

PBPG 957 Spring 2018 Yandell
QTL Mapping in Experimental Populations

Institution Name: University of Wisconsin-Madison

Course Subject, Number and Title: AGRONOMY/GENETICS/HORT 957 Seminar-Plant Breeding (Seminar)

Credits (#): 1

Canvas Course URL: <https://canvas.wisc.edu/courses/81468> (probably not used)

Course Designations and Attributes: NA

Meeting Time and Location: Friday 3:30-4:30pm Moore/PISci 351

Instructional Mode: face-to-face

Specify how Credit Hours are met by the Course: One hour per week contact plus two hours outside preparing for in-class presentation.

Instructor Title and Name: Professor [Brian Yandell](#) & Professor [Karl Broman](#)

Instructor Availability: Yandell and Broman are available by appointment or email

Instructor Email/Preferred Contact: brian.yandell@wisc.edu, kbroman@biostat.wisc.edu

Teaching Assistant: NA

Course Description: The overarching topic for this semester is **QTL Mapping in Experimental Populations**. Students either sign up for a topic-based or research presentations. We particularly encourage those with QTL mapping as part of their research to consider focusing on some aspect of QTL analysis. Here is a list of suggested topics, roughly in the order that makes sense for presentation (although we will likely introduce R/qtl early):

Requisites: For graduate students in the Plant Breeding & Plant Genetics PhD Program.

Course Learning Outcomes

- **Knowledge and Skills**

- Articulates research problems, potentials, and limits with respect to knowledge within the field of plant breeding and plant genetics.
- Formulates ideas, concepts, designs, and/or techniques beyond the current boundaries of knowledge within the field of plant breeding and plant genetics.
- Creates research that makes a substantive contribution.
- Demonstrates breadth within their learning experiences.
- Advances contributions of the field of plant breeding and plant genetics to society.
- Communicates complex ideas in a clear and understandable manner.

- **Professional Conduct**

- Fosters ethical and professional conduct.

Grading

Grading is based on attendance (10%), participation in discussion (20%) and quality of presentation and accompanying materials (70%).

Suggested topics

This seminar will work best if concepts are illustrated and grounded with data analysis and graphics. Sample data sets are indicated below;

- What is QTL mapping?
 - relation of genotype to phenotype across genome
 - genome scans
- How can we use R/qtl tools for QTL mapping?
 - linkage map diagnostics
 - model selection for multiple QTLs
 - estimating genetic effects and heritability
 - covariates and design considerations
- QTL mapping for multiparent experimental populations
 - What are the challenges and opportunities with?
 - How does R/qtl2 scale up to these larger crosses?
- Tour of available datasets (see Sample Datasets below)
- Tour of available packages
 - [R/qtl](#): see brief or shorter tour under [Tutorials](#)
 - [R/qtl2](#): see [User Guide](#) and [Differences between R/qtl & R/qtl2](#)
 - [Kyazma/MapQTL/JoinMap](#)
 - [GeneNetwork](#) & [GeneNetwork2](#)

Sample Datasets

- [listeria sample dataset in R/qtl package](#)
- [grav2 & iron sample datasets in R/qtl2geno package](#)
- [DO mouse data \(Dan Gatti\)](#)
- [Example data in R/qtl2data](#)
 - B6BTBR F2
 - DO from Gatti and Recla
 - Gough x WSB F2
- other data?

Selected References

- Broman KW (2001) [Review of statistical methods for QTL mapping in experimental crosses](#). Lab animal 30: 44-52.
- Broman & Sen (2009) [A Guide to QTL Mapping with R/qtl](#)
- Collard BCY, Jahufer MZZ, Brouwer JB, Pang ECK (2005) An introduction to markers, quantitative trait loci (QTL) mapping and marker-assisted selection for crop improvement: The basic concepts. Euphytica 142: 169-196. [\[doi:10.1007/s10681-005-1681-5\]](#)
- Doerge RW, Zeng ZB, Weir BS (1997) Statistical issues in the search for genes affecting quantitative traits in experimental populations. Statistical Science 12: 195-219. [\[doi:10.1214/ss/1030037909\]](#)
- [more QTL references](#)
 - **Overview:** Tanksley (1993); Lander, Schork (1994); Basten, Weir, Zeng (1995); Paterson (1995); Doerge, Zeng, Weir (1997); Kearsey, Farquhar (1998); Broman (2001); Mackay (2001a,b); Mauricio (2001); Asíns (2002); Boake et al. (2002); Phillips, Belknap (2002); Hackett (2003); FAO (2004); Collard et al. (2005); Swertz, Jansen (2007); Stein (2008); Xu, Crouch (2008)

- **From QTL to Gene:** Guo, Lange (2000); Nadeau, Frankel (2000); Flint, Mott (2001); Glazier, Nadeau, Aitman (2002); Korstanje, Paigen (2002); Botstein, Risch (2003); Page et al. (2003); Rebbeck, Spitz, Wu (2004); Barendse (2005); Darvasi (2005); Hirschorn, Daly (2005); Petretto, Liu, Aitman (2007); Verdugo et al. (2010)

The following are mostly about multiparental families

- [Magic Web talk \(Broman 2013, MAGIC Workshop, Cambridge\)](#)
- [Genetics.org Multiparental Populations site](#)
 - McIntyre & de Koning (2012) [Facilitating Discovery: The Role of Society Journals in Collaborative Science](#). *Genetics* 190: 285-286.
- [mouse:](#)
 - [The Diversity Outbred mouse population \(Mamm Genome 2012\)](#)
 - [High-resolution genetic mapping using the Mouse Diversity outbred population \(Genetics 2012\)](#)
 - [Quantitative trait locus mapping methods for diversity outbred mice \(G3 2014\)](#)
- [plants:](#)
 - Bandillo N et al. (2013) [Multi-parent advanced generation inter-cross \(MAGIC\) populations in rice: progress and potential for genetics research and breeding](#). *Rice* 6: 11.
 - Cavanagh C et al. (2008) [From mutations to MAGIC: resources for gene discovery, validation and delivery in crop plants](#). *Curr Opin Plant Biol.* 2008 Apr;11(2):215-21.
 - Cockram J et al. (2015) [Fine-Mapping the Wheat *Snn1* Locus Conferring Sensitivity to the *Parastagonospora nodorum* Necrotrophic Effector SnTox1 Using an Eight Founder Multiparent Advanced Generation Inter-Cross Population](#). *G3* 5: 2257-2266.
 - Higgins RH et al. (2014) [Multiparental Populations Multiparental Mapping of Plant Height and Flowering Time QTL in Partially Isogenic Sorghum Families](#). *G3* 4: 1593-1602.
 - Huang BE et al. (2012) [A multiparent advanced generation inter-cross population for genetic analysis in wheat](#). *Plant Biotechnol J* 10: 826-39.
 - Kover PX et al. (2009) A Multiparent Advanced Generation Inter-Cross to Fine-Map Quantitative Traits in *Arabidopsis thaliana*. *PLoS Genet* 5: e1000551. ([NASC Collection](#))
 - Liu Z, Garcia A, McMullen MD, Flint-Garcia SA (2016) [Genetic Analysis of Kernel Traits in Maize-Teosinte Introgression Populations](#). *G3* 6: 2523-2530.
 - Prado SA, López CG, Senior ML, Borrás L (2014) [Multiparental Populations The Genetic Architecture of Maize \(*Zea mays* L.\) Kernel Weight Determination](#). *G3* 4: 1611-1621.
 - Schmutzer T et al. (2015) [Species-wide genome sequence and nucleotide polymorphisms from the model allopolyploid plant *Brassica napus*](#). *Scientific Data* 2: 150072.
 - Würschum T et al. (2014) [Multiparental Populations Adult Plant Development in Triticale \(*× Triticosecale* Wittmack\) Is Controlled by Dynamic Genetic Patterns of Regulation](#). *G3* 4: 1585-1591.