

Prerequisite

- 1) make sure python 2.6 is install
- 2) make sure numpy and scipy are install
- 3) make sure GSL library is install

Installation:

- 1) download the caviar source code
- 2) unzip the source code
- 3) run make on the directory the code is downloaded

You can run CAVIAR on a single region or whole genome. We recommend running the CAVIAR to a region which consist of 50 variants (MORE THAN THAT WILL TAKE VERY LONG TIME NOW)

Run CAVIAR on single region:

```
python caviar.py -l input.LD -z input.Z -r 0.95 -o outputresults
```

Usage: caviar.py [options]

Options:

```
-h, --help          show this help message and exit
-o OUTFILE, --out=OUTFILE
                    specify the output file
-l LDFILE, --ld_file=LDFILE
                    the ld input file
-z ZFILE, --z_file=ZFILE
                    the z-score and rsID files
-r RHO, --rho-prob=RHO
                    set  $\rho$  probability
```

For running the caviar on a single region you need the LD between each pair of SNP and the marginal z-score.

The LD file should look like this for 3 SNPs, each row and column represent one SNP:

```
1 1 -0.245049
1 1 -0.255852
-0.245049 -0.255852 1
```

You can obtain this LD matrix using the plink command line:

```
plink --tfile testfile --r --matrix --snps snplist --chr  
chromname --noweb -out
```

For example:

```
plink --tfile finland.tped --r --matrix --snps  
rs3800406,rs236446,rs7741573 --chr 1 --noweb -out
```

You can obtain the Z-score using the plink:

```
plink --tfile testfile --assoc --pheno phenoFile --mpheno  
phenoNum --noweb --out outputFile
```

phenotFile is the phenotype file which is in the plink format.
phenoNum is a number which indicates which phenotype if more than
one phenotype exists in the phenotype file.

Running CAVIAR on whole Genome:

We provide a code which can run the caviar on the whole genome.

Usage: wholeGenomeCAVIAR.py [options]

Options:

```
-h, --help          show this help message and exit  
-o OUTFILE, --out=OUTFILE  
                    specify the output file  
-t TPEDFILE, --tped_file=TPEDFILE  
                    the tped file  
-p PHENOFIELD, --pheno_file=PHENOFIELD  
                    the phenotype files in PLINK format  
-m PHENONUM, --mpheno=PHENONUM  
                    the phenotype number  
-r RHO, --rho-prob=RHO  
                    set  $\rho$  probability
```