



## **AGRONOMY/AN SCI/GENETICS/HORT 615**

### **Genetic Mapping**

3 credits

**Course Designation:** Graduate

#### **Course Description**

Computing-intensive course to prepare students for genetic mapping research; linkage analysis and QTL mapping in designed crosses; linkage disequilibrium and association analysis (GWAS). Recommended preparation is undergraduate courses in genetics and statistics and prior experience with R scripting.

**Requisites:** Graduate/professional standing

#### **Meeting Time**

MWF 8:50 – 9:40 am, Room 128 Plant Sciences

**Instructional Modality:** Classroom Instruction

**Course Website:** <https://canvas.wisc.edu/courses/346435>

#### **How Credit Hours are met by the Course**

This course meets for three 50-minute periods per week, and students are expected to spend at least 6 hours per week on course learning activities outside the classroom.

**Instructor:** Jeffrey Endelman, Associate Professor

**Office Hours:** 3:30p – 4:30p Thursday, Room 473 Plant Sciences

**Contact Information:** [endelman@wisc.edu](mailto:endelman@wisc.edu)

#### **Learning outcomes**

1. Write scripts to curate marker data and analyze population structure
2. Explain the distinction between linkage and association mapping
3. Describe how population and model parameters affect statistical power
4. Construct genetic linkage maps and discover QTL in biparental populations
5. Perform a genome-wide association analysis and interpret the results

## Required Textbooks

Van Ooijen JW, Jansen J. 2013. Genetic Mapping in Experimental Populations. Cambridge University Press, Cambridge.

Broman KW, Sen S. 2009. A Guide to QTL Mapping with R/qtl. Springer, NY. **Available as e-book through UW library**

Lecture notes will be provided through Canvas.

## Grading

60% Homework (11 assignments, lowest grade dropped)

10% Midterm Exam (closed note, 8:50 – 9:40a March 10)

15% Final Exam: Computing (open note, 24 hr, due 5 pm May 5)

15% Final Exam: Conceptual (closed note, 5:05 – 7:05 pm May 10)

Course grades will be assigned based on the following breakpoints, where X is the final numeric grade. After reviewing the distribution, the breakpoints may be lowered.

A	$92 \leq X$
AB	$88 \leq X < 92$
B	$82 \leq X < 88$
BC	$78 \leq X < 82$
C	$70 \leq X < 78$
D	$60 \leq X < 70$
F	$X < 60$

## Exam Policy

- You may NOT discuss the exam with anyone while taking it
- Late submissions will be penalized 10% **for every hour** past the deadline

## Homework (HW) Policy

- There will be 11 HW assignments, and your lowest grade will be dropped.
- Unless indicated, HW must be submitted through Canvas in R markdown format: both the Rmd and compiled (HTML or PDF) files.
- Late homework assignments will be penalized 10% if received up to 1 day (24h) beyond the deadline and 20% for 24–48h beyond the deadline. **After 48h you will receive zero credit so that solutions can be posted.**
- You are encouraged to work in study groups but **do not copy code** from other students. This will result in zero credit for an assignment.

HW	Topic	Deadline, 5 pm
1	Genotyping-by-sequencing	Feb 3
2	Variant Call Format (VCF)	Feb 10
3	Linkage disequilibrium (LD)	Feb 17
4	Recombination Frequency	Feb 24
5	Linkage maps	March 3
6	Imputation	March 24
7	QTL Design	March 31
8	Single QTL discovery	April 7
9	Multi-QTL discovery	April 14
10	Multi-parental linkage mapping	April 21
11	Genome-wide association study	April 28

### UW-Madison Policies

For additional information on the following topics, please follow the link in the electronic version of the syllabus:

- [Teaching and Learning Data Transparency Statement](#)
- [Privacy of Student Records and the Use of Audio Recorded Lectures Statement](#)
- [Campus Resources for Academic Success](#)
- [Course Evaluations](#) and [Digital Course Evaluations](#)
- [Students' Rules, Rights and Responsibilities](#)
- [Diversity and Inclusion Statement](#)
- [Academic Integrity Statement](#)
- [Accommodations for Students with Disabilities](#)
- [Academic Calendar and Religious Observances](#)