Package ‘diffcyt’

April 3, 2024

Version 1.22.1
Title Differential discovery in high-dimensional cytometry via high-resolution clustering
Description Statistical methods for differential discovery analyses in high-dimensional cytometry data (including flow cytometry, mass cytometry or CyTOF, and oligonucleotide-tagged cytometry), based on a combination of high-resolution clustering and empirical Bayes moderated tests adapted from transcriptomics.
URL https://github.com/lmweber/diffcyt
BugReports https://github.com/lmweber/diffcyt/issues
License MIT + file LICENSE
biocViews ImmunoOncology, FlowCytometry, Proteomics, SingleCell, CellBasedAssays, CellBiology, Clustering, FeatureExtraction, Software
Depends R (>= 3.4.0)
Imports flowCore, FlowSOM, SummarizedExperiment, S4Vectors, limma, edgeR, lme4, multcomp, dplyr, tidyr, reshape2, magrittr, stats, methods, utils, grDevices, graphics, ComplexHeatmap, circlize, grid
VignetteBuilder knitr
Suggests BiocStyle, knitr, rmarkdown, testthat, HDCytoData, CATALYST
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Author Lukas M. Weber [aut, cre] (<https://orcid.org/0000-0002-3282-1730>)
Maintainer Lukas M. Weber <lmweberedu@gmail.com>
R topics documented:

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- topTable
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calcCounts

Calculate cluster cell counts

Description

Calculate number of cells per cluster-sample combination

Usage

calcCounts(d_se)

Arguments

d_se

Data object from previous steps, in SummarizedExperiment format, containing cluster labels as a column in the row meta-data (from generateClusters).

Details

Calculate number of cells per cluster-sample combination (referred to as cluster cell 'counts', 'abundances', or 'frequencies').

The cluster cell counts are required for testing for differential abundance of cell populations, and are also used for weights and filtering when testing for differential states within cell populations.

Results are returned as a new SummarizedExperiment object, where rows = clusters, columns = samples, assay = values (counts). (Note that this structure differs from the input data object.)
Value

d_counts: \textit{SummarizedExperiment} object, where rows = clusters, columns = samples, assay = values (counts).

Examples

# For a complete workflow example demonstrating each step in the 'diffcyt' pipeline,
# see the package vignette.

# Function to create random data (one sample)
d_random <- function(n = 20000, mean = 0, sd = 1, ncol = 20, cofactor = 5) {
  d <- sinh(matrix(rnorm(n, mean, sd), ncol = ncol)) * cofactor
  colnames(d) <- paste0("marker", sprintf("%02d", 1:ncol))
  d
}

# Create random data (without differential signal)
set.seed(123)
d_input <- list(
  sample1 = d_random(),
  sample2 = d_random(),
  sample3 = d_random(),
  sample4 = d_random()
)

experiment_info <- data.frame(
  sample_id = factor(paste0("sample", 1:4)),
  group_id = factor(c("group1", "group1", "group2", "group2")),
  stringsAsFactors = FALSE
)

marker_info <- data.frame(
  channel_name = paste0("channel", sprintf("%03d", 1:20)),
  marker_name = paste0("marker", sprintf("%02d", 1:20)),
  marker_class = factor(c(rep("type", 10), rep("state", 10)),
                        levels = c("type", "state", "none")),
  stringsAsFactors = FALSE
)

# Prepare data
d_se <- prepareData(d_input, experiment_info, marker_info)

# Transform data
d_se <- transformData(d_se)

# Generate clusters
d_se <- generateClusters(d_se)

# Calculate counts
d_counts <- calcCounts(d_se)
**calcMedians**  
*Calculate cluster medians*

**Description**  
Calculate cluster medians (median expression for each cluster-sample-marker combination)

**Usage**  
```
calcMedians(d_se)
```

**Arguments**  
- **d_se**: Data object from previous steps, in `SummarizedExperiment` format, containing cluster labels as a column in the row meta-data (from `generateClusters`). Column meta-data is assumed to contain a factor `marker_class`.

**Details**  
Calculate median marker expression for each cluster and sample (i.e. medians for each cluster-sample-marker combination).

The data object is assumed to contain a factor `marker_class` in the column meta-data (see `prepareData`), which indicates the protein marker class for each column of data ("type", "state", or "none").

The cluster medians are required for testing for differential states within cell populations, and for plotting purposes.

Variables `id_type_markers` and `id_state_markers` are saved in the metadata slot of the output object. These can be used to identify the 'cell type' and 'cell state' markers in the list of assays in the output `SummarizedExperiment` object, which is useful in later steps of the 'diffcyt' pipeline.

Results are returned as a new `SummarizedExperiment` object, where rows = clusters, columns = samples, sheets (assays slot) = markers. Note that there is a separate table of values (assay) for each marker. The metadata slot also contains variables `id_type_markers` and `id_state_markers`, which can be used to identify the sets of cell type and cell state markers in the list of assays.

**Value**  
- **d_medians**: `SummarizedExperiment` object, where rows = clusters, columns = samples, sheets (assays slot) = markers. The metadata slot contains variables `id_type_markers` and `id_state_markers`, which can be accessed with `metadata(d_medians)$id_type_markers` and `metadata(d_medians)$id_state_markers`.

**Examples**

```r
# For a complete workflow example demonstrating each step in the 'diffcyt' pipeline,
# see the package vignette.

# Function to create random data (one sample)
d_random <- function(n = 20000, mean = 0, sd = 1, ncol = 20, cofactor = 5) {
  d <- sinh(matrix(rnorm(n, mean, sd), ncol = ncol)) * cofactor
  d_se <- as.data.frame(d)
  d_se$marker_class <- sample(c("type", "state", "none"), n, replace = TRUE)
  d_se$cluster <- sample(1:10, n, replace = TRUE)
  d_se$replicate <- sample(1:10, n, replace = TRUE)
  d_se$assay <- sample(1:10, n, replace = TRUE)
  d_se$sample <- sample(1:10, n, replace = TRUE)
  d_se$group <- sample(c("group1", "group2"), n, replace = TRUE)
  d_se <- asित("summarizedExperiment", d_se)
  calculateMedians(d_se)
}
```

calcMediansByClusterMarker

Calculate medians (by cluster and marker)

Description

Calculate medians for each cluster-marker combination

Usage

calcMediansByClusterMarker(d_se)
Arguments

d_se Data object from previous steps, in SummarizedExperiment format, containing cluster labels as a column in the row meta-data (from generateClusters). Column meta-data is assumed to contain a factor marker_class.

Details

Calculate median marker expression for each cluster, across all samples (i.e. medians for each cluster-marker combination).

The data object is assumed to contain a factor marker_class in the column meta-data (see prepareData), which indicates the protein marker class for each column of data ("type", "state", or "none"). Cluster medians are calculated for all markers.

The medians by cluster and marker are required for plotting purposes.

Variables id_type_markers and id_state_markers are saved in the metadata slot of the output object. These can be used to identify the 'cell type' and 'cell state' markers in the sequence of markers (columns) in the output object, which is useful in later steps of the 'diffcyt' pipeline.

Results are returned as a new SummarizedExperiment object, where rows = clusters, columns = markers, assay = values (marker expression values). The metadata slot also contains variables id_type_markers and id_state_markers, which can be used to identify the sets of cell type and cell state markers in the columns.

Value

d_medians_by_cluster_marker: SummarizedExperiment object, where rows = clusters, columns = markers, assay = values (marker expression values). The metadata slot contains variables id_type_markers and id_state_markers, which can be accessed with metadata(d_medians)$id_type_markers and metadata(d_medians)$id_state_markers.

Examples

# For a complete workflow example demonstrating each step in the 'diffcyt' pipeline,
# see the package vignette.

# Function to create random data (one sample)

# Create random data (without differential signal)
set.seed(123)
d_input <- list(
sample1 = d_random(),
sample2 = d_random(),
sample3 = d_random(),
sample4 = d_random()
)
calcMediansBySampleMarker <- function(d_se) {
  # Prepare data
  d_se <- prepareData(d_input, experiment_info, marker_info)
  # Transform data
  d_se <- transformData(d_se)
  # Generate clusters
  d_se <- generateClusters(d_se)
  # Calculate medians (by cluster and marker)
  d_medians_by_cluster_marker <- calcMediansByClusterMarker(d_se)
}

Description

Calculate medians for each sample-marker combination

Usage

calcMediansBySampleMarker(d_se)

Arguments

d_se : Data object from previous steps, in SummarizedExperiment format, containing cluster labels as a column in the row meta-data (from generateClusters). Column meta-data is assumed to contain a factor marker_class.

Details

Calculate overall median marker expression for each sample (i.e. medians for each sample-marker combination).
The data object is assumed to contain a factor marker_class in the column meta-data (see `prepareData`), which indicates the protein marker class for each column of data ("type", "state", or "none"). Cluster medians are calculated for all markers.

The medians by sample and marker are required for plotting purposes. Variables `id_type_markers` and `id_state_markers` are saved in the metadata slot of the output object. These can be used to identify the 'cell type' and 'cell state' markers in the sequence of markers (columns) in the output object, which is useful in later steps of the 'diffcyt' pipeline.

Results are returned as a new `SummarizedExperiment` object, where rows = samples, columns = markers, assay = values (marker expression values). The metadata slot also contains variables `id_type_markers` and `id_state_markers`, which can be used to identify the sets of cell type and cell state markers in the columns.

**Value**

```r
d_medians_by_sample_marker: SummarizedExperiment object, where rows = samples, columns = markers, assay = values (marker expression values). The metadata slot contains variables `id_type_markers` and `id_state_markers`, which can be accessed with `metadata(d_medians)$id_type_markers` and `metadata(d_medians)$id_state_markers`.
```

**Examples**

```r
# For a complete workflow example demonstrating each step in the 'diffcyt' pipeline, 
# see the package vignette.

# Function to create random data (one sample)
d_random <- function(n = 20000, mean = 0, sd = 1, ncol = 20, cofactor = 5) {
  d <- sinh(matrix(rnorm(n, mean, sd), ncol = ncol)) * cofactor
  colnames(d) <- paste0("marker", sprintf("%02d", 1:ncol))
  d
}

# Create random data (without differential signal)
set.seed(123)
d_input <- list(
  sample1 = d_random(),
  sample2 = d_random(),
  sample3 = d_random(),
  sample4 = d_random()
)

experiment_info <- data.frame(
  sample_id = factor(paste0("sample", 1:4)),
  group_id = factor(c("group1", "group1", "group2", "group2")),
  stringsAsFactors = FALSE
)

marker_info <- data.frame(
  channel_name = paste0("channel", sprintf("%03d", 1:20)),
  marker_name = paste0("marker", sprintf("%02d", 1:20)),
  marker_class = factor(c(rep("type", 10), rep("state", 10)),
```
levels = c("type", "state", "none"),
stringsAsFactors = FALSE
)

# Prepare data
d_se <- prepareData(d_input, experiment_info, marker_info)

# Transform data
d_se <- transformData(d_se)

# Generate clusters
d_se <- generateClusters(d_se)

# Calculate medians (by sample and marker)
d_medians_by_sample_marker <- calcMediansBySampleMarker(d_se)

createContrast

Create contrast matrix

Description

Create contrast matrix for differential testing

Usage

createContrast(contrast)

Arguments

contrast Vector defining the contrast of interest. This should be a numeric vector specifying the combination of model parameters to test whether they are equal to zero. The entries correspond to the columns of the design matrix, or the levels of the fixed effect terms in the model formula. For example, using a design matrix:

c(0, 1, 0, 0, 0)
to test whether a single parameter corresponding to the second column in the design matrix is equal to zero.

Details

Creates a contrast matrix specifying the comparison of interest, in the correct format for the differential testing functions. This can then be provided to the differential testing functions, together with either a design matrix or model formula, and the data object.

The argument contrast defines the contrast of interest. This should be a numeric vector specifying the combination of model parameters to test whether they are equal to zero. In many cases, this will simply be a vector of zeros and a single entry equal to one; this will test whether a single parameter is equal to zero (e.g. c(0, 1, 0, 0, 0)).

If a design matrix has been used, the entries of contrast correspond to the columns of the design matrix; and the length of contrast equals the number of columns in the design matrix. If a model
formula has been used, the entries correspond to the levels of the fixed effect terms; and the length equals the number of levels of the fixed effect terms.

The contrast matrix is formatted as a matrix with a single column containing the contrast of interest. To perform tests for multiple contrasts, run this function and the corresponding differential testing function multiple times.

Value

contrast: Returns a contrast matrix containing the contrast of interest, formatted as a matrix with a single column.

Examples

# For a complete workflow example demonstrating each step in the 'diffcyt' pipeline,
# see the package vignette.

# Example: contrast matrix
createContrast(c(0, 1, 0, 0, 0))
createDesignMatrix

Details

Creates a design matrix specifying the models to be fitted. (Alternatively, createFormula can be used to generate a model formula instead of a design matrix.)

The design matrix can then be provided to the differential testing functions, together with the data object and contrast matrix.

The experiment_info input (which was also previously provided to prepareData) should be a data frame containing all factors and covariates of interest. For example, depending on the experimental design, this may include the following columns:

- group IDs (e.g. groups for differential testing)
- block IDs (e.g. patient IDs in a paired design)
- batch IDs (batch effects)
- continuous covariates

The argument cols_design specifies which columns in experiment_info to include in the design matrix. (For example, there may be an additional column of sample IDs, which should not be included.) This can be provided as a character vector of column names, a numeric vector of column indices, or a logical vector. By default, all columns are included.

Columns of indicator variables (e.g. group IDs, block IDs, and batch IDs) in experiment_info must be formatted as factors (otherwise they will be treated as numeric values). The indicator columns will be expanded into the design matrix format. The names for each parameter are taken from the column names of experiment_info.

All factors provided here will be included as fixed effect terms in the design matrix. Alternatively, to use random effects for some factors (e.g. for block IDs), see createFormula; or, depending on the method used, provide them directly to the differential testing function (testDA_voom and testDS_limma).

Value

design: Returns a design matrix (numeric matrix), with one row per sample, and one column per model parameter.

Examples

# For a complete workflow example demonstrating each step in the 'diffcyt' pipeline, # see the package vignette.

# Example: simple design matrix
experiment_info <- data.frame(
  sample_id = factor(paste0("sample", 1:4)),
  group_id = factor(c("group1", "group1", "group2", "group2")),
  stringsAsFactors = FALSE
)
createDesignMatrix(experiment_info, cols_design = "group_id")

# Example: more complex design matrix: patient IDs and batch IDs
experiment_info <- data.frame(
  sample_id = factor(paste0("sample", 1:8)),
  group_id = factor(paste0("group", 1:8)),
  batch_id = factor(paste0("batch", 1:4)),
  patient_id = factor(paste0("patient", 1:2))
)
createDesignMatrix(experiment_info, cols_design = c("group_id", "batch_id", "patient_id"))
createFormula

Create model formula and corresponding data frame of variables

Description

Create model formula and corresponding data frame of variables for model fitting

Usage

createFormula(experiment_info, cols_fixed = NULL, cols_random = NULL)

Arguments

- **experiment_info**: data.frame, DataFrame, or tbl_df of experiment information (which was also previously provided to prepareData). This should be a data frame containing all factors and covariates of interest; e.g. group IDs, block IDs, batch IDs, and continuous covariates.

- **cols_fixed**: Argument specifying columns of experiment_info to include as fixed effect terms in the model formula. This can be provided as a character vector of column names, a numeric vector of column indices, or a logical vector.

- **cols_random**: Argument specifying columns of experiment_info to include as random intercept terms in the model formula. This can be provided as a character vector of column names, a numeric vector of column indices, or a logical vector. Default = none.

Details

Creates a model formula and corresponding data frame of variables specifying the models to be fitted. (Alternatively, createDesignMatrix can be used to generate a design matrix instead of a model formula.)
The output is a list containing the model formula and corresponding data frame of variables (one column per formula term). These can then be provided to differential testing functions that require a model formula, together with the main data object and contrast matrix.

The experiment_info input (which was also previously provided to prepareData) should be a data frame containing all factors and covariates of interest. For example, depending on the experimental design, this may include the following columns:

- group IDs (e.g. groups for differential testing)
- block IDs (e.g. patient IDs in a paired design; these may be included as either fixed effect or random effects)
- batch IDs (batch effects)
- continuous covariates
- sample IDs (e.g. to include random intercept terms for each sample, to account for overdispersion typically seen in high-dimensional cytometry data; this is known as an 'observation-level random effect' (OLRE); see Nowicka et al., 2017, F1000Research for more details)

The arguments cols_fixed and cols_random specify the columns in experiment_info to include as fixed effect terms and random intercept terms respectively. These can be provided as character vectors of column names, numeric vectors of column indices, or logical vectors. The names for each formula term are taken from the column names of experiment_info.

Note that for some methods, random effect terms (e.g. for block IDs) must be provided directly to the differential testing function instead (testDA_voom and testDS_limma).

If there are no random effect terms, it will usually be simpler to use a design matrix instead of a model formula; see createDesignMatrix.

**Value**

- formula: Returns a list with three elements:
  - formula: model formula
  - data: data frame of variables corresponding to the model formula
  - random_terms: TRUE if model formula contains any random effect terms

**Examples**

# For a complete workflow example demonstrating each step in the 'diffcyt' pipeline,  
# see the package vignette.

# Example: model formula
experiment_info <- data.frame(  
  sample_id = factor(paste0("sample", 1:8)),  
  group_id = factor(rep(paste0("group", 1:2), each = 4)),  
  patient_id = factor(rep(paste0("patient", 1:4), 2)),  
  stringsAsFactors = FALSE)
createFormula(experiment_info, cols_fixed = "group_id", cols_random = c("sample_id", "patient_id"))
**diffcyt**

Run 'diffcyt' pipeline

**Description**

Wrapper function to run complete 'diffcyt' pipeline

**Usage**

```r
diffcyt(
  d_input,
  experiment_info = NULL,
  marker_info = NULL,
  design = NULL,
  formula = NULL,
  contrast,
  analysis_type = c("DA", "DS"),
  method_DA = c("diffcyt-DA-edgeR", "diffcyt-DA-voom", "diffcyt-DA-GLMM"),
  method_DS = c("diffcyt-DS-limma", "diffcyt-DS-LMM"),
  markers_to_test = NULL,
  clustering_to_use = NULL,
  cols_to_include = NULL,
  subsampling = FALSE,
  n_sub = NULL,
  seed_sub = NULL,
  transform = TRUE,
  cofactor = 5,
  cols_clustering = NULL,
  xdim = 10,
  ydim = 10,
  meta_clustering = FALSE,
  meta_k = 40,
  seed_clustering = NULL,
  min_cells = 3,
  min_samples = NULL,
  normalize = FALSE,
  norm_factors = "TMM",
  trend_method = "none",
  block_id = NULL,
  trend = TRUE,
  weights = TRUE,
  plot = FALSE,
  path = ".",
  verbose = TRUE
)
```
Arguments

d_input
Input data. Must be either: (i) a flowSet or list of flowFrames, DataFrames, data.frames, or matrices as input (one flowFrame or list item per sample) (see prepareData); or (ii) a CATALYST daFrame (containing cluster labels in rowData; see vignette for an example).

experiment_info
data.frame, DataFrame, or tbl_df of experiment information, for example sample IDs and group IDs. Must contain a column named sample_id. See prepareData. (Not required when providing a CATALYST daFrame for d_input.)

marker_info
data.frame, DataFrame, or tbl_df of marker information for each column of data. This should contain columns named marker_name and marker_class. The columns contain: (i) marker names (and any other column names); and (ii) a factor indicating the marker class for each column (with entries "type", "state", or "none"). See prepareData. (Not required when providing a CATALYST daFrame for d_input.)

design
Design matrix, created with createDesignMatrix. See createDesignMatrix.

formula
Model formula object, created with createFormula. See createFormula.

contrast
Contrast matrix, created with createContrast. See createContrast.

analysis_type
Type of differential analysis to perform: differential abundance (DA) of cell populations, or differential states (DS) within cell populations. Options are "DA" and "DS". See testDA_edgeR, testDA_voom, testDA_GLMM, testDS_limma, or testDS_LMM.

method_DA
Method to use for calculating differential abundance (DA) tests. Options are "diffcyt-DA-edgeR", "diffcyt-DA-voom", and "diffcyt-DA-GLMM". Default = "diffcyt-DA-edgeR". See testDA_edgeR, testDA_voom, or testDA_GLMM.

method_DS
Method to use for calculating differential state (DS) tests. Options are "diffcyt-DS-limma" and "diffcyt-DS-LMM". Default = "diffcyt-DS-limma". See testDS_limma or testDS_LMM.

markers_to_test
(Optional) Logical vector specifying which markers to test for differential expression (from the set of markers stored in the assays of d_medians; for method testDS_limma or testDS_LMM). Default = all 'cell state' markers, which are identified by the logical vector id_state_markers stored in the meta-data of d_medians. See testDS_limma or testDS_LMM.

clustering_to_use
(Optional) Column name indicating which set of cluster labels to use for differential testing, when input data are provided as a CATALYST daFrame object containing multiple sets of cluster labels. (In this case, the metadata of the daFrame object is assumed to contain a data frame named cluster_codes; clustering_to_use is the column name of the selected column in cluster_codes. If clustering_to_use is provided, an identifier clustering_name to identify this column will also be saved in the metadata of the output object.) Default = NULL, in which case cluster labels stored in column named cluster_id in the rowData of the daFrame object are used.
cols_to_include
Logical vector indicating which columns to include from the input data. Default = all columns. See prepareData.

subsampling
Whether to use random subsampling to select an equal number of cells from each sample. Default = FALSE. See prepareData.

n_sub
Number of cells to select from each sample by random subsampling, if subsampling = TRUE. Default = number of cells in smallest sample. See prepareData.

seed_sub
Random seed for subsampling. Set to an integer value to generate reproducible results. Default = NULL. See prepareData.

transform
Whether to apply 'arcsinh' transform. This may be set to FALSE if the input data has already been transformed. Default = TRUE. See transformData.

cofactor
Cofactor parameter for 'arcsinh' transform. Default = 5, which is appropriate for mass cytometry (CyTOF) data. For fluorescence flow cytometry, we recommend cofactor = 150 instead. See transformData.

cols_clustering
Columns to use for clustering. Default = NULL, in which case markers identified as 'cell type' markers (with entries "type") in the vector marker_class in the column meta-data of d_se will be used. See generateClusters.

xdim
Horizontal length of grid for self-organizing map for FlowSOM clustering (number of clusters = xdim * ydim). Default = 10 (i.e. 100 clusters). See generateClusters.

ydim
Vertical length of grid for self-organizing map for FlowSOM clustering (number of clusters = xdim * ydim). Default = 10 (i.e. 100 clusters). See generateClusters.

meta_clustering
Whether to include FlowSOM 'meta-clustering' step. Default = FALSE. See generateClusters.

meta_k
Number of meta-clusters for FlowSOM, if meta-clustering = TRUE. Default = 40. See generateClusters.

seed_clustering
Random seed for clustering. Set to an integer value to generate reproducible results. Default = NULL. See generateClusters.

min_cells
Filtering parameter. Default = 3. Clusters are kept for differential testing if they have at least min_cells cells in at least min_samples samples. See testDA_edgeR, testDA_voom, testDA_GLMM, testDS_limma, or testDS_LMM.

min_samples
Filtering parameter. Default = number of samples / 2, which is appropriate for two-group comparisons (of equal size). Clusters are kept for differential testing if they have at least min_cells cells in at least min_samples samples. See testDA_edgeR, testDA_voom, testDA_GLMM, testDS_limma, or testDS_LMM.

normalize
Whether to include optional normalization factors to adjust for composition effects. Default = FALSE. See testDA_edgeR, testDA_voom, or testDA_GLMM.

norm_factors
Normalization factors to use, if normalize = TRUE. Default = "TMM", in which case normalization factors are calculated automatically using the 'trimmed mean of M-values' (TMM) method from the edgeR package. Alternatively, a vector of values can be provided (the values should multiply to 1). See testDA_edgeR, testDA_voom, or testDA_GLMM.
trend_method  Method for estimating dispersion trend; passed to function `estimateDisp` from edgeR package (for method `testDA_edgeR`). Default = "none". (See `estimateDisp` help file from edgeR package for other options.) See `testDA_edgeR`.

block_id  (Optional) Vector or factor of block IDs (e.g. patient IDs) for paired experimental designs, to be included as random effects (for method `testDA_voom` or `testDS_limma`). If provided, the block IDs will be included as random effects using the limma `duplicateCorrelation` methodology. Alternatively, block IDs can be included as fixed effects in the design matrix (`createDesignMatrix`). See `testDA_voom` or `testDS_limma`.

trend  (Optional) Whether to fit a mean-variance trend when calculating moderated tests with function `eBayes` from limma package (for method `testDS_limma`). When `trend = TRUE`, this is known as the limma-trend method (Law et al., 2014; Phipson et al., 2016). Default = TRUE. See `testDS_limma`.

weights  (Optional) Whether to include precision weights (for method `testDS_limma` or `testDS_LMM`). For method `testDS_limma`, cluster cell counts will be used as precision weights (across all samples and clusters); this allows the limma model fitting functions to account for uncertainty due to the total number of cells per sample (library sizes) and total number of cells per cluster. For methods `testDS_LMM`, cluster cell counts will be used as precision weights within each model (across samples, i.e. within the model for each cluster); these represent the relative uncertainty in calculating each median value (within each model). Default = TRUE. See `testDS_limma` or `testDS_LMM`.

plot  Whether to save diagnostic plots (for method `testDA_voom` or `testDS_limma`). Default = FALSE. See `testDA_voom` or `testDS_limma`.

path  Path for diagnostic plots, if `plot = TRUE` (for method `testDA_voom` or `testDS_limma`). Default = current working directory. See `testDA_voom` or `testDS_limma`.

verbose  Whether to print status messages during each step of the pipeline. Default = TRUE.

Details

This wrapper function runs the complete 'diffcyt' analysis pipeline, by calling the functions for the individual steps in the pipeline in the correct sequence.

For more details about the functions for the individual steps, see the package vignette and the function help pages. Running the individual functions may provide additional flexibility, especially for complex analyses.

The input data can be provided as a `flowSet` or a list of `flowFrames`, `DataFrames`, `data.frames`, or matrices (one `flowFrame` or list item per sample). Alternatively, it is also possible to provide the input as a `daFrame` object from the CATALYST Bioconductor package (Chevrier, Crowell, Zanotelli et al., 2018). This can be useful when initial exploratory analyses and clustering have been performed using CATALYST; the `daFrame` object from CATALYST (containing cluster labels in the `rowData`) can then be provided directly to the `diffcyt` functions for differential testing.

Minimum required arguments when not providing a `flowSet` or list of `flowFrames`, `DataFrames`, `data.frames`, or matrices:

• `d_input`
• experiment_info
• marker_info
• either design or formula (depending on the differential testing method used)
• contrast
• analysis_type

Minimum required arguments when providing a CATALYST daFrame object:

• d_input
• either design or formula (depending on the differential testing method used)
• contrast
• analysis_type

Value

Returns a list containing the results object res, as well as the data objects d_se, d_counts, d_medians, d_medians_by_cluster_marker, and d_medians_by_sample_marker. (If a CATALYST daFrame object was used as input, the output list contains objects res, d_counts, and d_medians.) The structure of res depends on the differential testing method used. See testDA_edgeR, testDA_voom, testDA_GLMM, testDS_limma, or testDS_LMM.

Examples

# For a complete workflow example demonstrating each step in the 'diffcyt' pipeline,
# see the package vignette.

# Function to create random data (one sample)
d_random <- function(n = 20000, mean = 0, sd = 1, ncol = 20, cofactor = 5) {
d <- sinh(matrix(rnorm(n, mean, sd), ncol = ncol)) * cofactor
colnames(d) <- paste0("marker", sprintf("%02d", 1:ncol))
d
}

# Create random data (without differential signal)
set.seed(123)
d_input <- list(
sample1 = d_random(),
sample2 = d_random(),
sample3 = d_random(),
sample4 = d_random()
)

# Add differential abundance (DA) signal
d_input[[3]][ix_DA, ix_cols_type] <- d_random(n = 1000, mean = 2, ncol = 10)
d_input[[4]][ix_DA, ix_cols_type] <- d_random(n = 1000, mean = 2, ncol = 10)

# Add differential states (DS) signal
ix_DS <- 901:1000
ix_cols_DS <- 19:20
d_input[[1]][ix_DS, ix_cols_type] <- d_random(n = 1000, mean = 3, ncol = 10)
d_input[[2]][ix_DS, ix_cols_type] <- d_random(n = 1000, mean = 3, ncol = 10)
d_input[[3]][ix_DS, c(ix_cols_type, ix_cols_DS)] <- d_random(n = 1200, mean = 3, ncol = 12)
d_input[[4]][ix_DS, c(ix_cols_type, ix_cols_DS)] <- d_random(n = 1200, mean = 3, ncol = 12)

experiment_info <- data.frame(
    sample_id = factor(paste0("sample", 1:4)),
    group_id = factor(c("group1", "group1", "group2", "group2")),
    stringsAsFactors = FALSE
)

marker_info <- data.frame(
    channel_name = paste0("channel", sprintf("%03d", 1:20)),
    marker_name = paste0("marker", sprintf("%02d", 1:20)),
    marker_class = factor(c(rep("type", 10), rep("state", 10)),
        levels = c("type", "state", "none")),
    stringsAsFactors = FALSE
)

# Create design matrix
design <- createDesignMatrix(experiment_info, cols_design = "group_id")

# Create contrast matrix
contrast <- createContrast(c(0, 1))

# Test for differential abundance (DA) of clusters (using default method 'diffcyt-DA-edgeR')
out_DA <- diffcyt(d_input, experiment_info, marker_info,
    design = design, contrast = contrast,
    analysis_type = "DA", method_DA = "diffcyt-DA-edgeR",
    seed_clustering = 123, verbose = FALSE)

# Test for differential states (DS) within clusters (using default method 'diffcyt-DS-limma')
out_DS <- diffcyt(d_input, experiment_info, marker_info,
    design = design, contrast = contrast,
    analysis_type = "DS", method_DS = "diffcyt-DS-limma",
    seed_clustering = 123, verbose = FALSE)

# Display results for top DA clusters
topTable(out_DA, format_vals = TRUE)

# Display results for top DS cluster-marker combinations
topTable(out_DS, format_vals = TRUE)

# Plot heatmap for DA tests
plotHeatmap(out_DA, analysis_type = "DA")

# Plot heatmap for DS tests
plotHeatmap(out_DS, analysis_type = "DS"
generateClusters  Generate clusters

Description
Generate high-resolution clusters for diffcyt analysis

Usage
generateClusters(
  d_se,
  cols_clustering = NULL,
  xdim = 10,
  ydim = 10,
  meta_clustering = FALSE,
  meta_k = 40,
  seed_clustering = NULL,
  ...
)

Arguments
d_se  Transformed input data, from prepareData and transformData.
cols_clustering  Columns to use for clustering. Default = NULL, in which case markers identified as 'cell type' markers (with entries "type") in the vector marker_class in the column meta-data of d_se will be used.
xdim  Horizontal length of grid for self-organizing map for FlowSOM clustering (number of clusters = xdim * ydim). Default = 10 (i.e. 100 clusters).
ydim  Vertical length of grid for self-organizing map for FlowSOM clustering (number of clusters = xdim * ydim). Default = 10 (i.e. 100 clusters).
meta_clustering  Whether to include FlowSOM 'meta-clustering' step. Default = FALSE.
meta_k  Number of meta-clusters for FlowSOM, if meta-clustering = TRUE. Default = 40.
seed_clustering  Random seed for clustering. Set to an integer value to generate reproducible results. Default = NULL.
...  Other parameters to pass to the FlowSOM clustering algorithm (through the function BuildSOM).

Details
Performs clustering to group cells into clusters representing cell populations or subsets, which can then be further analyzed by testing for differential abundance of cell populations or differential
states within cell populations. By default, we use high-resolution clustering or over-clustering (i.e. we generate a large number of small clusters), which helps ensure that rare populations are adequately separated from larger ones.

Data is assumed to be in the form of a `SummarizedExperiment` object generated with `prepareData` and transformed with `transformData`.

The input data object `d_se` is assumed to contain a vector `marker_class` in the column meta-data. This vector indicates the marker class for each column ("type", "state", or "none"). By default, clustering is performed using the 'cell type' markers only. For example, in immunological data, this may be the lineage markers. The choice of cell type markers is an important design choice for the user, and will depend on the underlying experimental design and research questions. It may be made based on prior biological knowledge or using data-driven methods. For an example of a data-driven method of marker ranking and selection, see Nowicka et al. (2017), *F1000Research*.

By default, we use the FlowSOM clustering algorithm (Van Gassen et al. 2015, *Cytometry Part A*, available from Bioconductor) to generate the clusters. We previously showed that FlowSOM gives very good clustering performance for high-dimensional cytometry data, for both major and rare cell populations, and is extremely fast (Weber and Robinson, 2016, *Cytometry Part A*).

The clustering is run at high resolution to give a large number of small clusters (i.e. over-clustering). This is done by running only the initial 'self-organizing map' clustering step in the FlowSOM algorithm, i.e. without the final 'meta-clustering' step. This ensures that small or rare populations are adequately separated from larger populations, which is crucial for detecting differential signals for extremely rare populations.

The minimum spanning tree (MST) object from `BuildMST` is stored in the experiment metadata slot in the `SummarizedExperiment` object `d_se`, and can be accessed with `metadata(d_se)$MST`.

Value

`d_se`: Returns the `SummarizedExperiment` input object, with cluster labels for each cell stored in an additional column of row meta-data. Row meta-data can be accessed with `rowData`. The minimum spanning tree (MST) object is also stored in the `metadata` slot, and can be accessed with `metadata(d_se)$MST`.

Examples

```r
# For a complete workflow example demonstrating each step in the 'diffcyt' pipeline,
# see the package vignette.

# Function to create random data (one sample)

d_random <- function(n = 20000, mean = 0, sd = 1, ncol = 20, cofactor = 5) {
  d <- sinh(matrix(rnorm(n, mean, sd), ncol = ncol)) * cofactor
  colnames(d) <- paste0("marker", sprintf("%02d", 1:ncol))
  d
}

# Create random data (without differential signal)
set.seed(123)
d_input <- list(
  sample1 = d_random(),
  sample2 = d_random(),
  sample3 = d_random(),
)
plotHeatmap

Plot heatmap showing top clusters or cluster-marker combinations

Usage

plotHeatmap(
    out = NULL,
    analysis_type = c("DA", "DS"),
    top_n = 20,
    threshold = 0.1,
    res = NULL,
    d_se = NULL,
    d_counts = NULL,
    d_medians = NULL,
    d_medians_by_cluster_marker = NULL,
    sample_order = NULL
)
**plotHeatmap**

### Arguments

- **out**: Output object from `diffcyt` wrapper function, containing results object `res` and data objects `d_se`, `d_counts`, `d_medians`, and `d_medians_by_cluster_marker`. Alternatively, the results and data objects can be provided individually.
- **analysis_type**: Whether to plot heatmap for differential abundance (DA) or differential state (DS) test results.
- **top_n**: Number of top clusters (DA tests) or cluster-marker combinations (DS tests) to display. Default = 20.
- **threshold**: Threshold for significant adjusted p-values. Default = 0.1.
- **res**: Object containing differential test results. Alternatively, the combined output object from the wrapper function `diffcyt` can be provided.
- **d_se**: Data object. Alternatively, the combined output object from the wrapper function `diffcyt` can be provided.
- **d_counts**: Data object. Alternatively, the combined output object from the wrapper function `diffcyt` can be provided.
- **d_medians**: Data object. (Required for DS tests only.) Alternatively, the combined output object from the wrapper function `diffcyt` can be provided.
- **d_medians_by_cluster_marker**: Data object. Alternatively, the combined output object from the wrapper function `diffcyt` can be provided.
- **sample_order**: (Optional) Custom ordering for samples (columns) in right-hand panel of heatmap. (This is useful when the default ordering does not group samples by condition; e.g. samples are ordered alphabetically by sample IDs instead.)

### Details

Display heatmap to visualize results for the top (most highly significant) detected clusters or cluster-marker combinations.

For DA tests, the heatmap consists of the following panels:

- median (arcsinh-transformed) expression (across all samples) for 'cell type' markers
- cluster abundances by sample
- row annotation indicating significant detected clusters

For DS tests, the heatmap consists of:

- median (arcsinh-transformed) expression (across all samples) for 'cell type' markers
- median (arcsinh-transformed) expression (across all samples) for 'cell state' markers
- median (arcsinh-transformed) expression (by sample) for 'cell state' markers for the top cluster-marker combinations
- row annotation indicating significant detected cluster-marker combinations

Heatmaps are generated using the `ComplexHeatmap` package (Gu et al., 2016), and color scales are generated using the `circlize` package (Gu et al., 2014). Both packages are available from Bioconductor.
Value

Displays a heatmap.

Examples

# For a complete workflow example demonstrating each step in the 'diffcyt' pipeline,
# see the package vignette.

# Function to create random data (one sample)

d_random <- function(n = 20000, mean = 0, sd = 1, ncol = 20, cofactor = 5) {
  d <- sinh(matrix(rnorm(n, mean, sd), ncol = ncol)) * cofactor
  colnames(d) <- paste0("marker", sprintf("%02d", 1:ncol))
  d
}

# Create random data (without differential signal)
set.seed(123)
d_input <- list(
  sample1 = d_random(),
  sample2 = d_random(),
  sample3 = d_random(),
  sample4 = d_random()
)

# Add differential abundance (DA) signal
ix_DA <- 801:900
d_input[[3]][ix_DA, ix_cols_type] <- d_random(n = 1000, mean = 2, ncol = 10)
d_input[[4]][ix_DA, ix_cols_type] <- d_random(n = 1000, mean = 2, ncol = 10)

# Add differential states (DS) signal
ix_DS <- 901:1000
ix_cols_DS <- 19:20
d_input[[1]][ix_DS, c(ix_cols_type, ix_cols_DS)] <- d_random(n = 1200, mean = 3, ncol = 12)
d_input[[2]][ix_DS, c(ix_cols_type, ix_cols_DS)] <- d_random(n = 1200, mean = 3, ncol = 12)

experiment_info <- data.frame(
  sample_id = factor(paste0("sample", 1:4)),
  group_id = factor(c("group1", "group1", "group2", "group2")),
  stringsAsFactors = FALSE
)

marker_info <- data.frame(
  channel_name = paste0("channel", sprintf("%03d", 1:20)),
  marker_name = paste0("marker", sprintf("%02d", 1:20)),
  marker_class = factor(c(rep("type", 10), rep("state", 10)),
                        levels = c("type", "state", "none")),
  stringsAsFactors = FALSE
)
# Create design matrix
design <- createDesignMatrix(experiment_info, cols_design = "group_id")

# Create contrast matrix
contrast <- createContrast(c(0, 1))

# Test for differential abundance (DA) of clusters (using default method 'diffcyt-DA-edgeR')
out_DA <- diffcyt(d_input, experiment_info, marker_info,
                design = design, contrast = contrast,
                analysis_type = "DA", method_DA = "diffcyt-DA-edgeR",
                seed_clustering = 123, verbose = FALSE)

# Test for differential states (DS) within clusters (using default method 'diffcyt-DS-limma')
out_DS <- diffcyt(d_input, experiment_info, marker_info,
                design = design, contrast = contrast,
                analysis_type = "DS", method_DS = "diffcyt-DS-limma",
                seed_clustering = 123, verbose = FALSE)

# Display results for top DA clusters
topTable(out_DA, format_vals = TRUE)

# Display results for top DS cluster-marker combinations
topTable(out_DS, format_vals = TRUE)

# Plot heatmap for DA tests
plotHeatmap(out_DA, analysis_type = "DA")

# Plot heatmap for DS tests
plotHeatmap(out_DS, analysis_type = "DS")

---

**prepareData**

*Prepare data*

**Description**

Prepare data into format for diffcyt pipeline

**Usage**

```r
prepareData(
  d_input,
  experiment_info,
  marker_info,
  cols_to_include = NULL,
  subsampling = FALSE,
  n_sub = NULL,
  seed_sub = NULL
)
```
Arguments

d_input Input data. Must be a flowSet or list of flowFrames, dataFrames, or matrices as input (one flowFrame or list item per sample).

experiment_info data.frame, DataFrame, or tbl_df of experiment information, for example sample IDs and group IDs. Must contain a column named sample_id.

marker_info data.frame, DataFrame, or tbl_df of marker information for each column of data. This should contain columns named marker_name and marker_class. The columns contain: (i) marker names (and any other column names); and (ii) a factor indicating the marker class for each column (with entries "type", "state", or "none").

cols_to_include Logical vector indicating which columns to include from the input data. Default = all columns.

subsampling Whether to use random subsampling to select an equal number of cells from each sample. Default = FALSE.

n_sub Number of cells to select from each sample by random subsampling, if subsampling = TRUE. Default = number of cells in smallest sample.

seed_sub Random seed for subsampling. Set to an integer value to generate reproducible results. Default = NULL.

Details

Functions in the diffcyt analysis pipeline assume that input data is provided as a SummarizedExperiment object, which contains a single matrix of expression values, together with row and column meta-data.

This function accepts a flowSet or a list of flowFrames, data.frames, or matrices as input (i.e. one flowFrame or list item per sample). The function then concatenates the data tables into a single matrix of values, and adds row and column meta-data.

Row meta-data should be provided as a data frame named experiment_info, containing columns of relevant experiment information, such as sample IDs and group IDs (for each sample). This must contain at least a column named sample_id.

Column meta-data should be provided as a data frame named marker_info, containing the following columns of marker information. The column names must be as shown.

- marker_name: protein marker names (and column names for any other columns)
- marker_class: factor indicating the protein marker class for each column of data (usually, entries will be either "type", "state", or "none")

The split into 'cell type' and 'cell state' markers is crucial for the analysis. Cell type markers are used to define cell populations by clustering, and to test for differential abundance of cell populations; while cell state markers are used to test for differential states within cell populations.

The optional argument cols_to_include allows unnecessary columns (e.g. any columns not containing protein markers) to be discarded.
Optionally, random subsampling can be used to select an equal number of cells from each sample (subsampling = TRUE). This can be useful when there are large differences in total numbers of cells per sample, since it ensures that samples with relatively large numbers of cells do not dominate the clustering. However, subsampling should generally not be used when rare cell populations are of interest, due to the significant loss of information if cells from the rare population are discarded.

Value

d_se: Returns data as a SummarizedExperiment containing a single matrix of data (expression values) in the assays slot, together with row meta-data (experiment information) and column meta-data (marker information). The metadata slot also contains the experiment_info data frame, and a vector n_cells of the number of cells per sample; these can be accessed with metadata(d_se)$experiment_info and metadata(d_se)$n_cells.

Examples

# For a complete workflow example demonstrating each step in the 'diffcyt' pipeline,
# see the package vignette.

# Function to create random data (one sample)
d_random <- function(n = 20000, mean = 0, sd = 1, ncol = 20, cofactor = 5) {
  d <- sinh(matrix(rnorm(n, mean, sd), ncol = ncol)) * cofactor
  colnames(d) <- paste0("marker", sprintf("%02d", 1:ncol))
  d
}

# Create random data (without differential signal)
set.seed(123)
d_input <- list(
sample1 = d_random(),
sample2 = d_random(),
sample3 = d_random(),
sample4 = d_random()
)

experiment_info <- data.frame(
sample_id = factor(paste0("sample", 1:4)),
group_id = factor(c("group1", "group1", "group2", "group2")),
stringsAsFactors = FALSE
)

marker_info <- data.frame(
  channel_name = paste0("channel", sprintf("%03d", 1:20)),
  marker_name = paste0("marker", sprintf("%02d", 1:20)),
  marker_class = factor(c(rep("type", 10), rep("state", 10)),
                        levels = c("type", "state", "none")),
  stringsAsFactors = FALSE
)

# Prepare data
d_se <- prepareData(d_input, experiment_info, marker_info)
testDA_edgeR

Test for differential abundance: method 'diffcyt-DA-edgeR'

Description

Calculate tests for differential abundance of cell populations using method 'diffcyt-DA-edgeR'

Usage

testDA_edgeR(
  d_counts,
  design,
  contrast,
  trend_method = "none",
  min_cells = 3,
  min_samples = NULL,
  normalize = FALSE,
  norm_factors = "TMM"
)

Arguments

d_counts SummarizedExperiment object containing cluster cell counts, from calcCounts.
design Design matrix, created with createDesignMatrix. See createDesignMatrix for details.
contrast Contrast matrix, created with createContrast. See createContrast for details.
trend_method Method for estimating dispersion trend; passed to function estimateDisp from edgeR package. Default = "none". (See estimateDisp help file from edgeR package for other options.)
min_cells Filtering parameter. Default = 3. Clusters are kept for differential testing if they have at least min_cells cells in at least min_samples samples.
min_samples Filtering parameter. Default = number of samples / 2, which is appropriate for two-group comparisons (of equal size). Clusters are kept for differential testing if they have at least min_cells cells in at least min_samples samples.
normalize Whether to include optional normalization factors to adjust for composition effects (see details). Default = FALSE.
norm_factors Normalization factors to use, if normalize = TRUE. Default = "TMM", in which case normalization factors are calculated automatically using the 'trimmed mean of M-values' (TMM) method from the edgeR package. Alternatively, a vector of values can be provided (the values should multiply to 1).
Details

Calculates tests for differential abundance of clusters, using functions from the edgeR package.

This method uses the edgeR package (Robinson et al. 2010, Bioinformatics; McCarthy et al. 2012, Nucleic Acids Research) to fit models and calculate moderated tests at the cluster level. Moderated tests improve statistical power by sharing information on variability (i.e. variance across samples for a single cluster) between clusters. By default, we use the option trend.method = "none" to calculate dispersions, since the dispersion-mean relationship typically does not resemble RNA-sequencing data; see edgeR User’s Guide. The statistical methods implemented in the edgeR package were originally designed for the analysis of gene expression data such as RNA-sequencing counts. Here, we apply these methods to cluster cell counts.

The experimental design must be specified using a design matrix, which can be created with createDesignMatrix. Flexible experimental designs are possible, including blocking (e.g. paired designs), batch effects, and continuous covariates. See createDesignMatrix for more details.

The contrast matrix specifying the contrast of interest can be created with createContrast. See createContrast for more details.

Filtering: Clusters are kept for differential testing if they have at least min_cells cells in at least min_samples samples. This removes clusters with very low cell counts across conditions, to improve power.

Normalization for the total number of cells per sample (library sizes) and total number of cells per cluster is automatically performed by the edgeR functions. Optional normalization factors can also be included to adjust for composition effects in the cluster cell counts per sample. For example, in an extreme case, if several additional clusters are present in only one condition, while all other clusters are approximately equally abundant between conditions, then simply normalizing by the total number of cells per sample will create a false positive differential abundance signal for the non-differential clusters. (For a detailed explanation in the context of RNA sequencing gene expression, see Robinson and Oshlack, 2010.) Normalization factors can be calculated automatically using the 'trimmed mean of M-values' (TMM) method (Robinson and Oshlack, 2010), implemented in the edgeR package (see also the edgeR User’s Guide for details). Alternatively, a vector of values can be provided (the values should multiply to 1).

Value

Returns a new SummarizedExperiment object, with differential test results stored in the rowData slot. Results include raw p-values (p_val) and adjusted p-values (p_adj) from the edgeR moderated tests, which can be used to rank clusters by evidence for differential abundance. Additional output columns from the edgeR tests are also included. The results can be accessed with the rowData accessor function.

Examples

# For a complete workflow example demonstrating each step in the 'diffcyt' pipeline, # see the package vignette.

# Function to create random data (one sample)

```r
d_random <- function(n = 20000, mean = 0, sd = 1, ncol = 20, cofactor = 5) {
  d <- sinh(matrix(rnorm(n, mean, sd), ncol = ncol)) * cofactor
  colnames(d) <- paste0("marker", sprintf("%02d", 1:ncol))
}
```

# Create random data (without differential signal)
set.seed(123)
d_input <- list(
  sample1 = d_random(),
  sample2 = d_random(),
  sample3 = d_random(),
  sample4 = d_random()
)

# Add differential abundance (DA) signal
ix_DA <- 801:900
ix_cols_type <- 1:10
d_input[[3]][ix_DA, ix_cols_type] <- d_random(n = 1000, mean = 2, ncol = 10)
d_input[[4]][ix_DA, ix_cols_type] <- d_random(n = 1000, mean = 2, ncol = 10)

experiment_info <- data.frame(
  sample_id = factor(paste0("sample", 1:4)),
  group_id = factor(c("group1", "group1", "group2", "group2")),
  stringsAsFactors = FALSE
)

marker_info <- data.frame(
  channel_name = paste0("channel", sprintf("%03d", 1:20)),
  marker_name = paste0("marker", sprintf("%02d", 1:20)),
  marker_class = factor(c(rep("type", 10), rep("state", 10)),
                        levels = c("type", "state", "none")),
  stringsAsFactors = FALSE
)

# Prepare data
d_se <- prepareData(d_input, experiment_info, marker_info)

# Transform data
d_se <- transformData(d_se)

# Generate clusters
d_se <- generateClusters(d_se)

# Calculate counts
d_counts <- calcCounts(d_se)

# Create design matrix
design <- createDesignMatrix(experiment_info, cols_design = "group_id")

# Create contrast matrix
contrast <- createContrast(c(0, 1))

# Test for differential abundance (DA) of clusters
res_DA <- testDA_edgeR(d_counts, design, contrast)
testDA_GLMM

Test for differential abundance: method 'diffcyt-DA-GLMM'

Description

Calculate tests for differential abundance of cell populations using method 'diffcyt-DA-GLMM'

Usage

testDA_GLMM(
  d_counts,  
  formula,  
  contrast,  
  min_cells = 3,  
  min_samples = NULL,  
  normalize = FALSE,  
  norm_factors = "TMM"  
)

Arguments

d_counts SummarizedExperiment object containing cluster cell counts, from calcCounts.

formula Model formula object, created with createFormula. This should be a list containing three elements: formula, data, and random_terms: the model formula, data frame of corresponding variables, and variable indicating whether the model formula contains any random effect terms. See createFormula for details.

contrast Contrast matrix, created with createContrast. See createContrast for details.

min_cells Filtering parameter. Default = 3. Clusters are kept for differential testing if they have at least min_cells cells in at least min_samples samples.

min_samples Filtering parameter. Default = number of samples / 2, which is appropriate for two-group comparisons (of equal size). Clusters are kept for differential testing if they have at least min_cells cells in at least min_samples samples.

normalize Whether to include optional normalization factors to adjust for composition effects (see details). Default = FALSE.

norm_factors Normalization factors to use, if normalize = TRUE. Default = "TMM", in which case normalization factors are calculated automatically using the 'trimmed mean of M-values' (TMM) method from the edgeR package. Alternatively, a vector of values can be provided (the values should multiply to 1).

Details

Calculates tests for differential abundance of clusters, using generalized linear mixed models (GLMMs).
This methodology was originally developed and described by Nowicka et al. (2017), *F1000Research*, and has been modified here to make use of high-resolution clustering to enable investigation of rare cell populations. Note that unlike the original method by Nowicka et al., we do not attempt to manually merge clusters into canonical cell populations. Instead, results are reported at the high-resolution cluster level, and the interpretation of significant differential clusters is left to the user via visualizations such as heatmaps (see the package vignette for an example).

This method fits generalized linear mixed models (GLMMs) for each cluster, and calculates differential tests separately for each cluster. The response variables in the models are the cluster cell counts, which are assumed to follow a binomial distribution. There is one model per cluster. We also include a filtering step to remove clusters with very small numbers of cells, to improve statistical power.

For more details on the statistical methodology, see Nowicka et al. (2017), *F1000Research* (section 'Differential cell population abundance').

The experimental design must be specified using a model formula, which can be created with `createFormula`. Flexible experimental designs are possible, including blocking (e.g. paired designs), batch effects, and continuous covariates. Blocking variables can be included as either random intercept terms or fixed effect terms (see `createFormula`). For paired designs, we recommend using random intercept terms to improve statistical power; see Nowicka et al. (2017), *F1000Research* for details. Batch effects and continuous covariates should be included as fixed effects. In addition, we include random intercept terms for each sample to account for overdispersion typically seen in high-dimensional cytometry count data. The sample-level random intercept terms are known as 'observation-level random effects' (OLREs); see Nowicka et al. (2017), *F1000Research* for more details.

The contrast matrix specifying the contrast of interest can be created with `createContrast`. See `createContrast` for more details.

Filtering: Clusters are kept for differential testing if they have at least `min_cells` cells in at least `min_samples` samples. This removes clusters with very low cell counts across conditions, to improve power.

Normalization: Optional normalization factors can be included to adjust for composition effects in the cluster cell counts per sample. For example, in an extreme case, if several additional clusters are present in only one condition, while all other clusters are approximately equally abundant between conditions, then simply normalizing by the total number of cells per sample will create a false positive differential abundance signal for the non-differential clusters. (For a detailed explanation in the context of RNA sequencing gene expression, see Robinson and Oshlack, 2010.) Normalization factors can be calculated automatically using the 'trimmed mean of M-values' (TMM) method (Robinson and Oshlack, 2010), implemented in the `edgeR` package (see also the `edgeR` User’s Guide for details). Alternatively, a vector of values can be provided (the values should multiply to 1).

**Value**

Returns a new `SummarizedExperiment` object, with differential test results stored in the `rowData` slot. Results include raw p-values (`p_val`) and adjusted p-values (`p_adj`), which can be used to rank clusters by evidence for differential abundance. The results can be accessed with the `rowData` accessor function.

**Examples**

```r
# For a complete workflow example demonstrating each step in the 'diffcyt' pipeline,
```
# Function to create random data (one sample)
d_random <- function(n = 20000, mean = 0, sd = 1, ncol = 20, cofactor = 5) {
  d <- sinh(matrix(rnorm(n, mean, sd), ncol = ncol)) * cofactor
  colnames(d) <- paste0("marker", sprintf("%02d", 1:ncol))
  d
}

# Create random data (without differential signal)
set.seed(123)
d_input <- list(
  sample1 = d_random(),
  sample2 = d_random(),
  sample3 = d_random(),
  sample4 = d_random()
)

# Add differential abundance (DA) signal
ix_DA <- 801:900
ix_cols_type <- 1:10
d_input[[3]][ix_DA, ix_cols_type] <- d_random(n = 1000, mean = 2, ncol = 10)
d_input[[4]][ix_DA, ix_cols_type] <- d_random(n = 1000, mean = 2, ncol = 10)

experiment_info <- data.frame(
  sample_id = factor(paste0("sample", 1:4)),
  group_id = factor(c("group1", "group1", "group2", "group2")),
  stringsAsFactors = FALSE
)

marker_info <- data.frame(
  channel_name = paste0("channel", sprintf("%03d", 1:20)),
  marker_name = paste0("marker", sprintf("%02d", 1:20)),
  marker_class = factor(c(rep("type", 10), rep("state", 10)),
                        levels = c("type", "state", "none")),
  stringsAsFactors = FALSE
)

# Prepare data
d_se <- prepareData(d_input, experiment_info, marker_info)

# Transform data
d_se <- transformData(d_se)

# Generate clusters
d_se <- generateClusters(d_se)

# Calculate counts
d_counts <- calcCounts(d_se)

# Create model formula
formula <- createFormula(experiment_info, cols_fixed = "group_id", cols_random = "sample_id")
# Create contrast matrix
contrast <- createContrast(c(0, 1))

# Test for differential abundance (DA) of clusters
res_DA <- testDA_GLMM(d_counts, formula, contrast)

testDA_voom

Test for differential abundance: method 'diffcyt-DA-voom'

Description
Calculate tests for differential abundance of cell populations using method 'diffcyt-DA-voom'

Usage

```r
testDA_voom(
  d_counts, design, contrast, block_id = NULL, min_cells = 3, min_samples = NULL, normalize = FALSE, norm_factors = "TMM", plot = FALSE, path = "."
)
```

Arguments

- `d_counts` *SummarizedExperiment* object containing cluster cell counts, from `calcCounts`.
- `design` Design matrix, created with `createDesignMatrix`. See `createDesignMatrix` for details.
- `contrast` Contrast matrix, created with `createContrast`. See `createContrast` for details.
- `block_id` (Optional) Vector or factor of block IDs (e.g. patient IDs) for paired experimental designs, to be included as random effects. If provided, the block IDs will be included as random effects using the `limma duplicateCorrelation` methodology. Alternatively, block IDs can be included as fixed effects in the design matrix (`createDesignMatrix`). See details.
- `min_cells` Filtering parameter. Default = 3. Clusters are kept for differential testing if they have at least `min_cells` cells in at least `min_samples` samples.
- `min_samples` Filtering parameter. Default = `number of samples / 2`, which is appropriate for two-group comparisons (of equal size). Clusters are kept for differential testing if they have at least `min_cells` cells in at least `min_samples` samples.
**normalize**

Whether to include optional normalization factors to adjust for composition effects (see details). Default = FALSE.

**norm_factors**

Normalization factors to use, if normalize = TRUE. Default = "TMM", in which case normalization factors are calculated automatically using the 'trimmed mean of M-values' (TMM) method from the edgeR package. Alternatively, a vector of values can be provided (the values should multiply to 1).

**plot**

Whether to save diagnostic plots for the limma voom transformations. Default = FALSE.

**path**

Path for diagnostic plots, if plot = TRUE. Default = current working directory.

---

**Details**

Calculates tests for differential abundance of clusters, using functions from the limma package and voom method.

This method uses the limma package (Ritchie et al. 2015, Nucleic Acids Research) to fit models and calculate moderated tests at the cluster level. Moderated tests improve statistical power by sharing information on variability (i.e. variance across samples for a single cluster) between clusters. Since count data are often heteroscedastic, we use the voom method (Law et al. 2014, Genome Biology) to transform the raw cluster cell counts and estimate observation-level weights to stabilize the mean-variance relationship. Diagnostic plots are shown if plot = TRUE.

The experimental design must be specified using a design matrix, which can be created with createDesignMatrix. Flexible experimental designs are possible, including blocking (e.g. paired designs), batch effects, and continuous covariates. See createDesignMatrix for more details.

For paired designs, either fixed effects or random effects can be used. Fixed effects are simpler, but random effects may improve power in data sets with unbalanced designs or very large numbers of samples. To use fixed effects, provide the block IDs (e.g. patient IDs) to createDesignMatrix. To use random effects, provide the block_id argument here instead. This will make use of the limma duplicateCorrelation methodology. Note that >2 measures per sample are not possible in this case (fixed effects should be used instead). Block IDs should not be included in the design matrix if the limma duplicateCorrelation methodology is used.

The contrast matrix specifying the contrast of interest can be created with createContrast. See createContrast for more details.

Filtering: Clusters are kept for differential testing if they have at least min_cells cells in at least min_samples samples. This removes clusters with very low cell counts across conditions, to improve power.

Normalization for the total number of cells per sample (library sizes) and total number of cells per cluster is automatically performed by the limma and voom functions. Optional normalization factors can also be included to adjust for composition effects in the cluster cell counts per sample. For example, in an extreme case, if several additional clusters are present in only one condition, while all other clusters are approximately equally abundant between conditions, then simply normalizing by the total number of cells per sample will create a false positive differential abundance signal for the non-differential clusters. (For a detailed explanation in the context of RNA sequencing gene expression, see Robinson and Oshlack, 2010.) Normalization factors can be calculated automatically using the 'trimmed mean of M-values' (TMM) method (Robinson and Oshlack, 2010), implemented in the edgeR package (see also the edgeR User’s Guide for details). Alternatively, a vector of values can be provided (the values should multiply to 1).
Value

Returns a new `SummarizedExperiment` object, with differential test results stored in the `rowData` slot. Results include raw p-values (`p_val`) and adjusted p-values (`p_adj`) from the limma moderated tests, which can be used to rank clusters by evidence for differential abundance. Additional output columns from the limma tests are also included. The results can be accessed with the `rowData` accessor function.

Examples

```r
# For a complete workflow example demonstrating each step in the 'diffcyt' pipeline,
# see the package vignette.

# Function to create random data (one sample)

d_random <- function(n = 20000, mean = 0, sd = 1, ncol = 20, cofactor = 5) {
  d <- sinh(matrix(rnorm(n, mean, sd), ncol = ncol)) * cofactor
  colnames(d) <- paste0("marker", sprintf("%02d", 1:ncol))
  d
}

# Create random data (without differential signal)
set.seed(123)
d_input <- list(
  sample1 = d_random(),
  sample2 = d_random(),
  sample3 = d_random(),
  sample4 = d_random()
)

# Add differential abundance (DA) signal
ix_DA <- 801:900
ix_cols_type <- 1:10

d_input[[3]][ix_DA, ix_cols_type] <- d_random(n = 1000, mean = 2, ncol = 10)
d_input[[4]][ix_DA, ix_cols_type] <- d_random(n = 1000, mean = 2, ncol = 10)

experiment_info <- data.frame(
  sample_id = factor(paste0("sample", 1:4)),
  group_id = factor(c("group1", "group1", "group2", "group2")),
  stringsAsFactors = FALSE
)

marker_info <- data.frame(
  channel_name = paste0("channel", sprintf("%03d", 1:20)),
  marker_name = paste0("marker", sprintf("%02d", 1:20)),
  marker_class = factor(c(rep("type", 10), rep("state", 10)),
                        levels = c("type", "state", "none")),
  stringsAsFactors = FALSE
)

# Prepare data
d_se <- prepareData(d_input, experiment_info, marker_info)

# Transform data
```
testDS_limma <- transformData(d_se)

# Generate clusters
d_se <- generateClusters(d_se)

# Calculate counts
d_counts <- calcCounts(d_se)

# Create design matrix
design <- createDesignMatrix(experiment_info, cols_design = "group_id")

# Create contrast matrix
contrast <- createContrast(c(0, 1))

# Test for differential abundance (DA) of clusters
res_DA <- testDA_voom(d_counts, design, contrast)

testDS_limma

Test for differential states: method 'diffcyt-DS-limma'

Description

Calculate tests for differential states within cell populations using method 'diffcyt-DS-limma'

Usage

testDS_limma(
  d_counts,  
  d_medians,  
  design,  
  contrast,  
  block_id = NULL,  
  trend = TRUE,  
  weights = TRUE,  
  markers_to_test = NULL,  
  min_cells = 3,  
  min_samples = NULL,  
  plot = FALSE,  
  path = "."  
)

Arguments

d_counts SummarizedExperiment object containing cluster cell counts, from calcCounts.
d_medians SummarizedExperiment object containing cluster medians (median marker expression for each cluster-sample combination), from calcMedians. Assumed to contain a logical vector id_state_markers in the meta-data (accessed with
metadata(d_medians)$id_state_markers), which identifies the set of 'cell state' markers in the list of assays.

design
Design matrix, created with createDesignMatrix. See createDesignMatrix for details.

contrast
Contrast matrix, created with createContrast. See createContrast for details.

block_id
(Optional) Vector or factor of block IDs (e.g. patient IDs) for paired experimental designs, to be included as random effects. If provided, the block IDs will be included as random effects using the limma duplicateCorrelation methodology. Alternatively, block IDs can be included as fixed effects in the design matrix (createDesignMatrix). See details.

trend
(Optional) Whether to fit a mean-variance trend when calculating moderated tests with function eBayes from limma package. When trend = TRUE, this is known as the limma-trend method (Law et al., 2014; Phipson et al., 2016). Default = TRUE.

weights
(Optional) Whether to use cluster cell counts as precision weights (across all samples and clusters); this allows the limma model fitting functions to account for uncertainty due to the total number of cells per sample (library sizes) and total number of cells per cluster. Default = TRUE.

markers_to_test
(Optional) Logical vector specifying which markers to test for differential expression (from the set of markers stored in the assays of d_medians). Default = all 'cell state' markers, which are identified by the logical vector id_state_markers stored in the meta-data of d_medians.

min_cells
Filtering parameter. Default = 3. Clusters are kept for differential testing if they have at least min_cells cells in at least min_samples samples.

min_samples
Filtering parameter. Default = number of samples / 2, which is appropriate for two-group comparisons (of equal size). Clusters are kept for differential testing if they have at least min_cells cells in at least min_samples samples.

plot
Whether to save diagnostic plot. Default = FALSE.

path
Path for diagnostic plot, if plot = TRUE. Default = current working directory.

Details

Calculates tests for differential states within cell populations (i.e. differential expression of cell state markers within clusters). Clusters are defined using cell type markers, and cell states are characterized by the median transformed expression of cell state markers.

This method uses the limma package (Ritchie et al. 2015, Nucleic Acids Research) to fit models and calculate moderated tests at the cluster level. Moderated tests improve statistical power by sharing information on variability (i.e. variance across samples for a single cluster) between clusters. By default, we provide option trend = TRUE to the limma eBayes function; this fits a mean-variance trend when calculating moderated tests, which is also known as the limma-trend method (Law et al., 2014; Phipson et al., 2016). Diagnostic plots are shown if plot = TRUE.

The experimental design must be specified using a design matrix, which can be created with createDesignMatrix. Flexible experimental designs are possible, including blocking (e.g. paired designs), batch effects, and continuous covariates. See createDesignMatrix for more details.
For paired designs, either fixed effects or random effects can be used. Fixed effects are simpler, but random effects may improve power in data sets with unbalanced designs or very large numbers of samples. To use fixed effects, provide the block IDs (e.g. patient IDs) to `createDesignMatrix`. To use random effects, provide the block_id argument here instead. This will make use of the limma `duplicateCorrelation` methodology. Note that >2 measures per sample are not possible in this case (fixed effects should be used instead). Block IDs should not be included in the design matrix if the limma `duplicateCorrelation` methodology is used.

The contrast matrix specifying the contrast of interest can be created with `createContrast`. See `createContrast` for more details.

By default, differential tests are performed for all cell state markers (which are identified with the vector `id_state_markers` stored in the meta-data of the cluster medians input object). The optional argument `markers_to_test` allows the user to specify a different set of markers to test (e.g. to investigate differences for cell type markers).

Filtering: Clusters are kept for differential testing if they have at least `min_cells` cells in at least `min_samples` samples. This removes clusters with very low cell counts across conditions, to improve power.

Weights: By default, cluster cell counts are used as precision weights (across all samples and clusters); allowing the limma model fitting functions to account for uncertainty due to the total number of cells per sample (library sizes) and total number of cells per cluster. This option can also be disabled with `weights = FALSE`, if required.

Value

Returns a new `SummarizedExperiment` object, where rows = cluster-marker combinations, and columns = samples. In the rows, clusters are repeated for each cell state marker (i.e. the sheets or assays from the previous `d_medians` object are stacked into a single matrix). Differential test results are stored in the `rowData` slot. Results include raw p-values (`p_val`) and adjusted p-values (`p_adj`) from the limma moderated tests, which can be used to rank cluster-marker combinations by evidence for differential states within cell populations. Additional output columns from the limma tests are also included. The results can be accessed with the `rowData` accessor function.

Examples

```r
# For a complete workflow example demonstrating each step in the 'diffcyt' pipeline, # see the package vignette.

# Function to create random data (one sample)
d_random <- function(n = 20000, mean = 0, sd = 1, ncol = 20, cofactor = 5) {
  d <- sinh(matrix(rnorm(n, mean, sd), ncol = ncol)) * cofactor
  colnames(d) <- paste0("marker", sprintf("%02d", 1:ncol))
  d
}

# Create random data (without differential signal)
set.seed(123)
d_input <- list(
sample1 = d_random(),
sample2 = d_random(),
sample3 = d_random(),
)
```
sample4 = d_random()
)

# Add differential states (DS) signal
ix_DS <- 901:1000
ix_cols_type <- 1:10
ix_cols_DS <- 19:20
d_input[[1]][ix_DS, ix_cols_type] <- d_random(n = 1000, mean = 3, ncol = 10)
d_input[[2]][ix_DS, ix_cols_type] <- d_random(n = 1000, mean = 3, ncol = 10)
d_input[[3]][ix_DS, c(ix_cols_type, ix_cols_DS)] <- d_random(n = 1200, mean = 3, ncol = 12)
d_input[[4]][ix_DS, c(ix_cols_type, ix_cols_DS)] <- d_random(n = 1200, mean = 3, ncol = 12)

experiment_info <- data.frame(
  sample_id = factor(paste0("sample", 1:4)),
  group_id = factor(c("group1", "group1", "group2", "group2")),
  stringsAsFactors = FALSE
)

marker_info <- data.frame(
  channel_name = paste0("channel", sprintf("%03d", 1:20)),
  marker_name = paste0("marker", sprintf("%02d", 1:20)),
  marker_class = factor(c(rep("type", 10), rep("state", 10)),
    levels = c("type", "state", "none")),
  stringsAsFactors = FALSE
)

# Prepare data
d_se <- prepareData(d_input, experiment_info, marker_info)

# Transform data
d_se <- transformData(d_se)

# Generate clusters
d_se <- generateClusters(d_se)

# Calculate counts
d_counts <- calcCounts(d_se)

# Calculate medians
d_medians <- calcMedians(d_se)

# Create design matrix
design <- createDesignMatrix(experiment_info, cols_design = "group_id")

# Create contrast matrix
contrast <- createContrast(c(0, 1))

# Test for differential states (DS) within clusters
res_DS <- testDS_limma(d_counts, d_medians, design, contrast)
testDS_LMM

**Description**

Calculate tests for differential states within cell populations using method 'diffcyt-DS-LMM'

**Usage**

```r
testDS_LMM(
  d_counts,  # SummarizedExperiment object containing cluster cell counts, from calcCounts.
  d_medians,  # SummarizedExperiment object containing cluster medians (median marker expression for each cluster-sample combination), from calcMedians. Assumed to contain a logical vector id_state_markers in the meta-data (accessed with metadata(d_medians)$id_state_markers), which identifies the set of 'cell state' markers in the list of assays.
  formula,  # Model formula object, created with createFormula. This should be a list containing three elements: formula, data, and random_terms: the model formula, data frame of corresponding variables, and variable indicating whether the model formula contains any random effect terms. See createFormula for details.
  contrast,  # Contrast matrix, created with createContrast. See createContrast for details.
  weights = TRUE,  # (Optional) Whether to include precision weights within each model (across samples, i.e. within the model for each cluster); these represent the relative uncertainty in calculating each median value (within each model). Accepts values of TRUE, FALSE, or a numeric vector of custom weights. Default = TRUE, in which case cluster cell counts are used as weights.
  markers_to_test = NULL,  # (Optional) Logical vector specifying which markers to test for differential expression (from the set of markers stored in the assays of d_medians). Default = all 'cell state' markers, which are identified by the logical vector id_state_markers stored in the meta-data of d_medians.
  min_cells = 3,
  min_samples = NULL
)
```

**Arguments**

d_counts: SummarizedExperiment object containing cluster cell counts, from calcCounts.
d_medians: SummarizedExperiment object containing cluster medians (median marker expression for each cluster-sample combination), from calcMedians. Assumed to contain a logical vector id_state_markers in the meta-data (accessed with metadata(d_medians)$id_state_markers), which identifies the set of 'cell state' markers in the list of assays.
formula: Model formula object, created with createFormula. This should be a list containing three elements: formula, data, and random_terms: the model formula, data frame of corresponding variables, and variable indicating whether the model formula contains any random effect terms. See createFormula for details.
contrast: Contrast matrix, created with createContrast. See createContrast for details.
weights: (Optional) Whether to include precision weights within each model (across samples, i.e. within the model for each cluster); these represent the relative uncertainty in calculating each median value (within each model). Accepts values of TRUE, FALSE, or a numeric vector of custom weights. Default = TRUE, in which case cluster cell counts are used as weights.
markers_to_test: (Optional) Logical vector specifying which markers to test for differential expression (from the set of markers stored in the assays of d_medians). Default = all 'cell state' markers, which are identified by the logical vector id_state_markers stored in the meta-data of d_medians.
Details

Calculates tests for differential states within cell populations (i.e. differential expression of cell state markers within clusters), using linear mixed models (LMMs). Clusters are defined using cell type markers, and cell states are characterized by the median transformed expression of cell state markers.

This methodology was originally developed and described by Nowicka et al. (2017), *F1000Research*, and has been modified here to make use of high-resolution clustering to enable investigation of rare cell populations. Note that unlike the original method by Nowicka et al., we do not attempt to manually merge clusters into canonical cell populations. Instead, results are reported at the high-resolution cluster level, and the interpretation of significant differential clusters is left to the user via visualizations such as heatmaps (see the package vignette for an example).

This method fits linear mixed models (LMMs) for each cluster-marker combination (cell state markers only), and calculates differential tests separately for each cluster-marker combination. The response variable in each model is the median arcsinh-transformed marker expression of the cell state marker, which is assumed to follow a Gaussian distribution. There is one model per cluster per cell state marker. Within each model, sample-level weights are included (by default) for the number of cells per sample; these weights represent the relative uncertainty in calculating each median value. (Additional uncertainty exists due to variation in the total number of cells per cluster; however, it is not possible to account for this, since there are separate models for each cluster-marker combination.) We also include a filtering step to remove clusters with very small numbers of cells, to improve statistical power.

For more details on the statistical methodology, see Nowicka et al. (2017), *F1000Research* (section 'Differential analysis of marker expression stratified by cell population'.)

The experimental design must be specified using a model formula, which can be created with `createFormula`. Flexible experimental designs are possible, including blocking (e.g. paired designs), batch effects, and continuous covariates. Blocking variables can be included as either random intercept terms or fixed effect terms (see `createFormula`). For paired designs, we recommend using random intercept terms to improve statistical power; see Nowicka et al. (2017), *F1000Research* for details. Batch effects and continuous covariates should be included as fixed effects.

If no random intercept terms are included in the model formula, model fitting is performed using a linear model (LM) instead of a LMM.

The contrast matrix specifying the contrast of interest can be created with `createContrast`. See `createContrast` for more details.

By default, differential tests are performed for all cell state markers (which are identified with the vector `id_state_markers` stored in the meta-data of the cluster medians input object). The optional argument `markers_to_test` allows the user to specify a different set of markers to test (e.g. to investigate differences for cell type markers).
Filtering: Clusters are kept for differential testing if they have at least min_cells cells in at least min_samples samples. This removes clusters with very low cell counts across conditions, to improve power.

Weights: By default, cluster cell counts are used as precision weights within each model (across samples only, i.e. within the model for each cluster); these represent the relative uncertainty in calculating each median value (within each model). See above for details.

Value

Returns a new `SummarizedExperiment` object, where rows = cluster-marker combinations, and columns = samples. In the rows, clusters are repeated for each cell state marker (i.e. the sheets or assays from the previous `d_medians` object are stacked into a single matrix). Differential test results are stored in the `rowData` slot. Results include raw p-values (p_val) and adjusted p-values (p_adj), which can be used to rank cluster-marker combinations by evidence for differential states within cell populations. The results can be accessed with the `rowData` accessor function.

Examples

```r
# For a complete workflow example demonstrating each step in the 'diffcyt' pipeline, # see the package vignette.

# Function to create random data (one sample)
d_random <- function(n = 20000, mean = 0, sd = 1, ncol = 20, cofactor = 5) {
  d <- sinh(matrix(rnorm(n, mean, sd), ncol = ncol)) * cofactor
  colnames(d) <- paste0("marker", sprintf("%02d", 1:ncol))
  d
}

# Create random data (without differential signal)
set.seed(123)
d_input <- list(
  sample1 = d_random(),
  sample2 = d_random(),
  sample3 = d_random(),
  sample4 = d_random()
)

# Add differential states (DS) signal
ix_DS <- 901:1000
ix_cols_type <- 1:10
ix_cols_DS <- 19:20
d_input[[1]][ix_DS, ix_cols_type] <- d_random(n = 1000, mean = 3, ncol = 10)
d_input[[2]][ix_DS, ix_cols_type] <- d_random(n = 1000, mean = 3, ncol = 10)
d_input[[3]][ix_DS, c(ix_cols_type, ix_cols_DS)] <- d_random(n = 1200, mean = 3, ncol = 12)
d_input[[4]][ix_DS, c(ix_cols_type, ix_cols_DS)] <- d_random(n = 1200, mean = 3, ncol = 12)

experiment_info <- data.frame(
  sample_id = factor(paste0("sample", 1:4)),
  group_id = factor(c("group1", "group1", "group2", "group2")),
  stringsAsFactors = FALSE
)
```

marker_info <- data.frame(
  channel_name = paste0("channel", sprintf("%03d", 1:20)),
  marker_name = paste0("marker", sprintf("%02d", 1:20)),
  marker_class = factor(c(rep("type", 10), rep("state", 10)),
                        levels = c("type", "state", "none")),
  stringsAsFactors = FALSE
)

# Prepare data
d_se <- prepareData(d_input, experiment_info, marker_info)

# Transform data
d_se <- transformData(d_se)

# Generate clusters
d_se <- generateClusters(d_se)

# Calculate counts
d_counts <- calcCounts(d_se)

# Calculate medians
d_medians <- calcMedians(d_se)

# Create model formula
formula <- createFormula(experiment_info, cols_fixed = "group_id")

# Create contrast matrix
contrast <- createContrast(c(0, 1))

# Test for differential states (DS) within clusters
res_DS <- testDS_LMM(d_counts, d_medians, formula, contrast)

---

**topClusters**  
*Alias for 'topTable' (deprecated)*

**Description**

Alias for function 'topTable' (deprecated)

**Usage**

```r
topClusters(...)```

**Arguments**

```r
...  # See arguments for function topTable
```
**Details**

The function `topClusters` has been renamed to `topTable`, to more accurately reflect the structure of the results (results are returned for either clusters or cluster-marker combinations, depending on the type of differential tests performed).

This alias is provided for backward compatibility. The new function name `topTable` should be used whenever possible.

See `topTable` for details.

---

**topTable**  
*Show table of results for top clusters or cluster-marker combinations*

---

**Description**

Show table of results for top (most highly significant) clusters or cluster-marker combinations

**Usage**

```r
topTable(
  res,
  d_counts = NULL,
  d_medians = NULL,
  order = TRUE,
  order_by = "p_adj",
  all = FALSE,
  top_n = 20,
  show_counts = FALSE,
  show Props = FALSE,
  show_meds = FALSE,
  show_logFC = FALSE,
  show_all_cols = FALSE,
  sort_cols = TRUE,
  format_vals = FALSE,
  digits = 3
)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>res</code></td>
<td>Output object from either the <code>diffcyt</code> wrapper function or one of the individual differential testing functions (<code>testDA_edgeR</code>, <code>testDA_voom</code>, <code>testDA_GLMM</code>, <code>testDS_limma</code>, or <code>testDS_LMM</code>). If the output object is from the wrapper function, the objects <code>res</code> and <code>d_counts</code> will be automatically extracted. Alternatively, these can be provided directly.</td>
</tr>
<tr>
<td><code>d_counts</code></td>
<td>(Optional) <code>SummarizedExperiment</code> object containing cluster cell counts, from <code>calcCounts</code>. (If the output object from the wrapper function is provided, this will be be automatically extracted.)</td>
</tr>
</tbody>
</table>
### topTable

d_medians  (Optional) `SummarizedExperiment` object containing cluster medians (median marker expression for each cluster-sample combination), from `calcMedians`. Assumed to contain a logical vector `id_state_markers` in the meta-data (accessed with `metadata(d_medians)$id_state_markers`), which identifies the set of 'cell state' markers in the list of assays. (If the output object from the wrapper function is provided, this will be automatically extracted.)

order  Whether to order results by values in column `order_by` (default: column `p_adj` containing adjusted p-values). Default = TRUE.

order_by  Name of column to use to order rows by values, if `order = TRUE`. Default = "p_adj" (adjusted p-values); other options include "p_val", "cluster_id", and "marker_id".

all  Whether to display all clusters or cluster-marker combinations (instead of top `top_n`). Default = FALSE.

top_n  Number of clusters or cluster-marker combinations to display (if `all = FALSE`). Default = 20.

show_counts  Whether to display cluster cell counts by sample (from `d_counts`). Default = FALSE.

show_props  Whether to display cluster cell count proportions by sample (calculated from `d_counts`). Default = FALSE.

show_meds  Whether to display median expression values for each cluster-marker combination (from `d_medians`). Default = FALSE.

show_logFC  Whether to display log fold change (logFC) values. Default = FALSE.

show_all_cols  Whether to display all columns from output object (e.g. logFC, logCPM, LR, etc.) Default = FALSE.

sort_cols  Whether to sort columns of counts, proportions, and medians; by levels of factor `sample_id` in `colData` of `d_medians` (requires object `d_medians` to be provided). Default = TRUE.

format_vals  Whether to display rounded values in numeric columns. This improves readability of the summary table, but should not be used when exact numeric values are required for subsequent steps (e.g. plotting). Default = FALSE.

digits  Number of significant digits to show, if `format_vals = TRUE`. Default = 3. (Note: for percentages shown if `show_props = TRUE`, digits = 1 is used.)

### Details

Summary function to display table of results for top (most highly significant) detected clusters or cluster-marker combinations.

The differential testing functions return results in the form of p-values and adjusted p-values for each cluster (DA tests) or cluster-marker combination (DS tests), which can be used to rank the clusters or cluster-marker combinations by their evidence for differential abundance or differential states. The p-values and adjusted p-values are stored in the `rowData` of the output `SummarizedExperiment` object generated by the testing functions.

This function displays a summary table of results. By default, the `top_n` clusters or cluster-marker combinations are shown, ordered by adjusted p-values. Optionally, cluster counts, proportions, and
median expression by cluster-marker combination can also be included. The `format_vals` and `digits` arguments can be used to display rounded values to improve readability of the summary table.

**Value**

Returns a `DataFrame` table of results for the `top_n` clusters or cluster-marker combinations, ordered by values in column `order_by` (default: adjusted p-values). Optionally, cluster counts, proportions, and median expression by cluster-marker combination are also included.

**Examples**

For a complete workflow example demonstrating each step in the 'diffcyt' pipeline, see the package vignette.

```r
# Function to create random data (one sample)
d_random <- function(n = 20000, mean = 0, sd = 1, ncol = 20, cofactor = 5) {
  d <- sinh(matrix(rnorm(n, mean, sd), ncol = ncol)) * cofactor
  colnames(d) <- paste0("marker", sprintf("%02d", 1:ncol))
  d
}

# Create random data (without differential signal)
set.seed(123)
d_input <- list(
sample1 = d_random(),
  sample2 = d_random(),
  sample3 = d_random(),
  sample4 = d_random()
)

# Add differential abundance (DA) signal
topTable(d_input, top_n = 10, order_by = "adjusted_p", digits = 2)

# Add differential states (DS) signal

# Function to create random data (without differential signal)
sample1 = d_random()
sample2 = d_random()
sample3 = d_random()
sample4 = d_random()

# Add differential abundance (DA) signal
topTable(sample1, top_n = 10, order_by = "adjusted_p", digits = 2)

eperiment_info <- data.frame(
  sample_id = factor(paste0("sample", 1:4)),
  group_id = factor(c("group1", "group1", "group2", "group2")),
  stringsAsFactors = FALSE
)

marker_info <- data.frame(
  marker = factor(paste0("marker", 1:20)),
  expression = numeric(20)
)

# Add differential abundance (DA) signal
topTable(marker_info, top_n = 10, order_by = "adjusted_p", digits = 2)
```

channel_name = paste0("channel", sprintf("%03d", 1:20)),
marker_name = paste0("marker", sprintf("%02d", 1:20)),
marker_class = factor(c(rep("type", 10), rep("state", 10)),
levels = c("type", "state", "none"),
stringsAsFactors = FALSE)
)

# Create design matrix
design <- createDesignMatrix(experiment_info, cols_design = "group_id")

# Create contrast matrix
contrast <- createContrast(c(0, 1))

# Test for differential abundance (DA) of clusters (using default method 'diffcyt-DA-edgeR')
out_DA <- diffcyt(d_input, experiment_info, marker_info,
  design = design, contrast = contrast,
  analysis_type = "DA", method_DA = "diffcyt-DA-edgeR",
  seed_clustering = 123, verbose = FALSE)

# Test for differential states (DS) within clusters (using default method 'diffcyt-DS-limma')
out_DS <- diffcyt(d_input, experiment_info, marker_info,
  design = design, contrast = contrast,
  analysis_type = "DS", method_DS = "diffcyt-DS-limma",
  seed_clustering = 123, verbose = FALSE)

# Display results for top DA clusters
topTable(out_DA, format_vals = TRUE)

# Display results for top DS cluster-marker combinations
topTable(out_DS, format_vals = TRUE)

---

### transformData

**Transform data**

**Description**

Transform data prior to clustering

**Usage**

```r
transformData(d_se, cofactor = 5)
```

**Arguments**

- `d_se` Input data. Assumed to be in the form of a `SummarizedExperiment`, prepared with the function `prepareData`. Column meta-data is assumed to contain a factor `marker_class`, where entries "none" indicate non-marker columns.

- `cofactor` Cofactor parameter for 'arcsinh' transform. Default = 5, which is appropriate for mass cytometry (CyTOF) data. For fluorescence flow cytometry, we recommend cofactor = 150 instead.
Details

Flow and mass cytometry data should be transformed prior to clustering. The raw data follows an approximately log-normal distribution. Transforming with a log (or similar) function brings the data closer to a normal distribution, which improves clustering performance and allows positive and negative populations to be distinguished more clearly.

This function implements an inverse hyperbolic sine ('arcsinh') transform with adjustable 'cofactor' parameter. The arcsinh transform is widely used for CyTOF data. It behaves similarly to a log transform at high values, but is approximately linear near zero; so unlike the log, it can handle zeros or small negative values. The cofactor parameter controls the width of the linear region. Zero values and small negatives occur in CyTOF data when no ions are detected in a given channel (negatives are due to background subtraction and randomization of integer count values, which are performed by default by the CyTOF instrument software).

Recommended values for the cofactor parameter are 5 (mass cytometry, CyTOF) or 150 (fluorescence flow cytometry); see Bendall et al. (2011), *Science*, Supplementary Figure S2.

The transform should be applied to protein marker columns only. The *SummarizedExperiment* object created in the previous step (*prepareData*) is assumed to contain a factor *marker_class* in the column meta-data, where entries "none" indicate non-marker columns. (If this is not available, all columns will be transformed instead.)

Value

d_se: Data with transform applied to protein marker columns.

Examples

```r
# For a complete workflow example demonstrating each step in the 'diffcyt' pipeline,
# see the package vignette.

# Function to create random data (one sample)
 d_random <- function(n = 20000, mean = 0, sd = 1, ncol = 20, cofactor = 5) {
  d <- sinh(matrix(rnorm(n, mean, sd), ncol = ncol)) * cofactor
  colnames(d) <- paste0("marker", sprintf("%02d", 1:ncol))
  d
}

# Create random data (without differential signal)
set.seed(123)
d_input <- list(
  sample1 = d_random(),
  sample2 = d_random(),
  sample3 = d_random(),
  sample4 = d_random()
)

experiment_info <- data.frame(
  sample_id = factor(paste0("sample", 1:4)),
  group_id = factor(c("group1", "group1", "group2", "group2")),
  stringsAsFactors = FALSE
)
```

marker_info <- data.frame(  
  channel_name = paste0("channel", sprintf("%03d", 1:20)),
  marker_name = paste0("marker", sprintf("%02d", 1:20)),
  marker_class = factor(c(rep("type", 10), rep("state", 10)),
                       levels = c("type", "state", "none")),
  stringsAsFactors = FALSE
)

# Prepare data
d_se <- prepareData(d_input, experiment_info, marker_info)

# Transform data
d_se <- transformData(d_se)
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