Course Lay-Out - Genetic Epidemiology - 2012-2013 (non-Public Health)

Date	Key Term	Description	Project Assignment	Due
5/3	Software	- Introduction to Genetic Epidemiology (what it is and what it is not) - Each subfield of Genetic Epidemiology has a vast amount of software tools available - Zoom in on Population Genetics - Assignment 1: Software for population genetics and genetic association studies	Assignm1: - What is population genetics? Why is it important in the context of genetic epidemiology? - Compendium of software tools: where do they focus on? Can you classify them? What are the criteria to classify them? Highlight one or two of these tools and explain what they do in more detail. Use available information on the www. - Compare R GenABEL with R SNPassoc.	1/4
19/3	QC	- Garbage in garbage out principle. The importance of QC-ing - Introduction to Genetic Association Studies - In depth assessment of QC-ing criteria / classifications: ▪ Data generation step ▪ Data preprocessing step prior to • main effects analysis • multiple snp analysis • interaction analysis - Assignment 2: Describe and QC simulated data for subsequent genetic association analysis.	Assignm2: - Know your data using R: How is it composed? Do the data contain family structures or only involve unrelated individuals? How much family structure is there; what are the inbreeding coefficients? (e.g., "pedigree" package in R) How many non-genetic variables are there? How are their measurements distributed in the data? How many SNPs are there? What is the distribution of allele frequencies in the data? (e.g., "adegenet" package in R) - QC the data in the light of subsequent association analysis - Perform a genetic association analysis using all of the data. Use PLINK and use	15/4 Feedback meeting and group presentations of these assignments on or around 30/4 (to be discussed in class)

			R tools. Compare the results. When different, discuss how this can be explained and what the consequences may be for subsequent analysis	
16/4	Families	- Families lie at the basis of heritability assessments - Current association studies leave room for much unexplained heritability. Where did it go? - Introduction to family-based genetic association studies with illustration using the FBAT software - Assignment 3: Perform a genetic association study, explicitly acknowledging the family-structure in the data	Assignm3: - Exploit the nature of the data, this is, acknowledge the family-structure in the data, by performing a family-based association study using R (GenABEL) and FBAT. Compare the results. When different, discuss how this can be explained. - Is it possible to correct the GenABEL analysis for population stratification? If so, and when implementing such a correction, do the results change? Is population stratification an issue in GenABEL / in FBAT? Why or why not?	15/5
30/4	Environment	- Environment is key to epidemiology. Genetics gives added value to epidemiology, environment should not be forgotten in genetic epidemiology - Introduction to gene-gene and gene-environment interactions with illustration using the MB-MDR software	Assignm4: - Perform a gene-gene and gene-environment interaction study using GenABEL and discuss your results - Annotate hit findings (e.g., see http://www.biomedcentral.com/content/pdf/1471-2105-11-311.pdf) - Not mandatory: compare your gene-gene interaction results with those obtained from MB-MDR	20/5 Feedback meeting and group presentations of these assignments around 25/5 (to be discussed in class)