

# 2015 Genomic Epidemiology Workshop

## Agenda

Time	2015/8/17	2015/8/18	2015/8/19	2015/8/20	2015/8/21
9:00	<p><b>Keynote speech</b> (Prof. Chien-Jen Chen)</p>	<p><b>GWAS 1: Introduction GWAS study design and data structure</b> (Dr. Chia-Yen Chen [1]/ Dr. Hailliang Huang [2])</p> <p>1. GWAS study design: (30 mins)</p> <ul style="list-style-type: none"> <li>• Genotyping/batch effect</li> <li>• Data QC</li> <li>• Population structure</li> <li>• Association test</li> </ul> <p>2. GWAS data structure: (30 mins)</p> <ul style="list-style-type: none"> <li>• Phenotype (case-control or quantitative)</li> <li>• Genotype coding (intensity plot/hard call/dosage/type of variants)</li> <li>• Population stratification (PC/MDS)</li> <li>• Public available resource</li> </ul>	<p><b>NGS basics 1: Introduction to Sequencing Technology</b> (Dr. Wan-Ping Lee)</p> <p>1. Evolution of NGS (30min)</p> <ul style="list-style-type: none"> <li>• Comparison of next-generation sequencing methods</li> <li>• Emerging technologies (Nanopore, Hi-C)</li> </ul> <p>2. NGS human genome projects (30min); 1000 genomes project, Genomics England, Iceland, etc</p>	<p><b>Variant Analysis 3: Variant and Phenotype Association</b> (Dr. Hailliang Huang [1]/ Dr. Chia-Yen Chen [2])</p> <p>1. Single rare variant test (population stratification and rare variants/PIP)</p> <p>2. Set-based rare variant test (burden test, variable threshold, SKAT/raremetal)</p>	<p><b>Introduction for Epigenetics</b> (Dr. Chen-Yu Liu and Dr. Wen-Chi Pan)</p> <p>1. Introduction</p> <p>2. DNA Methylation</p> <p>3. Histone Modification</p> <p>4. microRNA</p> <p>5. EWAS/cell mixture</p>
10:00	Break	Break	Break	Break	Break
10:30	<p><b>Taiwan Biobank</b> (Prof. Chen-Yang Shen)</p>	<p><b>GWAS 2: GWAS association analysis: theory</b> (Dr. Yen-Feng Lin [1]/ Dr. Chia-Yen Chen [2]/ Dr. Hailliang Huang [3,4])</p> <p>Concept/lecture</p> <ol style="list-style-type: none"> <li>1. QC / Imputation</li> <li>2. Population admixture and sub-structure</li> <li>3. Common variants association</li> <li>4. Single variant meta-analysis</li> </ol>	<p><b>NGS basics 2: Alignment</b> (Dr. Wan-Ping Lee)</p> <ol style="list-style-type: none"> <li>1. UCSC genome browser BLAT</li> <li>2. FASTA/FASTQ input formats</li> <li>3. Popular working flows</li> <li>4. BAM output format</li> <li>5. Alignment visualization (IGV)</li> </ol>	<p><b>NGS Applications 1: ExomeSeq, RNASeq, ChIPSeq</b> (Dr. Yaoyu Wang)</p>	<p><b>Statistical Analysis in Epigenetics</b> (Dr. Chen-Yu Liu and Dr. Wen-Chi Pan)</p> <ol style="list-style-type: none"> <li>1. Software: R</li> <li>2. Dataset: Maternal smoking, DNA methylation, and birth weight; Case-control for eclampsia</li> <li>3. Mediation Analysis</li> <li>4. EWAS/cell mixture</li> </ol>
11:30	<p><b>Workshop introduction</b> (Dr. Yi-Hsiang Hsu and Dr. Hwai-I Yang)</p>				
12:00	Lunch	Lunch	Lunch	Lunch	Lunch

13:00	<b>Introduction to genetic association study (genetic epi 101): From candidate gene study to genome-wide association study</b> (Dr. Yi-Hsiang Hsu and others)	<b>GWAS 3: GWAS association analysis: practice</b> (Dr. Yen-Feng Lin [1]/ Dr. Chia-Yen Chen [2]/ Dr. Hailliang Huang [3,4])  Concept/lecture 1.QC / Imputation 2.Population admixture and sub-structure 3.Common variants association 4.Single variant meta-analysis	<b>Variant Analysis 1: Variant Calling</b> (Dr. Wan-Ping Lee)  1.Introduction to genomic variations 2.Alignment characteristic of distinct variations 3.Popular working flows 4.VCF/BED/gVCF output formats	<b>NGS Application 2: RNASeq Analysis</b> (Dr. Yaoyu Wang)	<b>Beyond GWAS lecture and handon 1: eQTL, sQTL, mQTL and functional annoation by ENCODE and ROADMAP)</b> (Dr. Yi-Hsiang Hsu and others)  1.eQTL introduction, analytical approaches, publicly available resources, functional annotation; 2.ENCODE, Roadmap, DNase-seq, Chip-seq, Hi-C, ChromHMM, publicly available resource
14:00	Break			<b>NGS basics 3: NGS Data Quality Control</b> (Dr. Yaoyu Wang)	
14:30	<b>Introduction to common analytic platform and software: LINUX and R</b> (Dr. Wan-Ping Lee, Dr. Chia-Yen Chen, Dr. Wen-Chi Pan and Dr. Yi-Hsiang Hsu etc.)				
15:00	1.Basic Unix commands 2.Basic R usage; plotting in R	Break	Break	Break	Break
15:30		<b>GWAS 4: Advanced Statistical analyses</b> (Dr. Chia-Yen Chen [1]/ Dr. Yen-Feng Lin [2]/ Dr. Hailliang Huang [3])  1.SNP-based heritability (GCTA/LD score regression) 2.Polygenic score prediction 3.Fine mapping (credible set)	<b>Variant Analysis 2: Variation Annotation</b> (Yu-Hsiang (Philippe) Lin)  1.Fuctional variation annotation 2.Clinical databases 3.The role of genomics variations in human diseaes	<b>NGS Applications 3: NGS for cancer genomics / Precision medicine</b> (Dr. Shann-Ching Chen)  1. Case study	<b>Beyond GWAS lecture and handon 2: Metabolomics</b> (Dr. Yi-Hsiang Hsu and others)  1.Introduction; analytical approaches, publicly available resource