

Package: conformeR (via r-universe)

October 19, 2026

Type Package

Title Conformalized differential expression analysis of
multi-condition single-cell data

Version 0.99.1

Description conformeR provides conformal prediction layers for the
cell neighborhood construction step of the LEMUR framework. It
implements two complementary approaches, conformal clustering
and conformal selection, to quantify uncertainty in the
resulting cell neighborhoods, together with tools for
visualizing and interpreting the resulting uncertainty sets.

URL <https://github.com/juslecl/conformeR>

BugReports <https://github.com/juslecl/conformeR/issues>

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Encoding UTF-8

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RoxygenNote 7.3.3

Suggests testthat (>= 3.0.0), S4Vectors, BiocStyle, tidyr, purrr,
knitr, rmarkdown, edgeR, MASS, utils

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SingleCellExperiment, BiocParallel, rsample, rlang, stats,
lemur, glmGamPoi, uwot, ggnewscale, cowplot, scales, grid,
methods, tidysselect

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VignetteBuilder knitr

LazyData false

BiocType Software

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DimensionReduction, Classification, Clustering,
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conformeR	<i>LEMUR analysis for neighborhoods on predicted gene differential expression with conformal methods</i>
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Description

Runs a LEMUR analysis, identifies differential-expression neighborhoods, and applies conformal procedures to a set of genes of interest. The data are split into training, calibration, and test sets based on the covariates specified in the LEMUR design formula.

Usage

```
conformeR(  
  sce,  
  design_lemur = ~1,  
  contrast_column,  
  contrast_levels = NULL,  
  n_embedding = 60,  
  use_assay = "logcounts",  
  test_fraction_lemur = 0.2,  
  cp_train_frac = 0.5,  
  cp_cal_frac = 0.25,  
  cp_alpha = 0.05,  
  genes_of_interest,  
  what = c("conf_selection", "conf_clustering"),  
  n_cores = 1,  
  verbose = TRUE  
)
```

Arguments

sce	A SingleCellExperiment object containing the single-cell expression data.
design_lemur	A formula specifying the design used by LEMUR.
contrast_column	A column name specifying the comparison used for differential-expression testing in LEMUR.
contrast_levels	when contrast_column has more than two levels, specify which two are tested again each other.
n_embedding	Number of dimensions in the LEMUR embedding.
use_assay	Character string specifying the assay to use.
test_fraction_lemur	Fraction of cells used as the LEMUR test set.
cp_train_frac	Fraction of cells used for conformal training.
cp_cal_frac	Fraction of cells used for conformal calibration.
cp_alpha	Miscoverage level for the conformal procedures.
genes_of_interest	Character vector containing the names of genes to include in the conformal analysis. They need to correspond to the row names of the sce.
what	Character vector specifying the conformal procedure(s) to run.
n_cores	Number of cores used for parallel processing.
verbose	Logical indicating whether to display progress information.

Details

The conformal procedures are applied to a subset of genes of interest. Genes are processed in chunks to allow parallel computation.

Value

A list containing:

`fit_lemur` The LEMUR test-set object restricted to the genes of interest.

`nei_lemur` The LEMUR neighborhoods for the genes of interest in the test set.

`conf_results` The results of the conformal procedures for the genes of interest.

Examples

```
data("sce_reduced")
out_conformer <- conformeR(sce_reduced,
  design_lemur = ~ patient_id + condition,
  contrast_column = "condition",
  n_embedding = 15,
  genes_of_interest = c(
    "ENSG00000163453",
```

```

      "ENSG00000163734"
    )
  )
  out_conformer

```

plotter_conformal_clustering

Plot conformal clustering results on the LEMUR embedding

Description

Visualizes gene-level differential expression and conformal clustering results on the aligned LEMUR UMAP embedding. Cells are displayed according to their LEMUR neighborhood membership and the size of the conformal prediction set. The cells inside and outside the conformal neighborhood prediction set are combined into a single stacked plot, annotated "Inside" / "Outside", with one shared "Set size" legend for the black/grey contours.

Usage

```
plotter_conformal_clustering(conformer_output, genes_to_plot)
```

Arguments

conformer_output A list returned by `run_replication`, containing the LEMUR fit, LEMUR neighborhoods, and conformal results.

genes_to_plot Character vector specifying the genes to plot.

Value

A single combined ggplot/cowplot object: the "Inside" panel row stacked above the "Outside" panel row, each row labeled accordingly, with one shared "Set size" legend (black = set size 1, grey = the other set size observed in the data) below the combined grid.

Examples

```

data("sce_reduced")
out_conformer <- conformeR(sce_reduced,
  design_lemur = ~ patient_id + condition,
  contrast_column = "condition",
  n_embedding = 15,
  genes_of_interest = c(
    "ENSG00000163453",
    "ENSG00000163734"
  )
)
plotter_conformal_clustering(out_conformer,
  genes_to_plot = c(

```

```

        "ENSG00000163453",
        "ENSG00000163734"
    )
)

```

plotter_conformal_selection

Plot conformal selection results on the LEMUR embedding

Description

Visualizes gene-level differential expression and conformal selection results on the aligned LEMUR UMAP embedding. For each selected gene, cells are shown according to their LEMUR neighborhood membership and conformal selection status (density contours).

Usage

```
plotter_conformal_selection(conformer_output, genes_to_plot)
```

Arguments

conformer_output

A list returned by conformerR, containing the LEMUR fit, LEMUR neighborhoods, and conformal results.

genes_to_plot Character vector specifying the genes to plot.

Value

A single combined ggplot/cowplot object showing differential expression and conformal selection results for all requested genes on the aligned LEMUR UMAP embedding, with one shared "Conformal selection" legend for the green contours below the grid of gene panels (instead of one legend per gene).

Examples

```

data("sce_reduced")
out_conformer <- conformerR(sce_reduced,
  design_lemur = ~ patient_id + condition,
  contrast_column = "condition",
  n_embedding = 15,
  genes_of_interest = c(
    "ENSG00000163453",
    "ENSG00000163734"
  )
)
plotter_conformal_selection(out_conformer,
  genes_to_plot = c(
    "ENSG00000163453",

```

```

    "ENSG00000163734"
  )
)

```

sce_reduced

Example single-cell dataset

Description

A small SingleCellExperiment object used to demonstrate the conformeR workflow. Random subset from a real dataset (see source). Code for reproducing from original dataset at: https://github.com/juslecl/conformeR-paper/tree/main/data_preparation 3k cells and 100 genes for 2 patients, 2 conditions, 3 cell-types.

Usage

```
data("sce_reduced")
```

Format

A SingleCellExperiment object.

Details

This object is a subset of the dataset from Zhao et al. (2021), processed for use as an example dataset in **conformeR**.

Source

Zhao, W., Dovas, A., Spinazzi, E., et al. (2021). Deconvolution of cell type-specific drug responses in human tumor tissue with single-cell RNA-seq. *Genome Medicine*, 13, 82. GEO accession: GSE148842.

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* **datasets**

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