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). 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]
3	Data manipulation	Command Line Command Line for Genomics Manipulating a VCF with VCFtools	VCFtools		
4	Human genetic variation and diversity	Variation in populations 1000 Genomes Project Introduction to Plink and Plink vs VCF	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. 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.
5	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).
6	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
7	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)
8	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)
9	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					
10	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
11	Computational analysis of evolutionary forces	Hardy-Weinberg Equilibrium Computationall analysis of evolutionary forces	plink		
12	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.
13	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
14	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				
15	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.
16	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
17	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
18	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
19	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
20	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.