

# Package ‘yriMulti’

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**Title** support for expression, methylation, DHS, VCF for YRI

**Version** 0.16.0

**Author** VJ Carey <stvjc@channing.harvard.edu>

**Description** expression, methylation, DHS for YRI

**Suggests** erma, BiocStyle, knitr, rmarkdown, gQTLstats (>= 1.9.2), doParallel, geuvPack, knitcitations, bibtex

**Imports** GenomicFiles (>= 1.13.6), VariantAnnotation (>= 1.23.1), gQTLBase, SummarizedExperiment, GenomicRanges, dsQTL, GenomeInfoDb

**Depends** Homo.sapiens, geuvPack, MultiAssayExperiment (>= 1.3.14)

**Maintainer** VJ Carey <stvjc@channing.harvard.edu>

**License** Artistic-2.0

**LazyLoad** yes

**VignetteBuilder** knitr

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yriMulti-package      *support for expression, methylation, DHS, VCF for YRI*

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### Description

expression, methylation, DHS for YRI

### Details

The DESCRIPTION file: This package was not yet installed at build time.

Index: This package was not yet installed at build time.

This is a relatively experimental package that is used to exercise aspects of MultiAssayExperiment and gQTLstats. The primary innovations are illustration of VcfStack class of GenomicFiles as a distributed on-disk (or in-cloud) resource for assay elements representing genotypes, and adoption of MultiAssayExperiment to unite relatively uncommonly integrated assays such as DnaseI hypersensitivity and 450k methylation.

### Author(s)

VJ Carey <stvjc@channing.harvard.edu>

Maintainer: VJ Carey <stvjc@channing.harvard.edu>

### Examples

```
# see the vignette
```

---

banovichSE      *Illumina 450k methylation assay applied to Yoruba cell lines*

---

### Description

Illumina 450k methylation assay applied to Yoruba cell lines

### Usage

```
data("banovichSE")
```

### Format

The format is:

```
Formal class 'RangedSummarizedExperiment' [package "SummarizedExperiment"] with 6 slots
..@ rowRanges :Formal class 'GRanges' [package "GenomicRanges"] with 6 slots
.. ..@ seqnames :Formal class 'Rle' [package "S4Vectors"] with 4 slots
.. .. ..@ values : Factor w/ 24 levels "chr1","chr2",...: 16 1 8 14 1 15 19 3 12 15 ...
.. .. ..@ lengths : int [1:301401] 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..@ elementMetadata: NULL
.. .. ..@ metadata : list()
```

```

.. ..@ ranges :Formal class 'IRanges' [package "IRanges"] with 6 slots
.. ..@ start : int [1:329469] 53468112 91194674 42263294 69341139 230560793 23034447
54695678 128902377 124086477 59785306 ...
.. ..@ width : int [1:329469] 2 2 2 2 2 2 2 2 ...
.. ..@ NAMES : chr [1:329469] "cg00000029" "cg00000165" "cg00000236" "cg00000289"
...
.. ..@ elementType : chr "integer"
.. ..@ elementMetadata: NULL
.. ..@ metadata : list()
.. ..@ strand :Formal class 'Rle' [package "S4Vectors"] with 4 slots
.. ..@ values : Factor w/ 3 levels "+","-","*": 3
.. ..@ lengths : int 329469
.. ..@ elementMetadata: NULL
.. ..@ metadata : list()
.. ..@ elementMetadata:Formal class 'DataFrame' [package "S4Vectors"] with 6 slots
.. ..@ rownames : NULL
.. ..@ nrows : int 329469
.. ..@ listData :List of 10
.. ..$ addressA : chr [1:329469] "14782418" "12637463" "12649348" "18766346" ...
.. ..$ addressB : chr [1:329469] "" "" "" "" ...
.. ..$ channel :Formal class 'Rle' [package "S4Vectors"] with 4 slots
.. ..@ values : Factor w/ 3 levels "Both","Grn","Red": 1 3 1 2 1 2 1 3 1 2 ...
.. ..@ lengths : int [1:140453] 5 1 2 1 3 1 1 1 2 1 ...
.. ..@ elementMetadata: NULL
.. ..@ metadata : list()
.. ..$ platform :Formal class 'Rle' [package "S4Vectors"] with 4 slots
.. ..@ values : Factor w/ 2 levels "BOTH","HM450": 2 1 2 1 2 1 2 1 2 1 ...
.. ..@ lengths : int [1:35429] 38 1 31 1 41 1 19 1 8 1 ...
.. ..@ elementMetadata: NULL
.. ..@ metadata : list()
.. ..$ percentGC : num [1:329469] 0.46 0.48 0.5 0.44 0.42 0.8 0.6 0.58 0.78 0.54 ...
.. ..$ sourceSeq :Formal class 'DNAStringSet' [package "Biostrings"] with 5 slots
.. ..@ pool :Formal class 'SharedRaw_Pool' [package "XVector"] with 2 slots
.. ..@ xp_list :List of 1
.. ..$ :<externalptr>
.. ..@ .link_to_cached_object_list:List of 1
.. ..$ :<environment: 0x7f87a4476990>
.. ..@ ranges :Formal class 'GroupedIRanges' [package "XVector"] with 7 slots
.. ..@ group : int [1:329469] 1 1 1 1 1 1 1 1 1 ...
.. ..@ start : int [1:329469] 1 151 201 251 401 451 551 651 701 851 ...
.. ..@ width : int [1:329469] 50 50 50 50 50 50 50 50 50 ...
.. ..@ NAMES : NULL
.. ..@ elementType : chr "integer"
.. ..@ elementMetadata: NULL
.. ..@ metadata : list()
.. ..@ elementType : chr "DNAString"
.. ..@ elementMetadata: NULL
.. ..@ metadata : list()
.. ..$ probeType :Formal class 'Rle' [package "S4Vectors"] with 4 slots
.. ..@ values : Factor w/ 3 levels "cg","ch","rs": 1 2
.. ..@ lengths : int [1:2] 327286 2183
.. ..@ elementMetadata: NULL

```

```

.. .. .. .. ..@ metadata : list()
.. .. .. .. ..$ probeStart : chr [1:329469] "53468112" "91194626" "42263246" "69341139" ...
.. .. .. .. ..$ probeEnd : chr [1:329469] "53468161" "91194675" "42263295" "69341188" ...
.. .. .. .. ..$ probeTarget: num [1:329469] 5.35e+07 9.12e+07 4.23e+07 6.93e+07 2.31e+08 ...
.. .. .. .. ..@ elementType : chr "ANY"
.. .. .. .. ..@ elementMetadata: NULL
.. .. .. .. ..@ metadata : list()
.. .. .. ..@ seqinfo :Formal class 'Seqinfo' [package "GenomeInfoDb"] with 4 slots
.. .. .. ..@ seqnames : chr [1:24] "chr1" "chr2" "chr3" "chr4" ...
.. .. .. ..@ seqlengths : int [1:24] 249250621 243199373 198022430 191154276 180915260
171115067 159138663 146364022 141213431 135534747 ...
.. .. .. ..@ is_circular: logi [1:24] FALSE FALSE FALSE FALSE FALSE FALSE ...
.. .. .. ..@ genome : chr [1:24] "hg19" "hg19" "hg19" "hg19" ...
.. .. ..@ metadata :List of 1
.. .. .. ..$ :Formal class 'DataFrame' [package "S4Vectors"] with 6 slots
.. .. .. ..@ rownames : NULL
.. .. .. ..@ nrows : int 13
.. .. .. ..@ listData :List of 2
.. .. .. .. ..$ name : chr [1:13] "Db type" "Supporting package" "data_nrow" "Db created by" ...
.. .. .. .. ..$ value: chr [1:13] "FeatureDb" "GenomicFeatures" "487173" "GenomicFeatures
package from Bioconductor" ...
.. .. .. ..@ elementType : chr "ANY"
.. .. .. ..@ elementMetadata: NULL
.. .. .. ..@ metadata : list()
..@ colData :Formal class 'DataFrame' [package "S4Vectors"] with 6 slots
.. .. ..@ rownames : chr [1:64] "NA18498" "NA18499" "NA18501" "NA18502" ...
.. .. ..@ nrows : int 64
.. .. ..@ listData :List of 35
.. .. .. ..$ title : Factor w/ 64 levels "GM18489","GM18498",...: 2 3 4 5 11 12 13 14 19 20 ...
.. .. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. .. ..$ geo_accession : Factor w/ 64 levels "GSM1383567","GSM1383568",...: 1 2 3 4 5 6 7 8 9
10 ...
.. .. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. .. ..$ status : Factor w/ 1 level "Public on May 09 2014": 1 1 1 1 1 1 1 1 1 1 ...
.. .. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. .. ..$ submission_date : Factor w/ 1 level "May 08 2014": 1 1 1 1 1 1 1 1 1 1 ...
.. .. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. .. ..$ last_update_date : Factor w/ 1 level "Aug 12 2014": 1 1 1 1 1 1 1 1 1 1 ...
.. .. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. .. ..$ type : Factor w/ 1 level "genomic": 1 1 1 1 1 1 1 1 1 1 ...
.. .. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. .. ..$ channel_count : Factor w/ 1 level "1": 1 1 1 1 1 1 1 1 1 1 ...
.. .. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. .. ..$ source_name_ch1 : Factor w/ 1 level "HapMap_Yoruba": 1 1 1 1 1 1 1 1 1 1 ...
.. .. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. .. ..$ organism_ch1 : Factor w/ 1 level "Homo sapiens": 1 1 1 1 1 1 1 1 1 1 ...
.. .. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. .. ..$ characteristics_ch1 : Factor w/ 2 levels "gender: Female",...: 2 1 2 1 2 1 2 1 2 ...
.. .. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. .. ..$ characteristics_ch1.1 : Factor w/ 1 level "cell type: Lymphoblastoid Cell Line": 1 1 1 1 1
1 1 1 1 1 ...
.. .. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...

```

```

.. .. ..$ molecule_ch1 : Factor w/ 1 level "genomic DNA": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ extract_protocol_ch1 : Factor w/ 1 level "DNA was extracted from lymphoblastoid Cell
Line": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ label_ch1 : Factor w/ 1 level "cy3 and cy5": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ label_protocol_ch1 : Factor w/ 1 level "Standard illumina protocols": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ taxid_ch1 : Factor w/ 1 level "9606": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ hyb_protocol : Factor w/ 1 level "The samples were bisulphite-converted and hybridized
to the Infinium HumanMethylation450 BeadChip at the University of Chicago "l__truncated__": 1
1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ scan_protocol : Factor w/ 1 level "not provided": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ description : Factor w/ 64 levels "Sample 1","Sample 10",...: 1 12 23 34 45 56 62 63 64 2
...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ data_processing : Factor w/ 1 level "To ensure high data quality, probes were mapped to a
bisulfite converted genome and only uniquely mapped probes were retained. "l__truncated__": 1 1
1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ data_processing.1 : Factor w/ 1 level "Normalized data: Normalized average beta (PCs
removed).": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ data_processing.2 : Factor w/ 1 level "Un-normalized data: Unmethylated and methylated
signal intensities and detection p-value.": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ platform_id : Factor w/ 1 level "GPL13534": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ contact_name : Factor w/ 1 level "Nicholas,E,Banovich": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ contact_laboratory : Factor w/ 1 level "Gilad": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ contact_department : Factor w/ 1 level "Human Genetics": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ contact_institute : Factor w/ 1 level "University of Chicago": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ contact_address : Factor w/ 1 level "920 E. 58th Street, CLSC 317": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ contact_city : Factor w/ 1 level "Chicago": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ contact_state : Factor w/ 1 level "IL": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ contact_zip.postal_code: Factor w/ 1 level "60453": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ contact_country : Factor w/ 1 level "USA": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. ..$ supplementary_file : Factor w/ 1 level "NONE": 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...

```

```

.. .. .. ..$ data_row_count : Factor w/ 1 level "329469": 1 1 1 1 1 1 1 1 1 1 ...
.. .. .. ..- attr(*, "names")= chr [1:64] "V2" "V3" "V4" "V5" ...
.. .. .. ..$ naid : chr [1:64] "NA18498" "NA18499" "NA18501" "NA18502" ...
.. .. ..@ elementType : chr "ANY"
.. .. ..@ elementMetadata: NULL
.. .. ..@ metadata : list()
..@ assays :Reference class 'ShallowSimpleListAssays' [package "GenomicRanges"] with 1 field
.. ..$ data: NULL
.. ..and 14 methods.
..@ NAMES : NULL
..@ elementMetadata:Formal class 'DataFrame' [package "S4Vectors"] with 6 slots
.. .. ..@ rownames : NULL
.. .. ..@ nrows : int 329469
.. .. ..@ listData : Named list()
.. .. ..@ elementType : chr "ANY"
.. .. ..@ elementMetadata: NULL
.. .. ..@ metadata : list()
..@ metadata : list()

```

## Examples

```
data(banovichSE)
```

---

mexGR

*combine expression data for a gene with nearby methylation data*


---

## Description

combine expression data for a gene with nearby methylation data,

## Usage

```
mexGR(methSE, exprSE, gradius = 0, symbol = "ORMDL3", etagname = "gene_name")
```

## Arguments

methSE	SummarizedExperiment instance
exprSE	SummarizedExperiment instance
gradius	number of base pairs around 'gene' to search
symbol	string selecting a gene
etagname	metadata column in which symbol can be found to select gene

## Value

GRanges instance with assay results in mcols

## Examples

```

data(geuFPKM)
data(banovichSE)
m1 = mexGR(banovichSE, geuFPKM, gradius=5000)
ii = bindElms(geuFPKM, banovichSE)

```

---

pwplot

*pairwise plot for components of MultiAssayExperiment*

---

### Usage

```
pwplot(fmla1, fmla2, mae, ytx = force, xtx = force, ...)
```

### Arguments

fmla1	a formula with one name in each of lhs and rhs. these are the names of the experiments to be extracted
fmla2	a formula with lhs the name of a feature in rowData(lhs(fmla1)) and rhs the name of a feature in rowData(rhs(fmla1)). these are the features to be plotted
mae	instance of MultiAssayExperiment
ytx	function to transform lhs(fmla2)
xtx	function to transform rhs(fmla2)
...	passed to plot

### Value

runs plot

### Author(s)

VJ Carey <stvjc@channing.harvard.edu>

### Examples

```
data(demoMAE)
pwplot(geuvRNAseq~yri450k, ENSG00000139618.9~cg20073910,
  demoMAE, ytx=log, main="demo")
```

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