Package 'lemur'

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Type Package

Title Latent Embedding Multivariate Regression

Version 1.10.2

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,
  ...,
  epsilon_harmony = 1e-04,
  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
`epsilon_harmony`	argument specific for `align_harmony`. Convergence threshold for the outer alignment loop. Default: `1e-4`
`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 `NA`s 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`	defines how the pseudobulks 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(...)`. The function automatically includes all variables that are referenced in the original design formula, so they don't need to be explicitly mentioned.
`contrast`	a specification of the contrast of interest. This defaults to the `contrast` argument that was used for `test_de` and is stored in `fit$contrast`.
`selection_procedure`	specify the algorithm that is used to select the neighborhoods for each gene. Broadly, `selection_procedure = "zscore"` is faster but less elaborate than `selection_procedure = "contrast"`.
`directions`	a string to define the algorithm to select the direction onto which the cells are projected before searching for the neighborhood. `directions = "random"` produces denser neighborhoods, whereas `directions = "contrast"` has usually more power. Alternatively, this can also be a matrix with one direction for each gene (i.e., a matrix of size `nrow(fit) * fit$n_embedding`).
`min_neighborhood_size`	the minimum number of cells per neighborhood. Default: `50`.

de_mat
: the matrix with the differential expression values. This 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 the counts. limma works on the continuous assay.

continuous_assay_name, count_assay_name
: the names of the assays that are used for the statistical test. By default, `continuous_assay_name` is the name that was specified in the original `lemur()` call and `count_assay_name`, which is used if `test_method` is `"glmGamPoi"` or `"edgeR"`, is `"counts"`.

size_factor_method
: the procedure to calculate the size factor after pseudobulking. This argument 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
: logical scalar to specify whether the logarithmic fold change (plus significance) of the DE in the neighborhood against the DE in the complement of the neighborhood is calculated. If `TRUE`, the result includes three additional columns starting with `"did_"` short for difference-in-difference..

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`.

`init_max_diversity_clustering` *Maximum diversity soft clustering*

Description

A pure R re-implementation of the maximum diversity clustering step from the Harmony batch-integration algorithm (Korsunsky et al. 2019, Nature Methods). Iteratively fits soft cluster assignments that maximize the diversity (in terms of a design/grouping variable, e.g. batch or patient) within each cluster, using an entropy-regularized penalty. This is the piece of Harmony that `align_harmony` uses; the rest of Harmony's algorithm (the ridge regression based correction) is implemented natively by lemur (see `align_impl()`).

Usage

```
init_max_diversity_clustering(
  embedding,
  design_matrix,
  theta = 2,
  sigma = 0.1,
  nclust = min(round(ncol(embedding)/30), 100),
  tau = 0,
  block_size = 0.05,
  max_iter_cluster = 200,
  epsilon_cluster = 1e-05,
  verbose = TRUE
)
```

Arguments

`embedding`	a matrix of size `n_features x n_cells`
`design_matrix`	a design matrix with `ncol(embedding)` rows that specifies which cells should be diverse within a cluster (typically the batch or patient variable).
`theta`	diversity penalty. Larger values encourage more diverse clusters. Can be a single value or one value per group in `design_matrix`. Default: `2`
`sigma`	width of the soft-clustering kernel. Default: `0.1`
`nclust`	number of clusters. Default: `min(round(ncol(embedding) / 30), 100)`
`tau`	protection against overclustering small groups. Default: `0`
`block_size`	fraction of cells to update per block in the online update of the cluster assignments. Default: `0.05`
`max_iter_cluster`	maximum number of iterations. Default: `200`
`epsilon_cluster`	convergence threshold for the clustering iterations. Default: `1e-5`
`verbose`	Should progress be printed. Default: `TRUE`

Value

A list with the state of the clustering procedure (Z_cos, Y, R, Phi, Pr_b, theta, sigma, E, O, K, N, B, and bookkeeping fields used by run_max_diversity_clustering).

See Also

run_max_diversity_clustering

---

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 fit produced by lemur. It is the class of the result returned 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 dimension of the latent space.

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

fit$base_point a matrix of size nrow(fit) x fit$n_embedding with the base point for the Grassmann exponential map.

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

fit$embedding a matrix of size fit$n_embedding x ncol(fit) with the latent space coordinates of each cell.

fit$design_matrix a matrix with the covariate values for each cell, of size ncol(fit) x ncol(fit$design_matrix).

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

fit$alignment_coefficients a 3-tensor with the coefficients for the alignment, of size fit$n_embedding x fit$n_embedding x ncol(fit$design_matrix).

fit$alignment_design an alternative specification of the alignment, using a design, typically a stats::formula.

fit$alignment_design_matrix an alternative specification of the alignment, using a design matrix.

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.

run_max_diversity_clustering *Run the maximum diversity clustering iterations*

Description

Alternates between updating the cluster centroids `Y` and the soft cluster assignment `R` (with the diversity penalty) until convergence or `state$max_iter_cluster` is reached.

Usage

```
run_max_diversity_clustering(state, embedding = NULL)
```

Arguments

`state`	the result of `init_max_diversity_clustering` or a previous call to `run_max_diversity_clustering`.
`embedding`	optionally, an updated embedding (e.g., after aligning the cells) that replaces `state$Z_cos` before the clustering iterations start. If `NULL` (default), the embedding of `state` is used unchanged.

Value

The updated `state` list (see `init_max_diversity_clustering`). `state$objective_kmeans` contains the trace of the objective function for this call (not accumulated across calls).

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` $\times$ `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

`update_diversity_clustering_R` *Update the soft cluster assignment matrix* `R` *with the diversity penalty*

Description

Cells are processed in randomly shuffled blocks of size `state$block_size * state$N`; within each block the diversity-adjusted assignment is recomputed from the batch-occupancy statistics `E/O` with the other blocks temporarily removed ("online" update).

Usage

```
update_diversity_clustering_R(state)
```

`%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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