Instructors: Liming Liang (course head), Dan Chasman, Pete Kraft, and Hughes Aschard

Course Materials: Will be drawn from the literature

Prerequisites: BST 227 (or equivalent) and either BST 231 (co-requisite) or Epi 511. Course is intended for doctoral students; Enrollment will be limited to 15.

Course Objectives: The course is a seminar style course with readings selected from the literature in areas of expertise of the participating faculty. Content may vary from year to year.

At the end of the course the student will be able to critically read foundational papers and current journal articles in statistical genetics; present sophisticated ideas to an audience of peers and engage in doctoral level research in the area.

Session Format
Each session of the course will focus on one topic selected by the participating faculty members. Reading material will be assigned ahead of class meeting. During class session, one student will present the assigned paper and the faculty members will coordinate discussion including important technical details, potential applications, limitation and extension of the statistical methods.

One week will be office hours by appointment; faculty can use their office or the classroom below
One week will be presentation of students; location will be classroom below.

Outcome Measures
Each student must carefully read all assigned papers and be prepared for an in-class discussion of the papers. In addition, each student is expected to prepare a
presentation of at least one paper during the course. The course grade will depend on presentations and class participation. Students are encouraged to read and discuss the papers together outside of class.

**Topics for 2018 Spring 2 and Schedule:**
Liming Liang  
Topic 1. Estimating heritability and co-heritability from GWAS data and pleiotropy

Hughes Aschard  
Topic 2. Multivariate analysis in genetic association studies

Pete Kraft  
Topic 3. Bayesian methods in genetic epidemiology

Daniel Chasman  
Topic 4. Extracting biological insight from GWAS

**Location and Time for Class meetings:**

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<tr>
<th>Date</th>
<th>Location</th>
<th>Time</th>
<th>Speaker</th>
<th>Topic</th>
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<td>5/10/2018  Thu</td>
<td>K204</td>
<td>presentation</td>
<td>Chasman</td>
<td>Topic 4</td>
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Reading Reference for Discussion Topics:
(may subject to slight modification by instructors):

**Topic 1. Estimating heritability and co-heritability from GWAS data and pleiotropy**


**Topic 2. Multivariate analysis in genetic association studies**

1. Stegle et al. 2010, PLoS Genet :: A Bayesian framework to account for complex non-genetic factors in gene expression levels greatly increases power in eQTL studies.


4. Zhu et al. 2015, Am J Hum Genet :: Meta-analysis of Correlated Traits via Summary Statistics from GWASs with an Application in Hypertension

5. Aschard et al. 2015, Am J Hum Gen :: Adjusting for heritable covariates can bias effect estimates in genome-wide association studies

6. Pickrell et al. 2016, Nat Gen :: Detection and interpretation of shared genetic influences on 42 human traits
**Topic 3. Bayesian methods in genetic epidemiology**


**Topic 4: Extracting biological insight from GWAS**

Genomic properties


Methods


Applied analysis
