

Package: gRaphiaExtra (via r-universe)

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Type Package

Title An R Package for Integrating 'Seurat' Objects into 'gRaphia'

Version 0.26.9

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Description Utilising graph-based network analysis frameworks, 'Graphia' <<https://graphia.app/>> is a powerful open source visual analytics application developed to aid the interpretation of large and complex datasets. For more details, see article by Freeman et al. (2022) <[doi:10.1371/journal.pcbi.1010310](https://doi.org/10.1371/journal.pcbi.1010310)>. 'gRaphia' is an extension of the 'Graphia' application within the R environment, providing tools for network analysis and visualisation. 'gRaphiaExtra' provides additional functionality specifically designed for single-cell RNA-sequencing data, enabling users to seamlessly integrate and utilise existing 'Seurat' analysis outputs in 'gRaphia'. The package also provides supplementary functions to support and enhance the 'gRaphia' analysis framework.

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Depends R (>= 4.4.2.0)

Imports checkmate, dplyr, stats, utils

Encoding UTF-8

RoxygenNote 7.3.3

NeedsCompilation no

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testSeuratClusterEnrichment	<i>testSeuratClusterEnrichment - Test Seurat Clusters for Enrichment</i>
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Description

Performs appropriate tests of enrichment of Seurat clusters for a specified set of genes.

Usage

```
testSeuratClusterEnrichment(
  markers_list,
  test_set,
  background_set,
  test = "fisher",
  alternative = "greater",
  p_adjust = "bonferroni"
)
```

Arguments

markers_list	Data frame. A data frame containing two columns: a gene column and a cluster column. Typically, output from the FindAllMarkers() function. If using a custom markers_list object, ensure no clusters are labelled as "0". If so, rename that cluster to prevent erroneous enrichment. "0" is a cluster label internally reserved for the background set.
test_set	Data frame or character. Either a data frame including two columns, "gene" and "group" (e.g., causal genes for different mouse diseases), or a vector of genes giving the test set (e.g., mouse breast cancer genes).
background_set	Character. A vector of genes that form the background population for the tests (e.g., all mouse protein coding genes).
test	Character. One of "fisher" (default) for fisher's exact test, "chi.sq" for the chi squared test, "hyper" for the hypergeometric test, and "conditional" for partial odds ratios from a multivariable logistic regression. Conditional is only applicable when groups are included in the test set and there is substantial overlap between the groups.
alternative	Character. One of "greater" (default), "two.sided", or "less".
p_adjust	Character. Correct for multiple testing using one of "holm", "hochberg", "hommel", "bonferroni" (default), "BH", "BY", or "fdr" methods.

Value

A data frame with enrichment test results.

Examples

[illegible]

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