

**PLANT GENOMICS
PBIO / PLPA 5301
FALL 2016**

TU/TH 1:30 - 2:45 pm
ROOM 146 McNEAL HALL
ST PAUL CAMPUS, UNIVERSITY OF MINNESOTA

INSTRUCTOR

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Office hours are flexible. Send an email to schedule an appointment or just visit with me before or after class. Students are also welcome to visit me in my office (320 Cargill) during regular office hours, Friday 9:00 – 10:00 am throughout the fall semester.

Overview

Plant Genomics is a course for graduate and advanced undergraduate students interested in the genomics and bioinformatics of plants. Students learn strategies for genomic analysis by exploring DNA sequencing technology, model plant systems, comparative genomics, sequence variation, genome expression, and genome evolution. Students also develop an understanding about the fundamentals of sequence analysis, database searches, and data-mining through case studies, computer labs and independent projects. Class sessions consist of lectures, discussions, small group activities, and hands-on computer labs.

Prerequisites

Introductory course in genetics – or – consent of instructor.

Requirements

Everyone who attends class *must* enroll formally, including students who are taking Plant Genomics for credit as well as those who plan to audit. Because class participation is a formal part of the final grade, students need to attend every class. If you expect to miss a class for a valid reason, please inform me by email a day or two ahead of time.

Moodle Site

Nearly all resources for Plant Genomics are found on the class Moodle site (<https://ay16.moodle.umn.edu/course/view.php?id=2547>). For example, a tentative class schedule is available in a shortened .pdf format on the Moodle site, corresponding closely to the layout of classes and teaching materials found on the site. Keep in mind that timing as well as modified versions of handouts and assignments become available on the site throughout the semester so be sure to visit regularly.

Readings

Practical Bioinformatics (Agostino) provides many of the readings in Fall 2016. This book can be purchased or rented at the UMN Bookstore or through Amazon. All other readings for Fall semester 2016 are accessed through the course Moodle site.

Grading

200 points	Two In-class Exams: 100 points each
50	One Take-home Exam: 50 points
40	Teaching Project and Presentation: 40 points
20	Data-Mining Homework: 20 points
20	In-Class Activities: 5 x 5 points total (Lowest one dropped)
20	Moodle & Homework: 5 x 5 points total (Lowest one dropped)

TOTAL: 350 points

NOTE: Point totals for Class Activities and Homework are projections and may be adjusted during the semester. In other words, **the point total of 350 is only an estimate.**

There are **NO plans for extra credit** in this class.

A	=>	95.0	–	100
A-	=>	90.0	–	94.9
B+	=>	87.0	–	89.9
B	=>	83.0	–	86.9
B-	=>	80.0	–	82.9
C+	=>	77.0	–	79.9
C	=>	73.0	–	76.9
C-	=>	70.0	–	72.9
D+	=>	67.0	–	69.9
D	=>	60.0	–	66.9
F	=>	59.9	or less	

Exams

There are two in-class exams – each approximately 60 minutes in length – on October 25 and December 1. Each exam will be preceded by a Review Session that takes place during the class period immediately before the exam. There are generally no make-ups, so in the case of a documented excused absence from an exam, the final semester grade may (at the discretion of the instructor) be based on remaining exams, quizzes, project, and assignments. In-class exam generally consist of four to six medium-length essay questions or problems.

There will also be a take-home exam starting on September 27. The take-home exam will be accessible through the class Moodle site, where answers should be submitted. More details about exams will be provided in class.

Class Activities and Homework

To provide practical experience with genome databases and data-mining, there will be a variety of in-class activities, computer labs, problem sets, and homework. These activities will be relatively short and frequently connected to specific labs. Many class activities require the use of laptop, tablet or smartphone technology and involve internet, Moodle or Voice Thread technologies. **In other words, always bring at least one internet-capable device with you to class each day.**

Group Teaching Project

The field of Plant Genomics is so rich and diverse there really isn't time to cover all of the essential material. Therefore, students will break into groups of three starting October 27 to investigate one of several different **special topics in Plant Genomics**. Groups will develop and present 25 minute teaching modules that consist of foundational material, an illustrative research paper, and example questions to include on the final exam. More details will be provided later in class.

Group Data-Mining Project

The final assignment will be a small group genome mining project in class on November 22nd. This will be followed by an individual homework where you identify a candidate gene for further analysis and then propose a series of genomics-based experiments that would help to confirm the biological role of your chosen candidate gene.

Handouts

Most classes are accompanied by lecture handouts, which are .pdf versions of material presented in class. These handouts can be downloaded from Moodle and are generally available before class. Some readings also have study guides.

For some classes, there is one or more video links providing deeper information about a specific topic. In certain cases, the video replaces class (due to instructor travel). Other videos are optional. Videos are accessible through the Moodle site and generally work on all computers or mobile devices.

Computer Labs and Electronic Technology

Several times during the semester, we have classes that are primarily computer lab activities. Therefore, students should bring laptops and/or tablet devices (laptops are better for genomics) to class whenever possible. Remember – during class, electronic devices can only be used for class activities, which will be clear from instructions given during class. Phones may never be used during class and should be set to airplane- or silent-mode before class begins.

Though unlikely, we may need to change the location of class if special facilities are required, something that will be announced ahead of time and also posted on the Moodle site. During lab classes, students should plan to work in pairs to explore different bioinformatic tools, websites, and databases. Generally, a handout with computer lab instructions will be available on the Moodle website ahead of time.

Course Communication

Electronic communication during the semester will primarily be through X500 email and the course Moodle site. Therefore, students should plan to read their X500 email account and visit the course Moodle site regularly (at least a times each week).

Late Assignments

In cases where an assignment or take-home exam is submitted after the deadline, the **grade will be reduced one letter grade if turned in one day late and two letter grades if turned in two days late. Late assignments submitted more than two days late will be accepted on a case-by-case basis only**, generally requiring documentation that justifies handing in a late assignment. Making arrangements with the instructor ahead of time is strongly encouraged.

Grade Disputes

Grade disputes for any assignment or exam should be submitted in writing or email to the instructor **within one week of receiving a disputed grade**. If the dispute can not be resolved satisfactorily, the assignment may be given to an expert outside of class to provide input. Please remember that re-graded exams and assignments can potentially be lowered as well as raised.

Students with Disabilities and Equal Access

All registered students, independent of race, gender, sexual preference, employment background, primary language, or disability, receive equal treatment and equal access to class materials in Plant Genomics. Students with a disability should contact University Disability Services (612-624-4037) or the instructor.

Student Code, Scholastic Honesty, and Appropriate Use of Course Materials

Students in Plant Genomics are expected to do their own work and submit their own assignments – so except when explicitly stated by the instructor or in an assignment’s instructions, students are prohibited from copying or pasting materials directly from the internet or copying material from another student.

Nevertheless, collaboration and communication among students is encouraged. I will make it clear when a graded activity can include collaboration and/or shared responses. Details about the University of Minnesota's student honor code are found at: <http://www1.umn.edu/regents/policies/academic/StudentConduct.pdf>.

When working together – and at all times during class – students should seek to:

- be comfortable sharing their unique experiences, values and beliefs
- be open to the views of others
- respect the contributions of colleagues
- appreciate the opportunity to learn from one another
- value one another’s opinions and communicate in a respectful manner
- keep discussions confidential when appropriate.

Plant Genomics 1501: Student Learning Outcomes

Examples of How Students Master the Principles of Genomics. Students master the principles of genomics by applying genome-based modes of inquiry to investigate essential plant processes. Students begin by learning the conceptual basis of genomics; a way of thinking that involves asking questions about all the genes or gene products in an organism simultaneously in order to explore biological

phenomena. Students gain mastery in interpreting genome data by learning the underlying technology behind DNA sequencing, elementary strategies to mine genomic datasets, and the skills to search genomic data through the use of sequence alignment algorithms. Students extend these foundational principles to explore sequenced plant genomes, gene families, gene expression and function, epigenetic phenomena (heritable change not involving DNA sequence), and genome variation within plant species. With these skills in place, students go on to examine the growing body of knowledge about plant genome architecture, evolution and function. They apply their skills by assembling genome sequences from preliminary data, annotating plant genomes to reveal the complement of genetic features, dissecting the topology of defense gene networks, and mapping target genes through the principles of association genetics.

Examples of How Class Work Relates to Learning Outcomes. Early in the semester, students begin with active learning exercises where they work in pairs to explore real-world DNA sequence data using the fundamental sequence alignment tool, "BLAST". They work together to determine what is significant (and what is not), how significance should be evaluated, and how genome searches can be improved. Their results form the basis of both class discussion, forums managed through Moodle, homework activities, and essay questions on exams. Later, students tackle the challenges of sequencing whole plant genomes, highlighting the pitfalls, and modeling the steps that eventually lead to a finished genome sequence. They experience first-hand why plant genomes tend to be more difficult to sequence and assemble than other biological organisms as a result of the high degree of sequence duplication found within plants. These exercises form the basis of in-class and Moodle activities, homework assignments, and exam questions. In other learning experiences, students work in small groups to read and critique the steps in classic studies about plant gene networks, disease resistance genes, and the development of a pan-genome, reproducing the steps and reasoning of the original authors. Finally, students perform one or more capstone experiences working individually and in small groups to: 1) Develop a teaching module about a specific aspect of plant genomics and present it to class, 2) Debate controversial scientific and/or public policy issues of current interest in the field of (plant) genomics, 3) Explore a small portion of a plant genome in order to discover the features found there, the quality of the gene annotation, the evidence for expression, comparisons and contrasts with homologous regions of related plant genomes, and discover possible causative trait loci. This final exercise leads to a saved video report that is presented in class, forming the basis for a question and answer session led by students.