

Title : Genome-wide association studies

Lecturers: Sungho Won¹, Wonil Chung², Sangsoo Kim³

Day: 15-16th of Jan, 2020

Affiliation:

¹Department of Public Health Sciences, Seoul National University

²Department of Statistics and Actuarial Science, Soongsil University

³Department of Bioinformatics and Life Science, Soongsil University

Outline: Recent advances in genome sequencing and microarray technology enabled us to conduct genome-wide association studies (GWAS). GWAS identified more than ten thousand SNPs associated with SNPs, and they increased our understanding about human diseases. Recently genome-wide SNPs have been utilized to predict their traits and these profiles have been useful resources to understand human diseases. In this course, attendees learn basic knowledge for data processing and analyses of the genetic association studies from different platforms of microarrays including Korean-chip. Attendees can learn the analytical skills for data processing procedures including quality control, normalization, annotation, and etc. Also, basic programming language skills for R, and PLINK under the Windows platform will be provided.

	Day	Lecture	Lecturer
Day1	Session 1 (09:00-10:30)	Introduction to Genetic Analysis	Sungho Won
	(10:30-10:45)	Break	
	Session 2 (10:45-12:15)	Genome-wide association Studies	Sungho Won
		Lunch	
	Session 3 (13:30-15:00)	Lab: GWAS	Sungho Won
	(15:00-15:15)	Break	
	Session 4 (15:15-16:45)	Heritability Estimation	Wonil Chung

Day2	Session 5 (09:00-10:30)	Gene-set Analysis	Sangsoo Kim
	(10:30-10:45)	Break	
	Session 6 (10:45-12:15)	Lab: Gene-set Analysis	Sangsoo Kim
		Lunch	
	Session 7 (13:30-15:00)	Polygenic Risk Score Estimation	Wonil Chung
	(15:00-15:15)	Break	
	Session 8 (15:15-16:45)	Lab: Polygenic Risk Score Estimation	Wonil Chung