Association Mapping: GWAS and Sequencing Data

Instructors: Timothy Thornton and Michael Wu

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Taipei, Taiwan

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Introduction: Course Aims

This is a course on statistical methods and software for genetic association studies of complex traits. We aim to cover:

- Case-Control Association Testing
- Genetic Association Testing with Quantitative Traits
- Gene and Pathway Level Analysis
- Population Structure/Ancestry Inference
- Genetic Association Testing in Samples with Structure
- Introduction to Rare Variant Analysis and Collapsing Tests
- Supervised Burden Tests and Variance Component Test for Rare Variants
- Omnibus Tests, Weighting, Design Considerations
- Gene Environment Interactions, Meta Analysis, Emerging Issues

Introduction: Resources

Importantly, the class site is:

http://faculty.washington.edu/tathornt/SISG2015.html

Contains (or will contain);

- PDF copies of slides (in color)
- Datasets needed for exercises
- Exercises for you to try
- Our solutions to exercises (later!)
- Links to software packages

Introduction: About Mike



- Assistant Member, FHCRC Public Health Sciences Division
- Affiliate Assistant Professor, UW Boistatistics
- Research in:

High dimensional data Kernel machine methods Variable selection and regularization Pathway and network based analysis Translational research Statistical genomics/genetics

Introduction: About Tim



... and you?

- Associate Professor, UW Biostatistics
- Affiliate Investigator, FHCRC Public Health Sciences Division
- Research in:

Genetic Association Studies Methods for Correlated Genetic Data Inferring Genetic Ancestry Relatedness Estimation Pharmacogenomics

Introduction: Course Structure

- 10 sessions over 2.5 days
- What to expect in a typical session;
 - 45 mins teaching/lecture
 - 30 mins hands-on exercises
 - 15 mins summary, discussion

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