Package 'lemur'

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Type Package

Title Latent Embedding Multivariate Regression

Version 1.4.0

Description Fit a latent embedding multivariate regression (LEMUR) model to multi-condition single-cell data. The model provides a parametric description of single-cell data measured with treatment vs. control or more complex experimental designs. The parametric model is used to (1) align conditions, (2) predict log fold changes between conditions for all cells, and (3) identify cell neighborhoods with consistent log fold changes. For those neighborhoods, a pseudobulked differential expression test is conducted to assess which genes are significantly changed.

URL https://github.com/const-ae/lemur

BugReports https://github.com/const-ae/lemur/issues

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Contents

.DollarNames.lemur_fit

                                Access values from a lemur_fit

---

Description

Access values from a lemur_fit

Usage

```
## S3 method for class 'lemur_fit'
.DollarNames(x, pattern = "")

## S4 method for signature 'lemur_fit'
x$name

## S4 replacement method for signature 'lemur_fit'
x$name <- value
```

Arguments

x	the lemur_fit
pattern	the pattern from looking up potential values interactively
name	the name of the value behind the dollar
value	the replacement value. This only works for colData and rowData.

Value

The respective value stored in the lemur_fit object.

See Also

lemur_fit for more documentation on the accessor functions.

---

align_harmony	*Enforce additional alignment of cell clusters beyond the direct differential embedding*

Description

Enforce additional alignment of cell clusters beyond the direct differential embedding

Usage

```
align_harmony(
  fit,
  design = fit$alignment_design,
  ridge_penalty = 0.01,
  max_iter = 10,
  ...,
  verbose = TRUE
)

align_by_grouping(
  fit,
  grouping,
  design = fit$alignment_design,
  ridge_penalty = 0.01,
  preserve_position_of_NAs = FALSE,
  verbose = TRUE
)
```

Arguments

`fit`	a `lemur_fit` object
`design`	a specification of the design (matrix or formula) that is used for the transformation. Default: `fit$design_matrix`
`ridge_penalty`	specification how much the flexibility of the transformation should be regularized. Default: `0.01`
`max_iter`	argument specific for `align_harmony`. The number of iterations. Default: `10`
`...`	additional parameters that are passed on to relevant functions
`verbose`	Should the method print information during the fitting. Default: `TRUE`.
`grouping`	argument specific for `align_by_grouping`. Either a vector which assigns each cell to one group or a matrix with `ncol(fit)` columns where the rows are a soft-assignment to a cluster (i.e., columns sum to 1). NA's are allowed.
`preserve_position_of_NAs`	
	argument specific for `align_by_grouping`. Boolean flag to decide if NAs in the grouping mean that these cells should stay where they are (if possible) or if they are free to move around. Default: FALSE

Value

The `fit` object with the updated `fit$embedding` and `fit$alignment_coefficients`.

Examples

```
data(glioblastoma_example_data)
fit <- lemur(glioblastoma_example_data, design = ~ patient_id + condition,
             n_emb = 5, verbose = FALSE)
# Creating some grouping for illustration
cell_types <- sample(c("tumor cell", "neuron", "leukocyte"), size = ncol(fit), replace = TRUE)
fit_al1 <- align_by_grouping(fit, grouping = cell_types)

# Alternatively, use harmony to automatically group cells
fit_al2 <- align_harmony(fit)
fit_al2

# The alignment coefficients are a 3D array
fit_al2$alignment_coefficients
```

---

align_impl	*Align the points according to some grouping*

Description

Align the points according to some grouping

Usage

```
align_impl(
  embedding,
  grouping,
  design_matrix,
  ridge_penalty = 0.01,
  preserve_position_of_NAs = FALSE,
  calculate_new_embedding = TRUE
)
```

Value

A list with the new embedding and the coefficients

---

find_de_neighborhoods *Find differential expression neighborhoods*

Description

Find differential expression neighborhoods

Usage

```
find_de_neighborhoods(
  fit,
  group_by,
  contrast = fit$contrast,
  selection_procedure = c("zscore", "contrast"),
  directions = c("random", "contrast", "axis_parallel"),
  min_neighborhood_size = 50,
  de_mat = SummarizedExperiment::assays(fit)[["DE"]],
  test_data = fit$test_data,
  test_data_col_data = NULL,
  test_method = c("glmGamPoi", "edgeR", "limma", "none"),
  continuous_assay_name = fit$use_assay,
  count_assay_name = "counts",
  size_factor_method = NULL,
  design = fit$design,
  alignment_design = fit$alignment_design,
  add_diff_in_diff = TRUE,
  make_neighborhoods_consistent = FALSE,
  skip_confounded_neighborhoods = FALSE,
  control_parameters = NULL,
  verbose = TRUE
)
```

Arguments

fit   the `lemur_fit` generated by `lemur()`

group_by   If the `independent_matrix` is provided, `group_by` defines how the pseudob-
                    ulks are formed. This is typically the variable in the column data that represents
                    the independent unit of replication of the experiment (e.g., the mouse or patient
                    ID). The argument has to be wrapped in `vars(...)`.

contrast   a specification which contrast to fit. This defaults to the `contrast` argument that
                    was used for `test_de` and is stored in `fit$contrast`.

selection_procedure
                    specify the algorithm that is used to select the neighborhoods for each gene.
                    Broadly, `selection_procedure = "zscore"` is faster but less precise than `selection_procedure`
                    `= "contrast"`.

directions   a string to define the algorithm to select the direction onto which the cells are
                    projected before searching for the neighborhood. `directions = "random"` pro-
                    duces denser neighborhoods, whereas `directions = "contrast"` has usually
                    more power.
                    Alternatively, this can also be a matrix with one direction for each gene (i.e., a
                    matrix of size `nrow(fit) * fit$n_embedding`).

min_neighborhood_size
                    the minimum number of cells per neighborhood. Default: 50.

de_mat   the matrix with the differential expression values and is only relevant if `selection_procedure`
                    `= "zscore"` or `directions = "random"`. Defaults to an assay called `"DE"` that
                    is produced by `lemur::test_de()`.

test_data   a `SummarizedExperiment` object or a named list of matrices. The data is used to
                    test if the neighborhood inferred on the training data contain a reliable significant
                    change. If `test_method` is `"glmGamPoi"` or `"edgeR"` a test using raw counts
                    is conducted and two matching assays are needed: (1) the continuous assay
                    (with `continuous_assay_name`) is projected onto the LEMUR fit to find the
                    latent position of each cell and (2) the count assay (`count_assay_name`) is used
                    for forming the pseudobulk. If `test_method == "limma"`, only the continuous
                    assay is needed.
                    The arguments defaults to the test data split of when calling `lemur()`.

test_data_col_data
                    additional column data for the `test_data` argument.

test_method   choice of test for the pseudobulked differential expression. glmGamPoi and
                    edgeR work on an count assay. limma works on the continuous assay.

continuous_assay_name, count_assay_name
                    the assay or list names of `independent_data`.

size_factor_method
                    Set the procedure to calculate the size factor after pseudobulking. This argu-
                    ment is only relevant if `test_method` is `"glmGamPoi"` or `"edgeR"`. If `fit` is
                    subsetted, using a vector with the sequencing depth per cell ensures reasonable
                    results. Default: `NULL` which means that `colSums(assay(fit$test_data,`
                    `count_assay_name))` is used.

design, alignment_design
                    the design to use for the fit. Default: `fit$design`

add_diff_in_diff
                    a boolean to specify if the log-fold change (plus significance) of the DE in the
                    neighborhood against the DE in the complement of the neighborhood is calcu-
                    lated. If `TRUE`, the result includes three additional columns starting with `"did_"`
                    short for difference-in-difference. Default: `TRUE`.

make_neighborhoods_consistent

Include cells from outside the neighborhood if they are at least 10 times in the k-nearest neighbors of the cells inside the neighborhood. Secondly, remove cells from the neighborhood which are less than 10 times in the k-nearest neighbors of the other cells in the neighborhood. Default FALSE

skip_confounded_neighborhoods

Sometimes the inferred neighborhoods are not limited to a single cell state; this becomes problematic if the cells of the conditions compared in the contrast are unequally distributed between the cell states. Default: FALSE

control_parameters

named list with additional parameters passed to underlying functions.

verbose   Should the method print information during the fitting. Default: TRUE.

Value

a data frame with one entry per gene

name The gene name.

neighborhood A list column where each element is a vector with the cell names included in that neighborhood.

n_cells the number of cells in the neighborhood (lengths(neighborhood)).

sel_statistic The statistic that is maximized by the selection_procedure.

pval, adj_pval, t_statistic, lfc The p-value, Benjamini-Hochberg adjusted p-value (FDR), the t-statistic, and the log2 fold change of the differential expression test defined by contrast for the cells inside the neighborhood (calculated using test_method). Only present if test_data is not NULL.

did_pval, did_adj_pval, did_lfc The measurement if the differential expression of the cells inside the neighborhood is significantly different from the differential expression of the cells outside the neighborhood. Only present if add_diff_in_diff = TRUE.

Examples

```
data(glioblastoma_example_data)
fit <- lemur(glioblastoma_example_data, design = ~ patient_id + condition,
             n_emb = 5, verbose = FALSE)
# Optional alignment
# fit <- align_harmony(fit)
fit <- test_de(fit, contrast = cond(condition = "panobinostat") - cond(condition = "ctrl"))
nei <- find_de_neighborhoods(fit, group_by = vars(patient_id))
head(nei)
```

---

fold_left   *Fold left over a sequence*

Description

Fold left over a sequence

Fold right over a sequence

Usage

```
fold_left(init)

fold_right(init)
```

Arguments

`init`	initial value. If not specified `NULL`
`x`	the sequence to iterate over
`FUN`	a function with first argument named `elem` and second argument named `accum`

Value

The final value of `accum`.

Examples

```
## Not run:
  # This produces ...
  fold_left(0)(1:10, \(elem, accum) accum + elem)
  # ... the same as
  sum(1:10)

## End(Not run)
```

---

glioblastoma_example_data

The glioblastoma_example_data *dataset*

Description

The dataset is a SingleCellExperiment object subset to 5,000 cells and 300 genes. The `colData` contain an entry for each cell from which patient it came and to which treatment condition it belonged (`"ctrl"` or `"panobinostat"`).

Details

The original data was collected by Zhao et al. (2021).

Value

A SingleCellExperiment object.

References

- Zhao, Wenting, Athanassios Dovas, Eleonora Francesca Spinazzi, Hanna Mendes Levitin, Matei Alexandru Banu, Pavan Upadhyayula, Tejaswi Sudhakar, et al. "Deconvolution of Cell Type-Specific Drug Responses in Human Tumor Tissue with Single-Cell RNA-Seq." Genome Medicine 13, no. 1 (December 2021): 82. https://doi.org/10.1186/s13073-021-00894-y.

grassmann_geodesic_regression

*Solve d(P, exp_p(V * x))^2 for V*

Description

Solve d(P, exp_p(V * x))^2 for V

Usage

```
grassmann_geodesic_regression(
  coordsystems,
  design,
  base_point,
  weights = 1,
  tangent_regression = FALSE
)
```

Value

A three-dimensional array with the coefficients V.

grassmann_lm   *Solve ||Y - exp_p(V * x) Y ||^2_2 for V*

Description

Solve ||Y - exp_p(V * x) Y ||^2_2 for V

Usage

```
grassmann_lm(data, design, base_point, tangent_regression = FALSE)
```

Value

A three-dimensional array with the coefficients V.

harmony_new_object   *Create an arbitrary Harmony object so that I can modify it later*

Description

Create an arbitrary Harmony object so that I can modify it later

Usage

```
harmony_new_object()
```

Value

The full harmony object (R6 reference class type).

lemur   *Main function to fit the latent embedding multivariate regression (LEMUR) model*

Description

Main function to fit the latent embedding multivariate regression (LEMUR) model

Usage

```
lemur(
  data,
  design = ~1,
  col_data = NULL,
  n_embedding = 15,
  linear_coefficient_estimator = c("linear", "mean", "cluster_median", "zero"),
  use_assay = "logcounts",
  test_fraction = 0.2,
  ...,
  verbose = TRUE
)
```

Arguments

data	a matrix with observations in the columns and features in the rows. Or a `SummarizedExperiment` / `SingleCellExperiment` object
design	a formula referring to global objects or column in the `colData` of data and `col_data` argument
col_data	an optional data frame with `ncol(data)` rows.
n_embedding	the dimension of the k-plane that is rotated through space.
linear_coefficient_estimator	
	specify which estimator is used to center the conditions. `"linear"` runs simple regression it works well in many circumstances but can produce poor results if the composition of the cell types changes between conditions (e.g., one cell type disappears). `"mean"`, `"cluster_median"` and `"zero"` are alternative estimators, which are each supposed to be more robust against compositional changes but cannot account for genes that change for all cells between conditions. `"linear"` is the default as it works best with subsequent alignment steps.
use_assay	if data is a `SummarizedExperiment` / `SingleCellExperiment` object, which assay should be used.
test_fraction	the fraction of cells that are split of before the model fit to keep an independent set of test observations. Alternatively, a logical vector of length `ncol(data)`. Default: 20% (`0.2`).
...	additional parameters that are passed on to the internal function `lemur_impl`.
verbose	Should the method print information during the fitting. Default: `TRUE`.

Value

An object of class `lemur_fit` which extends [SingleCellExperiment](#). Accordingly, all functions that work for `sce`'s also work for `lemur_fit`'s. In addition, we give easy access to the fitted values using the dollar notation (e.g., `fit$embedding`). For details see the [lemur_fit](#) help page.

References

- Ahlmann-Eltze, C. & Huber, W. (2023). Analysis of multi-condition single-cell data with latent embedding multivariate regression. bioRxiv https://doi.org/10.1101/2023.03.06.531268

See Also

align_by_grouping, align_harmony, test_de, find_de_neighborhoods

Examples

```
data(glioblastoma_example_data)
fit <- lemur(glioblastoma_example_data, design = ~ patient_id + condition, n_emb = 5)
fit
```

---

lemur_fit-class *The* lemur_fit *class*

Description

The lemur_fit class extends SingleCellExperiment and provides additional accessors to get the values of the values produced by lemur.

Usage

```
## S4 method for signature 'lemur_fit,ANY,ANY,ANY'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'lemur_fit'
design(object)
```

Arguments

x, i, j, ..., drop the lemur_fit object and indices for the [subsetting operator

object   the lemur_fit object for the BiocGenerics::design generic

Details

To access the values produced by lemur, use the dollar notation ($):

fit$n_embedding the number of embedding dimensions.

fit$design the specification of the design in lemur. Usually this is a stats::formula.

fit$base_point a matrix (nrow(fit) * fit$n_embedding) with the base point for the Grass-mann exponential map.

fit$coefficients a three-dimensional tensor (nrow(fit) * fit$n_embedding * ncol(fit$design_matrix)) with the coefficients for the exponential map.

fit$embedding a matrix (fit$n_embedding * ncol(fit)) with the low dimensional position for each cell.

fit$design_matrix a matrix with covariates for each cell (ncol(fit) * ncol(fit$design_matrix)).

fit$linear_coefficients a matrix (nrow(fit) * ncol(fit$design_matrix)) with the coefficients for the linear regression.

fit$alignment_coefficients a 3D tensor with the coefficients for the alignment (fit$n_embedding * fit$n_embedding * ncol(fit$design_matrix))

fit$alignment_design an alternative design specification for the alignment. This is typically a stats::formula.

fit$alignment_design_matrix an alternative design matrix specification for the alignment.

fit$contrast a parsed version of the contrast specification from the test_de function or NULL.

fit$colData the column annotation DataFrame.

fit$rowData the row annotation DataFrame.

Value

An object of class lemur_fit.

See Also

lemur, predict, residuals

Examples

```
# The easiest way to make a lemur_fit object, is to call `lemur`
data(glioblastoma_example_data)
fit <- lemur(glioblastoma_example_data, design = ~ patient_id + condition,
             n_emb = 5, verbose = FALSE)

fit$n_embedding
fit$embedding[,1:10]
fit$n_embedding
fit$embedding[,1:10]
fit$design_matrix[1:10,]
fit$coefficients[1:3,,]
```

---

mply_dbl   *Iterating function that returns a matrix*

Description

The length of x determines the number of rows. The length of FUN(x[i]) determines the number of columns. Must match ncol.

Usage

```
mply_dbl(x, FUN, ncol = 1, ...)

stack_rows(x)

stack_cols(x)
```

Arguments

x	the sequence that is mapped to a matrix
FUN	the function that returns a vector of length ncol
ncol	the length of the output vector
...	additional arguments that are passed to FUN

Value

A matrix with `length(x) / nrow(x)` rows and `ncol` columns. For `msply_dbl` the number of columns depends on the output of `FUN`.

Functions

- `stack_rows()`: Each list element becomes a row in a matrix
- `stack_cols()`: Each list element becomes a row in a matrix

---

one_hot_encoding *Take a vector and convert it to a one-hot encoded matrix*

Description

Take a vector and convert it to a one-hot encoded matrix

Usage

```
one_hot_encoding(groups)
```

Value

A matrix with `length(unique(groups))` rows and `length(groups)` columns.

---

predict.lemur_fit *Predict values from* lemur_fit *object*

Description

Predict values from `lemur_fit` object

Usage

```
## S3 method for class 'lemur_fit'
predict(
  object,
  newdata = NULL,
  newdesign = NULL,
  newcondition = NULL,
  embedding = object$embedding,
  with_linear_model = TRUE,
  with_embedding = TRUE,
  with_alignment = TRUE,
  ...
)
```

Arguments

`object`	an `lemur_fit` object
`newdata`	a data.frame which passed to `model.matrix` with design to make the `newdesign` matrix
`newdesign`	a matrix with the covariates for which the output is predicted. If NULL, the `object$design_matrix` is used. If it is a vector it is repeated `ncol(embedding)` times to create a design matrix with the same entry for each cell.
`newcondition`	an unquoted expression with a call to `cond()` specifying the covariates of the prediction. See the `contrast` argument in [test_de](#) for more details. Note that combinations of multiple calls to `cond()` are not allowed (e.g., `cond(a = 1) - cond(a = 2)`). If specified, `newdata` and `newdesign` are ignored.
`embedding`	the low-dimensional cell position for which the output is predicted.
`with_linear_model`	
	a boolean to indicate if the linear regression offset is included in the prediction.
`with_embedding`	a boolean to indicate if the embedding contributes to the output.
`with_alignment`	a boolean to indicate if the alignment effect is removed from the output.
`...`	additional parameters passed to `predict_impl`.

Value

A matrix with the same dimension `nrow(object) * nrow(newdesign)`.

See Also

[residuals](#)

Examples

```
data(glioblastoma_example_data)
fit <- lemur(glioblastoma_example_data, design = ~ patient_id + condition,
             n_emb = 5, verbose = FALSE)

pred <- predict(fit)

pred_ctrl <- predict(fit, newdesign = c(1, 0, 0, 0, 0, 0))
pred_trt <-  predict(fit, newdesign = c(1, 0, 0, 0, 0, 1))
# This is the same as the test_de result
fit <- test_de(fit, cond(condition = "panobinostat") - cond(condition = "ctrl"))
all.equal(SummarizedExperiment::assay(fit, "DE"), pred_trt - pred_ctrl,
          check.attributes = FALSE)
```

---

project_on_lemur_fit   *Project new data onto the latent spaces of an existing lemur fit*

Description

Project new data onto the latent spaces of an existing lemur fit

Usage

```
project_on_lemur_fit(
  fit,
  data,
  col_data = NULL,
  use_assay = "logcounts",
  design = fit$design,
  alignment_design = fit$alignment_design,
  return = c("matrix", "lemur_fit")
)
```

Arguments

fit
: an `lemur_fit` object

data
: a matrix with observations in the columns and features in the rows. Or a `SummarizedExperiment` / `SingleCellExperiment` object. The features must match the features in `fit`.

col_data
: col_data an optional data frame with `ncol(data)` rows.

use_assay
: if data is a `SummarizedExperiment` / `SingleCellExperiment` object, which assay should be used.

design, alignment_design
: the design formulas or design matrices that are used to project the data on the correct latent subspace. Both default to the designs from the `fit` object.

return
: which data structure is returned.

Value

Either a matrix with the low-dimensional embeddings of the `data` or an object of class `lemur_fit` wrapping that embedding.

Examples

```
data(glioblastoma_example_data)

subset1 <- glioblastoma_example_data[,1:2500]
subset2 <- glioblastoma_example_data[,2501:5000]

fit <- lemur(subset1, design = ~ condition, n_emb = 5,
             test_fraction = 0, verbose = FALSE)

# Returns a `lemur_fit` object with the projection of `subset2`
fit2 <- project_on_lemur_fit(fit, subset2, return = "lemur_fit")
fit2
```

---

pseudoinverse   *Moore-Penrose pseudoinverse calculated via SVD*

Description

In the simplest case, the pseudoinverse is

$$X^+ = (X^T X)^{-1} X^T.$$

Usage

```
pseudoinverse(X)
```

Arguments

X   a matrix X

Details

To handle the more general case, the pseudoinverse can expressed using a SVD $X = UDV^T$:

$$X^+ = VD^{-1}U^T$$

Value

The matrix X^+.

---

recursive_least_squares

Iteratively calculate the least squares solution

Description

Both functions are for testing purposes. There is a faster implementation called `cum_brls_which_abs_max`.

Usage

```
recursive_least_squares(y, X)

bulked_recursive_least_squares_contrast(
  y,
  X,
  group,
  contrast,
  ridge_penalty = 1e-06
)
```

Arguments

y   a vector with observations
X   a design matrix

Value

a matrix where column i is the solution to y[1:i] ~ X[1:i,].

---

reexports *Objects exported from other packages*

Description

These objects are imported from other packages. Follow the links below to see their documentation.

glmGamPoi [vars](#)

Value

see [glmGamPoi::vars.](#)

Examples

```
# `vars` quotes expressions (just like in dplyr)
vars(condition, sample)
```

---

residuals,lemur_fit-method
Predict values from lemur_fit *object*

Description

Predict values from lemur_fit object

Usage

```
## S4 method for signature 'lemur_fit'
residuals(object, with_linear_model = TRUE, with_embedding = TRUE, ...)
```

Arguments

object   an lemur_fit object

with_linear_model
                a boolean to indicate if the linear regression offset is included in the prediction.

with_embedding a boolean to indicate if the embedding contributes to the output.

...   ignored.

Value

A matrix with the same dimension dim(object).

See Also

[predict.lemur_fit](#)

Examples

```
data(glioblastoma_example_data)
fit <- lemur(glioblastoma_example_data, design = ~ patient_id + condition,
             n_emb = 5, verbose = FALSE)

resid <- residuals(fit)
dim(resid)
```

---

ridge_regression   *Ridge regression*

Description

The function does not treat the intercept special.

Usage

```
ridge_regression(Y, X, ridge_penalty = 0, weights = rep(1, nrow(X)))
```

Arguments

Y	the observations matrix (features x samples)
X	the design matrix (samples x covariates)
ridge_penalty	a numeric vector or matrix of size (covariates or covariates x covariates respectively)
weights	a vector of observation weights

Value

The matrix of coefficients.

---

stack_slice   *Make a cube from a list of matrices*

Description

The length of the list will become the third dimension of the cube.

Usage

```
stack_slice(x)

destack_slice(x)
```

Arguments

x	a list of vectors/matrices that are stacked

Value

A three-dimensional array.

Functions

- destack_slice(): Make a list of matrices from a cube

---

test_de   *Predict log fold changes between conditions for each cell*

Description

Predict log fold changes between conditions for each cell

Usage

```
test_de(
  fit,
  contrast,
  embedding = NULL,
  consider = c("embedding+linear", "embedding", "linear"),
  new_assay_name = "DE"
)
```

Arguments

fit	the result of calling [lemur()](#)
contrast	Specification of the contrast: a call to cond() specifying a full observation (e.g. cond(treatment = "A", sex = "male") - cond(treatment = "C", sex = "male") to compare treatment A vs C for male observations). Unspecified factors default to the reference level.
embedding	matrix of size n_embedding × n that specifies where in the latent space the differential expression is tested. It defaults to the position of all cells from the original fit.
consider	specify which part of the model are considered for the differential expression test.
new_assay_name	the name of the assay added to the fit object. Default: "DE".

Value

If is.null(embedding) the fit object with a new assay called "DE". Otherwise return a matrix with the differential expression values.

See Also

[find_de_neighborhoods](#)

Examples

```
library(SummarizedExperiment)
library(SingleCellExperiment)

data(glioblastoma_example_data)
fit <- lemur(glioblastoma_example_data, design = ~ patient_id + condition,
             n_emb = 5, verbose = FALSE)
# Optional alignment
# fit <- align_harmony(fit)
fit <- test_de(fit, contrast = cond(condition = "panobinostat") - cond(condition = "ctrl"))

# The fit object contains a new assay called "DE"
assayNames(fit)

# The DE assay captures differences between conditions
is_ctrl_cond <- fit$colData$condition == "ctrl"
mean(logcounts(fit)[1,!is_ctrl_cond]) - mean(logcounts(fit)[1,is_ctrl_cond])
mean(assay(fit, "DE")[1,])
```

| test_global | *Differential embedding for each condition* |

Description

Differential embedding for each condition

Usage

```
test_global(
  fit,
  contrast,
  reduced_design = NULL,
  consider = c("embedding+linear", "embedding", "linear"),
  variance_est = c("analytical", "resampling", "none"),
  verbose = TRUE,
  ...
)
```

Arguments

fit	the result of calling lemur()
contrast	Specification of the contrast: a call to cond() specifying a full observation (e.g. cond(treatment = "A", sex = "male") - cond(treatment = "C", sex = "male") to compare treatment A vs C for male observations). Unspecified factors default to the reference level.
reduced_design	an alternative specification of the null hypothesis.
consider	specify which part of the model are considered for the differential expression test.
variance_est	How or if the variance should be estimated. 'analytical' is only compatible with consider = "linear". 'resampling' is the most flexible (to adapt the number of resampling iterations, set n_resampling_iter. Default: 100)

verbose	should the method print information during the fitting. Default: `TRUE`.
`...`	additional arguments.

Value

a data.frame

`%zero_dom_mat_mult%`	*Helper function that makes sure that NA * 0 = 0 in matrix multiply*

Description

Helper function that makes sure that NA * 0 = 0 in matrix multiply

Usage

```
X %zero_dom_mat_mult% Y
```

Arguments

X	a matrix of size n*m
Y	a matrix of size m*p

Value

a matrix of size n*p

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