.
3. Nelson D.L. and Cox, M.M. (2017) Principles of Biochemistry. W.H. Freeman & Co., USA, ISBN:9781319108243.
4. Stryer L., et al. (2002) Biochemistry. W.H. Freeman & Co., USA, ISBN:9780716746843.
5. Ashihara, H., et al. (2011) Plant Metabolism and Biotechnology, Wiley, ISBN:9780470747032.
6. Piechulla, B. and Hans-Walter, H. (2024) Plant Biochemistry, 6th edition, Elsevier, Academic Press, ISBN:9780443266164.

PBSC203: Eukaryotic Gene Expression and Regulation

Course title & code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSC203: Eukaryotic Gene Expression and Regulation	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

This course provides a detailed understanding of eukaryotic genome structure, regulation, and function. It emphasizes advancements in genome sequencing, epigenetics, and functional genomics, including CRISPR-Cas technologies, while exploring their applications in agriculture and human health. Students will develop theoretical knowledge and practical skills to analyze and manipulate genomic systems.

Learning Outcomes

Upon successful completion of this course, students will gain a comprehensive understanding of genome organization, gene regulation, and functional genomics. It will equip them to interpret high-throughput genomic data and understand regulatory mechanisms at multiple levels. Students will be able to apply this knowledge to genome editing, crop improvement, and medical research. They will also be able to propose innovative solutions to agricultural and health-related challenges by leveraging insights from transcriptional regulation, epigenetics, and emerging genomic technologies.

Course Content (45 hours)

Unit 1: Genomes and Comparative Genomics -- Genome structure and organization; Structure of chromatin and chromosomes; Genome complexity; Nuclear territories; Chromosomal Conformation studies (Hi-C); Unique and repetitive DNA; Evolution of gene families; Advances in genome sequencing technologies (Next-gen and 3rd-gen methodologies, Illumina, PacBio, Nanopore, etc.) and assembly; Optical Genome mapping; Comparative genomics of model organisms (Arabidopsis, rice, humans, and non-model species); Functional annotation through phylogenetic footprinting and multi-genome alignment; Impact of repetitive and transposable elements on genome evolution. 15 hours

Essential Readings: Brown, T.A. (2023) Genomes 5. CRC Press, ISBN:9780367674076, Chapter 4 (Sequencing genomes), Chapter 5 (Genome annotation), Chapter 6 (Identifying gene functions), Chapter 7 (Eukaryotic nuclear genomes), Chapter 8 (Genomes of prokaryotes and eukaryotic organelles); Paterson, A.H., et al. (2010) Insights from the comparison of plant genome sequences. Annual Review of Plant Biology, 61:349–372, DOI:10.1146/annurev-arplant-042809-112235; Jayakodi, M., et al. (2025) What are we learning from plant pangenomes? Annual Review of Plant Biology, 76:663–686, DOI:10.1146/annurev-arplant-090823-015358; For Case Study: International Human Genome Sequencing Consortium. (2001) Initial sequencing and analysis of the human genome. Nature, 409:860–921, DOI:10.1038/35057062; Arabidopsis Genome Initiative. (2000) Analysis of the genome sequence of the flowering plant *Arabidopsis thaliana*. Nature, 408:796–815, DOI:10.1038/35048692; International Rice Genome Sequencing Project. (2005) The map-based sequence of the rice genome. Nature, 436:793–800, DOI:10.1038/nature03895; 3,000 Rice Genomes Project. (2014) The 3,000 Rice Genomes Project. GigaScience, 3:7, DOI:10.1186/2047-217X-3-7.

Unit 2: Epigenetic and Transcriptional Regulation of Gene Expression -- Mechanisms of DNA methylation and histone modifications; Role of non-coding RNAs and chromatin remodeling in transcriptional regulation; Environmental and developmental epigenetic reprogramming; Case studies: Epigenetic regulation in flowering and stress responses; Promoter and enhancer dynamics; Mechanisms of RNA polymerase recruitment and mediator complex functions; Latest insights into transcription factors, co-activators, and repressors; Chromatin looping and transcription factories. 10 hours

Essential Readings: Alberts, B. et al. (2022) Molecular Biology of the Cell, 7th edition, Garland Science/W.W. Norton, ISBN:9780393884821, Chapter 4 (DNA, Chromosomes, and Genomes), Chapter 7 (Control of Gene Expression); Hemenway, E.A. and Slotkin, R.K. (2023) Epigenetic regulation during plant development and the capacity for epigenetic memory. Annual Review of Plant Biology, 74:347–369, DOI:10.1146/annurev-arplant-070122-025047; Marand, A.P., et al. (2023) *cis*-Regulatory elements in plant development, adaptation, and evolution. Annual Review of Plant Biology, 74:111–137, DOI:10.1146/annurev-arplant-070122-030236.

Unit 3: Post-transcriptional, Translational, and Post-translational Regulation -- RNA splicing mechanisms and alternative splicing; RNA editing, stability, transport, and degradation pathways; Regulatory roles of microRNAs, siRNAs, and lncRNAs; Insights into translational regulation and protein synthesis; Global proteomics and functional characterization of protein complexes; Role of post-translational modifications (e.g. phosphorylation, ubiquitination, etc.) and degradation in cellular processes. 10 hours

Essential Readings: Lodish, H. et al. (2016/2021) Molecular Cell Biology, 8th /9th edition, W.H. Freeman, ISBN:9781464183393, Chapter 9 (Post-Transcriptional Gene Control); Wu, Q. and Bazzini, A.A. (2023) Translation and mRNA stability control. Annual Review of Biochemistry, 92:227–245, DOI:10.1146/annurev-biochem-052621-091808; Millar, A.H. et al. (2019) The scope, functions, and dynamics of posttranslational protein modifications. Annual Review of Plant Biology 70:119–151, DOI:10.1146/annurev-arplant-050718-100211.

Unit 4: Functional Genomics and Genome Editing and their Applications -- High-throughput RNA sequencing (single-cell transcriptomics); Spatial Transcriptomics; CRISPR-Cas technologies: principles and applications; Gene Function validation through knockouts, knockdowns, TILLING, and transposon-tagging; Engineering crops with enhanced traits (e.g., drought resistance, pest tolerance); Case studies in transcriptional regulation and its relevance to diseases (e.g., cancer, diabetes). 10 hours

Essential Readings: Brown, T.A. (2023) Genomes 5. CRC Press, ISBN:9780367674076 (print) and 9781003133162 (eBook), Chapter 6 (Identifying gene functions), Chapter 17 (Agricultural genomics); Chen, K. et al. (2019) CRISPR/Cas genome editing and precision plant breeding in agriculture. Annual Review of Plant Biology, 70:667–697, DOI:10.1146/annurev-arplant-050718-100049; Mackelprang, R. and Lemaux, P.G. (2020) Genetic engineering and editing of plants: An analysis of new and persisting questions. Annual Review of Plant Biology, 71:659–687, DOI:10.1146/annurev-arplant-081519-035916.

Practicals (30 hours)

1. Plant DNA extraction and quality assessment.
2. Plant RNA isolation and quality assessment.
3. Gene expression analysis by qRT-PCR.
4. Analysis and validation of qRT-PCR dataset by Student’s t-test.
5. Experimental designing of CRISPR-Cas9-mediated gene editing in plants.

Suggested Readings:

1. Berg, J.M, et al. (2012) Biochemistry. W.H. Freeman and Company, New York, ISBN:9781429229364.

2. Buchanan, B.B., et al. (2015) Biochemistry and Molecular Biology of Plants. 2nd edition, John Wiley & Sons, Ltd., ISBN:9780470714218.
3. Kahl, G. and Meksem, K. (2008) The handbook of plant functional genomics. Wiley-VCH Verlag, ISBN:9783527318848.
4. Krebs, J.E., et al. (2018) Lewin's Genes XII. 12th edition, Jones and Bartlett Learning, ISBN:9781284104493.
5. Latchman, D.S. and Cheriyath, V. (2025) Gene Control. 3rd edition, Garland Science New York, ISBN:9781003382225, DOI:10.1201/9781003382225.
6. Lodish, H., et al. (2016) Molecular Cell Biology. 8th edition, WH Freeman and Company, New York, ISBN: 978-1464183393.
7. Stewart Jr., C.N, (2025) Plant Biotechnology and Genetics: Principles, Techniques and Applications. 3rd edition, John Wiley & Sons Inc., ISBN:9781394217236.

PBSE204: Cell Signaling and Communication

Course title & code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE204: Cell Signaling and Communication	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

This course aims to provide a comprehensive understanding of cellular signaling and communication in different organisms. It will cover fundamental signaling pathways, receptor mechanisms, primary and second messengers, and their roles in cellular responses. Students will explore the molecular basis of cell cycle regulation and hormone signaling, with a special focus on plant hormones and their roles in stress responses, growth, and development. The course integrates key regulatory mechanisms, emphasizing experimental insights and biological relevance.

Learning Outcomes

The candidate would learn about cellular signaling and communication, controlling a myriad of cellular processes, and coupling the cellular processes with external and internal signals/stimuli. The candidate will develop a fundamental understanding of how cells communicate with one another and respond to external stimuli, which govern all cellular functions, including growth, development, and even cell death, making it essential to comprehend complex biological processes.

Course Content (45 hours)

Unit 1: Basic Understanding of Cellular Signaling and Communication -- External and internal signals; Different signaling pathways; Analogy of signaling pathways to electronic circuitry; Stimulus response-coupling; Cellular communication through receptors and plasmodesmata; Two-component system; G-protein coupled receptors, receptor tyrosine kinase, receptor-like kinase, ion channel receptor, other cell surface receptors, intracellular hormone receptors, intracellular ligand-receptor. 10 hours

Essential Readings: Gomperts, B.D., et al. (2009) Signal Transduction. Academic Press USA, ISBN: 9780123694416, Chapter 1 (Prologue: Signal transduction, origin and ancestors), Chapter 2 (First messengers); Buchanan, B.B., et al. (2015) Biochemistry and Molecular Biology of the Plants. American Society of Plant Biologists, ISBN:9780470714218, Chapter 18 (Signal transduction); Alberts, B., et al. (2015) Molecular Biology of the Cell. Garland Publishing, Taylor & Francis Group, USA, ISBN:9780815344322, Chapter 15 (Cell signaling).

Unit 2: Primary and Second Messengers -- Growth factors and hormones in animals (EGF, interleukins, cytokines, insulin, etc.); Plant hormones (auxins, cytokinins, gibberellins, abscisic acid, etc.); Second messengers (Ca^{2+}, ROS, IP_3, cAMP, cGMP, DAG, etc.). 5 hours

Essential Readings: Buchanan, B.B., et al. (2015) Biochemistry and Molecular Biology of the Plants. American Society of Plant Physiologists, USA, ISBN:9780470714218, Chapter 18 (Signal transduction); Alberts, B., et al. (2015) Molecular Biology of the Cell. Garland Publishing, Taylor & Francis Group, USA, ISBN:9780815344322, Chapter 15 (Cell signaling); Gomperts, B.D., et al. (2009) Signal Transduction, Academic Press, USA, ISBN:9780123694416, Chapter 2 (First messengers).

Unit 3: Signaling Pathway in Prokaryotes, Animals, and Plants -- Histidine kinase-based signaling, GPCR-based signaling, receptor tyrosine kinase-based signaling, receptor kinase-based signaling, MAP-kinase-based signaling, Ca^{2+} signaling, phospholipid-based signaling, cyclic nucleotide (cAMP/cGMP)-based signaling; Role of protein kinases and phosphatases in signaling pathways. 12 hours

Essential Readings: Gomperts, B.D., et al. (2009) Signal Transduction. Academic Press, ISBN:9780123694416, Chapter 3 (Receptors), Chapter 4 (GTP-binding proteins and signal transduction), Chapter 5 (Effector enzymes coupled to GTP binding proteins: Adenylyl cyclase and phospholipase), Chapter 6 (The regulation of visual transduction and olfaction), Chapter 20 (Signaling through receptor serine/threonine kinases); Buchanan, B. B. et al. (2015) Biochemistry and Molecular Biology of the Plants. American Society of Plant Physiologists, USA, ISBN:9780470714218, Chapter 18 (Signal transduction); Alberts, B., et al. (2015) Molecular Biology of the Cell. 6th edition, Garland Publishing, ISBN:9780815344322, DOI:10.1201/9781315735368, Chapter 15 (Cell signaling).

Unit 4: Plant Hormones Signaling and Regulation of Cell Cycle -- Signal perception of auxin, ABA, GA, cytokinins, ethylene, brassinosteroids, jasmonic acid, salicylic acid, strigolactones, etc.; Regulation of gene expression during signal transduction; Role of mutants in understanding hormone action; Regulation of biotic and abiotic stresses by phytohormones. Overview of cell cycle, progression to mitosis and meiosis; Cell cycle checkpoints, role of cyclin and cyclin-dependent kinases. 18 hours

Essential Readings: Buchanan, B.B., et al. (2015) Biochemistry and Molecular Biology of the Plants. American Society of Plant Biologists, USA, ISBN:9780470714218, Chapter 18 (Signal transduction), Chapter 11 (Cell division); Alberts, B. et al. (2015) Molecular Biology of the Cell. Garland Publishing, Taylor & Francis Group, USA, ISBN:9780815344322, Chapter 15 (Cell signaling), Chapter 17 (The cell cycle); Kleinsmith, L.J. and Kish, V.M. (1996) Principles of Cell and Molecular Biology. HarperCollins College Publishers, USA, ISBN:9780065004045, Chapter 12 (Cell cycles and cell division).

Practicals (30 hours)

1. Effect of stress signals on growth kinetics of *E. coli*.
2. Analysis of a calcium sensor and its effector kinase by yeast two-hybrid growth assay.
3. Effect of stress stimuli on plant signaling mutants by analyzing the growth phenotype.
4. Localization of cellular auxin biosensor, *DR5*::GFP, in the roots of Arabidopsis.
5. Effect of abiotic stress signals on key signaling gene expression in *Arabidopsis thaliana*.

Suggested Readings:

1. Gomperts B.D., et al. (2009) Signal Transduction. 2nd edition, Academic Press, USA, ISBN:9780123694416, DOI:10.1016/B978-0-12-369441-6.X0001-3.
2. Alberts, B., et al. (2015) Molecular Biology of the Cell. Garland Publishing, ISBN:9780815344322.
3. Buchanan, B.B., et al. (2015) Biochemistry and molecular biology of the plants. American Society of Plant Biologists and Wiley Blackwell, ISBN:9780470714218.
4. Karp, G., et al. (2019) Cell and Molecular Biology. 9th edition, John Wiley & Sons, USA, ISBN:781119598169.
5. Kleinsmith, L.J. and Kish, V.M. (1995) Principles of Cell & Molecular Biology. 2nd edition, Harper Collins College Publishers, USA, ISBN:9780065004045.
6. Lodish, H., et al. (2016) Molecular Cell Biology. Freeman & Co., USA, ISBN:9781464183393.

PBSE205: Plant-Environment Interactions

Course title & code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE205: Plant-Environment Interactions	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

Adverse environmental conditions significantly impact plant survival and productivity. The paper aims to provide an in-depth understanding of how plants perceive and interact with their environments. Students will learn about the effect of different stresses on plant growth and development, the impact of climate change on plant-environment interactions, and how plants adapt to these changing conditions. The course will introduce experimental approaches, modern techniques, and analytical tools for studying plant stress biology.

Learning Outcomes

Students will be able to understand the interactions between plants and their environment, and understand their significance in agriculture and ecology. They will be able to evaluate the changes that plants undergo under challenging conditions and differentiate between the responses to biotic and abiotic stresses. Students will design and execute experiments using physiological, biochemical, and molecular techniques to study plant responses and adaptations. Moreover, students will be able to propose innovative solutions to mitigate the adverse effects of environmental stress on crop productivity using advanced molecular biology and bioengineering approaches. Based on their knowledge, they can develop strategies for developing stress-tolerant plants and their applications in sustainable agriculture and environmental remediation.

Course Content (45 hours)

Unit 1: Plant-Environment Interactions and Plant Stress Responses -- Overview of abiotic and biotic factors and plant responses; Adaptation strategies in different ecosystems (desert, halophytes, aquatic plants, etc.); Role of plant microbiomes in environmental interactions; Stress perception; Stress signal transduction pathways; Role of phytohormones; Epigenetic modifications and non-coding RNAs in plant stress adaptation; Crosstalk between different signaling pathways; Concept of phenotypic plasticity and stress memory in plants. 8 hours

Essential Readings: Manghwar, H., et al. (2024) Plant Biotic and Abiotic Stresses. Life (Basel), 14(3):372, DOI:10.3390/life14030372; Hao, J-R., et al. (2024) Harnessing the plant microbiome for environmental sustainability: From ecological foundations to novel applications. Science of the Total Environment, 951:175766, DOI:10.1016/j.scitotenv.2024.175766; Ali, J., et al. (2024) Harnessing phytohormones: Advancing plant growth and defence strategies for sustainable agriculture. Physiologia Plantarum, 176:e14307, DOI:10.1111/ppl.14307; Ma, L., et al. (2025) Epigenetic control of plant abiotic stress responses. Journal of Genetics and Genomics, 52(2):129–144, DOI:10.1016/j.jgg.2024.09.008; Li, P., et al. (2025) Phenotypic plasticity and stability in plants: Genetic mechanisms, environmental adaptation, evolutionary implications, and future directions. Plant, Cell and Environment, 48(8):5847–5860, DOI:10.1111/pce.15566; Siddique, A.B., et al. (2024) Revisiting plant stress memory: mechanisms and contribution to stress adaptation. Physiology and Molecular Biology of Plants, 30:349–367, DOI:10.1007/s12298-024-01422-z.

Unit 2: **Abiotic Stress Responses** -- Types of abiotic stress factors; Climate change and pollution; Physiological, morphological, biochemical, and molecular changes in plants against different abiotic stresses; Stress tolerance in crops through allelic variation; Genomic and transcriptomic approaches in abiotic stress research; Engineering plants for abiotic stress resilience; Phytoremediation and environmental biotechnology. 12 hours

Essential Readings: Zhang, H., et al. (2022) Abiotic stress responses in plants. Nature Reviews Genetics, 23:104–119, DOI:10.1038/s41576-021-00413-0; Ahmad, P. and Prasad, M.N.V. (2011). Abiotic stress responses in plants. Springer New York, ISBN:9781461406334 (pages1–369); Varadharajan, V., et al. (2025) Multi-omics approaches against abiotic and biotic stress-A review. Plants (Basel), 14(6):865, DOI: 10.3390/plants14060865; Nedjimi, B., et al. (2021) Phytoremediation: a sustainable environmental technology for heavy metals decontamination. SN Applied Sciences, 3:286, DOI:10.1007/s42452-021-04301-4; Sinha, A., et al. (2020) Potential of allele mining for improving drought tolerance in crops. International Journal of Current Microbiology and Applied Sciences, 9(5):1098–1117. DOI:10.20546/ijcmas.2020.905.121.

Unit 3: **Biotic Stress Responses and Symbiotic Interactions** -- Types of biotic stresses; Molecular basis of plant-pathogen interactions (compatible vs. incompatible); Plant defense mechanisms against biotic agents (PTI and ETI); Plant disease resistance and susceptibility genes; Role of Systemic Acquired Resistance (SAR), Induced Systemic Resistance (ISR), and Hypersensitive Response (HR); Role of secondary metabolites; Plant immunity and priming; Effect of climate change on biotic interactions; Genetic and molecular basis of plant-insect interaction; Diversity in parasitic plants; Molecular mechanisms of host-parasite interactions, host plant pre- and post-attachment defense responses; Role of mobile RNAs and proteins in parasitism and defense responses; Rhizobial symbiosis and molecular regulation of nodule development; Interactions with arbuscular mycorrhizal fungi (AMF); Other mutualistic associations; Genomic insights into symbiotic relationships. 18 hours

Essential Readings: Buchanan, B.B., et al. (2015) Biochemistry and Molecular Biology of Plants, 2nd edition, Chapter-21 (Responses to plant pathogens), Wiley-Blackwell, ISBN:9781118502198; Wang, Y., et al. (2022) Evasion of plant immunity by microbial pathogens. Nature Reviews Microbiology, 20(8):449–464, DOI: 10.1038/s41579-022-00710-3; Lopez-Raez, J., et al. (2025) Molecular mechanisms modulating beneficial plant root-microbe interactions: What's common? Plant Communications, 101592, DOI:10.1016/j.xplc.2025.101592; Li, F., et al. (2025) Antiviral RNA interference in plants: Increasing complexity and integration with other biological processes. Plant Communications, 6(10):101490, DOI:10.1016/j.xplc.2025.101490; Castro, B. (2021) Stress-induced reactive oxygen species compartmentalization, perception and signalling. Nature Plants, 7(4):403–412, DOI:10.1038/s41477-021-00887-0; van Schie, C.C. and Takken, F.L. (2014) Susceptibility genes 101: how to be a good host. Annual Review of Phytopathology, 52:551–581. DOI:10.1146/annurev-phyto-102313-045854; Mahmood, M.A., et. al. (2024) Methyl-salicylate (MeSA)-mediated airborne defence. Trends in Plant Science, 29(4):391–393, DOI:10.1016/j.tplants.2023.12.001; Zou, J., et al. (2024) Plant-nematode battle: engagement of complex signaling network. Trends in Parasitology, 40(9):846–857, DOI:10.1016/j.pt.2024.07.010; Wani, K.A., et al. (2025) Evolutionarily ancient functions of enzymatic TIR proteins in innate immunity. Trends in Immunology, 46(6):441–454, DOI:10.1016/j.it.2025.04.005;; Zhang, X., et al. (2025) Networks of the symbiosis-immunity continuum in plants. Cell Host and Microbe, 33(8):125–1275, DOI:10.1016/j.chom.2025.06.009.

Unit 4: Experimental Approaches and Applications -- Techniques to study plant stress physiology; Utility of model plant systems (*Arabidopsis-Pseudomonas* interaction, Rice-*Magnaporthe* interaction, etc.); Advanced techniques in high-throughput phenotyping, multi-omics approaches, advanced imaging techniques; Use of bioinformatics and AI in predicting plant stress responses; Case studies for development of climate-smart crops; Applications of synthetic biology, breeding, and transgenic technology for sustainable agriculture. 7 hours

Essential Readings: Katagiri, F., et al. (2002) The *Arabidopsis thaliana-Pseudomonas syringae* interaction. *Arabidopsis* Book, 1:e0039, DOI:10.1199/tab.0039; Ragulakollu, S., et al. (2025) Unraveling the host-pathogen relationship between rice and *Magnaporthe oryzae*. Physiological and Molecular Plant Pathology, 140:102928, DOI:10.1016/j.pmpp.2025.102928; Angidi, S., et al. (2025) Advanced high-throughput phenotyping techniques for managing abiotic stress in agricultural crops-A comprehensive review. Crops, 5:8,

DOI:10.3390/crops5020008; Vishnoi, S. and Goel, R.K. (2024) Climate smart agriculture for sustainable productivity and healthy landscapes. Environmental Science & Policy, 151:103600, DOI:10.1016/j.envsci.2023.103600; Zhang, D., et al. (2025) Synthetic biology and artificial intelligence in crop improvement. Plant Communications, 6(2):101220, DOI:10.1016/j.xplc.2024.101220; Koja, Y., et al. (2024) Basic design of artificial membrane-less organelles using condensation-prone proteins in plant cells. Communications Biology, 7:1396, DOI:10.1038/s42003-024-07102-8.

Practicals (30 hours)

1. Effect of heat stress on seed germination of *Arabidopsis*.
2. Determination of membrane stability index (MSI) of plant tissues exposed to drought stress.
3. Detection of reactive oxygen species (ROS) in salt-stressed rice plants.
4. Detection of plant pathogen and disease diagnosis by loop-mediated isothermal amplification (LAMP).
5. Detection of hypersensitive response (HR) during R-Avr interaction in *Nicotiana benthamiana* leaves.

Suggested Readings:

1. Tuteja, N. and Gill, S.S. (2013) Climate change and plant abiotic stress tolerance. Wiley-VCH Verlag GmbH & Co. KgaA, eISBN:9783527675265.
2. Buchanan, B.B., et al. (2015) Biochemistry and Molecular Biology of Plants. 2nd edition, Wiley, USA, ISBN:9781118502198.
3. Dickinson, M. (2003) Molecular plant pathology.; BIOS Scientific Publishers, ISBN:9781859960448.
4. Wolpert, T., et al. (2017) Genome-enabled analysis of plant-pathogen interactions. APS Press, ISBN:9780890544983.
5. Hirt, H. (2009) Plant stress biology: From genomics to systems biology. 1st edition. Blackwell Publishers, ISBN:978352732290.
6. Hull, R. (2014) Plant Virology. 5th edition, Academic Press, USA, ISBN:9780123848710.
7. Jenks, M.A. and Hasegawa, P.M. (2014) Plant abiotic stress. 2nd edition, Wiley-Blackwell, ISBN:9781118412176.
8. Aftab, T. (2023) New frontiers in plant-environment interactions: Innovative technologies and developments (Environmental Science and Engineering). Springer International Publishing AG. 1st edition, ISBN:9783031437281.
9. Huang, B. (2006) Plant-Environment Interactions. 3rd edition. CRC Press, ISBN: 978084933727.
10. Jhu, M.Y., et al. (2025) From hosts to parasites: hormones driving symbiosis-induced *de novo* organogenesis. Trends in Plant Science, DOI:10.1016/j.tplants.2025.05.015.

PBSE206: Proteomics, Metabolomics, and Elementomics

This course is open to students of other departments as a GE course.

Course title & code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE206: Proteomics, Metabolomics, and Elementomics	4	3	1	0	B.Sc. in any branch of science	NA

Learning Objectives

Protein, metabolite, and ionic/element profiles in living systems are crucial for understanding the regulatory and metabolic capacity of the system. The primary objective of this course is to equip students with the principles of proteome, metabolome, and elementome. The course aims to develop knowledge of the application of state-of-the-art technologies to understand the proteome, metabolome, and elementome of different organisms; protein modification; and the complexities of protein-protein interactions and metabolic outcomes. There will be a strong emphasis on how these technologies are applied to the agriculture and health sectors.

Learning Outcomes

Students would develop a detailed understanding of the state-of-the-art techniques and analytical methods for studying the plant proteome, metabolome, and elementome. They will be able to design basic experiments for a given biological condition and compare methods to study proteomics, metabolomics, and elementomics. They will learn to perform data analysis and develop skills to interpret data, such as identifying peptides/proteins/metabolites and metabolites, and comparing proteomes, elementomes, and metabolomes across different groups of samples.

Course Content (45 hours)

Unit 1: Introduction to Proteomics, Metabolomics, and Elementomics -- Introduction to 'Omics'; Protein structure folding and function; Types of Proteomics: structural, functional, and expression; Basics and workflow design of proteomics technology; Comparative proteomics; Metabolites and their importance; Elements and their significance; Technological advancements in multi-omics studies; Importance in agriculture and health sciences. 6 hours

Essential Readings: Yan, S., et al. (2022) Recent advances in proteomics and metabolomics in plants. Molecular Horticulture, 2(1):17, DOI:10.1186/s43897-022-00038-9; van Wijk, K.J. (2001) Challenges and prospects of plant proteomics. Plant Physiology, 126(2):501–508. DOI:10.1104/pp.126.2.501; Salt, D.E., et al. (2008) Ionomics and the study of the plant ionome. Annual Review of Plant Biology, 59(1):709–733, DOI:10.1146/annurev.arplant.59.032607.092942.

Unit 2: Tools and Techniques in Proteomics -- Principles and applications of the separation technology; 1-D and 2-D Polyacrylamide Gel Electrophoresis (PAGE), workflow, high-throughput methods, importance and applications in proteomics; Proteomic Profiling: protein sequencing, Liquid Chromatography and Mass Spectrometry (LC-MS/MS), quantitative proteomics, advanced methods in proteomics; Isotope Coded Affinity Tag based Protein

Profiling (ICAT), Isobaric Tags for Relative and Absolute Quantitation: iTRAQ, AQUA, ESI-Q-IT-MS; SELDI-TOF-MS, SWATH, database search, protein identification, and pathway analysis; Post-translational modifications and their profiling; High-throughput methods for detection of protein-protein interactions and interactions of proteins with other biomolecules; Immunoproteomics: Overview of immune systems; Utility of antibodies in routine laboratory experiments; Serological proteome analysis; Protein microarrays (analytical and functional), protein array detection methods; Antigen identification by antigen capture and mass spectrometry; Characterization of the cell-mediated immune response by cytokine detection and quantification; Immuno-PCR; Immunoproteomics for major histocompatibility complex (MHC) peptides. 18 hours

Essential Readings: Lesk, A.M. (2010) Introduction to protein science: Architecture, function and genomics. Oxford University Press, ISBN:199541302; Loo, J.A. (2003) The tools of proteomics. Advances in protein chemistry, 65:25–56, DOI:10.1016/S0065-3233(03)01015-5; Righetti, P.G. (2024) Quantitative proteomics: a review of different methodologies. European Journal of Mass Spectrometry, 10(3):335–348; Patton, W.F., et al. (2002) Two-dimensional gel electrophoresis; better than a poke in the ICAT? Current Opinion in Biotechnology, 13(4):321–328, DOI:10.1016/S0958-1669(02)00333-6; Wiese, S., et al. (2007) Protein labeling by iTRAQ: a new tool for quantitative mass spectrometry in proteome research. Proteomics, 7(3):340–350, DOI:10.1002/pmic.200600422C; Mathur, M. et al. (2021) Advances in genomics and proteomics in agriculture. In Crop Improvement (pp. 23–35), CRC Press, ISBN:9781003099079; Fulton, K.M., et al. (2019) Immunoproteomics methods and techniques. Immunoproteomics: methods and protocols. ISBN:9781493995967.

Unit 3: Metabolomics -- Types of metabolites; Definition and scope of metabolomics; Sample preparation and extraction techniques; Separation and detection methods: gas chromatography (GC), high-performance liquid chromatography (HPLC), mass spectrometry (MS) secondary ion MS (SIMS), desorption electrospray ionization (DESI), laser ablation electrospray ionization (LAESI), Nuclear Magnetic Resonance (NMR); Statistical tools for data analysis. 11 hours

Essential Readings: Liu, X. and Locasale, J.W. (2017) Metabolomics:a primer. Trends in Biochemical Sciences, 42(4):274–284, DOI:10.1016/j.tibs.2017.01.004; Noack, S. and Wiechert, W. (2014) Quantitative metabolomics: a phantom? Trends in Biotechnology, 32:238–244, DOI:10.1016/j.tibtech.2014.03.006; Cajka, T. and Fiehn, O. (2016) Toward merging untargeted and targeted methods in mass spectrometry-based metabolomics and lipidomics. Analytical Chemistry, 88:524–545, DOI:10.1021/acs.analchem.5b04491; Wishart, D.S. (2016) Emerging applications of metabolomics in drug discovery and precision medicine. Nature Reviews Drug discovery, 15(7):473–484. DOI:10.1038/nrd.2016.32.

Unit 4: Elementomics -- Relevance of mineral nutrients and trace elements; Atomic absorption spectroscopy; High-throughput elemental profiling using inductively coupled plasma-mass spectroscopy (ICP-MS), inductively coupled plasma-optical emission spectroscopy (ICP-OES), Energy Dispersive X-ray Spectroscopy (EDS), X-Ray fluorescence spectroscopy, atomic neutron activation analysis; Elemental data analysis. 10 hours

Essential Readings: Kumar, V., et al. (2022) Plant nutrition and food security in the era of climate change. Academic Press, ISBN:9780128229163, Chapter 9 (Plant ionomics: toward high-throughput nutrient profiling); Huang, X.Y. and Salt, D.E. (2016) Plant Ionomics: From elemental profiling to environmental adaptation. Molecular Plant, 9(6):787–797, DOI:10.1016/j.molp.2016.05.003; Singh, U.M., et al. (2013) Plant Ionomics: a newer approach to study mineral transport and its regulation. Acta Physiologiae Plantarum, 35:2641–2653, DOI:10.1007/s11738-013-1316-8; Marguí, E. (2022) X-ray fluorescence spectrometry for environmental analysis: Basic principles, instrumentation, applications and recent trends. Chemosphere, 303:135006, DOI:10.1016/j.chemosphere.2022.135006; Wilschefski, S.C. and Baxter, M.R. (2019) Inductively Coupled Plasma Mass Spectrometry: Introduction to analytical aspects. The Clinical Biochemist Reviews, 40(3):115–133, DOI:10.33176/AACB-19-00024; Tromp, R.M. (2024) Energy-dispersive X-ray spectroscopy in a low energy electron microscope. Ultramicroscopy, 259:113935, DOI:10.1016/j.ultramic.2024.113935.

Tutorials (15 hours)

- A visit to Proteomics, Metabolomics, and Elementomics facility.
- Assignment on analysis of the protein data to understand protein function, interactions, and pathways.
- Assignment on analysis of metabolite data to understand metabolic pathways, identify biomarkers, and study the effects of various factors.
- Assignment on analysis of the elemental data to understand elemental homeostasis, identify elemental imbalances, and study the role of elements in biological processes.

Suggested Readings:

1. Antonio, C. (2018) Plant Metabolomics: Methods and Protocols (Methods in Molecular Biology). Humana Press, USA, ISBN:9781493992942.
2. Branden, C.I. and Tooze, T. (1999) Introduction to protein structure. Garland Publishing, USA, ISBN:9780815323051.
3. Saito, K., et al. (2006) Plant Metabolomics (Biotechnology in Agriculture and Forestry). Springer, USA, ISBN:9783540297819.
4. Lammerhofer, M. and Weckwerth, W. (2013) Metabolomics in practice: Successful strategies to generate and analyze metabolic data. Oxford University Press, UK, ISBN:9783527330898.
5. Weckwerth, W. (2007) Metabolomics: Methods and Protocols (Methods in Molecular Biology). Humana Press, USA, ISBN:9781588295613.
6. Tan, B.C., et al. (2017) Proteomics in commercial crops: An overview. Journal of Proteomics, 169:176–188, DOI:10.1016/j.jprot.2017.05.018.

PBSEC207: Plant Tissue Culture and Transformation Methodologies

Course title & code	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSEC207: Plant Tissue Culture and Transformation Methodologies	2	0	0	2	B.Sc. in any branch of science	NA

Learning Objectives

This course aims to provide hands-on training in plant biotechnology techniques, including plant tissue culture, haploid production, protoplast isolation, plant genetic transformation, and virus-induced gene silencing. Students will gain practical experience in media preparation, sterile techniques, regeneration protocols, and molecular screening for plant improvement and research applications.

Learning Outcomes

Upon completion of this course, students will develop proficiency in key plant biotechnology methods, enabling them to perform plant tissue culture, genetic transformation, and molecular validation independently. They will acquire skills in protoplast manipulation, haploid generation, plant transformation and gene silencing, preparing them for careers in plant tissue culture, crop improvement, and biotechnological innovations.

Hands-on Training (60 hours)

Unit 1: Plant Tissue Culture, Micropropagation, and Protoplast Isolation -- Media preparation, surface sterilization of leaf discs of tobacco/hypocotyls of tomato), callus induction and proliferation, shoot and root regeneration, establishment of plantlets; Haploid production through androgenesis: Selection of specific stages of anthers of tobacco/*Datura*, surface sterilization, axenic culture, haploid plant generation; Plant protoplast isolation and transfection: protoplast isolation from leaves/roots of wheat seedlings, viability check using dyes, transformation using PEG method, visualization under confocal microscope. 30 hours

Essential Readings: Bhojwani, S.S. and Razdan, M.K. (1986) Plant tissue culture: theory and practice. Elsevier, ISBN:0444421645; Bhojwani, S.S. and Dantu, P.K. (2013) Micropropagation. In Plant tissue culture: An introductory text (pp. 245–274). Springer India, ISBN:9788132210252; Davey, M.R., et al. (2010) Plant protoplasts: isolation, culture and plant regeneration. Plant cell culture essential methods. Wiley-Blackwell, New York, 153–173, ISBN:9780470686485; Eriksson, T.R. (2018) Protoplast isolation and culture. In Plant protoplasts (pp. 1–20), CRC Press, ISBN:9781351075770.

Unit 2: Plant Genetic Transformation and Virus-induced Gene Silencing (VIGS) -- *Agrobacterium tumefaciens*-mediated transformation of Arabidopsis plants using the floral dip method, transformants screening, transgene insertion validation by PCR; Agroinfiltration of TRV-*pds* constructs in tobacco leaves, phenotyping, and screening of VIGS lines. 30 hours

Essential Readings: Koh, H.-J., et al. (2015) Current technologies in plant molecular breeding: A guidebook of plant molecular breeding for researchers. ISBN:9789401799966, Springer Dordrecht, DOI:10.1007/978-94-017-9996-6, Chapter 9 (Plant transformation methods and applications); Birch, R.G. (1997) Plant transformation: problems and strategies for practical application. Annual Review of Plant Biology, 48(1):297–326, DOI:10.1146/annurev.arplant.48.1.297; Jeong, J.H., et al. (2025) Empowering *Agrobacterium*: Ternary vector

systems as a new arsenal for plant transformation and genome editing. Biotechnology Advances, 83:108631, DOI:10.1016/j.biotechadv.2025.108631; Rössner, C., et al. (2022) VIGS goes viral: How VIGS transforms our understanding of plant science. Annual Review of Plant Biology, 73:703–728, DOI:10.1146/annurev-arplant-102820-020542.

Suggested Readings:

1. Barresi, M.J.F. and Gilbert, S.F. (2023) Developmental Biology. 13th edition, Sinauer Associates, ISBN:9780197574591.
2. Westhoff, P. (1998) Molecular plant development: from gene to plant. The Bath Press, UK, ISBN:9780198502043.
3. Wolpert, L., et al. (2015) Principles of Development. Oxford Publishers, UK, ISBN:9780198709886.
4. Boisson-Dernier, A., et al. (2001) *Agrobacterium rhizogenes*-transformed roots of *Medicago truncatula* for the study of nitrogen-fixing and endomycorrhizal symbiotic associations. Molecular Plant-Microbe Interactions, 14(6):695–700, DOI:10.1094/MPMI.2001.14.6.695.

Structure 1 - PG with Coursework

SEMESTER 3

PBSC311: Plant Biotechnology

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSC311: Plant Biotechnology	4	3	0	1	B. Sc. in any branch of science	NA

Learning Objectives

This course will enable students to understand the core principles and milestones of plant biotechnology, including the molecular basis of crop domestication and Green Revolution traits, as well as concepts in tissue culture. Students will learn about the molecular toolbox for plant genetic engineering and be introduced to advanced approaches, including RNAi, genome editing, and synthetic biology, for pathway engineering. The course will build conceptual understanding of modern gene/QTL mapping, marker-assisted and genomic selection, speed breeding, and gene pyramiding, together with applications of plant biotechnology in molecular farming, biofortification, climate resilience, plant-microbe interactions, and industrial and environmental biotechnology. Finally, students will be sensitized to biosafety guidelines, GMO risk assessment, IPR, farmers' rights, and ethical and societal issues in plant biotechnology.

Learning Outcomes

On completing the course, students will be able to explain and apply tissue culture and related technologies for crop improvement. They will be able to outline and compare plant transformation and genome editing strategies, design genetic constructs and describe workflows for the generation and characterization of transgenic and edited plants. Students will be able to select appropriate molecular markers and mapping approaches for dissecting complex traits, and integrate marker-assisted selection, genomic selection, and breeding pipelines. They will be able to critically analyse case studies such as Golden rice, Bt cotton, virus-resistant papaya, and DH mustard, among others. In addition, they will be able to interpret biosafety and regulatory frameworks, IPR/PBR/farmer's rights provisions, and articulate ethical, social, and policy implications of deploying plant biotechnological innovations in agriculture.

Course Content (45 hours)

Unit 1: Fundamentals and Scope of Plant Biotechnology -- Concept, history, and milestones in plant biotechnology; Molecular basis of crop domestication and Green revolution; Principles of plant tissue culture, totipotency, and micropropagation; Somaclonal variation, somatic embryogenesis, and synthetic seeds; Protoplast fusion and somatic hybridization. 5 hours

Essential Readings: Stewart Jr., C.N. (2025) Biotechnology and Genetics: Principles, Techniques, and Applications. 3rd edition, John Wiley & Sons, ISBN:9781394217236, Chapter 1 (Plant Agriculture: The impact of biotechnology); Abdin, M.Z, et al. (2017) Plant Biotechnology: Principles and Applications, Springer Verlag,

Singapore, ISBN:9789811029592, Chapter 1 (Historical perspective and basic principles of plant tissue culture), Chapter 2 (Plant tissue culture: Applications in plant improvement and conservation); Pathirana, R. and Carimi, F. (2024) Plant biotechnology-an indispensable tool for crop improvement. Plants (Basel), 13(8):1133, DOI:10.3390/plants13081133.

Unit 2: Molecular Tools and Techniques -- Genetic cloning strategies and vector systems; Promoters, selectable markers, and reporter genes; Gene transfer methods; Chloroplast transformation; Characterization of transgenic plants at molecular, biochemical, and phenotypic level; Case studies: Golden rice, Bt cotton, virus-resistant papaya, herbicide-tolerant crops, Dhara Mustard, any other product; Virus-induced gene silencing (VIGS) methods; Genome editing technologies [Zinc Finger Nucleases, Transcription activator-like effector nucleases, Clustered Regularly Interspaced Short Palindromic Repeats or CRISPR)/CRISPR-associated (Cas) systems, prime editing, base editing, and miniature RNA-guided endonuclease]; Generation of marker-free transgenics; RNAi interference (RNAi); Introduction of synthetic biology and metabolic pathway engineering. 15 hours

Essential Readings: Li, B., et al. (2024) Targeted genome-modification tools and their advanced applications in crop breeding. Nature Reviews Genetics, 25(9):603–622, DOI:10.1038/s41576-024-00720-2; Liu, W., et al. (2013) Advanced genetic tools for plant biotechnology. Nature Review Genetics, 14:781–793, DOI:10.1038/nrg3583; Gupta, O.P. and Karkute, S.G. (2021) Genome editing in plants: Principles and applications, CRC Press, ISBN:9780367415907, Chapter 1 (Historical developments of genome editing in plants), Chapter 2 (Mechanism of ZFN mediated genome editing: scope and opportunities), Chapter 3 (TALEN: customizable molecular scissors for tailoring newer types of genomes in plants), Chapter 4 (Mechanism of CRISPR/Cas9 mediated genome editing: scope and opportunities); Koeppe, S., et al. (2023) RNA interference: past and future applications in plants, International J. Molecular Science, 24(11):9755, DOI: 10.3390/ijms24119755; Singh, R., et al. (2023) A prospective review on selectable marker-free genome engineered rice: past, present and future scientific realm, Frontiers in Genetics, 13:2022, DOI:10.3389/fgene.2022.882836; Aaron, S., et al. (2020) Metabolic engineering and synthetic biology of plant natural products – A minireview. Current Plant Biology, 24:100163, DOI:10.1016/j.cpb.2020.100163.

Unit 3: Mapping of Genes/QTLs -- High-throughput molecular markers and genotyping assays; Bulk segregant analysis (QTL-seq), Target-Sequence Enrichment and Sequencing (TEnSeq), Resistance gene enrichment sequencing (RenSeq), and Mutation mapping (MutMap, MutMap-Gap, etc); Genome-Wide Association Studies (GWAS); Marker-assisted plant breeding and genomic selection (GS); Speed breeding; Gene Pyramiding; Hybrid breeding and doubled haploid technologies. 15 hours

Essential Readings: Jaganathan, D., et al. (2020) Fine mapping and gene cloning in the post-NGS era: advances and prospects. Theoretical and Applied Genetics, 133(5):1791–1810, DOI:10.1007/s00122-020-03560-w; Wang, X., et al. (2023) Next-generation bulked segregant analysis for Breeding 4.0. Cell Reports, 42(9):113039, DOI:10.1016/j.celrep.2023.113039; Uffelmann, E., et al. (2021) Genome-wide association studies. Nature Reviews Methods Primers, 1:59, DOI:10.1038/s43586-021-00056-9; Kabade, P.G., et al. (2025) Speed breeding 3.0: mainstreaming light-driven plant breeding for sustainable genetic gains. Trends in Biotechnology, 43(10):2462–2478, DOI:10.1016/j.tibtech.2025.04.011; Crossa, J., et al. (2017) Genomic selection in plant breeding: methods, models, and perspectives, Trends in Plant Science, 22*(*11):961–975, DOI:10.1016/j.tplants.2017.08.011; Qu, Y., et al. (2024) Doubled haploid technology and synthetic apomixis: Recent advances and applications in future crop breeding. Molecular Plant, 17(7):1005–1018, DOI:10.1016/j.molp.2024.06.005.

Unit 4: Applications and Societal Aspects of Plant Biotechnology -- Molecular farming; Biofortification and nutritional enhancement; Manipulating and harnessing plant-microbe interactions: disease resistant plants, biofertilizers, biopesticides, and mycorrhizal biotechnology; Climate-resilient crops: generation of abiotic stress tolerant plants; Industrial Biotechnology: bioethanol and other products; Environmental biotechnology: phytoremediation; Regulatory frameworks: biosafety guidelines, GMO risk assessments, and

intellectual property rights (IPR); Plant breeders' rights (PBRs) and farmers' rights; Ethical, social, and policy implications of plant biotechnology. 10 hours

Essential Readings: Shanmugaraj, B., et al. (2020) Plant molecular farming: A viable platform for recombinant biopharmaceutical production. Plants, 9(7):842, DOI:10.3390/plants9070842; Garg, M., et al. (2024) Biofortification for nutrient-rich crops. ISBN:9781032690636, DOI:10.1201/9781032690636; Digel, I., et al. (2025) Introduction to Industrial Biotechnology, Springer Cham, ISBN:9783032079183, DOI:10.1007/978-3-032-07918-3; Abdin, M.Z., et al. (2017) Plant Biotechnology: Principles and Applications, Springer Verlag, Singapore, ISBN:9789811029592, Chapter 14 (Biosafety, Bioethics, and IPR Issues in Plant Biotechnology); Protection of plant varieties and farmers' right act (PPV & FR), 2001, Ministry of Agriculture and Farmers Welfare, GoI; Standard Operating Procedures for regulatory review of genome edited plants under SDN-1 and SDN-2 categories 2022 and Guidelines on genetically engineered plants containing stacked events 2025 by Department of Biotechnology, MoS&T, GoI.

Practicals (30 hours)

1. Assessment of promoter activity in transgenic plants using beta-glucuronidase (GUS) reporter through histochemical staining and fluorometric (MUG) assays.
2. To perform PCR-based screening of *Arabidopsis* T-DNA insertion lines to distinguish heterozygous and homozygous plants.
3. Genome editing of a target gene in a plant (GFP/transient assay).
4. T7E1/ Surveyor mismatch cleavage assays to detect mutated/edited genomic regions.
5. Construction of a plant genetic linkage map with molecular markers.

Suggested Readings:

1. Acquaah, G. (2020) Principles of Plant Genetics and Breeding, 3rd edition, Wiley-Blackwell, ISBN:9781119626695.
2. Al-Khayri, J.M., et al. (2025) Genome Editing for Crop Improvement - Theory and Methodology. CAB International, ISBN:9781800622494.
3. Hille, F., et al. (2018) The biology of CRISPR-Cas: Backward and forward. Cell, 172(6):1239–1259, DOI:10.1016/j.cell.2017.11.032.
4. Singh, B.D. and Singh, A.K. (2015) Marker-Assisted Plant Breeding: Principles and Practices, Springer New Delhi, ISBN:9788132223160, DOI:10.1007/978-81-322-2316-0.
5. Clauw, P., et al. (2025) Beyond the standard GWAS-A guide for plant biologists. Plant and Cell Physiology, 66(4):431–443, DOI:10.1093/pcp/pcae079.
6. Quiroz, L.F., et al. (2024) Haploid rhapsody: the molecular and cellular orchestra of *in vivo* haploid induction in plants. New Phytologist, 241(5):1936–1949, DOI:10.1111/nph.19523.
7. Ghosh, S., et al. (2018) Speed breeding in growth chambers and glasshouses for crop breeding and model plant research. Nature Protocols, 13:2944–2963, DOI:10.1038/s41596-018-0072-z.
8. Chen, J.T. (2024) Plant speed breeding and high-throughput technologies, CRC Press, ISBN: 9781003434733.
9. Xiong, J., et al. (2023) Synthetic apomixis: the beginning of a new era. Current Opinion in Biotechnology, 79:102877, DOI:10.1016/j.copbio.2022.102877.
10. WHO (2004) Laboratory Biosafety Manual, 3rd edition
11. FAO (2018) Biosafety Primer.
12. Department of Biotechnology (DBT), MoS&T, GoI (2023) Intellectual Property Guidelines.
13. Scientific Journals: Plant Biotechnology Reports; International Journal of Plant Biotechnology; Plant Biotechnology Journal; Transgenic Research; Journal of Plant Biotechnology; Plant Cell, Tissue and Organ Culture.
14. Singh, K.K. (2014) Biotechnology and intellectual property rights-legal and social implications. ISBN:9788132220596, DOI:10.1007/978-81-322-2059-6.

PBSC312: Molecular Plant Breeding

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSC312: Molecular Plant Breeding	4	3	0	1	B. Sc. in any branch of science	NA

Learning Objectives

Molecular breeding has greatly advanced human agriculture by enabling the continuous improvement of food and industrial crops. This paper introduces students to the foundations of classical breeding, quantitative genetics, and plant genetic resources, while also covering advanced molecular methods such as marker-assisted selection, QTL mapping, genomic selection, and hybrid breeding technologies. By integrating conventional and modern techniques, the course highlights how new, high-performing crop varieties are developed to meet global demands for productivity, quality, and stress resilience.

Learning Outcomes

Students will be able to understand the historical foundations and objectives of plant breeding and crop genetics beyond model plant systems. They will be able to distinguish breeding methods across reproductive systems and the application of molecular tools in enhancing crop quality at the field level. It will equip them with the capability to understand and evaluate global molecular breeding efforts, integrate genetic modification with modern breeding practices, and apply strategies to enhance yield, quality, and stress tolerance.

Course Contents (45 hours)

Unit 1: Plant breeding -- Introduction and history of breeding; Breeding objectives and crop traits; Principles of population and quantitative genetics; Plant genetic resources and crop domestication; Breeding in self-pollinated, cross-pollinated, and clonally propagated species; Concept of molecular breeding. 12 hours

Essential Readings: Acquaah, G. (2021) Principles of Plant Genetics and Breeding, 3rd Edition, Wiley Blackwell, ISBN:9781119626329; Singh, D.P., et al. (2021) Plant Breeding and Cultivar Development, Academic Press, ISBN:9780128175637, DOI:10.1016/C2018-0-01730-2.

Unit 2: Molecular markers and their Utilisation -- Molecular markers and genotyping methods; Linkage mapping of molecular markers; Mapping populations and quantitative trait loci mapping; Association mapping; Marker-assisted selection; Training population and statistical models in genomic selection; Phylogenetic relationships and genetic diversity; Mutation mapping and breeding; Process of variety release, Seed certification, and commercial release. 12 hours

Essential Readings: Singh, B.D. and Singh, A.K. (2015) Marker-Assisted Plant Breeding: Principles and Practices, ISBN:9788132223160, DOI:10.1007/978-81-322-2316-0; Amiteye, S. (2021) Basic concepts and methodologies of DNA marker systems in plant molecular breeding. Heliyon, 7(10):e08093, DOI: 10.1016/j.heliyon.2021.e08093; Al-Khayri, J.M., et al. (2024) Plant Molecular Breeding in Genomics Era - Concepts and Tools, Springer Cham, ISBN:9783031685866, DOI:10.1007/978-3-031-68586-6; Bhat, T.A. and Hakeem, K.R. (2023) Biotechnologies and genetics in plant mutation breeding (volume 1: Mutagenesis and Crop Improvement). Apple Academic Press, Inc., ISBN:9781003305064; Acquaah, G. (2021) Principles of Plant

Genetics and Breeding, 3rd edition, Wiley-Blackwell, ISBN:9781119626329, Section 12 (Variety release process in plant breeding).

Unit 3: Hybrid Breeding and Doubled haploid (DH) Technologies -- Genetic basis of heterosis and hybrid breeding strategies; Molecular aspects of three-line and two-line approaches (photoperiod- and thermo-sensitive genic male sterility); Transgenics in hybrid seed production; Role of DH lines in mapping and varietal improvement; Molecular mechanisms of haploid induction (maternal and paternal); Synthetic apomixis and fixing elite genotypes. 12 hours

Essential Readings: Chen, L. and Liu, Y.G. (2014) Male sterility and fertility restoration in crops. Annual Review of Plant Biology, 65:579–606, DOI:10.1146/annurev-arplant-050213-040119; Kim, Y.J. and Zhang, D. (2018) Molecular control of male fertility for crop hybrid breeding. Trends in Plant Science, 23(1):53–65, DOI: 10.1016/j.tplants.2017.10.001; Quiroz, L.F., et al. (2024) Haploid rhapsody: the molecular and cellular orchestra of *in vivo* haploid induction in plants. New Phytologist, 241(5):1936–1949, DOI: 10.1111/nph.19523.

Unit 4: Applications of Molecular Breeding -- International molecular breeding efforts; Improving crop yields, quality, biotic and abiotic stress tolerance; Enhancing shelf-life, nutritional value and flavor; Integration of genetic modification and molecular breeding.

9 hours

Essential Readings: Acquaah, G. (2021) Principles of plant genetics and breeding. 3rd edition, Wiley-Blackwell. ISBN:9781119626343, Chapter 14 (Breeding for resistance to disease and insect pests), Chapter 15 (Breeding for resistance to abiotic stresses), Chapter 35 (International plant breeding efforts); Lomax, J., et al. (2024) Multi-omic applications for understanding and enhancing tropical fruit flavour. Plant Molecular Biology, 114(4):83, DOI:10.1007/s11103-024-01480-7; Sharma, R., et al. (2025) Integrating molecular genetics with plant breeding to deliver impact. Plant Physiology, 198(3):kiaf087, DOI:10.1093/plphys/kiaf087.

Practicals (30 hours)

1. *In silico* analysis of crop genomes and identification of polymorphisms under known QTLs.
2. Designing markers and genotyping of locus-specific SNPs using CAPS and dCAPS markers.
3. Haplotype analysis from publicly available genomic data of a selected crop plant.
4. Verification of true F_1 hybrid with molecular markers in bi-parental crossed plants.
5. Association analysis of selected genotypes with their phenotype data.

Suggested Readings:

1. Koh, H.J., et al. (2015) Current technologies in plant molecular breeding - A guidebook of plant molecular breeding for Researchers. ISBN:9789401799966, DOI:10.1007/978-94-017-9996-6.
2. Al-Khayri, J.M., et al. (2016) Advances in plant breeding strategies: Breeding, Biotechnology and Molecular Tools, Springer Cham, ISBN:9783319225210, DOI:10.1007/978-3-319-22521-0.
3. Kang, M.S. (2020). Quantitative genetics, genomics and plant breeding, 2nd Edition, CABI, ISBN: 9781789242942.
4. Li, B., et al. (2024) Targeted genome-modification tools and their advanced applications in crop breeding. Nature Reviews Genetics, 25(9):603–622, DOI:10.1038/s41576-024-00720-2.
5. Bharadwaj, D.N. (2018) Advanced Molecular Plant Breeding- Meeting the challenge of food security. CRC Press. ISBN:9780203710654, DOI:10.1201/b22473.
6. Crossa, J., et al. (2017) Genomic selection in plant breeding: Methods, models, and perspectives. Trends in Plant Science, 22(11):961–975, DOI:10.1016/j.tplants.2017.08.011.
7. Alemu, A., et al. (2024) Genomic selection in plant breeding: Key factors shaping two decades of progress. Molecular Plant, 17(4):552–578, DOI:10.1016/j.molp.2024.03.007.
8. Chaudhary, N. and Sandhu, R. (2024) A comprehensive review on speed breeding methods and applications. Euphytica, 220:42, DOI:10.1007/s10681-024-03300-x.

9. Rajan, R., et al. (2025) Innovations in climate resilient agriculture, Springer Cham, ISBN:9783031848025, DOI:10.1007/978-3-031-84802-5.
10. Klee, H.J. and Tieman, D.M. (2018) The genetics of fruit flavour preferences. Nature Reviews Genetics, 19(6):347–356, DOI:10.1038/s41576-018-0002-5.
11. Kamaluddin, et al. (2022) Technologies in Plant biotechnology and breeding of field Crops. Springer Singapore, ISBN:9789811657672, DOI:10.1007/978-981-16-5767-2.

PBSE313: Metagenomics of Plant-associated Microbes

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE313: Metagenomics of Plant-associated Microbes	4	3	1	0	B.Sc. in any branch of science	NA

Learning Objectives

This course aims to introduce students to the fundamental concepts of metagenomics and the plant holobiont, with a focus on rhizosphere and aquatic microbiomes using environmental DNA (eDNA). It seeks to develop an understanding of sampling strategies and to familiarize students with the basics of metagenomic data analysis. This would help students appreciate how metagenomic approaches are applied in biodiversity assessment, plant pathology, environmental surveillance, and emerging areas such as space biology, integration of breeding and precision agriculture.

Learning Outcomes

By the end of the course, students should be able to explain key concepts of metagenomics and plant microbiomes and outline appropriate strategies for sampling and sequencing rhizosphere and aquatic environmental samples. They should be able to understand the components of the metagenomic analysis pipeline, interpret community and functional profiles, and critically read metagenomic datasets. Students will be able to relate metagenomic findings to practical applications in plant health, ecosystem monitoring, and sustainable agriculture.

Course Contents (45 hours)

Unit 1: Introduction to Metagenomics -- Concepts of microbiome, metagenome, holobiont, hologenome; Plant-associated microbiomes: Rhizosphere, phyllosphere, endosphere, etc.; Overview of metagenomics and integration with metatranscriptomics, metaproteomics, and metabolomics; Marker genes and DNA barcoding; Overview of workflow and sample preparation methodologies. 15 hours

Essential Readings: Nelson, K.E. (2020) Encyclopedia of metagenomics. Springer, New York, ISBN: 9781461464181, DOI:10.1007/978-1-4614-6418-1; Simon, J.C., et al. (2019) Host-microbiota interactions: from holobiont theory to analysis. Microbiome, 7:5, DOI:10.1186/s40168-019-0619-4; Vorholt, J. (2012) Microbial life in the phyllosphere. Nature Reviews Microbiology, 10:828–840, DOI:10.1038/nrmicro2910; Compant, S., et al. (2021) The plant endosphere world - bacterial life within plants. Environmental Microbiology, 23(4):1812–1829, DOI:10.1111/1462-2920.15240; Christopher, C.M., et al. (2016) Dissecting host-associated communities with DNA barcodes. Philosophical Transactions of the Royal Society Biological Sciences, 371(1702):20150328, DOI:10.1098/rstb.2015.0328.

Unit 2: Rhizosphere and Aquatic Metagenomics -- Environmental DNA (eDNA): sources, stability, sampling, limitations; Rhizosphere: structure, gradients, root exudates and microsome assembly; Aquatic plants-associated microbes; case studies. 10 hours

Essential Readings: Liu, S., et al. (2025) Analysis of metagenomic data. Nature Reviews Methods Primers, 5:5, DOI:10.1038/s43586-024-00376-6; Behera, B.K., et al. (2024) Metagenomics study in aquatic resource management: Recent trends, applied methodologies and future needs. Gene Reports, 25:101371, DOI:

10.1016/j.genrep.2021.101372; Wang, B., et al. (2021) Metagenomic insights into the effects of submerged plants on functional potential of microbial communities in wetland sediments. Marine Life Science & Technology, 3(4):405–415, DOI:10.1007/s42995-021-00100-3; Sahu, A., et al. (2023) Environmental DNA (eDNA): Powerful technique for biodiversity conservation. Journal for Nature Conservation, 71:126325, DOI: 10.1016/j.jnc.2022.126325; Pudake, R.N. et al. (2021) Omics science for rhizosphere biology. Springer Singapore, ISBN:9789811608896, DOI:10.1007/978-981-16-0889-6; Wani, A.K., et al. (2024) Metagenomic profiling of rhizosphere microbiota: Unravelling the plant-soil dynamics. Physiology and Molecular Plant Pathology, 133:10238, DOI:10.1016/j.pmpp.2024.102381.

Unit 3: Overview of Metagenomic Data Generation and Analysis -- Workflow overview, Selection of appropriate sequencing technologies (short and long-read); Demultiplexing, adapter and quality trimming, removal of contaminating DNA (host) sequences, metagenomic data assembly, taxonomic characterization (alignment based, alignment-free k-mer based, hybrid strategy); Gene prediction and functional analysis; Metagenomic data repositories. 10 hours

Essential Readings: Thomas T., et al. (2012) Metagenomics - a guide from sampling to data analysis. Microbial Informatics and Experimentation, 2:3, DOI:10.1186/2042-5783-2-3; Navgire, G.S., et al. (2022) Analysis and Interpretation of metagenomics data: an approach. Biological Procedures Online, 24:18, DOI:10.1186/s12575-022-00179-7; Aplakidou, E., et al. (2024) Visualizing metagenomic and metatranscriptomic data: A comprehensive review. Computational and Structural Biotechnology Journal, 23:2011–33, DOI:10.1016/j.csbj.2024.04.060.

Unit 4: Applications of Metagenomics -- Biodiversity assessment of plant-associated ecosystems; Plant pathology; Metagenomics in bioremediation and agro-ecosystem health; Metagenomics in controlled plant growth systems; Space biology; Future perspectives: integrating metagenomics with breeding and agriculture. 10 hours

Essential Readings: Charles, T.C., et al. (2017) Functional Metagenomics: Tools and Applications. Springer Cham, ISBN:9783319615103, DOI:10.1007/978-3-319-61510-3; Nagarajan, M. (2024) Metagenomics - Perspectives, Methods, and Applications. 2nd edition, Academic Press, ISBN:9780323917124; Roman-Reyna, V. and Crandall, S.G. (2024) Seeing in the dark: a metagenomic approach can illuminate the drivers of plant disease. Frontiers in Plant Science, 15:140502, DOI:10.3389/fpls.2024.1405042; Kumar, V. and Iram, S. (2024) Microbial Technology for Agro-Ecosystems. Academic Press, ISBN:9780443184468, Chapter 15 (Metagenomics: An approach for understanding microbe-microbe and plant-microbiome-interactions); Compant, S., et. al. (2025) Harnessing the plant microbiome for sustainable crop production. Nature Reviews Microbiology, 23(1):9–23, DOI:10.1038/s41579-024-01079-1.

Tutorials (15 hours)

1. Case study: Sargasso Sea.
2. Designing a rhizosphere metagenomics experiment.
3. Case study on how eDNA is used to track microbial biodiversity.
4. Survey of metagenomic databases.

Suggested Readings:

1. Chopra, R.S., et al. (2020) Metagenomics: techniques, applications, challenges and opportunities. Springer Singapore, ISBN:9789811565298, DOI:10.1007/978-981-15-6529-8.
2. Streit, W.R. and Daniel, R. (2017) Metagenomics: Methods and Protocols. Humana NY, ISBN: 9781493966912, DOI:10.1007/978-1-4939-6691-2.
3. Vacher, C., et al. (2016) The phyllosphere: microbial jungle at the plant–climate interface. Annual Review of Ecology, Evolution, and Systematics, 47:1–24, DOI:10.1146/annurev-ecolsys-121415-032238
4. Pudake, R.N., et al. (2021) Omics science for rhizosphere biology. Springer Singapore, ISBN:9789811608896, DOI:10.1007/978-981-16-0889-6.
5. Carter, D.O., et al. (2017) Forensic Microbiology. Wiley, ISBN:9781119062578, Chapter 5 (An introduction to metagenomic data generation, analysis, visualization, and interpretation).

PBSE314: Frontiers in Plant Molecular Biology

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE314: Frontiers in Plant Molecular Biology	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

This course has been designed to introduce students to state-of-the-art concepts, technologies, and experimental systems that define modern plant molecular biology and its translational applications. It aims to develop a rigorous understanding of plant signaling architectures, multi-omics driven functional genomics, structural advances in genome biology, and emerging domains such as epitranscriptomics, nanobiotechnology, and space biology. Furthermore, it aims to enable students to relate primary discoveries in calcium, ROS, hormone and retrograde signaling to crop improvement, biosensing, and stress resilience through synthetic and genome engineering approaches, supported by current literature in plant signaling and systems biology.

Learning Outcomes

After successful completion of the course, students will be able to critically interpret and integrate datasets from transcriptomic, proteomic, metabolomic, epigenomic, and phenomics platforms to elucidate gene function and regulatory networks in plants. They should be able to design and conceptualize CRISPR-based functional analyses, visualize and analyse gene interaction networks, and evaluate gene function prediction, stress-tolerance forecasting, and genome-assisted breeding. Students will also be able to assess emerging tools, such as optogenetics, targeted epigenome editing, and plant nanotechnology, for their feasibility in research or application in crops, thereby demonstrating their research readiness.

Course Content (45 hours)

Unit 1: Forefront of Plant Signaling -- Mechanosensing and electrosensing; Receptor dynamics and nanodomains; Phosphoswitches and dynamic network mapping; Organelle-to-nucleus signaling (retrograde signaling); Optogenetics and chemical biology tools; Live-cell imaging of Ca^{2+} and ROS dynamics; Phytohormone dynamics studies; Engineering synthetic receptors or signaling circuits for stress tolerance or biosensing. 11 hours

Essential Readings: Hamilton, E.S., et al. (2015) United in diversity: mechanosensitive ion channels in plants, Annual Review of Plant Biology, 66:113–37, DOI:10.1146/annurev-arplant-043014-114700; Fromm, J. and Lautner, S. (2007) Electrical signals and their physiological significance in plants. Plant Cell and Environment, 30(3):249–257, DOI:10.1111/j.1365-3040.2006.01614.x; Wang, L., et al. (2018) Exploring the spatiotemporal organization of membrane proteins in living plant cells. Annual Review of Plant Biology, 69:525–551, DOI:10.1146/annurev-arplant-042817-040233; Zhang, J., et al. (2023) Protein phosphorylation: A molecular switch in plant signaling. Cell Reports, 42(7):112729, DOI:10.1016/j.celrep.2023.112729; Tatjana, K. and Dario, L. (2016) Retrograde signaling: Organelles go networking. Biochimica et Biophysica Acta (BBA)–Bioenergetics, 1857(8):1313–1325, DOI:10.1016/j.bbabio.2016.03.017; Hiromasa, S. and Philipp, D. (2022) Plant optogenetics: Applications and perspectives. Current Opinion in Plant Biology, 68:102256, DOI:10.1016/j.pbi.2022.102256; Sarah, J., et al. (2011) *In vivo* imaging of Ca^{2+}, pH, and reactive oxygen species using fluorescent probes in plants. Annual Review of Plant Biology, 62:273–297, DOI:10.1146/annurev-arplant-042110-103832; Rainer, W. (2020) Phytohormone signaling mechanisms and genetic methods for their

modulation and detection, Current Opinion in Plant Biology, 57:31–40, DOI:10.1016/j.pbi.2020.05.011; Ondřej N., et al. (2017) Zooming in on plant hormone analysis: Tissue- and cell-specific approaches. Annual Review of Plant Biology, 68:323–348, DOI:10.1146/annurev-arplant-042916-040812; Alexander, R.L., et al. (2020) Engineering synthetic signaling in plants. Annual Review of Plant Biology, 71:767–788, DOI:10.1146/annurev-arplant-081519-035852.

Unit 2: Structural and Functional Genomics -- Third- and fourth-generation sequencing platforms and their applications in plant genome analysis, principles of transcriptomics and proteomics, including experimental design and data interpretation; Case study-based functional genomics strategies such as large-scale mutagenesis (T-DNA, CRISPR/Cas), RNAi, VIGS and activation tagging to elucidate gene function; Understanding advanced layers of regulation through RNA-seq, ribosome profiling, single-nucleus RNA-seq, and epigenomic assays such as ATAC-seq, ChIP-seq and DNA methylome analysis. 12 hours

Essential Readings: Brown, T.A. (2023) Genomes 5. CRC Press, ISBN:9781003133162, Chapter 4 (Sequencing Genomes), Chapter 9 (Transcriptomes and Proteomes), Chapter 10 (Genome Regulation); Mardis, E.R. (2008) Next-generation DNA sequencing methods. Annual Review of Genomics and Human Genetics, 9:387–402, DOI:10.1146/annurev.genom.9.081307.164359; Chappell, L., et al. (2018) Single-Cell (Multi)omics Technologies. Annual Review of Genomics and Human Genetics, 19:15–41, DOI: 10.1146/annurev-genom-091416-035324.

Unit 3: **Applied Aspects of Plant-Environment Interactions** -- Overview of plant responses to abiotic and biotic stresses; Molecular signaling pathways; Omics-driven discovery of stress tolerance genes; Engineering the plant microbiome; Spatial and integrative omics for stress biology: single cell vs. tissue level omics, transcriptomics and metabolite mapping of root-soil interface; Inter-kingdom communication; AI and ML in prediction of stress-tolerant genotypes.
11 hours

Essential Readings: Tuteja, N. and Gill, S.S. (2016) Abiotic stress responses in plants. ISBN:9783527339181, Wiley-VCH Verlag GmbH & Co., Chapter 1 (Abiotic stress signaling in plants: an overview); Zhang H., et al. (2022) Abiotic stress responses in plants. Nature Review Genetics, 23:104–119, DOI:10.1038/s41576-021-00413-0; Jiang Z., et al. (2025) Mechanisms of plant acclimation to multiple abiotic stresses. Communications Biology, 8:655, DOI:10.1038/s42003-025-08077-w; Mochida, K., et al. (2020) Decoding plant–environment interactions that influence crop agronomic traits. Plant and Cell Physiology, 61(8):1408–1418, DOI:10.1093/pcp/pcaa064; Du, B., et al. (2024) Strategies of plants to overcome abiotic and biotic stresses. Biological Reviews, 99(4):1524–1536, DOI: 10.1111/brv.13079; Varadharajan, V., et al. (2025) Multi-omics approaches against abiotic and biotic stress-A review. Plants, 14(6):865, DOI:10.3390/plants14060865; Afridi M.S., et al. (2022) New opportunities in plant microbiome engineering for increasing agricultural sustainability under stressful conditions. Frontiers in Plant Sciences, 13:899464, DOI:10.3389/fpls.2022.899464; Special issue on "Use of single cell and spatial multiomics for uncovering cellular and molecular mechanisms underlying plant stress responses". Stress Biology, 2025; Salem M.A., et al. (2022) Metabolomics of plant root exudates: From sample preparation to data analysis, Frontiers in Plant Sciences, 13:1062982, DOI:10.3389/fpls.2022.1062982; Singhal, R., et al. (2025) Using supervised machine-learning approaches to understand abiotic stress tolerance and design resilient crops. Philosophical Transactions of the Royal Society B, 380:2024.0252, DOI:10.1098/rstb.2024.0252.

Unit 4: Emerging Tools and Techniques -- Epitranscriptomics; Targeted epigenome editing: development of specific DNA-targeting systems, next-generation CRISPR activators, applications in agriculture; Nanotechnology and its applications in plant biology: types of nanomaterials, uptake and translocation, biological impact, applications of nanoparticles (NPs) in plant biology (biosensors, nutrient delivery, nanomaterials in plant genetic engineering (DNA / RNA delivery); Plant biology in space: growth and monitoring, effects of microgravity and ionizing radiations, applications, and benefits. 11 hours

Essential Readings: Kumari, A., et. al. (2023) Nanotechnology as a powerful tool in plant sciences: Recent developments, challenges and perspectives. Plant Nano Biology, 5:100046, DOI:10.1016/j.plana.2023.100046; Sanzari, I., et. al. (2019) Nanotechnology in plant science: To make a long story short. Frontiers in Bioengineering and Biotechnology, 7:120, DOI:10.3389/fbioe.2019.00120; Sharma, B., et al. (2023) The diversity and functions

of plant RNA modifications: what we know and where we go from here. Annual Review of Plant Biology, 74(1):53–85, DOI:10.1146/annurev-arplant-071122-085813; Shen, L., et al. (2019) Messenger RNA modifications in plants. Trends in Plant Science, 24(4):328–41, DOI:10.1016/j.tplants.2019.01.005; McCutcheon, S.R., et al. (2024) Epigenome editing technologies for discovery and medicine. Nature Biotechnology, 42:1199–1217, DOI:10.1038/s41587-024-02320-1; Kungulovski, G. and Jeltsch, A. (2016) Epigenome editing: state of the art, concepts, and perspectives. Trends in Genetics, 32(2):101–13, DOI:10.1016/j.tig.2015.12.001.

Practicals (30 hours)

1. To investigate the phenotypic responses in the calcium signaling mutants.
2. To investigate the transactivation or transrepression activity of a transcription factor.
3. To design CRISPR guide RNA primers using online tools (e.g., CHOPCHOP, CRISPOR).
4. Molecular probe-based pathogen detection.
5. To design functional genomics approaches for specific gene/phenotype questions and compare the strengths and limitations of different methods.

Suggested Readings:

1. Kramer, L.M. (2015) Signal Transduction. 3rd edition, Academic Press, ISBN:9780123948199.
2. Heldin, C.H. and Purton, M. (1996) Signal transduction: Modular texts in molecular and cell biology, Chapman & Hall, ISBN:0412708108.
3. Alberts, B., et al. (2022) Molecular Biology of the Cell. 7th edition, W.W. Norton & Company, ISBN:9780393884630.
4. Buchanan, B.B., et al. (2015) Biochemistry & Molecular Biology of the Plants. 2nd edition, Wiley Blackwell, ISBN:9781118502198.
5. Kleinsmith, L.J. and Kish, V.M. (1997) Principles of Cell & Molecular Biology. Harper Collins College Publishers, ISBN:9780065004045.
6. Taiz, L., et al. (2023). Plant Physiology and Development. 7th edition, Sinauer Associates, ISBN:9780197614204.
7. Glick, B.R. and Pasternak, J.J. (2022) Molecular Biotechnology: Principles and Applications of recombinant DNA. 6th edition, ASM Press, ISBN:9781683673668.
8. Brown, T.A. (2023) Genomes 5. 5th edition, CRC Press, ISBN:9781003133162.
9. Piechulla, B. (2025) Plant Biochemistry. 6th edition, Academic Press, ISBN:9780443266164.
10. Abd-Elsalam, K.A. and Prasad, R. (2018) Nanobiotechnology applications in plant protection. Springer Cham, ISBN:9783319911601, DOI:10.1007/978-3-319-91161-8.
11. Chen, J.T. (2024) Advanced Nanotechnology in Plants: Methods and Applications. CRC Press, ISBN:9781003368571.
12. Jeltsch, A., and Rots, M.G. (2018) Epigenome editing: Methods and Protocols. Humana New York, ISBN:9781493977741, DOI:10.1007/978-1-4939-7774-1.
13. Jurga, S. and Barciszewski, J. (2021) Epitranscriptomics. Springer Cham, ISBN:9783030716127, DOI:10.1007/978-3-030-71612-7.
14. Online Databases and Resources: NCBI, TAIR, Phytozome, EnsemblPlants and others, KEGG, STRING, Gene Ontology, CRISPR-Cas toolkits and others.

PBSE315: Introduction to Bioinformatics

This course is open to students of other departments as a GE course.

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE315: Introduction to Bioinformatics	4	3	1	0	B.Sc. in any branch of science	NA

Learning Objectives

The paper is devised to introduce the students to the field of bioinformatics and data analysis. The content is designed for students from any stream of life sciences. The course imparts basic and essential knowledge regarding the nature of life science data, including data formats, international databases and data repositories. It also helps to understand how different biological file formats facilitate storage, retrieval and analysis of biological sequences and structures. Furthermore, the unit is designed to familiarize the learner with the landscape of major international nucleotide and protein databases, understanding their scope, interrelationships, and specific applications (universal and organism-specific databases). Additionally, understand the structure, interoperability, and collaborative role of INSDC, and its importance in maintaining the global genomic data ecosystem. Furthermore, it will explain the fundamental principles of local and global alignment (pairwise sequence comparison) and the biological rationale behind scoring systems, including substitution matrices and gap penalties. It also focuses on interpreting results of Clustal-W, Clustal Omega, T-Coffee, and MultiAlign BLAST tools and how to optimize their parameters to draw biologically meaningful conclusions. The last unit of the course presents the fundamentals of RNA/ Protein secondary and tertiary structure prediction. It will be helpful to learn the basic principles of docking analysis and drug design workflows.

Learning Outcomes

After successfully completing the course, students will be able to identify and describe various biological data formats and their respective applications. They will be able to access and retrieve sequences and structural data from major databases, data repositories, and browsers like UCSC Genome Browser, linking data formats to visual genomic analysis. Furthermore, students will be able to utilize tools like BLAST for sequence comparison and evolutionary significance, as well as understand the conceptual difference between various substitution matrices and pairwise algorithms. They can perform and interpret the MSA of different biological sequences using different computational software and also visualize phylogenetic trees using various algorithms. Upon completing the last unit, students will be able to use computational tools for RNA and protein prediction, evaluate them, and analyse protein-ligand interaction and outcomes of docking.

Course Content (45 hours)

Unit 1: Biological Data Formats and Databases -- Overview of database management system, concept of 'structured' and 'semi-structured/unstructured' data, concept of 'flat-file' formats; Various file formats used in bioinformatics such as 'fasta', 'fastq', Phylip format, Newick, PDB file format, 'GFF3', SAM/BAM/CRAM formats; Universal nucleotide data repositories: NCBI-GenBank, EMBL-ENA, DDBJ; Details of the International Nucleotide Sequence Data Collaboration (INSDC); Universal Protein databases: UniprotKB, PDB. Organism specific databases (Flybase, Wormbase etc), UCSC Human Genome Browser; Molecular interaction databases such as KEGG and STRING. 10 hours

Essential Readings: Mount, D.W. (2004) Bioinformatics: Sequence and Genome Analysis. 2nd edition, Cold Spring Harbor Laboratory Press, ISBN:9780879697129, Chapter 1 (Historical Introduction and Overview), Chapter 2 (Collecting and Storing Sequences in the Laboratory); Zvelebil, M. and Baum, J.O. (2008) Understanding Bioinformatics. Garland Science, ISBN:9780815340249, Chapter 1 (The nucleic world) and chapter 3 (Dealing with databases); Sayers, E.W., et al. (2022) Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 50(D1):D20–D26, DOI:10.1093/nar/gkab1112; Cochrane, G., et al. (2016). The European Nucleotide Archive in 2016. Nucleic Acids Research, 44(D1):D32–D37, DOI:10.1093/nar/gkw1106; The UniProt Consortium (2023) UniProt: the Universal Protein Knowledgebase in 2023. Nucleic Acids Research, 51(D1):D523–D531, DOI:10.1093/nar/gkac1052; Berman, H.M., et al. (2000) The Protein Data Bank. Nucleic Acids Research, 28(1):235–242, DOI:10.1093/nar/28.1.235; Li, H., et al. (2009) The Sequence Alignment/Map format and SAMtools. Bioinformatics, 25(16):2078–2079, DOI:10.1093/bioinformatics/btp352; Cock, P.J.A., et al. (2010) The Sanger FASTQ file format for sequences with quality scores, and the Solexa/Illumina FASTQ variants. Nucleic Acids Research, 38(6):1767–1771, DOI:10.1093/nar/gkp1137; Kanehisa, M., et al. (2023) KEGG for taxonomy-based analysis of pathways and genomes. Nucleic Acids Research, 51(D1):D587–D592, DOI:10.1093/nar/gkac997; Szklarczyk, D., et al. (2023) The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome. Nucleic Acids Research, 51(D1):D638–D646, DOI:10.1093/nar/gkac1000; The FlyBase Consortium. (2022). FlyBase: updates to the *Drosophila melanogaster* knowledge base. Nucleic Acids Research, 50(D1):D1014–D1020, DOI:10.1093/nar/gkab1099; Haeussler, M., et al. (2019) The UCSC Genome Browser database: 2019 update. Nucleic Acids Research, 47(D1):D853–D858, DOI:10.1093/nar/gky1095.

Unit 2: Pairwise Sequence Alignment -- Concept of local and global sequence alignment; Pairwise sequence alignment algorithms such as Needleman and Wunsch, Smith-Waterman, scoring an alignment, linear and affine gap penalty, amino acid substitution scoring matrices (PAM and BLOSUM); Sequence alignment-based database search, BLAST and its variants, BLAST parameters (word size, E-value, scoring scheme, gap-penalty), bit/raw score. 10 hours

Essential Readings: Mount, D.W. (2004) Bioinformatics: Sequence and Genome Analysis. 2nd edition, Cold Spring Harbor Laboratory Press, ISBN:9780879697129, Chapter 3 (Alignment of pairs of sequences), Chapter 6 (Sequence database searching for similar sequences); Zvelebil, M. and Baum, J.O. (2008) Understanding Bioinformatics. Garland Science, ISBN:9780815340249, Chapter 4 (Producing and analyzing sequence alignments), Chapter 5 (Pairwise sequence alignment and database searching); Morrison, D.A. (2006). Multiple sequence alignment for phylogenetic purposes. Australian Systematic Botany, 19(6):479–539, DOI:10.1071/SB06020.

Unit 3: Multiple Sequence Alignment and Phylogenetic Analysis -- Global and local multiple sequence alignment, multiple sequence alignment algorithms (progressive and iterative algorithms), profile and block analysis; Softwares: Clustal-X, Clustal-W, Clustal-Omega, T-Coffee, MultiAlign; Basic concept of phylogenetic analysis, rooted and unrooted trees, approaches for phylogenetic tree construction; Basics of algorithm for UPGMA, neighbour joining (NJ), maximum parsimony, and maximum likelihood phylogenetic analysis. 15 hours

Essential Readings: Mount, D.W. (2004) Bioinformatics: Sequence and Genome Analysis. 2nd edition, Cold Spring Harbor Laboratory Press, ISBN:9780879697129, Chapter 5 (Multiple sequence alignment), Chapter 7 (Phylogenetic prediction); Zvelebil, M. and Baum, J.O. (2008) Understanding Bioinformatics. Garland Science, ISBN:9780815340249, Chapter 4 (Producing and analyzing sequence alignments), Chapter 5 (Pairwise sequence alignment and database searching), Chapter 6 (Patterns, profiles, and multiple alignments).

Unit 4: Structure Predictions for Nucleic Acids and Proteins -- Approaches for prediction of RNA secondary and tertiary predictions, energy minimization and base covariance models; Basic approaches for protein structure predictions, comparative modeling, fold recognition/'threading', and *ab-initio* prediction; Introduction to AlfaFold database; Docking analysis and drug designing. 10 hours

Essential Readings: Mount, D.W. (2004) Bioinformatics: Sequence and Genome Analysis. 2nd edition, Cold Spring Harbor Laboratory Press, ISBN:9780879697129, Chapter 8 (Prediction of RNA secondary structure), Chapter 10 (Protein classification and structure prediction); Zvelebil, M. and Baum, J.O. (2008) Understanding Bioinformatics. Garland Science, ISBN:9780815340249, Chapter 8 (Recovering evolutionary history), Chapter 11 (Obtaining secondary structure from sequence), Chapter 12 (Predicting secondary structures).

Tutorials (15 hours)

1. To perform 'text-based' database search
2. Sequence alignment-based database search.
3. Multiple sequence alignment and phylogenetic analysis.
4. Analysis of gene/protein interaction networks.

Suggested Readings:

1. Baxevanis, A.D., et al. (2020) Bioinformatics: A practical guide to the analysis of genes and proteins. 4th edition. John Wiley & Sons, Inc., ISBN:9781119335962.
2. Tramontano, A. (2018) Introduction to Bioinformatics. Chapman and Hall/CRC, ISBN:9781315276014, DOI:10.1201/9781420010886.
3. Lee, E. Tan, T.W. (2018) Beginners guide to bioinformatics for high throughput sequencing. World Scientific, ISBN:9789813231665, DOI:10.1142/10720.
4. Thompson, J.D., et al. (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Research, 22(22):4673–4680, DOI:10.1093/nar/22.22.4673.
5. Notredame, C., et al., (2000) T-Coffee: A novel method for fast and accurate multiple sequence alignment. Journal of Molecular Biology, 302(1):205–217, DOI:10.1006/jmbi.2000.4042.
6. Saitou, N. and Nei, M. (1987) The neighbor-joining method: a new method for reconstructing phylogenetic trees. Molecular Biology and Evolution, 4(4):406–425, DOI:10.1093/oxfordjournals.molbev.a040454.
7. Felsenstein, J. (1981) Evolutionary trees from DNA sequences: a maximum likelihood approach. Journal of Molecular Evolution, 17(6):368–376, DOI:10.1007/BF01734359.
8. JJumper, J., et al. (2021) Highly accurate protein structure prediction with AlphaFold2. Nature, 596:583–589, DOI:10.1038/s41586-021-03819-2.
9. Zhang, Y. (2008) Progress and challenges in protein structure prediction. Current Opinion in Structural Biology, 18(3):342–348, DOI:10.1016/j.sbi.2008.02.004.
10. Kryshtafovych, A., et al. (2021) Critical assessment of methods of protein structure prediction (CASP)—Round XIV. Proteins: Structure, Function, and Bioinformatics, 89(12):1607–1617, DOI:10.1002/prot.26237.
11. Zuker, M. (2003) Mfold web server for nucleic acid folding and hybridization prediction. Nucleic Acids Research, 31(13):3406–3415, DOI:10.1093/nar/gkg595.
12. Kitchen, D.B., et al. (2004) Docking and scoring in virtual screening for drug discovery: methods and applications. Nature Reviews Drug Discovery, 3(11):935–949, DOI:10.1038/nrd1549.

PBSE316: Molecular Plant Evolution and Biodiversity

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE316: Molecular Plant Evolution and Biodiversity	4	3	1	0	B.Sc. in any branch of science	NA

Learning Objectives

The course aims to establish a foundational understanding of the core principles of evolutionary biology from a plant-centric perspective. It explores how mechanisms like polyploidy and lateral gene transfer shape plant diversity, and covers the evolution of key plant structures, developmental processes, and metabolic pathways. The learner will investigate how abiotic (climate, soil) and biotic (herbivores, pollinators, microbes) interactions act as selective pressures, driving adaptation and diversification. The final unit introduces methods for assessing biodiversity using genomics (multi-omics data), phylogenomics, and environmental DNA (eDNA), and discusses global efforts in biodiversity data sharing and the Access and Benefit Sharing (ABS) mechanism.

Learning Outcomes

The course enables learners to describe the evolutionary biology of plants through genetic mechanisms, including mutation, drift, and natural selection. Upon completion, students will be able to explain homologies and analogies in plant phenotypes, metabolic evolution, and various evolutionary trends relevant to modern plant physiology and adaptation. Learners are able to discuss the roles of abiotic and biotic factors in shaping plant diversity and analyze the impact of domestication on genetic diversity. Furthermore, scholars are equipped to conduct analyses using whole-genome, pan-genome, and environmental DNA approaches. They also gain an understanding of the importance of FAIR data principles, Access and Benefit-Sharing (ABS) in biodiversity management, and the policy dimensions of Digital Sequence Information (DSI).

Course Contents (45 hours)

Unit 1: Basics of Evolution -- Overview of plant evolution; Natural selection, adaptation, lateral gene transfer, genetic drift, speciation, adaptive potential, polyploidy; Multicellularity in plants; Molecular basis of evolution. 5 hours

Essential Readings: Willis, K.J. and McElwain, J.C. (2021) The evolution of plants. 3rd edition, Oxford University Press, ISBN:9780199292233; Soltis, D.E. and Soltis, P.S. (2009) The role of hybridization in plant speciation. Annual Review of Plant Biology, 60:561–588, DOI:10.1146/annurev.arplant.043008.092039.

Unit 2: Introduction to Plant Evolution -- Evolution of land plants and plant stress response networks (terrestrialization), plant development and vasculature, homology and evolution of key phenotypic novelties of land plants, plant sexual diversity; Evolution of plant metabolism, photosynthesis, energy metabolism, and specialised metabolites. 15 hours

Essential Readings: Niklas, K.J. and Kutschera, U. (2022) The evolution of the land plants. University of Chicago Press, Chicago, ISBN:9780226784635; Raven, P.H., et al. (2016) Biology of Plants, 8th edition, W.H.

Freeman New York, ISBN:9781429219617; Bowman, J.L., et. al. (2019) Evolution and co-option of developmental regulatory pathways in early land plants. Current Topics in Developmental Biology, 131:35–53, DOI:10.1016/bs.ctdb.2018.10.001; Muggia, L., et. al. (2020) An Overview of genomics, phylogenomics and proteomics approaches in Ascomycota. Life (Basel). 10(12):356, DOI:10.3390/life10120356.

Unit 3: Drivers of Plant Evolution -- Impact of environmental factors on plant evolution and distribution; Role of biotic factors such as herbivores, pollinators, and microbes in plant evolution; Domestication; Impact of plant evolution on Earth's climate; Drivers of biodiversity loss. 10 hours

Essential Readings: Briggs, D. (2020) Plant Microevolution and Conservation in Human-Influenced Ecosystems, Cambridge University Press, ISBN:9780521818353; Doebley, J.F., et. al. (2006) The molecular genetics of crop domestication. Cell, 127(7):1309–1321, DOI:10.1016/j.cell.2006.12.006; Ehrlich, P.R. and Raven, P.H. (1964) Butterflies and plants: a study in coevolution. Evolution, 18(4):586–608, DOI:10.1111/j.1558-5646.1964.tb01674.x; Larson, G. and Fuller, D.Q. (2014) The evolution of animal domestication. Annual Review of Ecology, Evolution, and Systematics, 45:115-136, DOI:10.1146/annurev-ecolsys-110512-135813; Niklas, K.J. and Kutschera, U. (2022) The evolution of the land plants. University of Chicago Press, Chicago, ISBN:9780226784635; Willis, K.J. and McElwain, J.C. (2021) The Evolution of Plants. 3rd edition, Oxford University Press, ISBN:9780199292233; Ruiz, V.V., et. al., (2025). A new era in the discovery of biological control bacteria: Omics-driven bioprospecting. Soil Systems, 9(4):108, DOI:10.3390/soilsystems9040108.

Unit 4: Multi-omic Assessment of Plant Evolutionary Biodiversity -- Biodiversity hot-spots, monitoring and assessment of biodiversity, Whole genome sequencing; Phylogenomics; environmental DNA (eDNA) sequencing for diversity assessment, advantage of pangenome datasets, biodiversity cell atlas, global efforts to characterize plant molecular diversity; Metabolomics; Concept of digital forests; Implications of the Convention on Biological Diversity, concept of Digital Sequence Information (DSI) and Access Benefit Sharing mechanisms (ABS). 15 hours

Essential Readings: Deiner, K., et al. (2017) Environmental DNA metabarcoding: Transforming how we survey animal and plant communities. Molecular Ecology, 26(21):5872–95, DOI:10.1111/mec.14350; Exposito-Alonso, M., et al. (2022) The Earth BioGenome project: opportunities and challenges for plant genomics and conservation. The Plant Journal, 102(2):222–229, DOI:10.1111/tpj.14631; Golicz, A.A., et.al. (2016) The pangenome of an agronomically important crop plant *Brassica oleracea*. Nature Communications, 7:13390, DOI:10.1038/ncomms13390; Laird, S. and Wynberg, R. (2018) A fact-finding and scoping study on digital sequence information on genetic resources in the context of the Convention on Biological Diversity and the Nagoya Protocol, CBD/DSI/AHTEG/2018/1/3, Secretariat of the Convention on Biological Diversity, Montreal; Zhou, L., et. al. (2025) Estimating carbon biomass using DNA: Phytoplankton as a case study. DNA, 5(1):13, DOI:10.3390/dna5010013; Achieng, A.O., et al. (2023) Monitoring biodiversity loss in rapidly changing Afrotropical ecosystems: an emerging imperative for governance and research. Philosophical Transactions of the Royal Society B. 378:20220271, DOI:10.1098/rstb.2022.0271.

Tutorials (15 hours)

Case studies on:

1. Impact of horizontal gene transfer on plant evolution.
2. Evolution of 3D growth patterns in plants.
3. Plant biodiversity and modern drug discovery.
4. Insights into plant biodiversity of India.

Suggested Readings:

1. Doyle, J.J. and Gaut, B.S. (2000) Plant molecular evolution. Springer Dordrecht, ISBN:9780792360964, DOI:10.1007/978-94-011-4221-2.
2. Kenrick, P. and Crane, P.R. (1997) The origin and early evolution of plants on land. Nature, 389:33–39, DOI:10.1038/37918.
3. Weng, J.K., et al. (2012). The rise of chemodiversity in plants. Science, 336:1667–70, DOI:10.1126/science.1217411.

PBSEC317: Emerging Techniques in Plant Biology

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSEC317: Emerging Techniques in Plant Biology	2	1	0	1	B.Sc. in any branch of science	NA

Learning Objectives

The objective of this paper is to familiarize students with the latest advancements and methodologies in the field. The course offers insight into diverse imaging approaches and methodologies used to study plant systems at the cellular level. This course provides an in-depth understanding of emerging and state-of-the-art techniques used in contemporary research and applications.

Learning Outcomes

Students would acquire specific practical skills regarding various sample preparations and imaging techniques, which are essential for conducting advanced plant science research. They will acquire knowledge of the principles and applications of cutting-edge techniques relevant to modern research and innovation, and will learn to apply appropriate state-of-the-art tools and technologies to investigate complex scientific problems.

Course Content (15 hours)

Unit 1: Imaging Techniques -- Fundamental principles of microscope design, image formation, magnification, numerical aperture, resolution, and contrast; Components and optics of light microscopy; Transmitted light techniques: bright-field, phase contrast, and DIC; Fundamentals of fluorescence, excitation-emission principles, fluorescent probes and biosensors, photobleaching, and quenching; Confocal laser scanning microscopy–optical sectioning, Z-stack reconstruction, and 3D imaging, super-resolution microscopy (STED, SIM, PALM/STORM), and cryo-electron microscopy (Cryo-EM); Digital image recording, cameras, signal-to-noise ratio, and quantitative image analysis; Applications in plant cell and developmental biology using fluorescence-based imaging approaches. 7.5 hours

Essential Readings: Murphy, D.B. and Davidson, M.W. (2012) Fundamentals of light microscopy and electronic imaging, 2nd edition, Wiley-Blackwell, ISBN:9781118382905, Chapter 1 (Introduction to Microscopy), Chapter 2 (The Optical Microscope), Chapter 3 (Image Formation in the Microscope), Chapter 4 (Fluorescence Microscopy): Principles, Chapter 5 (Fluorescence Microscopy: Instrumentation), Chapter 6 (Digital Imaging Fundamentals), Chapter 9 (Confocal Microscopy), Chapter 13 (Electron Microscopy Fundamentals); Huang, B., et al. (2009) Super-resolution fluorescence microscopy. Annual Review of Biochemistry, 78:993–1016, DOI: 10.1146/annurev.biochem.77.061906.092014; Nogales, E. and Scheres, S.H.W. (2015) Cryo-EM: A unique tool for the visualization of macromolecular complexity. Molecular Cell, 58:677–689, DOI: 10.1016/j.molcel.2015.02.019.

Unit 2: Single Cell Biology -- Isolation and handling of single cells: Fluorescence-activated cell sorting (FACS); Microfluidics, Laser Capture Microdissection (LCM); Single-cell multi-omics analysis: Single-cell genomics (scDNA-seq), transcriptomics (scRNA-seq), proteomics (scProteomics), metabolomics (scMetabolomics); Multi-omics integration; Temporal and Spatial analysis: Spatial Transcriptomics, *in situ* subcellular localization of a metabolite;

Chromosomal immunostaining; Applications of single cell biology in plant molecular biology.

7.5 hours

Essential Readings: Hu, P., et al. (2016) Single cell isolation and analysis. Frontiers in Cell and Developmental Biology, 4:116, DOI:10.3389/fcell.2016.00116; Wang, D. and Bodovitz, S. (2010) Single-cell analysis: the new frontier in 'omics'. Trends in Biotechnology, 28(6):281–290, DOI:10.1016/j.tibtech.2010.03.002; Jackson, C.A., et al. (2022) New horizons in the stormy sea of multimodal single-cell data integration Molecular Cell, 82(2):248–259, DOI:10.1016/j.molcel.2021.12.012; Rahman, M.S., et al. (2024) Opportunities and challenges in advancing plant research with single-cell omics. Genomics, Proteomics & Bioinformatics, 22(2):qzae026, DOI:10.1093/gpbjnl/qzae026; Clark, N.M., et al. (2022) To the proteome and beyond: advances in single-cell omics profiling for plant systems. Plant Physiology, 188(2):726–737, DOI:10.1093/plphys/kiab429; Nobori, T. (2025) Exploring the untapped potential of single-cell and spatial omics in plant biology. The New Phytologist, 247(3):1098, DOI:10.1111/nph.70220; Chau, T.N., et al. (2024) Advancing plant single-cell genomics with foundation models. Current Opinion in Plant Biology, 82:102666, DOI:10.1016/j.pbi.2024.102666.

Practicals (30 hours)

1. To visualize a living plant specimen using bright-field, phase contrast, and (if available) DIC, and understand how each enhances different features.
2. Preparation of publication-quality microscopy figures: Brightfield–Fluorescence overlays and scale bars.
3. To navigate and annotate multi-dimensional images for preparing a figure using Image J.
4. Data analysis of targeted metabolite profiling.
5. Analysis of cell cycle stages using FACS.

Suggested Readings:

1. Wu, X., et al. (2024) Single-cell sequencing to multi-omics: technologies and applications. Biomarker Research, 12:110, DOI:10.1186/s40364-024-00643-4.
2. Zhu, M., et al. (2025) Single-cell transcriptomics reveal how root tissues adapt to soil stress. Nature, 642:721–729, DOI:10.1038/s41586-025-08941-z.
3. Lee, T.A., et al. (2025) A single-cell, spatial transcriptomic atlas of the *Arabidopsis* life cycle. Nature Plants, 11:1960–75, DOI:10.1038/s41477-025-02072-z.
4. Cold Spring Harbour Protocols- Imaging/Microscopy, general weblink: (https://cshprotocols.cshlp.org/cgi/collection/imaging_microscopy_general)
5. Paddock, S.W. (2014) Confocal Microscopy: Methods and Protocols. Humana New York, NY, eISBN:9781607618478, DOI:10.1007/978-1-60761-847-8.
6. Ruzin, S.E. (1999) Plant Microtechnique and Microscopy. Oxford University Press, USA, ISBN:9780195089561.
7. Pawley, J.B. (2006) Handbook of Biological Confocal Microscopy. 3rd Edition, Springer New York, NY, ISBN:9780387455242, DOI:10.1007/978-0-387-45524-2.
8. Markaki, Y. and Harz, H. (2017) Light microscopy: Methods and Protocols. Humana New York, NY, DOI:10.1007/978-1-4939-6810-7.
9. Yin, Z. et al. (2023) Mass spectrometry imaging techniques: a versatile toolbox for plant metabolomics. Trends in Plant Science, 289(2):250–251, DOI:10.1016/j.tplants.2022.10.009.
10. Pawlowski, W.P., et al. (2013) Plant Meiosis: Methods and Protocols. Humana Totowa, NJ, Chapter (Immunolocalization of meiotic proteins in *Brassicaceae*: method 1), ISBN:9781627033336, DOI:10.1007/978-1-62703-333-6_9.
11. Petrova, B. and Guler, A.T. (2025) Recent developments in single-cell metabolomics by mass Spectrometry- A perspective. Journal of Proteome Research, 24(4):1493–1518, DOI:10.1021/acs.jproteome.4c00646.
12. Shaw, R., et al. (2021) Single-cell transcriptome analysis in plants: advances and challenges. Molecular Plant, 14(1):115–126, DOI:10.1016/j.molp.2020.10.012.

SEMESTER 4

PBSC411: Advances in Crop Biotechnology

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSC411: Advances in Crop Biotechnology	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

This course aims to provide learners with an advanced and integrative understanding of modern crop biotechnology and its role in sustainable agriculture. Students will engage with emerging molecular tools, the development and significance of crop pan-genomes, and cutting-edge concepts such as *de novo* domestication and innovations in *in-planta* transformation. The course will also provide in-depth insights into translational strategies to enhance crop nutrition and improve resilience to biotic and abiotic stresses through sustainable, environmentally friendly approaches. Overall, learners will develop the scientific foundation and biotechnology skills required to address challenges in crop improvement.

Learning Outcomes

Upon completing this course, participants will be able to critically analyze crop genomes for domestication signatures and evaluate germplasm diversity for trait improvement. They will demonstrate practical knowledge of state-of-the-art plant transformation techniques and emerging delivery platforms for gene and RNA manipulation. Students will be able to assess and design strategies for enhancing stress tolerance, yield, and nutritional value in crop plants. They will also gain competence in applying biostimulants and other biofortification approaches.

Course Contents (45 hours)

Unit 1: Introduction to Crop Biotechnology -- Emerging tools and techniques in biotechnology; Crop pan-genomes and signatures of crop domestication; Germplasm diversity analysis; Concept of *de novo* crop domestication; Agro-morphological traits enhancement; Environmental challenges and food security; Plants as biofactories. 10 hours

Essential Readings: Mascher, M., et al. (2024) Promises and challenges of crop translational genomics. Nature, 636:585–593, DOI:10.1038/s41586-024-07713-5; Shi, J., et al. (2023) Plant pan-genomics and its applications. Molecular Plant, 16(1):168–186, DOI:10.1016/j.molp.2022.12.009; Curtin, S., et al. (2022) Pathways to *de novo* domestication of crop wild relatives. Plant Physiology, 188(4):1746–1756, DOI:10.1093/plphys/kiab554.

Unit 2: Genetic Transformation Techniques -- Ternary vector systems; Improved *in planta* transformation - *de novo* meristems induction, morphogenic regulators, particle bombardment of shoot apical meristem, composite plants, etc; Use of magnetic nanoparticles; Organelle genome transformation. 10 hours

Essential Readings: Chen, Z., et al. (2022) Recent advances in crop transformation technologies. Nature Plants, 8(12):1343–1351, DOI:10.1038/s41477-022-01295-8; Bélanger, J.G., et al. (2024) A comprehensive review of *in planta* stable transformation strategies. Plant Methods, 20(1):79, DOI:10.1186/s13007-024-01200-8.

Unit 3: Climate Resilience and Yield Enhancement -- Case studies on abiotic and biotic stress tolerance; RNA delivery against fungal pathogens; Probiotic-based gene silencing in polyphagous pests; Biofertilizers, Biopesticides; Cell-penetrating peptides; Concept of chronoculture; Synthetic circuits and rewiring for plant improvement; Enhancement of photosynthetic capacity; Carbon dots in plant (epi)genomics. 15 hours

Essential Readings: González Guzmán, M., et al. (2022) New approaches to improve crop tolerance to biotic and abiotic stresses. Physiologia Plantarum, 174(1):e13547, DOI:10.1111/ppl.13547; Al-Dossary, O., et al. (2025) Crop management to enhance plant resilience to abiotic stress using nanotechnology: towards more efficient and sustainable agriculture. Frontiers in Plant Science, 16:1626624, DOI:10.3389/fpls.2025.1626624; Afridi, M.S., et al. (2022) New opportunities in plant microbiome engineering for increasing agricultural sustainability under stressful conditions. Fronters in Plant Science 13:899464, DOI:10.3389/fpls.2022.899464; Shahwar, D., et al. (2023) Role of microbial inoculants as bio fertilizers for improving crop productivity: A review. Heliyon, 9(6):e16134, DOI:10.1016/j.heliyon.2023.e16134; Lloyd, J.P.B., et al. (2025) The switch-liker's guide to plant synthetic gene circuits. Plant Journal, 121(5):e70090, DOI: 10.1111/tpj.70090.

Unit 4: Enhancement of Nutrients -- Improved nutritional profile of crops; Enhancement of mineral nutrient uptake and distribution; Biofortification (Fe, Zn, Ca, K, Vitamins, proteins, essential oils, etc.), micronutrient-dense crops; Anti-nutrient reduction; Concept of Biostimulants. 10 hours

Essential Readings: Napier, J.A., et al. (2019) The challenges of delivering genetically modified crops with nutritional enhancement traits. Nature Plants, 5(6):563–567, DOI:10.1038/s41477-019-0430-z; Zhu, Q., et al. (2019) Plant synthetic metabolic engineering for enhancing crop nutritional quality. Plant Communications, 1(1):100017, DOI:10.1016/j.xplc.2019.100017; White, P.J. and Broadley, M.R. (2005) Biofortifying crops with essential mineral elements. Trends in Plant Science, 10(12):586–593, DOI:10.1016/j.tplants.2005.10.001.

Practicals (30 hours)

1. Transient gene expression using the particle bombardment method.
2. Measurement of photosynthetic efficiency using fluorescence-based system.
3. *In vivo* plant imaging under stress conditions.
4. Mineral nutrient profiling of plants.
5. Molecular detection of *Rhizobium* in root nodules of leguminous plants.

Suggested Readings:

1. Li, X., et al. (2025) The next Green Revolution: integrating crop architectype and physiotype. Trends in Biotechnology, 43(10):2479–2493, DOI:10.1016/j.tibtech.2025.04.002.
2. Della Coletta, R., et al. (2021) How the pan-genome is changing crop genomics and improvement. Genome Biology, 22(1):3, DOI:10.1186/s13059-020-02224-8.
3. Li, S., et al. (2021) Advancing organelle genome transformation and editing for crop improvement. Plant Communications, 2(2):100141, DOI:10.1016/j.xplc.2021.100141.
4. Jeong, J.H., et al. (2025). Empowering *Agrobacterium*: Ternary vector systems as a new arsenal for plant transformation and genome editing. Biotechnology Advances, 83:108631, DOI: 10.1016/j.biotechadv.2025.108631.
5. Shrawat, A., et al. (2018) Engineering nitrogen utilization in crop plants. Springer Cham, DOI: 10.1007/978-3-319-92958-3.
6. Basar, N.U., et al. (2025) Synergies between biostimulants and plant nutrients: a review of ecofriendly nutrient management in crop production. Discover Agriculture, 3:150, DOI:10.1007/s44279-025-00345-x.
7. Patel, P., et al. (2024) Cell-penetrating peptides for sustainable agriculture. Trends in Plant Science, 29(10):1131–44, DOI:10.1016/j.tplants.2024.05.011.
8. Jaswal, S., et al. (2025) Chloroplast engineering for enhancing photosynthetic efficiency and agronomic traits. Trends in Biotechnology, DOI:10.1016/j.tibtech.2025.09.011.
9. Tavakoli, M., et al. (2025) Emerging applications of carbon dots in plant (epi)genomics. Trends in Biotechnology, DOI:10.1016/j.tibtech.2025.09.005.

10. Hawkesford, M.J., et al. (2016) Nutrient use efficiency in plants. Springer Cham, ISBN:9783319106342, DOI:10.1007/978-3-319-10635-9.
11. Li, G., et al. (2025) Integrated biotechnological and AI innovations for crop improvement. Nature, 643:925–937, DOI:10.1038/s41586-025-09122-8.
12. Bartlett, M.E., et al. (2023) The power and perils of *De Novo* domestication using genome editing. Annual Review of Plant Biology, 74:727–750, DOI:10.1146/annurev-arplant-053122-030653.
13. Jian, L., et al. (2022) *De novo* domestication in the multi-omics era. Plant and Cell Physiology, 63(11): 1592–1606, DOI:10.1093/pcp/pcac077.
14. Altpeter, F., et al. (2016) Advancing crop transformation in the era of genome editing. The Plant cell, 28(7):1510–1520, DOI:10.1105/tpc.16.00196.
15. Olsen, K.M., and Wendel, J.F. (2013) A bountiful harvest: genomic insights into crop domestication phenotypes. Annual Review of Plant Biology, 64:47–70, DOI:10.1146/annurev-arplant-050312-120048.
16. Ayenew, B.M. et al. (2024) A review on the production of nanofertilizers and its application in agriculture. Heliyon, 11(1):e41243, DOI:10.1016/j.heliyon.2024.e41243.
17. Steed, G., et al. (2021) Chronoculture, harnessing the circadian clock to improve crop yield and sustainability. Science, 372:eabc9141, DOI:10.1126/science.abc9141.
18. Borowsky, A.T. and Bailey-Serres, J. (2024) Rewiring gene circuitry for plant improvement. Nature Genetics, 56(8):1574–1582, DOI:10.1038/s41588-024-01806-7.
19. Naik, B., et al. (2024) Biofortification as a solution for addressing nutrient deficiencies and malnutrition. Heliyon, 10(9):e30595, DOI:10.1016/j.heliyon.2024.e30595.

PBSC412: Plant Secondary Metabolism and Applications

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSC412: Plant Secondary Metabolism and Applications	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

This course aims to provide students with a comprehensive understanding of plant secondary metabolites, focusing on their biosynthesis, regulation, detection, and diverse applications. It is designed to equip students with knowledge in analytical techniques, molecular tools, and biotechnological approaches used to study and manipulate secondary metabolite pathways. The course also emphasizes the ecological significance and medicinal potential of these compounds, preparing students to apply metabolic engineering for research and development in areas such as plant defense, drug discovery, and sustainable bioproduction.

Learning Outcomes

Upon completing this course, students will understand the biosynthesis, regulation, and classification of key plant secondary metabolites, as well as their significance in molecular biology and biotechnology. Students will also learn to apply genetic and metabolic engineering tools, such as CRISPR/Cas and RNAi, to manipulate biosynthetic pathways to enhance the production of metabolites. Additionally, students will explore the ecological functions of these compounds in plant defense and pollination, including the role of VOCs. Through this course, students will be prepared for research and applied careers in plant molecular biology, biotechnology, and phytopharmaceuticals.

Course Content (45 hours)

Unit 1: Fundamentals of Plant Secondary Metabolism -- Overview of Primary vs. Secondary Metabolites; Different classes of secondary metabolites: Alkaloids, Terpenoids, Flavonoids, Phenolics, Glucosinolates; Regulation of secondary metabolism (transcriptional, post-transcriptional, epigenetic). 12 hours

Essential Readings: Dixon, R.A. (2001) Natural products and plant disease resistance. Nature, 411:843–847, DOI:10.1038/35081178; Rabeh, K., et al. (2025) A comprehensive review of transcription factor-mediated regulation of secondary metabolites in plants under environmental stress. Stress Biology, 5(1):15, DOI:10.1007/s44154-024-00201-w; Buchanan, B.B., et al. (2015) Biochemistry and Molecular Biology of Plants. John Wiley & Sons, ISBN:9780470714218, Chapter 24 (Natural Products); Strauss, J. and Reyes-Dominguez, Y. (2011) Regulation of secondary metabolism by chromatin structure and epigenetic codes. Fungal Genetics and Biology, 48(1):62–69, DOI:10.1016/j.fgb.2010.07.009.

Unit 2: Isolation, Detection, and Characterization of Secondary Metabolites -- Extraction techniques: Solvent extraction, hydrodistillation, supercritical CO_2; Detection techniques (Chromatographic and Spectroscopic methods); Large-scale metabolite profiling and data analysis. 10 hours

Essential Reading: Dettmer, K., et al. (2007) Mass spectrometry-based metabolomics. Mass Spectrometry Reviews, 26(1):51–78, DOI:10.1002/mas.20108; Sukumaran, S.T., et al. (2020) Plant metabolites: methods, applications and prospects. Springer, ISBN:9789811551352, DOI:10.1007/978-981-15-5136-9.

Unit 3: Metabolic Engineering of Secondary Metabolites -- Concepts and techniques in metabolic engineering; Understanding of Synthetic biology and pathway engineering; Large-scale production of metabolites; Case studies in *E. coli*, *Saccharomyces*, and *Nicotiana*. 12 hours

Essential Readings: Zhu, X., et al. (2021) Synthetic biology of plant natural products: from pathway elucidation to engineered biosynthesis in plant cells. Plant Communications, 2(5):100229, DOI:10.1016/j.xplc.2021.100229; Karaca, H., et al. (2024) Metabolic engineering of *Saccharomyces cerevisiae* for enhanced taxadiene production. Microbial Cell Factories, 23(1):241, DOI:10.1186/s12934-024-02512-z; Zhao, S., et al. (2024) The metabolic engineering of *Escherichia coli* for the high-yield production of hypoxanthine. Microbial Cell Factories, 23(1):309, DOI:10.1186/s12934-024-02576-x.

Unit 4: Applications in Plant Defense, Human Health, and Ecology -- Role of secondary metabolites in plant defense (phytoalexins, VOCs, allelopathy); Ecological significance: VOCs in pollination, plant-insect interactions; Secondary metabolites in human health: antimicrobial, anticancer, antioxidant; Secondary metabolites in nutraceuticals and pharmaceuticals. 11 hours

Essential Readings: George, B.P., et al. (2021) Role of phytochemicals in cancer chemoprevention: Insights. Antioxidants, 10(9):1455, DOI:10.3390/antiox10091455; Divekar, P.A., et al. (2022) Plant secondary metabolites as defense tools against herbivores for sustainable crop protection. International Journal of Molecular Sciences, 23(5):2690, DOI:10.3390/ijms23052690.

Practicals (30 hours)

1. Extraction and qualitative analysis of plant secondary metabolites-saponins, phenolics, lignin.
2. Induction of secondary metabolite production in callus culture.
3. Demonstration of antimicrobial activity of plant extracts.
4. Detection of flavonoids during pollen development.
5. Effect of glucosinolate-derived compound, indole-3-carbinol, in plant root growth and development.

Suggested Readings:

1. Crozier, A., et al. (2006) Plant secondary metabolites: Occurrence, structure and role in the human diet. Blackwell Publishing, ISBN:9780470988558, DOI:10.1002/9780470988558.
2. Wink, M. (2010) Annual Plant Reviews Vol. 39: Functions and biotechnology of plant secondary metabolites. Blackwell Publishing, ISBN:9781444318876, DOI:10.1002/9781444318876.
3. Verpoorte, R. and Memelink, J. (2002) Engineering secondary metabolite production in plants. Current Opinion in Biotechnology, 13(2):181–187, DOI:10.1016/S0958-1669(02)00308-7.
4. Dewick, P.M. (2009) Medicinal Natural Products: A Biosynthetic Approach. John Wiley & Sons, ISBN:9780470742761, DOI:10.1002/9780470742761.
5. Katz, E., et al. (2015) The glucosinolate breakdown product indole-3-carbinol acts as an auxin antagonist in roots of *Arabidopsis thaliana*. The Plant Journal, 82(4):547–555, DOI: 10.1111/tpj.12824.

PBSE413: Epigenetics and Small RNA Biology

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE413: Epigenetics and Small RNA Biology	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

The epigenetic landscape (including both DNA methylation and histone modifications) of an organism has a significant bearing in regulating various developmental and metabolic processes at the global level. Similarly, small RNAs (sRNAs) have emerged as major modulators of global gene expression patterns. Therefore, this course is designed to provide students with a clear understanding of key epigenetic mechanisms, including chromatin modelling, DNA methylation, and histone modifications, and how these processes regulate plant development and physiology. Students will learn how epigenetic regulation contributes to environmental responses, stress adaptation, and inheritance, as well as its relevance in human systems, including immunity, cancer, and cardiovascular diseases. The course also introduces the diversity, biogenesis, and regulatory roles of non-coding RNAs across organisms, including their mechanisms of action and trans-kingdom interactions. Additionally, students will become familiar with experimental and computational tools for detecting, predicting, and validating small RNAs, and will explore the applications of RNA-based technologies and CRISPR-Cas systems in crop improvement, diagnostics, and therapeutic development.

Learning Outcomes

By the end of this course, students will be able to understand major epigenetic mechanisms and evaluate their roles in plant development, environmental responses, and human diseases. They will be able to understand DNA methylation and histone modifications, classify non-coding RNAs, and describe how small RNAs regulate gene expression. Students will also be equipped to use molecular and bioinformatic approaches for small RNA analyses and apply RNA-based tools. Overall, they will be able to integrate epigenetics and small RNA biology concepts to address research problems and understand their practical applications in agriculture, biotechnology, and human health.

Course Content (45 hours)

Unit 1: Epigenetic Regulation -- Chromatin modeling and remodeling: polycomb complexes, SWI/SNF1 complexes and other chromatin modifiers; DNA methylation and its interpretation: methylated DNA-binding proteins, their structure and function; techniques of altering and analyzing DNA methylation; Histone modifications: types, modifying enzymes, histone deacetylase inhibitors; Chromatin modification and its influence on plant development: somatic embryogenesis, leaf development, photosynthesis, flowering, and ageing. 12 hours

Essential Readings: Jenuwein, T. and Allis, C.D. (2001) Translating the histone code. Science, 293(5532):1074-1080, DOI:10.1126/science.1063127; Zhang, H., et al. (2018). Dynamics and function of DNA methylation in plants. Nature Reviews Molecular Cell Biology, 19(8):489-506, DOI:10.1038/s41580-018-0016-z; Rajewsky, N., et al. (2018) Plant epigenetics. Springer International, ISBN:9783319555195, DOI:10.1007/978-3-319-55520-1;

Huang, Y., et al., (2025) Chromatin remodeling in plants: Complex composition, mechanistic diversity, and biological functions. Molecular Plant, 18(9):1436–1457, DOI:10.1016/j.molp.2025.08.004.

Unit 2: Environmental and Evolutionary Epigenetics -- Role of epigenetic regulation in plant stress responses and epigenetic memory; Epigenetic inheritance and adaptive responses to environmental cues; Epigenetics in human systems: regulation of immune responses, cancer, and cardiovascular diseases. 10 hours

Essential Readings: Chinnusamy, V. and Zhu, J.K. (2009) Epigenetic regulation of stress responses in plants. Current Opinion in Plant Biology, 12(2):133–139, DOI:10.1016/j.pbi.2008.12.006; Avramova, Z. (2015) Transcriptional 'memory' of a stress: transient chromatin and memory (epigenetic) marks at stress-response genes. The Plant Journal, 83(1):149–159, DOI:10.1111/tpj.12832; Ma, L., et al., (2025) Epigenetic control of plant abiotic stress responses. Journal of Genetics and Genomics, 52(2):129–44, DOI:10.1016/j.jgg.2024.09.008; Janson, P.C. and Winqvist, O. (2011) Epigenetics–the key to understand immune responses in health and disease. American Journal of Reproductive Immunology, 66:72–74, DOI:10.1111/j.1600-0897.2011.01050.x; Zoghbi, H.Y. and Beaudet, A.L. (2016) Epigenetics and human disease. Cold Spring Harbor Perspectives in Biology, 8(2): a019497, DOI:10.1101/cshperspect.a019497.

Unit 3: Biology of Non-coding RNAs -- Discovery, types, occurrence, and diversity of non-coding RNAs; Small RNA pathways in bacteria, plants, and animal systems; Biogenesis and functional components of different classes of small RNAs; Regulation of gene expression by small RNAs: transcriptional gene silencing (TGS), post-transcriptional gene silencing (PTGS), gene activation, and evolutionary transitions in RNA-target interactions; Functional roles of small RNAs in different organisms; Trans-kingdom cross-talk mediated by small RNAs.

13 hours

Essential Readings: Guleria, P. and Kumar, V. (2020) Plant Small RNA- Biogenesis, Regulation and Application. Academic Press, ISBN:9780128171127, DOI:10.1016/C2018-0-01900-3; Alquethamy S., et al. (2025). What makes a small RNA work. Nucleic Acids Research, 53(12):gkaf563, DOI:10.1093/nar/gkaf563; Mattick, J. and Amaral, P. (2022) RNA, the epicenter of genetic information. ISBN:9781003109242, CRC Press, DOI:10.1201/9781003109242; Wierzbiki, A.T., et al. (2021) Long non-coding RNAs in plants. Annual Review of Plant Biology, 72:245–271, DOI:10.1146/annurev-arplant-093020-035446; Zhan, J. and Meyers, B.C. (2023) Plant small RNAs: their biogenesis, Regulatory roles, and functions. Annual Review of Plant Biology, 74:21–51, DOI:10.1146/annurev-arplant-070122-035226; Barquist, L. and Vogel, J. (2015) Accelerating discovery and functional analysis of small RNAs with new technologies. Annual Review of Genetics, 49:367–394, DOI:10.1146/annurev-genet-112414-054804.

Unit 4: Tools, Applications, and Emerging Technologies -- Discovery, detection, and validation of small RNAs; Target prediction and validation approaches; Databases and bioinformatic tools for small RNA analysis; Applications: artificial miRNA (amiR) technology, siRNA and virus-induced gene silencing (VIGS); RNAi interference (RNAi), RNA activation (RNAa), target mimicry and STTM technologies; CRISPR-Cas-based genome editing guided by small RNAs; Applications in crop improvement, diagnostics, and therapeutics. 10 hours

Essential Readings: Tang, G., et al. (2021) RNA-based technologies for functional genomics in plants. Springer Cham, ISBN:9783030649937, DOI:10.1007/978-3-030-64994-4; Ting, P., et al. (2018) A resource for inactivation of microRNAs using short tandem target mimic technology in model and crop plants. Molecular Plant, 11(11):1400–1417, DOI:10.1016/j.molp.2018.09.003; Halloy, F., et al. (2022) Innovative developments and emerging technologies in RNA therapeutics. 19(1):313–332, DOI:10.1080/15476286.2022.2027150.

Practicals (30 hours)

1. To resolve and visualize low molecular weight RNAs by denaturing urea-PAGE.
2. To perform expression analysis of selected miRNAs using the quantitative PCR method.

3. To isolate, sonicate, and observe cross-linked chromatin to study histone modifications.
4. To enzymatically cleave and assess DNA to detect methylation patterns.
5. To predict and analyze the secondary structure and thermodynamic stability of the miRNA precursor sequence (pre-miRNA) using Mfold.

Suggested Readings:

1. Esteller, M. (2009) Epigenetics in biology and medicine. CRC Press, eISBN:9780429124921.
2. Workman, J.L. and Abmayr, S.M. (2014) Fundamentals of chromatin. Springer New York, ISBN:9781461486237, DOI:10.1007/978-1-4614-8624-4.
3. Dinkar, V., et al. (2024) Epigenetic regulations under plant stress: a cereals perspective. Environmental and Experimental Botany, 220:105688, DOI:10.1016/j.envexpbot.2024.105688.
4. He, L. (2025) The interplay between chromatin remodeling and DNA double-strand break repair: Implications for cancer biology and therapeutics. DNA Repair, 146:103811, DOI:10.1016/j.dnarep.2025.103811.
5. Muka, T., et al. (2016) The role of epigenetic modifications in cardiovascular disease: a systematic review. International Journal of Cardiology, 212:174–183, DOI:10.1016/j.ijcard.2016.03.062.
6. Mallick, B. and Ghosh, Z. (2012) Regulatory RNAs: Basics, Methods and Applications. Springer Berlin, Heidelberg, ISBN:9783642225161, DOI:10.1007/978-3-642-22517-8.
7. Nellan, W. and Hammann, C. (2007) Small RNAs: analysis and regulatory functions. Springer Berlin, Heidelberg, ISBN:9783540281306, DOI:10.1007/978-3-540-28130-6.
8. Gaur, R.K. and Rossi, J.J. (2009) Regulation of gene expression by small RNAs. CRC Press, USA, eISBN:9780429121692, DOI:10.1201/9781420008708.
9. Alquethamy, S., et al. (2025) What makes a small RNA work? Nucleic Acids Research, 53(12):gkaf563, DOI:10.1093/nar/gkaf563.
10. Rederstorff, M. (2021) Small non-coding RNAs: Methods and Protocols. Humana New York. eISBN:9781071613863, DOI:10.1007/978-1-0716-1386-3.

PBSE414: Data Analytics and Biocuration

This course is open to students of other departments as a GE course.

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE414: Data Analytics and Biocuration	4	3	1	0	B.Sc. in any branch of Science	

Learning Objectives

The paper aims to empower learners with foundational data analytics skills essential for modern bioinformatics by exposing them to the fundamentals of advanced operating systems, including the Linux command-line interface (CLI), file handling, permissions, and data manipulation. It also provides a brief exposure to the R programming environment, syntax, and functions for data analysis and packages available in the Bioconductor repository for statistical computing, data visualization, and genomic data analysis. It also provides a comprehensive overview of the primary computational workflows for analyzing next-generation sequencing (NGS) data. The learner will explore the concepts, applications, and key steps involved in major "big data" bioinformatics domains, including genome assembly, variant calling, pangenomics, metagenomics, transcriptomics (RNA-seq) and epigenomics (ChIP-seq, Bisulfite-seq). Besides, it also focuses on the behind-the-scenes work of biocuration that powers biological databases through processes of extracting, standardizing, and organizing biological data from literature and experiments. It provides an overview of BioDbCore, FAIRsharing, and ethical principles of open data management. The student will be able to interpret Gene Ontology and biomedical ontologies using OBO formats. In the last unit, there is a brief overview of foundational concepts of AI and machine learning (ML), along with the utility of domain-specific LLMs, their applications in genomics, drug design, and systems biology.

Learning Outcomes

The completion of the course will give expertise in essential Linux commands and in setting up and running ‘R’ scripts for statistical analysis and plotting. The learner can apply Bioconductor tools for biological data exploration, such as DESeq2, edgeR, and limma. Furthermore, students can analyse NGS data for variant calling, transcriptome quantification, and epigenomic data integration. They also understand the FAIR data principles, ontologies, and the curation of biological data from published sources. Moreover, students can work with LLMs, ML, and AI tools across domains such as genomic prediction, phenotype classification, drug discovery, and structure-based screening.

Course Content (45 hours)

Unit 1: Basic of Linux and ‘R’ -- Computer architecture, types of operating systems (Windows, Mac-OS and Linux), concept of networking (IP address); Basic fundamentals of working with Unix/Linux on CLI (Command Line Interface), Unix/Linux directory structure, file permissions, remote login; Linux commands (whoami, pwd, cd, ls, man, mkdir, rm, cat copy, mv, chmod, grep, sed, sep, sort, head, tail, wc); Introduction to the 'R' data analysis package, basic work environment, syntax, introduction to the 'Bioconductor' packages for data analysis. 15 hours

Essential Readings: Blum, R. and Bresnahan, A. (2021) Linux Command Line and Shell Scripting Bible. 4th edition, John Wiley & Sons, Inc., ISBN:9781119700913; Kabacoff, R.I. (2022) R in action: Data analysis and graphics with R. 3rd edition, Manning Publications, ISBN:9781617296055; Gentleman, R.C., et al. (2004) Bioconductor: open software development for computational biology and bioinformatics. Genome Biology, 5:R80, DOI:10.1186/gb-2004-5-10-r80.

Unit 2: Big Data Analysis -- Whole genome reference-based assembly, de-novo genome analysis, variant call analysis, Pangenomes, Metagenomic analysis, RNA-seq data analysis, ChIP (Chromatin Immunoprecipitation) data analysis; Whole genome bisulphite sequencing data analysis. 10 hours

Essential Readings: Compeau, P. and Pevzner, P. (2018) Bioinformatics algorithms: An active learning approach. 3rd edition, Active Learning Publishers, ISBN:9780990374633; Shendure, J. and Aiden, E.L. (2012) The expanding scope of DNA sequencing. Nature Biotechnology, 30(11):1084–1094, DOI:10.1038/nbt.2421; Conesa, A., et al. (2016) A survey of best practices for RNA-seq data analysis. Genome Biology, 17:13, DOI:10.1186/s13059-016-0881-8; Landt, S.G., et al. (2012) ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. Genome Research, 22(9):1813–31, DOI:10.1101/gr.136184.111.

Unit 3: Data Integration and Biocuration -- Overview of Biocuration, various approaches for biocuration, BioDbCore guidelines, FAIRsharing and ethics in data sharing, Text/Literature-based curation, text mining approaches, and an introduction to tools such as Textpresso. Basics and importance of ontology development, OBO (Open Biological and Biomedical Ontology) format, OBO foundary, biomedical and plant-based ontologies.

10 hours

Essential Readings: Gaudet, P., et al. (2011) Towards BioDBcore: a community-defined information specification for biological databases. Nucleic Acids Research, 39(s1):D7–D10, DOI:10.1093/nar/gkq1173; Open Biological and Biomedical Ontology Foundry: Community development of interoperable ontologies for the biological sciences, https://obofoundry.org/about-OBO-Foundry.html; FAIRsharing: A curated, informative and educational resource on data and metadata standards, inter-related to databases and data policies, https://fairsharing.org, DOI:10.1038/s41587-019-0080-8; Howe, D., et al. (2008) The future of biocuration. Nature, 455:47–50, DOI:10.1038/455047a; Wilkinson, M.D., et al. (2016) The FAIR Guiding Principles for scientific data management and stewardship. Scientific Data, 3:160018, DOI:10.1038/sdata.2016.18.

Unit 4: Artificial Intelligence in Life Sciences -- Introduction to Machine-Learning (ML) and Artificial Intelligence (AI); Supervised and unsupervised learning approaches in data integration, interpretation, and predictive modelling; Applications in genomic prediction, drug discovery, ecosystem modelling; Domain-specific Large Language Models (LLMs). 10 hours

Essential Readings: Cannataro, M., et al. (2022) Artificial Intelligence in Bioinformatics: from omics analysis to deep learning and network mining, 1st edition, Elsevier, eISBN:9780128229293; Jumper, J., et al. (2021) Highly accurate protein structure prediction with AlphaFold. Nature, 596:583–589, DOI:10.1038/s41586-021-03819-2.

Tutorials (15 hours)

1. Practice of working with Linux commands on the Command Line Interface (CLI).
2. Analysis of RNA-seq data:
    a. Quality and adapter trimming of Next Generation Sequencing (NGS) data.
    b. Reference-based genome mapping of NGS data.
    c. Identification of differentially expressed genes.
3. Use of Gene Ontology for gene function analysis.

Suggested Readings:

1. Bessant, C., et al. (2014) Building bioinformatics solutions with Perl, R, and SQL. 2nd edition, Oxford University Press, UK, ISBN:978019965855.
2. Buffalo, V. (2015) Bioinformatics data skills: Reproducible and robust research with open-source tools. O'Reilley Media, ISBN:9781449367374.
3. Quince, C., et al. (2017) Shotgun metagenomics, from sampling to analysis. Nature Biotechnology, 35(9):833–844, DOI:10.1038/nbt.3935.
4. Sansone, S.A., et al. (2019) FAIRsharing as a community approach to standards, repositories and policies, Nature Biotechnology, 37(4):358–367, DOI:10.1038/s41587-019-0080-8.
5. Smith, B., et al. (2007) The OBO Foundry: coordinated evolution of ontologies to support biomedical data integration, Nature Biotechnology, 25(11):1251–1255, DOI:10.1038/nbt1346.
6. Müller, H.M., et al. (2018) Textpresso Central: a customizable platform for searching, text mining, viewing, and curating biological literature. BMC Bioinformatics, 19:94, DOI:10.1186/s12859-018-2103-8.
7. Web link: www.bioconductor.org
8. Web link: www.obofoundary.org; www.oboedit.org
9. Web link: www.biocuration.org

PBSE415: Plant Phenomics

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE415: Plant Phenomics	4	3	1	0	B.Sc. in any branch of science	

Course Objectives

This course aims to introduce students to the conceptual and methodological foundations of plant phenomics, spanning trait ontology, G×E×M frameworks, and robust experimental design. It seeks to familiarise students with controlled-environment and field phenotyping platforms, diverse imaging modalities, and 3D architectural reconstruction. A further objective is to develop competence in end-to-end phenomics data pipelines, from image acquisition to quantitative trait extraction and machine-learning-based modelling, enabling critical engagement with current literature and applications in crop improvement and stress biology.

Learning Outcomes

Upon successful completion, students will be able to define and differentiate plant phenomics from classical phenotyping, design basic phenotyping experiments with appropriate traits, platforms and metadata, and justify these choices. They will interpret and compare outputs from RGB, fluorescence, thermal, spectral and 3D imaging in controlled and field settings. Students will execute simple image-analysis workflows, apply elementary machine learning for phenotypic data, critically evaluate published phenomics studies, and articulate how phenomics informs breeding, resilience and systems-level plant biology.

Course Content (45 hours)

Unit 1: Foundations of Plant Phenomics and Trait Biology -- Definition and scope of plant phenomics; Distinction between classical phenotyping and high-throughput phenomics; Links to functional genomics, systems biology, and crop improvement; Trait ontology (morphological, physiological, developmental, functional traits); G×E×M (genotype× environment×management) framework; Principles of experimental design (replication, randomisation, blocking, temporal sampling); Metadata standards and FAIR (Findable, Accessible, Interoperable, and Reusable) data; Evolution of phenotyping platforms and international phenomics networks; Ideotype concepts and gene-to-phenotype mapping.

12 hours

Essential Readings: Chen, J.T. (2025) Plant high-throughput phenotyping and functional phenomics. CRC Press, eISBN:9781003505631, DOI:10.1201/9781003505631, Chapter 2 (Plant high-throughput phenotyping and phenomics for accelerating crop breeding), Chapter 9 (High-throughput phenotyping and phenomics for exploration of plant growth and development), Chapter 13 (High-throughput plant phenotyping and phenomics: Advances and prospects); Fiorani, F. and Schurr, U. (2013) Future scenarios for plant phenotyping. Annual Review of Plant Biology, 64:267–291, DOI:10.1146/annurev-arplant-050312-120137; Papoutsoglou, E.A., et al. (2023) The benefits and struggles of FAIR data: the case of reusing plant phenotyping data. Scientific Data, 10(1):595, DOI:10.1038/s41597-023-02364-z.

Unit 2: Controlled-Environment Phenomics and Imaging Modalities -- Growth chamber and greenhouse phenotyping platforms; conveyor- and chamber-based systems; Longitudinal monitoring of growth and development; RGB (Red, Green, and Blue) imaging for morphology, colour indices, and growth curves; Chlorophyll fluorescence imaging (PSII efficiency, stress signatures); Thermal imaging (canopy temperature, transpiration proxies); Multispectral and hyperspectral imaging for pigment and biochemical traits; Controlled root phenotyping [rhizotrons, gel systems, CT (Computed Tomography)/MRI (Magnetic Resonance Imaging) concepts]; Calibration, illumination control, reference standards; Time-series design for controlled-environment stress and treatment experiments. 10 hours

Essential Readings: Lorence, A. and Jimenez, K.M. (2022) High-throughput plant phenotyping: Methods and Protocols. Methods in Molecular Biology. Humana New York, ISBN:9781071625361, DOI:10.1007/978-1-0716-2537-8, Chapter 5 (A straightforward high-throughput aboveground phenotyping platform for small- to medium-sized plants), Chapter 6 (Wireless fixed camera network for greenhouse-based plant phenotyping), Chapter 7 (Experimental design for controlled environment high-throughput plant phenotyping); Zhang, Y. and Zhang, N. (2018) Imaging technologies for plant high-throughput phenotyping: a review. Frontiers of Agricultural Science and Engineering, 5(4):406–419, DOI:10.15302/J-FASE-2018242; Mahlein, A.K., et al. (2018) Hyperspectral sensors and imaging technologies in phytopathology: state of the art. Annual Review of Phytopathology, 56:535–558, DOI:10.1146/annurev-phyto-080417-050100.

Unit 3: Field Phenomics, Remote Sensing, and 3D Architecture -- Fixed gantry, tractor-/robot-mounted and handheld phenotyping systems; UAV(Unmanned Aerial Vehicle)-based phenotyping with RGB, multispectral, and hyperspectral sensors; Vegetation indices (NDVI (Normalized Difference Vegetation Index), NDRE (Normalized Difference Red Edge Index), etc. for growth, water and nutrient status; Canopy temperature mapping; LiDAR and stereo vision for 3D reconstruction; Point clouds and structural traits; Integration of environmental data with phenotypic measurements; Spatial heterogeneity and experimental layout; Applications in breeding across diverse field environments. 12 hours

Essential Readings: Chen, J.T. (2025) Plant high-throughput phenotyping and functional phenomics. CRC Press, eISBN:9781003505631, DOI:10.1201/9781003505631, Chapter 3 (Remote sensing technologies for high-throughput in-field crop phenotyping, Chapter 4 (High-Throughput field phenotyping: Enhancing crop monitoring for food security), Chapter 10 (Root phenotyping for breeding of climate-resilient crops), Chapter 16 (Robotics and aerial vehicle for high-throughput phenotyping: technologies and prospects); Araus, J.L. and Cairns, J.E. (2014) Field high-throughput phenotyping: the new crop breeding frontier. Trends in Plant Science, 19(1):52–61, DOI:10.1016/j.tplants.2013.09.008; Guo, W., et al. (2021) UAS-based plant phenotyping for research and breeding applications. Plant Phenomics, 2021:9840192, DOI:10.34133/2021/9840192.

Unit 4: Data Pipelines, Image Analysis, and Machine Learning in Phenomics -- End-to-end phenomics data pipeline (acquisition, pre-processing, segmentation, feature extraction, trait computation); Use of ImageJ/Fiji, PlantCV and related open-source tools; Machine learning for phenotyping; Deep learning and CNNs for segmentation, Classification and regression; Model training, validation and evaluation; Phenomic features in GWAS, genomic prediction and phenomic selection; Data management, reproducibility, model transferability and interpretability. 11 hours

Essential Readings: Chen, J.T. (2025) Plant high-throughput phenotyping and functional phenomics. CRC Press, eISBN:9781003505631, DOI:10.1201/9781003505631, Chapter 1 (Bioinformatics tools and deep learning for plant high-throughput phenotyping and phenomics), Chapter 15 (Statistical tools and data analysis for organizing plant high-throughput phenomics); Murphy, K.M., et al. (2024) Deep learning in image-based plant phenotyping. Annual Review of Plant Biology, 75:771–795, DOI:10.1146/annurev-arplant-070523-042828; Danilevicz, M.F., et al. (2021) Resources for image-based high-throughput phenotyping in crops and data sharing challenges. Plant Physiology, 187(2):699–715, DOI:10.1093/plphys/kiab301.

Tutorials (15 hours)

1. Short presentations on landmark phenomics papers.
2. Designing a basic phenotyping experiment (traits, platform, experimental design, metadata sheet).
3. Hands-on demonstrations with sample image datasets.
4. Analysis of PSII efficiency (Fv/Fm) and photosynthetic activity [fluorescence decline ratio in steady state (Rfd_*Lss*)] in control and stressed plants.

Suggested Readings:

1. Chen, J.T. (2025) Plant high-throughput phenotyping and functional phenomics. CRC Press, ISBN:9781003505631, DOI:10.1201/9781003505631.
2. Lorence, A. and Jimenez, K.M. (2022) High-throughput plant phenotyping: Methods and Protocols. Methods in Molecular Biology, Humana New York, DOI:10.1007/978-1-0716-2537-8.
3. Awada, L., et al. (2024) The evolution of plant phenomics: Global insights, trends, and collaborations (2000-2021). Frontiers in Plant Science, 15:1410738, DOI:10.3389/fpls.2024.1410738.
4. Großkinsky, D.K., et al. (2023) The potential of integrative phenomics to harness underutilized crops for improving stress resilience. Frontiers in Plant Science, 14:1216337, DOI:10.3389/fpls.2023.1216337.
5. Singh, A., et al. (2016) Machine learning for high-throughput stress phenotyping in plants. Trends in Plant Science, 21(2):110–124, DOI:10.1016/j.tplants.2015.10.015.
6. Abebe, A.M., et al. (2023) Image-based high-throughput phenotyping in horticultural crops. Plants, 12(10):2061, DOI:10.3390/plants12102061.
7. Xu, R. and Li, C. (2022) A review of high-throughput field phenotyping systems: Focusing on ground robots. Plant Phenomics, 2022:9760269, DOI:10.34133/2022/9760269.
8. Gano, B., et al. (2024) Drone-based imaging sensors, techniques, and applications in plant phenotyping for crop breeding: A comprehensive review. The Plant Phenome Journal, 7(1): e20100, DOI:10.1002/ppj2.20100.
9. Li, S., et al. (2025) A review of optical-based three-dimensional reconstruction and multi-source fusion for plant phenotyping. Sensors, 25(11):3401, DOI:10.3390/s25113401.
10. Su, M., et al. (2025) Design and implementation of high-throughput field phenotyping robot for acquiring multisensory data in wheat. Plant Phenomics, 7(2):100014, DOI:10.1016/j.plaphe.2025.100014.
11. Adak, A., et al. (2023) Phenomic data-driven biological prediction of maize through field-base high-throughput phenotyping integration with genomic data. Journal of Experimental Botany, 74(17):5307–5326, DOI: 0.1093/jxb/erad216.
12. Zavafer, A., et al. (2023) Phenomics: conceptualization and importance for plant physiology. Trends in Plant Science, 28(9):1004–1013, DOI:10.1016/j.tplants.2023.03.023.
13. Lichtenthaler, H.K. and Miehé, J.A. (1997) Fluorescence imaging as a diagnostic tool for plant stress. Trends in Plant Science, 2(8):316–320, DOI:10.1016/S1360-1385(97)89954-2.

PBSE416: Synthetic Biology

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE416: Synthetic Biology	4	3	1	0	B.Sc. in any branch of science	NA

Learning Objectives

This course introduces the foundational and applied aspects of synthetic biology with a focus on plants and microbial chassis used in plant biotechnology. It integrates principles of genetic circuit design, genome refactoring, metabolic engineering, and synthetic ecosystems. Special emphasis is placed on synthetic *E. coli* as a design chassis and on plant-based biohybrid systems, such as photovoltaic cells, that merge biological and artificial components for sustainable energy and agricultural innovation.

Learning Outcomes

Students will understand theoretical and design principles of synthetic biology across systems. They will be able to apply genetic circuit and metabolic pathway engineering to plants and microbes. They will evaluate *E. coli* as a chassis for producing plant metabolites, explore biohybrid innovations like plant photovoltaic cells and synthetic photosynthesis, and recognize biosafety, ethical, and policy issues in synthetic biology research.

Course Content (45 hours)

Unit 1: Principles and Foundations of Synthetic Biology -- Definition, concept, and evolution of synthetic biology; Historical milestones; Comparison with conventional genetic engineering; Minimal genomes and synthetic cells; Jargons of Synbio: parts, devices, systems, modules, chassis, orthogonality, retroactivity; Modularity and chassis optimization for plants and microbes. 8 hours

Essential Readings: Brenner, S.A. and Sismour, A.M. (2005) Synthetic biology. Nature Reviews Genetics 6(7):533–543, DOI:10.1038/nrg1637; Andrianantoandro, E., et al. (2006) Synthetic biology: new engineering rules for an emerging discipline. Molecular Systems Biology, 2:MSB4100073, DOI:10.1038/msb4100073; Garner, K.L. (2021) Principles of synthetic biology. Essays in Biochemistry, 65(5):791–811, DOI:10.1042/EBC20200059; Wang, Y. and Demirer, G.S. (2023) Synthetic biology for plant genetic engineering and molecular farming. Trends in Biotechnology 41(9):1182–1198, DOI:10.1016/j.tibtech.2023.03.007; Nemhauser, J.L., and Torii, K.U. (2016) Plant synthetic biology for molecular engineering of signalling and development. Nature Plants, 2:16010, DOI:10.1038/nplants.2016.10; Kocaoglan, E.G., et al. (2023) Synthetic developmental biology: molecular tools to re-design plant shoots and roots. Journal of Experimental Botany, 74(13):3864–3876, DOI:10.1093/jxb/erad169.

Unit 2: Synthetic *E. coli* as a Model Chassis -- Genome refactoring and minimal *E. coli* genomes; Design and assembly of synthetic operons for metabolite production; Genetic circuits; Synthetic biosensors and quorum-sensing modules; Heterologous expression of plant pathways in *E. coli* for establishing biomanufacturing platform 10 hours

Essential Readings: Chi, H., et al. (2019) Engineering and modification of microbial chassis for systems and synthetic biology. Synthetic and Systems Biotechnology, 4(1):25–33, DOI:10.1016/j.synbio.2018.12.001; Reiter, M.A., et al. (2024) A synthetic methylotrophic *Escherichia coli* as a chassis for bioproduction from methanol. Nature Catalysis, 7:560–573, DOI:10.1038/s41929-024-01137-0.

Unit 3: Biological Circuits and Network Engineering -- Design of genetic circuits: requirements, tools, and techniques; Modelling of gene circuits (basic ODE modelling of biological systems with MATLAB, introduction to Cello: genetic circuit design automation software); Creating large-scale biological circuits and regulatory networks; Multi-gene network construction and *in silico* simulations. 12 hours

Essential Readings: Elnaggar, K.S., et al. (2025) A guide in synthetic biology: Designing genetic circuits and their applications in stem cells. SynBio 3(3):11. DOI:10.3390/synbio3030011; Müller, M.M., et al. (2025) Genetic circuits in synthetic biology: broadening the toolbox of regulatory devices. Frontiers in Synthetic Biology, 3:1548572. DOI:10.3389/fsybi.2025.1548572.

Unit 4: Plant Synthetic Biology and Biohybrid Systems -- Gene circuit design in plants: requirements, tools, and techniques; Engineering photosynthesis, photorespiration, and carbon fixation pathways; Chloroplast genome engineering and minimal plastomes; Metabolic engineering for nutraceuticals, industrial products, etc.; Plant-based photovoltaic cells; Case studies on Spinach leaf photovoltaic (PV) devices, cytochrome-based photoanodes; Synthetic nitrogen fixation and carbon sequestration in plants; Machine learning and AI-assisted circuit optimization; Biocontainment and genetic firewalls; Ethical, legal, and biosafety frameworks; Future prospects: cell-free systems, synthetic organelles. 15 hours

Essential Readings: Goshisht, M.K. (2024) Machine learning and deep learning in synthetic biology: Key architectures, applications, and challenges. ACS Omega, 9:9921–45, DOI:10.1021/acsomega.3c05913; Kurtoğlu, A., et al. (2024) The view of synthetic biology in the field of ethics: a thematic systematic review. Frontiers in Bioengineering and Biotechnology, 12:1397796, DOI:10.3389/fbioe.2024.1397796; Hynek, N. (2025) Synthetic biology/AI convergence (SynBioAI): security threats in frontier science and regulatory challenges. AI & Society, DOI:10.1007/s00146-025-02576-4; Arya, R., et al. (2025) New techniques of genetic engineering in agriculture: Innovations, applications, and future prospects. International Journal of Advanced Biochemistry Research, 9(4):166–174, DOI:10.33545/26174693.2025.v9.i4c.4066; Zhang, D., et al. (2025) Synthetic biology and artificial intelligence in crop improvement. Plant Communications, 6(2):101220, DOI:10.1007/s00146-025-02576-4.

Tutorials (15 hours)

Case studies of:

a. *Escherichia coli* as a chassis for the production of plant metabolites.
b. Synthetic photosynthesis.
c. Synthetic cell.
d. Carbon sequestration.

Suggested Readings:

1. Davies, J.A. (2018) Synthetic Biology: A very short introduction. Oxford University Press, ISBN:9780198803492, DOI:10.1093/actrade/9780198803492.001.0001.
2. Zhang, W. and Nielsen, D.R. (2014) Synthetic biology applications in industrial microbiology. Frontiers in Microbiology, 5(313):451, DOI:10.3389/fmicb.2014.00451.
3. Zhao, H. (2013) Synthetic biology: tools and applications. Academic Press, ISBN:9780123944306, DOI:10.1016/C2011-0-06857-6.
4. Freemont, P.S. and Kitney, R.I. (2015) Synthetic Biology - A Primer. Imperial College Press, ISBN:9781783268795.
5. Voigt, C.A. (2020) Synthetic biology 2020–2030: six commercially-available products that are changing our world. Nature Communications, 11:6379, DOI:10.1038/s41467-020-20122-2.

PBSEC417: Advanced Research Methodology

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSEC417: Advanced Research Methodology	2	1	0	1	B.Sc. in any branch of science	NA

Learning Objectives

This course aims to provide students with an in-depth conceptual understanding of advanced research methodologies applied in molecular plant sciences. It emphasizes experimental design, interpretation, and analysis in the context of gene function, regulatory networks, and crop improvement. The course also aims to establish a solid foundation for critically evaluating experimental data, formulating hypotheses, and communicating scientific findings in plant biology research.

Learning Outcomes

Upon successful completion of this course, students will develop a comprehensive understanding of advanced research methodologies in plant molecular biology. They will be able to conceptualize and design theoretical frameworks for gene function analysis, regulatory network mapping, and crop improvement experiments. Students will gain the ability to integrate bioinformatics insights with molecular and genetic approaches to interpret gene and protein function. Furthermore, they will gain an understanding of the conceptual underpinnings of genome editing, regulatory pathway analysis, and experimental data validation. The course will enhance their skills in critical thinking and experimental design in plant molecular biology research.

Course Content (15 hours)

Unit 1: Experimental Design for Gene Function Analysis -- Experimental frameworks for dissecting gene function and regulatory cascade in plants; Conceptual foundations of gene/protein function prediction, principles of homology, conserved domain identification, integration networks and database search; Principles of experimental design for gene over-expression and knock-out/knock-down studies, mutant analysis, and genetic mapping; Protein localization studies; Elucidation of genetic regulatory cascades. 10 hours

Essential Readings: Robles, J.A., et al. (2012) Efficient experimental design and analysis strategies for the detection of differential expression using RNA-Sequencing. BMC Genomics, 13:484, DOI:10.1186/1471-2164-13-484; Grondin, A., et al. (2024) A case study from the overexpression of OsTZF5, encoding a CCCH tandem zinc finger protein, in rice plants across nineteen yield trials. Rice, 17(1):25, DOI:10.1186/s12284-024-00705-z; Tang, M., et al. (2021) A genome-scale TF–DNA interaction network of transcriptional regulation of *Arabidopsis* primary and specialized metabolism. Molecular Systems Biology, 17(11):e10625, DOI:10.15252/msb.202110625; https://www.goldenhelix.com/blog/stop-ignoring-experimental-design-or-my-head-will-explode/; https://www.ncbi.nlm.nih.gov/books/NBK26818/; Wagner, M.R., and Kleiner, M. (2025) How thoughtful experimental design can empower biologists in the omics era. Nature Communications, 16(1):7263, DOI:10.1038/s41467-025-62616-x; Boadu, F., (2025) Deep learning methods for protein function prediction. Proteomics, 25(1-2):e2300471, DOI:10.1002/pmic.202300471; Goodin, M.M. (2018) Advances in virus research. 100:117-144, DOI:10.1016/bs.aivir.2017.10.004, Chapter 6 (Protein localization and interaction studies in plants: Toward defining complete proteomes by visualization).

Unit 2: Experimental Frameworks for Crop Improvement by Genome Editing -- Experimental frameworks for designing molecular and genetic strategies for crop improvement; CRISPR-based strategies for gain-of-function and loss-of-function of genes for enhanced agronomic traits; Validation of transgene-free plants, Field trials and regulations regarding the release of genome-edited crops. 5 hours

Essential Readings: Graham, D.B. and Root, D.E. (2015) Resources for the design of CRISPR gene editing experiments. Genome Biology, 16:260, DOI:10.1186/s13059-015-0823-x; Zhou, J., et al. (2023) An efficient CRISPR–Cas12a promoter editing system for crop improvement. Nature Plants, 9(4):588–604, DOI:10.1038/s41477-023-01384-2; Han, X., et al. (2025) Genetic engineering, including genome editing, for enhancing broad-spectrum disease resistance in crops. Plant Communications, 6(2):101195, DOI:10.1016/j.xplc.2024.101195; Hanna, R.E. and Doench, J.G. (2020) Design and analysis of CRISPR-Cas experiments. Nature Biotechnology, 38(7):813–823, DOI:10.1038/s41587-020-0490-7.

Practicals (30 hours)

1. Analysis of conserved protein motifs using WebLogo and interpreting functional domains of a protein family.
2. Development of transgenic hairy roots using RNAi or promoter–*uidA* binary vector constructs.
3. Analysis of stress-induced promoter activity *in planta* using non-destructive methods.
4. *In silico* design of a vector for transgene-free plant genome editing using TnpB.
5. Design and application of CAPS/dCAPS markers to identify and validate single-base substitutions or targeted genome edits.

Suggested Readings:

1. Buchanan, B.B. et al. (2015) Biochemistry and molecular biology of the plants. 2nd edition, WILEY Blackwell, ISBN:9780470714218.
2. Singh, P.P., and Benayoun, B.A. (2023) Considerations for reproducible omics in aging research. Nature Aging, 3(8):921–930, DOI:10.1038/s43587-023-00448-4;
3. Conesa, A., et al. (2016) A survey of best practices for RNA-seq data analysis. Genome Biology, 17:13, DOI:10.1186/s13059-016-0881-8.
4. Haas, R., et al. (2017) Designing and interpreting 'multi-omic' experiments that may change our understanding of biology. Current Opinion in Systems Biology, 6:37–45, DOI:10.1016/j.coisb.2017.08.009.
5. Strotmann, V.I. and Stahl, Y. (2022) Visualization of *in vivo* protein-protein interactions in plants. Journal of Experimental Botany, 73(12):3866–3880, DOI:10.1093/jxb/erac139.
6. Quattrocchio, F.M., et al. (2013) Transgenes and protein localization: myths and legends. Trends in Plant Science, 18(9):473–476, DOI:10.1016/j.tplants.2013.07.003.
7. Lichocka, M. and Schmelzer, E. (2014) Subcellular localization experiments and FRET-FLIM measurements in plants. Bio-Protocol, 4(1):e1018, DOI:10.21769/BioProtoc.1018.
8. Zhang, Y., et al. (2023) Investigating the dynamics of protein-protein interactions in plants. The Plant Journal, 114(4):965–983, DOI:10.1111/tpj.16182.
9. Teng, C. (2024) Killing two birds with one stone: A breakthrough in transgene-free gene editing in soybean. Plant Physiology, 196(4):2263–2265, DOI:10.1093/plphys/kiae526.
10. Ricroch, A., et al. (2024) Worldwide study on field trials of biotechnological crops: new promises but old policy hurdles. Frontiers in Plant Science, 15:1452767, DOI:10.3389/fpls.2024.1452767.
11. https://dbtindia.gov.in/sites/default/files/Final_%2011052022_Annexure-I%2C%20Genome_Edited_Plants_2022_Hyperlink.pdf

Structure 2 - PG with Coursework & Research

SEMESTER 3

PBSC321: Plant Biotechnology

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSC321: Plant Biotechnology	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

This course will enable students to understand the core principles and milestones of plant biotechnology, including the molecular basis of crop domestication and Green Revolution traits, as well as concepts in tissue culture. Students will learn about the molecular toolbox for plant genetic engineering and be introduced to advanced approaches, including RNAi, genome editing, and synthetic biology, for pathway engineering. The course will build conceptual understanding of modern gene/QTL mapping, marker-assisted and genomic selection, speed breeding, and gene pyramiding, together with applications of plant biotechnology in molecular farming, biofortification, climate resilience, plant-microbe interactions, and industrial and environmental biotechnology. Finally, students will be sensitized to biosafety guidelines, GMO risk assessment, IPR, farmers' rights, and ethical and societal issues in plant biotechnology.

Learning Outcomes

On completing the course, students will be able to explain and apply tissue culture and related technologies for crop improvement. They will be able to outline and compare plant transformation and genome editing strategies, design genetic constructs and describe workflows for the generation and characterization of transgenic and edited plants. Students will be able to select appropriate molecular markers and mapping approaches for dissecting complex traits, and integrate marker-assisted selection, genomic selection, and breeding pipelines. They will be able to critically analyse case studies such as Golden rice, Bt cotton, virus-resistant papaya, and DH mustard, among others. In addition, they will be able to interpret biosafety and regulatory frameworks, IPR/PBR/farmer's rights provisions, and articulate ethical, social, and policy implications of deploying plant biotechnological innovations in agriculture.

Course Content (45 hours)

Unit 1: Fundamentals and Scope of Plant Biotechnology -- Concept, history, and milestones in plant biotechnology; Molecular basis of crop domestication and Green revolution; Principles of plant tissue culture, totipotency, and micropropagation; Somaclonal variation, somatic embryogenesis, and synthetic seeds; Protoplast fusion and somatic hybridization. 5 hours

Essential Readings: Stewart Jr., C.N. (2025) Biotechnology and Genetics: Principles, Techniques, and Applications. 3rd edition, John Wiley & Sons, ISBN:9781394217236, Chapter 1 (Plant Agriculture: The impact of biotechnology); Abdin, M.Z, et al. (2017) Plant Biotechnology: Principles and Applications, Springer Verlag,

Singapore, ISBN:9789811029592, Chapter 1 (Historical perspective and basic principles of plant tissue culture), Chapter 2 (Plant tissue culture: Applications in plant improvement and conservation); Pathirana, R. and Carimi, F. (2024) Plant biotechnology-an indispensable tool for crop improvement. Plants (Basel), 13(8):1133, DOI:10.3390/plants13081133.

Unit 2: Molecular Tools and Techniques -- Genetic cloning strategies and vector systems; Promoters, selectable markers, and reporter genes; Gene transfer methods; Chloroplast transformation; Characterization of transgenic plants at molecular, biochemical, and phenotypic level; Case studies: Golden rice, Bt cotton, virus-resistant papaya, herbicide-tolerant crops, Dhara Mustard, any other product; Virus-induced gene silencing (VIGS) methods; Genome editing technologies [Zinc Finger Nucleases, Transcription activator-like effector nucleases, Clustered Regularly Interspaced Short Palindromic Repeats or CRISPR)/CRISPR-associated (Cas) systems, prime editing, base editing, and miniature RNA-guided endonuclease]; Generation of marker-free transgenics; RNAi interference (RNAi); Introduction of synthetic biology and metabolic pathway engineering. 15 hours

Essential Readings: Li, B., et al. (2024) Targeted genome-modification tools and their advanced applications in crop breeding. Nature Reviews Genetics, 25(9):603–622, DOI:10.1038/s41576-024-00720-2; Liu, W., et al. (2013) Advanced genetic tools for plant biotechnology. Nature Review Genetics, 14:781–793, DOI:10.1038/nrg3583; Gupta, O.P. and Karkute, S.G. (2021) Genome editing in plants: Principles and applications, CRC Press, ISBN:9780367415907, Chapter 1 (Historical developments of genome editing in plants), Chapter 2 (Mechanism of ZFN mediated genome editing: scope and opportunities), Chapter 3 (TALEN: customizable molecular scissors for tailoring newer types of genomes in plants), Chapter 4 (Mechanism of CRISPR/Cas9 mediated genome editing: scope and opportunities); Koeppe, S., et al. (2023) RNA interference: past and future applications in plants, International J. Molecular Science, 24(11):9755, DOI: 10.3390/ijms24119755; Singh, R., et al. (2023) A prospective review on selectable marker-free genome engineered rice: past, present and future scientific realm, Frontiers in Genetics, 13:2022, DOI:10.3389/fgene.2022.882836; Aaron, S., et al. (2020) Metabolic engineering and synthetic biology of plant natural products – A minireview. Current Plant Biology, 24:100163, DOI:10.1016/j.cpb.2020.100163.

Unit 3: Mapping of Genes/QTLs -- High-throughput molecular markers and genotyping assays; Bulk segregant analysis (QTL-seq), Target-Sequence Enrichment and Sequencing (TEnSeq), Resistance gene enrichment sequencing (RenSeq), and Mutation mapping (MutMap, MutMap-Gap, etc); Genome-Wide Association Studies (GWAS); Marker-assisted plant breeding and genomic selection (GS); Speed breeding; Gene Pyramiding; Hybrid breeding and doubled haploid technologies. 15 hours

Essential Readings: Jaganathan, D., et al. (2020) Fine mapping and gene cloning in the post-NGS era: advances and prospects. Theoretical and Applied Genetics, 133(5):1791–1810, DOI:10.1007/s00122-020-03560-w; Wang, X., et al. (2023) Next-generation bulked segregant analysis for Breeding 4.0. Cell Reports, 42(9):113039, DOI:10.1016/j.celrep.2023.113039; Uffelmann, E., et al. (2021) Genome-wide association studies. Nature Reviews Methods Primers, 1:59, DOI:10.1038/s43586-021-00056-9; Kabade, P.G., et al. (2025) Speed breeding 3.0: mainstreaming light-driven plant breeding for sustainable genetic gains. Trends in Biotechnology, 43(10):2462–2478, DOI:10.1016/j.tibtech.2025.04.011; Crossa, J., et al. (2017) Genomic selection in plant breeding: methods, models, and perspectives, Trends in Plant Science, 22(11):961–975, DOI:10.1016/j.tplants.2017.08.011; Qu, Y., et al. (2024) Doubled haploid technology and synthetic apomixis: Recent advances and applications in future crop breeding. Molecular Plant, 17(7):1005–1018, DOI:10.1016/j.molp.2024.06.005.

Unit 4: Applications and Societal Aspects of Plant Biotechnology -- Molecular farming; Biofortification and nutritional enhancement; Manipulating and harnessing plant-microbe interactions: disease resistant plants, biofertilizers, biopesticides, and mycorrhizal biotechnology; Climate-resilient crops: generation of abiotic stress tolerant plants; Industrial Biotechnology: bioethanol and other products; Environmental biotechnology: phytoremediation; Regulatory frameworks: biosafety guidelines, GMO risk assessments, and

intellectual property rights (IPR); Plant breeders' rights (PBRs) and farmers' rights; Ethical, social, and policy implications of plant biotechnology. 10 hours

Essential Readings: Shanmugaraj, B., et al. (2020) Plant molecular farming: A viable platform for recombinant biopharmaceutical production. Plants, 9(7):842, DOI:10.3390/plants9070842; Garg, M., et al. (2024) Biofortification for nutrient-rich crops. ISBN:9781032690636, DOI:10.1201/9781032690636; Digel, I., et al. (2025) Introduction to Industrial Biotechnology, Springer Cham, ISBN:9783032079183, DOI:10.1007/978-3-032-07918-3; Abdin, M.Z., et al. (2017) Plant Biotechnology: Principles and Applications, Springer Verlag, Singapore, ISBN:9789811029592, Chapter 14 (Biosafety, Bioethics, and IPR Issues in Plant Biotechnology); Protection of plant varieties and farmers' right act (PPV & FR), 2001, Ministry of Agriculture and Farmers Welfare, GoI; Standard Operating Procedures for regulatory review of genome edited plants under SDN-1 and SDN-2 categories 2022 and Guidelines on genetically engineered plants containing stacked events 2025 by Department of Biotechnology, MoS&T, GoI.

Practicals (30 hours)

1. Assessment of promoter activity in transgenic plants using beta-glucuronidase (GUS) reporter through histochemical staining and fluorometric (MUG) assays.
2. To perform PCR-based screening of *Arabidopsis* T-DNA insertion lines to distinguish heterozygous and homozygous plants.
3. Genome editing of a target gene in a plant (GFP/transient assay).
4. T7E1/ Surveyor mismatch cleavage assays to detect mutated/edited genomic regions.
5. Construction of a plant genetic linkage map with molecular markers.

Suggested Readings:

1. Acquaah, G. (2020) Principles of Plant Genetics and Breeding, 3rd edition, Wiley-Blackwell, ISBN:9781119626695.
2. Al-Khayri, J.M., et al. (2025) Genome Editing for Crop Improvement - Theory and Methodology. CAB International, ISBN:9781800622494.
3. Hille, F., et al. (2018) The biology of CRISPR-Cas: Backward and forward. Cell, 172(6):1239–1259, DOI:10.1016/j.cell.2017.11.032.
4. Singh, B.D. and Singh, A.K. (2015) Marker-Assisted Plant Breeding: Principles and Practices, Springer New Delhi, ISBN:9788132223160, DOI:10.1007/978-81-322-2316-0.
5. Clauw, P., et al. (2025) Beyond the standard GWAS-A guide for plant biologists. Plant and Cell Physiology, 66(4):431–443, DOI:10.1093/pcp/pcae079.
6. Quiroz, L.F., et al. (2024) Haploid rhapsody: the molecular and cellular orchestra of *in vivo* haploid induction in plants. New Phytologist, 241(5):1936–1949, DOI:10.1111/nph.19523.
7. Ghosh, S., et al. (2018) Speed breeding in growth chambers and glasshouses for crop breeding and model plant research. Nature Protocols, 13:2944–2963, DOI:10.1038/s41596-018-0072-z.
8. Chen, J.T. (2024) Plant speed breeding and high-throughput technologies, CRC Press, ISBN: 9781003434733.
9. Xiong, J., et al. (2023) Synthetic apomixis: the beginning of a new era. Current Opinion in Biotechnology, 79:102877, DOI:10.1016/j.copbio.2022.102877.
10. WHO (2004) Laboratory Biosafety Manual, 3rd edition
11. FAO (2018) Biosafety Primer.
12. Department of Biotechnology (DBT), MoS&T, GoI (2023) Intellectual Property Guidelines.
13. Scientific Journals: Plant Biotechnology Reports; International Journal of Plant Biotechnology; Plant Biotechnology Journal; Transgenic Research; Journal of Plant Biotechnology; Plant Cell, Tissue and Organ Culture.
14. Singh, K.K. (2014) Biotechnology and intellectual property rights-legal and social implications. ISBN:9788132220596, DOI:10.1007/978-81-322-2059-6.

PBSC322: Molecular Plant Breeding

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSC322: Molecular Plant Breeding	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

Molecular breeding has greatly advanced human agriculture by enabling the continuous improvement of food and industrial crops. This paper introduces students to the foundations of classical breeding, quantitative genetics, and plant genetic resources, while also covering advanced molecular methods, including marker-assisted selection, QTL mapping, genomic selection, and hybrid breeding technologies. By integrating conventional and modern techniques, the course highlights how new, high-performing crop varieties are developed to meet global demands for productivity, quality, and stress resilience.

Learning Outcomes

Students will be able to understand the historical foundations and objectives of plant breeding and crop genetics beyond model plant systems. They will be able to distinguish between breeding methods across reproductive systems and the application of molecular tools to enhance crop quality at the field level. It will equip them to understand and evaluate global molecular breeding efforts, integrate genetic modification with modern breeding practices, and apply strategies to enhance yield, quality, and stress tolerance.

Course Contents (45 hours)

Unit 1: Plant breeding -- Introduction and history of breeding; Breeding objectives and crop traits; Principles of population and quantitative genetics; Plant genetic resources and crop domestication; Breeding in self-pollinated, cross-pollinated, and clonally propagated species; Concept of molecular breeding. 12 hours

Essential Readings: Acquaah, G. (2021) Principles of Plant Genetics and Breeding, 3rd Edition, Wiley Blackwell, ISBN:9781119626329; Singh, D.P., et al. (2021) Plant Breeding and Cultivar Development, Academic Press, ISBN:9780128175637, DOI:10.1016/C2018-0-01730-2.

Unit 2: Molecular markers and their Utilisation -- Molecular markers and genotyping methods; Linkage mapping of molecular markers; Mapping populations and quantitative trait loci mapping; Association mapping; Marker-assisted selection; Training population and statistical models in genomic selection; Phylogenetic relationships and genetic diversity; Mutation mapping and breeding; Process of variety release, Seed certification, and commercial release. 12 hours

Essential Readings: Singh, B.D. and Singh, A.K. (2015) Marker-Assisted Plant Breeding: Principles and Practices, ISBN:9788132223160, DOI:10.1007/978-81-322-2316-0; Amiteye, S. (2021) Basic concepts and methodologies of DNA marker systems in plant molecular breeding. Heliyon, 7(10):e08093, DOI: 10.1016/j.heliyon.2021.e08093; Al-Khayri, J.M., et al. (2024) Plant Molecular Breeding in Genomics Era - Concepts and Tools, Springer Cham, ISBN:9783031685866, DOI:10.1007/978-3-031-68586-6; Bhat, T.A. and Hakeem, K.R. (2023) Biotechnologies and genetics in plant mutation breeding (volume 1: Mutagenesis and Crop Improvement). Apple Academic Press, Inc., ISBN:9781003305064; Acquaah, G. (2021) Principles of Plant

Genetics and Breeding, 3rd edition, Wiley-Blackwell, ISBN:9781119626329, Section 12 (Variety release process in plant breeding).

Unit 3: Hybrid Breeding and Doubled haploid (DH) Technologies -- Genetic basis of heterosis and hybrid breeding strategies; Molecular aspects of three-line and two-line approaches (photoperiod- and thermo-sensitive genic male sterility); Transgenics in hybrid seed production; Role of DH lines in mapping and varietal improvement; Molecular mechanisms of haploid induction (maternal and paternal); Synthetic apomixis and fixing elite genotypes. 12 hours

Essential Readings: Chen, L. and Liu, Y.G. (2014) Male sterility and fertility restoration in crops. Annual Review of Plant Biology, 65:579–606, DOI:10.1146/annurev-arplant-050213-040119; Kim, Y.J. and Zhang, D. (2018) Molecular control of male fertility for crop hybrid breeding. Trends in Plant Science, 23(1):53–65, DOI: 10.1016/j.tplants.2017.10.001; Quiroz, L.F., et al. (2024) Haploid rhapsody: the molecular and cellular orchestra of *in vivo* haploid induction in plants. New Phytologist, 241(5):1936–1949, DOI: 10.1111/nph.19523.

Unit 4: Applications of Molecular Breeding -- International molecular breeding efforts; Improving crop yields, quality, biotic and abiotic stress tolerance; Enhancing shelf-life, nutritional value and flavor; Integration of genetic modification and molecular breeding.

9 hours

Essential Readings: Acquaah, G. (2021) Principles of plant genetics and breeding. 3rd edition, Wiley-Blackwell. ISBN:9781119626343, Chapter 14 (Breeding for resistance to disease and insect pests), Chapter 15 (Breeding for resistance to abiotic stresses), Chapter 35 (International plant breeding efforts); Lomax, J., et al. (2024) Multi-omic applications for understanding and enhancing tropical fruit flavour. Plant Molecular Biology, 114(4):83, DOI:10.1007/s11103-024-01480-7; Sharma, R., et al. (2025) Integrating molecular genetics with plant breeding to deliver impact. Plant Physiology, 198(3):kiaf087, DOI:10.1093/plphys/kiaf087.

Practicals (30 hours)

1. *In silico* analysis of crop genomes and identification of polymorphisms under known QTLs.
2. Designing markers and genotyping of locus-specific SNPs using CAPS and dCAPS markers.
3. Haplotype analysis from publicly available genomic data of a selected crop plant.
4. Verification of true F_1 hybrid with molecular markers in bi-parental crossed plants.
5. Association analysis of selected genotypes with their phenotype data.

Suggested Readings:

1. Koh, H.J., et al. (2015) Current technologies in plant molecular breeding - A guidebook of plant molecular breeding for Researchers. ISBN:9789401799966, DOI:10.1007/978-94-017-9996-6.
2. Al-Khayri, J.M., et al. (2016) Advances in plant breeding strategies: Breeding, Biotechnology and Molecular Tools, Springer Cham, ISBN:9783319225210, DOI:10.1007/978-3-319-22521-0.
3. Kang, M.S. (2020). Quantitative genetics, genomics and plant breeding, 2nd Edition, CABI, ISBN: 9781789242942.
4. Li, B., et al. (2024) Targeted genome-modification tools and their advanced applications in crop breeding. Nature Reviews Genetics, 25(9):603–622, DOI:10.1038/s41576-024-00720-2.
5. Bharadwaj, D.N. (2018) Advanced Molecular Plant Breeding- Meeting the challenge of food security. CRC Press. ISBN:9780203710654, DOI:10.1201/b22473.
6. Crossa, J., et al. (2017) Genomic selection in plant breeding: Methods, models, and perspectives. Trends in Plant Science, 22(11):961–975, DOI:10.1016/j.tplants.2017.08.011.
7. Alemu, A., et al. (2024) Genomic selection in plant breeding: Key factors shaping two decades of progress. Molecular Plant, 17(4):552–578, DOI:10.1016/j.molp.2024.03.007.
8. Chaudhary, N. and Sandhu, R. (2024) A comprehensive review on speed breeding methods and applications. Euphytica, 220:42, DOI:10.1007/s10681-024-03300-x.

9. Rajan, R., et al. (2025) Innovations in climate resilient agriculture, Springer Cham, ISBN:9783031848025, DOI:10.1007/978-3-031-84802-5.
10. Klee, H.J. and Tieman, D.M. (2018) The genetics of fruit flavour preferences. Nature Reviews Genetics, 19(6):347–356, DOI:10.1038/s41576-018-0002-5.
11. Kamaluddin, et al. (2022) Technologies in Plant biotechnology and breeding of field Crops. Springer Singapore, ISBN:9789811657672, DOI:10.1007/978-981-16-5767-2.

PBSE323: Metagenomics of Plant-associated Microbes

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE323: Metagenomics of Plant-associated Microbes	4	3	1	0	B.Sc. in any branch of science	NA

Learning Objectives

This course aims to introduce students to the fundamental concepts of metagenomics and the plant holobiont, with a focus on rhizosphere and aquatic microbiomes using environmental DNA (eDNA). It seeks to develop an understanding of sampling strategies and to familiarize students with the basics of metagenomic data analysis. This would help students appreciate how metagenomic approaches are applied in biodiversity assessment, plant pathology, environmental surveillance, and emerging areas such as space biology, integration of breeding and precision agriculture.

Learning Outcomes

By the end of the course, students should be able to explain key concepts of metagenomics and plant microbiomes and outline appropriate strategies for sampling and sequencing rhizosphere and aquatic environmental samples. They should be able to understand the components of the metagenomic analysis pipeline, interpret community and functional profiles, and critically read metagenomic datasets. Students will be able to relate metagenomic findings to practical applications in plant health, ecosystem monitoring, and sustainable agriculture.

Course Contents (45 hours)

Unit 1: Introduction to Metagenomics -- Concepts of microbiome, metagenome, holobiont, hologenome; Plant-associated microbiomes: Rhizosphere, phyllosphere, endosphere, etc.; Overview of metagenomics and integration with metatranscriptomics, metaproteomics, and metabolomics; Marker genes and DNA barcoding; Overview of workflow and sample preparation methodologies. 15 hours

Essential Readings: Nelson, K.E. (2020) Encyclopedia of metagenomics. Springer, New York, ISBN: 9781461464181, DOI:10.1007/978-1-4614-6418-1; Simon, J.C., et al. (2019) Host-microbiota interactions: from holobiont theory to analysis. Microbiome, 7:5, DOI:10.1186/s40168-019-0619-4; Vorholt, J. (2012) Microbial life in the phyllosphere. Nature Reviews Microbiology, 10:828–840, DOI:10.1038/nrmicro2910; Compant, S., et al. (2021) The plant endosphere world - bacterial life within plants. Environmental Microbiology, 23(4):1812–1829, DOI:10.1111/1462-2920.15240; Christopher, C.M., et al. (2016) Dissecting host-associated communities with DNA barcodes. Philosophical Transactions of the Royal Society Biological Sciences, 371(1702):20150328, DOI:10.1098/rstb.2015.0328.

Unit 2: Rhizosphere and Aquatic Metagenomics -- Environmental DNA (eDNA): sources, stability, sampling, limitations; Rhizosphere: structure, gradients, root exudates and microsome assembly; Aquatic plants-associated microbes; case studies. 10 hours

Essential Readings: Liu, S., et al. (2025) Analysis of metagenomic data. Nature Reviews Methods Primers, 5:5, DOI:10.1038/s43586-024-00376-6; Behera, B.K., et al. (2024) Metagenomics study in aquatic resource management: Recent trends, applied methodologies and future needs. Gene Reports, 25:101371, DOI:

10.1016/j.genrep.2021.101372; Wang, B., et al. (2021) Metagenomic insights into the effects of submerged plants on functional potential of microbial communities in wetland sediments. Marine Life Science & Technology, 3(4):405–415, DOI:10.1007/s42995-021-00100-3; Sahu, A., et al. (2023) Environmental DNA (eDNA): Powerful technique for biodiversity conservation. Journal for Nature Conservation, 71:126325, DOI: 10.1016/j.jnc.2022.126325; Pudake, R.N. et al. (2021) Omics science for rhizosphere biology. Springer Singapore, ISBN:9789811608896, DOI:10.1007/978-981-16-0889-6; Wani, A.K., et al. (2024) Metagenomic profiling of rhizosphere microbiota: Unravelling the plant-soil dynamics. Physiology and Molecular Plant Pathology, 133:10238, DOI:10.1016/j.pmpp.2024.102381.

Unit 3: Overview of Metagenomic Data Generation and Analysis -- Workflow overview, Selection of appropriate sequencing technologies (short and long-read); Demultiplexing, adapter and quality trimming, removal of contaminating DNA (host) sequences, metagenomic data assembly, taxonomic characterization (alignment based, alignment-free k-mer based, hybrid strategy); Gene prediction and functional analysis; Metagenomic data repositories. 10 hours

Essential Readings: Thomas T., et al. (2012) Metagenomics - a guide from sampling to data analysis. Microbial Informatics and Experimentation, 2:3, DOI:10.1186/2042-5783-2-3; Navgire, G.S., et al. (2022) Analysis and Interpretation of metagenomics data: an approach. Biological Procedures Online, 24:18, DOI:10.1186/s12575-022-00179-7; Aplakidou, E., et al. (2024) Visualizing metagenomic and metatranscriptomic data: A comprehensive review. Computational and Structural Biotechnology Journal, 23:2011–33, DOI:10.1016/j.csbj.2024.04.060.

Unit 4: Applications of Metagenomics -- Biodiversity assessment of plant-associated ecosystems; Plant pathology; Metagenomics in bioremediation and agro-ecosystem health; Metagenomics in controlled plant growth systems; Space biology; Future perspectives: integrating metagenomics with breeding and agriculture. 10 hours

Essential Readings: Charles, T.C., et al. (2017) Functional Metagenomics: Tools and Applications. Springer Cham, ISBN:9783319615103, DOI:10.1007/978-3-319-61510-3; Nagarajan, M. (2024) Metagenomics - Perspectives, Methods, and Applications. 2nd edition, Academic Press, ISBN:9780323917124; Roman-Reyna, V. and Crandall, S.G. (2024) Seeing in the dark: a metagenomic approach can illuminate the drivers of plant disease. Frontiers in Plant Science, 15:140502, DOI:10.3389/fpls.2024.1405042; Kumar, V. and Iram, S. (2024) Microbial Technology for Agro-Ecosystems. Academic Press, ISBN:9780443184468, Chapter 15 (Metagenomics: An approach for understanding microbe-microbe and plant-microbiome-interactions); Compant, S., et. al. (2025) Harnessing the plant microbiome for sustainable crop production. Nature Reviews Microbiology, 23(1):9–23, DOI:10.1038/s41579-024-01079-1.

Tutorials (15 hours)

1. Case study: Sargasso Sea.
2. Designing a rhizosphere metagenomics experiment.
3. Case study on how eDNA is used to track microbial biodiversity.
4. Survey of metagenomic databases.

Suggested Readings:

1. Chopra, R.S., et al. (2020) Metagenomics: techniques, applications, challenges and opportunities. Springer Singapore, ISBN:9789811565298, DOI:10.1007/978-981-15-6529-8.
2. Streit, W.R. and Daniel, R. (2017) Metagenomics: Methods and Protocols. Humana NY, ISBN: 9781493966912, DOI:10.1007/978-1-4939-6691-2.
3. Vacher, C., et al. (2016) The phyllosphere: microbial jungle at the plant–climate interface. Annual Review of Ecology, Evolution, and Systematics, 47:1–24, DOI:10.1146/annurev-ecolsys-121415-032238
4. Pudake, R.N., et al. (2021) Omics science for rhizosphere biology. Springer Singapore, ISBN:9789811608896, DOI:10.1007/978-981-16-0889-6.
5. Carter, D.O., et al. (2017) Forensic Microbiology. Wiley, ISBN:9781119062578, Chapter 5 (An introduction to metagenomic data generation, analysis, visualization, and interpretation).

PBSE324: Frontiers in Plant Molecular Biology

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE324: Frontiers in Plant Molecular Biology	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

This course has been designed to introduce students to state-of-the-art concepts, technologies, and experimental systems that define modern plant molecular biology and its translational applications. It aims to develop a rigorous understanding of plant signaling architectures, multi-omics driven functional genomics, structural advances in genome biology, and emerging domains such as epitranscriptomics, nanobiotechnology, and space biology. Furthermore, it aims to enable students to relate primary discoveries in calcium, ROS, hormone and retrograde signaling to crop improvement, biosensing, and stress resilience through synthetic and genome engineering approaches, supported by current literature in plant signaling and systems biology.

Learning Outcomes

After successful completion of the course, students will be able to critically interpret and integrate datasets from transcriptomic, proteomic, metabolomic, epigenomic, and phenomics platforms to elucidate gene function and regulatory networks in plants. They should be able to design and conceptualize CRISPR-based functional analyses, visualize and analyse gene interaction networks, and evaluate gene function prediction, stress-tolerance forecasting, and genome-assisted breeding. Students will also be able to assess emerging tools, such as optogenetics, targeted epigenome editing, and plant nanotechnology, for their feasibility for research or crop applications, thereby demonstrating their research readiness.

Course Content (45 hours)

Unit 1: Forefront of Plant Signaling -- Mechanosensing and electrosensing; Receptor dynamics and nanodomains; Phosphoswitches and dynamic network mapping; Organelle-to-nucleus signaling (retrograde signaling); Optogenetics and chemical biology tools; Live-cell imaging of Ca^{2+} and ROS dynamics; Phytohormone dynamics studies; Engineering synthetic receptors or signaling circuits for stress tolerance or biosensing. 11 hours

Essential Readings: Hamilton, E.S., et al. (2015) United in diversity: mechanosensitive ion channels in plants, Annual Review of Plant Biology, 66:113–37, DOI:10.1146/annurev-arplant-043014-114700; Fromm, J. and Lautner, S. (2007) Electrical signals and their physiological significance in plants. Plant Cell and Environment, 30(3):249–257, DOI:10.1111/j.1365-3040.2006.01614.x; Wang, L., et al. (2018) Exploring the spatiotemporal organization of membrane proteins in living plant cells. Annual Review of Plant Biology, 69:525–551, DOI:10.1146/annurev-arplant-042817-040233; Zhang, J., et al. (2023) Protein phosphorylation: A molecular switch in plant signaling. Cell Reports, 42(7):112729, DOI:10.1016/j.celrep.2023.112729; Tatjana, K. and Dario, L. (2016) Retrograde signaling: Organelles go networking. Biochimica et Biophysica Acta (BBA)–Bioenergetics, 1857(8):1313–1325, DOI:10.1016/j.bbabio.2016.03.017; Hiromasa, S. and Philipp, D. (2022) Plant optogenetics: Applications and perspectives. Current Opinion in Plant Biology, 68:102256, DOI:10.1016/j.pbi.2022.102256; Sarah, J., et al. (2011) *In vivo* imaging of Ca^{2+}, pH, and reactive oxygen species using fluorescent probes in plants. Annual Review of Plant Biology, 62:273–297, DOI:10.1146/annurev-arplant-042110-103832; Rainer, W. (2020) Phytohormone signaling mechanisms and genetic methods for their

modulation and detection, Current Opinion in Plant Biology, 57:31–40, DOI:10.1016/j.pbi.2020.05.011; Ondřej N., et al. (2017) Zooming in on plant hormone analysis: Tissue- and cell-specific approaches. Annual Review of Plant Biology, 68:323–348, DOI:10.1146/annurev-arplant-042916-040812; Alexander, R.L., et al. (2020) Engineering synthetic signaling in plants. Annual Review of Plant Biology, 71:767–788, DOI:10.1146/annurev-arplant-081519-035852.

Unit 2: Structural and Functional Genomics -- Third- and fourth-generation sequencing platforms and their applications in plant genome analysis, principles of transcriptomics and proteomics, including experimental design and data interpretation; Case study-based functional genomics strategies such as large-scale mutagenesis (T-DNA, CRISPR/Cas), RNAi, VIGS and activation tagging to elucidate gene function; Understanding advanced layers of regulation through RNA-seq, ribosome profiling, single-nucleus RNA-seq, and epigenomic assays such as ATAC-seq, ChIP-seq and DNA methylome analysis. 12 hours

Essential Readings: Brown, T.A. (2023) Genomes 5. CRC Press, ISBN:9781003133162, Chapter 4 (Sequencing Genomes), Chapter 9 (Transcriptomes and Proteomes), Chapter 10 (Genome Regulation); Mardis, E.R. (2008) Next-generation DNA sequencing methods. Annual Review of Genomics and Human Genetics, 9:387–402, DOI:10.1146/annurev.genom.9.081307.164359; Chappell, L., et al. (2018) Single-Cell (Multi)omics Technologies. Annual Review of Genomics and Human Genetics, 19:15–41, DOI: 10.1146/annurev-genom-091416-035324.

Unit 3: **Applied Aspects of Plant-Environment Interactions** -- Overview of plant responses to abiotic and biotic stresses; Molecular signaling pathways; Omics-driven discovery of stress tolerance genes; Engineering the plant microbiome; Spatial and integrative omics for stress biology: single cell vs. tissue level omics, transcriptomics and metabolite mapping of root-soil interface; Inter-kingdom communication; AI and ML in prediction of stress-tolerant genotypes. 11 hours

Essential Readings: Tuteja, N. and Gill, S.S. (2016) Abiotic stress responses in plants. ISBN:9783527339181, Wiley-VCH Verlag GmbH & Co., Chapter 1 (Abiotic stress signaling in plants: an overview); Zhang H., et al. (2022) Abiotic stress responses in plants. Nature Review Genetics, 23:104–119, DOI:10.1038/s41576-021-00413-0; Jiang Z., et al. (2025) Mechanisms of plant acclimation to multiple abiotic stresses. Communications Biology, 8:655, DOI:10.1038/s42003-025-08077-w; Mochida, K., et al. (2020) Decoding plant–environment interactions that influence crop agronomic traits. Plant and Cell Physiology, 61(8):1408–1418, DOI:10.1093/pcp/pcaa064; Du, B., et al. (2024) Strategies of plants to overcome abiotic and biotic stresses. Biological Reviews, 99(4):1524–1536, DOI: 10.1111/brv.13079; Varadharajan, V., et al. (2025) Multi-omics approaches against abiotic and biotic stress-A review. Plants, 14(6):865, DOI:10.3390/plants14060865; Afridi M.S., et al. (2022) New opportunities in plant microbiome engineering for increasing agricultural sustainability under stressful conditions. Frontiers in Plant Sciences, 13:899464, DOI:10.3389/fpls.2022.899464; Special issue on "Use of single cell and spatial multiomics for uncovering cellular and molecular mechanisms underlying plant stress responses". Stress Biology, 2025; Salem M.A., et al. (2022) Metabolomics of plant root exudates: From sample preparation to data analysis, Frontiers in Plant Sciences, 13:1062982, DOI:10.3389/fpls.2022.1062982; Singhal, R., et al. (2025) Using supervised machine-learning approaches to understand abiotic stress tolerance and design resilient crops. Philosophical Transactions of the Royal Society B, 380:2024.0252, DOI:10.1098/rstb.2024.0252.

Unit 4: Emerging Tools and Techniques -- Epitranscriptomics; Targeted epigenome editing: development of specific DNA-targeting systems, next-generation CRISPR activators, applications in agriculture; Nanotechnology and its applications in plant biology: types of nanomaterials, uptake and translocation, biological impact, applications of nanoparticles (NPs) in plant biology (biosensors, nutrient delivery, nanomaterials in plant genetic engineering (DNA / RNA delivery); Plant biology in space: growth and monitoring, effects of microgravity and ionizing radiations, applications, and benefits. 11 hours

Essential Readings: Kumari, A., et. al. (2023) Nanotechnology as a powerful tool in plant sciences: Recent developments, challenges and perspectives. Plant Nano Biology, 5:100046, DOI:10.1016/j.plana.2023.100046; Sanzari, I., et. al. (2019) Nanotechnology in plant science: To make a long story short. Frontiers in Bioengineering and Biotechnology, 7:120, DOI:10.3389/fbioe.2019.00120; Sharma, B., et al. (2023) The diversity and functions

of plant RNA modifications: what we know and where we go from here. Annual Review of Plant Biology, 74(1):53–85, DOI:10.1146/annurev-arplant-071122-085813; Shen, L., et al. (2019) Messenger RNA modifications in plants. Trends in Plant Science, 24(4):328–41, DOI:10.1016/j.tplants.2019.01.005; McCutcheon, S.R., et al. (2024) Epigenome editing technologies for discovery and medicine. Nature Biotechnology, 42:1199–1217, DOI:10.1038/s41587-024-02320-1; Kungulovski, G. and Jeltsch, A. (2016) Epigenome editing: state of the art, concepts, and perspectives. Trends in Genetics, 32(2):101–13, DOI:10.1016/j.tig.2015.12.001.

Practicals (30 hours)

1. To investigate the phenotypic responses in the calcium signaling mutants.
2. To investigate the transactivation or trans-repression activity of a transcription factor.
3. To design CRISPR guide RNA primers using online tools (e.g., CHOPCHOP, CRISPOR).
4. Molecular probe-based pathogen detection.
5. To design functional genomics approaches for specific gene/phenotype questions and compare the strengths and limitations of different methods.

Suggested Readings:

1. Kramer, L.M. (2015) Signal Transduction. 3rd edition, Academic Press, ISBN:9780123948199.
2. Heldin, C.H. and Purton, M. (1996) Signal transduction: Modular texts in molecular and cell biology, Chapman & Hall, ISBN:0412708108.
3. Alberts, B., et al. (2022) Molecular Biology of the Cell. 7th edition, W.W. Norton & Company, ISBN:9780393884630.
4. Buchanan, B.B., et al. (2015) Biochemistry & Molecular Biology of the Plants. 2nd edition, Wiley Blackwell, ISBN:9781118502198.
5. Kleinsmith, L.J. and Kish, V.M. (1997) Principles of Cell & Molecular Biology. Harper Collins College Publishers, ISBN:9780065004045.
6. Taiz, L., et al. (2023). Plant Physiology and Development. 7th edition, Sinauer Associates, ISBN:9780197614204.
7. Glick, B.R. and Pasternak, J.J. (2022) Molecular Biotechnology: Principles and Applications of recombinant DNA. 6th edition, ASM Press, ISBN:9781683673668.
8. Brown, T.A. (2023) Genomes 5. 5th edition, CRC Press, ISBN:9781003133162.
9. Piechulla, B. (2025) Plant Biochemistry. 6th edition, Academic Press, ISBN:9780443266164.
10. Abd-Elsalam, K.A. and Prasad, R. (2018) Nanobiotechnology applications in plant protection. Springer Cham, ISBN:9783319911601, DOI:10.1007/978-3-319-91161-8.
11. Chen, J.T. (2024) Advanced Nanotechnology in Plants: Methods and Applications. CRC Press, ISBN:9781003368571.
12. Jeltsch, A., and Rots, M.G. (2018) Epigenome editing: Methods and Protocols. Humana New York, ISBN:9781493977741, DOI:10.1007/978-1-4939-7774-1.
13. Jurga, S. and Barciszewski, J. (2021) Epitranscriptomics. Springer Cham, ISBN:9783030716127, DOI:10.1007/978-3-030-71612-7.
14. Online Databases and Resources: NCBI, TAIR, Phytozome, EnsemblPlants and others, KEGG, STRING, Gene Ontology, CRISPR-Cas toolkits and others.

PBSE325: Introduction to Bioinformatics

This course is open to students of other departments as a GE course.

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE325: Introduction to Bioinformatics	4	3	1	0	B.Sc. in any branch of science	NA

Learning Objectives

The paper is devised to introduce the students to the field of bioinformatics and data analysis. The content is designed for students from any stream of life sciences. The course imparts basic and essential knowledge regarding the nature of life science data, including data formats, international databases and data repositories. It also helps to understand how different biological file formats facilitate storage, retrieval and analysis of biological sequences and structures. Furthermore, the unit is designed to familiarize the learner with the landscape of major international nucleotide and protein databases, understanding their scope, interrelationships, and specific applications (universal and organism-specific databases). Additionally, understand the structure, interoperability, and collaborative role of INSDC, as well as its importance in maintaining the global genomic data ecosystem. Furthermore, it will explain the fundamental principles of local and global alignment (pairwise sequence comparison) and the biological rationale behind scoring systems, including substitution matrices and gap penalties. It also focuses on interpreting results of Clustal-W, Clustal Omega, T-Coffee, and MultiAlign BLAST tools and how to optimize their parameters to draw biologically meaningful conclusions. The last unit of the course presents the fundamentals of RNA/ Protein secondary and tertiary structure prediction. It will be helpful to learn the basic principles of docking analysis and drug design workflows.

Learning Outcomes

After successfully completing the course, students will be able to identify and describe various biological data formats and their respective applications. They will be able to access and retrieve sequences and structural data from major databases, data repositories, and browsers such as the UCSC Genome Browser, linking these data formats to visual genomic analysis. Furthermore, students will be able to utilize tools like BLAST for sequence comparison and evolutionary significance, as well as understand the conceptual difference between various substitution matrices and pairwise algorithms. They can perform and interpret the MSA of different biological sequences using different computational software and also visualize phylogenetic trees using various algorithms. Upon completing the last unit, students will be able to use computational tools for RNA and protein prediction, evaluate them, and analyse protein-ligand interaction and outcomes of docking.

Course Content (45 hours)

Unit 1: Biological Data Formats and Databases -- Overview of database management system, concept of 'structured' and 'semi-structured/unstructured' data, concept of 'flat-file' formats; Various file formats used in bioinformatics such as 'fasta', 'fastq', Phylip format, Newick, PDB file format, 'GFF3', SAM/BAM/CRAM formats; Universal nucleotide data repositories: NCBI-GenBank, EMBL-ENA, DDBJ; Details of the International Nucleotide Sequence Data Collaboration (INSDC); Universal Protein databases: UniprotKB, PDB. Organism specific databases (Flybase, Wormbase etc), UCSC Human Genome Browser; Molecular interaction databases such as KEGG and STRING. 10 hours

Essential Readings: Mount, D.W. (2004) Bioinformatics: Sequence and Genome Analysis. 2nd edition, Cold Spring Harbor Laboratory Press, ISBN:9780879697129, Chapter 1 (Historical Introduction and Overview), Chapter 2 (Collecting and Storing Sequences in the Laboratory); Zvelebil, M. and Baum, J.O. (2008) Understanding Bioinformatics. Garland Science, ISBN:9780815340249, Chapter 1 (The nucleic world) and chapter 3 (Dealing with databases); Sayers, E.W., et al. (2022) Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 50(D1):D20–D26, DOI:10.1093/nar/gkab1112; Cochrane, G., et al. (2016). The European Nucleotide Archive in 2016. Nucleic Acids Research, 44(D1):D32–D37, DOI:10.1093/nar/gkw1106; The UniProt Consortium (2023) UniProt: the Universal Protein Knowledgebase in 2023. Nucleic Acids Research, 51(D1):D523–D531, DOI:10.1093/nar/gkac1052; Berman, H.M., et al. (2000) The Protein Data Bank. Nucleic Acids Research, 28(1):235–242, DOI:10.1093/nar/28.1.235; Li, H., et al. (2009) The Sequence Alignment/Map format and SAMtools. Bioinformatics, 25(16):2078–2079, DOI:10.1093/bioinformatics/btp352; Cock, P.J.A., et al. (2010) The Sanger FASTQ file format for sequences with quality scores, and the Solexa/Illumina FASTQ variants. Nucleic Acids Research, 38(6):1767–1771, DOI:10.1093/nar/gkp1137; Kanehisa, M., et al. (2023) KEGG for taxonomy-based analysis of pathways and genomes. Nucleic Acids Research, 51(D1):D587–D592, DOI:10.1093/nar/gkac997; Szklarczyk, D., et al. (2023) The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome. Nucleic Acids Research, 51(D1):D638–D646, DOI:10.1093/nar/gkac1000; The FlyBase Consortium. (2022). FlyBase: updates to the *Drosophila melanogaster* knowledge base. Nucleic Acids Research, 50(D1):D1014–D1020, DOI:10.1093/nar/gkab1099; Haeussler, M., et al. (2019) The UCSC Genome Browser database: 2019 update. Nucleic Acids Research, 47(D1):D853–D858, DOI:10.1093/nar/gky1095.

Unit 2: Pairwise Sequence Alignment -- Concept of local and global sequence alignment; Pairwise sequence alignment algorithms such as Needleman and Wunsch, Smith-Waterman, scoring an alignment, linear and affine gap penalty, amino acid substitution scoring matrices (PAM and BLOSUM); Sequence alignment-based database search, BLAST and its variants, BLAST parameters (word size, E-value, scoring scheme, gap-penalty), bit/raw score. 10 hours

Essential Readings: Mount, D.W. (2004) Bioinformatics: Sequence and Genome Analysis. 2nd edition, Cold Spring Harbor Laboratory Press, ISBN:9780879697129, Chapter 3 (Alignment of pairs of sequences), Chapter 6 (Sequence database searching for similar sequences); Zvelebil, M. and Baum, J.O. (2008) Understanding Bioinformatics. Garland Science, ISBN:9780815340249, Chapter 4 (Producing and analyzing sequence alignments), Chapter 5 (Pairwise sequence alignment and database searching); Morrison, D.A. (2006). Multiple sequence alignment for phylogenetic purposes. Australian Systematic Botany, 19(6):479–539, DOI:10.1071/SB06020.

Unit 3: Multiple Sequence Alignment and Phylogenetic Analysis -- Global and local multiple sequence alignment, multiple sequence alignment algorithms (progressive and iterative algorithms), profile and block analysis; Softwares: Clustal-X, Clustal-W, Clustal-Omega, T-Coffee, MultiAlign; Basic concept of phylogenetic analysis, rooted and unrooted trees, approaches for phylogenetic tree construction; Basics of algorithm for UPGMA, neighbour joining (NJ), maximum parsimony, and maximum likelihood phylogenetic analysis. 15 hours

Essential Readings: Mount, D.W. (2004) Bioinformatics: Sequence and Genome Analysis. 2nd edition, Cold Spring Harbor Laboratory Press, ISBN:9780879697129, Chapter 5 (Multiple sequence alignment), Chapter 7 (Phylogenetic prediction); Zvelebil, M. and Baum, J.O. (2008) Understanding Bioinformatics. Garland Science, ISBN:9780815340249, Chapter 4 (Producing and analyzing sequence alignments), Chapter 5 (Pairwise sequence alignment and database searching), Chapter 6 (Patterns, profiles, and multiple alignments).

Unit 4: Structure Predictions for Nucleic Acids and Proteins -- Approaches for prediction of RNA secondary and tertiary predictions, energy minimization and base covariance models; Basic approaches for protein structure predictions, comparative modeling, fold recognition/'threading', and *ab-initio* prediction; Introduction to AlfaFold database; Docking analysis and drug designing. 10 hours

Essential Readings: Mount, D.W. (2004) Bioinformatics: Sequence and Genome Analysis. 2nd edition, Cold Spring Harbor Laboratory Press, ISBN:9780879697129, Chapter 8 (Prediction of RNA secondary structure), Chapter 10 (Protein classification and structure prediction); Zvelebil, M. and Baum, J.O. (2008) Understanding Bioinformatics. Garland Science, ISBN:9780815340249, Chapter 8 (Recovering evolutionary history), Chapter 11 (Obtaining secondary structure from sequence), Chapter 12 (Predicting secondary structures).

Tutorials (15 hours)

1. To perform 'text-based' database search.
2. Sequence alignment-based database search.
3. Multiple sequence alignment and phylogenetic analysis.
4. Analysis of gene/protein interaction networks.

Suggested Readings:

1. Baxevanis, A.D., et al. (2020) Bioinformatics: A practical guide to the analysis of genes and proteins. 4th edition. John Wiley & Sons, Inc., ISBN:9781119335962.
2. Tramontano, A. (2018) Introduction to Bioinformatics. Chapman and Hall/CRC, ISBN:9781315276014, DOI:10.1201/9781420010886.
3. Lee, E. Tan, T.W. (2018) Beginners guide to bioinformatics for high throughput sequencing. World Scientific, ISBN:9789813231665, DOI:10.1142/10720.
4. Thompson, J.D., et al. (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Research, 22(22):4673–4680, DOI:10.1093/nar/22.22.4673.
5. Notredame, C., et al., (2000) T-Coffee: A novel method for fast and accurate multiple sequence alignment. Journal of Molecular Biology, 302(1):205–217, DOI:10.1006/jmbi.2000.4042.
6. Saitou, N. and Nei, M. (1987) The neighbor-joining method: a new method for reconstructing phylogenetic trees. Molecular Biology and Evolution, 4(4):406–425, DOI:10.1093/oxfordjournals.molbev.a040454.
7. Felsenstein, J. (1981) Evolutionary trees from DNA sequences: a maximum likelihood approach. Journal of Molecular Evolution, 17(6):368–376, DOI:10.1007/BF01734359.
8. JJumper, J., et al. (2021) Highly accurate protein structure prediction with AlphaFold2. Nature, 596:583–589, DOI:10.1038/s41586-021-03819-2.
9. Zhang, Y. (2008) Progress and challenges in protein structure prediction. Current Opinion in Structural Biology, 18(3):342–348, DOI:10.1016/j.sbi.2008.02.004.
10. Kryshtafovych, A., et al. (2021) Critical assessment of methods of protein structure prediction (CASP)—Round XIV. Proteins: Structure, Function, and Bioinformatics, 89(12):1607–1617, DOI:10.1002/prot.26237.
11. Zuker, M. (2003) Mfold web server for nucleic acid folding and hybridization prediction. Nucleic Acids Research, 31(13):3406–3415, DOI:10.1093/nar/gkg595.
12. Kitchen, D.B., et al. (2004) Docking and scoring in virtual screening for drug discovery: methods and applications. Nature Reviews Drug Discovery, 3(11):935–949, DOI:10.1038/nrd1549.

PBRE326: Dissertation-I

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBRE326: Dissertation-I	6	0	0	6	B.Sc. in any branch of science	NA

Learning Objectives

The students will identify and select a relevant research problem in consultation with the faculty members, ensuring alignment with current advances in Plant Molecular Biology and Biotechnology. They will conduct a thorough and critical appraisal of the existing literature on the problem, enabling them to understand the depth of current knowledge. Students will learn to formulate well-defined research questions and develop testable hypotheses in the context of scientific reasoning. Under faculty mentorship, they will design an experimentally feasible and scientifically structured research plan, complete with realistic timelines, appropriate methodologies, and anticipated outcomes. In addition, the students will gain training in scientific writing through preparation of a detailed literature review, and they will enhance their communication skills by effectively presenting and discussing their research survey in laboratory group discussions and structured oral presentations.

Learning Outcomes

Upon successful completion of the course, the student will be able to independently conduct a comprehensive survey of scientific literature and critically analyse it to identify significant knowledge gaps within the research field. They will demonstrate the ability to justify the importance and relevance of selected research problems using evidence-based reasoning. Students will prepare a well-structured synopsis that includes an in-depth literature review, clearly articulated research questions, hypotheses, and a coherent experimental plan to be executed in Semester 4. Additionally, they will acquire proficiency in scientific writing, including organization, clarity, and synthesis of complex information, and will develop strong oral communication skills necessary for presenting research findings and engaging in scientific discourse. Overall, the students will hone their ability to think independently, plan research systematically, and communicate their work confidently in both written and verbal formats.

Suggested Readings:

1. Latest research and review articles from scientific journals and book chapters on a chosen research problem.

SEMESTER 4

PBSC421: Advances in Crop Biotechnology

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSC421: Advances in Crop Biotechnology	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

This course aims to provide learners with an advanced and integrative understanding of modern crop biotechnology and its role in sustainable agriculture. Students will engage with emerging molecular tools, the development and significance of crop pan-genomes, and cutting-edge concepts such as *de novo* domestication and innovations in *in-planta* transformation. The course will also provide in-depth insights into translational strategies to enhance crop nutrition and improve resilience to biotic and abiotic stresses through sustainable, environmentally friendly approaches. Overall, learners will develop the scientific foundation and biotechnology skills required to address challenges in crop improvement.

Learning Outcomes

Upon completing this course, participants will be able to critically analyze crop genomes for domestication signatures and evaluate germplasm diversity for trait improvement. They will demonstrate practical knowledge of state-of-the-art plant transformation techniques and emerging delivery platforms for gene and RNA manipulation. Students will be able to assess and design strategies for enhancing stress tolerance, yield, and nutritional value in crop plants. They will also gain competence in applying biostimulants and other biofortification approaches.

Course Contents (45 hours)

Unit 1: Introduction to Crop Biotechnology -- Emerging tools and techniques in biotechnology; Crop pan-genomes and signatures of crop domestication; Germplasm diversity analysis; Concept of *de novo* crop domestication; Agro-morphological traits enhancement; Environmental challenges and food security; Plants as biofactories. 10 hours

Essential Readings: Mascher, M., et al. (2024) Promises and challenges of crop translational genomics. Nature, 636:585–593, DOI:10.1038/s41586-024-07713-5; Shi, J., et al. (2023) Plant pan-genomics and its applications. Molecular Plant, 16(1):168–186, DOI:10.1016/j.molp.2022.12.009; Curtin, S., et al. (2022) Pathways to *de novo* domestication of crop wild relatives. Plant Physiology, 188(4):1746–1756, DOI:10.1093/plphys/kiab554.

Unit 2: Genetic Transformation Techniques -- Ternary vector systems; Improved *in planta* transformation - *de novo* meristems induction, morphogenic regulators, particle bombardment of shoot apical meristem, composite plants, etc; Use of magnetic nanoparticles; Organelle genome transformation. 10 hours

Essential Readings: Chen, Z., et al. (2022) Recent advances in crop transformation technologies. Nature Plants, 8(12):1343–1351, DOI:10.1038/s41477-022-01295-8; Bélanger, J.G., et al. (2024) A comprehensive review of *in planta* stable transformation strategies. Plant Methods, 20(1):79, DOI:10.1186/s13007-024-01200-8.

Unit 3: Climate Resilience and Yield Enhancement -- Case studies on abiotic and biotic stress tolerance; RNA delivery against fungal pathogens; Probiotic-based gene silencing in polyphagous pests; Biofertilizers, Biopesticides; Cell-penetrating peptides; Concept of chronoculture; Synthetic circuits and rewiring for plant improvement; Enhancement of photosynthetic capacity; Carbon dots in plant (epi)genomics. 15 hours

Essential Readings: González Guzmán, M., et al. (2022) New approaches to improve crop tolerance to biotic and abiotic stresses. Physiologia Plantarum, 174(1):e13547, DOI:10.1111/ppl.13547; Al-Dossary, O., et al. (2025) Crop management to enhance plant resilience to abiotic stress using nanotechnology: towards more efficient and sustainable agriculture. Frontiers in Plant Science, 16:1626624, DOI:10.3389/fpls.2025.1626624; Afridi, M.S., et al. (2022) New opportunities in plant microbiome engineering for increasing agricultural sustainability under stressful conditions. Fronters in Plant Science 13:899464, DOI:10.3389/fpls.2022.899464; Shahwar, D., et al. (2023) Role of microbial inoculants as bio fertilizers for improving crop productivity: A review. Heliyon, 9(6):e16134, DOI:10.1016/j.heliyon.2023.e16134; Lloyd, J.P.B., et al. (2025) The switch-liker's guide to plant synthetic gene circuits. Plant Journal, 121(5):e70090, DOI: 10.1111/tpj.70090.

Unit 4: Enhancement of Nutrients -- Improved nutritional profile of crops; Enhancement of mineral nutrient uptake and distribution; Biofortification (Fe, Zn, Ca, K, Vitamins, proteins, essential oils, etc.), micronutrient-dense crops; Anti-nutrient reduction; Concept of Biostimulants. 10 hours

Essential Readings: Napier, J.A., et al. (2019) The challenges of delivering genetically modified crops with nutritional enhancement traits. Nature Plants, 5(6):563–567, DOI:10.1038/s41477-019-0430-z; Zhu, Q., et al. (2019) Plant synthetic metabolic engineering for enhancing crop nutritional quality. Plant Communications, 1(1):100017, DOI:10.1016/j.xplc.2019.100017; White, P.J. and Broadley, M.R. (2005) Biofortifying crops with essential mineral elements. Trends in Plant Science, 10(12):586–593, DOI:10.1016/j.tplants.2005.10.001.

Practicals (30 hours)

1. Transient gene expression using the particle bombardment method.
2. Measurement of photosynthetic efficiency using fluorescence-based system.
3. *In vivo* plant imaging under stress conditions.
4. Mineral nutrient profiling of plants.
5. Molecular detection of *Rhizobium* in root nodules of leguminous plants.

Suggested Readings:

1. Li, X., et al. (2025) The next Green Revolution: integrating crop architectype and physiotype. Trends in Biotechnology, 43(10):2479–2493, DOI:10.1016/j.tibtech.2025.04.002.
2. Della Coletta, R., et al. (2021) How the pan-genome is changing crop genomics and improvement. Genome Biology, 22(1):3, DOI:10.1186/s13059-020-02224-8.
3. Li, S., et al. (2021) Advancing organelle genome transformation and editing for crop improvement. Plant Communications, 2(2):100141, DOI:10.1016/j.xplc.2021.100141.
4. Jeong, J.H., et al. (2025). Empowering *Agrobacterium*: Ternary vector systems as a new arsenal for plant transformation and genome editing. Biotechnology Advances, 83:108631, DOI: 10.1016/j.biotechadv.2025.108631.
5. Shrawat, A., et al. (2018) Engineering nitrogen utilization in crop plants. Springer Cham, DOI: 10.1007/978-3-319-92958-3.
6. Basar, N.U., et al. (2025) Synergies between biostimulants and plant nutrients: a review of ecofriendly nutrient management in crop production. Discover Agriculture, 3:150, DOI:10.1007/s44279-025-00345-x.
7. Patel, P., et al. (2024) Cell-penetrating peptides for sustainable agriculture. Trends in Plant Science, 29(10):1131–44, DOI:10.1016/j.tplants.2024.05.011.
8. Jaswal, S., et al. (2025) Chloroplast engineering for enhancing photosynthetic efficiency and agronomic traits. Trends in Biotechnology, DOI:10.1016/j.tibtech.2025.09.011.
9. Tavakoli, M., et al. (2025) Emerging applications of carbon dots in plant (epi)genomics. Trends in Biotechnology, DOI:10.1016/j.tibtech.2025.09.005.

10. Hawkesford, M.J., et al. (2016) Nutrient use efficiency in plants. Springer Cham, ISBN:9783319106342, DOI:10.1007/978-3-319-10635-9.
11. Li, G., et al. (2025) Integrated biotechnological and AI innovations for crop improvement. Nature, 643:925–937, DOI:10.1038/s41586-025-09122-8.
12. Bartlett, M.E., et al. (2023) The power and perils of *De Novo* domestication using genome editing. Annual Review of Plant Biology, 74:727–750, DOI:10.1146/annurev-arplant-053122-030653.
13. Jian, L., et al. (2022) *De novo* domestication in the multi-omics era. Plant and Cell Physiology, 63(11): 1592–1606, DOI:10.1093/pcp/pcac077.
14. Altpeter, F., et al. (2016) Advancing crop transformation in the era of genome editing. The Plant cell, 28(7):1510–1520, DOI:10.1105/tpc.16.00196.
15. Olsen, K.M., and Wendel, J.F. (2013) A bountiful harvest: genomic insights into crop domestication phenotypes. Annual Review of Plant Biology, 64:47–70, DOI:10.1146/annurev-arplant-050312-120048.
16. Ayenew, B.M. et al. (2024) A review on the production of nanofertilizers and its application in agriculture. Heliyon, 11(1):e41243, DOI:10.1016/j.heliyon.2024.e41243.
17. Steed, G., et al. (2021) Chronoculture, harnessing the circadian clock to improve crop yield and sustainability. Science, 372:eabc9141, DOI:10.1126/science.abc9141.
18. Borowsky, A.T. and Bailey-Serres, J. (2024) Rewiring gene circuitry for plant improvement. Nature Genetics, 56(8):1574–1582, DOI:10.1038/s41588-024-01806-7.
19. Naik, B., et al. (2024) Biofortification as a solution for addressing nutrient deficiencies and malnutrition. Heliyon, 10(9):e30595, DOI:10.1016/j.heliyon.2024.e30595.

PBSC422: Plant Secondary Metabolism and Applications

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSC422: Plant Secondary Metabolism and Applications	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

This course aims to provide students with a comprehensive understanding of plant secondary metabolites, focusing on their biosynthesis, regulation, detection, and diverse applications. It is designed to equip students with knowledge in analytical techniques, molecular tools, and biotechnological approaches used to study and manipulate secondary metabolite pathways. The course also emphasizes the ecological significance and medicinal potential of these compounds, preparing students to apply metabolic engineering for research and development in areas such as plant defense, drug discovery, and sustainable bioproduction.

Learning Outcomes

Upon completing this course, students will understand the biosynthesis, regulation, and classification of key plant secondary metabolites, as well as their significance in molecular biology and biotechnology. Students will also learn to apply genetic and metabolic engineering tools, such as CRISPR/Cas and RNAi, to manipulate biosynthetic pathways and enhance metabolite production. Additionally, students will explore the ecological functions of these compounds in plant defense and pollination, including the role of VOCs. Through this course, students will be prepared for research and applied careers in plant molecular biology, biotechnology, and phytopharmaceuticals.

Course Content (45 hours)

Unit 1: Fundamentals of Plant Secondary Metabolism -- Overview of Primary vs. Secondary Metabolites; Different classes of secondary metabolites: Alkaloids, Terpenoids, Flavonoids, Phenolics, Glucosinolates; Regulation of secondary metabolism (transcriptional, post-transcriptional, epigenetic). 12 hours

Essential Readings: Dixon, R.A. (2001) Natural products and plant disease resistance. Nature, 411:843–847, DOI:10.1038/35081178; Rabeh, K., et al. (2025) A comprehensive review of transcription factor-mediated regulation of secondary metabolites in plants under environmental stress. Stress Biology, 5(1):15, DOI:10.1007/s44154-024-00201-w; Buchanan, B.B., et al. (2015) Biochemistry and Molecular Biology of Plants. John Wiley & Sons, ISBN:9780470714218, Chapter 24 (Natural Products); Strauss, J. and Reyes-Dominguez, Y. (2011) Regulation of secondary metabolism by chromatin structure and epigenetic codes. Fungal Genetics and Biology, 48(1):62–69, DOI:10.1016/j.fgb.2010.07.009.

Unit 2: Isolation, Detection, and Characterization of Secondary Metabolites -- Extraction techniques: Solvent extraction, hydrodistillation, supercritical CO_2; Detection techniques (Chromatographic and Spectroscopic methods); Large-scale metabolite profiling and data analysis. 10 hours

Essential Reading: Dettmer, K., et al. (2007) Mass spectrometry-based metabolomics. Mass Spectrometry Reviews, 26(1):51–78, DOI:10.1002/mas.20108; Sukumaran, S.T., et al. (2020) Plant metabolites: methods, applications and prospects. Springer, ISBN:9789811551352, DOI:10.1007/978-981-15-5136-9.

Unit 3: Metabolic Engineering of Secondary Metabolites -- Concepts and techniques in metabolic engineering; Understanding of Synthetic biology and pathway engineering; Large-scale production of metabolites; Case studies in *E. coli*, *Saccharomyces*, and *Nicotiana*. 12 hours

Essential Readings: Zhu, X., et al. (2021) Synthetic biology of plant natural products: from pathway elucidation to engineered biosynthesis in plant cells. Plant Communications, 2(5):100229, DOI:10.1016/j.xplc.2021.100229; Karaca, H., et al. (2024) Metabolic engineering of *Saccharomyces cerevisiae* for enhanced taxadiene production. Microbial Cell Factories, 23(1):241, DOI:10.1186/s12934-024-02512-z; Zhao, S., et al. (2024) The metabolic engineering of *Escherichia coli* for the high-yield production of hypoxanthine. Microbial Cell Factories, 23(1):309, DOI:10.1186/s12934-024-02576-x.

Unit 4: Applications in Plant Defense, Human Health, and Ecology -- Role of secondary metabolites in plant defense (phytoalexins, VOCs, allelopathy); Ecological significance: VOCs in pollination, plant-insect interactions; Secondary metabolites in human health: antimicrobial, anticancer, antioxidant; Secondary metabolites in nutraceuticals and pharmaceuticals. 11 hours

Essential Readings: George, B.P., et al. (2021) Role of phytochemicals in cancer chemoprevention: Insights. Antioxidants, 10(9):1455, DOI:10.3390/antiox10091455; Divekar, P.A., et al. (2022) Plant secondary metabolites as defense tools against herbivores for sustainable crop protection. International Journal of Molecular Sciences, 23(5):2690, DOI:10.3390/ijms23052690.

Practicals (30 hours)

1. Extraction and qualitative analysis of plant secondary metabolites-saponins, phenolics, lignin.
2. Induction of secondary metabolite production in callus culture.
3. Demonstration of antimicrobial activity of plant extracts.
4. Detection of flavonoids during pollen development.
5. Effect of glucosinolate-derived compound, indole-3-carbinol, in plant root growth and development.

Suggested Readings:

1. Crozier, A., et al. (2006) Plant secondary metabolites: Occurrence, structure and role in the human diet. Blackwell Publishing, ISBN:9780470988558, DOI:10.1002/9780470988558.
2. Wink, M. (2010) Annual Plant Reviews Vol. 39: Functions and biotechnology of plant secondary metabolites. Blackwell Publishing, ISBN:9781444318876, DOI:10.1002/9781444318876.
3. Verpoorte, R. and Memelink, J. (2002) Engineering secondary metabolite production in plants. Current Opinion in Biotechnology, 13(2):181–187, DOI:10.1016/S0958-1669(02)00308-7.
4. Dewick, P.M. (2009) Medicinal Natural Products: A Biosynthetic Approach. John Wiley & Sons, ISBN:9780470742761, DOI:10.1002/9780470742761.
5. Katz, E., et al. (2015) The glucosinolate breakdown product indole-3-carbinol acts as an auxin antagonist in roots of *Arabidopsis thaliana*. The Plant Journal, 82(4):547–555, DOI: 10.1111/tpj.12824.

PBSE423: Epigenetics and Small RNA Biology

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE423: Epigenetics and Small RNA Biology	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

The epigenetic landscape (including both DNA methylation and histone modifications) of an organism has a significant bearing in regulating various developmental and metabolic processes at the global level. Similarly, small RNAs (sRNAs) have emerged as major modulators of global gene expression patterns. Therefore, this course is designed to provide students with a clear understanding of key epigenetic mechanisms, including chromatin modeling, DNA methylation, and histone modifications, and how these processes regulate plant development and physiology. Students will learn how epigenetic regulation contributes to environmental responses, stress adaptation, and inheritance, and its relevance in human systems, including immunity, cancer, and cardiovascular diseases. The course also introduces the diversity, biogenesis, and regulatory roles of non-coding RNAs across organisms, including their mechanisms of action and trans-kingdom interactions. Additionally, students will become familiar with experimental and computational tools for detecting, predicting, and validating small RNAs, and will explore the applications of RNA-based technologies and CRISPR-Cas systems in crop improvement, diagnostics, and therapeutic development.

Learning Outcomes

By the end of this course, students will be able to understand major epigenetic mechanisms and evaluate their roles in plant development, environmental responses, and human diseases. They will be able to understand DNA methylation and histone modifications, classify non-coding RNAs, and describe how small RNAs regulate gene expression. Students will also be equipped to use molecular and bioinformatic approaches for small RNA analyses and apply RNA-based tools. Overall, they will be able to integrate epigenetics and small RNA biology concepts to address research problems and understand their practical applications in agriculture, biotechnology, and human health.

Course Content (45 hours)

Unit 1: Epigenetic Regulation -- Chromatin modeling and remodeling: polycomb complexes, SWI/SNF1 complexes and other chromatin modifiers; DNA methylation and its interpretation: methylated DNA-binding proteins, their structure and function; techniques of altering and analyzing DNA methylation; Histone modifications: types, modifying enzymes, histone deacetylase inhibitors; Chromatin modification and its influence on plant development: somatic embryogenesis, leaf development, photosynthesis, flowering, and ageing. 12 hours

Essential Readings: Jenuwein, T. and Allis, C.D. (2001) Translating the histone code. Science, 293(5532):1074-1080, DOI:10.1126/science.1063127; Zhang, H., et al. (2018). Dynamics and function of DNA methylation in plants. Nature Reviews Molecular Cell Biology, 19(8):489-506, DOI:10.1038/s41580-018-0016-z; Rajewsky, N., et al. (2018) Plant epigenetics. Springer International, ISBN:9783319555195, DOI:10.1007/978-3-319-55520-1;

Huang, Y., et al., (2025) Chromatin remodeling in plants: Complex composition, mechanistic diversity, and biological functions. Molecular Plant, 18(9):1436–1457, DOI:10.1016/j.molp.2025.08.004.

Unit 2: Environmental and Evolutionary Epigenetics -- Role of epigenetic regulation in plant stress responses and epigenetic memory; Epigenetic inheritance and adaptive responses to environmental cues; Epigenetics in human systems: regulation of immune responses, cancer, and cardiovascular diseases. 10 hours

Essential Readings: Chinnusamy, V. and Zhu, J.K. (2009) Epigenetic regulation of stress responses in plants. Current Opinion in Plant Biology, 12(2):133–139, DOI:10.1016/j.pbi.2008.12.006; Avramova, Z. (2015) Transcriptional 'memory'of a stress: transient chromatin and memory (epigenetic) marks at stress-response genes. The Plant Journal, 83(1):149–159, DOI:10.1111/tpj.12832; Ma, L., et al., (2025) Epigenetic control of plant abiotic stress responses. Journal of Genetics and Genomics, 52(2):129–44, DOI:10.1016/j.jgg.2024.09.008; Janson, P.C. and Winqvist, O. (2011) Epigenetics–the key to understand immune responses in health and disease. American Journal of Reproductive Immunology, 66:72–74, DOI:10.1111/j.1600-0897.2011.01050.x; Zoghbi, H.Y. and Beaudet, A.L. (2016) Epigenetics and human disease. Cold Spring Harbor Perspectives in Biology, 8(2): a019497, DOI:10.1101/cshperspect.a019497.

Unit 3: Biology of Non-coding RNAs -- Discovery, types, occurrence, and diversity of non-coding RNAs; Small RNA pathways in bacteria, plants, and animal systems; Biogenesis and functional components of different classes of small RNAs; Regulation of gene expression by small RNAs: transcriptional gene silencing (TGS), post-transcriptional gene silencing (PTGS), gene activation, and evolutionary transitions in RNA-target interactions; Functional roles of small RNAs in different organisms; Trans-kingdom cross-talk mediated by small RNAs.

13 hours

Essential Readings: Guleria, P. and Kumar, V. (2020) Plant Small RNA- Biogenesis, Regulation and Application. Academic Press, ISBN:9780128171127, DOI:10.1016/C2018-0-01900-3; Alquethamy S., et al. (2025). What makes a small RNA work. Nucleic Acids Research, 53(12):gkaf563, DOI:10.1093/nar/gkaf563; Mattick, J. and Amaral, P. (2022) RNA, the epicenter of genetic information. ISBN:9781003109242, CRC Press, DOI:10.1201/9781003109242; Wierzbiki, A.T., et al. (2021) Long non-coding RNAs in plants. Annual Review of Plant Biology, 72:245–271, DOI:10.1146/annurev-arplant-093020-035446; Zhan, J. and Meyers, B.C. (2023) Plant small RNAs: their biogenesis, Regulatory roles, and functions. Annual Review of Plant Biology, 74:21–51, DOI:10.1146/annurev-arplant-070122-035226; Barquist, L. and Vogel, J. (2015) Accelerating discovery and functional analysis of small RNAs with new technologies. Annual Review of Genetics, 49:367–394, DOI:10.1146/annurev-genet-112414-054804.

Unit 4: Tools, Applications, and Emerging Technologies -- Discovery, detection, and validation of small RNAs; Target prediction and validation approaches; Databases and bioinformatic tools for small RNA analysis; Applications: artificial miRNA (amiR) technology, siRNA and virus-induced gene silencing (VIGS); RNAi interference (RNAi), RNA activation (RNAa), target mimicry and STTM technologies; CRISPR-Cas-based genome editing guided by small RNAs; Applications in crop improvement, diagnostics, and therapeutics. 10 hours

Essential Readings: Tang, G., et al. (2021) RNA-based technologies for functional genomics in plants. Springer Cham, ISBN:9783030649937, DOI:10.1007/978-3-030-64994-4; Ting, P., et al. (2018) A resource for inactivation of microRNAs using short tandem target mimic technology in model and crop plants. Molecular Plant, 11(11):1400–1417, DOI:10.1016/j.molp.2018.09.003; Halloy, F., et al. (2022) Innovative developments and emerging technologies in RNA therapeutics. 19(1):313–332, DOI:10.1080/15476286.2022.2027150.

Practicals (30 hours)

1. To resolve and visualize low molecular weight RNAs by denaturing urea-PAGE.
2. To perform expression analysis of selected miRNAs using the quantitative PCR method.

3. To isolate, sonicate, and observe cross-linked chromatin to study histone modifications.
4. To enzymatically cleave and assess DNA to detect methylation patterns.
5. To predict and analyze the secondary structure and thermodynamic stability of the miRNA precursor sequence (pre-miRNA) using Mfold.

Suggested Readings:

1. Esteller, M. (2009) Epigenetics in biology and medicine. CRC Press, eISBN:9780429124921.
2. Workman, J.L. and Abmayr, S.M. (2014) Fundamentals of chromatin. Springer New York, ISBN:9781461486237, DOI:10.1007/978-1-4614-8624-4.
3. Dinkar, V., et al. (2024) Epigenetic regulations under plant stress: a cereals perspective. Environmental and Experimental Botany, 220:105688, DOI:10.1016/j.envexpbot.2024.105688.
4. He, L. (2025) The interplay between chromatin remodeling and DNA double-strand break repair: Implications for cancer biology and therapeutics. DNA Repair, 146:103811, DOI:10.1016/j.dnarep.2025.103811.
5. Muka, T., et al. (2016) The role of epigenetic modifications in cardiovascular disease: a systematic review. International Journal of Cardiology, 212:174–183, DOI:10.1016/j.ijcard.2016.03.062.
6. Mallick, B. and Ghosh, Z. (2012) Regulatory RNAs: Basics, Methods and Applications. Springer Berlin, Heidelberg, ISBN:9783642225161, DOI:10.1007/978-3-642-22517-8.
7. Nellan, W. and Hammann, C. (2007) Small RNAs: analysis and regulatory functions. Springer Berlin, Heidelberg, ISBN:9783540281306, DOI:10.1007/978-3-540-28130-6.
8. Gaur, R.K. and Rossi, J.J. (2009) Regulation of gene expression by small RNAs. CRC Press, USA, eISBN:9780429121692, DOI:10.1201/9781420008708.
9. Alquethamy, S., et al. (2025) What makes a small RNA work? Nucleic Acids Research, 53(12):gkaf563, DOI:10.1093/nar/gkaf563.
10. Rederstorff, M. (2021) Small non-coding RNAs: Methods and Protocols. Humana New York. eISBN:9781071613863, DOI:10.1007/978-1-0716-1386-3.

PBSE424: Data Analytics and Biocuration

<u>This course is open to students of other departments as a GE course.</u>

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE424: Data Analytics and Biocuration	4	3	1	0	B.Sc. in any branch of science	

Learning Objectives

The paper aims to empower learners with foundational data analytics skills essential to modern bioinformatics by exposing them to the fundamentals of advanced operating systems, including the Linux command-line interface (CLI), file handling, permissions, and data manipulation. It also provides a brief exposure to the R programming environment, syntax, and functions for data analysis and packages available in the Bioconductor repository for statistical computing, data visualization, and genomic data analysis. It also provides a comprehensive overview of the primary computational workflows for analyzing next-generation sequencing (NGS) data. The learner will explore the concepts, applications, and key steps involved in major "big data" bioinformatics domains, including genome assembly, variant calling, pangenomics, metagenomics, transcriptomics (RNA-seq) and epigenomics (ChIP-seq, Bisulfite-seq). Besides, it also focuses on the behind-the-scenes work of biocuration that powers biological databases through processes of extracting, standardizing, and organizing biological data from literature and experiments. It provides an overview of BioDbCore, FAIRsharing, and ethical principles of open data management. The student will be able to interpret Gene Ontology and biomedical ontologies using OBO formats. In the last unit, there is a brief overview of foundational concepts of AI and machine learning (ML), along with the utility of domain-specific LLMs, their applications in genomics, drug design, and systems biology.

Learning Outcomes

The completion of the course will give expertise in essential Linux commands, set up and run 'R' scripts for statistical analysis and plotting. The learner can apply Bioconductor tools for biological data exploration, such as DESeq2, edgeR, and limma. Furthermore, students can analyse NGS data for variant calling, transcriptome quantification, and epigenomic data integration. They also now understand the FAIR data principles, ontologies, and the curation of biological data from published sources. Moreover, students can work with LLMs, ML, and AI tools across domains such as genomic prediction, phenotype classification, drug discovery, and structure-based screening.

Course Content (45 hours)

Unit 1: Basic of Linux and 'R' -- Computer architecture, types of operating systems (Windows, Mac-OS and Linux), concept of networking (IP address); Basic fundamentals of working with Unix/Linux on CLI (Command Line Interface), Unix/Linux directory structure, file permissions, remote login; Linux commands (whoami, pwd, cd, ls, man, mkdir, rm, cat copy, mv, chmod, grep, sed, sep, sort, head, tail, wc); Introduction to the 'R' data analysis package, basic work environment, syntax, introduction to the 'Bioconductor' packages for data analysis. 15 hours

Essential Readings: Blum, R. and Bresnahan, A. (2021) Linux Command Line and Shell Scripting Bible. 4th edition, John Wiley & Sons, Inc., ISBN:9781119700913; Kabacoff, R.I. (2022) R in action: Data analysis and graphics with R. 3rd edition, Manning Publications, ISBN:9781617296055; Gentleman, R.C., et al. (2004) Bioconductor: open software development for computational biology and bioinformatics. Genome Biology, 5:R80, DOI:10.1186/gb-2004-5-10-r80.

Unit 2: Big Data Analysis -- Whole genome reference-based assembly, de-novo genome analysis, variant call analysis, Pangenomes, Metagenomic analysis, RNA-seq data analysis, ChIP (Chromatin Immunoprecipitation) data analysis; Whole genome bisulphite sequencing data analysis. 10 hours

Essential Readings: Compeau, P. and Pevzner, P. (2018) Bioinformatics algorithms: An active learning approach. 3rd edition, Active Learning Publishers, ISBN:9780990374633; Shendure, J. and Aiden, E.L. (2012) The expanding scope of DNA sequencing. Nature Biotechnology, 30(11):1084–1094, DOI:10.1038/nbt.2421; Conesa, A., et al. (2016) A survey of best practices for RNA-seq data analysis. Genome Biology, 17:13, DOI:10.1186/s13059-016-0881-8; Landt, S.G., et al. (2012) ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. Genome Research, 22(9):1813–31, DOI:10.1101/gr.136184.111.

Unit 3: Data Integration and Biocuration -- Overview of Biocuration, various approaches for biocuration, BioDbCore guidelines, FAIRsharing and ethics in data sharing, Text/Literature-based curation, text mining approaches, introduction to tools such as Textpresso. Basics and importance of ontology development, OBO (Open Biological and Biomedical Ontology) format, OBO foundary, biomedical and plant-based ontologies.

10 hours

Essential Readings: Gaudet, P., et al. (2011) Towards BioDBcore: a community-defined information specification for biological databases. Nucleic Acids Research, 39(s1):D7–D10, DOI:10.1093/nar/gkq1173; Open Biological and Biomedical Ontology Foundry: Community development of interoperable ontologies for the biological sciences, https://obofoundry.org/about-OBO-Foundry.html; FAIRsharing: A curated, informative and educational resource on data and metadata standards, inter-related to databases and data policies, https://fairsharing.org, DOI:10.1038/s41587-019-0080-8; Howe, D., et al. (2008) The future of biocuration. Nature, 455:47–50, DOI:10.1038/455047a; Wilkinson, M.D., et al. (2016) The FAIR Guiding Principles for scientific data management and stewardship. Scientific Data, 3:160018, DOI:10.1038/sdata.2016.18.

Unit 4: Artificial Intelligence in Life Sciences -- Introduction to Machine-Learning (ML) and Artificial Intelligence (AI); Supervised and un-supervised learning approaches in data integration, interpretation, and predictive modelling; Applications in genomic prediction, drug discovery, ecosystem modelling; Domain-specific Large Language Models (LLMs). 10 hours

Essential Readings: Cannataro, M., et al. (2022) Artificial Intelligence in Bioinformatics: from omics analysis to deep learning and network mining, 1st edition, Elsevier, eISBN:9780128229293; Jumper, J., et al. (2021) Highly accurate protein structure prediction with AlphaFold. Nature, 596:583–589, DOI:10.1038/s41586-021-03819-2.

Tutorials (15 hours)

1. Practice of working with Linux commands on the Command Line Interface (CLI).
2. Analysis of RNA-seq data:
    a. Quality and adapter trimming of Next Generation Sequencing (NGS) data.
    b. Reference-based genome mapping of NGS data.
    c. Identification of differentially expressed genes.
3. Use of Gene Ontology for gene function analysis.

Suggested Readings:

1. Bessant, C., et al. (2014) Building bioinformatics solutions with Perl, R, and SQL. 2nd edition, Oxford University Press, UK, ISBN:978019965855.
2. Buffalo, V. (2015) Bioinformatics data skills: Reproducible and robust research with open-source tools. O'Reilley Media, ISBN:9781449367374.
3. Quince, C., et al. (2017) Shotgun metagenomics, from sampling to analysis. Nature Biotechnology, 35(9):833–844, DOI:10.1038/nbt.3935.
4. Sansone, S.A., et al. (2019) FAIRsharing as a community approach to standards, repositories and policies, Nature Biotechnology, 37(4):358–367, DOI:10.1038/s41587-019-0080-8.
5. Smith, B., et al. (2007) The OBO Foundry: coordinated evolution of ontologies to support biomedical data integration, Nature Biotechnology, 25(11):1251–1255, DOI:10.1038/nbt1346.
6. Müller, H.M., et al. (2018) Textpresso Central: a customizable platform for searching, text mining, viewing, and curating biological literature. BMC Bioinformatics, 19:94, DOI:10.1186/s12859-018-2103-8.
7. Web link: www.bioconductor.org
8. Web link: www.obofoundary.org; www.oboedit.org
9. Web link: www.biocuration.org

PBSE425: Plant Phenomics

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE425: Plant Phenomics	4	3	1	0	B.Sc. in any branch of science	

Course Objectives

This course aims to introduce students to the conceptual and methodological foundations of plant phenomics, spanning trait ontology, G×E×M frameworks, and robust experimental design. It seeks to familiarise students with controlled-environment and field phenotyping platforms, diverse imaging modalities, and 3D architectural reconstruction. A further objective is to develop competence in end-to-end phenomics data pipelines, from image acquisition to quantitative trait extraction and machine-learning-based modelling, enabling critical engagement with current literature and applications in crop improvement and stress biology.

Learning Outcomes

Upon successful completion, students will be able to define and differentiate plant phenomics from classical phenotyping, design basic phenotyping experiments with appropriate traits, platforms and metadata, and justify these choices. They will interpret and compare outputs from RGB, fluorescence, thermal, spectral and 3D imaging in controlled and field settings. Students will execute simple image-analysis workflows, apply elementary machine learning for phenotypic data, critically evaluate published phenomics studies, and articulate how phenomics informs breeding, resilience and systems-level plant biology.

Course Content (45 hours)

Unit 1: Foundations of Plant Phenomics and Trait Biology -- Definition and scope of plant phenomics; Distinction between classical phenotyping and high-throughput phenomics; Links to functional genomics, systems biology, and crop improvement; Trait ontology (morphological, physiological, developmental, functional traits); G×E×M (genotype× environment×management) framework; Principles of experimental design (replication, randomisation, blocking, temporal sampling); Metadata standards and FAIR (Findable, Accessible, Interoperable, and Reusable) data; Evolution of phenotyping platforms and international phenomics networks; Ideotype concepts and gene-to-phenotype mapping.

12 hours

Essential Readings: Chen, J.T. (2025) Plant high-throughput phenotyping and functional phenomics. CRC Press, eISBN:9781003505631, DOI:10.1201/9781003505631, Chapter 2 (Plant high-throughput phenotyping and phenomics for accelerating crop breeding), Chapter 9 (High-throughput phenotyping and phenomics for exploration of plant growth and development), Chapter 13 (High-throughput plant phenotyping and phenomics: Advances and prospects); Fiorani, F. and Schurr, U. (2013) Future scenarios for plant phenotyping. Annual Review of Plant Biology, 64:267–291, DOI:10.1146/annurev-arplant-050312-120137; Papoutsoglou, E.A., et al. (2023) The benefits and struggles of FAIR data: the case of reusing plant phenotyping data. Scientific Data, 10(1):595, DOI:10.1038/s41597-023-02364-z.

Unit 2: Controlled-Environment Phenomics and Imaging Modalities -- Growth chamber and greenhouse phenotyping platforms; conveyor- and chamber-based systems; Longitudinal monitoring of growth and development; RGB (Red, Green, and Blue) imaging for morphology, colour indices, and growth curves; Chlorophyll fluorescence imaging (PSII efficiency, stress signatures); Thermal imaging (canopy temperature, transpiration proxies); Multispectral and hyperspectral imaging for pigment and biochemical traits; Controlled root phenotyping [rhizotrons, gel systems, CT (Computed Tomography)/MRI (Magnetic Resonance Imaging) concepts]; Calibration, illumination control, reference standards; Time-series design for controlled-environment stress and treatment experiments. 10 hours

Essential Readings: Lorence, A. and Jimenez, K.M. (2022) High-throughput plant phenotyping: Methods and Protocols. Methods in Molecular Biology. Humana New York, ISBN:9781071625361, DOI:10.1007/978-1-0716-2537-8, Chapter 5 (A straightforward high-throughput aboveground phenotyping platform for small- to medium-sized plants), Chapter 6 (Wireless fixed camera network for greenhouse-based plant phenotyping), Chapter 7 (Experimental design for controlled environment high-throughput plant phenotyping); Zhang, Y. and Zhang, N. (2018) Imaging technologies for plant high-throughput phenotyping: a review. Frontiers of Agricultural Science and Engineering, 5(4):406–419, DOI:10.15302/J-FASE-2018242; Mahlein, A.K., et al. (2018) Hyperspectral sensors and imaging technologies in phytopathology: state of the art. Annual Review of Phytopathology, 56:535–558, DOI:10.1146/annurev-phyto-080417-050100.

Unit 3: Field Phenomics, Remote Sensing, and 3D Architecture -- Fixed gantry, tractor-/robot-mounted and handheld phenotyping systems; UAV (Unmanned Aerial Vehicle)-based phenotyping with RGB, multispectral, and hyperspectral sensors; Vegetation indices (NDVI (Normalized Difference Vegetation Index), NDRE (Normalized Difference Red Edge Index), etc. for growth, water and nutrient status; Canopy temperature mapping; LiDAR and stereo vision for 3D reconstruction; Point clouds and structural traits; Integration of environmental data with phenotypic measurements; Spatial heterogeneity and experimental layout; Applications in breeding across diverse field environments. 12 hours

Essential Readings: Chen, J.T. (2025) Plant high-throughput phenotyping and functional phenomics. CRC Press, eISBN:9781003505631, DOI:10.1201/9781003505631, Chapter 3 (Remote sensing technologies for high-throughput in-field crop phenotyping, Chapter 4 (High-Throughput field phenotyping: Enhancing crop monitoring for food security), Chapter 10 (Root phenotyping for breeding of climate-resilient crops), Chapter 16 (Robotics and aerial vehicle for high-throughput phenotyping: technologies and prospects); Araus, J.L. and Cairns, J.E. (2014) Field high-throughput phenotyping: the new crop breeding frontier. Trends in Plant Science, 19(1):52–61, DOI:10.1016/j.tplants.2013.09.008; Guo, W., et al. (2021) UAS-based plant phenotyping for research and breeding applications. Plant Phenomics, 2021:9840192, DOI:10.34133/2021/9840192.

Unit 4: Data Pipelines, Image Analysis, and Machine Learning in Phenomics -- End-to-end phenomics data pipeline (acquisition, pre-processing, segmentation, feature extraction, trait computation); Use of ImageJ/Fiji, PlantCV and related open-source tools; Machine learning for phenotyping; Deep learning and CNNs for segmentation, Classification and regression; Model training, validation and evaluation; Phenomic features in GWAS, genomic prediction and phenomic selection; Data management, reproducibility, model transferability and interpretability. 11 hours

Essential Readings: Chen, J.T. (2025) Plant high-throughput phenotyping and functional phenomics. CRC Press, eISBN:9781003505631, DOI:10.1201/9781003505631, Chapter 1 (Bioinformatics tools and deep learning for plant high-throughput phenotyping and phenomics), Chapter 15 (Statistical tools and data analysis for organizing plant high-throughput phenomics); Murphy, K.M., et al. (2024) Deep learning in image-based plant phenotyping. Annual Review of Plant Biology, 75:771–795, DOI:10.1146/annurev-arplant-070523-042828; Danilevicz, M.F., et al. (2021) Resources for image-based high-throughput phenotyping in crops and data sharing challenges. Plant Physiology, 187(2):699–715, DOI:10.1093/plphys/kiab301.

Tutorials (15 hours)

1. Short presentations on landmark phenomics papers.
2. Designing a basic phenotyping experiment (traits, platform, experimental design, metadata sheet).
3. Hands-on demonstrations with sample image datasets.
4. Analysis of PSII efficiency (Fv/Fm) and photosynthetic activity [fluorescence decline ratio in steady state (Rfd_*Lss*)] in control and stress plants.

Suggested Readings:

1. Chen, J.T. (2025) Plant high-throughput phenotyping and functional phenomics. CRC Press, ISBN:9781003505631, DOI:10.1201/9781003505631.
2. Lorence, A. and Jimenez, K.M. (2022) High-throughput plant phenotyping: Methods and Protocols. Methods in Molecular Biology, Humana New York, DOI:10.1007/978-1-0716-2537-8.
3. Awada, L., et al. (2024) The evolution of plant phenomics: Global insights, trends, and collaborations (2000-2021). Frontiers in Plant Science, 15:1410738, DOI:10.3389/fpls.2024.1410738.
4. Großkinsky, D.K., et al. (2023) The potential of integrative phenomics to harness underutilized crops for improving stress resilience. Frontiers in Plant Science, 14:1216337, DOI:10.3389/fpls.2023.1216337.
5. Singh, A., et al. (2016) Machine learning for high-throughput stress phenotyping in plants. Trends in Plant Science, 21(2):110–124, DOI:10.1016/j.tplants.2015.10.015.
6. Abebe, A.M., et al. (2023) Image-based high-throughput phenotyping in horticultural crops. Plants, 12(10):2061, DOI:10.3390/plants12102061.
7. Xu, R. and Li, C. (2022) A review of high-throughput field phenotyping systems: Focusing on ground robots. Plant Phenomics, 2022:9760269, DOI:10.34133/2022/9760269.
8. Gano, B., et al. (2024) Drone-based imaging sensors, techniques, and applications in plant phenotyping for crop breeding: A comprehensive review. The Plant Phenome Journal, 7(1): e20100, DOI:10.1002/ppj2.20100.
9. Li, S., et al. (2025) A review of optical-based three-dimensional reconstruction and multi-source fusion for plant phenotyping. Sensors, 25(11):3401, DOI:10.3390/s25113401.
10. Su, M., et al. (2025) Design and implementation of high-throughput field phenotyping robot for acquiring multisensory data in wheat. Plant Phenomics, 7(2):100014, DOI:10.1016/j.plaphe.2025.100014.
11. Adak, A., et al. (2023) Phenomic data-driven biological prediction of maize through field-base high-throughput phenotyping integration with genomic data. Journal of Experimental Botany, 74(17):5307–5326, DOI: 0.1093/jxb/erad216.
12. Zavafer, A., et al. (2023) Phenomics: conceptualization and importance for plant physiology. Trends in Plant Science, 28(9):1004–1013, DOI:10.1016/j.tplants.2023.03.023.
13. Lichtenthaler, H.K. and Miehé, J.A. (1997) Fluorescence imaging as a diagnostic tool for plant stress. Trends in Plant Science, 2(8):316–320, DOI:10.1016/S1360-1385(97)89954-2.

PBRE426: Dissertation-II

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBRE426: Dissertation-II	6	0	0	6	B.Sc. in any branch of science	NA

Learning Objectives

The students will work independently on the research problem chosen in Semester 3 and will apply appropriate molecular, biochemical, physiological and/or computational approaches to address the defined objectives and hypotheses. They will learn to design and execute experiments with suitable controls and replicates, systematically collect, document, and analyse data using relevant statistical and bioinformatic tools, and interpret the results in the context of existing knowledge. They will further strengthen their skills in scientific writing by updating and refining the literature review and by preparing a well-organized dissertation adhering to standard formats, citation styles, and ethical guidelines. The student will also develop competencies in scientific communication by regularly discussing their work in lab meetings and presenting their findings through formal oral presentations.

Learning Outcomes

On successful completion of the dissertation, the student will be able to independently plan and conduct the experiments with appropriate controls, optimize and adapt protocols, and troubleshoot technical problems in response to experimental challenges. They will maintain systematic and complete laboratory records, generate reproducible datasets, and carry out quantitative/qualitative analyses, including appropriate statistical tests and data visualization. They will be able to critically interpret and integrate their experimental findings with published literature to draw logical, evidence-based conclusions, identify limitations, and suggest future directions. The student will be able to prepare a coherent dissertation that includes an updated literature review, methodology, results, discussion, and references in a standard format. They will exhibit professional research attitudes, including scientific rigor, ethical conduct, teamwork, and responsible data and time management in the laboratory to meet defined timelines and submission deadlines.

Suggested Readings:

Latest research and review articles on the chosen research topic.

Structure 3 - PG with Research

SEMESTER 3

PBSC331: Plant Biotechnology

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSC331: Plant Biotechnology	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

This course will enable students to understand the core principles and milestones of plant biotechnology, including the molecular basis of crop domestication and Green Revolution traits, as well as concepts in tissue culture. Students will learn about the molecular toolbox for plant genetic engineering and be introduced to advanced approaches, including RNAi, genome editing, and synthetic biology, for pathway engineering. The course will build conceptual understanding of modern gene/QTL mapping, marker-assisted and genomic selection, speed breeding, and gene pyramiding, together with applications of plant biotechnology in molecular farming, biofortification, climate resilience, plant-microbe interactions, and industrial and environmental biotechnology. Finally, students will be sensitized to biosafety guidelines, GMO risk assessment, IPR, farmers' rights, and ethical and societal issues in plant biotechnology.

Learning Outcomes

On completing the course, students will be able to explain and apply tissue culture and related technologies for crop improvement. They will be able to outline and compare plant transformation and genome editing strategies, design genetic constructs and describe workflows for the generation and characterization of transgenic and edited plants. Students will be able to select appropriate molecular markers and mapping approaches for dissecting complex traits, and integrate marker-assisted selection, genomic selection, and breeding pipelines. They will be able to critically analyse case studies such as Golden rice, Bt cotton, virus-resistant papaya, and DH mustard, among others. In addition, they will be able to interpret biosafety and regulatory frameworks, IPR/PBR/farmer's rights provisions, and articulate ethical, social, and policy implications of deploying plant biotechnological innovations in agriculture.

Course Content (45 hours)

Unit 1: Fundamentals and Scope of Plant Biotechnology -- Concept, history, and milestones in plant biotechnology; Molecular basis of crop domestication and Green revolution; Principles of plant tissue culture, totipotency, and micropropagation; Somaclonal variation, somatic embryogenesis, and synthetic seeds; Protoplast fusion and somatic hybridization. 5 hours

Essential Readings: Stewart Jr., C.N. (2025) Biotechnology and Genetics: Principles, Techniques, and Applications. 3rd edition, John Wiley & Sons, ISBN:9781394217236, Chapter 1 (Plant Agriculture: The impact of biotechnology); Abdin, M.Z, et al. (2017) Plant Biotechnology: Principles and Applications, Springer Verlag,

Singapore, ISBN:9789811029592, Chapter 1 (Historical perspective and basic principles of plant tissue culture), Chapter 2 (Plant tissue culture: Applications in plant improvement and conservation); Pathirana, R. and Carimi, F. (2024) Plant biotechnology-an indispensable tool for crop improvement. Plants (Basel), 13(8):1133, DOI:10.3390/plants13081133.

Unit 2: Molecular Tools and Techniques -- Genetic cloning strategies and vector systems; Promoters, selectable markers, and reporter genes; Gene transfer methods; Chloroplast transformation; Characterization of transgenic plants at molecular, biochemical, and phenotypic level; Case studies: Golden rice, Bt cotton, virus-resistant papaya, herbicide-tolerant crops, Dhara Mustard, any other product; Virus-induced gene silencing (VIGS) methods; Genome editing technologies [Zinc Finger Nucleases, Transcription activator-like effector nucleases, Clustered Regularly Interspaced Short Palindromic Repeats or CRISPR)/CRISPR-associated (Cas) systems, prime editing, base editing, and miniature RNA-guided endonuclease]; Generation of marker-free transgenics; RNAi interference (RNAi); Introduction of synthetic biology and metabolic pathway engineering. 15 hours

Essential Readings: Li, B., et al. (2024) Targeted genome-modification tools and their advanced applications in crop breeding. Nature Reviews Genetics, 25(9):603–622, DOI:10.1038/s41576-024-00720-2; Liu, W., et al. (2013) Advanced genetic tools for plant biotechnology. Nature Review Genetics, 14:781–793, DOI:10.1038/nrg3583; Gupta, O.P. and Karkute, S.G. (2021) Genome editing in plants: Principles and applications, CRC Press, ISBN:9780367415907, Chapter 1 (Historical developments of genome editing in plants), Chapter 2 (Mechanism of ZFN mediated genome editing: scope and opportunities), Chapter 3 (TALEN: customizable molecular scissors for tailoring newer types of genomes in plants), Chapter 4 (Mechanism of CRISPR/Cas9 mediated genome editing: scope and opportunities); Koeppe, S., et al. (2023) RNA interference: past and future applications in plants, International J. Molecular Science, 24(11):9755, DOI: 10.3390/ijms24119755; Singh, R., et al. (2023) A prospective review on selectable marker-free genome engineered rice: past, present and future scientific realm, Frontiers in Genetics, 13:2022, DOI:10.3389/fgene.2022.882836; Aaron, S., et al. (2020) Metabolic engineering and synthetic biology of plant natural products – A minireview. Current Plant Biology, 24:100163, DOI:10.1016/j.cpb.2020.100163.

Unit 3: Mapping of Genes/QTLs -- High-throughput molecular markers and genotyping assays; Bulk segregant analysis (QTL-seq), Target-Sequence Enrichment and Sequencing (TEnSeq), Resistance gene enrichment sequencing (RenSeq), and Mutation mapping (MutMap, MutMap-Gap, etc); Genome-Wide Association Studies (GWAS); Marker-assisted plant breeding and genomic selection (GS); Speed breeding; Gene Pyramiding; Hybrid breeding and doubled haploid technologies. 15 hours

Essential Readings: Jaganathan, D., et al. (2020) Fine mapping and gene cloning in the post-NGS era: advances and prospects. Theoretical and Applied Genetics, 133(5):1791–1810, DOI:10.1007/s00122-020-03560-w; Wang, X., et al. (2023) Next-generation bulked segregant analysis for Breeding 4.0. Cell Reports, 42(9):113039, DOI:10.1016/j.celrep.2023.113039; Uffelmann, E., et al. (2021) Genome-wide association studies. Nature Reviews Methods Primers, 1:59, DOI:10.1038/s43586-021-00056-9; Kabade, P.G., et al. (2025) Speed breeding 3.0: mainstreaming light-driven plant breeding for sustainable genetic gains. Trends in Biotechnology, 43(10):2462–2478, DOI:10.1016/j.tibtech.2025.04.011; Crossa, J., et al. (2017) Genomic selection in plant breeding: methods, models, and perspectives, Trends in Plant Science, 22*(*11):961–975, DOI:10.1016/j.tplants.2017.08.011; Qu, Y., et al. (2024) Doubled haploid technology and synthetic apomixis: Recent advances and applications in future crop breeding. Molecular Plant, 17(7):1005–1018, DOI:10.1016/j.molp.2024.06.005.

Unit 4: Applications and Societal Aspects of Plant Biotechnology -- Molecular farming; Biofortification and nutritional enhancement; Manipulating and harnessing plant-microbe interactions: disease resistant plants, biofertilizers, biopesticides, and mycorrhizal biotechnology; Climate-resilient crops: generation of abiotic stress tolerant plants; Industrial Biotechnology: bioethanol and other products; Environmental biotechnology: phytoremediation; Regulatory frameworks: biosafety guidelines, GMO risk assessments, and

intellectual property rights (IPR); Plant breeders' rights (PBRs) and farmers' rights; Ethical, social, and policy implications of plant biotechnology. 10 hours

Essential Readings: Shanmugaraj, B., et al. (2020) Plant molecular farming: A viable platform for recombinant biopharmaceutical production. Plants, 9(7):842, DOI:10.3390/plants9070842; Garg, M., et al. (2024) Biofortification for nutrient-rich crops. ISBN:9781032690636, DOI:10.1201/9781032690636; Digel, I., et al. (2025) Introduction to Industrial Biotechnology, Springer Cham, ISBN:9783032079183, DOI:10.1007/978-3-032-07918-3; Abdin, M.Z., et al. (2017) Plant Biotechnology: Principles and Applications, Springer Verlag, Singapore, ISBN:9789811029592, Chapter 14 (Biosafety, Bioethics, and IPR Issues in Plant Biotechnology); Protection of plant varieties and farmers' right act (PPV & FR), 2001, Ministry of Agriculture and Farmers Welfare, GoI; Standard Operating Procedures for regulatory review of genome edited plants under SDN-1 and SDN-2 categories 2022 and Guidelines on genetically engineered plants containing stacked events 2025 by Department of Biotechnology, MoS&T, GoI.

Practicals (30 hours)

1. Assessment of promoter activity in transgenic plants using beta-glucuronidase (GUS) reporter through histochemical staining and fluorometric (MUG) assays.
2. To perform PCR-based screening of *Arabidopsis* T-DNA insertion lines to distinguish heterozygous and homozygous plants.
3. Genome editing of a target gene in a plant (GFP/transient assay).
4. T7E1/ Surveyor mismatch cleavage assays to detect mutated/edited genomic regions.
5. Construction of a plant genetic linkage map with molecular markers.

Suggested Readings:

1. Acquaah, G. (2020) Principles of Plant Genetics and Breeding, 3rd edition, Wiley-Blackwell, ISBN:9781119626695.
2. Al-Khayri, J.M., et al. (2025) Genome Editing for Crop Improvement - Theory and Methodology. CAB International, ISBN:9781800622494.
3. Hille, F., et al. (2018) The biology of CRISPR-Cas: Backward and forward. Cell, 172(6):1239–1259, DOI:10.1016/j.cell.2017.11.032.
4. Singh, B.D. and Singh, A.K. (2015) Marker-Assisted Plant Breeding: Principles and Practices, Springer New Delhi, ISBN:9788132223160, DOI:10.1007/978-81-322-2316-0.
5. Clauw, P., et al. (2025) Beyond the standard GWAS-A guide for plant biologists. Plant and Cell Physiology, 66(4):431–443, DOI:10.1093/pcp/pcae079.
6. Quiroz, L.F., et al. (2024) Haploid rhapsody: the molecular and cellular orchestra of *in vivo* haploid induction in plants. New Phytologist, 241(5):1936–1949, DOI:10.1111/nph.19523.
7. Ghosh, S., et al. (2018) Speed breeding in growth chambers and glasshouses for crop breeding and model plant research. Nature Protocols, 13:2944–2963, DOI:10.1038/s41596-018-0072-z.
8. Chen, J.T. (2024) Plant speed breeding and high-throughput technologies, CRC Press, ISBN: 9781003434733.
9. Xiong, J., et al. (2023) Synthetic apomixis: the beginning of a new era. Current Opinion in Biotechnology, 79:102877, DOI:10.1016/j.copbio.2022.102877.
10. WHO (2004) Laboratory Biosafety Manual, 3rd edition
11. FAO (2018) Biosafety Primer.
12. Department of Biotechnology (DBT), MoS&T, GoI (2023) Intellectual Property Guidelines.
13. Scientific Journals: Plant Biotechnology Reports; International Journal of Plant Biotechnology; Plant Biotechnology Journal; Transgenic Research; Journal of Plant Biotechnology; Plant Cell, Tissue and Organ Culture.
14. Singh, K.K. (2014) Biotechnology and intellectual property rights-legal and social implications. ISBN:9788132220596, DOI:10.1007/978-81-322-2059-6.

PBSE334: Frontiers in Plant Molecular Biology

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE334: Frontiers in Plant Molecular Biology	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

This course has been designed to introduce students to state-of-the-art concepts, technologies, and experimental systems that define modern plant molecular biology and its translational applications. It aims to develop a rigorous understanding of plant signaling architectures, multi-omics-driven functional genomics, structural advances in genome biology, and emerging domains such as epitranscriptomics, nanobiotechnology, and space biology. Furthermore, it aims to enable students to relate primary discoveries in calcium, ROS, hormone and retrograde signaling to crop improvement, biosensing, and stress resilience through synthetic and genome engineering approaches, supported by current literature in plant signaling and systems biology.

Learning Outcomes

After successful completion of the course, students will be able to critically interpret and integrate datasets from transcriptomic, proteomic, metabolomic, epigenomic, and phenomics platforms to elucidate gene function and regulatory networks in plants. They should be able to design and conceptualize CRISPR-based functional analyses, visualize and analyse gene interaction networks, and evaluate gene function prediction, stress-tolerance forecasting, and genome-assisted breeding. Students will also be able to assess emerging tools, such as optogenetics, targeted epigenome editing, and plant nanotechnology, for their feasibility for research or crop applications, thereby demonstrating their research readiness.

Course Content (45 hours)

Unit 1: Forefront of Plant Signaling -- Mechanosensing and electrosensing; Receptor dynamics and nanodomains; Phosphoswitches and dynamic network mapping; Organelle-to-nucleus signaling (retrograde signaling); Optogenetics and chemical biology tools; Live-cell imaging of Ca^{2+} and ROS dynamics; Phytohormone dynamics studies; Engineering synthetic receptors or signaling circuits for stress tolerance or biosensing. 11 hours

Essential Readings: Hamilton, E.S., et al. (2015) United in diversity: mechanosensitive ion channels in plants, Annual Review of Plant Biology, 66:113–37, DOI:10.1146/annurev-arplant-043014-114700; Fromm, J. and Lautner, S. (2007) Electrical signals and their physiological significance in plants. Plant Cell and Environment, 30(3):249–257, DOI:10.1111/j.1365-3040.2006.01614.x; Wang, L., et al. (2018) Exploring the spatiotemporal organization of membrane proteins in living plant cells. Annual Review of Plant Biology, 69:525–551, DOI:10.1146/annurev-arplant-042817-040233; Zhang, J., et al. (2023) Protein phosphorylation: A molecular switch in plant signaling. Cell Reports, 42(7):112729, DOI:10.1016/j.celrep.2023.112729; Tatjana, K. and Dario, L. (2016) Retrograde signaling: Organelles go networking. Biochimica et Biophysica Acta (BBA)–Bioenergetics, 1857(8):1313–1325, DOI:10.1016/j.bbabio.2016.03.017; Hiromasa, S. and Philipp, D. (2022) Plant optogenetics: Applications and perspectives. Current Opinion in Plant Biology, 68:102256, DOI:10.1016/j.pbi.2022.102256; Sarah, J., et al. (2011) *In vivo* imaging of Ca^{2+}, pH, and reactive oxygen species using fluorescent probes in plants. Annual Review of Plant Biology, 62:273–297, DOI:10.1146/annurev-arplant-042110-103832; Rainer, W. (2020) Phytohormone signaling mechanisms and genetic methods for their

modulation and detection, Current Opinion in Plant Biology, 57:31–40, DOI:10.1016/j.pbi.2020.05.011; Ondřej N., et al. (2017) Zooming in on plant hormone analysis: Tissue- and cell-specific approaches. Annual Review of Plant Biology, 68:323–348, DOI:10.1146/annurev-arplant-042916-040812; Alexander, R.L., et al. (2020) Engineering synthetic signaling in plants. Annual Review of Plant Biology, 71:767–788, DOI:10.1146/annurev-arplant-081519-035852.

Unit 2: Structural and Functional Genomics -- Third- and fourth-generation sequencing platforms and their applications in plant genome analysis, principles of transcriptomics and proteomics, including experimental design and data interpretation; Case study-based functional genomics strategies such as large-scale mutagenesis (T-DNA, CRISPR/Cas), RNAi, VIGS and activation tagging to elucidate gene function; Understanding advanced layers of regulation through RNA-seq, ribosome profiling, single-nucleus RNA-seq, and epigenomic assays such as ATAC-seq, ChIP-seq and DNA methylome analysis. 12 hours

Essential Readings: Brown, T.A. (2023) Genomes 5. CRC Press, ISBN:9781003133162, Chapter 4 (Sequencing Genomes), Chapter 9 (Transcriptomes and Proteomes), Chapter 10 (Genome Regulation); Mardis, E.R. (2008) Next-generation DNA sequencing methods. Annual Review of Genomics and Human Genetics, 9:387–402, DOI:10.1146/annurev.genom.9.081307.164359; Chappell, L., et al. (2018) Single-Cell (Multi)omics Technologies. Annual Review of Genomics and Human Genetics, 19:15–41, DOI: 10.1146/annurev-genom-091416-035324.

Unit 3: **Applied Aspects of Plant-Environment Interactions** -- Overview of plant responses to abiotic and biotic stresses; Molecular signaling pathways; Omics-driven discovery of stress tolerance genes; Engineering the plant microbiome; Spatial and integrative omics for stress biology: single cell vs. tissue level omics, transcriptomics and metabolite mapping of root-soil interface; Inter-kingdom communication; AI and ML in prediction of stress-tolerant genotypes. 11 hours

Essential Readings: Tuteja, N. and Gill, S.S. (2016) Abiotic stress responses in plants. ISBN:9783527339181, Wiley-VCH Verlag GmbH & Co., Chapter 1 (Abiotic stress signaling in plants: an overview); Zhang H., et al. (2022) Abiotic stress responses in plants. Nature Review Genetics, 23:104–119, DOI:10.1038/s41576-021-00413-0; Jiang Z., et al. (2025) Mechanisms of plant acclimation to multiple abiotic stresses. Communications Biology, 8:655, DOI:10.1038/s42003-025-08077-w; Mochida, K., et al. (2020) Decoding plant–environment interactions that influence crop agronomic traits. Plant and Cell Physiology, 61(8):1408–1418, DOI:10.1093/pcp/pcaa064; Du, B., et al. (2024) Strategies of plants to overcome abiotic and biotic stresses. Biological Reviews, 99(4):1524–1536, DOI: 10.1111/brv.13079; Varadharajan, V., et al. (2025) Multi-omics approaches against abiotic and biotic stress-A review. Plants, 14(6):865, DOI:10.3390/plants14060865; Afridi M.S., et al. (2022) New opportunities in plant microbiome engineering for increasing agricultural sustainability under stressful conditions. Frontiers in Plant Sciences, 13:899464, DOI:10.3389/fpls.2022.899464; Special issue on "Use of single cell and spatial multiomics for uncovering cellular and molecular mechanisms underlying plant stress responses". Stress Biology, 2025; Salem M.A., et al. (2022) Metabolomics of plant root exudates: From sample preparation to data analysis, Frontiers in Plant Sciences, 13:1062982, DOI:10.3389/fpls.2022.1062982; Singhal, R., et al. (2025) Using supervised machine-learning approaches to understand abiotic stress tolerance and design resilient crops. Philosophical Transactions of the Royal Society B, 380:2024.0252, DOI:10.1098/rstb.2024.0252.

Unit 4: Emerging Tools and Techniques -- Epitranscriptomics; Targeted epigenome editing: development of specific DNA-targeting systems, next-generation CRISPR activators, applications in agriculture; Nanotechnology and its applications in plant biology: types of nanomaterials, uptake and translocation, biological impact, applications of nanoparticles (NPs) in plant biology (biosensors, nutrient delivery, nanomaterials in plant genetic engineering (DNA / RNA delivery); Plant biology in space: growth and monitoring, effects of microgravity and ionizing radiations, applications, and benefits. 11 hours

Essential Readings: Kumari, A., et. al. (2023) Nanotechnology as a powerful tool in plant sciences: Recent developments, challenges and perspectives. Plant Nano Biology, 5:100046, DOI:10.1016/j.plana.2023.100046; Sanzari, I., et. al. (2019) Nanotechnology in plant science: To make a long story short. Frontiers in Bioengineering and Biotechnology, 7:120, DOI:10.3389/fbioe.2019.00120; Sharma, B., et al. (2023) The diversity and functions

of plant RNA modifications: what we know and where we go from here. Annual Review of Plant Biology, 74(1):53–85, DOI:10.1146/annurev-arplant-071122-085813; Shen, L., et al. (2019) Messenger RNA modifications in plants. Trends in Plant Science, 24(4):328–41, DOI:10.1016/j.tplants.2019.01.005; McCutcheon, S.R., et al. (2024) Epigenome editing technologies for discovery and medicine. Nature Biotechnology, 42:1199–1217, DOI:10.1038/s41587-024-02320-1; Kungulovski, G. and Jeltsch, A. (2016) Epigenome editing: state of the art, concepts, and perspectives. Trends in Genetics, 32(2):101–13, DOI:10.1016/j.tig.2015.12.001.

Practicals (30 hours)

1. To investigate the phenotypic responses in the calcium signaling mutants.
2. To investigate the transactivation or transrepression activity of a transcription factor.
3. To design CRISPR guide RNA primers using online tools (e.g., CHOPCHOP, CRISPOR).
4. Molecular probe-based pathogen detection.
5. To design functional genomics approaches for specific gene/phenotype questions and compare the strengths and limitations of different methods.

Suggested Readings:

1. Kramer, L.M. (2015) Signal Transduction. 3rd edition, Academic Press, ISBN:9780123948199.
2. Heldin, C.H. and Purton, M. (1996) Signal transduction: Modular texts in molecular and cell biology, Chapman & Hall, ISBN:0412708108.
3. Alberts, B., et al. (2022) Molecular Biology of the Cell. 7th edition, W.W. Norton & Company, ISBN:9780393884630.
4. Buchanan, B.B., et al. (2015) Biochemistry & Molecular Biology of the Plants. 2nd edition, Wiley Blackwell, ISBN:9781118502198.
5. Kleinsmith, L.J. and Kish, V.M. (1997) Principles of Cell & Molecular Biology. Harper Collins College Publishers, ISBN:9780065004045.
6. Taiz, L., et al. (2023). Plant Physiology and Development. 7th edition, Sinauer Associates, ISBN:9780197614204.
7. Glick, B.R. and Pasternak, J.J. (2022) Molecular Biotechnology: Principles and Applications of recombinant DNA. 6th edition, ASM Press, ISBN:9781683673668.
8. Brown, T.A. (2023) Genomes 5. 5th edition, CRC Press, ISBN:9781003133162.
9. Piechulla, B. (2025) Plant Biochemistry. 6th edition, Academic Press, ISBN:9780443266164.
10. Abd-Elsalam, K.A. and Prasad, R. (2018) Nanobiotechnology applications in plant protection. Springer Cham, ISBN:9783319911601, DOI:10.1007/978-3-319-91161-8.
11. Chen, J.T. (2024) Advanced Nanotechnology in Plants: Methods and Applications. CRC Press, ISBN:9781003368571.
12. Jeltsch, A., and Rots, M.G. (2018) Epigenome editing: Methods and Protocols. Humana New York, ISBN:9781493977741, DOI:10.1007/978-1-4939-7774-1.
13. Jurga, S. and Barciszewski, J. (2021) Epitranscriptomics. Springer Cham, ISBN:9783030716127, DOI:10.1007/978-3-030-71612-7.
14. Online Databases and Resources: NCBI, TAIR, Phytozome, EnsemblPlants and others, KEGG, STRING, Gene Ontology, CRISPR-Cas toolkits and others.

PBSE335: Introduction to Bioinformatics

<u>This course is open to students of other departments as a GE course.</u>

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE335: Introduction to Bioinformatics	4	3	1	0	B.Sc. in any branch of science	NA

Learning Objectives

The paper is devised to introduce the students to the field of bioinformatics and data analysis. The content is designed for students from any stream of life sciences. The course imparts basic and essential knowledge regarding the nature of life science data, including data formats, international databases and data repositories. It also helps to understand how different biological file formats facilitate storage, retrieval and analysis of biological sequences and structures. Furthermore, the unit is designed to familiarize the learner with the landscape of major international nucleotide and protein databases, understanding their scope, interrelationships, and specific applications (universal and organism-specific databases). Additionally, understand the structure, interoperability, and collaborative role of INSDC, as well as its importance in maintaining the global genomic data ecosystem. Furthermore, it will explain the fundamental principles of local and global alignment (pairwise sequence comparison) and the biological rationale behind scoring systems, including substitution matrices and gap penalties. It also focuses on interpreting results of Clustal-W, Clustal Omega, T-Coffee, and MultiAlign BLAST tools and how to optimize their parameters to draw biologically meaningful conclusions. The last unit of the course presents the fundamentals of RNA/ Protein secondary and tertiary structure prediction. It will be helpful to learn the basic principles of docking analysis and drug design workflows.

Learning Outcomes

After successfully completing the course, students will be able to identify and describe various biological data formats and their respective applications. They will be able to access and retrieve sequences and structural data from major databases, data repositories, and browsers like UCSC Genome Browser, linking data formats to visual genomic analysis. Furthermore, students will be able to utilize tools like BLAST for sequence comparison and evolutionary significance, as well as understand the conceptual difference between various substitution matrices and pairwise algorithms. They can perform and interpret the MSA of different biological sequences using different computational software and also visualize phylogenetic trees using various algorithms. Upon completing the last unit, students will be able to use computational tools for RNA and protein prediction, evaluate them, and analyse protein-ligand interaction and outcomes of docking.

Course Content (45 hours)

Unit 1: Biological Data Formats and Databases -- Overview of database management system, concept of 'structured' and 'semi-structured/unstructured' data, concept of 'flat-file' formats; Various file formats used in bioinformatics such as 'fasta', 'fastq', Phylip format, Newick, PDB file format, 'GFF3', SAM/BAM/CRAM formats; Universal nucleotide data repositories: NCBI-GenBank, EMBL-ENA, DDBJ; Details of the International Nucleotide Sequence Data Collaboration (INSDC); Universal Protein databases: UniprotKB, PDB. Organism specific databases (Flybase, Wormbase etc), UCSC Human Genome Browser; Molecular interaction databases such as KEGG and STRING. 10 hours

Essential Readings: Mount, D.W. (2004) Bioinformatics: Sequence and Genome Analysis. 2nd edition, Cold Spring Harbor Laboratory Press, ISBN:9780879697129, Chapter 1 (Historical Introduction and Overview), Chapter 2 (Collecting and Storing Sequences in the Laboratory); Zvelebil, M. and Baum, J.O. (2008) Understanding Bioinformatics. Garland Science, ISBN:9780815340249, Chapter 1 (The nucleic world) and chapter 3 (Dealing with databases); Sayers, E.W., et al. (2022) Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 50(D1):D20–D26, DOI:10.1093/nar/gkab1112; Cochrane, G., et al. (2016). The European Nucleotide Archive in 2016. Nucleic Acids Research, 44(D1):D32–D37, DOI:10.1093/nar/gkw1106; The UniProt Consortium (2023) UniProt: the Universal Protein Knowledgebase in 2023. Nucleic Acids Research, 51(D1):D523–D531, DOI:10.1093/nar/gkac1052; Berman, H.M., et al. (2000) The Protein Data Bank. Nucleic Acids Research, 28(1):235–242, DOI:10.1093/nar/28.1.235; Li, H., et al. (2009) The Sequence Alignment/Map format and SAMtools. Bioinformatics, 25(16):2078–2079, DOI:10.1093/bioinformatics/btp352; Cock, P.J.A., et al. (2010) The Sanger FASTQ file format for sequences with quality scores, and the Solexa/Illumina FASTQ variants. Nucleic Acids Research, 38(6):1767–1771, DOI:10.1093/nar/gkp1137; Kanehisa, M., et al. (2023) KEGG for taxonomy-based analysis of pathways and genomes. Nucleic Acids Research, 51(D1):D587–D592, DOI:10.1093/nar/gkac997; Szklarczyk, D., et al. (2023) The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome. Nucleic Acids Research, 51(D1):D638–D646, DOI:10.1093/nar/gkac1000; The FlyBase Consortium. (2022). FlyBase: updates to the *Drosophila melanogaster* knowledge base. Nucleic Acids Research, 50(D1):D1014–D1020, DOI:10.1093/nar/gkab1099; Haeussler, M., et al. (2019) The UCSC Genome Browser database: 2019 update. Nucleic Acids Research, 47(D1):D853–D858, DOI:10.1093/nar/gky1095.

Unit 2: Pairwise Sequence Alignment -- Concept of local and global sequence alignment; Pairwise sequence alignment algorithms such as Needleman and Wunsch, Smith-Waterman, scoring an alignment, linear and affine gap penalty, amino acid substitution scoring matrices (PAM and BLOSUM); Sequence alignment-based database search, BLAST and its variants, BLAST parameters (word size, E-value, scoring scheme, gap-penalty), bit/raw score. 10 hours

Essential Readings: Mount, D.W. (2004) Bioinformatics: Sequence and Genome Analysis. 2nd edition, Cold Spring Harbor Laboratory Press, ISBN:9780879697129, Chapter 3 (Alignment of pairs of sequences), Chapter 6 (Sequence database searching for similar sequences); Zvelebil, M. and Baum, J.O. (2008) Understanding Bioinformatics. Garland Science, ISBN:9780815340249, Chapter 4 (Producing and analyzing sequence alignments), Chapter 5 (Pairwise sequence alignment and database searching); Morrison, D.A. (2006). Multiple sequence alignment for phylogenetic purposes. Australian Systematic Botany, 19(6):479–539, DOI:10.1071/SB06020.

Unit 3: Multiple Sequence Alignment and Phylogenetic Analysis -- Global and local multiple sequence alignment, multiple sequence alignment algorithms (progressive and iterative algorithms), profile and block analysis; Softwares: Clustal-X, Clustal-W, Clustal-Omega, T-Coffee, MultiAlign; Basic concept of phylogenetic analysis, rooted and unrooted trees, approaches for phylogenetic tree construction; Basics of algorithm for UPGMA, neighbour joining (NJ), maximum parsimony, and maximum likelihood phylogenetic analysis. 15 hours

Essential Readings: Mount, D.W. (2004) Bioinformatics: Sequence and Genome Analysis. 2nd edition, Cold Spring Harbor Laboratory Press, ISBN:9780879697129, Chapter 5 (Multiple sequence alignment), Chapter 7 (Phylogenetic prediction); Zvelebil, M. and Baum, J.O. (2008) Understanding Bioinformatics. Garland Science, ISBN:9780815340249, Chapter 4 (Producing and analyzing sequence alignments), Chapter 5 (Pairwise sequence alignment and database searching), Chapter 6 (Patterns, profiles, and multiple alignments).

Unit 4: Structure Predictions for Nucleic Acids and Proteins -- Approaches for prediction of RNA secondary and tertiary predictions, energy minimization and base covariance models; Basic approaches for protein structure predictions, comparative modeling, fold recognition/'threading', and *ab-initio* prediction; Introduction to AlfaFold database; Docking analysis and drug designing. 10 hours

Essential Readings: Mount, D.W. (2004) Bioinformatics: Sequence and Genome Analysis. 2nd edition, Cold Spring Harbor Laboratory Press, ISBN:9780879697129, Chapter 8 (Prediction of RNA secondary structure), Chapter 10 (Protein classification and structure prediction); Zvelebil, M. and Baum, J.O. (2008) Understanding Bioinformatics. Garland Science, ISBN:9780815340249, Chapter 8 (Recovering evolutionary history), Chapter 11 (Obtaining secondary structure from sequence), Chapter 12 (Predicting secondary structures).

Tutorials (15 hours)

1. To perform 'text-based' database search.
2. Sequence alignment-based database search.
3. Multiple sequence alignment and phylogenetic analysis.
4. Analysis of gene/protein interaction networks.

Suggested Readings:

1. Baxevanis, A.D., et al. (2020) Bioinformatics: A practical guide to the analysis of genes and proteins. 4th edition. John Wiley & Sons, Inc., ISBN:9781119335962.
2. Tramontano, A. (2018) Introduction to Bioinformatics. Chapman and Hall/CRC, ISBN:9781315276014, DOI:10.1201/9781420010886.
3. Lee, E. Tan, T.W. (2018) Beginners guide to bioinformatics for high throughput sequencing. World Scientific, ISBN:9789813231665, DOI:10.1142/10720.
4. Thompson, J.D., et al. (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Research, 22(22):4673–4680, DOI:10.1093/nar/22.22.4673.
5. Notredame, C., et al., (2000) T-Coffee: A novel method for fast and accurate multiple sequence alignment. Journal of Molecular Biology, 302(1):205–217, DOI:10.1006/jmbi.2000.4042.
6. Saitou, N. and Nei, M. (1987) The neighbor-joining method: a new method for reconstructing phylogenetic trees. Molecular Biology and Evolution, 4(4):406–425, DOI:10.1093/oxfordjournals.molbev.a040454.
7. Felsenstein, J. (1981) Evolutionary trees from DNA sequences: a maximum likelihood approach. Journal of Molecular Evolution, 17(6):368–376, DOI:10.1007/BF01734359.
8. JJumper, J., et al. (2021) Highly accurate protein structure prediction with AlphaFold2. Nature, 596:583–589, DOI:10.1038/s41586-021-03819-2.
9. Zhang, Y. (2008) Progress and challenges in protein structure prediction. Current Opinion in Structural Biology, 18(3):342–348, DOI:10.1016/j.sbi.2008.02.004.
10. Kryshtafovych, A., et al. (2021) Critical assessment of methods of protein structure prediction (CASP)—Round XIV. Proteins: Structure, Function, and Bioinformatics, 89(12):1607–1617, DOI:10.1002/prot.26237.
11. Zuker, M. (2003) Mfold web server for nucleic acid folding and hybridization prediction. Nucleic Acids Research, 31(13):3406–3415, DOI:10.1093/nar/gkg595.
12. Kitchen, D.B., et al. (2004) Docking and scoring in virtual screening for drug discovery: methods and applications. Nature Reviews Drug Discovery, 3(11):935–949, DOI:10.1038/nrd1549.

PBRM332: Advanced Research Methodology

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBRM332: Advanced Research Methodology	2	1	0	1	B.Sc. in any branch of science	NA

Learning Objectives

This course aims to provide students with an in-depth conceptual understanding of advanced research methodologies applied in molecular plant sciences. It emphasizes experimental design, interpretation, and analysis in the context of gene function, regulatory networks, and crop improvement. The course also aims to establish a solid foundation for critically evaluating experimental data, formulating hypotheses, and communicating scientific findings in plant biology research.

Learning Outcomes

Upon successful completion of this course, students will develop a comprehensive understanding of advanced research methodologies in plant molecular biology. They will be able to conceptualize and design theoretical frameworks for gene function analysis, regulatory network mapping, and crop improvement experiments. Students will gain the ability to integrate bioinformatics insights with molecular and genetic approaches to interpret gene and protein functions. Furthermore, they will gain an understanding of the conceptual underpinnings of genome editing, regulatory pathway analysis, and experimental data validation. The course will enhance their skills in critical thinking and experimental design in plant molecular biology research.

Course Content (15 hours)

Unit 1: Experimental Design for Gene Function Analysis -- Experimental frameworks for dissecting gene function and regulatory cascade in plants; Conceptual foundations of gene/protein function prediction, principles of homology, conserved domain identification, integration networks and database search; Principles of experimental design for gene over-expression and knock-out/knock-down studies, mutant analysis, and genetic mapping; Protein localization studies; Elucidation of genetic regulatory cascades. 10 hours

Essential Readings: Robles, J.A., et al. (2012) Efficient experimental design and analysis strategies for the detection of differential expression using RNA-Sequencing. BMC Genomics, 13:484, DOI:10.1186/1471-2164-13-484; Grondin, A., et al. (2024) A case study from the overexpression of OsTZF5, encoding a CCCH tandem zinc finger protein, in rice plants across nineteen yield trials. Rice, 17(1):25, DOI:10.1186/s12284-024-00705-z; Tang, M., et al. (2021) A genome-scale TF–DNA interaction network of transcriptional regulation of *Arabidopsis* primary and specialized metabolism. Molecular Systems Biology, 17(11):e10625, DOI:10.15252/msb.202110625; https://www.goldenhelix.com/blog/stop-ignoring-experimental-design-or-my-head-will-explode/; https://www.ncbi.nlm.nih.gov/books/NBK26818/; Wagner, M.R., and Kleiner, M. (2025) How thoughtful experimental design can empower biologists in the omics era. Nature Communications, 16(1):7263, DOI:10.1038/s41467-025-62616-x; Boadu, F., (2025) Deep learning methods for protein function prediction. Proteomics, 25(1-2):e2300471, DOI:10.1002/pmic.202300471; Goodin, M.M. (2018) Advances in virus research. 100:117-144, DOI:10.1016/bs.aivir.2017.10.004, Chapter 6 (Protein localization and interaction studies in plants: Toward defining complete proteomes by visualization).

Unit 2: Experimental Frameworks for Crop Improvement by Genome Editing -- Experimental frameworks for designing molecular and genetic strategies for crop improvement; CRISPR-based strategies for gain-of-function and loss-of-function of genes for enhanced agronomic traits; Validation of transgene-free plants, Field trials and regulations regarding the release of genome-edited crops. 5 hours

Essential Readings: Graham, D.B. and Root, D.E. (2015) Resources for the design of CRISPR gene editing experiments. Genome Biology, 16:260, DOI:10.1186/s13059-015-0823-x; Zhou, J., et al. (2023) An efficient CRISPR–Cas12a promoter editing system for crop improvement. Nature Plants, 9(4):588–604, DOI:10.1038/s41477-023-01384-2; Han, X., et al. (2025) Genetic engineering, including genome editing, for enhancing broad-spectrum disease resistance in crops. Plant Communications, 6(2):101195, DOI:10.1016/j.xplc.2024.101195; Hanna, R.E. and Doench, J.G. (2020) Design and analysis of CRISPR-Cas experiments. Nature Biotechnology, 38(7):813–823, DOI:10.1038/s41587-020-0490-7.

Practicals (30 hours)

1. Analysis of conserved protein motifs using WebLogo and interpreting functional domains of a protein family.
2. Development of transgenic hairy roots using RNAi or promoter–*uidA* binary vector constructs.
3. Analysis of stress-induced promoter activity *in planta* using non-destructive methods.
4. *In silico* design of a vector for transgene-free plant genome editing using TnpB.
5. Design and application of CAPS/dCAPS markers to identify and validate single base substitutions or targeted genome edits.

Suggested Readings:

1. Buchanan, B.B. et al. (2015) Biochemistry and molecular biology of the plants. 2nd edition, WILEY Blackwell, ISBN:9780470714218.
2. Singh, P.P., and Benayoun, B.A. (2023) Considerations for reproducible omics in aging research. Nature Aging, 3(8):921–930, DOI:10.1038/s43587-023-00448-4;
3. Conesa, A., et al. (2016) A survey of best practices for RNA-seq data analysis. Genome Biology, 17:13, DOI:10.1186/s13059-016-0881-8.
4. Haas, R., et al. (2017) Designing and interpreting 'multi-omic' experiments that may change our understanding of biology. Current Opinion in Systems Biology, 6:37–45, DOI:10.1016/j.coisb.2017.08.009.
5. Strotmann, V.I. and Stahl, Y. (2022) Visualization of *in vivo* protein-protein interactions in plants. Journal of Experimental Botany, 73(12):3866–3880, DOI:10.1093/jxb/erac139.
6. Quattrocchio, F.M., et al. (2013) Transgenes and protein localization: myths and legends. Trends in Plant Science, 18(9):473–476, DOI:10.1016/j.tplants.2013.07.003.
7. Lichocka, M. and Schmelzer, E. (2014) Subcellular localization experiments and FRET-FLIM measurements in plants. Bio-Protocol, 4(1):e1018, DOI:10.21769/BioProtoc.1018.
8. Zhang, Y., et al. (2023) Investigating the dynamics of protein-protein interactions in plants. The Plant Journal, 114(4):965–983, DOI:10.1111/tpj.16182.
9. Teng, C. (2024) Killing two birds with one stone: A breakthrough in transgene-free gene editing in soybean. Plant Physiology, 196(4):2263–2265, DOI:10.1093/plphys/kiae526.
10. Ricroch, A., et al. (2024) Worldwide study on field trials of biotechnological crops: new promises but old policy hurdles. Frontiers in Plant Science, 15:1452767, DOI:10.3389/fpls.2024.1452767.
11. https://dbtindia.gov.in/sites/default/files/Final_%2011052022_Annexure-I%2C%20Genome_Edited_Plants_2022_Hyperlink.pdf

PBRM333: Emerging Techniques in Plant Biology

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBRM333: Emerging Techniques in Plant Biology	2	1	0	1	B.Sc. in any branch of science	NA

Learning Objectives

The objective of this paper is to familiarize students with the latest advancements and methodologies in the field. The course offers insight into diverse imaging approaches and methodologies used to study plant systems at the cellular level. This course provides an in-depth understanding of emerging and state-of-the-art techniques used in contemporary research and applications.

Learning Outcomes

Students would acquire specific practical skills regarding various sample preparations and imaging techniques, which are essential for conducting advanced plant science research. They will acquire knowledge of the principles and applications of cutting-edge techniques relevant to modern research and innovation, and will learn to apply appropriate state-of-the-art tools and technologies to investigate complex scientific problems.

Course Content (15 hours)

Unit 1: Imaging Techniques -- Fundamental principles of microscope design, image formation, magnification, numerical aperture, resolution, and contrast; Components and optics of light microscopy; Transmitted light techniques: bright-field, phase contrast, and DIC; Fundamentals of fluorescence, excitation-emission principles, fluorescent probes and biosensors, photobleaching, and quenching; Confocal laser scanning microscopy–optical sectioning, Z-stack reconstruction, and 3D imaging, super-resolution microscopy (STED, SIM, PALM/STORM), and cryo-electron microscopy (Cryo-EM); Digital image recording, cameras, signal-to-noise ratio, and quantitative image analysis; Applications in plant cell and developmental biology using fluorescence-based imaging approaches. 7.5 hours

Essential Readings: Murphy, D.B. and Davidson, M.W. (2012) Fundamentals of light microscopy and electronic imaging, 2nd edition, Wiley-Blackwell, ISBN:9781118382905, Chapter 1 (Introduction to Microscopy), Chapter 2 (The Optical Microscope), Chapter 3 (Image Formation in the Microscope), Chapter 4 (Fluorescence Microscopy): Principles, Chapter 5 (Fluorescence Microscopy: Instrumentation), Chapter 6 (Digital Imaging Fundamentals), Chapter 9 (Confocal Microscopy), Chapter 13 (Electron Microscopy Fundamentals); Huang, B., et al. (2009) Super-resolution fluorescence microscopy. Annual Review of Biochemistry, 78:993–1016, DOI: 10.1146/annurev.biochem.77.061906.092014; Nogales, E. and Scheres, S.H.W. (2015) Cryo-EM: A unique tool for the visualization of macromolecular complexity. Molecular Cell, 58:677–689, DOI: 10.1016/j.molcel.2015.02.019.

Unit 2: Single Cell Biology -- Isolation and handling of single cells: Fluorescence-activated cell sorting (FACS); Microfluidics, Laser Capture Microdissection (LCM); Single-cell multi-omics analysis: Single-cell genomics (scDNA-seq), transcriptomics (scRNA-seq), proteomics (scProteomics), metabolomics (scMetabolomics); Multi-omics integration; Temporal and Spatial analysis: Spatial Transcriptomics, *in situ* subcellular localization of a metabolite;

Chromosomal immunostaining; Applications of single cell biology in plant molecular biology.

7.5 hours

Essential Readings: Hu, P., et al. (2016) Single cell isolation and analysis. Frontiers in Cell and Developmental Biology, 4:116, DOI:10.3389/fcell.2016.00116; Wang, D. and Bodovitz, S. (2010) Single-cell analysis: the new frontier in 'omics'. Trends in Biotechnology, 28(6):281–290, DOI:10.1016/j.tibtech.2010.03.002; Jackson, C.A., et al. (2022) New horizons in the stormy sea of multimodal single-cell data integration Molecular Cell, 82(2):248–259, DOI:10.1016/j.molcel.2021.12.012; Rahman, M.S., et al. (2024) Opportunities and challenges in advancing plant research with single-cell omics. Genomics, Proteomics & Bioinformatics, 22(2):qzae026, DOI:10.1093/gpbjnl/qzae026; Clark, N.M., et al. (2022) To the proteome and beyond: advances in single-cell omics profiling for plant systems. Plant Physiology, 188(2):726–737, DOI:10.1093/plphys/kiab429; Nobori, T. (2025) Exploring the untapped potential of single-cell and spatial omics in plant biology. The New Phytologist, 247(3):1098, DOI:10.1111/nph.70220; Chau, T.N., et al. (2024) Advancing plant single-cell genomics with foundation models. Current Opinion in Plant Biology, 82:102666, DOI:10.1016/j.pbi.2024.102666.

Practicals (30 hours)

1. To visualize a living plant specimen using bright-field, phase contrast, and (if available) DIC, and understand how each enhances different features.
2. Preparation of publication-quality microscopy figures: Brightfield–Fluorescence overlays and scale bars.
3. To navigate and annotate multi-dimensional images for preparing a figure using Image J.
4. Data analysis of targeted metabolite profiling.
5. Analysis of cell cycle stages using FACS.

Suggested Readings:

1. Wu, X., et al. (2024) Single-cell sequencing to multi-omics: technologies and applications. Biomarker Research, 12:110, DOI:10.1186/s40364-024-00643-4.
2. Zhu, M., et al. (2025) Single-cell transcriptomics reveal how root tissues adapt to soil stress. Nature, 642:721–729, DOI:10.1038/s41586-025-08941-z.
3. Lee, T.A., et al. (2025) A single-cell, spatial transcriptomic atlas of the *Arabidopsis* life cycle. Nature Plants, 11:1960–75, DOI:10.1038/s41477-025-02072-z.
4. Cold Spring Harbour Protocols- Imaging/Microscopy, general weblink: (https://cshprotocols.cshlp.org/cgi/collection/imaging_microscopy_general)
5. Paddock, S.W. (2014) Confocal Microscopy: Methods and Protocols. Humana New York, NY, eISBN:9781607618478, DOI:10.1007/978-1-60761-847-8.
6. Ruzin, S.E. (1999) Plant Microtechnique and Microscopy. Oxford University Press, USA, ISBN:9780195089561.
7. Pawley, J.B. (2006) Handbook of Biological Confocal Microscopy. 3rd edition, Springer New York, NY, ISBN:9780387455242, DOI:10.1007/978-0-387-45524-2.
8. Markaki, Y. and Harz, H. (2017) Light microscopy: Methods and Protocols. Humana New York, NY, DOI:10.1007/978-1-4939-6810-7.
9. Yin, Z. et al. (2023) Mass spectrometry imaging techniques: a versatile toolbox for plant metabolomics. Trends in Plant Science, 289(2):250–251, DOI:10.1016/j.tplants.2022.10.009.
10. Pawlowski, W.P., et al. (2013) Plant Meiosis: Methods and Protocols. Humana Totowa, NJ, Chapter (Immunolocalization of meiotic proteins in *Brassicaceae*: method 1), ISBN:9781627033336, DOI:10.1007/978-1-62703-333-6_9.
11. Petrova, B. and Guler, A.T. (2025) Recent developments in single-cell metabolomics by mass Spectrometry- A perspective. Journal of Proteome Research, 24(4):1493–1518, DOI:10.1021/acs.jproteome.4c00646.
12. Shaw, R., et al. (2021) Single-cell transcriptome analysis in plants: advances and challenges. Molecular Plant, 14(1):115–126, DOI:10.1016/j.molp.2020.10.012.

PBRE336: Dissertation-I

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBRE336: Dissertation-I	6	0	0	6	B.Sc. in any branch of science	NA

Learning Objectives

The students will identify and select a relevant research problem in consultation with the faculty members, ensuring alignment with current advances in Plant Molecular Biology and Biotechnology. They will conduct a thorough and critical appraisal of the existing literature on the problem, enabling them to understand the depth of current knowledge. Students will learn to formulate well-defined research questions and develop testable hypotheses in the context of scientific reasoning. Under faculty mentorship, they will design an experimentally feasible and scientifically structured research plan, complete with realistic timelines, appropriate methodologies, and anticipated outcomes. In addition, the students will gain training in scientific writing through preparation of a detailed literature review, and they will enhance their communication skills by effectively presenting and discussing their research survey in laboratory group discussions and structured oral presentations.

Learning Outcomes

Upon successful completion of the course, the student will be able to independently conduct a comprehensive survey of scientific literature and critically analyse it to identify significant knowledge gaps within the research field. They will demonstrate the ability to justify the importance and relevance of selected research problems using evidence-based reasoning. Students will prepare a well-structured synopsis that includes an in-depth literature review, clearly articulated research questions, hypotheses, and a coherent experimental plan to be executed in Semester 4. Additionally, they will acquire proficiency in scientific writing, including organization, clarity, and synthesis of complex information, and will develop strong oral communication skills necessary for presenting research findings and engaging in scientific discourse. Overall, the students will hone their ability to think independently, plan research systematically, and communicate their work confidently in both written and verbal formats.

Suggested Readings:

1. Latest research and review articles from scientific journals and book chapters on a chosen research problem.

SEMESTER 4

PBSE433: Epigenetics and Small RNA Biology

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE433: Epigenetics and Small RNA Biology	4	3	0	1	B.Sc. in any branch of science	NA

Learning Objectives

The epigenetic landscape (including both DNA methylation and histone modifications) of an organism has a significant bearing in regulating various developmental and metabolic processes at the global level. Similarly, small RNAs (sRNAs) have emerged as major modulators of global gene expression patterns. Therefore, this course is designed to provide students with a clear understanding of key epigenetic mechanisms, including chromatin modeling, DNA methylation, and histone modifications, and how these processes regulate plant development and physiology. Students will learn how epigenetic regulation contributes to environmental responses, stress adaptation, and inheritance, as well as its relevance in human systems, including immunity, cancer, and cardiovascular diseases. The course also introduces the diversity, biogenesis, and regulatory roles of non-coding RNAs across organisms, including their mechanisms of action and trans-kingdom interactions. Additionally, students will become familiar with experimental and computational tools for detecting, predicting, and validating small RNAs, and will explore the applications of RNA-based technologies and CRISPR-Cas systems in crop improvement, diagnostics, and therapeutic development.

Learning Outcomes

By the end of this course, students will be able to understand major epigenetic mechanisms and evaluate their roles in plant development, environmental responses, and human diseases. They will be able to understand DNA methylation and histone modifications, classify non-coding RNAs, and describe how small RNAs regulate gene expression. Students will also be equipped to use molecular and bioinformatic approaches for small RNA analyses and apply RNA-based tools. Overall, they will be able to integrate epigenetics and small RNA biology concepts to address research problems and understand their practical applications in agriculture, biotechnology, and human health.

Course Content (45 hours)

Unit 1: Epigenetic Regulation -- Chromatin modeling and remodeling: polycomb complexes, SWI/SNF1 complexes and other chromatin modifiers; DNA methylation and its interpretation: methylated DNA-binding proteins, their structure and function; techniques of altering and analyzing DNA methylation; Histone modifications: types, modifying enzymes, histone deacetylase inhibitors; Chromatin modification and its influence on plant development: somatic embryogenesis, leaf development, photosynthesis, flowering, and ageing. 12 hours

Essential Readings: Jenuwein, T. and Allis, C.D. (2001) Translating the histone code. Science, 293(5532):1074-1080, DOI:10.1126/science.1063127; Zhang, H., et al. (2018). Dynamics and function of DNA methylation in plants. Nature Reviews Molecular Cell Biology, 19(8):489-506, DOI:10.1038/s41580-018-0016-z; Rajewsky, N., et al. (2018) Plant epigenetics. Springer International, ISBN:9783319555195, DOI:10.1007/978-3-319-55520-1; Huang, Y., et al., (2025) Chromatin remodeling in plants: Complex composition, mechanistic diversity, and biological functions. Molecular Plant, 18(9):1436–1457, DOI:10.1016/j.molp.2025.08.004.

Unit 2: Environmental and Evolutionary Epigenetics -- Role of epigenetic regulation in plant stress responses and epigenetic memory; Epigenetic inheritance and adaptive responses to environmental cues; Epigenetics in human systems: regulation of immune responses, cancer, and cardiovascular diseases. 10 hours

Essential Readings: Chinnusamy, V. and Zhu, J.K. (2009) Epigenetic regulation of stress responses in plants. Current Opinion in Plant Biology, 12(2):133–139, DOI:10.1016/j.pbi.2008.12.006; Avramova, Z. (2015) Transcriptional 'memory'of a stress: transient chromatin and memory (epigenetic) marks at stress-response genes. The Plant Journal, 83(1):149–159, DOI:10.1111/tpj.12832; Ma, L., et al., (2025) Epigenetic control of plant abiotic stress responses. Journal of Genetics and Genomics, 52(2):129–44, DOI:10.1016/j.jgg.2024.09.008; Janson, P.C. and Winqvist, O. (2011) Epigenetics–the key to understand immune responses in health and disease. American Journal of Reproductive Immunology, 66:72–74, DOI:10.1111/j.1600-0897.2011.01050.x; Zoghbi, H.Y. and Beaudet, A.L. (2016) Epigenetics and human disease. Cold Spring Harbor Perspectives in Biology, 8(2): a019497, DOI:10.1101/cshperspect.a019497.

Unit 3: Biology of Non-coding RNAs -- Discovery, types, occurrence, and diversity of non-coding RNAs; Small RNA pathways in bacteria, plants, and animal systems; Biogenesis and functional components of different classes of small RNAs; Regulation of gene expression by small RNAs: transcriptional gene silencing (TGS), post-transcriptional gene silencing (PTGS), gene activation, and evolutionary transitions in RNA-target interactions; Functional roles of small RNAs in different organisms; Trans-kingdom cross-talk mediated by small RNAs.

13 hours

Essential Readings: Guleria, P. and Kumar, V. (2020) Plant Small RNA- Biogenesis, Regulation and Application. Academic Press, ISBN:9780128171127, DOI:10.1016/C2018-0-01900-3; Alquethamy S., et al. (2025). What makes a small RNA work. Nucleic Acids Research, 53(12):gkaf563, DOI:10.1093/nar/gkaf563; Mattick, J. and Amaral, P. (2022) RNA, the epicenter of genetic information. ISBN:9781003109242, CRC Press, DOI:10.1201/9781003109242; Wierzbiki, A.T., et al. (2021) Long non-coding RNAs in plants. Annual Review of Plant Biology, 72:245–271, DOI:10.1146/annurev-arplant-093020-035446; Zhan, J. and Meyers, B.C. (2023) Plant small RNAs: their biogenesis, Regulatory roles, and functions. Annual Review of Plant Biology, 74:21–51, DOI:10.1146/annurev-arplant-070122-035226; Barquist, L. and Vogel, J. (2015) Accelerating discovery and functional analysis of small RNAs with new technologies. Annual Review of Genetics, 49:367–394, DOI:10.1146/annurev-genet-112414-054804.

Unit 4: Tools, Applications, and Emerging Technologies -- Discovery, detection, and validation of small RNAs; Target prediction and validation approaches; Databases and bioinformatic tools for small RNA analysis; Applications: artificial miRNA (amiR) technology, siRNA and virus-induced gene silencing (VIGS); RNAi interference (RNAi), RNA activation (RNAa), target mimicry and STTM technologies; CRISPR-Cas-based genome editing guided by small RNAs; Applications in crop improvement, diagnostics, and therapeutics. 10 hours

Essential Readings: Tang, G., et al. (2021) RNA-based technologies for functional genomics in plants. Springer Cham, ISBN:9783030649937, DOI:10.1007/978-3-030-64994-4; Ting, P., et al. (2018) A resource for inactivation of microRNAs using short tandem target mimic technology in model and crop plants. Molecular Plant, 11(11):1400–1417, DOI:10.1016/j.molp.2018.09.003; Halloy, F., et al. (2022) Innovative developments and emerging technologies in RNA therapeutics. 19(1):313–332, DOI:10.1080/15476286.2022.2027150.

Practicals (30 hours)

1. To resolve and visualize low molecular weight RNAs by denaturing urea-PAGE.

2. To perform expression analysis of selected miRNAs using the quantitative PCR method.
3. To isolate, sonicate, and observe cross-linked chromatin to study histone modifications.
4. To enzymatically cleave and assess DNA to detect methylation patterns.
5. To predict and analyze the secondary structure and thermodynamic stability of the miRNA precursor sequence (pre-miRNA) using Mfold.

Suggested Readings:

1. Esteller, M. (2009) Epigenetics in biology and medicine. CRC Press, eISBN:9780429124921.
2. Workman, J.L. and Abmayr, S.M. (2014) Fundamentals of chromatin. Springer New York, ISBN:9781461486237, DOI:10.1007/978-1-4614-8624-4.
3. Dinkar, V., et al. (2024) Epigenetic regulations under plant stress: a cereals perspective. Environmental and Experimental Botany, 220:105688, DOI:10.1016/j.envexpbot.2024.105688.
4. He, L. (2025) The interplay between chromatin remodeling and DNA double-strand break repair: Implications for cancer biology and therapeutics. DNA Repair, 146:103811, DOI:10.1016/j.dnarep.2025.103811.
5. Muka, T., et al. (2016) The role of epigenetic modifications in cardiovascular disease: a systematic review. International Journal of Cardiology, 212:174–183, DOI:10.1016/j.ijcard.2016.03.062.
6. Mallick, B. and Ghosh, Z. (2012) Regulatory RNAs: Basics, Methods and Applications. Springer Berlin, Heidelberg, ISBN:9783642225161, DOI:10.1007/978-3-642-22517-8.
7. Nellan, W. and Hammann, C. (2007) Small RNAs: analysis and regulatory functions. Springer Berlin, Heidelberg, ISBN:9783540281306, DOI:10.1007/978-3-540-28130-6.
8. Gaur, R.K. and Rossi, J.J. (2009) Regulation of gene expression by small RNAs. CRC Press, USA, eISBN:9780429121692, DOI:10.1201/9781420008708.
9. Alquethamy, S., et al. (2025) What makes a small RNA work? Nucleic Acids Research, 53(12):gkaf563, DOI:10.1093/nar/gkaf563.
10. Rederstorff, M. (2021) Small non-coding RNAs: Methods and Protocols. Humana New York. eISBN:9781071613863, DOI:10.1007/978-1-0716-1386-3.

PBSE434: Data Analytics and Biocuration

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBSE434: Data Analytics and Biocuration	4	3	1	0	B.Sc. in any branch of science	

Learning Objectives

The paper aims to empower learners with foundational data analytics skills essential to modern bioinformatics by exposing them to the fundamentals of advanced operating systems, including the Linux command-line interface (CLI), file handling, permissions, and data manipulation. It also provides a brief exposure to the R programming environment, syntax, and functions for data analysis and packages available in the Bioconductor repository for statistical computing, data visualization, and genomic data analysis. It also provides a comprehensive overview of the primary computational workflows for analyzing next-generation sequencing (NGS) data. The learner will explore the concepts, applications, and key steps involved in major "big data" bioinformatics domains, including genome assembly, variant calling, pangenomics, metagenomics, transcriptomics (RNA-seq) and epigenomics (ChIP-seq, Bisulfite-seq). Besides, it also focuses on the behind-the-scenes work of biocuration that powers biological databases through processes of extracting, standardizing, and organizing biological data from literature and experiments. It provides an overview of BioDbCore, FAIRsharing, and ethical principles of open data management. The student will be able to interpret Gene Ontology and biomedical ontologies using OBO formats. In the last unit, there is a brief overview of foundational concepts in AI and machine learning (ML), along with the utility of domain-specific LLMs and their applications in genomics, drug design, and systems biology.

Learning Outcomes

The completion of the course will give expertise in essential Linux commands and in setting up and running ‘R’ scripts for statistical analysis and plotting. The learner can apply Bioconductor tools for biological data exploration, such as DESeq2, edgeR, and limma. Furthermore, students can analyse NGS data for variant calling, transcriptome quantification, and epigenomic data integration. They also now understand the FAIR data principles, ontologies, and the curation of biological data from published sources. Moreover, students can work with LLMs, ML, and AI tools across domains such as genomic prediction, phenotype classification, drug discovery, and structure-based screening.

Course Content (45 hours)

Unit 1: Basic of Linux and ‘R’ -- Computer architecture, types of operating systems (Windows, Mac-OS and Linux), concept of networking (IP address); Basic fundamentals of working with Unix/Linux on CLI (Command Line Interface), Unix/Linux directory structure, file permissions, remote login; Linux commands (whoami, pwd, cd, ls, man, mkdir, rm, cat copy, mv, chmod, grep, sed, sep, sort, head, tail, wc); Introduction to the ‘R’ data analysis package, basic work environment, syntax, introduction to the 'Bioconductor' packages for data analysis. 15 hours

Essential Readings: Blum, R. and Bresnahan, A. (2021) Linux Command Line and Shell Scripting Bible. 4th edition, John Wiley & Sons, Inc., ISBN:9781119700913; Kabacoff, R.I. (2022) R in action: Data analysis and graphics with R. 3rd edition, Manning Publications, ISBN:9781617296055; Gentleman, R.C., et al. (2004) Bioconductor: open software development for computational biology and bioinformatics. Genome Biology, 5:R80, DOI:10.1186/gb-2004-5-10-r80.

Unit 2: Big Data Analysis -- Whole genome reference-based assembly, de-novo genome analysis, variant call analysis, Pangenomes, Metagenomic analysis, RNA-seq data analysis, ChIP (Chromatin Immunoprecipitation) data analysis; Whole genome bisulphite sequencing data analysis. 10 hours

Essential Readings: Compeau, P. and Pevzner, P. (2018) Bioinformatics algorithms: An active learning approach. 3rd edition, Active Learning Publishers, ISBN:9780990374633; Shendure, J. and Aiden, E.L. (2012) The expanding scope of DNA sequencing. Nature Biotechnology, 30(11):1084–1094, DOI:10.1038/nbt.2421; Conesa, A., et al. (2016) A survey of best practices for RNA-seq data analysis. Genome Biology, 17:13, DOI:10.1186/s13059-016-0881-8; Landt, S.G., et al. (2012) ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. Genome Research, 22(9):1813–31, DOI:10.1101/gr.136184.111.

Unit 3: Data Integration and Biocuration -- Overview of Biocuration, various approaches to biocuration, BioDbCore guidelines, FAIRsharing and ethics in data sharing, Text/Literature-based curation, text mining approaches, and an introduction to tools such as Textpresso. Basics and importance of ontology development, OBO (Open Biological and Biomedical Ontology) format, OBO foundary, biomedical and plant-based ontologies.

10 hours

Essential Readings: Gaudet, P., et al. (2011) Towards BioDBcore: a community-defined information specification for biological databases. Nucleic Acids Research, 39(s1):D7–D10, DOI:10.1093/nar/gkq1173; Open Biological and Biomedical Ontology Foundry: Community development of interoperable ontologies for the biological sciences, https://obofoundry.org/about-OBO-Foundry.html; FAIRsharing: A curated, informative and educational resource on data and metadata standards, inter-related to databases and data policies, https://fairsharing.org, DOI:10.1038/s41587-019-0080-8; Howe, D., et al. (2008) The future of biocuration. Nature, 455:47–50, DOI:10.1038/455047a; Wilkinson, M.D., et al. (2016) The FAIR Guiding Principles for scientific data management and stewardship. Scientific Data, 3:160018, DOI:10.1038/sdata.2016.18.

Unit 4: Artificial Intelligence in Life Sciences -- Introduction to Machine-Learning (ML) and Artificial Intelligence (AI); Supervised and un-supervised learning approaches in data integration, interpretation, and predictive modelling; Applications in genomic prediction, drug discovery, ecosystem modelling; Domain-specific Large Language Models (LLMs). 10 hours

Essential Readings: Cannataro, M., et al. (2022) Artificial Intelligence in Bioinformatics: from omics analysis to deep learning and network mining, 1st edition, Elsevier, eISBN:9780128229293; Jumper, J., et al. (2021) Highly accurate protein structure prediction with AlphaFold. Nature, 596:583–589, DOI:10.1038/s41586-021-03819-2.

Tutorials (15 hours)

1. Practice of working with Linux commands on the Command Line Interface (CLI).
2. Analysis of RNA-seq data:
    a. Quality and adapter trimming of Next Generation Sequencing (NGS) data.
    b. Reference-based genome mapping of NGS data.
    c. Identification of differentially expressed genes.
3. Use of Gene Ontology for gene function analysis.

Suggested Readings:

1. Bessant, C., et al. (2014) Building bioinformatics solutions with Perl, R, and SQL. 2nd edition, Oxford University Press, UK, ISBN:978019965855.
2. Buffalo, V. (2015) Bioinformatics data skills: Reproducible and robust research with open-source tools. O'Reilley Media, ISBN:9781449367374.
3. Quince, C., et al. (2017) Shotgun metagenomics, from sampling to analysis. Nature Biotechnology, 35(9):833–844, DOI:10.1038/nbt.3935.
4. Sansone, S.A., et al. (2019) FAIRsharing as a community approach to standards, repositories and policies, Nature Biotechnology, 37(4):358–367, DOI:10.1038/s41587-019-0080-8.
5. Smith, B., et al. (2007) The OBO Foundry: coordinated evolution of ontologies to support biomedical data integration, Nature Biotechnology, 25(11):1251–1255, DOI:10.1038/nbt1346.
6. Müller, H.M., et al. (2018) Textpresso Central: a customizable platform for searching, text mining, viewing, and curating biological literature. BMC Bioinformatics, 19:94, DOI:10.1186/s12859-018-2103-8.
7. Web link: www.bioconductor.org
8. Web link: www.obofoundary.org; www.oboedit.org
9. Web link: www.biocuration.org

PBRM431: Research Presentation and Communication

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBRM431: Research Presentation and Communication	2	1	0	1	B.Sc. in any branch of science	NA

Learning Objectives

This course aims to outline the key principles and approaches in science communication. The course will blend theoretical insights with practical exercises to ensure that learners are prepared for the real-world challenges of science communication. The curriculum is structured to ensure that students gain the skills needed to communicate science accurately, compellingly, and responsibly.

Learning Outcomes

This course equips students with the skills to effectively communicate scientific concepts to diverse groups of audiences including experts as well as non-experts in the field. Students will learn to craft clear, engaging, and accurate messages and interact confidently with the media. They will learn to apply effective visual and verbal communication strategies to enhance the impact of the message and will also understand the role of science in society, policy, and public engagement.

Course Content (15 hours)

Unit 1: Foundations of Effective Science Communication -- Key principles of Science Communication (clarity, simplicity, accuracy, and engagement); History and evolution of science communication; Role of Science in Society (science policy, public perception, and media; Importance of science communication in shaping public understanding and policy), audience analysis, role of visuals in enhancing understanding (e.g., graphs, infographics, videos), evaluating the impact of Science Communication; Ethics in Science Communication.

7.5 hours

Essential Readings: National Academies of Sciences, Engineering, and Medicine (2017). Communicating Science Effectively: A Research Agenda. Washington, DC: National Academies Press, ISBN:0309451035, DOI:10.17226/23674, Chapter 1 (Using science to improve science communication), Chapter 2 (The complexities of communicating science), Chapter 3 (The nature of science-related public controversies), Chapter 4 (Communicating science in a complex, competitive communication environment); Bucchi, M. and Trench, B. (2021) Routledge handbook of public communication of science and technology. 3rd edition, Routledge, ISBN:9781003039242, Chapter 1 (Introduction: science communication as the social conversation around science), Chapter 9 (Risk, science and public communication: Third-order thinking about scientific culture).

Unit 2: Writing and Oral Communication -- Scientific and Technical Writing (scientific articles, thesis, project report, and research proposal, abstracts, preparing CVs, and research statements), Popular Science Writing; Presentation Skills (infographics, animation and slide design and organization); Public Speaking, Q&A Management; Digital Media and Social

Media in Science Communication: Science Blogging, Creative Video Production, Science Journalism, Science Communication for Crisis Management. 7.5 hours

Essential Readings: Hofmann, A.H. (2022) Scientific writing and communication. 5th edition, Oxford University Press, ISBN:9780197613795; Okwemba, R.K. (2022) Introduction to scientific writing A Review. International Journal of Scientific Research in Science and Technology, 9(1):56–63, DOI:10.32628/IJSRST218631; Vogel, W.H. and Viale, P.H. (2018) Presenting with confidence. Journal of the Advanced Practitioner in Oncology, 9(5):545–548, DOI:10.6004/jadpro.2018.9.5.9; Wallwork, A. and Southern, A. (2020) 100 Tips to avoid mistakes in academic writing and presenting. Springer Cham, eISBN:9783030442149, DOI:10.1007/978-3-030-44214-9, Chapter 9 (Presentations); Traboco, L., et al. (2022) Designing infographics: visual representations for enhancing education, communication, and scientific research. Journal of Korean Medical Science, 37(27):e214, DOI:10.3346/jkms.2022.37.e214; Wang, Y., et al. (2021) Animated presentation of static infographics with InfoMotion. Computer Graphics Forum, 40(3):507–518, DOI:10.1111/cgf.14325; León, B. and Bourk, M. (2018) Communicating science and technology through online video. Routledge, eISBN:9781351054584, DOI:10.4324/9781351054584, Chapter 3 (Producing science online video, by Erviti, M.C.); Bucchi, M. and Trench, B. (2021) Routledge handbook of public communication of science and technology. Routledge, eISBN:9781003039242, DOI:10.4324/9781003039242, Chapter 2 (Science journalism); Vadapalli, R., et al. (2018) Sci-Blogger: A step towards automated science journalism. Proceedings of the 27th ACM International Conference on Information and Knowledge Management, 1787–90, DOI: 10.1145/3269206.3269303.

Practicals (30 hours)

1. Conceptualization, designing, and assembly of a scientific poster presenting research objectives, methodology, results, and conclusions.
2. To design and develop a documentary-style video presenting the mission, key projects, and scientific contributions of a research group.
3. To prepare and publish a science blog.

Suggested Readings:

1. van Dam, F., et al. (2020) Science Communication- An Introduction. World Scientific, ISBN:9789811209871, DOI:10.1142/11541.
2. Kim, Y.S.G., et al. (2025) The science of teaching reading is incomplete without the science of writing: A randomized control trial of integrated teaching of reading and writing. Scientific Studies of Reading. 29(1):32–54, DOI:10.1080/10888438.2024.2380272.
3. Bowater, L. and Yeoman, K. (2012) Science communication: A practical guide for scientists. Wiley-Blackwell, ISBN:978111840666-3.
4. Plaxco, K.W. (2010) The art of writing science. Protein Science, 19(12):2261–66, DOI: 10.1002/pro.514.
5. Adair, J. (2011) John Adair's 100 Greatest Ideas for Brilliant Communication. John Wiley & Sons, ISBN:9780857082244.
6. Bewersdorff, A., et al. (2025) Taking the next step with generative artificial intelligence: The transformative role of multimodal large language models in science education. Learning and Individual Differences, 118:102601, DOI:10.1016/j.lindif.2024.102601.
7. Monavarian, M. (2021) Basics of scientific and technical writing. MRS Bulletin, 46:284–286, DOI:10.1557/s43577-021-00070-y.
8. Reid, C.P.P. (2000) Handbook for preparing and writing research proposals. IUFRO Special Programme for Developing Countries. ISBN:3901347232.
9. Brown, P. (2014) An explosion of alternatives: considering the future of science journalism. EMBO Reports, 15(8):827–832, DOI:10.15252/embr.201439130.

PBRE432: Dissertation-II

Course code & title	Credits	Credit distribution of the course			Eligibility criteria	Pre-requisite of the course (if any)
		Theory/ Lecture	Tutorial	Practical		
PBRE432: Dissertation-II	16	0	0	16	B.Sc. in any branch of science	NA

Learning Objectives

The students will work independently on the research problem chosen in Semester 3 and will apply appropriate molecular, biochemical, physiological and/or computational approaches to address the defined objectives and hypotheses. They will learn to design and execute experiments with suitable controls and replicates, systematically collect, document, and analyse data using relevant statistical and bioinformatic tools, and interpret the results in the context of existing knowledge. They will further strengthen their skills in scientific writing by updating and refining the literature review and by preparing a well-organized dissertation adhering to standard formats, citation styles, and ethical guidelines. The student will also develop competencies in scientific communication by regularly discussing their work in lab meetings and presenting their findings through formal oral presentations.

Learning Outcomes

On successful completion of the dissertation, the student will be able to independently plan and conduct the experiments with appropriate controls, optimize and adapt protocols, and troubleshoot technical problems in response to experimental challenges. They will maintain systematic and complete laboratory records, generate reproducible datasets, and carry out quantitative/qualitative analyses, including appropriate statistical tests and data visualization. They will be able to critically interpret and integrate their experimental findings with published literature to draw logical, evidence-based conclusions, identify limitations, and suggest future directions. The student will be able to prepare a coherent dissertation that includes an updated literature review, methodology, results, discussion, and references in a standard format. They will exhibit professional research attitudes, including scientific rigor, ethical conduct, teamwork, and responsible data and time management in the laboratory to meet defined timelines and submission deadlines.

Suggested Readings:

Latest research and review articles on the chosen research topic.

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