Package: altmem (via r-universe)

May 15, 2026

Title Alternative Interface to cytoMEM Marker Enrichment Modeling

Version 0.0.0.9000

Description Automatically generate and display quantitative labels for cell populations that have been identified from flow cytometry, mass cytometry, and single-cell RNA-seq data.

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URL `https://igordot.github.io/altmem/`

Depends R (>= 4.4)

Imports circlize, ComplexHeatmap, cytoMEM, RColorBrewer, SummarizedExperiment

Suggests CATALYST, HDCytoData, testthat (>= 3.0.0)

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Repository https://igordot.r-universe.dev

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Contents

`altmem` *Marker Enrichment Modeling*

Description

A wrapper around `cytoMEM::MEM()` that accepts a matrix, data frame, SummarizedExperiment, or SingleCellExperiment, and supports non-numeric cluster labels.

Usage

```
altmem(
  x,
  cluster_col,
  assay_name = "exprs",
  markers = "all",
  transform = FALSE,
  cofactor = 1,
  choose.markers = FALSE,
  choose.ref = FALSE,
  zero.ref = FALSE,
  IQR.thresh = NULL
)
```

Arguments

`x`	A matrix, data frame, SummarizedExperiment, or SingleCellExperiment.
`cluster_col`	Name of the column containing cluster labels.
`assay_name`	Name of the assay to use for the expression matrix. Only used for SummarizedExperiment input. Defaults to `"exprs"`.
`markers`	Character vector of marker names to include, or `"all"` to use all markers.
`transform`, `cofactor`, `choose.markers`, `choose.ref`, `zero.ref`, `IQR.thresh`	Passed to `cytoMEM::MEM()`.

Value

A list of matrices (the return value of `cytoMEM::MEM()`).

`mem_heatmap` *Heatmap of MEM scores*

Description

Visualizes MEM enrichment scores as a heatmap.

Usage

```
mem_heatmap(
  x,
  show_mem_labels = FALSE,
  min_label_score = 1,
  max_label_markers = 5,
  show_label_scores = FALSE,
  min_heatmap_score = 0,
  filename = NULL,
  width = 15,
  height = 8,
  cluster_rows = TRUE,
  cluster_columns = TRUE,
  ...
)
```

Arguments

`x`	The return value of `altmem()` or `cytoMEM::MEM()`.
`show_mem_labels`	Whether to annotate rows with MEM labels. When `TRUE`, labels are generated via `mem_labels()` using `min_label_score`, `max_label_markers`, and `show_label_scores`. Defaults to `FALSE`.
`min_label_score`	Minimum absolute MEM score for a marker to be included in the label. Defaults to `1`.
`max_label_markers`	Maximum number of markers to include per direction (positive and negative) in each label. Defaults to `5`.
`show_label_scores`	Whether to include MEM scores alongside marker names in the MEM labels. Defaults to `FALSE`.
`min_heatmap_score`	Minimum absolute MEM score across any cluster for a marker to be shown as a column in the heatmap. Increase this to remove low variance markers. Defaults to `0` (show all markers).
`filename`	Optional file path to save the heatmap. The format is inferred from the extension (e.g., `".png"`, `".pdf"`, `".svg"`). Defaults to `NULL` (no file saved).

`width, height`	Plot dimensions in inches. Only used when `filename` is provided.
`cluster_rows`	Whether to cluster rows. Defaults to `TRUE`.
`cluster_columns`	Whether to cluster columns. Defaults to `TRUE`.
`...`	Additional arguments passed to `ComplexHeatmap::Heatmap()`.

Value

A ComplexHeatmap::Heatmap object, invisibly.

`mem_labels` *MEM-enriched cluster labels*

Description

Generates descriptive labels for each cluster that include measured features specifically enriched on the population based on MEM scores, following the cytoMEM format. Markers are ranked by absolute MEM score and separated into positively and negatively enriched groups.

Usage

```
mem_labels(
  x,
  min_label_score = 1,
  max_label_markers = 5,
  show_label_scores = TRUE
)
```

Arguments

`x`	The return value of `altmem()` or `cytoMEM::MEM()`.
`min_label_score`	Minimum absolute MEM score for a marker to be included in the label. Defaults to `1`.
`max_label_markers`	Maximum number of markers to include per direction (positive and negative) in each label. Defaults to `5`.
`show_label_scores`	Whether to include MEM scores alongside marker names. Defaults to `TRUE`.

Value

A named character vector.

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