



**MEMORANDUM**

**TO: Health Care Colleges Council**

**FROM: William G. Pfeifle, EdD**  
**Associate Dean for Academic Affairs**

**SUBJECT: New Course Proposal – BST/STA 655 Statistical Genetics**

**DATE: April 26, 2011**

The Department of Biostatistics has submitted a course change proposal for BST 655 Statistical Genetics. It is to be cross listed as STA 655.

This course change proposal has been reviewed and approved by the Academic Affairs Committee and the Faculty Council, according to our college's established bylaws. It has also been reviewed and approved by the Department of Statistics (Dr. Arne Bathke, Department Chair).

Further information about this course can be obtained by contacting the course director, Dr. David Fardo, via phone at 218-2070 or via email at [david.fardo@uky.edu](mailto:david.fardo@uky.edu).

## **MEMO**

**DATE: April 18, 2011**

TO: Associate Dean for Academic Affairs

FROM: Chair, Faculty Council

SUBJECT: New Course Approval

The new course proposal for BST 655 (STA 655) Introduction to Statistical Genetics was approved unanimously.

## **MEMO**

**DATE: December 15, 2010**

TO: Associate Dean for Academic Affairs

FROM: Chair, Academic Affairs Committee

SUBJECT: New Course Approval

The new course proposal for BST 655 (STA 655) Introduction to Statistical Genetics was approved unanimously by those voting electronically.

# NEW COURSE FORM

<b>1. General Information</b>				
a.	Submitted by the College of: <u>Public Health</u>	Today's Date:	<u>11/30/2010</u>	
b.	Department/Division: <u>Biostatistics</u>			
c.	Contact person name: <u>Dave Fardo</u>	Email: <u>David.fardo@uky.edu</u>	Phone:	<u>218-2070</u>
d.	Requested Effective Date:	<input type="checkbox"/> Semester following approval	OR	<input checked="" type="checkbox"/> Specific Term/Year <sup>1</sup> <u>Fall 2011</u>
<b>2. Designation and Description of Proposed Course</b>				
a.	Prefix and Number: <u>BST 655</u>			
b.	Full Title: <u>Introduction to Statistical Genetics</u>			
c.	Transcript Title (if full title is more than 40 characters): <u>same</u>			
d.	To be Cross-Listed <sup>2</sup> with (Prefix and Number): <u>STA 655</u>			
e.	Courses must be described by <u>at least one</u> of the meeting patterns below. Include number of actual contract hours <sup>3</sup> for each meeting pattern type.			
	<u>45</u> Lecture	<u>    </u> Laboratory <sup>1</sup>	<u>    </u> Recitation	<u>    </u> Discussion
	<u>    </u> Clinical	<u>    </u> Colloquium	<u>    </u> Practicum	<u>    </u> Research
	<u>    </u> Seminar	<u>    </u> Studio	<u>    </u> Other – Please explain:	
f.	Identify a grading System:	<input checked="" type="checkbox"/> Letter (A, B, C, etc.)	<input type="checkbox"/> Pass/Fail	
g.	Number of credits: <u>3</u>			
h.	Is this course repeatable for additional credit?	YES <input type="checkbox"/>	NO <input checked="" type="checkbox"/>	
	If YES: Maximum number of credit hours: <u>    </u>			
	If YES: Will this course allow multiple registrations during the same semester?	YES <input type="checkbox"/>	NO <input type="checkbox"/>	
i.	Course Description for Bulletin: BST 655 presents an introduction to the statistical methodologies used today to investigate genetic susceptibility to complex diseases. The course focuses on linkage and association analysis with applications to real-world data. Commonly used (and freely available) software will be presented and used throughout. Because the field is constantly evolving, a focus of the material for this course will be recent statistical human genetics literature			
j.	Prerequisites, if any: <u>STA 580 or equivalent</u>			
k.	Will this course be offered through Distance Learning?	YES <sup>4</sup> <input type="checkbox"/>	NO <input checked="" type="checkbox"/>	
l.	Supplementary teaching component, if any:	<input type="checkbox"/> Community-Based Experience	<input type="checkbox"/> Service Learning	<input type="checkbox"/> Both
3.	Will this course be taught off campus?	YES <input type="checkbox"/>	NO <input checked="" type="checkbox"/>	
<b>4. Frequency of Course Offering</b>				
a.	Course will be offered (check all that apply):	<input checked="" type="checkbox"/> Fall	<input checked="" type="checkbox"/> Spring	<input type="checkbox"/> Summer
b.	Will the course be offered every year?	YES <input checked="" type="checkbox"/>	NO <input type="checkbox"/>	

<sup>1</sup>Courses are typically made effective for the semester following approval. No course will be made effective until all approvals are received

<sup>2</sup>The chair of the cross-listing department must sign off on the Signature Routing Log.

## NEW COURSE FORM

<b>5.</b>	Are facilities and personnel necessary for the proposed new course available?	YES <input checked="" type="checkbox"/>	NO <input type="checkbox"/>
	If NO, explain: _____		
<b>6.</b>	What enrollment (per section per semester) may reasonably be expected?	<u>10</u>	
<b>7.</b>	<b>Anticipated Student Demand</b>		
<b>a.</b>	Will this course serve students primarily within the degree program?	YES <input checked="" type="checkbox"/>	NO <input type="checkbox"/>
<b>b.</b>	Will it be of interest to a significant number of students outside the degree program?	YES <input checked="" type="checkbox"/>	NO <input type="checkbox"/>
	If YES, explain: <u>Epi/Biostats, computer science, dentistry, nursing</u>		
<b>8.</b>	<b>Check the category most applicable to this course:</b>		
	<input type="checkbox"/> Traditional – Offered in Corresponding Departments at Universities Elsewhere		
	<input checked="" type="checkbox"/> Relatively New – Now Being Widely Established		
	<input type="checkbox"/> Not Yet Found in Many (or Any) Other Universities		
<b>9.</b>	<b>Course Relationship to Program(s)</b>		
<b>a.</b>	Is this course part of a proposed new program?	YES <input type="checkbox"/>	NO <input checked="" type="checkbox"/>
	If YES, name the proposed new program: _____		
<b>b.</b>	Will this course be a new requirement <sup>5</sup> for ANY program?	YES <input type="checkbox"/>	NO <input checked="" type="checkbox"/>
	If YES <sup>5</sup> , list affected programs: _____		
<b>10.</b>	<b>Information to be Placed on Syllabus</b>		
<b>a.</b>	Is the course 400G or 500?	YES <input type="checkbox"/>	NO <input checked="" type="checkbox"/>
	If YES, the <i>differentiation for undergraduate students must be included</i> in the information required in <b>10.b</b> . You must include: (i) identification of additional assignments by the graduate students; and /or (ii) Establishment of different grading criteria in the course for graduate students. (See <i>SR 3.1.4.</i> )		
<b>b.</b>	<input checked="" type="checkbox"/> The syllabus, including course description, student learning outcomes, and grading policies (and 400G-/500 level grading differentiation if applicable, from <b>10.a</b> above) are attached.	NO <input type="checkbox"/>	

<sup>5</sup>In order to change a program, a program change form must also be submitted.

# NEW COURSE FORM

## Signature Routing Log

**General Information:**

Course Prefix and Number: BST/STA 655

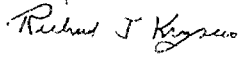
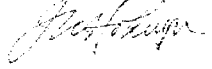



Proposal Contact Person Name: David Fardo Phone: 218-2070 Email: david.fardo@uky.edu

Becki Flanagan Phone: 218-2092 Email: becki@uky.edu

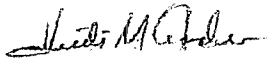
**INSTRUCTIONS:**

Identify the groups or individuals reviewing the proposal; note the date of approval; offer a contact person for each entry; and obtain signature of person authorized to report approval.

**Internal College Approvals and Course Cross-listing Approvals:**

Reviewing Group	Date Approved	Contact Person (name/phone/email)	Signature
Department of Biostatistics	11/30/2010	Richard Kryscio/218-2097/kryscio@uky.edu	
Academic Affairs Committee	12/15/2010	Jim Holsinger/323-6314/jwh@email.uky.edu	
Faculty Council	4/18/2011	Graham Rowles/218-0145/growl2@email.uky.edu	
Department of Statistics	4/25/2011	Arne Bathke/257-3610/arne@uky.edu	
Academic Dean	4/26/2011	William Pfeifle/218-2054/pfeifle@uky.edu	

**External-to-College Approvals:**

Council	Date Approved	Signature	Approval of Revision <sup>6</sup>
Undergraduate Council			
Graduate Council			
Health Care Colleges Council	5/17/11		
Senate Council Approval		University Senate Approval	

**Comments:**

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<sup>6</sup> Councils use this space to indicate approval of revisions made subsequent to that council's approval, if deemed necessary by the revising council.

# BST / STA 655 ~ Spring 2011

## Introduction to Statistical Genetics

### Lectures

M 12:00-2:30pm (CPH207)

### Instructor

David Fardo, PhD

### Contact Info

Office: CPH, Room 201-C  
Office Hours: By appointment  
Phone: 218.2070  
Email: david.fardo AT uky.edu  
Website: <http://db.tt/blUoXHJ>

### Texts (none required)

#### Strongly Recommended

*A Statistical Approach to Genetic Epidemiology: Concepts and Applications* – A Ziegler and I Koenig

#### Recommended

*Genetic Analysis of Complex Disease* – J Haines and M Pericak-Vance  
*Human Genome Epidemiology* – M Khoury, J Little and W Burke  
*Mathematical and Statistical Methods for Genetic Analysis* – K Lange  
*Statistical Genetics* – B Neale, M Ferreira, S Medland and D Posthuma  
*Statistics in Human Genetics* – P Sham  
*Statistics in Human Genetics and Molecular Biology* – C Reilly  
*Statistical Methods in Genetic Epidemiology* – DC Thomas  
*The Statistics of Gene Mapping* – D Siegmund and B Yakir

**Course Description:** BST 655 /STA 655 presents an introduction to the statistical methodologies used today to investigate genetic susceptibility to complex diseases in humans. The course focuses on linkage and association analysis with applications to real-world data. Commonly used (and freely available) software will be presented and used throughout. Because the field is constantly evolving, a focus of the material for this course will be recent statistical human genetics literature.

**Course Objectives:** Upon successful completion of this course, a student will be able to identify appropriate statistical methods for the analysis of genetic data. Specifically, the student objectives of this course are as follows:

1. Learn basic principles of human genetics (e.g., Mendelian inheritance, meiotic recombination, Hardy-Weinberg equilibrium, etc.)
2. Learn and apply methods for linkage analysis
3. Learn and apply methods for genetic association analysis
4. Learn about current trends in statistical genetics (e.g., genome-wide association studies, copy number variant analysis, SNP panel imputation, etc.)

### Grading

- 25% – Problem Sets & Participation
- 25% – Literature Presentation
- 25% – Software/Resource Tutorial
- 25% – Final Project

### Grading Scale\*

A 90 – 100  
B 75 – 89  
C 60 – 74  
E 0 – 59

\* Note that the lowest number in each range is a minimum so that, for example, you are guaranteed a B with a 75.

### Expectations for the...

#### Instructor

- Be accessible
- Be a resource
- Give examples
- Introduce procedures
- Be respectful
- Be patient
- Provide slides

#### Students

- Be prepared
- Be respectful
- Ask pertinent questions
- Turn in assignments on time
- Attend class
- Help one another
- Be patient

**Philosophical Statement:** Although statistical genetics is often considered a rapidly advancing and relatively young field, its history can be traced back as far as Karl Pearson, who founded the journals *Biometrika* (1901) and the *Annals of Human Genetics* (1925), and R.A. Fisher, who, along with J.B.S Haldane and Sewall Wright, is considered to have founded the field of population genetics (~1918). Currently, as biological advances have made studying entire genomes financially and logistically feasible, the field has entered a new era. Funding bodies have recognized this and many resources have been devoted to investigating the genetic underpinnings of many complex diseases in humans. This course offers students the opportunity to revisit the history of methodological advancements in this area and to be exposed to the cutting edge of the field. Real-world data will be analyzed in order to acclimate students to the scientific approaches currently being utilized. Various freeware software packages will be presented and employed.

## **Policies**

**Accommodations:** If you have a documented disability that requires academic accommodations, please see me as soon as possible. In order to receive accommodations in this course, you must provide me with a Letter of Accommodation from the Disability Resource Center ([www.uky.edu/TLC/grants/uk\\_ed/services/drc.html](http://www.uky.edu/TLC/grants/uk_ed/services/drc.html)). If you have not already done so, please register with the Disability Resource Center (Room 2 Alumni Gym, 257-2754, [jkarnes@uky.edu](mailto:jkarnes@uky.edu)) for coordination of campus disability services available to students with disabilities.

**Attendance Policy:** The course is designed so that students should be successful with active participation and regular, punctual attendance. It is understandable that students may miss class; however, it is the student's responsibility to determine what activities were missed and what material was covered. A student will only be allowed make-up work if the absence is excused. Also, students missing more than three class periods (excused or unexcused) will receive an E for the course.

**Make-up Work:** Only students with documented excused absences will be allowed to make-up work and examinations. Excused absences are defined as follows (S.R. 5.2.4.2):

1. *Illness of the student or serious illness of a member of the student's immediate family.*
2. *The death of a member of the student's immediate family.*
3. *Trips for members of student organizations sponsored by an academic unit, trips for University classes, and trips for participation in intercollegiate athletic events.*
4. *Major Religious Holidays.*
5. *Any circumstance which the instructor finds a reasonable cause for non-attendance. These circumstances must be presented to the instructor via email prior to the missed class.*

It is the student's responsibility to make arrangements for determining and handing in missed work, preferably in advance, but no later than three days after the missed class.

**Unforeseen Contingencies:** In the unlikely event that an unforeseen contingency requires additional course policies, you will be promptly notified in an e-mail memorandum.



**Academic Integrity:** Academic integrity is expected from all students. A violation of academic integrity involves any communication of information, verbal or nonverbal, during tests or quizzes, or sharing of homework and is not limited to these examples. Students are reminded that possible University penalties for such violations are an “E” for the course, suspension, and dismissal.

<http://www.uky.edu/StudentAffairs/Code/part2.html>

Academic relationships between students and the University are covered in [Part II](#) entitled, “Selected Rules of the University Senate Governing Academic Relationships.” Rules in [Part II](#) have been adopted and may be amended by the University Senate.

6.3.0 – Academic Offenses and Procedures: Students shall not plagiarize, cheat, or falsify or misuse academic records. (US: 3/7/88; 3/20/89)

6.3.1 – Plagiarism: All academic work, written or otherwise, submitted by students to their instructors or other academic supervisors, is expected to be the result of their own thought, research, or self-expression. **In cases where students feel unsure about a question of plagiarism involving their work, they are obliged to consult their instructors on the matter before submission.**

When students submit work purporting to be their own, but which in any way borrows ideas, organization, wording or anything else from another source without appropriate acknowledgment of the fact, the students are guilty of plagiarism.

Plagiarism includes **reproducing someone else’s work**, whether it be published article, chapter of a book, a paper from a friend or some file, or whatever. Plagiarism also includes the practice of employing or **allowing another person to alter or revise the work which a student submits as his/her own**, whoever that other person may be. Students may discuss assignments among themselves or with an instructor or tutor, but when the actual work is done, it must be done by the student, and the student alone.

When a student’s assignment involves research in outside sources or information, the student must carefully acknowledge exactly what, where and how he/she has employed them. If the words of someone else are used, the student must put quotation marks around the passage in question and add an appropriate indication of its origin. Making simple changes while leaving the organization, content and phraseology intact is plagiaristic. However, nothing in these Rules shall apply to those ideas which are so generally and freely circulated as to be a part of the public domain.

6.3.2 – Cheating: **Cheating is defined by its general usage. It includes, but is not limited to, the wrongfully giving, taking, or presenting any information or material by a student with the intent of aiding himself/herself or another on any academic work which is considered in any way in the determination of the final grade.** The fact that a student could not have benefited from an action is not by itself proof that the action does not constitute cheating. Any question of definition shall be referred to the University Appeals Board.

## **ASSIGNMENT DESCRIPTIONS**

### **• Problem Sets & Participation** (25% of grade)

**Purpose:** Much of what is learned in this class must be learned outside of lecture hours. Problem sets provide an opportunity to solidify concepts and gain first-hand experience conducting genetic research.

**Assignment:** Assignments will be given regularly throughout the course. Participation will include, but is not limited to, discussions of assigned readings and active dialogue during lectures and presentations.

**Logistics:** Specific instructions will accompany each problem set, however you will generally be given ~1 week to complete work relating to the concepts presented during lecture and in course readings/presentations.

**Grading:** You will be graded on each problem set (due at 12:00pm on the specified due date) as well as your active participation throughout the entirety of the semester.

### **• Literature Presentation** (25% of grade)

**Purpose:** A couple keys to success in most any profession are the ability to digest information from multiple, sometimes unfamiliar sources and the complementary ability to convey to others that which you have learned. The goal of this assignment is to foster these abilities by providing an opportunity to study a selected journal article and then present the material to our class. You can view this project as preparing a lesson or lecture for the class.

**Assignment:** As a group of two or three, you will select a journal article that is of particular interest to you. You are encouraged to discuss this choice with me so that the topic you will study fits well your scientific/educational interests. You will read the article and any additional material necessary for you to have a sufficient understanding of the work. You will individually write a short summary (no more than two pages) of the article and as a group deliver a 15-30 minute presentation during our course.

**Logistics:** Possibly with my help, you will choose an article to present on a first contacted, first served basis. That is, whoever first selects a topic and lets me know will have precedence. The presenters and I will determine at what point of the lecture will best suit the particular talks. Note that some lecture meetings have multiple papers that could be presented on the same day.

**Grading:** You will be graded on the paper (due at 12:00pm on the day of your presentation), the presentation materials, the presentation itself and your evaluations of

other student presentations. Fellow students will evaluate each presentation, and this will make up a small portion of the presentation grade.

- **Software/Resource Tutorial** (25% of grade)

**Purpose:** The goal of this assignment is to foster the same abilities mentioned above by providing the experience of learning a new resource and then presenting a tutorial to our class. You can view this project as preparing an interactive lesson or lecture for the class.

**Assignment:** As a group of two or three, you will select a software or web resource that is of particular interest to you. You are encouraged to discuss this choice with me so that the resource you will investigate fits well your scientific/educational interests. You will familiarize yourself with the resource and any additional resources necessary for you to have a sufficient understanding. You will develop and deliver a 30-60 minute interactive tutorial during our course.

**Logistics:** Possibly with my help, you will choose a resource to present on a first-contacted, first served basis. That is, whoever first selects a topic and lets me know will have precedence. The presenters and I will determine at what point of the lecture will best suit the particular tutorials. Note that some lecture meetings have multiple tutorials that could be presented on the same day.

**Grading:** You will be graded on tutorial material to be disseminated electronically (due at 12:00pm on the day of your tutorial), the presentation of your tutorial to the class and your evaluations of other student tutorials. Fellow students will evaluate each presentation, and this will make up a small portion of the tutorial grade.

- **Final Project** (25% of grade)

**Purpose:** Another crucial ability is that of assimilation. The goal of this assignment is provide a culminating experience as some say, from soup to nuts. You will choose a suitable data analytic project that you will then write up as a scientific report and present to the class.

**Assignment:** As a group, you will select a suitable data analytic project that is of particular interest to your group. You must discuss this choice with me in order to determine the project's feasibility. You will acquire necessary data, develop an analysis plan and then conduct the relevant study. You will write a scientific report (at least two pages not including tables and graphs) and present your findings in a presentation during our final lecture.

**Logistics:** Groups of between three and five students (with no more than two students from the same program) will form prior to choosing a project. I encourage both that this

is done early in the course and that the groups are made of students with diverse interests and skills. Once a group is formed, the group should come to a consensus regarding a proposed project that will be then discussed with me in order to determine feasibility. I will work with each group to help revise the project so that it is suitable.

**Grading:** You will be graded on the report (due at 12:00pm on May 2<sup>nd</sup>), the presentation and your evaluations of other group presentations. Fellow students will evaluate each presentation, and this will make up a small portion of the presentation grade.

# TENTATIVE SCHEDULE

Date (#)	Topics, Readings & Software & Resources	Presenter
Jan 24 (1)	<p><b>Introduction; Course Overview; Basic Genetics</b></p> <p><b>Readings</b></p> <ul style="list-style-type: none"> <li>• Genomics 101: A Primer <a href="http://www.ornl.gov/sci/techresources/Human_Genome/publicat/primer2001/1.shtml">http://www.ornl.gov/sci/techresources/Human_Genome/publicat/primer2001/1.shtml</a></li> </ul> <p><b>Software &amp; Resources</b></p> <ul style="list-style-type: none"> <li>• Roche Genetic Education Program (link to order form): <a href="http://www.roche.com/research_and_development/r_d_overview/education/order_form_roche_genetics_education_programm.htm">http://www.roche.com/research_and_development/r_d_overview/education/order_form_roche_genetics_education_programm.htm</a></li> <li>• Learn Genetics <a href="http://learn.genetics.utah.edu/">http://learn.genetics.utah.edu/</a></li> <li>• Eric Lander's Intro Biology Lectures (MIT) <a href="http://ocw.mit.edu/OcwWeb/Biology/7-012Fall-2004/CourseHome/index.htm">http://ocw.mit.edu/OcwWeb/Biology/7-012Fall-2004/CourseHome/index.htm</a></li> </ul>	
	<p><b>Populations Genetics</b></p> <p><b>Readings</b></p> <ul style="list-style-type: none"> <li>• Genetic Dissection of Complex Diseases (Lander &amp; Schork; Science 1994) <span style="float: right;">TBD</span></li> <li>• The essence of SNPs (Brookes; Gene 1999) <span style="float: right;">TBD</span></li> <li>• Key concepts in genetic epidemiology (Burton et al.; Lancet 2005) <span style="float: right;">TBD</span></li> <li>• Heritability in the genomics era - concepts and misconceptions (Visscher et al.; Nature Reviews Genetics 2008) <span style="float: right;">TBD</span></li> </ul> <p><b>Software &amp; Resources</b></p> <ul style="list-style-type: none"> <li>• Online Mendelian Inheritance in Man (OMIM) <span style="float: right;">TBD</span> <a href="http://www.ncbi.nlm.nih.gov/sites/entrez?db=omim">http://www.ncbi.nlm.nih.gov/sites/entrez?db=omim</a></li> <li>• dbSNP Database <span style="float: right;">TBD</span> <a href="http://www.ncbi.nlm.nih.gov/projects/SNP/index.html">http://www.ncbi.nlm.nih.gov/projects/SNP/index.html</a></li> <li>• The International HapMap Project <span style="float: right;">TBD</span> <a href="http://hapmap.ncbi.nlm.nih.gov/">http://hapmap.ncbi.nlm.nih.gov/</a></li> </ul>	
Jan 31 (2)	<p><b>Linkage Analysis – Parametric &amp; Non-Parametric</b></p> <p><b>Readings</b></p> <ul style="list-style-type: none"> <li>• Genetic linkage studies (Teare &amp; Barrett; Lancet 2005) <span style="float: right;">TBD</span></li> <li>• Construction of multilocus genetic linkage maps in humans (Lander &amp; Green; PNAS 1987) <span style="float: right;">TBD</span></li> <li>• The Power of Identity-by-State Methods for Linkage Analysis (Bishop &amp; Williamson; AJHG 1990) <span style="float: right;">TBD</span></li> <li>• Linkage Strategies for Genetically Complex Traits: II- The Power of Affected Relative Pairs (Risch; AJHG 1990) <span style="float: right;">TBD</span></li> </ul> <p><b>Software &amp; Resources</b></p> <ul style="list-style-type: none"> <li>• MERLIN <span style="float: right;">TBD</span></li> <li>• Online Mendelian Inheritance in Man (OMIM) <span style="float: right;">TBD</span> <a href="http://www.ncbi.nlm.nih.gov/sites/entrez?db=omim">http://www.ncbi.nlm.nih.gov/sites/entrez?db=omim</a></li> </ul>	
Feb 7 (3)	<p><b>Linkage Analysis – Quantitative Traits</b></p> <p><b>Readings</b></p> <ul style="list-style-type: none"> <li>• The Investigation of Linkage Between a Quantitative Trait and a Marker Locus (Haseman &amp; Elston; Behavior Genetics 1972) <span style="float: right;">TBD</span></li> <li>• Common disorders are quantitative traits (Plomin et al.; Nature <span style="float: right;">TBD</span></li> </ul>	
Feb 14 (4)	<p><b>Linkage Analysis – Quantitative Traits</b></p> <p><b>Readings</b></p> <ul style="list-style-type: none"> <li>• The Investigation of Linkage Between a Quantitative Trait and a Marker Locus (Haseman &amp; Elston; Behavior Genetics 1972) <span style="float: right;">TBD</span></li> <li>• Common disorders are quantitative traits (Plomin et al.; Nature <span style="float: right;">TBD</span></li> </ul>	

	<u>Reviews Genetics 2009)</u> <u>Software &amp; Resources</u> ● <b>S.A.G.E.</b>	TBD
	<b>Linkage Analysis – Wrap-up &amp; Future Directions</b>	
<b>Feb 21</b>	<u>Readings</u> ● Parametric and Nonparametric Linkage Analysis: A Unified Multipoint Approach (Kruglyak, Daly, Reeve-Daly & Lander; AJHG 1996)	TBD
<b>(5)</b>	● The genetics of quantitative traits: challenges and prospects (Mackay et al.; Nature Reviews Genetics 2009)	TBD
	<u>Software &amp; Resources</u> ● R/qtl	TBD
	<b>Association Analysis – Fundamentals</b>	
<b>Feb 28</b>	<u>Readings</u> ● Association study designs for complex diseases (Cardon & Bell; Nature Reviews Genetics 2001)	TBD
<b>(6)</b>	● Genetic association studies (Cordell & Clayton; Lancet 2005)	TBD
	<u>Software &amp; Resources</u> ● UCSC Genome Browser	TBD
	<b>Association Analysis – Population-based</b>	
<b>Mar 7</b>	<u>Readings</u> ● Shaking the tree: mapping complex disease genes with linkage disequilibrium (Palmer & Cardon; Lancet 2005)	TBD
<b>(7)</b>	● A tutorial on statistical methods for population association studies (Balding; Nature Reviews Genetics 2006)	TBD
	<u>Software &amp; Resources</u> ● HapMap ● Haploview	TBD TBD
<b>Mar 14</b>	<b>NO CLASS – SPRING BREAK</b>	
<b>***** **Mar 21** Need to re-schedule *****</b>	<b>Association Analysis – Population-based</b>	
<b>(8)</b>	<u>Readings</u> ● Linkage disequilibrium - understanding the evolutionary past and mapping the medical future (Slatkin; Nature Reviews Genetics 2008)	TBD
	<u>Software &amp; Resources</u> ● QUANTO	TBD
	<b>Association Analysis – Family-based</b>	
<b>Mar 28</b>	<u>Readings</u> ● The family based association test method: strategies for studying general genotype-phenotype associations (Horvath et al.; EJHG 2001)	TBD
<b>(9)</b>	<u>Software &amp; Resources</u> ● TBD	
	<b>Association Analysis – Family-based</b>	
<b>Apr 4</b>	<u>Readings</u> ● Family-based designs in the age of large-scale gene-association studies (Laird & Lange; Nature Reviews Genetics 2006)	TBD
<b>(10)</b>	<u>Software &amp; Resources</u> ● FBAT	TBD
	<b>Association Analysis – Genome-wide</b>	
<b>Apr 11</b>	<u>Readings</u> ● GENOME-WIDE ASSOCIATION STUDIES FOR COMMON DISEASES AND COMPLEX TRAITS (Hirschhorn & Daly; Nature Reviews Genetics 2005)	TBD
<b>(11)</b>		

	<ul style="list-style-type: none"> <li>• Genome-wide association studies for complex traits: consensus, uncertainty and challenges (McCarthy et al.; Nature Reviews Genetics, 2008)</li> </ul>	TBD
	<ul style="list-style-type: none"> <li>• Genome-wide association scan for diabetic nephropathy susceptibility genes in type 1 diabetes (Pezzolesi et al.; Diabetics 2009)</li> </ul>	TBD
	<p><b><u>Software &amp; Resources</u></b></p> <ul style="list-style-type: none"> <li>• PLINK</li> <li>• genomeSIM/genomeSIMLA (?)</li> <li>• SimPed (?)</li> </ul>	TBD TBD TBD
	<p><b>Association Analysis – Current &amp; Future Directions</b></p> <p><b><u>Readings</u></b></p> <ul style="list-style-type: none"> <li>• What makes a good genetic association study? (Hattersley &amp; McCarthy; Lancet 2005)</li> <li>• Genetic Mapping of Human Disease (Altshuler, Daly &amp; Lander; Science 2008)</li> <li>• Copy number variants and genetic traits: closer to the resolution of phenotypic to genotypic variability (Beckmann et al.; Nature Reviews Genetics 2007)</li> <li>• Identifying Relationships among Genomic Disease Regions: Predicting Genes at Pathogenic SNP Associations and Rare Deletions (Raychaudhur et al.; PLoS Genetics 2009)</li> <li>• Gene-Environment Interaction in Genome-Wide Association Studies (Murcray et al.; AJE 2008)</li> </ul> <p><b><u>Software &amp; Resources</u></b></p> <ul style="list-style-type: none"> <li>• MDR (?)</li> <li>• GRAIL</li> <li>• 1000 Genomes</li> </ul>	TBD TBD TBD TBD TBD TBD TBD
	<p><b>Other Topics</b></p> <p><b><u>Readings</u></b></p> <ul style="list-style-type: none"> <li>• Epigenetics (TIME MAGAZINE) <a href="http://www.time.com/time/health/article/0,8599,1951968,00.html">http://www.time.com/time/health/article/0,8599,1951968,00.html</a></li> <li>• Genome-wide association study identifies common variants at four loci as genetic risk factors for Parkinson’s disease (Satake et al.; Nature Genetics 2009)</li> <li>• Genome-wide association study reveals genetic risk underlying Parkinson’s disease (Simon-Sanchez et al.; Nature Genetics 2009)</li> </ul> <p><b><u>Software &amp; Resources</u></b></p> <ul style="list-style-type: none"> <li>• TBD</li> </ul>	TBD TBD TBD
Apr 18 (12)		
Apr 25 (13)		
May 2	EXAM WEEK – Project Presentations	Everyone!

## Course Outline

1. Basic Genetics
  - a. Central Dogma of Molecular Biology
  - b. Mitosis and Meiosis
  - c. Mendel's Laws
  - d. Modes of Inheritance
  - e. Genotyping
  - f. Haplotypes
2. Population Genetics
  - a. Hardy-Weinberg Equilibrium
  - b. Genetic Drift
  - c. Linkage Disequilibrium
  - d. Segregation
3. Parametric Linkage Analysis
  - a. Two-point Analysis
  - b. Multi-point Analysis
  - c. Model-based Linkage Analysis
  - d. Software Application: MERLIN
4. Non-parametric Linkage Analysis
  - a. Identity by State
  - b. Identity by Descent
  - c. Linkage Analysis with Affected Sib Pairs
  - d. LOD Scores
  - e. Maximum LOD Scores
  - f. Triangle Test
5. Population-based Association Analysis
  - a. Case-control Studies
  - b. Population Stratification and Admixture
  - c. Gene-environment Interaction
  - d. Gene-gene Interaction
  - e. Software Applications: PLINK, Haploview
6. Family-based Association Analysis
  - a. Haplotype Relative Risk
  - b. Transmission Disequilibrium Test
  - c. Quantitative Transmission Disequilibrium Test
  - d. Family-based Association Tests
  - e. Software Applications: fbat, pbat
7. Other Topics
  - a. Genome-wide Association Studies
  - b. Copy Number Variant Analysis
  - c. Rare Variant Analysis
  - d. Imputation

## Competency attainment

Your attainment after completing CPH 738 (655) will be at least the following and perhaps more, depending on the other courses in which you have enrolled. The numbers 0, 1, 2, and 3 indicate Unaware (No information or skill in this area), Aware (Basic mastery; able to identify the concept or skill but with limited ability to perform or apply it independently), Knowledgeable (Intermediate level of mastery; able to apply and describe the concept or skill), and Proficient (Advanced mastery; able to synthesize, critique, or teach the concept or skill), respectively.





	e. Fit a simple linear regression model;	2
	f. Construct Kaplan Meier curves for right censored observations and compute the log rank statistic to compare these curves between two groups.	1
5. Apply statistical methods commonly encountered in multivariate data analysis.	a. Identify and apply appropriate multivariate statistical models including multiple linear regression, logistic regression, Poisson regression, proportional hazards regression, and mixed models; b. Critically interpret the outcomes of the multivariate analysis; c. Conduct graphical and analytical model diagnostics, and recommend remedies based on the diagnostics; d. Integrate the outcomes of multiple studies using meta analysis.	
6. Gather, organize, and manage health survey data.	a. Design a health survey instrument; b. Assess instrument/item reliability and validity; c. Draw and analyze a simple random sample of measurements; d. Implement and analyze more complex survey designs including stratified samples, clustered samples, and multistage samples; e. Process incomplete data using imputation; f. Adopt an appropriate weighting scheme for observations in a health survey.	1 1 1
7. Effectively use statistical software to collect, manage, and analyze Public Health data.	a. Master the use of SAS analyst, a click and point statistical software; b. Acquire the skills necessary to write code for SAS programs; c. Understand the principles of data acquisition, verification, and validation; d. Become skilled at editing, combining, and linking data sets; e. Learn the fundamentals of data manipulation and analysis; f. Efficiently create tables, graphs, and reports; g. Learn the fundamentals of the SAS macro facility; h. Learn to use nQuery Advisor, a sample size calculation software program.	2 1 2 2
8. Critically review biostatistical issues arising in Public Health literature.	a. Demonstrate they can select appropriate statistical methods for the problem; b. Resolve controversial issues associated with competing solutions in biostatistics for the same problem (discussing strengths and weaknesses).	1 1
9. Interpret and clearly express findings.	a. Interpret univariate statistical models; b. Interpret complex multivariate statistical models; c. Express their findings clearly both verbally and in writing.	2 1 2
10. Integrate principles of biostatistics in the practice of Public Health.	a. Use statistical methodology to analyze public health data; b. Recognize the potential for statistics to aid in the development of guidelines and policies, the implementation and management of programs, and the evaluation of programs.	1