

yriMulti – HapMap YRI population, multiassay interfaces

Vincent J. Carey, *stvjc at channing.harvard.edu*

May 2016

Contents

1	Introduction	1
2	Basic data resources	1
2.1	Expression data	1
2.2	Methylation data	2
2.3	DnaseI hypersensitivity data	2
2.4	Genotype data	2
3	Some computations focused on methylation-expression association	3
3.1	Gene-centric selection	4
3.2	DNA-methylation association with expression	4
4	Using the MultiAssayExperiment infrastructure	5
4.1	Construction of the MultiAssayExperiment	6
4.2	Restriction by range	6
4.3	All pairwise regressions	7
4.4	Integrating dense genotypes in a VcfStack instance	10

1 Introduction

The EBV-transformed B-cells from Yoruban donors are assayed for genotype and various genomic features in a number of prominent studies. This package helps work with relevant datasets and data structures as use cases for MultiAssayExperiment package development. A particular concern is accommodation of distributed genotype data, in this case, based on the 1000 genomes VCF files in an S3 bucket.

2 Basic data resources

2.1 Expression data

We will use the RNA-seq expression data in the *geuvPack* package.

```
library(geuvPack)
data(geuFPKM)
```

```
geuFPKM
## class: RangedSummarizedExperiment
## dim: 23722 462
## metadata(3): MIAME constrHist colDataSource
## assays(1): exprs
## rownames(23722): ENSG00000152931.6 ENSG00000183696.9 ...
## ENSG00000257337.1 ENSG00000177494.5
## rowData names(18): source type ... tag ccidsid
```

```
## colnames(462): HG00096 HG00097 ... NA20826 NA20828
## colData names(35): Source.Name Comment.ENA_SAMPLE. ...
##   Factor.Value.laboratory. popcode
```

2.2 Methylation data

We have added 450k data from Banovich, Lan, McVicker, van de Geijn, Degner, Blischak, Roux, Pritchard, and Gilad (2014) paper to the yriMulti package.

```
library(yriMulti)
data(banovichSE)
```

```
banovichSE
## class: RangedSummarizedExperiment
## dim: 329469 64
## metadata(0):
## assays(1): betas
## rownames(329469): cg00000029 cg00000165 ... ch.9.98989607R
##   ch.9.991104F
## rowData names(10): addressA addressB ... probeEnd probeTarget
## colnames(64): NA18498 NA18499 ... NA18489 NA18909
## colData names(35): title geo_accession ... data_row_count naid
```

2.3 Dnase hypersensitivity data

```
library(dsQTL)
if (!exists("DHStop5_hg19")) data(DHStop5_hg19)
```

```
DHStop5_hg19
## class: RangedSummarizedExperiment
## dim: 1465442 70
## metadata(2): MIAME annotation
## assays(1): scores
## rownames(1465442): dhs_chr1_10402 dhs_chr1_10502 ...
##   dhs_chr22_51228236 dhs_chr22_51234736
## rowData names(0):
## colnames(70): NA18486 NA18498 ... NA19239 NA19257
## colData names(9): naid one ... male isFounder
```

2.4 Genotype data

We take advantage of a function (`gtpath`) that generates paths to S3-resident VCF from the 1000 genomes project.

```
litvcf = readVcf(gtpath(20),
  param=ScanVcfParam(which=GRanges("20",
    IRanges(3.7e7,3.701e7))), genome="hg19")
```

```
litvcf
## class: CollapsedVCF
## dim: 347 2504
## rowRanges(vcf):
##   GRanges with 5 metadata columns: paramRangeID, REF, ALT, QUAL, FILTER
```

```
## info(vcf):
##   DataFrame with 27 columns: CIEND, CIPOS, CS, END, IMPRECISE, MC, MEIN...
## info(header(vcf)):
##           Number Type   Description
##   CIEND      2      Integer Confidence interval around END for impr...
##   CIPOS      2      Integer Confidence interval around POS for impr...
##   CS         1      String   Source call set.
##   END        1      Integer End coordinate of this variant
##   IMPRECISE  0      Flag     Imprecise structural variation
##   MC         .      String   Merged calls.
##   MEINFO     4      String   Mobile element info of the form NAME,ST...
##   MEND       1      Integer Mitochondrial end coordinate of inserte...
##   MLEN       1      Integer Estimated length of mitochondrial insert
##   MSTART     1      Integer Mitochondrial start coordinate of inser...
##   SVLEN      .      Integer SV length. It is only calculated for st...
##   SVTYPE     1      String   Type of structural variant
##   TSD        1      String   Precise Target Site Duplication for bas...
##   AC         A      Integer Total number of alternate alleles in ca...
##   AF         A      Float   Estimated allele frequency in the range...
##   NS         1      Integer Number of samples with data
##   AN         1      Integer Total number of alleles in called genot...
##   EAS_AF     A      Float   Allele frequency in the EAS populations...
##   EUR_AF     A      Float   Allele frequency in the EUR populations...
##   AFR_AF     A      Float   Allele frequency in the AFR populations...
##   AMR_AF     A      Float   Allele frequency in the AMR populations...
##   SAS_AF     A      Float   Allele frequency in the SAS populations...
##   DP         1      Integer Total read depth; only low coverage dat...
##   AA         1      String   Ancestral Allele. Format: AA|REF|ALT|In...
##   VT         .      String   indicates what type of variant the line...
##   EX_TARGET  0      Flag     indicates whether a variant is within t...
##   MULTI_ALLELIC 0      Flag     indicates whether a site is multi-allelic
## geno(vcf):
##   SimpleList of length 1: GT
## geno(header(vcf)):
##           Number Type   Description
##   GT      1      String Genotype
length(colnames(litvcf))
## [1] 2504
length(intersect(colnames(litvcf), colnames(banovichSE)))
## [1] 52
length(intersect(colnames(litvcf), colnames(geuFPKM)))
## [1] 445
length(intersect(colnames(litvcf), colnames(DHStop5_hg19)))
## [1] 59
```

3 Some computations focused on methylation-expression association

The yriMulti package is currently a scratch-pad for some integrative infrastructure thoughts.

3.1 Gene-centric selection

With `mexGR`, a `GRanges` instance is formed with methylation scores for CpG near a gene. The assay data are placed in the `mcols`, with one range devoted to the expression measures.

```
m1 = mexGR(banovichSE, geuFPKM, symbol="ORMDL3")
m1
## mexGR instance with 44 metadata columns:
## NA18498, NA18499, ..., NA18909, type
## and 7 ranges
mcols(m1)[1:4,1:4]
## DataFrame with 4 rows and 4 columns
##      NA18498  NA18499  NA18502  NA18517
##      <numeric> <numeric> <numeric> <numeric>
## 1 -0.5920581 -0.1775026 -0.00553931 -1.5660101
## 2 -0.4633549  0.2876612  0.55386303 -1.0968065
## 3 -0.2245340 -1.1792216  1.09071357  0.4539331
## 4 -0.1583621 -0.8991156  1.02087023  0.5399715
table(mcols(m1)$type)
##
## expr meth
##      1      6
```

3.2 DNA-methylation association with expression

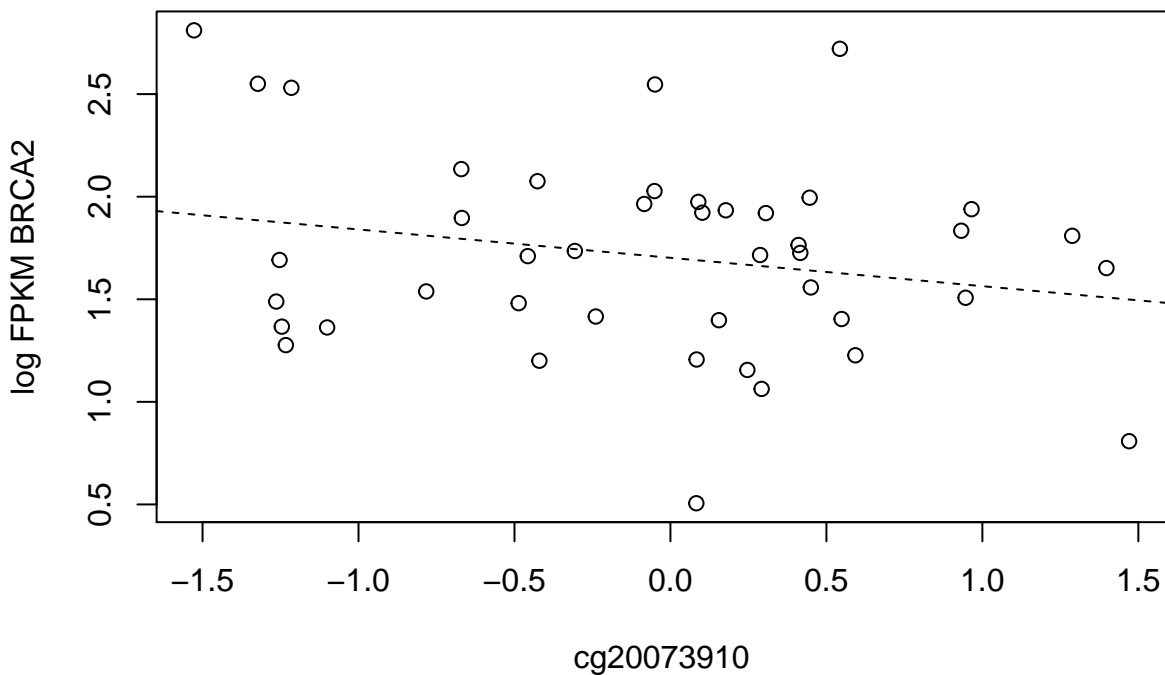
`bindelms` computes the regressions of the selected gene's expression values on the methylation scores. We have options to transform the expression value (parameter `ytx` is a function) and can indicate the radius around the gene coding region to search for CpG (parameter `gradius`).

We'll examine a region around gene `BRCA2` for a CpG whose methylation score is negatively associated with `BRCA2` expression.

```
b1 = bindelms(geuFPKM, banovichSE, symbol="BRCA2", ytx=log,
             gradius=20000)
b1
## class: RangedSummarizedExperiment
## dim: 29 43
## metadata(6): theCall symbol ... pwd txexpr
## assays(1): betas
## rownames(29): cg00031759 cg00214044 ... cg26458617 cg26941801
## rowData names(15): addressA addressB ... t p
## colnames(43): NA18498 NA18499 ... NA18489 NA18909
## colData names(35): title geo_accession ... data_row_count naid
mcols(b1)[1:3,]
## DataFrame with 3 rows and 15 columns
##      addressA  addressB channel platform percentGC
##      <character> <character> <Rle> <Rle> <numeric>
## 1 11602350          Both    HM450    0.50
## 2 33707391          Both    HM450    0.62
## 3 12675375          Both    HM450    0.54
##           sourceSeq probeType  probeStart  probeEnd probeTarget
##           <DNAStringSet> <Rle> <character> <character> <numeric>
## 1 CGGGTATTTTC...GCATCCCAAC      cg    32889486    32889535    32889534
## 2 CGGGCACCAG...ACCCATATTT      cg    32885906    32885955    32885906
```

```
## 3 GCCCACCTGA...TTCATTCCCG      cg      32984237      32984286      32984237
##
##
## 1 c(1.71061243102637, 0.00740906714807691),c(0.219325797562873, 1.01220892062976, -0.547746926935716, 0
## 2 c(1.70619587753478, 0.0396189079256385),c(0.233507135447547, 1.02347152679434, -0.564098505822397, 0
## 3 c(1.71120579164398, -0.0241223781711239),c(0.216715043465388, 0.982080901541917, -0.5555072909
##      slope      se      t      p
##      <numeric> <numeric> <numeric> <numeric>
## 1 0.007409067 0.10065080 0.07361161 0.9416774
## 2 0.039618908 0.10276459 0.38553072 0.7018374
## 3 -0.024122378 0.08494654 -0.28397129 0.7778616
summary(mcols(b1)$t)
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.
## -1.4740 -0.3809  0.3426  0.2091  0.5894  1.6640
mintind = which.min(mcols(b1)$t)
mincpgr = names(b1)[mintind]
mincpgr
## [1] "cg20073910"
```

```
plotEvM(b1)
```



4 Using the MultiAssayExperiment infrastructure

4.1 Construction of the MultiAssayExperiment

We will use a unified object design to reproduce the BRCA2 display just obtained.

We need a list of relevant objects and a phenodata component.

```
library(MultiAssayExperiment)
myobjs = list(geuvRNAseq=geuFPKM, yri450k=banovichSE, yriDHS=DHStop5_hg19)
cold = colData(geuFPKM)
suppressWarnings({
  library(MultiAssayExperiment)
  mm = MultiAssayExperiment(myobjs, as.data.frame(cold))
})
mm
## A MultiAssayExperiment object of 3 listed
## experiments with user-defined names and respective classes.
## Containing an ExperimentList class object of length 3:
## [1] geuvRNAseq: RangedSummarizedExperiment with 23722 rows and 462 columns
## [2] yri450k: RangedSummarizedExperiment with 329469 rows and 43 columns
## [3] yriDHS: RangedSummarizedExperiment with 1465442 rows and 50 columns
## To access:
## experiments() - to obtain the ExperimentList instance
## pData() - for the primary/phenotype DataFrame
## sampleMap() - for the sample availability DataFrame
## metadata() - for the metadata object of ANY class
## See also: subsetByAssay(), subsetByRow(), subsetByColumn()
```

4.2 Restriction by range

We compute the BRCA2 'gene range'.

```
library(erma)
brr = range(genemodel("BRCA2"))
## 'select()' returned 1:many mapping between keys and columns
brr
## GRanges object with 1 range and 0 metadata columns:
##      seqnames          ranges strand
##      <Rle>             <IRanges> <Rle>
## [1] chr13 [32889617, 32973809] +
## -----
## seqinfo: 1 sequence from hg19 genome
```

Subset the multiassay structure to features in the vicinity of this range.

```
.subsetByRanges = function(ma, r) {
  subsetByRow(ma,r)
}
newmm = .subsetByRanges(mm, brr+20000)
newmm
## A MultiAssayExperiment object of 3 listed
## experiments with user-defined names and respective classes.
## Containing an ExperimentList class object of length 3:
## [1] geuvRNAseq: RangedSummarizedExperiment with 3 rows and 462 columns
## [2] yri450k: RangedSummarizedExperiment with 29 rows and 43 columns
## [3] yriDHS: RangedSummarizedExperiment with 32 rows and 50 columns
```

```
## To access:
## experiments() - to obtain the ExperimentList instance
## pData() - for the primary/phenotype DataFrame
## sampleMap() - for the sample availability DataFrame
## metadata() - for the metadata object of ANY class
## See also: subsetByAssay(), subsetByRow(), subsetByColumn()
```

We now have all the relevant features and samples. In fact we have more genes than we really wanted. But we will proceed with this selection.

4.3 All pairwise regressions

We will introduce a formula idiom to specify a collection of models of interest.

```
library(doParallel)
## Loading required package: foreach
## Loading required package: iterators
registerDoSEQ()
allLM_pw = function(fmla, mae, xtx=force, ytx=force) {
#
# formula specifies dependent and independent assays
# form all regressions of ytx(dep) on xtx(indep) for all
# pairs of dependent and independent variables defined by
# assays for samples held in common
#
lf = as.list(fmla)
nms = lapply(lf, as.character)
yel = experiments(mae)[[nms[[2]]]]
xel = experiments(mae)[[nms[[3]]]]
sy = colnames(yel)
sx = colnames(xel)
sb = intersect(sy,sx)
yel = yel[,sb]
xel = xel[,sb]
vdf = as.matrix(expand.grid(rownames(yel),
rownames(xel), stringsAsFactors=FALSE ))
allf = apply(vdf, 1, function(x) as.formula(paste(x, collapse="~")))
alllm = foreach (i = 1:length(allf)) %dopar% {
df = data.frame(ytx(assay(yel)[vdf[i,1],]), xtx(assay(xel)[vdf[i,2],]))
names(df) = vdf[i,]
lm(allf[[i]], data=df)
}
names(alllm) = apply(vdf,1,function(x) paste(x, collapse="~"))
allts = lapply(alllm, function(x) summary(x)$coef[2, "t value"])
list(mods=alllm, tslopes=allts)
}
pwplot = function(fmla1, fmla2, mae, ytx=force, xtx=force, ...) {
#
# use fmla1 with assays as components to identify
# two assays to regard as sources of y and x
# fmla2 indicates which features to plot
#
lf = as.list(fmla1)
```



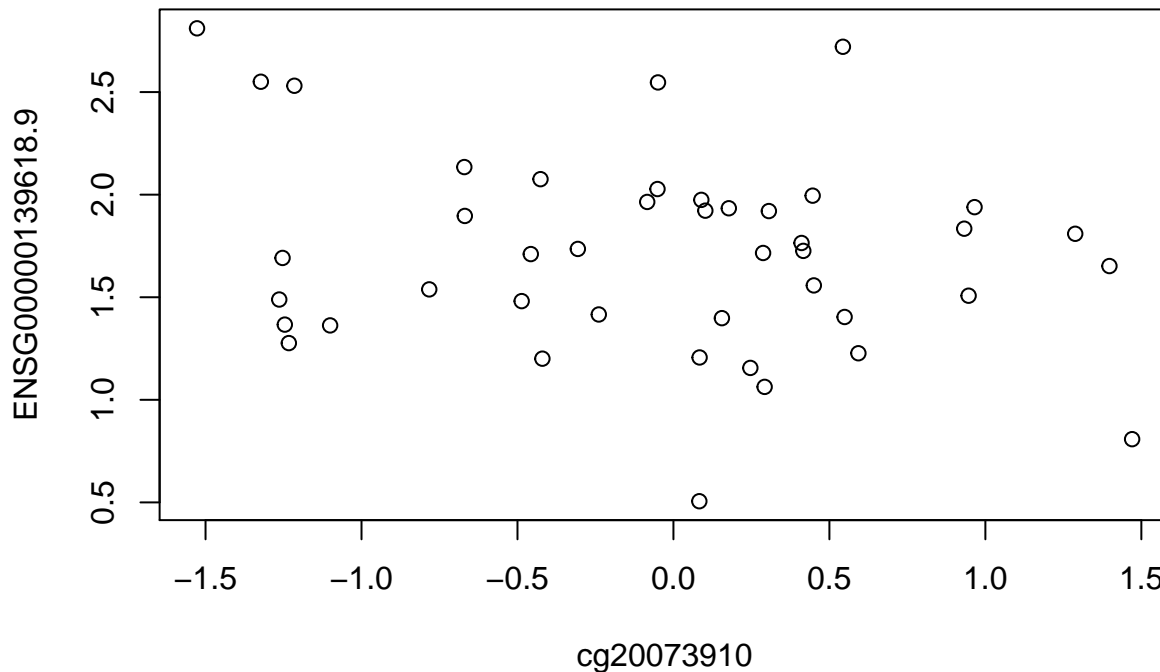
```

## Warning in ytx(assay(yel)[vdf[i, 1], ]): NaNs produced
## Warning in ytx(assay(yel)[vdf[i, 1], ]): NaNs produced
## Warning in ytx(assay(yel)[vdf[i, 1], ]): NaNs produced
## Warning in ytx(assay(yel)[vdf[i, 1], ]): NaNs produced
## Warning in ytx(assay(yel)[vdf[i, 1], ]): NaNs produced
## Warning in ytx(assay(yel)[vdf[i, 1], ]): NaNs produced
## Warning in ytx(assay(yel)[vdf[i, 1], ]): NaNs produced
## Warning in ytx(assay(yel)[vdf[i, 1], ]): NaNs produced
## Warning in ytx(assay(yel)[vdf[i, 1], ]): NaNs produced
## Warning in ytx(assay(yel)[vdf[i, 1], ]): NaNs produced
names(pp)
## [1] "mods"      "tslopes"
summary(pp[[1]][[1]])
##
## Call:
## lm(formula = allf[[i]], data = df)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.20112 -0.30856  0.00553  0.24330  1.10330
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.710612   0.074777  22.876  <2e-16 ***
## cg00031759   0.007409   0.100651   0.074   0.942
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4898 on 41 degrees of freedom
## Multiple R-squared:  0.0001321, Adjusted R-squared:  -0.02425
## F-statistic: 0.005419 on 1 and 41 DF,  p-value: 0.9417
which.min(unlist(pp[[2]])) # not BRCA2 but FRY
## ENSG0000073910.13~cg05918473
##
##              23

```

The formula idiom can be used to isolate assays and features.

```
pwplot(geuvRNAseq~yri450k, ENSG00000139618.9~cg20073910, newmm, ytx=log)
```



4.4 Integrating dense genotypes in a VcfStack instance

We set up a reference to a collection of VCF. We'll use 1000 genomes VCF for chr21, and chr22. At present (16 Oct 2016) chrY must be kept out of the stack as it does not have the full set of samples for other chromosomes.

```
library(gQTLstats)
library(VariantAnnotation)
library(GenomicFiles)
## Loading required package: BiocParallel
## Loading required package: rtracklayer
##
## Attaching package: 'GenomicFiles'
## The following objects are masked from 'package:Matrix':
##
##   pack, unpack
pa = paths1kg(paste0("chr", c(21:22))) #,"Y"))
sn = vcfSamples(scanVcfHeader(TabixFile(pa[1])))
library(Homo.sapiens) # necessary?
stopifnot(requireNamespace("GenomeInfoDb"))
ob = RangedVcfStack(VcfStack(pa, seqinfo(Homo.sapiens)))
cd = DataFrame(id1kg=sn)
rownames(cd) = sn
colData(ob) = cd
```

Now we set up a region of interest and bind it to the stack. This yields an instance of RangedVcfStack, for which we have samples, features, and assay methods defined in gQTLstats.

```

myr = GRanges("chr22", IRanges(20e6,20.01e6))
rowRanges(ob) = myr
colData(ob) = DataFrame(colData(ob), zz=runif(nrow(colData(ob))))
hasInternetConnectivity = function()
  !is.null(nsl("www.r-project.org"))
#if (hasInternetConnectivity()) lka = assay(ob)
myobs = list(geuvRNAseq=geuFPKM, yri450k=banovichSE, yriDHS=DHStop5_hg19,
  yriGeno=ob)
suppressWarnings({
mm = MultiAssayExperiment(myobs)
})
mm
## A MultiAssayExperiment object of 4 listed
## experiments with user-defined names and respective classes.
## Containing an ExperimentList class object of length 4:
## [1] geuvRNAseq: RangedSummarizedExperiment with 23722 rows and 462 columns
## [2] yri450k: RangedSummarizedExperiment with 329469 rows and 64 columns
## [3] yriDHS: RangedSummarizedExperiment with 1465442 rows and 70 columns
## [4] yriGeno: RangedVcfStack with 2 rows and 2504 columns
## To access:
## experiments() - to obtain the ExperimentList instance
## pData() - for the primary/phenotype DataFrame
## sampleMap() - for the sample availability DataFrame
## metadata() - for the metadata object of ANY class
## See also: subsetByAssay(), subsetByRow(), subsetByColumn()

```

References

[1] N. E. Banovich, X. Lan, G. McVicker, et al. "Methylation QTLs Are Associated with Coordinated Changes in Transcription Factor Binding, Histone Modifications, and Gene Expression Levels". In: *PLoS Genetics* 10.9 (2014), p. e1004663. ISSN: 1553-7404. DOI: 10.1371/journal.pgen.1004663. <URL: <http://dx.plos.org/10.1371/journal.pgen.1004663>>.