Package ‘hermes’

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Title Preprocessing, analyzing, and reporting of RNA-seq data
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Description Provides classes and functions for quality control, filtering, normalization and differential expression analysis of pre-processed `RNA-seq` data. Data can be imported from `SummarizedExperiment` as well as `matrix` objects and can be annotated from `BioMart`. Filtering for genes without too low expression or containing required annotations, as well as filtering for samples with sufficient correlation to other samples or total number of reads is supported. The standard normalization methods including cpm, rpkm and tpm can be used, and 'DESeq2' as well as voom differential expression analyses are available.

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URL https://github.com/insightsengineering/hermes/

BugReports https://github.com/insightsengineering/hermes/issues

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hermes-package

Description

hermes facilitates preprocessing, analyzing, and reporting of RNA-seq data.

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See Also

Useful links:

- [https://github.com/insightsengineering/hermes/](https://github.com/insightsengineering/hermes/)

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add_quality_flags  Add Quality Flags

Description

**[Stable]**

The function `add_quality_flags()` adds quality flag information to a `AnyHermesData` object:

- `low_expression_flag`: for each gene, counts how many samples don't pass a minimum expression Counts per Million (CPM) threshold. If too many, then it flags this gene as a "low expression" gene.

- `tech_failure_flag`: first calculates the Pearson correlation matrix of the sample wise CPM values, resulting in a matrix measuring the correlation between samples. Then compares the average correlation per sample with a threshold - if it is too low, then the sample is flagged as a "technical failure" sample.

- `low_depth_flag`: computes the library size (total number of counts) per sample. If this number is too low, the sample is flagged as a "low depth" sample.

Separate helper functions are internally used to create the flags, and separate getter functions allow easy access to the quality control flags in an object.
add_quality_flags

Usage

add_quality_flags(object, control = control_quality(), overwrite = FALSE)

h_low_expression_flag(object, control = control_quality())

h_low_depth_flag(object, control = control_quality())

h_tech_failure_flag(object, control = control_quality())

get_tech_failure(object)

get_low_depth(object)

get_low_expression(object)

Arguments

object (AnyHermesData)
  input.

control (list)
  list of settings (thresholds etc.) used to compute the quality control flags, produced by control_quality().

overwrite (flag)
  whether previously added flags may be overwritten.

Details

While object already has the variables mentioned above as part of the rowData and colData (as this is enforced by the validation method for AnyHermesData), they are usually still NA after the initial object creation.

Value

The input object with added quality flags.

Functions

- h_low_expression_flag(): creates the low expression flag for genes given control settings.
- h_low_depth_flag(): creates the low depth (library size) flag for samples given control settings.
- h_tech_failure_flag(): creates the technical failure flag for samples given control settings.
- get_tech_failure(): get the technical failure flags for all samples.
- get_low_depth(): get the low depth failure flags for all samples.
- get_low_expression(): get the low expression failure flags for all genes.
See Also

- `control_quality()` for the detailed settings specifications;
- `set_tech_failure()` to manually flag samples as technical failures.

Examples

```r
# Adding default quality flags to `AnyHermesData` object.
object <- hermes_data
result <- add_quality_flags(object)
which(get_tech_failure(result) != get_tech_failure(object))
head(get_low_expression(result))
head(get_tech_failure(result))
head(get_low_depth(result))

# It is possible to overwrite flags if needed, which will trigger a message.
result2 <- add_quality_flags(result, control_quality(min_cpm = 1000), overwrite = TRUE)

# Separate calculation of low expression flag.
low_expr_flag <- h_low_expression_flag(
  object,
  control_quality(min_cpm = 500, min_cpm_prop = 0.9)
)
length(low_expr_flag) == nrow(object)
head(low_expr_flag)

# Separate calculation of low depth flag.
low_depth_flag <- h_low_depth_flag(object, control_quality(min_depth = 5))
length(low_depth_flag) == ncol(object)
head(low_depth_flag)

# Separate calculation of technical failure flag.
technique_flag <- h_tech_failure_flag(object, control_quality(min_corr = 0.35))
length(technique_flag) == ncol(object)
head(technique_flag)
head(get_tech_failure(object))
head(get_low_depth(object))
head(get_low_expression(object))
```

---

**all_na**  
**Checks Whether All Missing**

**Description**

Internal function to check whether a whole vector is `NA`.

**Usage**

```r
all_na(x)
```
Arguments

\[ x \text{ (vector)} \]
vector to check.

Value

Corresponding flag.

---

**Annotation Accessor and Setter**

**Description**

[Stable]
These methods access and set the gene annotations stored in a `AnyHermesData` object.

**Usage**

```r
## S4 method for signature 'AnyHermesData'
annotation(object, ...)

.row_data_annotation_cols

## S4 replacement method for signature 'AnyHermesData,DataFrame'
annotation(object) <- value
```

**Arguments**

- `object` (AnyHermesData)
  object to access the annotations from.
- `...` not used.
- `value` (DataFrame)
  what should the annotations be replaced with.

**Format**

The annotation column names are available in the exported character vector `.row_data_annotation_cols`.

**Value**

The `S4Vectors::DataFrame` with the gene annotations:

- symbol
- desc
- chromosome
- size
### Note

When trying to replace the required annotations with completely missing values for any genes, a warning will be given and the corresponding gene IDs will be saved in the attribute `annotation.missing.genes`. Note also that additional annotations beyond the required ones may be supplied and will be stored.

### Examples

```r
object <- hermes_data
head(annotation(object))
```

### Description

**[Experimental]**
We provide additional assertion functions which can be used together with `assertthat::assert_that()`.

**[Experimental]**
We provide additional assertion functions which can be used together with the `checkmate` functions. These are described in individual help pages linked below.

### Usage

```r
is_class(x, class2)

is_hermes_data(x)

is_counts_vector(x)

is_list_with(x, elements)

one_provided(one, two)

is_constant(x)
```

### Arguments

- **x**: an object to check.
- **class2**: (character or class definition) the class to which `x` could belong.
- **elements**: (character) names of elements which should be in the list `x`.
- **one**: first input.
- **two**: second input.
Value

Depending on the function prefix.

- `assert_` functions return the object invisibly if successful, and otherwise throw an error message.
- `check_` functions return `TRUE` if successful, otherwise a string with the error message.
- `test_` functions just return `TRUE` or `FALSE`.

Functions

- `is_class()`: checks the class.
- `is_hermes_data()`: checks whether `x` is an `AnyHermesData` object.
- `is_counts_vector()`: checks for a vector of counts (positive integers).
- `is_list_with()`: checks for a list containing elements.
- `one_provided()`: checks that exactly one of the two inputs `one`, `two` is not `NULL`.
- `is_constant()`: checks whether the vector `x` is constant (only supports numeric, factor, character, logical). NAs are removed first.

See Also

`assert_proportion()`

Examples

```
# Assert a general class.
a <- 5
is_class(a, "character")

# Assert a `AnyHermesData` object.
is_hermes_data(hermes_data)
is_hermes_data(42)

# Assert a counts vector.
a <- 5L
is_counts_vector(a)

# Assert a list containing certain elements.
b <- list(a = 5, b = 3)
is_list_with(b, c("a", "c")){
is_list_with(b, c("a", "b")){

# Assert that exactly one of two arguments is provided.
a <- 10
b <- 10
one_provided(a, b)
one_provided(a, NULL)

# Assert a constant vector.
is_constant(c(1, 2))
```
assertion_arguments

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is_constant(c(NA, 1))
is_constant(c("a", "a"))
is_constant(factor(c("a", "a")))

assertion_arguments  Standard Assertion Arguments

Description
The documentation to this function lists all the conventional arguments in additional checkmate assertions.

Arguments

x  an object to check.
null.ok (flag) whether x may also be NULL.
.var.name (string) name of the checked object to print in assertions; defaults to the heuristic implemented in checkmate::vname().
add (AssertCollection or NULL) collection to store assertion messages, see checkmate::AssertCollection.
info (string) extra information to be included in the message for the testthat reporter, see testthat::expect_that().
label (string) name of the checked object to print in messages. Defaults to the heuristic implemented in checkmate::vname().

autoplot,AnyHermesData-method

All Standard Plots in Default Setting

Description
[Experimental]
This generates all standard plots - histogram and q-q plot of library sizes, density plot of the (log) counts distributions, boxplot of the number of non-zero expressed genes per sample, and a stacked barplot of low expression genes by chromosome at default setting.

Usage

## S4 method for signature 'AnyHermesData'
autoplot(object)
Arguments

object (AnyHermesData) input.

Value

A list with the ggplot objects from `draw_libsize_hist()`, `draw_libsize_qq()`, `draw_libsize_densities()`, `draw_nonzero_boxplot()` and `draw_genes_barplot()` functions with default settings.

Examples

```
result <- hermes_data
autoplot(result)
```

calc_pca Principal Components Analysis Calculation

Description

[Experimental]

The `calc_pca()` function performs principal components analysis of the gene count vectors across all samples.

A corresponding `autoplot()` method then can visualize the results.

Usage

```
calc_pca(object, assay_name = "counts", n_top = NULL)
```

Arguments

object (AnyHermesData) input.

assay_name (string) name of the assay to use.

n_top (count or NULL) filter criteria based on number of genes with maximum variance.

Details

- PCA should be performed after filtering out low quality genes and samples, as well as normalization of counts.
- In addition, genes with constant counts across all samples are excluded from the analysis internally in `calc_pca()`. Centering and scaling is also applied internally.
- Plots can be obtained with the `ggplot2::autoplot()` function with the corresponding method from the ggfortify package to plot the results of a principal components analysis saved in a `HermesDataPca` object. See `ggfortify::autoplot.prcomp()` for details.
Value

A `HermesDataPca` object which is an extension of the `stats::prcomp` class.

See Also

Afterwards correlations between principal components and sample variables can be calculated, see `pca_cor_samplevar`.

Examples

```r
object <- hermes_data %>%
    add_quality_flags() %>%
    filter() %>%
    normalize()

result <- calc_pca(object, assay_name = "tpm")
summary(result)

result1 <- calc_pca(object, assay_name = "tpm", n_top = 500)
summary(result1)

# Plot the results.
autoplot(result)
autoplot(result, x = 2, y = 3)
autoplot(result, variance_percentage = FALSE)
autoplot(result, label = TRUE, label.repel = TRUE)
```

---

**cat_with_newline**  
*Concatenate and Print with Newline*

Description

[Experimental]

This function concatenates inputs like `cat()` and prints them with newline.

Usage

```r
cat_with_newline(...)```

Arguments

`...`  
inputs to concatenate.

Value

None, only used for the side effect of producing the concatenated output in the R console.
See Also

This is similar to cli::cat_line().

Examples

cat_with_newline("hello", "world")

---

cbind

Column Binding of AnyHermesData Objects

Description

[Stable]
This method combines AnyHermesData objects with the same ranges but different samples (columns in assays).

Arguments

... (AnyHermesData)
objects to column bind.

Value

The combined AnyHermesData object.

Note

- Note that this just inherits SummarizedExperiment::cbind,SummarizedExperiment-method(). When binding a AnyHermesData object with a SummarizedExperiment::SummarizedExperiment object, then the result will be a SummarizedExperiment::SummarizedExperiment object (the more general class).
- Note that the combined object needs to have unique sample IDs (column names).

See Also

rbind to row bind objects.

Examples

a <- hermes_data[, 1:10]
b <- hermes_data[, 11:20]
result <- cbind(a, b)
class(result)
**check_proportion**  
*Check for proportion*

---

**Description**

[Experimental]

Check whether \(x\) is a (single) proportion.

**Usage**

```r
check_proportion(x, null.ok = FALSE)

assert_proportion(  
  x,  
  null.ok = FALSE,  
  .var.name = checkmate::vname(x),  
  add = NULL
)

test_proportion(x, null.ok = FALSE)

expect_proportion(x, null.ok = FALSE, info = NULL, label = vname(x))
```

**Arguments**

- **x**  
an object to check.

- **null.ok**  
(flag)  
whether \(x\) may also be NULL.

- **.var.name**  
(string)  
name of the checked object to print in assertions; defaults to the heuristic implemented in `checkmate::vname()`.

- **add**  
(AssertCollection or NULL)  
collection to store assertion messages, see `checkmate::AssertCollection`.

- **info**  
(string)  
extra information to be included in the message for the `testthat` reporter, see `testthat::expect_that()`.

- **label**  
(string)  
name of the checked object to print in messages. Defaults to the heuristic implemented in `checkmate::vname()`.

**Value**

TRUE if successful, otherwise a string with the error message.
See Also

assertions for more details.

Examples

check_proportion(0.25)

\[
\begin{array}{ll}
\text{colMeanZscores} & \text{Mean Z-score Gene Signature} \\
\end{array}
\]

Description

[Experimental]

This helper function returns the Z-score from an assay stored as a matrix.

Usage

\[\text{colMeanZscores}(x)\]

Arguments

\[x \quad \text{(matrix)}\]

containing numeric data with genes in rows and samples in columns, no missing values are allowed.

Value

A numeric vector containing the mean Z-score values for each column in \(x\).

Examples

\[
\begin{align*}
\text{object} & \leftarrow \text{hermes_data} \%>\%
\text{add_quality_flags()} \%>\%
\text{filter()} \%>\%
\text{normalize()} \%>\%
\text{assay("counts")}
\end{align*}
\]

\[\text{colMeanZscores}(\text{object})\]
colPrinComp1

First Principal Component (PC1) Gene Signature

Description

[Experimental]

This helper function returns the first principal component from an assay stored as a matrix.

Usage

colPrinComp1(x, center = TRUE, scale = TRUE)

Arguments

x (matrix) containing numeric data with genes in rows and samples in columns, no missing values are allowed.
center (flag) whether the variables should be zero centered.
scale (flag) whether the variables should be scaled to have unit variance.

Value

A numeric vector containing the principal component values for each column in x.

Examples

```r
object <- hermes_data %>%
  add_quality_flags() %>%
  filter() %>%
  normalize() %>%
  assay("counts")

colPrinComp1(object)
```

col_data_with_genes Sample Variables with Selected Gene Information

Description

[Experimental]

This obtains the sample variables of a HermesData object together with selected gene information.
Usage

```r
col_data_with_genes(object, assay_name, genes)
```

Arguments

- **object** `(AnyHermesData)`
  - input experiment.
- **assay_name** `(string)`
  - which assay to use.
- **genes** `(GeneSpec)`
  - which genes or which gene signature should be extracted.

Value

The combined data set, where the additional attribute `gene_cols` contains the names of the columns obtained by extracting the genes information.

Note

The class of the returned data set will depend on the class of `colData`, so usually will be `S4Vectors::DFrame`.

Examples

```r
result <- col_data_with_genes(hermes_data, "counts", gene_spec("GeneID:1820"))
tail(names(result))
result$GeneID.1820
```

---

**connect_biomart**  
*Connection to BioMart*

Description

[Experimental]

`connect_biomart()` creates a connection object of class `ConnectionBiomart` which contains the `biomaRt` object of class `biomaRt::Mart` and the prefix of the object which is used downstream for the query.

Usage

```r
connect_biomart(prefix = c("ENSG", "GeneID"), version = NULL)
```

Arguments

- **prefix** `(string)`
  - gene ID prefix.
- **version** `(string or NULL)`
  - optional Ensembl version to use. If NULL the latest available release is used.
**control_normalize**  

**Details**

This connects to the Ensembl data base of BioMart for human genes. A specific version can be optionally chosen to ensure reproducibility of results once a new release is available, as accessed data might then change.

**Value**

`ConnectionBiomart` object.

**Examples**

```r
if (interactive()) {
  connection <- connect_biomart("ENSG")
}
```

---

**control_normalize**  

*Control Settings for Counts Normalization*

**Description**

[Stable]

This control function allows for easy customization of the normalization settings.

**Usage**

```r
control_normalize(
  log = TRUE,
  lib_sizes = NULL,
  prior_count = 1,
  fit_type = "parametric"
)
```

**Arguments**

- **log**  
  (flag)
  whether log2 values are returned, otherwise original scale is used.

- **lib_sizes**  
  (NULL or counts)
  library sizes, if NULL the vector with the sum of the counts for each of the samples will be used.

- **prior_count**  
  (non-negative number)
  average count to be added to each observation to avoid taking log of zero, used only when log = TRUE.

- **fit_type**  
  (string)
  method to estimate dispersion parameters in Negative Binomial model, used only when normalize() methods include vst and/or rlog. See `estimateDispersions` for details.
Value

List with the above settings used to perform the normalization procedure.

Note

To be used with the `normalize()` function.

Examples

```r
control_normalize()
control_normalize(log = FALSE, lib_sizes = rep(1e6L, 20))
```

---

### control_quality

*Control for Specified Quality Flags*

**Description**

[Stable]

Control function which specifies the quality flag settings. One or more settings can be customized. Not specified settings are left at defaults.

**Usage**

```r
control_quality(
  min_cpm = 1,
  min_cpm_prop = 0.25,
  min_corr = 0.5,
  min_depth = NULL
)
```

**Arguments**

- `min_cpm` *(non-negative number)*
  minimum Counts per Million (CPM) for each gene within the sample.

- `min_cpm_prop` *(proportion)*
  minimum proportion of samples with acceptable CPM of certain gene for low expression flagging.

- `min_corr` *(proportion)*
  minimum Pearson correlation coefficient of CPM between samples for technical failure flagging.

- `min_depth` *(non-negative count or NULL)*
  minimum library depth for low depth flagging. If NULL, this will be calculated as the first quartile minus 1.5 times the inter-quartile range of the library size (depth) of all samples. (So anything below the usual lower boxplot whisker would be too low.)
correlate

Value
List with the above criteria to flag observations.

Note
To be used with the add_quality_flags() function.

Examples
# Default settings.
control_quality()

# One or more settings can be customized.
control_quality(min_cpm = 5, min_cpm_prop = 0.001)

correlate Generic Function for Correlation Calculations

description
[Experimental]
New generic function to calculate correlations for one or two objects.

Usage
correlate(object, ...)

Arguments
object input of which the class will be used to decide the method.
...
additional arguments.

Value
Corresponding object that contains the correlation results.

See Also
pca_cor_samplevar and calc_cor which are the methods included for this generic function.

Examples
sample_cors <- correlate(hermes_data)
autoplot(sample_cors)

calc_pca(hermes_data), hermes_data)
autoplot(pca_sample_var_cors)
Correlation between Sample Counts of AnyHermesData

Description

[Experimental]
The `correlate()` method can calculate the correlation matrix between the sample vectors of counts from a specified assay. This produces a `HermesDataCor` object, which is an extension of a `matrix` with additional quality flags in the slot `flag_data` (containing the `tech_failure_flag` and `low_depth_flag` columns describing the original input samples).

An `autoplot()` method then afterwards can produce the corresponding heatmap.

Usage

```
## S4 method for signature 'AnyHermesData'
correlate(object, assay_name = "counts", method = "pearson", ...)

## S4 method for signature 'HermesDataCor'
autoplot(
  object,
  flag_colors = c('FALSE' = "green", 'TRUE' = "red"),
  cor_colors = circlize::colorRamp2(c(0, 0.5, 1), c("red", "yellow", "green")),
  ...
)
```

Arguments

- `object` (AnyHermesData): object to calculate the correlation.
- `assay_name` (string): the name of the assay to use.
- `method` (string): the correlation method, see `stats::cor()` for details.
- `...`: other arguments to be passed to `ComplexHeatmap::Heatmap()`.
- `flag_colors` (named character): a vector that specifies the colors for TRUE and FALSE flag values.
- `cor_colors` (function): color scale function for the correlation values in the heatmap, produced by `circlize::colorRamp2()`.

Value

A `HermesDataCor` object.
Functions

- `autoplot(HermesDataCor)`: This `autoplot()` method uses the `ComplexHeatmap::Heatmap()` function to plot the correlations between samples saved in a `HermesDataCor` object.

Examples

```r
object <- hermes_data

# Calculate the sample correlation matrix.
correlate(object)

# We can specify another correlation coefficient to be calculated.
result <- correlate(object, method = "spearman")

# Plot the correlation matrix.
autoplot(result)

# We can customize the heatmap.
autoplot(result, show_column_names = FALSE, show_row_names = FALSE)

# Including changing the axis label text size.
autoplot(result,
         row_names_gp = grid::gpar(fontsize = 8),
         column_names_gp = grid::gpar(fontsize = 8))
```

---

**correlate,HermesDataPca-method**

Correlation of Principal Components with Sample Variables

**Description**

[Stable]

This `correlate()` method analyses the correlations (in R^2 values) between all sample variables in a `AnyHermesData` object and the principal components of the samples.

A corresponding `autoplot()` method then can visualize the results in a heatmap.

**Usage**

```r
## S4 method for signature 'HermesDataPca'
correlate(object, data)

## S4 method for signature 'HermesDataPcaCor'
autoplot(
    object,
    cor_colors = circlize::colorRamp2(c(-1, 0, 1), c("blue", "white", "red")),
    ...
)
```
correlate.HermesDataPca-method

Arguments

- **object** *(HermesDataPca)*
  - Input. It can be generated using `calc_pca()` function on `AnyHermesData`.
- **data** *(AnyHermesData)*
  - Input that was used originally for the PCA.
- **cor_colors** *(function)*
  - Color scale function for the correlation values in the heatmap, produced by `circlize::colorRamp2()`.
- ... other arguments to be passed to `ComplexHeatmap::Heatmap()`.

Value

A `HermesDataPcaCor` object with R2 values for all sample variables.

Functions

- `autoplot(HermesDataPcaCor)`: This plot method uses the `ComplexHeatmap::Heatmap()` function to visualize a `HermesDataPcaCor` object.

See Also

- `h_pca_df_r2_matrix()` which is used internally for the details.

Examples

```r
object <- hermes_data %>%
  add_quality_flags() %>%
  filter() %>%
  normalize()

# Perform PCA and then correlate the principal components with the sample variables.
object_pca <- calc_pca(object)
result <- correlate(object_pca, object)

# Visualize the correlations in a heatmap.
autoplot(result)

# We can also choose to not reorder the columns.
autoplot(result, cluster_columns = FALSE)

# We can also choose break-points for color customization.
autoplot(result, cor_colors = circlize::colorRamp2(
  c(-0.5, -0.25, 0, 0.25, 0.5, 0.75, 1),
  c("blue", "green", "purple", "yellow", "orange", "red", "brown")
))
```
Counts Accessor and Setter

Description

[Stable]

These methods access and set the counts assay in a AnyHermesData object.

Usage

```r
## S4 method for signature 'AnyHermesData'
counts(object, ...)

## S4 replacement method for signature 'AnyHermesData,matrix'
counts(object, ..., withDimnames = TRUE) <- value
```

Arguments

- `object` (AnyHermesData): object to access the counts from.
- `...` (not used).
- `withDimnames` (flag): setting withDimnames =FALSE in the setter (counts<-) is required when the dimnames on the supplied counts assay are not identical to the dimnames on the AnyHermesData object; it does not influence actual assignment of dimnames to the assay (they’re always stored as-is).
- `value` (matrix): what should the counts assay be replaced with.

Value

The counts assay.

Methods (by class)

- `counts(object = AnyHermesData) <- value`

Examples

```r
a <- hermes_data
test <- counts(a)
class(test)
head(test)
counts(a) <- counts(a) + 100L
head(counts(a))
```
cut_quantile  

Cutting a Numeric Vector into a Factor of Quantile Bins

Description

[Experimental]

This function transforms a numeric vector into a factor corresponding to the quantile intervals. The intervals are left-open and right-closed.

Usage

cut_quantile(x, percentiles = c(1/3, 2/3), digits = 0)

Arguments

- **x** (numeric)  
  the continuous variable values which should be cut into quantile bins. NA values are not taken into account when computing quantiles and are attributed to the NA interval.

- **percentiles** (proportions)  
  the required percentiles for the quantile intervals to be generated. Duplicated values are removed.

- **digits** (integer)  
  the precision to use when formatting the percentages.

Value

The factor with a description of the available quantiles as levels.

Examples

```r
set.seed(452)
x <- runif(10, -10, 10)
cut_quantile(x, c(0.33333333, 0.66666666), digits = 4)
x[1:4] <- NA
cut_quantile(x)
```
df_cols_to_factor

Conversion of Eligible Columns to Factor Variables in a DataFrame

Description

[Experimental]
This utility function converts all eligible character and logical variables in a `S4Vectors::DataFrame` to factor variables. All factor variables get amended with an explicit missing level. This includes both NA and empty strings.

Usage

```
df_cols_to_factor(data, omit_columns = NULL, na_level = "<Missing>")
```

Arguments

- `data` (DataFrame): input `S4Vectors::DataFrame`.
- `omit_columns` (character or NULL): which columns should be omitted from the possible conversion to factor and explicit missing level application.
- `na_level` (string): explicit missing level to be used for factor variables.

Value

The modified data.

Note

All required rowData and colData variables cannot be converted to ensure proper downstream behavior. These are automatically omitted if found in `data` and therefore do not need to be specified in `omit_columns`.

Examples

```
dat <- colData(summarized_experiment)
any(vapply(dat, is.character, logical(1)))
any(vapply(dat, is.logical, logical(1)))
dat_converted <- df_cols_to_factor(dat)
any(vapply(dat_converted, function(x) is.character(x) || is.logical(x), logical(1)))
```
diff_expression  Differential Expression Analysis

Description

[Experimental]

The `diff_expression()` function performs differential expression analysis using a method of preference.

A corresponding `autoplot()` method is visualizing the results as a volcano plot.

Usage

```r
diff_expression(object, group, method = c("voom", "deseq2"), ...)
```

```r
## S4 method for signature 'HermesDataDiffExpr'
autoplot(object, adj_p_val_thresh = 0.05, log2_fc_thresh = 2.5)
```

Arguments

- **object** (AnyHermesData)
  input. Note that this function only uses the original counts for analysis, so this does not need to be normalized.

- **group** (string)
  name of factor variable with 2 levels in `colData(object)`. These 2 levels will be compared in the differential expression analysis.

- **method** (string)
  method for differential expression analysis, see details below.

- **...** additional arguments passed to the helper function associated with the selected method.

- **adj_p_val_thresh** (proportion)
  threshold on the adjusted p-values (y-axis) to flag significance.

- **log2_fc_thresh** (number)
  threshold on the absolute log2 fold-change (x-axis) to flag up- or down-regulation of transcription.

Details

Possible method choices are:

- **voom**: uses `limma::voom()`, see `h_diff_expr_voom()` for details.
- **deseq2**: uses `DESeq2::DESeq()`, see `h_diff_expr_deseq2()` for details.
**Value**

A `HermesDataDiffExpr` object which is a data frame with the following columns for each gene in the `HermesData` object:

- `log2_fc` (the estimate of the log2 fold change between the 2 levels of the provided factor)
- `stat` (the test statistic, which one depends on the method used)
- `p_val` (the raw p-value)
- `adj_p_val` (the multiplicity adjusted p-value value)

**Functions**

- `autoplot(HermesDataDiffExpr)`: generates a volcano plot for a `HermesDataDiffExpr` object.

**Note**

- We provide the `df_cols_to_factor()` utility function that makes it easy to convert the `colData()` character and logical variables to factors, so that they can be subsequently used as group inputs. See the example.
- In order to avoid a warning when using `deseq2`, it can be necessary to specify `fitType = "local"` as additional argument. This could e.g. be the case when only few samples are present in which case the default parametric dispersions estimation will not work.

**Examples**

```r
object <- hermes_data %>%
  add_quality_flags() %>%
  filter()

# Convert character and logical to factor variables in `colData`,
# including the below used `group` variable.
colData(object) <- df_cols_to_factor(colData(object))
res1 <- diff_expression(object, group = "SEX", method = "voom")
head(res1)
res2 <- diff_expression(object, group = "SEX", method = "deseq2")
head(res2)

# Pass method arguments to the internally used helper functions.
res3 <- diff_expression(object, group = "SEX", method = "voom", robust = TRUE, trend = TRUE)
head(res3)
res4 <- diff_expression(object, group = "SEX", method = "deseq2", fitType = "local")
head(res4)

# Create the corresponding volcano plots.
autoplot(res1)
autoplot(res3)
```
draw_barplot  

**Barplot for Gene Expression Percentiles**

**Description**

*Experimental*

This produces a barplot of the dichotomized gene expression counts into two or three categories based on custom defined percentiles.

**Usage**

```r
draw_barplot(
  object,
  assay_name,
  x_spec,
  facet_var = NULL,
  fill_var = NULL,
  percentiles = c(1/3, 2/3)
)
```

**Arguments**

- `object` *(AnyHermesData)*  
  input.
- `assay_name` *(string)*  
  selects assay from input.
- `x_spec` *(GeneSpec)*  
  gene specification for the x-axis.
- `facet_var` *(string or NULL)*  
  optional faceting variable, taken from input sample variables.
- `fill_var` *(string or NULL)*  
  optional fill variable, taken from input sample variables.
- `percentiles` *(vector)*  
  lower and upper percentiles to dichotomize the gene counts into two or three categories.

**Value**

The `ggplot` barplot.

**Examples**

```r
object <- hermes_data

g <- genes(object)
```
**draw_boxplot**  

```r
draw_boxplot(
    object,
    assay_name = "counts",
    x_spec = gene_spec(g[1]),
    facet_var = "SEX",
    fill_var = "AGE18"
)

draw_boxplot(
    object,
    assay_name = "counts",
    x_spec = gene_spec(g[1:3], colMedians, "Median"),
    facet_var = "SEX",
    fill_var = "AGE18"
)

draw_boxplot(
    object,
    assay_name = "counts",
    x_spec = gene_spec(g[1:3], colMeans, "Mean"),
    facet_var = "SEX",
    fill_var = "AGE18",
    percentiles = c(0.1, 0.9)
)
```

---

**Boxplot for Gene Expression Values**

---

**Description**

*[Experimental]*

This produces boxplots of the gene expression values of a single gene, multiple genes or a gene signature.

**Usage**

```r
draw_boxplot(
    object,
    assay_name,
    genes,
    x_var = NULL,
    color_var = NULL,
    facet_var = NULL,
    violin = FALSE,
    jitter = FALSE
)

h_draw_boxplot_df(object, assay_name, genes, x_var, color_var, facet_var)
```
Arguments

- **object** (AnyHermesData): input.
- **assay_name** (string): selects assay from input for the y-axis.
- **genes** (GeneSpec): for which genes or which gene signature to produce boxplots.
- **x_var** (string or NULL): optional stratifying variable for the x-axis, taken from input sample variables.
- **color_var** (string or NULL): optional color variable, taken from input sample variables.
- **facet_var** (string or NULL): optional faceting variable, taken from input sample variables.
- **violin** (flag): whether to draw a violin plot instead of a boxplot.
- **jitter** (flag): whether to add jittered original data points.

Value

The ggplot boxplot.

Functions

- **h_draw_boxplot_df()**: Helper function to prepare the data frame required for plotting.

Examples

```r
object <- hermes_data
draw_boxplot(
  object,
  assay_name = "counts",
  genes = gene_spec(c(A = genes(object)[1]),
  violin = TRUE
)

object2 <- object %>%
  add_quality_flags() %>%
  filter() %>%
  normalize()

draw_boxplot(
  object2,
  assay_name = "tpm",
  x_var = "SEX",
  genes = gene_spec(setNames(genes(object2)[1:10], 1:10), fun = colMeans),
  facet_var = "RACE",
  color_var = "AGE18",
  jitter = TRUE
)```
draw_genes_barplot

) 

draw_boxplot(
  object,
  assay_name = "counts",
  x_var = "SEX",
  genes = gene_spec(genes(object)[1:3]),
  jitter = TRUE,
  facet_var = "AGE18"
)

draw_boxplot(
  object,
  assay_name = "counts",
  genes = gene_spec(c(A = "GeneID:11185", B = "GeneID:10677")),
  violin = TRUE
)

draw_genes_barplot  Stacked Barplot of Low Expression Genes by Chromosome

Description

[Experimental]
This creates a barplot of chromosomes for the AnyHermesData object with the proportions of low expression genes.

Usage

draw_genes_barplot(
  object,
  chromosomes = c(seq_len(22), "X", "Y", "MT"),
  include_others = TRUE
)

Arguments

object  (AnyHermesData)
  input.

chromosomes  (character)
  names of the chromosomes which should be displayed.

include_others  (flag)
  option to show the chromosomes not in chromosomes as "Others".

Value

The ggplot object with the histogram.
Examples

```r
object <- hermes_data

# Display chromosomes 1-22, X, Y, and MT. Other chromosomes are displayed in "Others".
# To increase readability, we can have flip the coordinate axes.
draw_genes_barplot(object) + coord_flip()

# Alternatively we can also rotate the x-axis tick labels.
draw_genes_barplot(object) + theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust = 1))

# Display chromosomes 1 and 2. Other chromosomes are displayed in "Others".
draw_genes_barplot(object, chromosomes = c("1", "2"))

# Display chromosomes 1 and 2 only.
draw_genes_barplot(object, chromosomes = c("1", "2"), include_others = FALSE)
```

---

**draw_heatmap**

*Heatmap for Gene Expression Counts*

Description

[Experimental]

This produces a heatmap of the chosen assay and groups by various sample variables.

Usage

```r
draw_heatmap(
  object,
  assay_name,
  color_extremes = c(0.01, 0.99),
  col_data_annotation = NULL,
  ...
)
```

Arguments

- **object** *(AnyHermesData)*
  - input.
- **assay_name** *(string)*
  - selects assay from input.
- **color_extremes** *(numeric)*
  - min and max percentiles to inform the color scheme of the heatmap as blue and red respectively.
- **col_data_annotation** *(character or NULL)*
  - optional grouping variable(s), taken from input sample variables.
- **...**
  - additional arguments to pass to `ComplexHeatmap::Heatmap()`.
draw_libsize_densities

Value

The ComplexHeatmap::Heatmap heatmap

Examples

```r
result <- hermes_data %>%
  normalize(methods = "voom") %>%
  add_quality_flags() %>%
  filter(what = "genes")

draw_heatmap(
  object = result[1:10, ],
  assay_name = "counts",
  col_data_annotation = "COUNTRY"
)

draw_heatmap(
  object = result[1:10, ],
  assay_name = "counts",
  color_extremes = c(0.001, 0.999),
  col_data_annotation = "AGEGRP"
)
```

draw_libsize_densities

_Density Plot of (Log) Counts Distributions_

Description

[Experimental]
This creates a density plot of the (log) counts distributions of the AnyHermesData object where each line on the plot corresponds to a sample.

Usage

draw_libsize_densities(object, log = TRUE)

Arguments

- **object** (AnyHermesData): input.
- **log** (flag): should the counts be log transformed (log2).

Value

The ggplot object with the density plot.
Examples

```r
result <- hermes_data
draw_libsize_densities(result)
draw_libsize_densities(result, log = FALSE)
```

---

draw_libsize_hist | Histogram of Library Sizes

Description

[Experimental]

This creates a histogram of the library sizes of the AnyHermesData object.

Usage

```r
draw_libsize_hist(object, bins = 30L, fill = "darkgrey")
```

Arguments

- **object** (AnyHermesData): input.
- **bins** (count): number of evenly distributed groups desired.
- **fill** (string): color of the bars filling.

Value

The ggplot object with the histogram.

Examples

```r
result <- hermes_data
draw_libsize_hist(result)
draw_libsize_hist(result, bins = 10L, fill = "blue")
```
**draw_libsize_qq**

*Q-Q Plot of Library Sizes*

**Description**

[Experimental]

This creates a Q-Q plot of the library sizes of the `AnyHermesData` object.

**Usage**

```r
draw_libsize_qq(object, color = "grey", linetype = "dashed")
```

**Arguments**

- `object` (AnyHermesData)
  - Input.
- `color` (string)
  - Color of Q-Q line.
- `linetype` (string)
  - Line type of Q-Q line.

**Value**

The ggplot object with the Q-Q Plot.

**Examples**

```r
result <- hermes_data
draw_libsize_qq(result)
draw_libsize_qq(result, color = "blue", linetype = "solid")

# We can also add sample names as labels.
library(ggrepel)
draw_libsize_qq(result) + geom_text_repel(label = colnames(result), stat = "qq")
```

---

**draw_nonzero_boxplot**

*Boxplot of Non-Zero Genes*

**Description**

[Experimental]

This draws a boxplot, with overlaid data points, of the number of non-zero expressed genes per sample.
### draw_nonzero_boxplot

**Usage**

```r
draw_nonzero_boxplot(object, position = position_jitter(0.2), alpha = 0.25)
```

**Arguments**

- `object` *(AnyHermesData)*
  - Input.
- `position` *(Position)*
  - Specifies x-axis position of points, e.g., for jittering.
- `alpha` *(proportion)*
  - Specifies transparency of points.

**Value**

The ggplot object with the boxplot.

**Examples**

```r
# Default boxplot.
result <- hermes_data
draw_nonzero_boxplot(result)

# Reusing the same position for labeling.
library(ggrepel)
pos <- position_jitter(0.5)
draw_nonzero_boxplot(result, position = pos) +
  geom_text_repel(aes(label = samples(result)), position = pos)
```

---

### draw_scatterplot

**Scatterplot for Gene Expression Values**

**Description**

[Experimental]

This produces a scatterplot of two genes or gene signatures.

**Usage**

```r
draw_scatterplot(
  object,
  assay_name,
  x_spec,
  y_spec,
  color_var = NULL,
  facet_var = NULL,
  smooth_method = c("lm", "loess", "none")
)
```
Arguments

- **object** *(AnyHermesData)*
  - Input.
- **assay_name** *(string)*
  - Selects assay from input.
- **x_spec** *(GeneSpec)*
  - Gene specification for the x-axis.
- **y_spec** *(GeneSpec)*
  - Gene specification for the y-axis.
- **color_var** *(string or NULL)*
  - Optional color variable, taken from input sample variables.
- **facet_var** *(string or NULL)*
  - Optional faceting variable, taken from input sample variables.
- **smooth_method** *(string)*
  - Smoothing method to use, either linear regression line (*lm*), local polynomial regression (*loess*) or none.

Value

The ggplot scatterplot.

Examples

```R
object <- hermes_data
g <- genes(object)
draw_scatterplot(
  object,
  assay_name = "counts",
  facet_var = NULL,
  x_spec = gene_spec(c(A = g[1]),
  y_spec = gene_spec(g[2]),
  color = "RACE"
)

object2 <- object %>%
  add_quality_flags() %>%
  filter() %>%
  normalize()
g2 <- genes(object2)
draw_scatterplot(
  object2,
  assay_name = "tpm",
  facet_var = "SEX",
  x_spec = gene_spec(g2[1:10], colMeans, "Mean"),
  y_spec = gene_spec(g2[11:20], colMedians, "Median"),
  smooth_method = "loess"
)```

### expression_set

#### Example ExpressionSet Data

**Description**

[Stable]

This example data can be used to try out conversion of a `Biobase::ExpressionSet` object into a `HermesData` object.

**Usage**

```
expression_set
```

**Format**

A `Biobase::ExpressionSet` object with 20 samples covering 5085 features (Entrez gene IDs).

**Source**

This is an artificial dataset designed to resemble real data.

**See Also**

- `SummarizedExperiment::makeSummarizedExperimentFromExpressionSet()` to convert into a `SummarizedExperiment::SummarizedExperiment`.
- `summarized_experiment` which contains similar data already as a `SummarizedExperiment::SummarizedExperiment`.

---

### extra_data_names

#### Extra Variable Names Accessor Methods

**Description**

[Experimental]

The methods access the names of the variables in `colData()` and `rowData()` of the object which are not required by design. So these can be additional sample or patient characteristics, or gene characteristics.
Usage

extraColDataNames(x, ...)

## S4 method for signature 'AnyHermesData'
extraColDataNames(x, ...)

extraRowDataNames(x, ...)

## S4 method for signature 'AnyHermesData'
extraRowDataNames(x, ...)

Arguments

x (AnyHermesData)
  object.

... not used.

Value

The character vector with the additional variable names in either colData() or rowData().

Examples

object <- hermes_data
extraColDataNames(object)
extraRowDataNames(object)

filter Filter AnyHermesData on Subset Passing Default QC Flags

Description

[Stable]

This filters a AnyHermesData object using the default QC flags and required annotations.

Usage

filter(object, ...)

## S4 method for signature 'AnyHermesData'
filter(object, what = c("genes", "samples"), annotation_required = "size")

## S4 method for signature 'data.frame'
filter(object, ...)

## S4 method for signature 'ts'
filter(object, ...)
Arguments

object (AnyHermesData)
object to filter.

... additional arguments.

what (character)
specify whether to apply the filter on genes and/or samples.

annotation_required
(character)
names of required annotation columns for genes. Only used when genes are filtered.

Details

- Only genes without low expression (low_expression_flag) and samples without low depth (low_depth_flag) or technical failure (tech_failure_flag) remain in the returned filtered object.
- Also required gene annotation columns can be specified, so that genes which are not complete for these columns are filtered out. By default this is the size column, which is needed for default normalization of the object.

Value

The filtered AnyHermesData object.

Note

The internal implementation cannot use the subset() method since that requires non-standard evaluation of arguments.

Examples

```r
a <- hermes_data
dim(a)

# Filter genes and samples on default QC flags.
result <- filter(a)
dim(result)

# Filter only genes without low expression.
result <- filter(a, what = "genes")

# Filter only samples with low depth and technical failure.
result <- filter(a, what = "samples")

# Filter only genes, and require certain annotations to be present.
result <- filter(a, what = "genes", annotation_required = c("size"))
```
genes

<table>
<thead>
<tr>
<th>Genes Accessor</th>
</tr>
</thead>
</table>

**Description**

**[Stable]**

Access the gene IDs, i.e., row names, of a `AnyHermesData` object with a nicely named accessor method.

**Usage**

```r
genes(object)
```

```r
## S4 method for signature 'AnyHermesData'
genes(object)
```

**Arguments**

- `object` *(AnyHermesData)*
  - input.

**Value**

The character vector with the gene IDs.

**See Also**

- `samples()` to access the sample IDs.

**Examples**

```r
a <- hermes_data
genes(a)
```

---

**Genespec**

*R6 Class Representing a Gene (Signature) Specification*

**Description**

**[Experimental]**

A GeneSpec consists of the gene IDs (possibly named with labels), the summary function and the name of the summary function.
Methods

Public methods:

- `GeneSpec$new()`
- `GeneSpec$get_genes()`
- `GeneSpec$get_gene_labels()`
- `GeneSpec$returns_vector()`
- `GeneSpec$get_label()`
- `GeneSpec$extract()`
- `GeneSpec$extract_data_frame()`
- `GeneSpec$clone()`

Method `new()`: Creates a new `GeneSpec` object.

Usage:
```r
GeneSpec$new(genes = NULL, fun = NULL, fun_name = deparse(substitute(fun)))
```

Arguments:
- `genes` (named character or NULL)
  - the gene IDs, where the names are used as labels if available.
- `fun` (function or NULL)
  - summary function. If NULL is used then multiple genes are not summarized but returned as a matrix from the `extract` method.
- `fun_name` (string)
  - name of the summary function.

Returns: A new `GeneSpec` object.

Method `get_genes()`: Returns the genes.

Usage:
```r
GeneSpec$get_genes()
```

Method `get_gene_labels()`: Returns the gene labels (substituted by gene IDs if not available).

Usage:
```r
GeneSpec$get_gene_labels(genes = self$get_genes())
```

Arguments:
- `genes` (character)
  - for which subset of genes the labels should be returned.

Method `returns_vector()`: Predicate whether the `extract` returns a vector or not.

Usage:
```r
GeneSpec$returns_vector()
```

Method `get_label()`: Returns a string which can be used e.g. for plot labels.

Usage:
```r
GeneSpec$get_label(genes = self$get_genes())
```

Arguments:
genes (character)
  for which subset of genes the labels should be returned.

Method extract(): Extract the gene values from an assay as specified.
  
Usage:
  GeneSpec$extract(assay)

Arguments:
  assay (matrix)
    original matrix with rownames containing the specified genes.

Returns: Either a vector with one value per column, or a matrix with multiple genes in the rows.

Method extract_data_frame(): Extract the gene values as a data.frame.
  
Usage:
  GeneSpec$extract_data_frame(assay)

Arguments:
  assay (matrix)
    original matrix with rownames containing the specified genes.

Returns: A data.frame with the genes in the columns and the samples in the rows.

Method clone(): The objects of this class are cloneable with this method.
  
Usage:
  GeneSpec$clone(deep = FALSE)

Arguments:
  deep Whether to make a deep clone.

Examples

  # Minimal specification if only one gene is used.
  x_spec <- gene_spec("GeneID:1820")

  # Using multiple genes with a signature.
  x_spec <- gene_spec(c("GeneID:1820", "GeneID:52"), fun = colMeans)
  x_spec <- gene_spec(c("GeneID:1820", "GeneID:52"), fun = colPrinComp1)
  x_spec$returns_vector()
  x_spec$get_genes()
  x_spec$get_gene_labels()
  x_spec$get_label()

  # Using multiple genes with partial labels, without a signature.
  x_spec <- gene_spec(c(A = "GeneID:1820", "GeneID:52"))
  x_spec$returns_vector()
  x_spec$get_gene_labels()

  # Use the gene specification to extract genes from a matrix.
  mat <- matrix(
    data = rpois(15, 10),
    nrow = 15, ncol = 10, byrow = TRUE)
  x_spec$extract(mat)
  x_spec$extract_data_frame(mat)
gene_spec
	nrow = 3, ncol = 5,
dimnames = list(c("GeneID:1820", "GeneID:52", "GeneID:523"), NULL)
x_spec$extract(mat)

# We can also extract these as a `data.frame`.
x_spec$extract_data_frame(mat)

gene_spec GeneSpec Constructor

Description

[Experimental]

Creates a new GeneSpec object.

Usage

gene_spec(genes = NULL, fun = NULL, fun_name = deparse(substitute(fun)))

Arguments

genes (named character or NULL)
the gene IDs, where the names are used as labels if available.

fun (function or NULL)
summary function. If NULL is used then multiple genes are not summarized but
returned as a matrix from the extract method.

fun_name (string)
name of the summary function.

Value

A new GeneSpec object.

Examples

gene_spec("GeneID:11185")
Description

[Experimental]

The **HermesData** class is an extension of **SummarizedExperiment::SummarizedExperiment** with additional validation criteria.

Usage

HermesData(object)

HermesDataFromMatrix(counts, ...)

Arguments

- **object** (SummarizedExperiment)
  input to create the **HermesData** object from. If this is a RangedSummarizedExperiment, then the result will be **RangedHermesData**.

- **counts** (matrix)
  counts to create the **HermesData** object from.

- **...** additional arguments, e.g. **rowData**, **colData**, etc. passed to **SummarizedExperiment::SummarizedExperiment()** internally. Note that if **rowRanges** is passed instead of **rowData**, then the result will be a **RangedHermesData** object.

Details

The additional criteria are:

- The first assay must be counts containing non-missing, integer, non-negative values. Note that **rename()** can be used to edit the assay name to counts if needed.

- The following columns must be in **rowData**:
  - symbol (also often called HGNC or similar, example: "INMT")
  - desc (the gene name, example: "indolethylamine N-methyltransferase")
  - chromosome (the chromosome as string, example: "7")
  - size (the size of the gene in base pairs, e.g 5468)
  - low_expression_flag (can be populated with **add_quality_flags()**)

- The following columns must be in **colData**:
  - low_depth_flag (can be populated with **add_quality_flags()**)
  - tech_failure_flag (can be populated with **add_quality_flags()**)

- The object must have unique row and column names. The row names are the gene names and the column names are the sample names.
Analogously, `RangedHermesData` is an extension of `SummarizedExperiment::RangedSummarizedExperiment` and has the same additional validation requirements. Methods can be defined for both classes at the same time with the `AnyHermesData` signature.

A `Biobase::ExpressionSet` object can be imported by using the `SummarizedExperiment::makeSummarizedExperimentFromExpressionSet()` function to first convert it to a `SummarizedExperiment::SummarizedExperiment` object before converting it again into a `HermesData` object.

Value

An object of class `AnyHermesData` (`HermesData` or `RangedHermesData`).

Slots

`prefix` common prefix of the gene IDs (row names).

Note

- Note that we use `S4Vectors::setValidity2()` to define the validity method, which allows us to turn off the validity checks in internal functions where intermediate objects may not be valid within the scope of the function.
- It can be helpful to convert character and logical variables to factors in `colData()` (before or after the `HermesData` creation). We provide the utility function `df_cols_to_factor()` to simplify this task, but leave it to the user to allow for full control of the details.

See Also

`rename()` for renaming columns of the input data.

Examples

```r
# Convert an "ExpressionSet" to a "RangedSummarizedExperiment".
ranged_summarized_experiment <- makeSummarizedExperimentFromExpressionSet(expression_set)

# Then convert to "RangedHermesData".
HermesData(ranged_summarized_experiment)

# Create objects starting from a "SummarizedExperiment".
hermes_data <- HermesData(summarized_experiment)
hermes_data

# Create objects from a matrix. Note that additional arguments are not required but possible.
counts_matrix <- assay(summarized_experiment)
counts_hermes_data <- HermesDataFromMatrix(counts_matrix)
```
hermes_data  Example HermesData Data

Description

[Stable]

This example HermesData is created from the underlying SummarizedExperiment::SummarizedExperiment object by renaming descriptors to align with standard specification. It already contains the required columns in rowData and colData.

Usage

hermes_data

Format

A HermesData object with 20 samples covering 5085 features (Entrez gene IDs).

Source

This is an artificial dataset designed to resemble real data.

See Also

summarized_experiment for the underlying SummarizedExperiment::SummarizedExperiment object.

h_all_duplicated  Finding All Duplicates in Vector

Description

The difference here to duplicated() is that also the first occurrence of a duplicate is flagged as TRUE.

Usage

h_all_duplicated(x)

Arguments

x a vector or a data frame or an array or NULL.

Value

Logical vector flagging all occurrences of duplicate values as TRUE.
**Examples**

```r
h_all_duplicated(c("a", "a", "b"))
duplicated(c("a", "a", "b"))
```

---

**h_df_factors_with_explicit_na**

*Conversion to Factors with Explicit Missing Level in a data.frame*

**Description**

[Experimental]

This helper function converts all character and logical variables to factor variables in a `data.frame`. It also sets an explicit missing data level for all factor variables that have at least one `NA`. Empty strings are handled as `NA`.

**Usage**

```r
h_df_factors_with_explicit_na(data, na_level = "<Missing>")
```

**Arguments**

- `data` *(data.frame)*
  - input data with at least one column.
- `na_level` *(string)*
  - explicit missing level to be used.

**Value**

The modified data.

**Examples**

```r
dat <- data.frame(
a = c(NA, 2),
b = c("A", NA),
c = c("C", "D"),
d = factor(c(NA, "X")),
e = factor(c("Y", "Z"))
)
h_df_factors_with_explicit_na(dat)
```
**h_diff_expr_deseq2**  

DESeq2 Differential Expression Analysis

---

**Description**

[Experimental]  
This helper function performs the differential expression analysis with `DESeq2::DESeq()` for a given AnyHermesData input and design matrix.

**Usage**

`h_diff_expr_deseq2(object, design, ...)`

**Arguments**

- **object** (HermesData) input.  
- **design** (matrix) design matrix.  
- **...** additional arguments internally passed to `DESeq2::DESeq()` (fitType, sfType, minReplicatesForReplace, useT, minmu).

**Value**

A data frame with columns log2_fc (estimated log2 fold change), stat (Wald statistic), p_val (raw p-value), adj_p_pval (Benjamini-Hochberg adjusted p-value).

**References**


**Examples**

```r
object <- hermes_data

# Create the design matrix corresponding to the factor of interest.
design <- model.matrix(~SEX, colData(object))

# Then perform the `DESeq2` differential expression analysis.
result <- h_diff_expr_deseq2(object, design)
head(result)

# Change of the `fitType` can be required in some cases.
result2 <- h_diff_expr_deseq2(object, design, fitType = "local")
head(result2)
```
**h_diff_expr_voom**

### Description

[Experimental]

This helper function performs the differential expression analysis with the voom method from the limma package (via `limma::voom()`, `limma::lmFit()` and `limma::eBayes()`) for given counts in a AnyHermesData object and a corresponding design matrix.

### Usage

```r
h_diff_expr_voom(object, design, ...)
```

### Arguments

- **object** (AnyHermesData)
  - input.
- **design** (matrix)
  - design matrix.
- **...**
  - additional arguments internally passed to `limma::eBayes()` (robust, trend, proportion, winsor.tail.p, stdev.coef.lim).

### Value

A data frame with columns `log2_fc` (estimated log2 fold change), `stat` (moderated t-statistic), `p_val` (raw p-value), `adj_p_pval` (Benjamini-Hochberg adjusted p-value).

### References


### Examples

```r
object <- hermes_data

# Create the design matrix corresponding to the factor of interest.
design <- model.matrix(~SEX, colData(object))

# Then perform the differential expression analysis.
result <- h_diff_expr_voom(object, design)
head(result)
```
h_ensembl_to_entrez_ids

Translation of Ensembl to Entrez Gene IDs

Description

[Experimental]

This helper function queries BioMart to translate Ensembl to Entrez Gene IDs.

Usage

h_ensembl_to_entrez_ids(gene_ids, mart)

Arguments

gene_ids (character)
Ensembl gene IDs.
mart (Mart)
given biomaRt::Mart object.

Value

Character vector of Entrez gene IDs.

Examples

if (interactive()) {
  mart <- biomaRt::useMart("ensembl", dataset = "hsapiens_gene_ensembl")
  h_ensembl_to_entrez_ids(c("ENSG00000135407", "ENSG00000241644"), mart)
}

h_get_annotation_biomart

Get Annotations from BioMart

Description

[Experimental]

Helper function to query annotations from biomaRt, for cleaned up gene IDs of a specific ID variable and given biomaRt::Mart.
Usage

h_get_granges_by_id(coords, id)

Description

[Experimental]
This function extracts the chromosome number, the start position and the end position of transcripts in given data.frame with coordinates as returned by biomaRt::getBM() and converts them to a GRanges object.

Usage

h_get_granges_by_id(coords, id)
Arguments

coords  
(data.frame) 
as returned by biomaRt::getBM(), containing the columns ensembl_gene_id, 
chromosome_name, exon_chrom_start, exon_chrom_end.

id  
(string) 
single Ensembl gene ID to convert the coordinates for.

Value

GRange objects for the respective single gene ID.

Examples

if (interactive()) {
  mart <- biomaRt::useMart("ensembl", dataset = "hsapiens_gene_ensembl")
  attrs <- c(
    "ensembl_gene_id",
    "ensembl_exon_id",
    "chromosome_name",
    "exon_chrom_start",
    "exon_chrom_end"
  )
  coords <- biomaRt::getBM(
    filters = "entrezgene_id",
    attributes = attrs,
    values = c("11185", "10677"),
    mart = mart
  )
  h_get_granges_by_id(coords, "ENSG00000135407")
}

Description

[Experimental]

This helper function queries BioMart for lengths of genes by adding up all exon lengths after reducing overlaps.

Usage

h_get_size_biomart(gene_ids, id_var, mart)
Arguments

gene_ids (character)
gene IDs, e.g. 10329, i.e. already without the Entrez GeneID prefix, or ENSG00000241644 for Ensembl gene ID.

id_var (string)
corresponding gene ID variable name in BiolR, i.e. entrezgene_id or ensembl_gene_id.

mart (Mart)
given BioR::Mart object.

Value
Named integer vector indicating the gene lengths.

Examples
if (interactive()) {
  mart <- biomaR::useMart("ensembl", dataset = "hsapiens_gene_ensembl")
  h_get_size_biomart("11185", "entrezgene_id", mart)
  h_get_size_biomart("ENSG00000215417", "ensembl_gene_id", mart)
  h_get_size_biomart(c("11185", "10677"), "entrezgene_id", mart)
  h_get_size_biomart(c("ENSG00000135407", "ENSG00000215417"), "ensembl_gene_id", mart)
}

h_has_req_annotations  Predicate for Required Annotations

Description
[Experimental]
This helper function determines for each gene in the object whether all required annotation columns are filled.

Usage
h_has_req_annotations(object, annotation_required)

Arguments

object (AnyHermesData)
input object.

annotation_required (character)
names of required annotation columns for genes.

Value
Named logical vector with one value for each gene in object, which is TRUE if all required annotation columns are filled, and otherwise FALSE.
**h_map_pos**

**See Also**

`filter()` where this is used internally.

**Examples**

```r
object <- hermes_data
result <- h_has_req_annotations(object, "size")
all(result)
rowData(object)$size[1] <- NA # nolint
which(!h_has_req_annotations(object, "size"))
```

---

**h_map_pos**  
*Helper Function For Matching Map Values to Names*

**Description**

This is used by the `rename` method. It wraps the assertions and the matching used several times.

**Usage**

```r
h_map_pos(names, map)
```

**Arguments**

- `names` *(character)*  
  original names.
- `map` *(named character)*  
  the mapping vector from old (value) to new (name) names. All values must be included in `names`.

**Value**

Integer vector of the positions of the map values in the names.

**Examples**

```r
h_map_pos(c("a", "b"), c(d = "b"))
```
**h_parens**  
Parenthesize a Character Vector

**Description**

[Experimental]  
This helper function adds parentheses around each element of a character vector.

**Usage**

```r
h_parens(x)
```

**Arguments**

- `x` (character)  
  inputs which should be parenthesized.

**Value**

Character vector with parentheses, except when `x` is a blank string in which case it is returned unaltered.

**Examples**

```r
h_parens("bla")  
h_parens("")  
h_parens(c("bla", "bli"))
```

---

**h_pca_df_r2_matrix**  
Calculation of R2 Matrix between Sample Variables and Principal Components

**Description**

[Stable]  
This function processes sample variables from `AnyHermesData` and the corresponding principal components matrix, and then generates the matrix of R2 values.

**Usage**

```r
h_pca_df_r2_matrix(pca, df)
```
Arguments

pca
(matrix)
comprises principal components generated by `calc_pca()`.

df
(data.frame)
from the `SummarizedExperiment::colData()` of a `AnyHermesData` object.

Details

- Note that only the df columns which are numeric, character, factor or logical are included in the resulting matrix, because other variable types are not supported.
- In addition, df columns which are constant, all NA, or character or factor columns with too many levels are also dropped before the analysis.

Value

A matrix with R2 values for all combinations of sample variables and principal components.

See Also

`h_pca_var_rsquared()` which is used internally to calculate the R2 for one sample variable.

Examples

```r
object <- hermes_data %>%
  add_quality_flags() %>%
  filter() %>%
  normalize()

# Obtain the principal components.
pca <- calc_pca(object)$x

# Obtain the `colData` as a `data.frame`.
df <- as.data.frame(colData(object))

# Correlate them.
r2_all <- h_pca_df_r2_matrix(pca, df)
str(r2_all)

# We can see that only about half of the columns from `df` were
# used for the correlations.
ncol(r2_all)
ncol(df)
```
h_pca_var_r_squared  

Calculation of R2 between Sample Variable and Principal Components

Description

[Stable]

This helper function calculates R2 values between one sample variable from AnyHermesData and all Principal Components (PCs) separately (one linear model is fit for each PC).

Usage

h_pca_var_r_squared(pca, x)

Arguments

pca  (matrix)
principal components matrix generated by calc_pca().

x  (vector)
values of one sample variable from a AnyHermesData object.

Details

Note that in case there are estimation problems for any of the PCs, then NA will be returned for those.

Value

A vector with R2 values for each principal component.

Examples

```
object <- hermes_data %>%
  add_quality_flags() %>%
  filter() %>%
  normalize()

# Obtain the principal components.
pca <- calc_pca(object)$x

# Obtain the sample variable.
x <- colData(object)$AGE18

# Correlate them.
r2 <- h_pca_var_r_squared(pca, x)
```
Description

[Experimental]
This helper function makes a short list string, e.g. "a, b, ..., z" out of a character vector, e.g. letters.

Usage

```r
h_short_list(x, sep = "", thresh = 3L)
```

Arguments

- **x**: (character) input which should be listed.
- **sep**: (string) separator to use.
- **thresh**: (count) threshold to use, if the length of x is larger then the list will be shortened using the ... ellipsis.

Value

String with the short list.

Examples

```r
h_short_list(letters)
h_short_list(letters[1:3])
h_short_list(LETTERS[1:5], sep = ";", thresh = 5L)
```

---

Description

[Experimental]
This helper function removes the prefix and possible delimiter from a vector of gene IDs, such that only the digits are returned.

Usage

```r
h_strip_prefix(gene_ids, prefix)
```
Arguments

gene_ids (character)
original gene IDs including prefix and optional delimiter before the digits.

prefix (string)
common prefix to be stripped away from gene_ids.

Value

Character vector that contains only the digits for each gene ID.

Note

This is currently used to strip away the GeneID prefix from Entrez gene IDs so that they can be queried from BioMart

Examples

h_strip_prefix(c("GeneID:11185", "GeneID:10677"), prefix = "GeneID")

h_unique_labels (Creation of Unique Labels)

Description

This helper function generates a set of unique labels given unique IDs and not necessarily unique names.

Usage

h_unique_labels(ids, nms = NULL)

Arguments

ids (character or NULL)
unique IDs.

nms (character or NULL)
not necessarily unique names if provided.

Value

Character vector where empty names are replaced by the IDs and non-unique names are made unique by appending the IDs in parentheses.

Examples

h_unique_labels(c("1", "2", "3"), c("A", "B", "A"))
h_unique_labels(NULL)
h_unique_labels(c("1", "2", "3"))
inner_join_cdisc

Description
[Experimental]
This is a useful function when trying to join genetic with CDISC data sets.

Usage
inner_join_cdisc(
  gene_data,  
gene_data,  
cdisc_data,  
  patient_key = "USUBJID",  
  additional_keys = character()
)

Arguments
  gene_data (data.frame or DataFrame)
  genetic data.
  cdisc_data (data.frame)
  CDISC data (typically patient level data).
  patient_key (string)
  patient identifier.
  additional_keys (character)
  potential additional keys for the two data sets.

Value
A data.frame which contains columns from both data sets merged by the keys.

Note
Columns which are contained in both data sets but are not specified as keys are taken from gene_data
and not from cdisc_data.

Examples
  gene_data <- col_data_with_genes(hermes_data, "counts", gene_spec("GeneID:1820"))
  cdisc_data <- data.frame(  
    USUBJID = head(gene_data$USUBJID, 10),
    extra = 1:10
  )
  result <- inner_join_cdisc(gene_data, cdisc_data)
  result
### Description

[Experimental]

This method checks whether a `SummarizedExperiment::SummarizedExperiment` object is empty.

### Usage

```r
## S4 method for signature 'SummarizedExperiment'
isEmpty(x)
```

### Arguments

- **x** 
  
  (SummarizedExperiment) object to check.

### Value

Flag whether the object is empty.

### Examples

```r
isEmpty(summarized_experiment)
isEmpty(summarized_experiment[NULL, ])
isEmpty(hermes_data)
```

### Description

[Experimental]

Apply a function on all experiments in an MAE.

### Usage

```r
## S4 method for signature 'MultiAssayExperiment'
lapply(X, FUN, safe = TRUE, ...)
```
**Arguments**

- **X**
  (MultiAssayExperiment)
  input.
- **FUN**
  (function) to be applied to each experiment in X.
- **safe**
  (flag)
  whether this method should skip experiments where the function fails.
- ... additional arguments passed to FUN.

**Value**

MultiAssayExperiment object with specified function applied.

**Examples**

```r
object <- multi_assay_experiment
result <- lapply(object, normalize, safe = TRUE)
# Similarly, all experiments in an MAE can be converted to HermesData class:
result <- lapply(object, HermesData, safe = TRUE)
```

---

**metadata**

*Metadata Accessor and Setter*

**Description**

[Stable]

These methods access or set the metadata in a AnyHermesData object.

**Arguments**

- **x**
  (AnyHermesData)
  object to access the metadata from.
- **value**
  (list)
  the list to replace the current metadata with.

**Value**

The metadata which is a list.

**Note**

Note that this just inherits S4Vectors::metadata,Annotated-method().

**Examples**

```r
a <- hermes_data
metadata(a)
metadata(a) <- list(new = "my metadata")
metadata(a)
```
Example MultiAssayExperiment Data

Description

[Experimental]
This example MultiAssayExperiment::MultiAssayExperiment can be used as test data.

Usage

multi_assay_experiment

Format

A MultiAssayExperiment::MultiAssayExperiment object with 3 separate HermesData objects.

- The first object contains 5 samples and covers 1000 features (Entrez gene IDs).
- The second object contains 9 samples with 2500 features.
- The third object contains 6 samples with 1300 features.

Source

This is an artificial dataset designed to resemble real data.

Normalization of AnyHermesData Objects

Description

[Stable]
The normalize() method is normalizing the input AnyHermesData according to one or more specified normalization methods. The results are saved as additional assays in the object.

Possible normalization methods (which are implemented with separate helper functions):

- cpm: Counts per Million (CPM). Separately by sample, the original counts of the genes are divided by the library size of this sample, and multiplied by one million. This is the appropriate normalization for between-sample comparisons.

- rpkm: Reads per Kilobase of transcript per Million reads mapped (RPKM). Each gene count is divided by the gene size (in kilobases) and then again divided by the library sizes of each sample (in millions). This allows for within-sample comparisons, as it takes into account the gene sizes - longer genes will always have more counts than shorter genes.
- **tpm**: Transcripts per Million (TPM). This addresses the problem of RPKM being inconsistent across samples (which can be seen that the sum of all RPKM values will vary from sample to sample). Therefore here we divide the RPKM by the sum of all RPKM values for each sample, and multiply by one million.
- **voom**: VOOM normalization. This is essentially just a slight variation of CPM where a prior_count of 0.5 is combined with lib_sizes increased by 1 for each sample. Note that this is not required for the corresponding differential expression analysis, but just provided as a complementary experimental normalization approach here.
- **vst**: Variance stabilizing transformation. This is to transform the normalized count data for all genes into approximately homoskedastic values (having constant variance).
- **rlog**: The transformation to the log2 scale values with approximately homoskedastic values.

### Usage
```r
## S4 method for signature 'AnyHermesData'
normalize(
  object,
  methods = c("cpm", "rpkm", "tpm", "voom", "vst"),
  control = control_normalize(),
  ...
)

h_cpm(object, control = control_normalize())

h_rpkm(object, control = control_normalize())

h_tpm(object, control = control_normalize())

h_voom(object, control = control_normalize())

h_vst(object, control = control_normalize())

h_rlog(object, control = control_normalize())
```

### Arguments

- **object** *(AnyHermesData)*
  object to normalize.
- **methods** *(character)*
  which normalization methods to use, see details.
- **control** *(named list)*
  settings produced by `control_normalize()`.
- **...**
  not used.

### Value

The `AnyHermesData` object with additional assays containing the normalized counts. The control is saved in the metadata of the object for future reference.
Functions

- `h_cpm()`: calculates the Counts per Million (CPM) normalized counts.
- `h_rpkm()`: calculates the Reads per Kilobase per Million (RPKM) normalized counts.
- `h_tpm()`: calculates the Transcripts per Million (TPM) normalized counts.
- `h_voom()`: calculates the VOOM normalized counts. [Experimental]
- `h_vst()`: variance stabilizing transformation (vst) from DESeq2 package.
- `h_rlog()`: regularized log transformation (rlog) from DESeq2 package.

See Also

`control_normalize()` to define the normalization method settings.

Examples

```r
a <- hermes_data

# By default, log values are used with a prior count of 1 added to original counts.
result <- normalize(a)
assayNames(result)
tpm <- assay(result, "tpm")
  tpm[1:3, 1:3]

# We can also work on original scale.
result_orig <- normalize(a, control = control_normalize(log = FALSE))
tpm_orig <- assay(result_orig, "tpm")
tpm_orig[1:3, 1:3]

# Separate calculation of the CPM normalized counts.
counts_cpm <- h_cpm(a)
str(counts_cpm)

# Separate calculation of the RPKM normalized counts.
counts_rpkm <- h_rpkm(a)
str(counts_rpkm)

# Separate calculation of the TPM normalized counts.
counts_tpm <- h_tpm(a)
str(counts_tpm)

# Separate calculation of the VOOM normalized counts.
counts_voom <- h_voom(a)
str(counts_voom)

# Separate calculation of the vst transformation.
counts_vst <- h_vst(a)
str(counts_vst)

# Separate calculation of the rlog transformation.
counts_rlog <- h_rlog(a)
str(counts_rlog)
```
Description

Prefix Accessor

[Experimental]

Generic function to access the prefix from an object.

Usage

prefix(object, ...)

Arguments

object (AnyHermesData)
  input.

... additional arguments.

Value

The prefix slot contents.

Examples

a <- hermes_data
prefix(a)

query

Query Gene Annotations from a Connection

Description

[Experimental]

The generic function `query()` is the interface for querying gene annotations from a data base connection.

Usage

query(genes, connection)

## S4 method for signature 'character,ConnectionBiomart'
query(genes, connection)
Arguments

genes (character)
gene IDs.
connection (connection class)
data base connection object.

Details

• A method is provided for the `ConnectionBiomart` class. However, the framework is extensible: It is simple to add new connections and corresponding query methods for other data bases, e.g. company internal data bases. Please make sure to follow the required format of the returned value.

• The BioMart queries might not return information for all the genes. This can be due to different versions being used in the gene IDs and the queried Ensembl data base.

Value

A `S4Vectors::DataFrame` with the gene annotations. It is required that:

• The rownames are identical to the input genes.

• The colnames are equal to the annotation columns `.row_data_annotation_cols`.

• Therefore, missing information needs to be properly included in the DataFrame with NA entries.

Examples

```r
if (interactive()) {
  object <- hermes_data
  connection <- connect_biomart(prefix(object))
  result <- query(genes(object), connection)
  head(result)
  head(annotation(object))
}
```

---

**rbind**

*Row Binding of AnyHermesData Objects*

Description

[Stable]

This method combines `AnyHermesData` objects with the same samples but different features of interest (rows in assays).

Arguments

... (AnyHermesData)
objects to row bind.
Value

The combined **AnyHermesData** object.

Note

- Note that this just inherits `SummarizedExperiment::rbind,SummarizedExperiment-method()`. When binding a **AnyHermesData** object with a **SummarizedExperiment** object, then the result will be a **SummarizedExperiment** object (the more general class).
- Note that we need to have unique gene IDs (row names) and the same prefix across the combined object.

See Also

`cbind` to column bind objects.

Examples

```r
a <- hermes_data[1:2542, ]
b <- hermes_data[2543:5085, ]
result <- rbind(a, b)
class(result)
```

Description

**Renaming Contents of SummarizedExperiment Objects**

This method renames columns of the rowData and colData, as well as assays, of **SummarizedExperiment** objects. This increases the flexibility since renaming can be done before conversion to a **HermesData** object.

Usage

```r
## S4 method for signature 'SummarizedExperiment'
rename(
  x,
  row_data = character(),
  col_data = character(),
  assays = character(),
  ...
)

## S4 method for signature 'data.frame'
rename(x, ...)
```
Arguments

- **x** *(SummarizedExperiment)*
  object to rename contents in.

- **row_data** *(named character)*
  mapping from existing (right-hand side values) to new (left-hand side names) column names of rowData.

- **col_data** *(named character)*
  mapping from existing (right-hand side values) to new (left-hand side names) column names of colData.

- **assays** *(named character)*
  mapping from existing (right-hand side values) to new (left-hand side names) assay names.

- ... additional arguments (not used here).

Value

The `SummarizedExperiment::SummarizedExperiment` object with renamed contents.

Examples

```
x <- summarized_experiment
# Use deliberately a non-standard assay name in this example.
assayNames(x) <- "count"

# Rename `HGNC` to `symbol` in the `rowData`.
x <- rename(x, row_data = c(symbol = "HGNC"))
head(names(rowData(x)))

# Rename `LowDepthFlag` to `low_depth_flag` in `colData`.
x <- rename(x, col_data = c(low_depth_flag = "LowDepthFlag"))
tail(names(colData(x)))

# Rename assay `count` to `counts`.
x <- rename(x, assays = c(counts = "count"))
assayNames(x)
```

---

**samples,AnyHermesData-method**

*Sample IDs Accessor*

**Description**

[Stable]
Access the sample IDs, i.e. col names, of a `AnyHermesData` object with a nicely named accessor method.
set_tech_failure

Usage

## S4 method for signature 'AnyHermesData'
samples(object)

Arguments

object (AnyHermesData)
  input.

Value

The character vector with the sample IDs.

See Also

genes() to access the gene IDs.

Examples

a <- hermes_data
samples(a)

---

set_tech_failure  Set Technical Failure Flags

Description

[Experimental]

Setter function which allows the user to define a sample manually as a technical failure.

Usage

set_tech_failure(object, sample_ids)

Arguments

object (AnyHermesData)
  input.

sample_ids (character)
  sample IDs to be flagged as technical failures.

Value

AnyHermesData object with modified technical failure flags.
See Also

`add_quality_flags()` which automatically sets all (gene and sample) quality flags, including these technical failure flags.

Examples

```r
# Manually flag technical failures in a `AnyHermesData` object.
object <- hermes_data
get_tech_failure(object)["06520101B0017R"]
result <- set_tech_failure(object, c("06520101B0017R", "06520047C0017R"))
get_tech_failure(result)["06520101B0017R"]
```

Description

[Experimental]
A show method that displays high-level information of `AnyHermesData` objects.

Usage

```r
## S4 method for signature 'HermesData'
show(object)

## S4 method for signature 'RangedHermesData'
show(object)
```

Arguments

- `object` (AnyHermesData): input.

Value

None (invisible NULL), only used for the side effect of printing to the console.

Note

The same method is used for both `HermesData` and `RangedHermesData` objects. We need to define this separately to have this method used instead of the one inherited from `SummarizedExperiment::SummarizedExperiment`.

Examples

```r
object <- hermes_data
object
```
Description

[Stable]

This method subsets `AnyHermesData` objects, based on expressions involving the `rowData` columns and the `colData` columns.

Arguments

- `x` (AnyHermesData) object to subset from.
- `subset` (expression) logical expression based on the `rowData` columns to select genes.
- `select` (expression) logical expression based on the `colData` columns to select samples.

Value

The subsetted `AnyHermesData` object.

Note

Note that this just inherits `SummarizedExperiment::subset,SummarizedExperiment-method()`.

Examples

```r
a <- hermes_data
a

# Subset both genes and samples.
subset(a, subset = low_expression_flag, select = DISCSTUD == "N")

# Subset only genes.
subset(a, subset = chromosome == "2")

# Subset only samples.
subset(a, select = AGE > 18)
```
Example SummarizedExperiment Data

Description

[Stable]
This example SummarizedExperiment::SummarizedExperiment can be used to create a HermesData object. It already contains the required columns in rowData and colData.

Usage

summarized_experiment

Format

A SummarizedExperiment::SummarizedExperiment object with 20 samples covering 5085 features (Entrez gene IDs).

Source

This is an artificial dataset designed to resemble real data.

See Also

eexpression_set which contains similar data as a Biobase::ExpressionSet.

Summary Method for AnyHermesData Objects

Description

[Experimental]
Provides a concise summary of the content of AnyHermesData objects.

Usage

summary(object, ...)

## S4 method for signature 'AnyHermesData'
summary(object)

## S4 method for signature 'HermesDataSummary'
show(object)
Arguments

object \hspace{1cm} (HermesDataSummary)
result from the summary method applied to \texttt{AnyHermesData} object.

... not used.

Value

An object of the corresponding summary class, here \texttt{HermesDataSummary}.

Methods (by class)

\begin{itemize}
  \item \textbf{summary(AnyHermesData):} A summary method for \texttt{AnyHermesData} object that creates a \texttt{HermesDataSummary} object.
  \item \textbf{show(HermesDataSummary):} A show method prints summary description of \texttt{HermesDataSummary} object generated by the \texttt{summary()} method.
\end{itemize}

Examples

\begin{verbatim}
object <- hermes_data
object_summary <- summary(object)

# We can access parts of this S4 object with the `slot` function.
str(object_summary)
slotNames(object_summary)
slot(object_summary, "lib_sizes")

# Just calling the summary method like this will use the `show()` method.
summary(object)
\end{verbatim}

---

\begin{tabular}{ll}
\hline
\textbf{top_genes} & \textit{Derivation of Top Genes} \\
\hline
\end{tabular}

Description

\textbf{[Experimental]}

top\_genes() creates a \texttt{HermesDataTopGenes} object, which extends \texttt{data.frame}. It contains two columns:

\begin{itemize}
  \item \textbf{expression}: containing the statistic values calculated by \texttt{summary\_fun} across columns.
  \item \textbf{name}: the gene names.
\end{itemize}

The corresponding \texttt{autoplot()} method then visualizes the result as a barplot.
Usage

```r
top_genes(
  object,
  assay_name = "counts",
  summary_fun = rowMeans,
  n_top = if (is.null(min_threshold)) 10L else NULL,
  min_threshold = NULL
)
```

## S4 method for signature 'HermesDataTopGenes'

```r
autoplot(
  object,
  x_lab = "HGNC gene names",
  y_lab = paste0(object@summary_fun_name, "(" , object@assay_name, ")"),
  title = "Top most expressed genes"
)
```

Arguments

- **object** *(AnyHermedData)*
  - Input.
- **assay_name** *(string)*
  - Name of the assay to use for the sorting of genes.
- **summary_fun** *(function)*
  - Summary statistics function to apply across the samples in the assay resulting in a numeric vector with one value per gene.
- **n_top** *(count or NULL)*
  - Selection criteria based on number of entries.
- **min_threshold** *(number or NULL)*
  - Selection criteria based on a minimum summary statistics threshold.
- **x_lab** *(string)*
  - X-axis label.
- **y_lab** *(string)*
  - Y-axis label.
- **title** *(string)*
  - Plot title.

Details

- The data frame is sorted in descending order of expression and only the top entries according to the selection criteria are included.
- Note that exactly one of the arguments `n_top` and `min_threshold` must be provided.

Value

A `HermesDataTopGenes` object.
validate

Functions

- `autoplot(HermesDataTopGenes)`: Creates a bar plot from a `HermesDataTopGenes` object, where the y axis shows the expression statistics for each of the top genes on the x-axis.

Examples

```r
object <- hermes_data
# Default uses average of raw counts across samples to rank genes.
top_genes(object)
# Instead of showing top 10 genes, can also set a minimum threshold on average counts.
top_genes(object, n_top = NULL, min_threshold = 50000)
# We can also use the maximum of raw counts across samples, by specifying a different
# summary statistics function.
result <- top_genes(object, summary_fun = rowMax)
# Finally we can produce barplots based on the results.
autoplot(result, title = "My top genes")
autoplot(result, y_lab = "Counts", title = "My top genes")
```

validate  

Internal Helper Functions for Validation of AnyHermesData Objects

Description

These functions are used internally only and therefore not exported. They work on `SummarizedExperiment::SummarizedExperiment` objects, and `AnyHermesData` objects are defined by successfully passing these validation checks.

Usage

```r
validate_counts(object)
validate_cols(required, actual)
validate_row_data(object)
validate_col_data(object)
validate_names(object)
validate_prefix(object)
```
Arguments

object  (SummarizedExperiment) object to validate.
required  (character) required column names.
actual  (actual) actual column names.

Value

A character vector with the validation failure messages, or NULL in case validation passes.

Functions

- validate_counts(): validates that the first assay is counts containing non-missing, integer, non-negative values.
- validate_cols(): validates that required column names are contained in actual column names.
- validate_row_data(): validates that the object contains rowData with required columns.
- validate_col_data(): validates that the object contains colData with required columns.
- validate_names(): validates that the object contains row and column names.
- validate_prefix(): validates that the object prefix is a string and only contains alphabetic characters.

Description

[Experimental]

This helper function wraps SummarizedExperiment objects into an a MultiAssayExperiment (MAE) object.

Usage

wrap_in_mae(x, name = deparse(substitute(x)))

Arguments

x  (SummarizedExperiment) input to create the MAE object from.
name  (string) experiment name to use in the MAE for x.
Value

The MAE object with the only experiment being x having the given name.

Examples

```r
mae <- wrap_in_mae(summarized_experiment)
mae[["summarized_experiment"]]
```

---

Pipe operator

Description

[Stable]

See magrittr::%>% for details.

Usage

```r
lhs %>% rhs
```

Value

The result of the corresponding function call.

Examples

```r
hermes_data %>%
  filter() %>%
  normalize() %>%
  summary()
```
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