

Package: HDStIM (via r-universe)

September 12, 2024

Type Package

Title High Dimensional Stimulation Immune Mapping ('HDStIM')

Version 1.0.0

Description A method for identifying responses to experimental stimulation in mass or flow cytometry that uses high dimensional analysis of measured parameters and can be performed with an end-to-end unsupervised approach. In the context of in vitro stimulation assays where high-parameter cytometry was used to monitor intracellular response markers, using cell populations annotated either through automated clustering or manual gating for a combined set of stimulated and unstimulated samples, 'HDStIM' labels cells as responding or non-responding. The package also provides auxiliary functions to rank intracellular markers based on their contribution to identifying responses and generating diagnostic plots.

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Encoding UTF-8

LazyData true

LazyDataCompression xz

RoxygenNote 7.2.3

URL <https://github.com/niaid/HDStIM>, <https://niaid.github.io/HDStIM/>

BugReports <https://github.com/niaid/HDStIM/issues>

Depends R (>= 3.6.0)

biocViews ComplexHeatmap

Imports tibble, ggplot2, uwot, dplyr, tidyr, magrittr, broom, tidyselect, gggridges, Boruta, scales, circlize, ComplexHeatmap

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr, rmarkdown

Language en-US

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

RemoteUrl <https://github.com/niaid/hdstim>

RemoteRef HEAD

RemoteSha b42e3d83871fe6077362e5a36ab065360a25184e

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chi11	<i>Sample data set for CyTOF Stimulation Assay</i>
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Description

A list with the CyTOF stimulation assay data.

Usage

```
chi11
```

Format

A list with one tibble containig CyTOF expression data. And four character vectors for arguments in the `HDSstIM` function.

chi11\$expr_data A 7,000 X 36 tibble. Cells are on the rows and variables on the columns. The first 6 columns contain for each cell `cluster_id` (from FlowSOM clustering), `sample_id` (unique for each FSC file), `condition` (comparison groups), `patient_id` (unique for each subject), `stim_type` (labels for types of stimulation assays including the unstim), `merging1` (meta culster labels from ConsensusClusterPlus). The last 30 columns contain the archsinh transformed CyTOF expression values for the 30 markers (20 type and 10 state) used in the sitmulation panel.

chi11\$type_markers A character vector with the labels for type markers used in the stimulation panel.

chi11\$state_markers A character vector with the labels for state markers used in the stimulation panel.

chi11\$cluster_col A character label of the meta-cluster/cluster ID column in `chi11$expr_dat` tibble.

chi11\$stim_label A character vector with the label(s) for the stimulation types corresponding to the labels in the `stim_type` column in `chi11$expr_data`.

chi11\$unstim_label A character label for the unstim cells corresponding to the labels in the `stim_type` column in `chi11$expr_data`.

 HDStIM

HDStIM: High Dimensional Stimulation Immune Mapping

Description

Function to select cells from the stimulated samples that have likely responded to the stimulant.

Usage

```
HDStIM(
  dat,
  state_markers,
  cellpop_col,
  stim_lab,
  unstim_lab,
  p_value = 0.05,
  seed_val = NULL,
  umap = FALSE,
  umap_cells = NULL,
  verbose = FALSE
)
```

Arguments

<code>dat</code>	A tibble with the single cell data. Cells on rows and variables/markers on columns.
<code>state_markers</code>	A character vector with the labels of state markers from the stimulation panel.
<code>cellpop_col</code>	Column in the tibble with the cell population IDs.
<code>stim_lab</code>	A character vector of stim label(s).
<code>unstim_lab</code>	A character of unstim label(s).
<code>p_value</code>	The P-value for Fisher's exact test. Default is 0.05.
<code>seed_val</code>	Seed value (integer) for kmeans clustering. Default is <code>NULL</code> for no seed value.
<code>umap</code>	Boolean (T/F) to carry out UMAP on the selected cells. Default is <code>FALSE</code> to skip UMAP calculation.
<code>umap_cells</code>	An integer; for calculating UMAPs take a minimum of <code>umap_cells</code> per cluster or the total number of cells if the cluster size is smaller than <code>umap_cells</code> . Default is <code>NULL</code> .
<code>verbose</code>	Logical. To make function more verbose. Default is <code>FALSE</code> .

Value

A list with tibbles for expression data for the selected cells, data to plot stacked bar plots, data to plot UMAP plots, and parameters passed to the function.

Examples

```
mapped_data <- HDStIM(chi11$expr_data, chi11$state_markers,
  chi11$cluster_col, chi11$stim_label,
  chi11$unstim_label, seed_val = 123, umap = FALSE, umap_cells = NULL,
  verbose = FALSE)
```

marker_ranking_boruta *Marker Ranking by Boruta*

Description

Function to run Boruta on the stimulation - cell population combinations that passed the Fisher's exact test to rank the markers according to their contribution to the response.

Usage

```
marker_ranking_boruta(
  mapped_data,
  path = NULL,
  n_cells = NULL,
  max_runs = 100,
  seed_val = 123,
  verbose = 0
)
```

Arguments

mapped_data	Returned list from the HDStIM function.
path	Path to the folder to save figures generated by this function.
n_cells	Number of cells to down sample the data. Default is NULL to include all the cells.
max_runs	Maximum number of runs for the random forest algorithm. Default is 100.
seed_val	Seed value for Boruta. Default is 123.
verbose	0, 1, or 2. Default is 0.

Value

A list with a tibble containing attribute statistics calculated by Boruta and ggplot objects. If the path is not NULL, plots are also rendered and saved in the specified folder in PNG format.

Examples

```
mapped_data <- HDStIM(chi11$expr_data, chi11$state_markers,
  chi11$cluster_col, chi11$stim_label,
  chi11$unstim_label, seed_val = 123, umap = FALSE, umap_cells = NULL,
  verbose = FALSE)

marker_ranking <- marker_ranking_boruta(mapped_data, path = NULL, n_cells = NULL,
  max_runs = 1000, seed_val = 123,
  verbose = 0)
```

plot_exprs	<i>Diagnostic plots showing individual marker distribution before and after mapping by HDStIM</i>
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Description

Diagnostic plots showing individual marker distribution before and after mapping by HDStIM

Usage

```
plot_exprs(mapped_data, path = NULL, verbose = FALSE)
```

Arguments

mapped_data	List output of the HDStIM function.
path	Path to the folder to save figures generated by this function.
verbose	Logical. To make function more verbose. Default is FALSE.

Value

A list of ggplot objects. If the path is not NULL, PNG files of the plots are saved in the specified folder.

Examples

```
mapped_data <- HDStIM(chi11$expr_data, chi11$state_markers,
  chi11$cluster_col, chi11$stim_label,
  chi11$unstim_label, seed_val = 123, umap = FALSE, umap_cells = NULL,
  verbose = FALSE)

pe <- plot_exprs(mapped_data, path = NULL, verbose = FALSE)
```

plot_K_Fisher	<i>Diagnostic plots explaining K-means clustering and Fisher's exact test carried out by HDStIM</i>
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Description

Diagnostic plots explaining K-means clustering and Fisher's exact test carried out by HDStIM

Usage

```
plot_K_Fisher(mapped_data, path = NULL, verbose = FALSE)
```

Arguments

mapped_data	Returned list from the HDStIM function.
path	Path to the folder to save figures generated by this function NULL by default.
verbose	Logical. To make function more verbose. Default is FALSE.

Value

A list of ggplot objects. If the path is not NULL, PNG files of the plots are saved in the specified folder.

Examples

```
mapped_data <- HDStIM(chi11$expr_data, chi11$state_markers,
  chi11$cluster_col, chi11$stim_label,
  chi11$unstim_label, seed_val = 123, umap = FALSE, umap_cells = NULL,
  verbose = FALSE)

pk <- plot_K_Fisher(mapped_data, path = NULL, verbose = FALSE)
```

plot_marker_ranking_heatmap	<i>Marker ranking heatmap</i>
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Description

A consolidated heatmap showing the importance scores of all the state markers (X-axis) from all the stimulation-cell population combinations that passed the Fisher's exact test (Y-axis).

Usage

```
plot_marker_ranking_heatmap(marker_ranking)
```

Arguments

marker_ranking Returned list from the [marker_ranking_boruta](#) function.

Value

A ComplexHeatmap object

Examples

```
mapped_data <- HDStIM(chi11$expr_data, chi11$state_markers,
                     chi11$cluster_col, chi11$stim_label,
                     chi11$unstim_label, seed_val = 123, umap = TRUE,
                     umap_cells = 50, verbose = FALSE)

marker_ranking <- marker_ranking_boruta(mapped_data, path = NULL, n_cells = NULL,
                                       max_runs = 1000, seed_val = 123,
                                       verbose = 0)

pht <- plot_marker_ranking_heatmap(marker_ranking)
```

plot_umap	<i>Diagnostic UMAP plots showing the partitioning of cells into responding and non-responding groups by HDStIM</i>
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Description

Diagnostic UMAP plots showing the partitioning of cells into responding and non-responding groups by HDStIM

Usage

```
plot_umap(mapped_data, path = NULL, verbose = FALSE)
```

Arguments

mapped_data Returned list from the [HDStIM](#) function.

path Path to the folder to save figures generated by this function.

verbose Logical. To make function more verbose. Default is FALSE.

Value

A list of ggplot objects. If the path is not NULL, PNG files of the plots are saved in the specified folder.

Examples

```
mapped_data <- HDStIM(chi11$expr_data, chi11$state_markers,  
                     chi11$cluster_col, chi11$stim_label,  
                     chi11$unstim_label, seed_val = 123, umap = TRUE,  
                     umap_cells = 50, verbose = FALSE)  
  
pu <- plot_umap(mapped_data, path = NULL, verbose = FALSE)
```


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