Genetic Epidemiology
Population Health 904 Section 002
Fall 2008, 10/27/08 – 12/19/08

Instructor: Corinne Engelman, MSPH, PhD
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Office Hours: ½ hour before each lecture class in the HSLC atrium right outside of 1222 HSLC or inside 1222 if it is available (or by appointment)

Lecture Time: Monday and Wednesday, 9:55-11:15
Location: 1222 HSLC

Discussion Time: Friday, 9:55-10:55
Location: G5/142 CSC

Course Description:
This course will provide an introduction to genetic epidemiology. Topics will include a general overview of genetics and Mendelian and complex inheritance. We will discuss the various elements of study design, including definition of study population, participant ascertainment, phenotype definition, selection of genetic markers, determination of the type of biologic sample to be collected for extraction of the DNA, data collection and management, and choice of analytic methods. We will briefly discuss some of the original study designs (e.g., linkage analysis) and will then focus on current study designs (e.g., association analysis) for the remainder of the class. We will cover analysis methods for case-control and family data, single marker and haplotype tests of association in the context of single gene, candidate region, and genome-wide association studies. Throughout, we will demonstrate the application of these methods both by hand calculation and by using available statistical software. We will use real data examples and examples from the literature. Additional topics will be touched upon, including copy number variation (CNV), gene expression studies, epigenomics, proteomics, comparative genomics, bioinformatics, systems biology, nutrigenomics, pharmacogenomics, public health genomics, and ethical, legal, and social issues (ELSI). At the completion of this course students will be able to critically review and discuss genetic epidemiologic literature, provide input on the design of genetic epidemiologic studies, identify and apply appropriate tests of association between genetic markers and both qualitative and quantitative outcomes using either unrelated individuals or families, and summarize and interpret the results of these tests of association.

Lecture:
The reading(s) and a short homework assignment will need to be completed before each lecture class time. The homework from the previous class will be distributed at the beginning of each lecture class and the first 20-30 minutes of class will be spent reviewing/discussing the homework answers, especially any problems that a number of students had difficulty with. This will be followed by a 50-60 minute lecture.

Discussion:
The objective of the discussion class time is to critically review current literature in genetic epidemiology and discuss study design, data collection, statistical analysis and interpretation, and other issues with your peers.

The discussion class time in weeks 2-7 will be spent discussing published journal articles. Each journal discussion will be led by one or more students. The student(s) leading the topic will search the literature to find a recent (within the last 2 years) original research (not review, commentary, meta-analysis, etc)
article related to the topic. (Note: for some topics – ethical, legal, and social issues in particular – a commentary article may be appropriate; please consult the instructor.) If you would like help selecting an article, please ask the instructor. The student(s) leading the discussion should email the instructor with the article chosen by Thursday of the week prior to the discussion for verification of article appropriateness. The instructor will then put the article up on the Learn@UW website by Friday of the week prior to the discussion so all students can access it.

Each student should read the paper in Nature, Vol 447 (7) 655-660 by the NCI-NHGRI Working Group, “Replicating genotype-phenotype associations”, before reading their first journal article and use Boxes 1-3 as a guide in reviewing all original research articles for the discussion class time. The student(s) leading the discussion should spend 25-30 minutes presenting the paper. The rest of the time (25-30 minutes) should be spent in discussion either as questions arise, or at the end of the presentation.

For those leading the discussion: While everyone should have read the paper, don’t assume that everyone will remember everything, let alone understand it. Give an overview of the paper (e.g. purpose, general approach, conclusions) and follow with specifics, including going through what you think might be the hardest parts to understand. You do not have to follow the format of the paper if you find it easier or more intuitive to go through things in a different order than the authors did in the paper. If you don't understand everything, focus on what you do understand. Try to identify for the class both what is important about the paper and what you didn’t understand and/or would like to know more about. Develop a set of questions to facilitate discussion. You will be evaluated on the clarity of your presentation and your efforts to facilitate discussion. Last year the student(s) leading the discussion did not use PowerPoint, but instead brought a 1-2 page handout for the other students – this seemed to work very well.

For those not leading the discussion: All students not leading the discussion will prepare a typed short paragraph summarizing the paper (1-2 sentences each for purpose, general approach, and conclusions) along with 3-4 questions for discussion (including, but not limited to items from Boxes 1-3 of the Nature paper above), which will be handed in to the instructor at the end of the discussion. You will be evaluated on your preparation (handing in your summary and discussion questions) and participation.

Exam
For the final exam, each student will select a disease or trait and find a recent (within the last 2 years) original research paper and a paper reviewing the genetic epidemiology of the disease or trait (OMIM can also be used for this). Selection of these two papers can begin at any time, but it is highly recommended that it be done before the exam is distributed. Once you have selected the two papers, you will email the references to the instructor. On Friday, December 12th, I will provide you with 10 questions from which you must choose 6 to answer; additional questions answered correctly will be extra credit. These questions will all be answered using the two papers you have selected. You may use no more than an average of ½ page per question including tables and figures (11 point font; e.g., 3 pages for 6 questions) so your answers must be concise and not include extraneous information. You will then have the chance to meet with the instructor for 30 minutes during finals week to help you with any of the questions you need help with (e.g., using a public database, interpreting results, calculations, conceptual clarifications). You can ask a variety of questions, but you cannot ask me if your response to the question is right or wrong and I will not tell you exactly how to answer a particular question. Think of this as a meeting with your thesis advisor where you would ask conceptual questions that would help you write you thesis or thesis proposal, but you would not ask your advisor to write a paragraph for you. Since you will only have 30 minutes, it would be to your advantage to have attempted to complete the entire exam and come with your questions organized because I will cut you off after 30 minutes. The
motivation behind this odd type of exam (including the meeting with the instructor) is that I want this to be a good learning experience, not merely a test of what you know.

**Required readings:**
The field of genetic epidemiology is evolving rapidly so the few text books that are written quickly become out of date and no one text book adequately covers the material that will be presented in this class. Therefore, we will use selected chapters from the text books below and original research and review articles as supplements to the lecture notes. These will be available at Learn@UW.

Although the required readings from the text books below will be available at Learn@UW, purchasing one or both of these text books is highly recommended for anyone who plans to be involved in a genetic study in the future. These books can be purchased from [http://www.addall.com/](http://www.addall.com/) (this website searches for the best price) or other textbook sources and they are also on reserve at Ebling Library.

Jonathan L. Haines and Margaret A. Pericak-Vance  
*Genetic Analysis of Complex Disease*  
John Wiley and Sons Inc 05 May 2006  
ISBN: 0471-08952-4  
List price is $99.95, but you can find it for as low as $56.07 at [http://www.addall.com/](http://www.addall.com/).

**Genetic Analysis of Complex Disease**

by Jonathan L. Haines, Margaret A. Pericak-Vance

*About this title:* Second Edition features the latest tools for uncovering the genetic basis of human disease

The "Second Edition" of this landmark publication brings together a team of leading experts in the field to thoroughly update the publication. Readers will discover the tremendous advances made in human genetics in the seven years that have elapsed since the "First Edition." Once again, the editors have assembled a comprehensive introduction to the strategies, designs, and methods of analysis for the discovery of genes in common and genetically complex traits. The growing social, legal, and ethical issues surrounding the field are thoroughly examined as well.

Rather than focusing on technical details or particular methodologies, the editors take a broader approach that emphasizes concepts and experimental design. Readers familiar with the "First Edition" will find new and cutting-edge material incorporated into the text: Updated presentations of bioinformatics, multiple comparisons, sample size requirements, parametric linkage analysis, case-control and family-based approaches, and genomic screening; New methods for analysis of gene-gene and gene-environment interactions; A completely rewritten and updated chapter on determining genetic components of disease; New chapters covering molecular genomic approaches such as microarray and SAGE analyses using single nucleotide polymorphism (SNP) and cDNA expression data, as well as quantitative trait loci (QTL) mapping.

The editors, two of the world's leading genetic epidemiologists, have ensured that each chapter adheres to a consistent and high standard. Each one includes all-new discussion questions and practical examples. Chapter summaries highlight key points, and a list of references for each chapter opens the door to further investigation of specific topics.

Molecular biologists, human geneticists, genetic epidemiologists, and clinical and pharmaceutical researchers will find the "Second Edition" a helpful guide to understanding the genetic basis of human disease, with its new tools for detecting risk factors and discovering treatment strategies.
Covering the latest developments, this advanced textbook focuses on introducing the relevant statistical methods applied in this field. Written by the prize-winning scientist Andreas Ziegler, President of the German Region of the International Biometric Society, and Inke R. König, who contributes more than five years of teaching experience, this is ideal for epidemiologists, geneticists, statistics specialists, biomathematicians, graduate and undergraduate students.

After providing a concise introduction to genetic fundamentals, the authors explain both linkage analysis and association analysis in detail. This includes novel techniques such as haplotype tagging or linkage disequilibrium maps. The textbook features more than 100 problems and solutions.

### Evaluation:

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<th>Component</th>
<th>Percentage</th>
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<tr>
<td>Exam</td>
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<tr>
<td>Assignments</td>
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<td>Journal article presentation and participation</td>
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### Academic Integrity:

Students may discuss and/or work together on homework assignments unless otherwise stated. However, please realize that the homework assignments serve as preparation for the exam so it is to your benefit to solve as many of the homework problems as you possibly can on your own to simulate the exam environment. Students may not work together on or discuss the exam. Students are expected to be in class unless extreme circumstances arise. Please let me know before class whenever possible if you will be unable to attend due to such circumstances.
<table>
<thead>
<tr>
<th>Date</th>
<th>Topic</th>
<th>Required Readings and Homework</th>
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| 10/27/08 | Course overview, intro to genetic epidemiology and basic concepts in genetics | Ziegler chapter 1 (skip 1.3.2)  
Online genetic tutorial chapter 3 topics 1, 2, 3 and 5 |
| 10/29/08 | Inheritance and the genetic component of diseases/trait               | Ziegler chapter 2-2.2.2  
Online genetic tutorial chapter 2 topic 1,2 and chapter 5 topic 2  
Haines chapter 3 pgs 91-92 and 100-110 |
| 10/31/08 | Complex inheritance                                                  | Ziegler chapter 2.3  
Online genetic tutorial chapter 2 topic 3 |
| 11/03/08 | Study design, DNA collection and genotyping                          | Haines chapter 3 pgs 92-99  
HW1 due |
| 11/05/08 | SNP selection and public databases                                   | HW2 due |
| 11/07/08 | Journal article discussion: Genetic epidemiology of a disease/trait   | Journal Discussion Week 2 reading on Learn@UW |
| 11/10/08 | Data collection, management and analysis                             | Ziegler chapter 4-4.3.1  
HW3 due |
| 11/12/08 | Unrelated case-control association analysis (Kristin Meyers)          | Ziegler chapter 9-9.1.2, 10-10.1  
Haines chapter 12 pgs 335-338  
HW4 due |
| 11/14/08 | Journal article discussion: Complex inheritance                      | Journal Discussion Week 3 reading on Learn@UW |
| 11/17/08 | Population stratification                                            | Ziegler chapter 10.4-10.4.4  
HW5 due |
| 11/19/08 | Family-based association analysis                                     | Haines chapter 12 pgs 340-344  
HW6 due |
| 11/21/08 | Journal article discussion: Case-control association analysis and population stratification | Journal Discussion Week 4 reading on Learn@UW |
| 11/24/08 | Linkage disequilibrium                                                | Haines chapter 12 pgs 330-333  
HW7 due |
| 11/26/08 | Journal article discussion: Family-based association analysis         | Journal Discussion Week 5 reading on Learn@UW |
| 11/28/08 | No class – Thanksgiving recess                                       | Pearson and Manolio 2008  
HW8 due |
| 12/1/08  | Guest lecture by Kristin Meyers: Genome-wide association studies (GWAS) | Pearson and Manolio 2008  
HW8 due |
| 12/3/08  | Special topics 1: Beyond GWAS                                        | Ziegler chapter 12-12.2 (skip 12.2.1-12.2.2)  
View 13 minute [PBS NOVA video on Epigenomics](https://www.pbs.org/wgbh/nova/epigenomics)  
HW9 due |
| 12/5/08  | Journal article discussion: GWAS                                     | Journal Discussion Week 6 reading on Learn@UW |
| 12/8/08  | Special topics 2: “Omics” and related fields                         | HW10 due |
| 12/10/08 | Special topics 3: Public health genomics                             | HW10 due |
| 12/12/08 | Journal article discussion: Special topics                           | Journal Discussion Week 7 reading on Learn@UW  
Exam distributed |
| 12/15/08 | No class – Finals week                                                | Exam due Saturday, Dec 20th |
| 12/17/08 | No class – Finals week                                                | Exam due Saturday, Dec 20th |
| 12/19/08 | No class – Finals week                                                | Exam due Saturday, Dec 20th |