

课程大纲

COURSE SYLLABUS

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| 1. | 课程代码/名称 Course Code/Title | 植物转录组学与基因组学前沿 Advanced Studies in Plant Transcriptomics and Genomics |
| 2. | 课程性质 Compulsory/Elective | 选修课 Elective |
| 3. | 开课单位 Offering Dept. | 生命科学学院 / School of Life Sciences |
| 4. | 课程学分/学时 Course Credit/Hours | 3 学分/48 学时 3 points/48 hours |
| 5. | 授课语言 Teaching Language | 中英文 Chinese and English |
| 6. | 授课教师 Instructor(s) | 翟继先 Jixian Zhai |
| 7. | 开课学期 Semester | 春季 Spring |
| 8. | 是否面向本科生开放 Open to undergraduates or not | |
| 9. | 先修要求 Pre-requisites | (如面向本科生开放, 请注明区分内容。 If the course is open to undergraduates, please indicate the difference.) 《普通生物学》 General Biology |
| 10. | 教学目标 Course Objectives | (如面向本科生开放, 请注明区分内容。 If the course is open to undergraduates, please indicate the difference.) 植物分子生物学和基因组学课程旨在深入研究基因在分子水平上的结构和功能。课程的目标是为学生提供坚实而严谨的基础, 使其能够深刻理解基因表达及其调控。课程将从蛋白质和核酸的结构开始进行回顾, 重点介绍驱动蛋白质与核酸相互作用的物理和化学性质。接着, 将学习应用于基因研究的方法和技术。随后, 将深入研究 DNA 复制、DNA 损伤修复、原核生物和真核生物的转录等分子层面的机制, 重点关注基因活性是如何通过核酸-蛋白质相互作用在分子水平上调控的。最后, 课程还将介绍基因组学和系统生物学, 并回顾正在改变我们对分子生物学理解的基因组学项目的进展。 Plant Molecular Biology and Genomics is a course is about genes - their structure and function at the molecular level. The objective is to give you a firm and rigorous foundation in understanding gene expression and its regulation. We will begin with a review of structure of protein and nucleic acid, and the physical and chemical properties that drive interactions of protein with nucleic acid. Then we will study methods and technologies applied to study genes. Next, we will study the molecular mechanics of DNA replication, DNA damage repair, transcription in both prokaryotic and eukaryotic organisms, with an emphasis on how the activity of genes is regulated at the molecular level through nucleic acid-protein interactions. Lastly, genomics and systems biology will also be introduced and we will review advances in genomics projects that are altering our understanding of molecular biology. |
| 11. | 教学方法 Teaching Methods | (如面向本科生开放, 请注明区分内容。 If the course is open to undergraduates, please indicate the difference.) 1. 教授授课 1. Lectures by Professor 2. 小组讨论 由教师指导学生就问题发表自己的看法, 让学生进行交流和学。通过讨论, 学生们可以互相帮助、互相学习, 加深对知识的认识和理解, 获得更多新知识。此外, 还可以鼓励学生自主学习, 共同解决问题。 |

2. Group Discussion

The teacher instructs students to give their own opinions about the issue, and make them to communicate and learn. Through discussion, students will help each other and learn from each other, deepen their knowledge, understanding and gain more new knowledge. Besides, their autonomy will also be encouraged in order to solve problems together.

12. 教学内容

Course Contents

(如面向本科生开放, 请注明区分内容。 If the course is open to undergraduates, please indicate the difference.)

1. Sanger 测序与早期植物基因组计划 (2 课时)

- a) DNA 和染色体的结构
- b) DNA 复制
- c) 早期低通量核酸测序技术发展历史
- d) 完成植物基因组计划

1. Sanger sequencing and early plant Genome Projects (2h)

- a) The structures of DNA & Chromosome
- b) DNA replication
- c) Early history in developing low-throughput DNA sequencing methods
- d) Completion of the plant genome projects.

2. 二代测序与植物基因组组装 (2 课时)

- a) 过去十年各种下一代测序平台的发展和竞争, 以及 Illumina 如何成为垄断者。
- b) 个性化基因组学、基因组编辑工具 (CRISPR) 的应用

2. Next-generation sequencing and the plant genome assembly (2h)

- a) Developments and competition of various next-generation sequencing platforms over the past decade, and how Illumina became the monopoly.
- b) Application for personalized genomics, Tools for genome editing (CRISPR)

3. 三代测序、植物组学大数据等 (2 课时)

- a) 长读长测序 (Nanopore 和 PacBio) 如何彻底改变基因组组装领域。
- b) 使用纳米孔技术对 RNA 和蛋白质进行直接测序

3. Third-generation sequencing, bigdata in plant transcriptomics (2h)

- a) How long-read sequencing (Nanopore and PacBio) revolutionize the field of genome assembly.
- b) Direct sequencing of RNA and protein using Nanopore technology

4. 植物基因组学科研思维与技术策略(2h)

- a) 植物基因组学与生物信息学研究进展
- b) 植物基因组学与生物信息学经典案例分享
- c) 科学思维与技术策略制定

4. Scientific research thinking and technological strategy of plant genomics (2h)

- a) advances in plant genomics and bioinformatics
- b) classic cases of plant genomics and bioinformatics
- c) scientific thinking and formulation of technical strategies

5. 学生报告展示-0

5. Students' presentation-0

6. 计算机基础 (linux+编程) (2h)

- a) 语言编程与字符串处理: 正则表达式
- b) 数据分析流程搭建: 模块化与流程化, 工程学思想

6. Computer basics (Linux + programming) (2h)

- a) string processing: regular expressions
- b) data analysis process building: modularization and routing, engineering ideas

7. 常用软件和植物数据库介绍，包括常用文件格式（2h）

- a) 实操 1: 包括 fasta、fastq、bam、vcf 格式介绍
- b) 功能分析与进化分析软件
- c) 实操 2: 包括 newick 格式介绍
- d) 常用植物生物数据库

7. Introduction to common software and database (2h)

- a) operation 1: introduction of fasta, fastq, bam and VCF formats
- b) functional analysis and evolutionary analysis softwares
- c) operation 2: introduction of newick format
- d) commonly used plant databases

8. 学生报告展示-1

8. Students' presentation-1

9. 大数据和云计算(2h)

- a) 生物大数据
- b) 生物云计算
- c) Galaxy 系统安装
- d) 搭建你的第一个云流程
- e) 比较几款常见的生物信息云平台
- f) 优化或扩展你的云流程

9. Big data and cloud computing (2h)

- a) biological big data
- b) biological cloud computing
- c) Galaxy system installation
- d) build your first cloud process
- e) comparison of several common biological cloud platforms
- f) optimize or extend your cloud processes

10. 植物基因组 De novo 分析（2h）

- a) 基因组组装问题建模
- b) 组装软件与应用场景
- c) 基因组组装：单个细菌基因组
- d) 组装评价：指标体系、QUAST 软件
- e) 基因组注释与比较基因组分析
- f) 宏基因组组装与分析

10. Plant genome de novo analysis (2h)

- a) modeling of genome assembly problems
- b) assembly software and application scenarios
- c) genome assembly: single bacterial genome
- d) assembly evaluation: indicator system and QUAST software
- e) genome annotation and comparative genome analysis
- f) macronomic assembly and analysis

11. 学生报告展示-2

11. Students' presentation-2

12. 植物小分子 RNA (2h)

- a) microRNA
 - b) small interfering RNA
 - c) trans-acting siRNA
12. Plant small RNA (2h)
- d) microRNA
 - e) small interfering RNA
 - f) trans-acting siRNA
13. 表观遗传学 (2h)
- a) 表观遗传研究与高通量技术
 - b) 表观遗传研究技术: ATAC-seq
 - c) 上机实操: 数据质控与分析软件安装
 - d) 上机实操: 修饰位点注释与差异分析
 - e) 上机实操: 信息整合与统计绘图
 - f) 综合实操: 表观组学研究方案设计与讨论
13. Epigenetics (2h)
- a) epigenetic research and high-throughput techniques
 - b) epigenetic research techniques: ATAC-seq
 - c) actual operation: data quality control and analysis software installation
 - d) computer operation: modification site annotation and difference analysis
 - e) computer operation: information integration and statistical drawing
 - f) comprehensive practice: design and discussion of the research scheme of apparent omics
14. 转录组学 (2h)
- a) 转录组测序技术: ncRNA、sRNA、降解组
 - b) 转录组组装与结构分析: SNP 检测、SSR 预测、可变剪接
 - c) 表达定量与差异分析: SEQC, ERCC,
 - d) 模式聚类与富集分析: 共表达网络
 - e) ncRNA、sRNA、降解组测序分析
 - f) 转录组研究方案设计与讨论
14. Transcriptome (2h)
- a) transcriptome sequencing technology: ncRNA, sRNA, degradation group
 - b) transcriptome assembly and structure analysis: SNP detection, SSR prediction, variable splicing
 - c) expression quantitative and differential analysis: SEQC, ERCC
 - d) pattern clustering and enrichment analysis: co-expression network
 - e) ncRNA, sRNA and degradation group sequencing analysis
 - f) design and discussion of transcriptome research scheme
15. 植物转基因技术 (2h)
- a) 植物转化技术的发展历程
 - b) 转基因技术在农业中的应用
 - c) 未来发展趋势
15. Metagenome (2h)
- a) history of plant transformation
 - b) Application of plant transgene technology in agriculture
 - c) future of transgenic plants
16. 学生报告展示-3
16. Students' presentation-3
17. 植物系统生物学网络分析和可视化(2h)

- a) 生物网络的类型简介
- b) 复杂网络中的关键概念
- c) 蛋白-蛋白相互作用网络
- d) 基因调控网络
- e) 基因集富集与网络分析
- f) 可视化降维

17. Network analysis and visualization for plant system biology(2h)

- a) Introduce types of biological networks
- b) Key concept in complex network
- c) Protein-Protein Interaction network
- d) Gene Regulatory Network
- e) Gene Set Enrichment and network analysis
- f) Dimensionality reduction for visualization

18. 机器学习在植物基因组学中的应用(2h)

- a) 机器学习在从头组装中的应用
- b) 机器学习在建立电子健康档案中的应用
- c) 基因组学中的深度神经网络
- d) 深度学习在生物网络中的应用

18. Machine learning in plant genomics(2h)

- a) Machine learning in *de novo* assembly
- b) Machine learning in electronic health record
- c) Deep neural network in genomics
- d) Deep learning for network biology

19. 植物单细胞组学技术简介 (2 学时)

- a) 单细胞技术发展历史
- b) 单细胞多组学
- c) 植物空间转录组技术

19. Introduction to plant Single Cell Omics (2h)

- a) Development history of single-cell technology
- b) Single-cell multi-omics
- c) Spatial Transcriptome Technology in plants

20. 学生报告展示-4

20. Students' presentation-4

21. 植物单细胞转录组学数据分析 1 (2 学时)

- a) 单细胞转录组数据结构
- b) 单细胞数据分析简要流程
- c) 单细胞转录组分析软件介绍

21. Plant Single-cell Transcriptomic Data Analysis-1 (2h)

- a) Single-cell transcriptome data structure
- b) Brief process of single-cell data analysis
- c) Introduction to single-cell transcriptome analysis software

22. 植物单细胞转录组学数据分析 2 (2 学时)

- a) 单细胞转录组数据质量控制和预处理
- b) 单细胞转录组分析范例
- c) 单细胞 RNA 动力学分析

22. Plant Single-cell Transcriptomic Data Analysis-2 (2h)

- a) 4. Single-cell transcriptome data quality control and preprocessing
- b) 5. Single-cell transcriptome analysis paradigm
- c) 6. Single-cell RNA kinetic analysis

23. 单细胞组学在植物生命科学研究中的应用（2 学时）

23. Application of single-cell omics in plant life science research (2h)

24. 学生报告展示-5

24. Students' presentation-5

13. 课程考核

Course Assessment

（① 考核形式 Form of examination; ②. 分数构成 grading policy; ③ 如面向本科生开放，请注明区分内容。
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考勤（10 分）、演讲（60 分）、报告（30 分）

Attendance (10 points), Presentation (60 points), Report (30 points)

14. 教材及其它参考资料

Textbook and Supplementary Readings

在线课本-拟南芥书籍，免费下载

Online text book – Arabidopsis Book, free download.