Lecture 9 Exercises:

ALL of the code and scripts are inside of the file: Lecture_9_code.txt. Because the code for doing some of these tasks is quite involved, please copy and paste from that file, but do make efforts to understand what the code is generally doing.

Exercise 1. Read in the variants in Gene2 and read in trait2. Then use SKAT to test for an association between the variants in Gene2 and Trait2.

Please check to see if SKAT is installed first. If not, then click on "Packages" in the menu and go to "Install Packages".

Exercise 2. Just for fun (woohoo!), let's dichotomize trait 2 and run SKAT with a dichotomous outcome. Specifically, for each sample, if the trait value is above the 75th percentile, call the sample a case (score it as a 1). If the trait value is below the 25th percentile, call the sample a control (score it as a 0). Omit the samples with intermediate trait values.

Run SKAT with the new, dichotomous outcome.

Exercise 3. Apply the C-alpha test to analyze the association between quantitative trait 2 and Gene 2 using the connection with SKAT.

Exercise 4. Now run the omnibus SKAT, but consider setting rho (r.corr) = 0 and rho = 1 and rho = 0.5. Compare the results to using count based collapsing and weighted count based collapsing where the weights are the same as in SKAT (i.e. beta density function with parameters 1 and 25). What do you notice?

Exercise 5. Run the omnibus version of SKAT, but use the "optimal" approach which searches across a range of rho values.

Exercise 6. SKAT can directly take in PLINK formats. Look inside the PlinkExample folder and note that files that are there. It's basically all of the standard files you would have from a GWAS.

The one additional file is the SetID file. Look at what is contained within this.

Now let's analyze the example data.