

Package: express (via r-universe)

June 3, 2026

Title Visualise Gene-Level Expression Data

Version 0.0.0.9000

Description Simple analysis and visualisation of tabular gene-level expression data.

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Suggests Rtsne, testthat (>= 3.0.0)

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RoxygenNote 7.3.1

URL <https://github.com/selkamand/express>

BugReports <https://github.com/selkamand/express/issues>

Imports assertions (>= 0.0.0.9000), ggiraph, ggplot2

Remotes selkamand/assertions

Config/pak/sysreqs

libcairo2-dev cmake libfontconfig1-dev libfreetype6-dev make libpng-dev libuv1-dev

Repository <https://selkamand.r-universe.dev>

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express_available_datasets

List Available Datasets

Description

This function lists all available datasets for use with the express package. It reads a predefined TSV file containing dataset information and returns it as a data frame.

Usage

```
express_available_datasets(url = FALSE)
```

Arguments

url show the URL from which the data will be pulled

Value

A data frame containing the available datasets. The data frame includes columns such as name, type, url, and description.

Examples

```
# List all available datasets
datasets <- express_available_datasets()
print(datasets)
```

express_precomputed *Fetch and Plot Precomputed Dataset*

Description

This function retrieves and visualizes precomputed t-SNE data from a specified dataset. It fetches the data from a URL associated with the dataset name provided, and then either returns the data directly or creates a ggplot2 visualization of the t-SNE dimensions.

Usage

```
express_precomputed(
  dataset,
  datatype = c("expression", "methylation"),
  interactive = FALSE,
  just_return_data = FALSE,
  title = "auto",
  show_axis_titles = FALSE
)
```

Arguments

dataset	A string specifying the name of the dataset to be retrieved. The dataset must be one of the available datasets listed by <code>express_available_datasets()</code> .
datatype	A string indicating whether to retrieve expression or methylation data
interactive	A logical value indicating whether the plot should be interactive. Currently, this parameter is not used in the function.
just_return_data	A logical value indicating whether to return only the dataset without generating a plot. Defaults to FALSE.
show_axis_titles	A boolean indicating whether to show axis titles

Value

If `just_return_data` is TRUE, a `data.table` containing the dataset is returned. If `just_return_data` is FALSE and the dataset type is "tsne", a `ggplot2` object representing the t-SNE plot is returned. If the dataset type is not "tsne", an error is raised.

Examples

```
# Retrieve and plot the
express_precomputed("GBM")

# Retrieve only the data without plotting
data <- express_precomputed_tsne("GBM", just_return_data = TRUE)
```

```
express_sample_relatedness
  Title
```

Description

Title

Usage

```
express_sample_relatedness(
  data,
  method = "TSNE",
  gene_selector = "most_variable",
  sample_metadata = NULL,
  colour_by = NULL,
  perplexity = 30
)
```

Arguments

perplexity if NULL, autocalculate

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