Package ‘biobroom’

March 28, 2017

Title Turn Bioconductor objects into tidy data frames
Version 1.6.0
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Description This package contains methods for converting standard objects
constructed by bioinformatics packages, especially those in Bioconductor,
and converting them to tidy data. It thus serves as a complement to the broom
package, and follows the same the tidy, augment, glance division of tidying
methods. Tidying data makes it easy to recombine, reshape and visualize
bioinformatics analyses.
biocViews MultipleComparison, DifferentialExpression, Regression,
GeneExpression, Proteomics, DataImport
Depends R (>= 3.0.0), broom
License LGPL
LazyData true
Imports dplyr, tidyr, Biobase
Suggests limma, DESeq2, airway, ggplot2, plyr, GenomicRanges,
testthat, magrittr, edgeR, qvalue, knitr, data.table, MSnbase,
SummarizedExperiment
VignetteBuilder knitr
URL https://github.com/StoreyLab/biobroom
BugReports https://github.com/StoreyLab/biobroom/issues
RoxygenNote 5.0.1
NeedsCompilation no

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augment_sva

Tidying methods for a sva list

Description

These are methods for turning a sva list, from the sva package, into a tidy data frame. tidy returns a data.frame of the estimated surrogate variables, glance returns a data.frame of the posterior probabilities, and glance returns a data.frame with only the number of surrogate variables.

Usage

augment_sva(x, data, ...)
tidy_sva(x, addVar = NULL, ...)
glance_sva(x, ...)

Arguments

x sva list
data Original data
... extra arguments (not used)
addVar add additional coefficients to the estimated surrogate variables

Value

All tidying methods return a data.frame without rownames. The structure depends on the method chosen.

augment returns one row per gene. It always contains the columns

pprob.gam Posterior probability each gene is affected by heterogeneity
pprob.b Posterior probability each gene is affected by model

tidy returns the estimate surrogate variables.
glance returns the estimate surrogate variables.
biobroom  

Convert Bioconductor Object into Tidy Data Frames

Description

This package contains methods for converting standard objects constructed by bioinformatics packages, especially those in Bioconductor, and converting them to tidy data. It thus serves as a complement to the broom package, and follows the same tidy, augment, glance division of tidying methods. Tidying data makes it easy to recombine, reshape and visualize bioinformatics analyses.

DESeq2_tidiers  

Tidying methods for DESeq2 DESeqDataSet objects

Description

This reshapes a DESeq2 expressionset object into a tidy format. If the dataset contains hypothesis test results (p-values and estimates), this summarizes one row per gene per possible contrast.

Usage

## S3 method for class 'DESeqDataSet'
tidy(x, colData = FALSE, intercept = FALSE, ...)

## S3 method for class 'DESeqResults'
tidy(x, ...)

Arguments

- **x**: DESeqDataSet object
- **colData**: whether colData should be included in the tidied output for those in the DESeqDataSet object. If dataset includes hypothesis test results, this is ignored
- **intercept**: whether to include hypothesis test results from the (Intercept) term. If dataset does not include hypothesis testing, this is ignored
- **...**: extra arguments (not used)

Details

colDat=TRUE adds covariates from colData to the data frame.

Value

If the dataset contains results (p-values and log2 fold changes), the result is a data frame with the columns

- **term**: The contrast being tested, as given to results
- **gene**: gene ID
- **baseMean**: mean abundance level
- **estimate**: estimated log2 fold change
stderr  standard error in log2 fold change estimate
statistic  test statistic
p.value  p-value
p.adjusted  adjusted p-value

If the dataset does not contain results (DESeq has not been run on it), tidy defaults to tidying the counts in the dataset:
gene  gene ID
sample  sample ID
count  number of reads in this gene in this sample

If colData = TRUE, it also merges this with the columns present in colData(x).

Examples

# From DESeq2 documentation

if (require("DESeq2")) {
  dds <- makeExampleDESeqDataSet(betaSD = 1)

  tidy(dds)
  # With design included
  tidy(dds, colData=TRUE)

  # add a noise confounding effect
  colData(dds)$noise <- rnorm(nrow(colData(dds)))
  design(dds) <- (~ condition + noise)

  # perform differential expression tests
  ddsres <- DESeq(dds, test = "Wald")
  # now results are per-gene, per-term
  tidied <- tidy(ddsres)
  tidied

  if (require("ggplot2")) {
    ggplot(tidied, aes(p.value)) + geom_histogram(binwidth = .05) +
    facet_wrap(~ term, scale = "free_y")
  }
}

edgeR_tidiers  Tidiers for edgeR’s differential expression objects

Description

Tidy, augment and glance methods for turning edgeR objects into tidy data frames, where each row represents one observation and each column represents one column.
edgeR_tidiers

Usage

## S3 method for class 'DGEExact'
tidy(x, ...)

## S3 method for class 'DGEList'
tidy(x, addSamples = FALSE, ...)

## S3 method for class 'DGEList'
augment(x, data = NULL, ...)

## S3 method for class 'DGEExact'
glance(x, alpha = 0.05, p.adjust.method = "fdr", ...)

Arguments

x  DGEEexact, DGEList object
...
extra arguments (not used)
addSamples  Merge information from samples. Default is FALSE.
data  merge data to augment. This is particularly useful when merging gene names or other per-gene information. Default is NULL.
alpha  Confidence level to test for significance
p.adjust.method  Method for adjusting p-values to determine significance; can be any in p.adjust.methods

Value

tidy defaults to tidying the counts in the dataset:

gene  gene ID
sample  sample ID
count  number of reads in this gene in this sample

If addSamples = TRUE, it also merges this with the sample information present in x$samples.
augment returns per-gene information (DGEList only)
glance returns one row with the columns (DGEEexact only)
significant  number of significant genes using desired adjustment method and confidence level
comparison  The pair of groups compared by edgeR, delimited by /

Examples

if (require("edgeR")) {
  library(Biobase)
data(hammer)
hammer.counts <- exprs(hammer)[, 1:4]
hammer.treatment <- phenoData(hammer)$protocol[1:4]
y <- DGEList(counts=hammer.counts, group=hammer.treatment)
y <- calcNormFactors(y)
y <- estimateCommonDisp(y)
y <- estimateTagwiseDisp(y)
et <- exactTest(y)

head(tidy(et))
head(glance(et))

---

**ExpressionSet_tidiers**  
*Tidying methods for Biobase’s ExpressionSet objects*

**Description**

Tidying methods for Biobase’s ExpressionSet objects

**Usage**

```r
## S3 method for class 'ExpressionSet'
tidy(x, addPheno = FALSE,
    assay = Biobase::assayDataElementNames(x)[1L], ...)
```

**Arguments**

- `x` ExpressionSet object
- `addPheno` whether columns should be included in the tidied output for those in the ExpressionSet’s phenoData
- `assay` The name of the `assayDataElement` to use as the values to tidy. Defaults to `assayDataElementNames(x)[1L]`, which is usually equivalent to `exprs(x)`.
- `...` extra arguments (not used)

**Details**

`addPheno=TRUE` adds columns that are redundant (since they add per-sample information to a per-sample-per-gene data frame), but that are useful for some kinds of graphs and analyses.

**Value**

tidy returns a data frame with one row per gene-sample combination, with columns

- `gene` gene name
- `sample` sample name (from column names)
- `value` expressions on log2 scale

**Examples**

```r
library(Biobase)
# import ExpressionSet object
data(hammer)

# Use tidy to extract genes, sample ids and measured value
tidy(hammer)
# add phenoType data
tidy(hammer, addPheno=TRUE)
```
**Description**

An ExpressionSet containing the results of the Hammer et al 2010 RNA-Seq study on the nervous system of rats (Hammer et al 2010).

This was downloaded from the ReCount database of analysis-ready RNA-Seq datasets (Frazee et al 2011).


**Usage**

hammer

**Format**

An object of class ExpressionSet with 29516 rows and 8 columns.

**Value**

ExpressionSet

---

**Description**

Tidy, augment, and glance methods for MArrayLM objects, which contain the results of gene-wise linear models to microarray datasets. This class is the output of the lmFit and eBayes functions.

Tidying method for a MA list

Tidy an EList expression object

**Usage**

```r
## S3 method for class 'MArrayLM'
tidy(x, intercept = FALSE, ...)

## S3 method for class 'MArrayLM'
augment(x, data, ...)

## S3 method for class 'MArrayLM'
```

---
limma_tidiers

glance(x, ...)

## S3 method for class 'MAList'
tidy(x, ...)

## S3 method for class 'EList'
tidy(x, addTargets = FALSE, ...)

### Arguments

- **x** MArrayLM, MAList, EList object
- **intercept** whether the (Intercept) term should be included (default FALSE)
- **...** extra arguments, not used
- **data** original expression matrix; if missing, augment returns only the computed per-gene statistics
- **addTargets** Add sample level information. Default is FALSE.

### Details

Tidying this fit computes one row per coefficient per gene, while augmenting returns one row per gene, with per-gene statistics included. (This is thus a rare case where the augment output has more rows than the tidy output. This is a side effect of the fact that the input to limma is not tidy but rather a one-row-per-gene matrix).

### Value

The output of tidying functions is always a data frame without rownames.

tidy returns one row per gene per coefficient. It always contains the columns

- **gene** The name of the gene (extracted from the rownames of the input matrix)
- **term** The coefficient being estimated
- **estimate** The estimate of each per-gene coefficient

Depending on whether the object comes from eBayes, it may also contain

- **statistic** Empirical Bayes t-statistic
- **p.value** p-value computed from t-statistic
- **lod** log-of-odds score

augment returns one row per gene, containing the original gene expression matrix if provided. It then adds columns containing the per-gene statistics included in the MArrayLM object, each prepended with a .:

- **.gene** gene ID, obtained from the rownames of the input
- **.sigma** per-gene residual standard deviation
- **.df.residual** per-gene residual degrees of freedom

The following columns may also be included, depending on which have been added by lmFit and eBayes:

- **.AMean** average intensity across probes
- **.statistic** moderated F-statistic
.p.value  p-value generated from moderated F-statistic
.df.total total degrees of freedom per gene
.df.residual residual degrees of freedom per gene
.s2.post posterior estimate of residual variance

glance returns one row, containing
rank       rank of design matrix
df.prior   empirical Bayesian prior degrees of freedom
s2.prior   empirical Bayesian prior residual standard deviation

tidy returns a data frame with one row per gene-sample combination, with columns
gene       gene name
sample     sample name (from column names)
value      expressions on log2 scale

tidy returns a data frame with one row per gene-sample combination, with columns
gene       gene name
sample     sample name (from column names)
value      expressions on log2 scale
weight     present if weights is set
other columns if present and if addTargets is set

Examples
if (require("limma")) {
    # create random data and design
    set.seed(2014)
    dat <- matrix(rnorm(1000), ncol=4)
    dat[, 1:2] <- dat[, 1:2] + .5  # add an effect
    rownames(dat) <- paste0("g", 1:nrow(dat))
    des <- data.frame(treatment = c("a", "a", "b", "b"),
                      confounding = rnorm(4))

    lfit <- lmFit(dat, model.matrix(~ treatment + confounding, des))
    eb <- eBayes(lfit)
    head(tidy(lfit))
    head(tidy(eb))

    if (require("ggplot2")) {
        # the tidied form puts it in an ideal form for plotting
        ggplot(tidy(lfit), aes(estimate)) + geom_histogram(binwidth=1) +
            facet_wrap(~ term)
        ggplot(tidy(eb), aes(p.value)) + geom_histogram(binwidth=.2) +
            facet_wrap(~ term)
    }
}
list_tidders  
_Tidiers for return values from functions that aren't S3 objects_

**Description**

This method handles the return values of functions that return lists rather than S3 objects, such as sva, and therefore cannot be handled by S3 dispatch.

**Usage**

```r
## S3 method for class 'list'
tidy(x, ...)

## S3 method for class 'list'
glance(x, ...)
```

**Arguments**

- `x`  list object
- `...`  extra arguments, passed to the tidying function

**Details**

Those tiders themselves are implemented as functions of the form tidy_<function> that are not exported.

---

**MSnSet_tidders**  
_Tidying methods for Biobase’s ExpressionSet objects_

**Description**

Tidying methods for Biobase’s ExpressionSet objects

**Usage**

```r
## S3 method for class 'MSnSet'
tidy(x, addPheno = FALSE, ...)
```

**Arguments**

- `x`  MSnSet object
- `addPheno`  whether columns should be included in the tidied output for those in the MSnSet’s phenoData
- `...`  extra arguments (not used)

**Details**

addPheno=TRUE adds columns that are redundant (since they add per-sample information to a per-sample-per-gene data frame), but that are useful for some kinds of graphs and analyses.
**Value**

`tidy` returns a data frame with one row per gene-sample combination, with columns

- **protein**: protein name
- **sample**: sample name (from column names)
- **value**: protein quantitation data

**Examples**

```r
if (require("MSnbase")) {
  library(MSnbase)
  # import MSnSet object
data(msnset)

  # Use tidy to extract genes, sample ids and measured value
  tidy(msnset)
  # add phenoType data
  tidy(msnset, addPheno=TRUE)
}
```

---

**qvalue_tidiers**

_Tidying methods for a qvalue object_

**Description**

These are methods for turning a qvalue object, from the `qvalue` package for false discovery rate control, into a tidy data frame. `augment` returns a data.frame of the original p-values combined with the computed q-values and local false discovery rates, `tidy` constructs a table showing how the estimate of pi0 (the proportion of true nulls) depends on the choice of the tuning parameter lambda, and `glance` returns a data.frame with only the chosen pi0 value.

**Usage**

```r
## S3 method for class 'qvalue'
tidy(x, ...)

## S3 method for class 'qvalue'
augment(x, data, ...)

## S3 method for class 'qvalue'
glance(x, ...)
```

**Arguments**

- **x**: qvalue object
- **data**: Original data
- **...**: extra arguments (not used)
Value

All tidying methods return a data.frame without rownames. The structure depends on the method chosen.

**tidy** returns one row for each choice of the tuning parameter lambda that was considered (argument lambda to qvalue), containing

- **lambda**: the tuning parameter
- **pi0**: corresponding estimate of pi0
- **smoothed**: whether the estimate has been spline-smoothed)

If pi0.method="smooth", the pi0 estimates and smoothed values both appear in the table. If pi0.method="bootstrap", smoothed is FALSE for all entries.

**augment** returns a data.frame with

- **p.value**: the original p-values given to qvalue
- **q.value**: the computed q-values
- **lfr**: the local false discovery rate

**glance** returns a one-row data.frame containing

- **pi0**: the estimated pi0 (proportion of nulls)
- **lambda**: lambda used to compute pi0. Note that if pi0 is 1, this may be NA since it can be ambiguous which lambda was used

Examples

```r
library(ggplot2)
if (require("qvalue")) {
  set.seed(2014)

  # generate p-values from many one sample t-tests: half of them null
  oracle <- rep(c(0, .5), each=1000)
pvals <- sapply(oracle, function(mu) t.test(rnorm(15, mu))$p.value)
qplot(pvals)

  q <- qvalue(pvals)
tidy(q)
  head(augment(q))
  glance(q)

  # use augmented data to compare p-values to q-values
  ggplot(augment(q), aes(p.value, q.value)) + geom_point()

  # use tidy see how pi0 estimate changes with lambda, comparing
  # to smoothed version
  g <- ggplot(tidy(q), aes(lambda, pi0, color=smoothed)) + geom_line()
g

  # show the chosen value
  g + geom_hline(yintercept=q$pi0, lty=2)
}
```
SummarizedExperiment_tidiers

Tidying methods for Biobase’s SummarizedExperiment objects

Description

Tidying methods for Biobase’s SummarizedExperiment objects

Usage

## S3 method for class 'RangedSummarizedExperiment'
tidy(x, addPheno = FALSE, 
    assay = SummarizedExperiment::assayNames(x)[1L], ...)

Arguments

x SummarizedExperiment object

addPheno whether columns should be included in the tidied output for those in the SummarizedExperiment colData

assay Which assay to return as the value column. Defaults to assays(x)[[1L]]

... extra arguments (not used)

Details

addPheno=TRUE adds columns that are redundant (since they add per-sample information to a per-sample-per-gene data frame), but that are useful for some kinds of graphs and analyses.

Value

tidy returns a data frame with one row per gene-sample combination, with columns
gene gene name
gene name (from column names)

If addPheno is TRUE then information from colData is added.

Examples

if (require("SummarizedExperiment", "airway")) {
  data(airway)
  se <- airway
tidy(se)
}
**Description**

Tidying methods for edge's deSet object

**Usage**

```r
## S3 method for class 'deSet'
tidy(x, addPheno = FALSE, ...)
```

```r
## S3 method for class 'deSet'
augment(x, data, ...)
```

```r
## S3 method for class 'deSet'
.glance(x, ...)
```

**Arguments**

- `x` deSet object
- `addPheno` whether columns should be included in the tidied output for those in the ExpressionSet's phenoData
- `...` extra arguments (not used)
- `data` Original data can be added. Default is NULL.

**Details**

`addPheno=TRUE` adds columns that are redundant (since they add per-sample information to a per-sample-per-gene data frame), but that are useful for some kinds of graphs and analyses.

**Value**

tidy returns a data frame with one row per gene-sample combination, with columns

- `gene` gene name
- `sample` sample name (from column names)
- `value` expressions on log2 scale

augment returns a data frame with

- `p.value` the original p-values given to qvalue
- `q.value` the computed q-values
- `lfdr` the local false discovery rate

.glance returns a data frame with the model fits
Tidying methods for GRanges and GRangesList objects.

Usage

## S3 method for class 'GRanges'
tidy(x, ...)

## S3 method for class 'GRangesList'
tidy(x, ...)

## S3 method for class 'GRanges'
glance(x, ...)

## S3 method for class 'GRangesList'
glance(x, ...)

Arguments

x  GRanges or GRangesList object
...
Not used.

Value

All tidying methods return a data.frame without rownames. tidy returns one row for each range, which contains

- start of the range
- end of the range
- width (or length) of the range
- names of the range
- strand
- seqname Name of the sequence from which the range comes (usually the chromosome)
- metadata Any included metadata, (ie, score, GC content)

For GRangesList, there will also be a column representing which group the ranges comes from. glance returns a data.frame with the number of ranges, the number of sequences, and the number of groups (if applicable).

Examples

```r
if (require("GenomicRanges", "airway")) {
  data(airway)

  # GRangesList object
  air_gr <- rowRanges(airway)
```
tidy(air_gr)
glance(air_gr)

# GRanges object
air_gr <- rowRanges(airway)@unlistData

tidy(air_gr)
glance(air_gr)

)
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