Package 'HDStIM'

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Type Package

Title High Dimensional Stimulation Immune Mapping ('HDStIM')

Version 0.1.0

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 7.1.2

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

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

Depends R (>= 3.6.0)

Imports tibble, ggplot2, uwot, dplyr, tidyr, broom, tidyselect, ggridges, Boruta, scales

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr, rmarkdown

Language en-US

NeedsCompilation no

Author Rohit Farmer [aut, cre] (ORCID: <https://orcid.org/0000-0003-4197-3047>), Richard Apps [aut] (ORCID: <https://orcid.org/0000-0001-5140-0141>), John Tsang [aut, pdr] (ORCID: <https://orcid.org/0000-0003-3186-3047>)

Maintainer Rohit Farmer <rohit.farmer@gmail.com>

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Contents

`chi11` *Sample data set for CyTOF Stimulation Assay*

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 `HDStIM` 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,
  seed_val = NULL,
  umap = FALSE,
  umap_cells = NULL,
  verbose = FALSE
)
```

Arguments

dat	A tibble with the single cell data. Cells on rows and variables/markers on columns.
state_markers	A character vector with the labels of state markers from the stimulation panel.
cellpop_col	Column in the tibble with the cell population IDs.
stim_lab	A character vector of stim label(s).
unstim_lab	A character of unstim label(s).
seed_val	Seed value (integer) for kmeans clustering. Default is NULL for no seed value.
umap	Boolean (T/F) to carry out UMAP on the selected cells. Default is FALSE to skip UMAP calculation.
umap_cells	An integer; for calculating UMAPs take a minimum of umap_cells per cluster or the total number of cells if the cluster size is smaller than umap_cells. Default is NULL.
verbose	Logical. To make function more verbose. Default is FALSE.

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)

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

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

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

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

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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