

Package ‘ggtut’

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Title support for tutorial on genetics of gene expression ISMB 2011

Version 0.0.46

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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

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LazyLoad yes

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ggtut-package *support for tutorial on genetics of gene expression ISMB 2011*

Description

various resources for genetics of expression with R/bioc

Details

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) ...

```

observed17ceu

obtain access to ff-based archives of eQTL test results

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) { s1 = smList(sms) summs = lapply(s1, 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) s1[[i]] = s1[[i]][,-todrop[[i]]] sms@sm1Env$smList = s1
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_per")
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

Description

SNP locations for chr 17

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(snpgr17)
snpgr17
## maybe str(snpgr17) ; plot(snpgr17) ...
```

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