

PLNT 7164, Genetic Mapping in Plants

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Office Hours: immediately following lectures, however setting an appointment time is recommended.

Course Description: Application of genetic mapping analyses for the dissection of traits in plant species. Linkage mapping, quantitative trait locus (QTL) mapping, association mapping, and related analyses will be reviewed in detail. Emphasis will be placed on practical applications in genetic studies. The analysis and interpretation of real data will be conducted in computer tutorials sessions.

Goal: To understand and implement modern genetic analysis techniques to study the genetic control of plant traits.

Objectives: To acquire knowledge needed to conduct various genetic mapping analyses:

- 1) Linkage mapping
 - a. Determining linkage groups
 - b. Marker ordering methods
 - c. Error detection
- 2) QTL mapping
 - a. Mapping algorithms
 - b. Key statistics, significance thresholds for LOD scores
- 3) Association mapping
 - a. Population structure
 - b. Kinship
 - c. LD decay
- 4) Ability to design experiments with a working knowledge of different genetic analyses and their strengths and weaknesses.

Format: The class will meet on a weekly basis for approximately three hours. The course will consist of formal lectures, discussion periods, and computer tutorials. Meeting times and locations will be determined at the first class meeting to ensure no conflicts with other classes.

Textbook: None. Assigned readings will be provided for class discussions.

Software: BRING A LAPTOP TO CLASS!

MapDisto (http://mapdisto.free.fr/Download_Soft/), linkage analysis, robust features for refining linkage maps.

QGene (<http://www.qgene.org/qgene/download.php>), QTL mapping, user-friendly

QTL IciMapping (<http://www.isbreeding.net/software/>), placing markers into linkage bins to remove redundant markers (critical step of linkage analysis), linkage analysis (limited features), QTL mapping (includes epistatic QTL analysis)

TASSEL (<http://www.maizegenetics.net/tassel>), Genome Wide Association Study

CIMMYT Software (<https://data.cimmyt.org/dataverse/cimmytswdvn>), useful but not needed.

GEA-R (Genotype x Environment Analysis with R for Windows)

META-R (Multi Environment Trial Analysis with R for Windows)

Spatial META-R (Spatial Multi-Environment Trial Analysis with R for Windows)

Evaluation:

<u>Method</u>	<u>%</u>
Assignments	60%
Presentations	30%
Discussion/Participation	10%
Total	100%

Late Submissions: Assignments that are submitted after the deadline will be reduced by 10% of the value of the assignment per day.

General Academic Regulations: Please refer to the University of Manitoba General Calendar for regulations regarding plagiarism, cheating, and examination impersonation.

Assignments: Three assignments will be completed over the duration of the course. Tentative due dates are:

October 9, 2020

November 6, 2020

December 4, 2020

Presentations: Each student will be assigned two papers to present to the class. A presentation schedule will be determined at the beginning of the term. Presentations will be 15 minutes in length, with 5 minutes for discussion. Presentations will include a brief introduction, key results, and a summary/conclusions. Students must read all papers and have 1 to 2 questions prepared for discussion.

Evaluative feedback will be given to the students prior to the voluntary withdrawal deadline.

Course Schedule

Lecture	Date	Topics
1	Sept 11	Introduction to course
2	Sept 18	Linkage analysis
3	Sept 25	Linkage analysis
4	Oct 2	Linkage analysis
5	Oct 9	QTL analysis
6	Oct 16	QTL analysis
7	Oct 23	QTL analysis
8	Oct 30	QTL analysis
9	Nov 6	Association Mapping
-	Nov 13	No Class (Fall Term Break)
10	Nov 20	Association Mapping
-	Nov 23	Voluntary Withdrawal Deadline
11	Nov 27	Association Mapping
12	Dec 4	Wrap-up, Q & A

Grading Scale

Grade	Percentage
A+	90-100
A	80-89
B+	75-79
B	70-74
C+	65-69
C	60-64
D	50-59
F	0-49