



Universidad
Pontificia
Bolivariana



Workshop: Human Genomic Data Analysis

Course and Workshop: Human Genomic Data Analysis

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Place: July 19th-july 21th pending confirmation.
July 21th,24th to 28th Universidad Pontificia Bolivariana,
Sede El Poblado, carrera 43C #72a-173, Patio Bonito, Medellín

Basic requirements:

- Basic concepts of genetic transmission and population genetics
- All participants should bring their own computers
- English level B1: 25% of the course will be taught in English

Directed to master and PhD students in Medical Sciences, Basic Sciences, Biology and Microbiology, or related areas that require analyzing human genomic data, and professors. Students and professors of Universidad Pontificia Bolivariana will have priority for the course.

Invited speakers:

Dr. Marc Via, Universidad de Barcelona
Dr. Ana Victoria Valencia, Universidad Pontificia Bolivariana.
Dr. Candelaria Vergara, Johns Hopkins University
Dr. Paul McLaren, Public Health Agency Canada, University of Manitoba
Dr. Yoav Keynan, University of Manitoba



Schedule

July 19th, 2017. Day 1.

Hour	Subject	Speaker
8:30 – 10:00 a.m.	General concepts in Population Genetics: Genetic polymorphisms, allelic and genotypic frequencies, Hardy-Weinberg equilibrium, Linkage disequilibrium (LD), haplotype and linkage phase determination, tagSNPs.	Dr. Ana Victoria Valencia, Universidad Pontificia Bolivariana.
10:00 – 10:30 a.m.	Coffee break	
10:30 a.m. - 12 m.	A primer in General concepts in Genetic epidemiology: The concept of causality Outcomes of interest, risks factors. Type I and type II errors. Statistical power.	Dra. Ana Victoria Valencia, Universidad Pontificia Bolivariana.
12:00-1:30 p.m.	Lunch	
1:30-5:30 p.m.	Introduction to LINUX and software installation.	Dr. Juan Pablo Isaza.

July 21th, 2017. Day 2: Genetic Association Studies.

8:30-10 a.m.	Bias in genetic association studies Measures of association Confounding and interaction (GxG & GxE).	Dra. Ana Victoria Valencia, Universidad Pontificia Bolivariana.
10:00–10:30 a.m.	Coffee break	
10:30 a.m. -12:00 m.	Design of genetic association studies based on hypothesis (candidate genes) Genetic variation Phenotype definition.	Dr. Ana Victoria Valencia, Universidad Pontificia Bolivariana.
12:00-1:30 p.m.	Lunch	



1:30-2:30 p.m.	Exposure measurement: genotyping methods and platforms. Databases of genetic variation: dbSNP, 1000 genomes.	Dr. Ana Victoria Valencia, Universidad Pontificia Bolivariana.
2:30-5:30 p.m.	Workshop: Selection of genes and functional variants or tagging SNPs. Size of sample (Genetic power calculator, Quanto). Conventional Data formats (VCF, PED, MAP, DAT, INFO) Navigating through 1000 genomes: Allelic frequencies identification Download genotypes in a region of interest. LD visualization (Haploview) Tag SNPs identification.	Dr. Ana Victoria Valencia, Universidad Pontificia Bolivariana.
July 24th, 2017. Day 3: Genetic Association Studies.		
8:30 – 10:00 a.m.	Talk: Genome wide association studies versus candidate gene association Design of GWAS: statistical power and sample size. Multiple test correction Massive genotyping methods Available platforms.	
10:00 – 10:30 a.m.	Coffee break	
10:30a.m. -12:00 m.	Workshop: Descriptive statistics in genetics (PLINK and R) Data management: Database fusion, To merge file sets, filter file sets by SNPs and individuals, Pruning based on LD.	Dr. Candelaria Vergara, Johns Hopkins University.
12:30 – 2:00 p.m.	Lunch	
2:00-3:00 p.m.	Quality control data in genomic projects.	Dr. Candelaria Vergara, Johns Hopkins University.
3:00 – 5:30 p.m.	Practical workshop: Detection of related individuals and outliers using IBD (PLINK) Quality control data in genomic projects and descriptive statistics.	Dr. Candelaria Vergara, Johns Hopkins University.



July 25th, 2017. Day 4: Genomic Association Studies and Genetic Structuration.

8:30 – 9:30 a.m.	Talk: Genetic association test.	Dr. Candelaria Vergara, Johns Hopkins University.
9:30-10:00 a.m.	Coffee break	
10:00 a.m.-12:00 m.	Practical workshop: GWAS and Dr. Candelaria Vergara, graphical visualization of results.	Dr. Candelaria Vergara, Johns Hopkins University.
12:00 – 1:30 p.m.	Lunch	
1:30-2:30 p.m.	Talk: Identification of genetic structuration: genomic inflation factor, QQ-plot.	Dr. Marc Via, Universidad de Barcelona.
2:30-5:30 p.m.	Practical workshop: Identification of genetic structuration: genomic inflation factor, QQ-plot.	Dr. Marc Via, Universidad de Barcelona.

July 26th, 2017. Day 5: Adjusted association and interaction.

8:30 – 9:15 a.m.	Talk: Genomic structuration correction: Principal component analysis Ancestry estimation.	Dr. Marc Via, Universidad de Barcelona.
9:15-9:45 a.m.	Coffee break	
9:45 a.m. -12:00 m.	Practical workshop: Principal component analysis (EIGENSOFT) and Ancestry estimation: global and regional (STRUCTURE.)	Dr. Marc Via, Universidad de Barcelona.



12:00-1:30 p.m.	Lunch	
1:30-3:00 p.m.	Talk: Adjusted association test, Genomic structuration correction: Principal component analysis or Ancestry estimation.	Dr. Marc Via, Universidad de Barcelona.
3:00-3:30 p.m.	Coffee break	
3:30-4:30 p.m.	Translational medicine: From bench to bedside.	Dr. Yoav Keynan, University of Manitoba.
4:30-5:30 p.m.	Discussion among speakers and students of clinical application of genetic approaches to diseases.	All speakers.
July 27th, 2017. Day 6: Adjusted association and interaction.		
8:30-10:30 p.m.	Practical workshop: Adjusted analysis by population structuration.	Dr. Marc Via, Universidad de Barcelona.
10:00 – 10:30 a.m.	Coffee break	
10:30 a.m. – 12:00 m.	Practical workshop: Adjusted by other covariables Interaction: gen x gen, and gen x environment.	Dr. Marc Via, Universidad de Barcelona.
12:00-1:30 p.m.	Lunch	
2:00 – 3:30 p.m.	Talk: Meta-analysis of individual data.	
3:30 – 4:00 p.m.	Coffee break	
4:00-5:30 p.m.	Talk and workshop: Imputation methods of genotypes and Meta-analysis.	Dr. Candelaria Vergara, Johns Hopkins University.



**July 28th, 2017. Day 7:
Exome analysis.**

7:00 a.m.	Talk: Next generation sequencing platforms and data types.	Dr. Paul McLaren, Public Health Agency Canada, University of Manitoba
10:00 – 10:30 a.m.	Coffee break	
10:30 a.m. – 12:00 m.	Talk: Exome and genome sequencing to identify disease associated loci.	Dr. Paul McLaren, Public Health Agency Canada, University of Manitoba.
12:00 – 1:30 p.m.	Lunch	
1:30 – 4:00 p.m.	Practical workshop: Processing and analysis of exome sequencing data, annotation of variant function and association methods.	Dr. Paul McLaren, Public Health Agency Canada, University of Manitoba.