

Package: lemur (via r-universe)

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Type Package

Title Latent Embedding Multivariate Regression

Version 1.11.2

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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.DollarNames.lemur_fit
<i>Access values from a lemur_fit</i>

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	<i>Enforce additional alignment of cell clusters beyond the direct differential embedding</i>
---------------	---

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

<code>fit</code>	a <code>lemur_fit</code> object
<code>design</code>	a specification of the design (matrix or formula) that is used for the transformation. Default: <code>fit\$design_matrix</code>
<code>ridge_penalty</code>	specification how much the flexibility of the transformation should be regularized. Default: <code>0.01</code>
<code>max_iter</code>	argument specific for <code>align_harmony</code> . The number of iterations. Default: <code>10</code>
<code>...</code>	additional parameters that are passed on to relevant functions
<code>epsilon_harmony</code>	argument specific for <code>align_harmony</code> . Convergence threshold for the outer alignment loop. Default: <code>1e-4</code>
<code>verbose</code>	Should the method print information during the fitting. Default: <code>TRUE</code> .
<code>grouping</code>	argument specific for <code>align_by_grouping</code> . Either a vector which assigns each cell to one group or a matrix with <code>ncol(fit)</code> columns where the rows are a soft-assignment to a cluster (i.e., columns sum to 1). NA's are allowed.
<code>preserve_position_of_NAs</code>	argument specific for <code>align_by_grouping</code> . 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: <code>FALSE</code>

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)
# Create 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
```

compute_contrasts	<i>Predict log fold changes between conditions for each cell. Both names compute_contrasts and test_de bind to the same function, but the former is more evocative.</i>
-------------------	---

Description

Predict log fold changes between conditions for each cell. Both names `compute_contrasts` and `test_de` bind to the same function, but the former is more evocative.

Usage

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

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

Arguments

<code>fit</code>	the result of calling <code>lemur()</code>
<code>contrast</code>	Specification of the contrast: a call to <code>cond()</code> specifying a full observation (e.g. <code>cond(treatment = "A", sex = "male") - cond(treatment = "C", sex = "male")</code>) to compare treatment A vs C for male observations). Unspecified factors default to the reference level.
<code>embedding</code>	matrix of size $n_{\text{embedding}} \times n$ that specifies where in the latent space the differential expression is tested. It defaults to the position of all cells from the original fit.
<code>consider</code>	specify which part of the model are considered for the differential expression test.
<code>new_assay_name</code>	the name of the assay added to the <code>fit</code> 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 <- compute_contrasts(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,])
```

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

<code>fit</code>	the <code>lemur_fit</code> generated by <code>lemur()</code>
<code>group_by</code>	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 <code>vars(...)</code> . The function automatically includes all variables that are referenced in the original design formula, so they don't need to be explicitly mentioned.
<code>contrast</code>	a specification of the contrast of interest. This defaults to the contrast argument that was used for <code>compute_contrasts</code> and is stored in <code>fit\$contrast</code> .
<code>selection_procedure</code>	specify the algorithm that is used to select the neighborhoods for each gene. Broadly, <code>selection_procedure = "zscore"</code> is faster but less elaborate than <code>selection_procedure = "contrast"</code> .
<code>directions</code>	a string to define the algorithm to select the direction onto which the cells are projected before searching for the neighborhood. <code>directions = "random"</code> produces denser neighborhoods, whereas <code>directions = "contrast"</code> has usually more power. Alternatively, this can also be a matrix with one direction for each gene (i.e., a matrix of size <code>nrow(fit) * fit\$n_embedding</code>).
<code>min_neighborhood_size</code>	the minimum number of cells per neighborhood. Default: 50.
<code>de_mat</code>	the matrix with the differential expression values. This is only relevant if <code>selection_procedure = "zscore"</code> or <code>directions = "random"</code> . Defaults to an assay called "DE" that is produced by <code>lemur::compute_contrasts()</code> .
<code>test_data</code>	a <code>SummarizedExperiment</code> 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 <code>test_method</code> is <code>"glmGamPoi"</code> or <code>"edgeR"</code> a test using raw counts is conducted and two matching assays are needed: (1) the continuous assay (with <code>continuous_assay_name</code>) is projected onto the LEMUR fit to find the latent position of each cell and (2) the count assay (<code>count_assay_name</code>) is used for forming the pseudobulk. If <code>test_method == "limma"</code> , only the continuous assay is needed. The arguments defaults to the test data split of when calling <code>lemur()</code> .
<code>test_data_col_data</code>	additional column data for the <code>test_data</code> argument.
<code>test_method</code>	choice of test for the pseudobulked differential expression. <code>glmGamPoi</code> and <code>edgeR</code> work on the counts. <code>limma</code> works on the continuous assay.

<code>continuous_assay_name, count_assay_name</code>	the names of the assays that are used for the statistical test. By default, <code>continuous_assay_name</code> is the name that was specified in the original <code>lemur()</code> call and <code>count_assay_name</code> , which is used if <code>test_method</code> is "glmGamPoi" or "edgeR", is "counts".
<code>size_factor_method</code>	the procedure to calculate the size factor after pseudobulking. This argument is only relevant if <code>test_method</code> is "glmGamPoi" or "edgeR". If <code>fit</code> is sub-setted, using a vector with the sequencing depth per cell ensures reasonable results. Default: NULL which means that <code>colSums(assay(fit\$test_data, count_assay_name))</code> is used.
<code>design, alignment_design</code>	the design to use for the fit. Default: <code>fit\$design</code>
<code>add_diff_in_diff</code>	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..
<code>make_neighborhoods_consistent</code>	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
<code>skip_confounded_neighborhoods</code>	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
<code>control_parameters</code>	named list with additional parameters passed to underlying functions.
<code>verbose</code>	Should the method print information during the fitting. Default: TRUE.

Value

a data frame with one entry per gene
<code>name</code> The gene name.
<code>neighborhood</code> A list column where each element is a vector with the cell names included in that neighborhood.
<code>n_cells</code> the number of cells in the neighborhood (<code>lengths(neighborhood)</code>).
<code>sel_statistic</code> The statistic that is maximized by the <code>selection_procedure</code> .
<code>pval, adj_pval, t_statistic, lfc</code> 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 <code>test_method</code>). Only present if <code>test_data</code> is not NULL.
<code>did_pval, did_adj_pval, did_lfc</code> 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 <code>add_diff_in_diff = TRUE</code> .

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 <- compute_contrasts(fit, contrast = cond(condition = "panobinostat") - cond(condition = "ctrl"))
nei <- find_de_neighborhoods(fit, group_by = vars(patient_id))
head(nei)
```

glioblastoma_example_data

The glioblastoma_example_data dataset

Description

The dataset is a `SingleCellExperiment::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::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>.

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

<code>data</code>	a matrix with observations in the columns and features in the rows. Or a <code>SummarizedExperiment</code> / <code>SingleCellExperiment</code> object
<code>design</code>	a formula referring to global objects or column in the <code>colData</code> of <code>data</code> and <code>col_data</code> argument
<code>col_data</code>	an optional data frame with <code>ncol(data)</code> rows.
<code>n_embedding</code>	the dimension of the k -plane that is rotated through space.
<code>linear_coefficient_estimator</code>	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.
<code>use_assay</code>	if <code>data</code> is a <code>SummarizedExperiment</code> / <code>SingleCellExperiment</code> object, which assay should be used.
<code>test_fraction</code>	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 <code>ncol(data)</code> . Default: 20% (0.2).
<code>...</code>	additional parameters that are passed on to the internal function <code>lemur_impl</code> .
<code>verbose</code>	Should the method print information during the fitting. Default: TRUE.

Value

An object of class `lemur_fit` which extends `SingleCellExperiment::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](#), [compute_contrasts](#), [find_de_neighborhoods](#)

Examples

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

lemur_fit-class	<i>The lemur_fit class</i>
-----------------	----------------------------

Description

The `lemur_fit` class extends `SingleCellExperiment::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 `compute_contrasts` 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,,]
```

predict.lemur_fit	<i>Predict values from lemur_fit object</i>
-------------------	---

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 compute_contrasts 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 compute_contrasts result
fit <- compute_contrasts(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
```

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)
```

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 <code>cond()</code> specifying a full observation (e.g. <code>cond(treatment = "A", sex = "male") - cond(treatment = "C", sex = "male")</code>) 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.

<code>variance_est</code>	How or if the variance should be estimated. 'analytical' is only compatible with <code>consider = "linear"</code> . 'resampling' is the most flexible (to adapt the number of resampling iterations, set <code>n_resampling_iter</code> . Default: 100)
<code>verbose</code>	should the method print information during the fitting. Default: TRUE.
<code>...</code>	additional arguments.

Value

a `data.frame`

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