ANSC 545, CPSC 545, IB 507
Statistical Genomics

Second-half Spring 2011
3 or 4 hours

Course Information
Instructor: Sandra Rodriguez Zas, Ph. D.
Office: Room 30 Animal Sciences Laboratory (ASL)
Email: rodrgzzs@uiuc.edu

Lectures and Labs: W, F. 10:00AM – 11:30PM
Second-half session March 14-May4, 2011
Room: 30 LIAC (ACES Library building Computer Lab)

Office hours: After class Room 30 LIAC

Course web address: http://compass.illinois.edu
Web page login: NetID; password: AD password

Every student is responsible for frequently reviewing the content of course ANSC 545 webpage for class notes, assignments, course related materials, calendar of events, updated information or messages.

Prerequisites
One applied statistical methods course (for example, CPSC 440, ANSC 445, STAT 200, STAT 425) or equivalent course on statistics and experience using the statistical software SAS.

Background
Nucleic microarray studies measure the level of expression of thousands of genes simultaneously. Results from this type of studies can help identify genes differentially expressed between conditions, discover common gene expression patterns, and characterize samples based on unique gene expression profiles.
Another important area of genomic studies is the identification of significant associations between phenotypic variation and genome location or quantitative trait loci. Together with information from quantitative trait loci mapping, nucleic microarray studies are helping to understand the genetic architecture of complex traits and are being used in academia, pharmaceutical and biotechnology industries. The volume and complexity of this data challenges the analysis, interpretation and application of the results.

Description
The goal of ANSC 545 is to provide the skills necessary to analyze data from nucleic microarray and quantitative trait loci studies in livestock, plants, model organisms, and humans.

Lectures and hands on activities using real data and annotated statistical software code will cover the key aspects of the analysis.
This capstone course combines concepts in statistics, molecular and quantitative genetics. The theoretical rationale of some statistical and mathematical concepts is complemented or substituted with intuitive explanations to facilitate the understanding.

Objectives

During the course, students will: a) be introduced to approaches for the analysis of gene expression and molecular marker genetic data, b) reflect on the interpretation of the results of the analyses, c) develop critical thinking skills while using relevant computer packages, and d) exercise problem solving capabilities and communication skills for effective research These objectives will be accomplished through lectures, lab activities, and homework assignments.

Topics

Microarray studies

1) Introduction to two-dye microarray data 2) Normalization 3) Detection of differentially expressed genes 4) Experimental design 5) Identification of relationships between genes and samples 6) Classification of samples, 7) One-dye microarray data, 8) Functional analysis, 9) Network visualization

QTL mapping studies

10) Detection of genes controlling complex traits in backcross and F2 inbred line crosses using single marker and linkage analysis, 11) Detection of genes controlling complex traits in outbred populations, 12) Association studies

Genetical genomics (as time permits)

13) Integration of gene expression and QTL data

References

Required reading material: class notes and lab activities available at the ANSC 545 webpage. Lectures will highlight some aspects from the class notes. Students are expected to read the class notes before the lecture to make the most of the lectures. Lab activities are directly related to the homework assignments.

Suggested reading material:

* Dov Stekel. 2003. Microarray Bioinformatics. Cambridge University Press. [U of I Library call number 572.8636 St37m]
* Joel Ira Weller. 2001. Quantitative Trait Loci Analysis in Animals. Oxford University Press. [U of I Library call number 636.0821 W458q]
* B M Neale, M A R Ferreira, S E Medland, D Posthuma (Eds). 2009. Statistical Genetics. Gene Mapping Through Linkage and Association. Taylor and Francis [U of I Library call number 572.8633 St296]

Additional reading materials:

Geoffrey J. McLachlan, Kim-Anh Do, Christophe Ambroise. 2003. Analyzing Microarray Gene Expression Data (Wiley Series in Probality and Statisics).

Richard M. Simon, Edward L. Korn, George W. Wright, Yingdong Zhao, Michael D. Radmacher, Lisa M. McShane. 2004. Design and Analysis of DNA Microarray Investigations (Statistics for Biology and Health). Springer.
Mark Schena, Mark Schena. 2002. Microarray Analysis. Wiley, John & Sons, Incorporated
Sorin Draghici, Alexander Kuklin 2002. Data Analysis Tools for DNA Microarrays. CRC Press.
Terry P. Speed. 2003. Statistical Analysis of Gene Expression Microarray Data. CRC Press.
Pierre Baldi, G. Wesley Hatfield. 2002. DNA Microarrays and Gene Expression: From Experiments to Data Analysis and Modeling. Cambridge University Press. Ben-Hui Liu. 1998. Statistical Genomics. CRC Press, Boca Raton, FL. Michael Lynch and Bruce Walsh. 1998. Genetics and analysis of quantitative traits. Sinauer Associates, Inc. Sunderland, MA
Jurg Ott. 1992. Analysis of Human Genetic Linkage. The Johns Hopkins University Press. Baltimore, MY

*On reserve at the ACES library (LIAC), 1101 S. Goodwin.

Grading
For students registered for 3 hours, grading will be based on three homework assignments (assignments 1 to 3).
For students registered for 4 hours, grading will be based on four homework assignments (assignments 1 to 4).

	Assignment due day	Points
1	Friday April 8 at 10:00AM	300 points
2	Friday April 22 at 10:00AM	400 points
3	Friday May 6 at 10:00AM	300 points
Total		1000 points
4	Wednesday May 11 at 10:00AM	333 points
Total:		1333 points

All homework assignments must be electronically submitted using the course ANSC 545 Compass webpage by the respective due day deadlines (10:00AM of each corresponding day). Electronic mail attachments or printed homework submissions will not be accepted or graded.

Study groups
Study groups of 4 students have been created. Group number and composition is available in the course website. Students are encouraged to work with their study group on the homework assignments. Every student must submit a homework assignment individually. Each student's homework file to be submitted must be named starting with the netid of the student, followed by study group number, followed by the homework number (e.g. rodrgzzs_group2_hwk1).

Deadline extension
Only one homework assignment can be submitted up to 5 days after the deadline. This exception must be arranged with the ANSC 545 instructor at least 2 days before the

deadline of the homework.

Academic Integrity
The *Code of Policies and Regulations Applying to All Students* at the University of Illinois is available at http://www.uiuc.edu/admin_manual/code) and includes the rules, policies and regulations governing the student's integrity and academic aspects. The students attending ANSC 545 are responsible for knowing and abiding by these rules.

Policies on software packages, computer labs and copyrights
All students attending ANSC 545 must comply with the rules and policies indicated by the software, websites and computer laboratories used for course related purposes. The ACES Academic Computing Facility Policies can be found at http://acf.aces.illinois.edu/policy/index.html. The policy on course notes and related printed and internet materials (e.g. published articles, website information) copyrights follows The General Rules Concerning University Organization and Procedure (University of Illinois Board of Trustees, 1998) and can be found at http://www.vpaa.uillinois.edu/policies and any other rule mentioned in the materials.