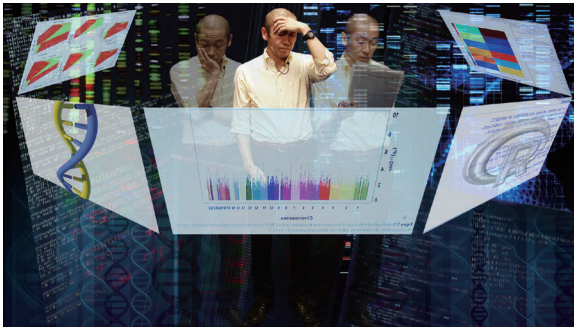


“Introduction to Statistical Methods for Gene Mapping”

Learn about statistical methods used to identify genetic variants responsible for phenotypes.



April 2, 2020 – March 4, 2021

Length: **Self-paced (4 weeks)**

Instructor: **Ryo Yamada, Ph.D.**

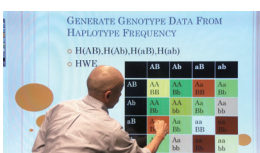
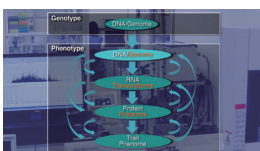
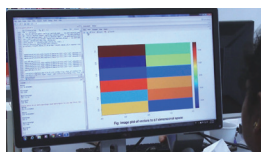
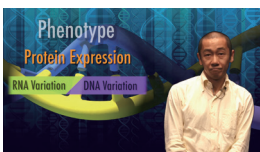
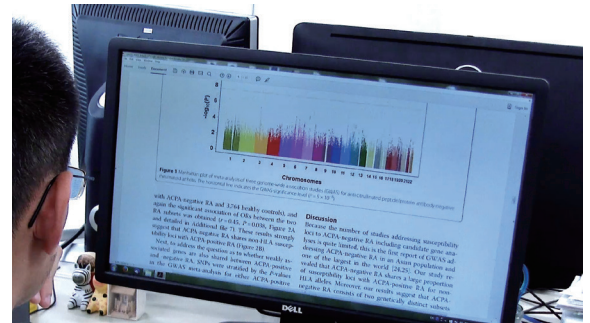
Professor of Statistical Genetics, Kyoto University

This data course is a primer to statistical genetics and covers an approach called linkage disequilibrium mapping, which analyzes non-familial data and has been successfully used to identify genetic variants associated with common and complex genetic traits.

We hope many students find this introductory course interesting and are motivated to study further topics in statistical genetics to understand biological variation from statistical standpoints.

Previous knowledge of molecular genetics and basic statistical concepts, such as statistical tests and estimation, is required. Basic knowledge on genetic variations is offered at the start of the course.

- 1st week**
Basic Knowledge for Gene Mapping
- Genetics**
Gene, Heritage, Monogenic diseases, Complex genetic diseases
- Molecular genetics**
DNA, mRNA, Protein, Genome, Omics, Phenotypes
- Statistics**
Probability, Likelihood, Statistical tests, Estimation
- Computation**
Realization of Statistical Ideas in Computer Language. Free software R.



Section 1 Basic Knowledge for Gene Mapping

Section 2 Linkage Disequilibrium

Section 3 GWAS and Multiple Testing

Section 4 Common Variants and Rare Variants

<https://www.edx.org/course/introduction-to-statistical-methods-for-gene-mappi>
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