INTRODUCTION TO COMPUTATIONAL GENETICS					
Week	**Topic**	**Important concepts**	**Computation**	**Hum. Evolutionary genetics chapter**	**Recommended readings**
1	Introduction	Introduction to the course DNA, chromosomes and central dogma Next-Generation Sequencing Visualization of genes and proteins	Genomic browser	**Chapter 2** Organization and Inheritance of the Human Genome (2.1 -2.5)	Nurk S, Koren S, Rhie A, Rautiainen M, Bzikadze AV, Mikheenko A, Vollger MR, Altemose N, Uralsky L, Gershman A, Aganezov S. The complete sequence of a human genome. Science. 2022 Apr 1;376(6588):44-53.
2	Genetic sequencing	Data generation, from DNA to VCF Variant Call Formatting Files Understanding the information in a VCF file	Linea de Comandos	**Chapter 3** Human Genome Variation (3.1 and 3.2)	The Variant Call Format (VCF) Version 4.2 Specification. Danecek, P., Auton, A., Abecasis, G., Albers, C. A., Banks, E., DePristo, M. A., ... & 1000 Genomes Project Analysis Group. (2011).
3	Data manipulation	Command Line Command Line for Genomics Manipulating a VCF with VCFtools	VCFtools		The variant call format and VCFtools. Bioinformatics, 27(15), 2156-2158. Chaitankar, Vijender, et al. "Next generation sequencing technology and genomewide data analysis: Perspectives for retinal research." Progress in retinal and eye research 55 (2016): 1-31 [Semana 2]
4	Human genetic variation and diversity	Variation in populations 1000 Genomes Project Introduction to Plink	Plink	**Chapter 4** Finding and Assaying Genome Diversity (from 4.1 to 4.6)	Auton et al.- A global reference for human genetic variation (2015). Genomes are failing on diversity- Alice popejoy.
5	Manipulating genetic data with Plink	Genotyping rate and other quality metrics Plink vs. VCFtools Multiallelic Variants	Plink		Data Management and Summary Statistics with PLINK. Christopher Chang in Julien Y. Dutheil, Statistical Population Genomics, Methods in Molecular Biology, vol. 2090, https://doi.org/10.1007/978-1-0716-0199-0_3.
6	Haplotypes and recombination	Chromosome recombination and Linkage Disequilibrium (LD) Identity by State and Identity by Descent Haplotypes and LD Patterns Phasing	VCFtools/Plink	**Chapter 2** Organization and Inheritance of the Human Genome (**2.6-2.7**) **Chapter 4** Finding and Assaying Genome Diversity (**Seccion 4.9**)	The Structure of Haplotype Blocks in the Human Genome. SB Gabriel 2002. Browning & Browning - Identity by Descent Between Distant Relatives Detection and Applications (2012).
7	Data imputation	SNP array sequencing Data Imputation Using population references to infer data	TopMed server		Das et al. 2018 - Genotype Imputation from Large Reference Panels. Li et al. 2009 - Genotype Imputation
8	Quality control	CARE and FAIR Principles Quality control of genetic data	Plink, R		CARE principles, The FAIR Guiding Principles for scientific data management and stewardship. Anderson - Data quality control for association studies Nature Protocols (2010).
9	Kinship and genetic relateedness	How to interpret pedigrees Genetic kinship and calculation of the "kinship coefficient" Using software to infer kinship	KING	**Chapter 2** Organization and Inheritance of the Human Genome (2.6-2.7). **Chapter 18.3** Deducing Family and Genealogical Relationships	**Browning & Browning - Identity by Descent Between Distant Relatives Detection and Applications (2012) [otra vez!].** Speed, Balding - 2015 - Relatedness in the post-genomic era Is it still useful? Manichaikul - Robust relationship inference in genome-wide association studies (2010)
10	Non-recombining segments of DNA	Mitochondrial chromosome and Y chromosome Haplogroups	haplogrep	**Chapter 2** Organization and Inheritance of the Human Genome (2.8). Chapter 3 Human Genome Variation (3.3). Appendix	
POPULATION GENETICS					
11	Introduction to population genetics	Forces of Evolution Genetic Drift, Mutation, Migration, and Selection	No	**Chapter 5** Processes Shaping Diversity. **Chapter 16** Evolutionary Insights into Simple Genetic Disease	Benton et al. - 2021 - The influence of evolutionary history on human health and disease. Prohaska et al. - 2019 - Human Disease Variation in the Light of Population Genomics. Ceballos et al. - 2018 - Runs of homozygosity Windows into population history and trait architecture
12	Computational analysis of evolutionary forces	Hardy-Weinberg Equilibrium Computationall analysis of evolutionary forces	plink		
13	Population stratification	Population Stratification Principal Component Analysis (PCA)	Plink (PCA), R	**Chapter 14** What Happens When Populations Meet	Novembre et al. - 2008 - Genes mirror geography within Europe Acosta-Uribe, Juliana, et al. "A neurodegenerative disease landscape of rare mutations in Colombia due to founder effects." Genome Medicine 14.1 (2022): 1-22.
14	Global ancestry	Global Ancestry and ADMIXTURE How to model a population	ADMIXTURE Pong		Moreno-Estrada et al. - 2013 - Reconstructing the Population Genetic History of the Caribbean
15	Local ancestry	Phasing Local Ancestry Determination Long-read Sequencing	RFMix2 Shapeit5		Blue et al. - 2019 - Local ancestry at APOE modifies Alzheimer's disease risk in Caribbean Hispanics. Maples et al. Maples et al. - 2013 - RFMix A discriminative modeling approach for rapid and robust local-ancestry inference
GENETIC EPIDELMIOLOGY					
16	Introduction to genetic epidemiology	Design of genetic studies Determining the genetic component of a disease Genome annotation and population databases	noGnomAD, ExAC, 100GP	Ghosh et al. 2017 In Silico prediction algorithms. Gunning et al. 2020 - Assessing performance of pathogenicity predictors using clinically relevant variant datasets. Rojano, Regulatory variants from detection to predicting impact.	
17	Variant curation	ACMG guidelines for variant interpretation In-silico pathogenicity analysis	wANNOVAR CADD, SIFT, Polyphen	Richards et al. - 2015 - Standards and guidelines for the interpretation of sequence variants A joint consensus recommendation of the AMCG/AMP. Strande et al. 2018 - Navigating the nuances of clinical sequence variant interpretation in Mendelian disease	
18	Gene-disease association	Guidelines for Gene-Disease association Mendelian segregation studies (zygosity mapping) Linkage and LOD Score	Plink	Strande et al. - 2017 - Evaluating the Clinical Validity of Gene-Disease Associations An Evidence-Based Framework Developed by the Clinical genome Resource Ott 2011 - Family-based designs for genome-wide association studies Ott, Wang, Leal - 2015 - Genetic linkage analysis in the age of whole-genome sequencing	
19	Case-control studies	Case-Control Studies Statistical risk approach Genome Wide Association Studies (GWAS) Rare variant collapsing tests	Plink	A tutorial on statistical methods for population association studies **Benefits and limitations of genome-wide association studies** Clarke et al. - 2011 - Basic statistical analysis in genetic case-control studies Gene Clinical Validity Curation Process	
20	Genome Wide Association Studies (GWAS)	Design and statistics of GWAS Discrete vs. continuous phenotypes Linear regression	Plink R	Uffelmann, E., Huang, Q.Q., Munung, N.S. et al. Genome-wide association studies. Nat Rev Methods Primers 1, 59 (2021). https://doi.org/10.1038/s43586-021-00056-9 Abdellaoui, Abdel et al. "15 years of GWAS discovery: Realizing the promise." American journal of human genetics vol. 110,2 (2023): 179-194. doi:10.1016/j.ajhg.2022.12.011	
21	Polygenic Risk Score (PRS)	Utility of PRS Extrapolating PRS between populations	Plink R	Torkamani, Ali, Nathan E. Wineinger, and Eric J. Topol. "The personal and clinical utility of polygenic risk scores." Nature Reviews Genetics 19.9 (2018): 581-590.	