Running DMR code procedure

1. Run DMR.m

Input to program:

Change these in DMR.m accordingly:

1. Infinium 450K data in original format [j1 = GSE30870\_dmr.csv; name of test file = GSE30870\_sub.csv]

1. Phenotype [variable: pheno]

\*GSE30870\_dmr are 2 newborns versus 2 nonagenarian dataset from Heyn *et al.*

Optional changes:

1. Number of simulations for null distribution [in get\_permu.m change nS=50]

DMR.m program output

1. AAREA

: Area of region (test statistic)

1. DIFF

: Length of region

1. CRR

: Region’s chromosome number

1. Sstart

: Chromosome start position of region

1. HOWpr

: Number of probes in region

1. GGENE

: Genes covered by chromosomal position of DMR

1. CCPG

: CpGs covered by chromosomal position of DMR

1. p

: p-value of region

1. q

: q-value of region

Running VMR code procedure

*Run all in the same directory*

1. Run VMR.m
2. Run VMR\_simu\_1.m
   1. Generate cluster\_vmr.csv and tt\_vmr.csv
3. Run R code burg\_code.R
   1. Generate coef.csv and stddev.csv
4. Run VMR\_simu\_2.m

Input to program:

Change these in VMR.m accordingly:

Infinium 450K data in original format [j1=load('GSE30870\_vmr.csv'); j1=j1(2:485578,:); name of test file = GSE30870\_1.csv]

\*GSE30870\_vmr are 4 nonagenarians from Heyn *et al.*

Optional changes:

1. Number of simulations for null distribution [in vmr\_get\_permu.m change nS=50]

VMR.m program output

1. AAREA

: Area of region (test statistic)

1. DIFF

: Length of region

1. CRR

: Region’s chromosome number

1. Sstart

: Chromosome start position of region

1. HOWpr

: Number of probes in region

1. GGENE

: Genes covered by chromosomal position of DMR

1. CCPG

: CpGs covered by chromosomal position of DMR

1. p

: p-value of region

1. q

: q-value of region