

Package ‘ggtut’

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Title support for tutorial on genetics of gene expression ISMB 2011

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

Description various resources for genetics of expression with R/bioc

Suggests rtracklayer, GenomicFeatures, ChIPpeakAnno,
TxDb.Hsapiens.UCSC.hg18.knownGene

Depends R (>= 2.14.0), GGtools (>= 3.11.32), ff, GenomicRanges,
snpStats, GGdata, GenomicFeatures, ChIPpeakAnno, Rsamtools(>=
1.5.35), cheung2010, SNPlocs.Hsapiens.dbSNP.20120608, hmyriB36

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

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LazyLoad yes

biocViews SequencingData, MicroarrayData, SNPData

NeedsCompilation no

R topics documented:

ggtut-package	2
c17imp	3
g17rngsnr	3
observed17ceu	4
rules.n43	5
snpgr17	6
Index	8

`c17imp`*SnpMatrix instance with imputations from 1KG to CEU chr 17*

Description

SnpMatrix instance with imputations from 1KG to CEU chr 17

Usage

```
data(c17imp)
```

Format

The format is:

Formal class 'SnpMatrix' [package "snpStats"] with 1 slots

..@ .Data: raw [1:90, 1:175170] 77 d6 77 2d ...

.. .. attr(*, "dimnames")=List of 2

..\$: chr [1:90] "NA06985" "NA06991" "NA06993" "NA06994" ...

..\$: chr [1:175170] "chr17:1869" "rs17055023" "rs6565733" "rs34663111" ...

Source

uses rules.n43

Examples

```
library(snpStats)
data(c17imp)
c17imp
```

`g17rngsnr`*ranges of genes on chrom 17 (uses hg18)*

Description

ranges of genes on chrom 17 (uses hg18)

Usage

```
data(g17rngsnr)
```

Format

The format is:

```
Formal class 'GRanges' [package "GenomicRanges"] with 6 slots
..@ seqnames :Formal class 'Rle' [package "IRanges"] with 4 slots
.. ..@ values : Factor w/ 1 level "chr17": 1
.. ..@ lengths : int 475
.. ..@ elementMetadata: NULL
.. ..@ metadata : list()
..@ ranges :Formal class 'IRanges' [package "IRanges"] with 6 slots
.. ..@ start : int [1:475] 39509647 50333051 46294586 77439016 38229969 37098653 45133689
58981554 44263371 17349602 ...
.. ..@ width : int [1:475] 46894 61277 5753 3743 19335 2772 6839 43820 33858 86118 ...
.. ..@ NAMES : chr [1:475] "GI_21237796-A" "GI_4885638-S" "GI_22035666-S" "GI_17572809-
S" ...
.. ..@ elementType : chr "integer"
.. ..@ elementMetadata: NULL
.. ..@ metadata : list()
..@ strand :Formal class 'Rle' [package "IRanges"] with 4 slots
.. ..@ values : Factor w/ 3 levels "+","-","*": 3
.. ..@ lengths : int 475
.. ..@ elementMetadata: NULL
.. ..@ metadata : list()
..@ elementMetadata:Formal class 'DataFrame' [package "IRanges"] with 6 slots
.. ..@ rownames : NULL
.. ..@ nrows : int 475
.. ..@ listData :List of 1
.. .. ..$ probeid: chr [1:475] "GI_21237796-A" "GI_4885638-S" "GI_22035666-S" "GI_17572809-
S" ...
.. ..@ elementType : chr "ANY"
.. ..@ elementMetadata: NULL
.. ..@ metadata : list()
..@ seqinfo :Formal class 'Seqinfo' [package "GenomicRanges"] with 3 slots
.. ..@ seqnames : chr "chr17"
.. ..@ seqlengths : int NA
.. ..@ is_circular: logi NA
..@ metadata : list()
```

Examples

```
data(g17rngsnr)
g17rngsnr
## maybe str(g17rngsnr) ; plot(g17rngsnr) ...
```

Description

obtain access to ff-based archives of eQTL test results

Usage

```
observed17ceu()
onePerm17ceu()
```

Details

The underlying ff data were obtained as follows

```
dropMonomorphies = function(sms) { sl = smList(sms) summs = lapply(sl, col.summary)
todrop = lapply(summs, function(x) which(x[, "RAF"]==1 | x[, "RAF"]==0)) for (i in 1:length(todrop))
if (length(todrop[[i]])>0) sl[[i]] = sl[[i]][,-todrop[[i]]] sms@smEnv$smList = sl
sms } library(GGdata) library(multicore) data(eset) ex library(genefilter) exf1 = nsFilter(ex)
length(get("17", revmap(illuminaHumanv1CHR))->ZZ) kp = intersect(ZZ, featureNames(exf1[[1]]))
c17 = getSS("GGdata", "17", renameChrs="chr17", probesToKeep=kp, wrapperEndo=dropMonomorphies)
f1dm = eqtlTests(c17, ~male, targdir="c17c", genegran=1, geneApply=mclapply)
save(f1dm, file="f1dm.rda") set.seed(1234); permf1dm = eqtlTests(permEx(c17), ~male, targdir="c17c_p")
save(permf1dm, file="permf1dm.rda")
```

Value

an instance of [eqtlTestsManager-class](#)

Examples

```
f1 = observed17ceu()
f1
f1@call
f1[ rsid("rs7502145"), probeId("GI_10190685-S")]
pf1 = onePerm17ceu()
pf1[ rsid("rs7502145"), probeId("GI_10190685-S")]
```

rules.n43

snpStats imputation rules instance

Description

snpStats imputation rules instance

Usage

```
data(rules.n43)
```

Format

The format is:
 Formal class 'ImputationRules' [package "snpStats"] with 1 slots
 ..@ .Data:List of 470806
\$: NULL
\$:List of 4
\$ maf : num 0.128
\$ r.squared: num 0.901
\$ snps : chr [1:4] "rs11654695" "rs9789059" "rs8073513" "rs7225087"
\$ hap.probs: num [1:32] 0.00 1.02e-21 0.00 1.45e-07 1.52e-07 ...
\$:List of 4
\$ maf : num 0.163
\$ r.squared: num 0.802
\$ snps : chr [1:4] "rs11654695" "rs12449775" "rs8078223" "rs9907102"
\$ hap.probs: num [1:32] 0.02863 0.0253 0.00342 0.07866 0.01717 ...
\$:List of 4
\$ maf : num 0.116
\$ r.squared: num 0.881
\$ snps : chr [1:4] "rs11654695" "rs9789059" "rs8073513" "rs4968164"
\$ hap.probs: num [1:32] 0.00 1.96e-13 0.00 4.91e-05 1.05e-06 ...
\$: NULL
 [list output truncated]

Examples

```
library(snpStats)
data(rules.n43)
rules.n43[1:4]
## maybe str(rules.n43) ; plot(rules.n43) ...
```

snpgr17

SNP locations for chr 17: hg18 coordinates

Description

SNP locations for chr 17: hg18 coordinates

Usage

```
data(snpgr17)
```

Format

The format is:
 Formal class 'GRanges' [package "GenomicRanges"] with 6 slots
 ..@ seqnames :Formal class 'Rle' [package "IRanges"] with 4 slots

```

.. ..@ values : Factor w/ 1 level "chr17": 1
.. ..@ lengths : int 316396
.. ..@ elementMetadata: NULL
.. ..@ metadata : list()
..@ ranges :Formal class 'IRanges' [package "IRanges"] with 6 slots
.. ..@ start : int [1:316396] 6934 7214 7242 8611 11743 11830 13546 13905 14122 14300 ...
.. ..@ width : int [1:316396] 1 1 1 1 1 1 1 1 1 1 ...
.. ..@ NAMES : chr [1:316396] "rs1106176" "rs6420494" "rs6420495" "rs62054996" ...
.. ..@ elementType : chr "integer"
.. ..@ elementMetadata: NULL
.. ..@ metadata : list()
..@ strand :Formal class 'Rle' [package "IRanges"] with 4 slots
.. ..@ values : Factor w/ 3 levels "+","-","*": 3
.. ..@ lengths : int 316396
.. ..@ elementMetadata: NULL
.. ..@ metadata : list()
..@ elementMetadata:Formal class 'DataFrame' [package "IRanges"] with 6 slots
.. ..@ rownames : NULL
.. ..@ nrows : int 316396
.. ..@ listData : Named list()
.. ..@ elementType : chr "ANY"
.. ..@ elementMetadata: NULL
.. ..@ metadata : list()
..@ seqinfo :Formal class 'Seqinfo' [package "GenomicRanges"] with 3 slots
.. ..@ seqnames : chr "chr17"
.. ..@ seqlengths : int NA
.. ..@ is_circular: logi NA
..@ metadata : list()

```

Examples

```

data(snpr17)
snpr17
## maybe str(snpr17) ; plot(snpr17) ...

```

Index

*Topic **datasets**

- c17imp, 3
- g17rngsnr, 3
- rules.n43, 5
- snpgpr17, 6

*Topic **models**

- observed17ceu, 4

*Topic **package**

- ggtut-package, 2

bestGenesPerSNP_obs (ggtut-package), 2

bestGenesPerSNP_perm (ggtut-package), 2

c17imp, 3

CPS17 (ggtut-package), 2

g17rngsnr, 3

getFixedBFL (ggtut-package), 2

ggtut (ggtut-package), 2

ggtut-package, 2

hg18tx (ggtut-package), 2

observed17ceu, 4

onePerm17ceu (observed17ceu), 4

PERMCPS17 (ggtut-package), 2

permsb1 (ggtut-package), 2

rsb2_list (ggtut-package), 2

rsb2_perm_list (ggtut-package), 2

rules.n43, 5

sb1 (ggtut-package), 2

snpgpr17, 6

SVA1 (ggtut-package), 2

tr17_1_9 (observed17ceu), 4

tr17_1_9_perm (observed17ceu), 4