**Installation and operation of non-normally distributed phenotype code on LISA**

Last rev sep 20, 2016

This script will run an association analysis on LISA using Rscript code.

**Installation for LISA**

**R Libraries**

Install the VGAM/Rserve libraries (code below). Needs only be run once.  
  
module load c/intel  
module load fortran/intel  
module load intel-studio/2015.2  
module load R  
  
R  
install.packages('VGAM')  
install.packages('Rserve')  
80  
q('no')

**Scripts**

Next put the following files into your working directory

analyze\_data\_v2.script

make\_phenotype\_file\_v2\_sep19\_2016.R

ologit\_rserve\_v1\_may25\_2016.R

Rserve.R

trauma\_analysis\_v1.pbs

**Script modifications**

Open analyze\_data\_v2.script and set the variables

Notes on variable settings

**famfile**

The .fam file should be pulled from the genotype data. If data is split into multiple chunks (e.g. by chromosome), this assumes that all .fam files are the same.

**Phenotypes and covariates**

Phenotypes and covariates files should be tab delimited, and contain FID, IID, and all relevant data. Missing data should follow the PLINK format for missing data.

Phenotypes and covariates can be extracted from the same file (in other words, it's fine to have a single table with both).

FIDs and IIDs should be study submitted IDs. There is a script built in that will make them compatible with the Ricopili modified FIDS and IIDs:

Namely, a study submitted FID and IID will look like e.g.

4511 1

and the ricopili ID will look like

con\_pts\_mrsa\_mix\_am\_OMEX\*4511 1

Job walltime may need to be modified. Default is 2 hours (03:00:00). This is more than adequate for a single 3MB chunk, but may need to be lengthened if all data is in a single PLINK binary. I recommend going by either chunk or chromosome. If output data is truncated (fewer SNPs than expected), try lengthening the walltime.

**Operation**

After the script has been modified, copy and past the code into the console. A job array ID will be returned. Check the job status periodically by writing

qsub -t writejobarrayhere[]

Error logs/console outputs are stored in the errandout folder.