Course Information for (SU2007) M21-515
Fundamentals of Genetic Epidemiology

Course Masters
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Website
http://www.biostat.wustl.edu/~treva/ (M21-515 course link)

Grading Criteria
Numerical score based on computer lab assignments (75%), pop-quizzes (5%) and final exam (20%)

Computer Programs
Software packages may include (among others):
SEGPATH, SOLAR, PAP, MERLIN, FBAT, QTDT

Textbook
A Statistical Approach to Genetic Epidemiology by
Andreas Ziegler and Inke R. König (2006; Wiley-VCH)

Format:
2-week INTENSIVE course, Monday-Friday 9am-5pm
Typically, a.m. lectures and p.m. computer labs

1st Homework
Due on FIRST DAY OF CLASS
(1) Read 1st chapter of book
(2) Online genetic tutorial, Chapters 1, 2, 3, 5
http://anthro.palomar.edu/tutorials/biological.htm

Course Overview:
This course features basic concepts and methods in quantitative genetics and genetic epidemiology, with a focus on methods to determine and characterize the nature of a genetic component to human disease using standard software packages to analyze family data. The course is partitioned into 2 components:

Week 1: Involves basic quantitative genetics, family designs, preparing family data for analysis, and defining and computing heritability (correlations, variance components, path analysis) and segregation models. Most topics will be illustrated with hands-on computer practice using some standard software packages. SAS is used as the data manager.

Week 2: Provides an introduction to linkage and association, including the use of some standard software packages.

NOTE on syllabus (following pages), the reading assignments should be completed prior to class on the day listed. READING ASSIGNMENTS ARE DUE ON THE FIRST DAY OF CLASS.
### Syllabus: SU2007, M21-515

<table>
<thead>
<tr>
<th>Week 1</th>
<th>Morning (Lecture)</th>
<th>Reading / Homework</th>
<th>Afternoon (Computer Lab)</th>
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<tbody>
<tr>
<td>Day 1</td>
<td>Basic review of genetics, statistics, and quantitative genetics. Familial resemblance part I (familial correlations), maximum likelihood, hypothesis testing, model fitting</td>
<td>Chapter 1 and website tutorial (see above)</td>
<td>Familial correlation model using <strong>SEGPATH</strong></td>
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<td>Day 2</td>
<td>Familial resemblance part II (path analysis (TAU model) and variance components models, including pleiotropy, oligogenic, epistasis and genetic correlations)</td>
<td>Refs 1,2</td>
<td>TAU path model using <strong>SEGPATH</strong>; variance components models using <strong>SOLAR</strong></td>
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<td>Day 3</td>
<td>Characterizing genetic effects part I: Segregation of genes (Mendelian genetics, modes of inheritance, complications of Mendelian segregation, HW law) and mixed model of segregation (major gene + polygenic), hypothesis testing</td>
<td>Chapter 2 and Refs 3,4</td>
<td>Univariate segregation analysis of quantitative traits using <strong>PAP</strong></td>
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<td>Day 4</td>
<td>Characterizing genetic effects part II: Segregation and more complex effects (revisiting pleiotropy, oligogenic, epistasis and genetic correlations)</td>
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<td>GxE and bivariate segregation models of quantitative traits using <strong>PAP</strong></td>
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<td>Day 5</td>
<td>Theory meets practice: Family designs and family structures and family data: data preparation, covariate adjustments, nuclearization and triplet codes, outputting analysis dataset and summary statistics</td>
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<td>Manipulation of family data using <strong>SAS</strong>, including macros to perform repetitive functions</td>
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**Required Reading Assignments Outside of Textbook (see handouts):**


<table>
<thead>
<tr>
<th>Week 2</th>
<th>Morning (Lecture)</th>
<th>Reading / Homework</th>
<th>Afternoon (Computer Lab)</th>
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<tbody>
<tr>
<td>Day 6</td>
<td>Linkage: Basic principles (Revisiting Mendelian segregation), genetic markers and maps, model-based linkage models</td>
<td>Chapters 3, 5, 6</td>
<td>Linkage analysis using <strong>MERLIN</strong> &amp; <strong>SOLAR</strong></td>
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<td>Day 7</td>
<td>Model-free linkage analysis</td>
<td>Chapter 7</td>
<td>Linkage analysis using <strong>MERLIN</strong> &amp; <strong>SOLAR</strong></td>
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<td>Day 8</td>
<td>Linkage of quantitative traits, including Haseman-Elston and variance components approaches</td>
<td>Chapter 8</td>
<td>Linkage analysis using <strong>MERLIN</strong> &amp; <strong>SOLAR</strong></td>
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<td>Day 9</td>
<td>Fundamentals of association analysis, linkage disequilibrium, unrelated individuals, family-based models</td>
<td>Chapters 9, 10, 11</td>
<td>Association analysis using <strong>FBAT</strong> &amp; <strong>QTDT</strong> Review for Final</td>
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<td>Day 10</td>
<td>Haplotypes, multiple comparisons problems and empirical determination of p-values, data quality (phenotype and genotype)</td>
<td>Chapter 4, 12</td>
<td>Final Exam</td>
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**Optional Reference Books:**


The *Handbook for Statistical Genetics* is widely regarded as the reference work in the field. However, the field has developed considerably over the past three years. In particular the modeling of genetic networks has advanced considerably via the evolution of microarray analysis. As a consequence the 3rd edition of the handbook contains a much expanded section on Network Modeling, including 5 new chapters covering metabolic networks, graphical modeling and inference and simulation of pedigrees and genealogies. Other chapters new to the 3rd edition include Human Population Genetics, Genome-wide Association Studies, Family-based Association Studies, Pharmacogenetics, Epigenetics, Ethics and Insurance.

