Estimating permutation p-values using MatrixEQTL

In our pipeline we first reformat the data per gene and then for each preprocessed gene run step4\_MatrixEQTL script which runs multiple bootstraps.

step4\_submitMatrixEQTL.R will call step4\_MatrixEQTL.R with several options: chromosome (in this example 9), number of samples inthe dataset (this can be taken from specification file) random seed 1565691 window - 5e+05 is used in this example and which model is used - shorter model for this example and optional parameter - how much paralellization you want to introduce (if your cluster supports submitting multiple jobs, for this example set to 1 meaning that every job will be run sequentially)

We load the data for MatrixEQTL

args = c("9", "704", "1565691", "5e+05", "short", "1")  
args

## [1] "9" "704" "1565691" "5e+05" "short" "1"

chri = as.numeric(args[1])  
nsub = as.numeric(args[2])  
seedval = as.numeric(args[3])  
cis\_window = as.numeric(args[4])  
model = args[5]  
if(length(args)>5){  
 paral = as.numeric(args[6])  
}else{  
 paral = 1e6  
}  
  
specf = "specifications.txt"  
  
specs = unlist(read.table(specf, as.is=T))  
pref = specs[1]  
nsam = specs[2]  
queue = specs[3]  
days = specs[4]  
days = 2  
bmem = as.numeric(specs[5])  
mem = "4g"  
if(length(specs)>20){  
 mem = specs[21]  
}  
mem

## V121   
## "4g"

seedval = specs[13]  
wrk.dir = specs[14]  
lib.dir = specs[15]  
bas.dir = specs[16]  
eigenMTdir = specs[9]  
rprog = specs[19];rprog

## V119   
## "R"

pyth = specs[20];pyth

## V120   
## "python"

setwd(wrk.dir)  
wrk.dir

## V114   
## "C:/Users/Vasyl/Documents/GitHub/asSeq/pipeline\_GTEx/v8/example/Muscle\_Skeletal"

library(MatrixEQTL)  
library(Matrix)  
useModel = modelLINEAR;   
source(sprintf("%s/helpers.R", lib.dir))  
  
  
numpoints = 100  
maf = 0.05  
   
set.seed(seedval)  
  
  
routdir = sprintf("%s/rout\_%s", wrk.dir, pref)  
boutdir = sprintf("%s/bout\_%s", wrk.dir, pref)  
if(!file.exists(routdir))dir.create(routdir)  
if(!file.exists(boutdir))dir.create(boutdir)  
  
int.dir = sprintf("%s\_%s\_%s", pref, nsub, cis\_window)  
  
  
cnt.dir = sprintf("%s\_prepr", pref);cnt.dir;file.exists(cnt.dir)

## [1] "Muscle\_Skeletal\_prepr"

## [1] TRUE

out.dir = sprintf("oneperm\_%s\_%s\_%s\_%s", pref, nsub, cis\_window, model)  
perm.dir = sprintf("boot\_%s\_%s\_%s\_%s\_%s", pref, nsub, cis\_window, model, numpoints)  
if(!file.exists(out.dir))dir.create(out.dir)  
if(!file.exists(perm.dir))dir.create(perm.dir)

Once initial setup is done we read relevant (multigene) data

genepos\_file\_name = sprintf("%s/geneInfo\_prepr\_%s.txt", cnt.dir, model)  
geneInfo = read.table(genepos\_file\_name,   
 header = T, as.is = T)  
genepos = geneInfo[geneInfo$chr==sprintf("chr%s", chri),1:4]  
genepos[,2] = gsub("chr", "", genepos[,2])  
for(coli in 3:4)genepos[,coli] = as.numeric(genepos[,coli])  
genepos

## Name chr start end  
## 15011 ENSG00000181404.15 9 14521 25004

covariates\_file\_name = sprintf("%s/Xmat\_%s.csv", int.dir, model)   
covar = read.csv(covariates\_file\_name, as.is=T, header=F)  
covar = as.matrix(covar)  
  
converge = 1e-4  
vari = apply(covar,2,var)  
  
updvar = which(vari<converge)  
for(i in updvar){  
 if(length(vari[-updvar]>0)>0){  
 correct = sqrt(median(vari[-updvar]))/sqrt(vari[i])  
 }else{  
 correct = 1/sqrt(vari[i])  
 }   
 xm = mean(covar[,i])   
 covar[,i] = xm+(covar[,i]-xm)\*correct  
}

Load gene specific data

blocki = 1  
  
 suff0 = sprintf("%s\_%s", chri, blocki)  
 timout = sprintf("%s/time\_%s.csv", perm.dir, suff0)  
   
 output\_file\_name = sprintf("%s/output\_norm\_%s.txt", int.dir, suff0)  
 output\_file\_name2 = sprintf("%s/output\_eigenMT\_%s.txt", out.dir, suff0)  
 expression\_file\_name = sprintf("%s/GE\_norm\_%s\_%s.dat", int.dir, model, suff0)  
 output\_file\_name\_min = sprintf("%s/output\_norm\_min\_%s.txt", perm.dir, suff0)  
  
 genotype\_file\_name = sprintf("%s/genotypes\_%s.dat", int.dir, suff0)  
 cvrt = SlicedData$new()  
 cvrt = cvrt$CreateFromMatrix(t(covar))  
   
 g.ini = read.table(genotype\_file\_name, header=T)  
 g.ini[g.ini==3] = 1  
 g.ini[g.ini==4] = 2  
 snpspos\_file\_name = sprintf("%s/genotypei\_%s.dat", int.dir, suff0)  
 snpspos = read.table(snpspos\_file\_name, header=T, as.is=T)  
 for(coli in 3:3)snpspos[,coli] = as.numeric(snpspos[,coli])  
 rownames(g.ini) = snpspos[,1]  
  
 kp = rowMeans(g.ini)/2  
   
 converge=5e-5  
 varZ = apply(g.ini, 1, var)  
 wVar = (varZ >= converge)  
 kp = wVar #& ((a0&a1)|(a2&a1)|(a0&a2))  
   
   
 g.ini = read.table(genotype\_file\_name, header=T)  
 g.ini[g.ini==3] = 1  
 g.ini[g.ini==4] = 2  
 snpspos\_file\_name = sprintf("%s/genotypei\_%s.dat", int.dir, suff0)  
 snpspos = read.table(snpspos\_file\_name, header=T, as.is=T)  
 for(coli in 3:3)snpspos[,coli] = as.numeric(snpspos[,coli])  
 rownames(g.ini) = snpspos[,1]  
  
 kp = rowMeans(g.ini)/2  
   
 converge=5e-5  
 varZ = apply(g.ini, 1, var)  
 wVar = (varZ >= converge)  
 kp = wVar   
  
 exprj = read.table(expression\_file\_name)  
   
   
 pvOutputThreshold = 1;  
 errorCovariance = numeric();  
   
 snps = SlicedData$new();  
 snps$fileSliceSize = 2000; # read file in pieces of 2,000 rows  
 snps = snps$CreateFromMatrix(as.matrix(g.ini))  
   
 genepos\_file\_name = sprintf("%s/genepos\_%s.dat", int.dir, suff0)  
 colnames(snpspos) = c("snpid", "chr", "pos")  
 colnames(genepos) = c("geneid", "chr", "left", "right")  
 write.table(genepos[blocki,], file=genepos\_file\_name, row.names=F, col.names=T, quote=F, sep="\t")  
  
 rownames(exprj) = genepos$geneid[blocki]  
 gene = SlicedData$new();  
 gene = gene$CreateFromMatrix(as.matrix(exprj))

Load information for the relevant chromosome

genepos\_file\_name = sprintf("%s/geneInfo\_prepr\_%s.txt", cnt.dir, model)  
geneInfo = read.table(genepos\_file\_name,   
 header = T, as.is = T)  
genepos = geneInfo[geneInfo$chr==sprintf("chr%s", chri),1:4]  
genepos[,2] = gsub("chr", "", genepos[,2])  
for(coli in 3:4)genepos[,coli] = as.numeric(genepos[,coli])  
genepos

## Name chr start end  
## 15011 ENSG00000181404.15 9 14521 25004

covariates\_file\_name = sprintf("%s/Xmat\_%s.csv", int.dir, model)   
covar = read.csv(covariates\_file\_name, as.is=T, header=F)  
covar = as.matrix(covar)  
  
converge = 1e-4  
vari = apply(covar,2,var)  
  
updvar = which(vari<converge)  
for(i in updvar){  
 if(length(vari[-updvar]>0)>0){  
 correct = sqrt(median(vari[-updvar]))/sqrt(vari[i])  
 }else{  
 correct = 1/sqrt(vari[i])  
 }   
 xm = mean(covar[,i])   
 covar[,i] = xm+(covar[,i]-xm)\*correct  
}

Load gene specific data

blocki = 1  
countjobs = 0  
  
 suff0 = sprintf("%s\_%s", chri, blocki)  
 timout = sprintf("%s/time\_%s.csv", perm.dir, suff0)  
   
 output\_file\_name = sprintf("%s/output\_norm\_%s.txt", int.dir, suff0)  
 output\_file\_name2 = sprintf("%s/output\_eigenMT\_%s.txt", out.dir, suff0)  
 expression\_file\_name = sprintf("%s/GE\_norm\_%s\_%s.dat", int.dir, model, suff0)  
 output\_file\_name\_min = sprintf("%s/output\_norm\_min\_%s.txt", perm.dir, suff0)  
  
 genotype\_file\_name = sprintf("%s/genotypes\_%s.dat", int.dir, suff0)  
 cvrt = SlicedData$new()  
 cvrt = cvrt$CreateFromMatrix(t(covar))  
   
 g.ini = read.table(genotype\_file\_name, header=T)  
 g.ini[g.ini==3] = 1  
 g.ini[g.ini==4] = 2  
 snpspos\_file\_name = sprintf("%s/genotypei\_%s.dat", int.dir, suff0)  
 snpspos = read.table(snpspos\_file\_name, header=T, as.is=T)  
 for(coli in 3:3)snpspos[,coli] = as.numeric(snpspos[,coli])  
 rownames(g.ini) = snpspos[,1]  
  
 kp = rowMeans(g.ini)/2  
   
 converge=5e-5  
 varZ = apply(g.ini, 1, var)  
 wVar = (varZ >= converge)  
 kp = wVar #& ((a0&a1)|(a2&a1)|(a0&a2))  
   
   
 g.ini = read.table(genotype\_file\_name, header=T)  
 g.ini[g.ini==3] = 1  
 g.ini[g.ini==4] = 2  
 snpspos\_file\_name = sprintf("%s/genotypei\_%s.dat", int.dir, suff0)  
 snpspos = read.table(snpspos\_file\_name, header=T, as.is=T)  
 for(coli in 3:3)snpspos[,coli] = as.numeric(snpspos[,coli])  
 rownames(g.ini) = snpspos[,1]  
  
 kp = rowMeans(g.ini)/2  
   
 converge=5e-5  
 varZ = apply(g.ini, 1, var)  
 wVar = (varZ >= converge)  
 kp = wVar   
  
 SNP\_file\_name = sprintf("%s/SNP\_%s.txt", int.dir, suff0)  
  
 write.table(g.ini, SNP\_file\_name, row.names=T, col.names=T, quote=F, sep="\t")  
  
 exprj = read.table(expression\_file\_name)  
   
   
 pvOutputThreshold = 1;  
 errorCovariance = numeric();  
   
 snps = SlicedData$new();  
 snps$fileSliceSize = 2000; # read file in pieces of 2,000 rows  
 snps = snps$CreateFromMatrix(as.matrix(g.ini))  
   
 genepos\_file\_name = sprintf("%s/genepos\_%s.dat", int.dir, suff0)  
 colnames(snpspos) = c("snpid", "chr", "pos")  
 colnames(genepos) = c("geneid", "chr", "left", "right")  
 write.table(genepos[blocki,], file=genepos\_file\_name, row.names=F, col.names=T, quote=F, sep="\t")  
  
 rownames(exprj) = genepos$geneid[blocki]  
 gene = SlicedData$new();  
 gene = gene$CreateFromMatrix(as.matrix(exprj))

Rewrite permutation estimate as a function Run permutation estimate (calling newscript runboot to produce 1000 iterations for 100 points) with the refitting on the same data MatrixEQTL) Note, here we disabled submission to the cluster, so example gene will be run directly on the local machine.

#will now create an object which would contained required information  
permEst = list(snpM=as.matrix(g.ini), geneM=as.matrix(exprj), cvrtM=as.matrix(covar),   
 snpspos=snpspos, genepos=genepos, outpf=sprintf("%s\_mEQTL.txt", rownames(exprj)[1]),   
 pvOutputThreshold=1e-300, pvOutputThreshold.csv=1, cisDist=1e9,  
 effNumGuess=nrow(g.ini)/4,  
 verbose=FALSE, pvalue.hist=FALSE, min.pv.by.genesnp = FALSE, noFDRsaveMemory=FALSE,  
 outdir="unreduced")  
#updNtests=sprintf("%s\_updtests.csv", rownames(exprj)[1])  
me = getPermP(permEst)

## 1 of 1 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 1,613 cis-eQTLs, 0 trans-eQTLs

## No significant associations were found.  
## 5

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 1 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 2 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 3 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 4 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 5 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 6 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 7 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 8 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 9 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 10 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 11 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 12 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 13 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 14 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 15 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 16 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 17 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 18 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 19 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 20 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 21 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 22 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 23 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 24 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 25 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 26 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 27 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 28 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 29 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 30 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 31 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 32 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 33 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 34 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 35 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 36 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 37 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 38 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 39 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 40 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 41 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 42 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 43 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 44 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 45 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 46 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 47 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 48 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 49 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 50 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 51 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 52 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 53 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 54 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 55 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 56 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 57 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 58 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 59 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 60 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 61 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 62 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 63 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 64 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 65 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 66 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 67 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 68 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 69 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 70 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 71 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 72 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 73 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 74 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 75 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 76 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 77 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 78 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 79 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 80 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 81 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 82 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 83 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 84 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 85 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 86 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 87 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 88 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 89 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 90 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 91 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 92 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 93 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 94 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 95 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 96 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 97 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 98 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 99 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 100 out of 100

## time per iter: 0.3439

## attempt 1: 0.52 and 0.01

## 1 47

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 1 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 2 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 3 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 4 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 5 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 6 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 7 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 8 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 9 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 10 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 11 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 12 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 13 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 14 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 15 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 16 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 17 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 18 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 19 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 20 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 21 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 22 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 23 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 24 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 25 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 26 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 27 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 28 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 29 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 30 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 31 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 32 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 33 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 34 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 35 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 36 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 37 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 38 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 39 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 40 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 41 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 42 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 43 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 44 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 45 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 46 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 47 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 48 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 49 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 50 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 51 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 52 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 53 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 54 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 55 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 56 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 57 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 58 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 59 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 60 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 61 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 62 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 63 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 64 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 65 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 66 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 67 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 68 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 69 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 70 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 71 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 72 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 73 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 74 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 75 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 76 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 77 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 78 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 79 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 80 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 81 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 82 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 83 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 84 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 85 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 86 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 87 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 88 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 89 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 90 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 91 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 92 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 93 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 94 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 95 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 96 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 97 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 98 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 99 out of 100

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 100 out of 100

## time per iter: 0.4123

## attempt 2: 0.285714285714286 and 0.0204081632653061

## 52 1 47 34.39

## 42 3 102 41.23

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 101 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 102 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 103 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 104 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 105 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 106 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 107 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 108 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 109 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 110 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 111 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 112 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 113 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 114 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 115 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 116 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 117 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 118 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 119 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 120 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 121 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 122 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 123 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 124 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 125 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 126 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 127 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 128 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 129 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 130 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 131 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 132 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 133 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 134 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 135 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 136 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 137 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 138 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 139 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 140 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 141 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 142 out of 1000

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## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 969 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 970 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 971 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 972 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 973 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 974 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 975 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 976 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 977 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 978 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 979 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 980 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 981 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 982 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 983 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 984 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 985 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 986 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 987 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 988 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 989 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 990 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 991 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 992 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 993 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 994 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 995 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 996 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 997 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 998 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 999 out of 1000

## 147 of 147 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 1000 out of 1000

## time per iter: 0.4417

## attempt 2: 0.0680272108843537 and 0.0136054421768707

names(me)

## [1] "summ" "tim" "vals" "mEQTL" "min.snp"

me$summ

## SNP gene beta t.stat p.value  
## 1 chr9\_520337\_T\_G\_b38 ENSG00000181404.15 0.9185603 14.08248 8.582963e-40  
## FDR BF TESTS chr snppos genestart geneend ntest  
## 1 1.384432e-36 3.46108e-37 403.25 9 520337 14521 25004 1613  
## TESTSupd pred.permGLM pred.permLM LM.i LM.s GLM.i GLM.s  
## 1 201.625 1.526859e-33 2.372658e-32 -2.126765 0.8639537 5.319358 -2.07036  
## numpts  
## 1 135

#if you ran eigenMT outside, you can use that result to get a better guess of effective number of tests  
#but it can be skipped, in that case  
#simple number of SNPs will be used as a proxy for initial guess of effective number of steps  
  
#now, same but imagine reduced effect size  
eigenMT = me$summ  
eigenMT$TESTS = eigenMT$TESTSupd  
gen.sub = me$min.snp  
redboot = get\_reduced\_boot(1, target.perm.ps=1e-2, i=1, mQTL.fit=eigenMT, expr.mat = permEst$geneM,   
 min.SNP=gen.sub, covars=permEst$cvrtM, nsam=ncol(gen.sub))  
permEstR = permEst  
permEstR$geneM = redboot  
rownames(permEstR$geneM) = rownames(permEst$geneM)  
  
permEstR$effNumGuess=eigenMT$TESTSupd   
permEstR$outdir="reduced"  
  
meR = getPermP(permEstR)

## 1 of 1 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 1,613 cis-eQTLs, 0 trans-eQTLs

## No significant associations were found.  
## 5

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 1 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 2 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 3 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 4 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 5 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 6 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 7 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 8 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 9 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 10 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 11 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 12 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 13 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 14 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 15 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 16 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 17 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 18 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 19 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 20 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 21 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 22 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 23 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 24 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 25 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 26 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 27 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 28 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 29 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 30 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 31 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 32 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 33 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 34 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 35 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 36 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 37 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 38 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 39 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 40 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 41 out of 100

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## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 42 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 43 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 44 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 45 out of 100

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## 1613 of 1613 SNPs matched

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## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

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## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 48 out of 100

## 100 of 100 genes matched

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## 49 out of 100

## 100 of 100 genes matched

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## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 50 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 51 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 52 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 53 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 54 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 55 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 56 out of 100

## 100 of 100 genes matched

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## 57 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 58 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 59 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 60 out of 100

## 100 of 100 genes matched

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## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 61 out of 100

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## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 63 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

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## 64 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 65 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 66 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 67 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 68 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 69 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 70 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 71 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 72 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 73 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 74 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 75 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 76 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 77 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 78 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 79 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 80 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 81 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 82 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 83 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 84 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 85 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 86 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 87 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 88 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 89 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 90 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 91 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 92 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 93 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 94 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 95 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 96 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 97 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 98 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 99 out of 100

## 100 of 100 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 100 out of 100

## time per iter: 0.3385

## attempt 1: 0.32 and 0.02

## 1 66

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 1 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 2 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 3 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 4 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 5 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 6 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 7 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 8 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 9 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 10 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 11 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 12 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 13 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 14 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 15 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 16 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 17 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 18 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

## 19 out of 100

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

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## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

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## 166 of 166 genes matched

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## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

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## time per iter: 0.7037

## attempt 2: 0.283132530120482 and 0.0240963855421687

## 32 2 66 33.85

## 47 4 115 70.37

## 166 of 166 genes matched

## 1613 of 1613 SNPs matched

## 100.00% done, 0 cis-eQTLs, 0 trans-eQTLs

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## 1000 out of 1000

## time per iter: 0.50158

## attempt 2: 0.0240963855421687 and 0.0180722891566265

meR$summ

## SNP gene beta t.stat p.value  
## 1 chr9\_521172\_A\_C\_b38 ENSG00000181404.15 0.2772655 4.39478 1.282664e-05  
## FDR BF TESTS chr snppos genestart geneend ntest  
## 1 0.008789618 0.002586172 201.625 9 521172 14521 25004 1613  
## TESTSupd pred.permGLM pred.permLM LM.i LM.s GLM.i GLM.s  
## 1 201.625 0.007402141 0.007182481 -2.207039 0.8893836 5.605652 -2.147271  
## numpts  
## 1 159

Lets illustrate calculation of permutation p-value estimate. We take the values generated in step4\_runboot.R and fit glm predicting probability of observing more extreme result (then observed in bootstrap) by log10(minimum p-value). After fitting glm, predict permutation p-value based on log10(minimum p-value) Effective number of tests will be ratio of predicted permutation p-value and minimum p-value (trimmed between 1 and number of SNPs)

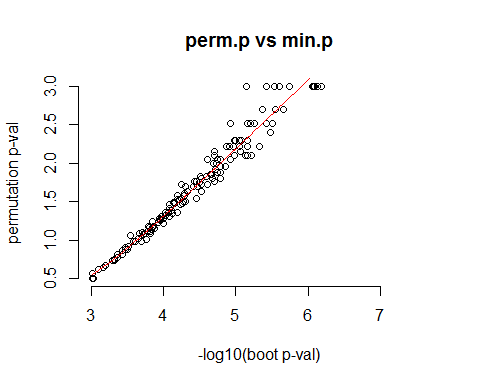
#boots = read.csv(sprintf("%s/short\_boot\_pval\_9\_1.csv", perm.dir), as.is=T)  
#eigenMT = read.csv(sprintf("%s/upd\_eigenMT\_9\_1.csv", out.dir), as.is=T)  
nperm = 1000  
y = me$vals$permp\*nperm  
pvalb = me$vals$pvalb  
kp3 = (y/nperm)>=0 & (y/nperm)<=0.3  
kp3a = (y/nperm)>0 & (y/nperm)<=0.3  
   
y1 = log10(y/nperm)  
x1 = log10(pvalb)  
glmi3 = glm(cbind(y[kp3],nperm-y[kp3])~x1[kp3], family="binomial")  
summary(glmi3)

##   
## Call:  
## glm(formula = cbind(y[kp3], nperm - y[kp3]) ~ x1[kp3], family = "binomial")  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -3.05450 -0.64409 -0.05165 0.49232 2.25401   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 5.31936 0.10488 50.72 <2e-16 \*\*\*  
## x1[kp3] 2.07036 0.02768 74.80 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 8722.30 on 144 degrees of freedom  
## Residual deviance: 124.67 on 143 degrees of freedom  
## AIC: 773.55  
##   
## Number of Fisher Scoring iterations: 4

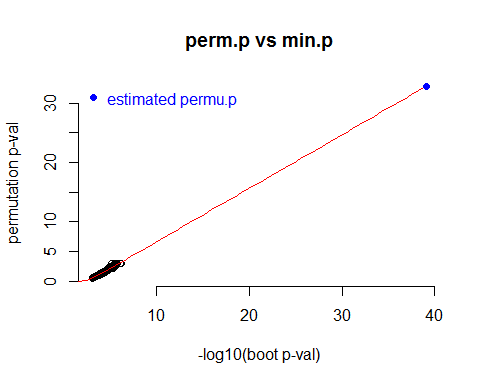
xval = log10(eigenMT$p.value)  
pred.perm = logiti(glmi3$coef[1]+glmi3$coef[2]\*xval)  
c(xval, pred.perm)

## (Intercept)   
## -3.906636e+01 1.526859e-33

xlim = range(-c(x1, xval))  
ylim = range(-log10(y/nperm))  
ylim[2] = -log10(pred.perm)  
  
plot(-x1, -log10(y/nperm), xlab="-log10(boot p-val)", ylab="permutation p-val", bty="n", main="perm.p vs min.p")  
o = order(x1[kp3])  
xf = x1[kp3][o]  
yf = glmi3$fitted.values[o]  
lines(-xf, -log10(yf), col="red")



fit = seq(0, xval, length.out=50)  
pred.perm0 = logiti(glmi3$coef[1]+glmi3$coef[2]\*fit)  
plot(-x1, -log10(y/nperm), xlab="-log10(boot p-val)", ylab="permutation p-val", bty="n", main="perm.p vs min.p", xlim=xlim,ylim=ylim)  
lines(-fit, -log10(pred.perm0), col="red")  
points(-xval, -log10(pred.perm), col="blue", cex=1, pch=19)  
legend("topleft", "estimated permu.p", text.col="blue", pch=19, col="blue", bty="n")



Or using less extreme efect size: Lets illustrate calculation of permutation p-value estimate. We take the values generated in step4\_runboot.R and fit glm predicting probability of observing more extreme result (then observed in bootstrap) by log10(minimum p-value). After fitting glm, predict permutation p-value based on log10(minimum p-value) Effective number of tests will be ratio of predicted permutation p-value and minimum p-value (trimmed between 1 and number of SNPs)

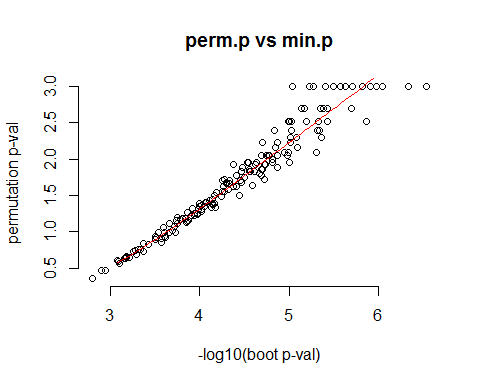
nperm = 1000  
eigenMT = meR$summ  
y = meR$vals$permp\*nperm  
pvalb = meR$vals$pvalb  
kp3 = (y/nperm)>=0 & (y/nperm)<=0.3  
kp3a = (y/nperm)>0 & (y/nperm)<=0.3  
   
y1 = log10(y/nperm)  
x1 = log10(pvalb)  
glmi3 = glm(cbind(y[kp3],nperm-y[kp3])~x1[kp3], family="binomial")  
summary(glmi3)

##   
## Call:  
## glm(formula = cbind(y[kp3], nperm - y[kp3]) ~ x1[kp3], family = "binomial")  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -2.56893 -0.77416 -0.03343 0.68899 2.69706   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 5.60565 0.09047 61.96 <2e-16 \*\*\*  
## x1[kp3] 2.14727 0.02442 87.92 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 11853.9 on 162 degrees of freedom  
## Residual deviance: 203.2 on 161 degrees of freedom  
## AIC: 965.49  
##   
## Number of Fisher Scoring iterations: 4

xval = log10(eigenMT$p.value)  
pred.perm = logiti(glmi3$coef[1]+glmi3$coef[2]\*xval)  
c(xval, pred.perm)

## (Intercept)   
## -4.891887051 0.007402141

xlim = range(-c(x1, xval))  
ylim = range(-log10(y/nperm))  
ylim[2] = -log10(pred.perm)  
  
plot(-x1, -log10(y/nperm), xlab="-log10(boot p-val)", ylab="permutation p-val", bty="n", main="perm.p vs min.p")  
o = order(x1[kp3])  
xf = x1[kp3][o]  
yf = glmi3$fitted.values[o]  
lines(-xf, -log10(yf), col="red")



fit = seq(0, xval, length.out=50)  
pred.perm0 = logiti(glmi3$coef[1]+glmi3$coef[2]\*fit)  
plot(-x1, -log10(y/nperm), xlab="-log10(boot p-val)", ylab="permutation p-val", bty="n", main="perm.p vs min.p", xlim=xlim,ylim=ylim)  
lines(-fit, -log10(pred.perm0), col="red")  
points(-xval, -log10(pred.perm), col="blue", cex=1, pch=19)  
legend("topleft", "estimated permu.p", text.col="blue", pch=19, col="blue", bty="n")

