Package 'pipeComp'

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Type Package

Title pipeComp pipeline benchmarking framework

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Description A simple framework to facilitate the comparison of pipelines involving various steps and parameters.
The `pipelineDefinition` class represents pipelines as, minimally, a set of functions consecutively executed on
the output of the previous one, and optionally accompanied by stepwise evaluation and aggregation functions.
Given such an object, a set of alternative parameters/methods, and benchmark datasets, the `runPipeline` function
then proceeds through all combinations arguments, avoiding recomputing the same step twice and compiling evaluations
on the fly to avoid storing potentially large intermediate data.

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pipeComp-package *pipeComp - a framework for pipeline benchmarking*

Description

pipeComp is a simple framework to facilitate the comparison of pipelines involving various steps and parameters. It was initially developed to benchmark single-cell RNA sequencing pipelines, and contains pre-defined PipelineDefinitions and functions to that effect, but could be applied to any context. See ‘vignette("pipeComp")‘ for an introduction.

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addPipelineStep *addPipelineStep*

Description

Add a step to an existing PipelineDefinition

Usage

```
addPipelineStep(object, name, after = NULL, slots = list())
```

Arguments

object	A PipelineDefinition
name	The name of the step to add
after	The name of the step after which to add the new step. If NULL, will add the step at the beginning of the pipeline.
slots	A optional named list with slots to fill for that step (i.e. ‘functions‘, ‘evaluation‘, ‘aggregation‘, ‘descriptions‘ - will be parsed)

Value

A PipelineDefinition

See Also

PipelineDefinition, PipelineDefinition-methods

Examples

```
pd <- mockPipeline()
pd
pd <- addPipelineStep(pd, name="newstep", after="step1",
                      slots=list(description="Step that does nothing..."))
pd
```

aggregatePipelineResults *aggregatePipelineResults*

Description

Aggregates the evaluation and running times of ‘runPipeline‘ results. Results should be indicated either as a ‘path“ prefix or as a vector of paths to ‘evaluation\.rds‘ files (‘resfiles‘).

Usage

```
aggregatePipelineResults(res, pipDef = NULL)
```

Arguments

res	A (named) list of results (per dataset), as produced by readPipelineResults (or ‘mergePipelineResults‘).
pipDef	An optional PipelineDefinition containing the aggregation methods. If omitted, that from the results will be used.

Value

A list with a slot for each step for which there is an aggregation method, or (if no aggregation method available) a list of the ‘stepIntermediateReturnObjects‘ of ‘runPipeline‘

Examples

```
# we produce mock pipeline results:
pip <- mockPipeline()
datasets <- list( ds1=1:3, ds2=c(5,10,15) )
tmpdir1 <- paste0(tempdir(),'/')
res <- runPipeline(datasets, pipelineDef=pip, output.prefix=tmpdir1,
                   alternatives=list() )
# we read the evaluation files:
res <- readPipelineResults(tmpdir1)
# we aggregate the results (equivalent to the output of `runPipeline`):
res <- aggregatePipelineResults(res)
```

buildCombMatrix *buildCombMatrix*

Description

Builds a matrix of parameter combinations from a list of alternative values.

Usage

```
buildCombMatrix(alt, returnIndexMatrix = FALSE)
```

Arguments

alt	A named list of alternative parameter values
returnIndexMatrix	Logical; whether to return a matrix of indices, rather than a data.frame of factors.

Value

a matrix or data.frame

Examples

```
buildCombMatrix(list(param1=LETTERS[1:3], param2=1:2))
```

---

checkPipelinePackages *checkPipelinePackages*

Description

Checks whether the packages required by a pipeline and its alternative methods are available.

Usage

```
checkPipelinePackages(alternatives, pipDef = NULL)
```

Arguments

alternatives	A named list of alternative parameter values
pipDef	An object of class 'PipelineDefinition'.

Value

Logical.

Examples

```
checkPipelinePackages(list(argument1="mean"), scrna_pipeline())
```

---

clustMetricsCorr *Correlations across clustering evaluation metrics*

Description

A list of two matrices containing, respectively, the Pearson and Spearman pairwise correlations between various clustering evalution metrics, computed across a wide range of scRNAseq clustering analyses (see reference).

Value

a list.

References

See https://doi.org/10.1101/2020.02.02.930578

colCenterScale *colCenterScale*

Description

Matrix scaling by centering columns separately and then performing variance scaling on the whole matrix, in a NA-robust fashion. With the default arguments, the output will be the number of (matrix-)median absolute deviations from the column-median.

Usage

```
colCenterScale(
  x,
  centerFn = median,
  scaleFn = function(x, na.rm) median(abs(x), na.rm = na.rm)
)
```

Arguments

x	A numeric matrix.
centerFn	The function for calculating centers. Should accept the 'na.rm' argument. E.g. 'centerFn=mean' or 'centerFn=median'.
scaleFn	The function for calculating the (matrix-wise) scaling factor. Should accept the 'na.rm' argument. Default 'median(abs(x))'.

Value

A scaled matrix of the same dimensions as 'x'.

Examples

```
# random data with column mean differences
d <- cbind(A=rnorm(5, 10, 2), B=rnorm(5, 20, 2), C=rnorm(5,30, 2))
colCenterScale(d)
```

ctrlgenes *Lists of control genes*

Description

Lists of mouse and human control genes (mitochondrial, ribosomal, protein-coding), as ensembl gene ids or official symbols, for computing cell QC.

Value

a list.

dea_evalPlot_curve *dea_evalPlot_curve*

Description

dea_evalPlot_curve

Usage

```
dea_evalPlot_curve(
  res,
  scales = "free",
  agg.by = NULL,
  agg.fn = mean,
  xlim = c(NA, NA),
  colourBy = "method",
  shapeBy = NULL,
  pointsize = 4
)
```

Arguments

res	Aggregated results of the DEA pipeline
scales	Passed to 'facet_grid'
agg.by	Aggregate results by these columns (default no aggregation)
agg.fn	Function for aggregation (default mean)
xlim	Optional vector of x limits
colourBy	Name of column by which to colour
shapeBy	Name of column determining the shape of the points. If omitted, the shape will indicate whether the nominal FDR is below or equal the real FDR.
pointsize	Size of the points

Value

A ggplot.

Examples

```
data("exampleDEAresults", package="pipeComp")
dea_evalPlot_curve(exampleDEAresults, agg.by=c("sva.method"))
```

dea_pipeline *dea_pipeline*

Description

The 'PipelineDefinition' for bulk RNAseq differential expression analysis (DEA).

Usage

```
dea_pipeline()
```

Value

A 'PipelineDefinition' object to be used with 'runPipeline'.

Examples

```
pip <- dea_pipeline()
pip
```

defaultStepAggregation *defaultStepAggregation*

Description

defaultStepAggregation

Usage

```
defaultStepAggregation(x)
```

Arguments

x	A list of results per dataset, each containing a list (1 element per combination of parameters) of evaluation metrics (coercible to vectors or matrix).

Value

A data.frame.

evalHeatmap *evalHeatmap*

Description

General heatmap representation of aggregated evaluation results. By default, the actual metric values are printed in the cells, and while the coloring is determined by `colCenterScale` (number of matrix-median absolute deviations from the column means). Unless the total number of analyses is small, it is strongly recommended to use the 'agg.by' argument to limit the size and improve the readability of the heatmap.

Usage

```
evalHeatmap(
  res,
  step = NULL,
  what,
  what2 = NULL,
  agg.by = NULL,
  agg.fn = mean,
  filterExpr = NULL,
  scale = "colCenterScale",
  value_format = "%.2f",
  reorder_rows = FALSE,
  show_heatmap_legend = FALSE,
  show_column_names = FALSE,
  col = NULL,
  font_factor = 0.9,
  row_split = NULL,
  shortNames = TRUE,
  value_cols = c("black", "white"),
  title = NULL,
  name = NULL,
  anno_legend = TRUE,
  ...
)
```

Arguments

`res`	Aggregated pipeline results (i.e. the output of 'runPipeline' or 'aggregateResults')
`step`	Name of the step for which to plot the evaluation results. If unspecified, will use the latest step that has evaluation results.
`what`	What metric to plot.
`what2`	If the step has more than one benchmark data.frame, which one to use. The function will attempt to guess that automatically based on 'what', and will notify in case of ambiguity.
`agg.by`	Aggregate results by these columns (default no aggregation)
`agg.fn`	Function for aggregation (default mean)

filterExpr	An optional filtering expression based on the columns of the target dataframe, (e.g. 'filterExpr=param1=="value1"').
scale	Controls the scaling of the columns for the color mapping. Can either be a logical (TRUE will use NA-safe column z-scores, FALSE will not scale) or a function performing the scaling. The default uses the 'colCenterScale' function (per-column centering, but per-matrix variance scaling).
value_format	Format for displaying cells' values (use 'value_format=""' to disable)
reorder_rows	Logical; whether to sort rows (default FALSE). The row names themselves can also be passed to specify an order, or a 'ComplexHeatmap'.
show_heatmap_legend	Passed to 'Heatmap' (default FALSE)
show_column_names	Passed to 'Heatmap' (default FALSE)
col	Colors for the heatmap, or a color-mapping function as produced by 'colorRamp2'. If passing a vector of colors and the data is scaled, there should be an odd number of colors. By default, will apply linear mapping (if the data is not scaled) or signed sqrt mapping (if scaled) on the 'viridisLite::inferno' palette.
font_factor	A scaling factor applied to fontsizes (default 1)
row_split	Optional column (included in 'agg.by') by which to split the rows. Alternatively, an expression using the columns (retained after aggregation) can be passed.
shortNames	Logical; whether to use short row names (with only the parameter values instead of the parameter name and value pairs), default TRUE.
value_cols	A vector of length 2 indicating the colors of the values (above and below the mean), if printed
title	Plot title
name	Heatmap name (e.g. used for the legend)
anno_legend	Logical; whether to plot the legend for the datasets
...	Passed to 'Heatmap'

Value

A Heatmap

Examples

```
data("exampleResults", package="pipeComp")
evalHeatmap( exampleResults, step="clustering", what=c("ARI","MI","min_pr"),
             agg.by=c("filt", "norm"), row_split = "norm" ) +
evalHeatmap( exampleResults, step="clustering", what="ARI",
             agg.by=c("filt", "norm"), filterExpr=n_clus==true.nbClusts,
             name="ARI at true k", title="ARI at
true K" )
```

evaluateClustering *evaluateClustering*

Description

Evaluates a clustering using 'true' labels. Entries with missing true labels (i.e. NA) are excluded from calculations. If using 'evaluteClustering' in a custom pipeline, you might want to use the corresponding 'pipeComp:::.aggregateClusterEvaluation' aggregation function.

Usage

```
evaluateClustering(x, tl = NULL)
```

Arguments

x	The clustering labels
tl	The true labels

Value

A numeric vector of metrics (see the 'pipeComp_scRNA' vignette for details)

Examples

```
# random data
dat <- data.frame(
 cluster=rep(LETTERS[1:3], each=10),
 x=c(rnorm(20, 0), rnorm(10, 1)),
 y=c(rnorm(10, 1), rnorm(20, 0))
)
# clustering
dat$predicted <- kmeans(dist(dat[,-1]),3)$cluster
# evaluation
evaluateClustering(dat$predicted, dat$cluster)
```

evaluateDEA *evaluateDEA*

Description

Evaluates a differential expression analysis (DEA).

Usage

```
evaluateDEA(dea, truth = NULL, th = c(0.01, 0.05, 0.1))
```

Arguments

dea	Expects a data.frame with logFC and FDR, as produced by 'edgeR::topTags', 'limma::topTable' or 'DESeq2::results'.
truth	A data.frame containing the columns 'expected.beta' (real logFC) and 'isDE' (logical indicating whether there is a difference or not; accepts NA values)
th	The significance thresholds for which to compute the metrics.

Value

A list with two slots: 'logFC' (vector of metrics on logFC) and 'significance' table of significance-related statistics.

Examples

```
# fake DEA results
dea <- data.frame( row.names=paste0("gene",1:10), logFC=rnorm(10) )
dea$PValue <- dea$FDR <- c(2:8/100, 0.2, 0.5, 1)
truth <- data.frame( row.names=paste0("gene",1:10), expected.beta=rnorm(10),
                     isDE=rep(c(TRUE,FALSE,TRUE,FALSE), c(3,1,2,4)) )
evaluateDEA(dea, truth)
```

---

evaluateDimRed *evaluateDimRed*

Description

Gathers evaluation statistics on a reduced space using known cell labels. If using 'evaluteDimRed' in a custom pipeline, you will probably want to use 'pipeComp:::.aggregateDR' as the corresponding aggregation function.

Usage

```
evaluateDimRed(x, clusters = NULL, n = c(10, 20, 50), covars)
```

Arguments

x	The matrix of the reduced space, with cells as rows and components as columns
clusters	The vector indicating each cell's cluster.
n	A numeric vector indiciating the number of top dimensions at which to gather statistics (default 'c(10,20,50)'). Will use all available dimensions if a higher number is given.
covars	A character vectors containing any additional covariates (column names of 'colData') to track during evalutation. If missing, will attempt to use default covariates. To disable, set 'covars=c()'.

Value

A list with the following components: * silhouettes: a matrix of the silhouette for each cell-cluster pair at each value of 'n' * clust.avg.silwidth: a matrix of the cluster average width at each value of 'n' * R2: the proportion of variance in each component (up to 'max(n)') that is explained by the clusters (i.e. R-squared of a linear model).

Examples

```
# random data
library(scater)
sce <- runPCA(logNormCounts(mockSCE(ngenes = 500)))
sce <- addPerCellQC(sce)
# random population labels
sce$cluster <- sample(LETTERS[1:3], ncol(sce), replace=TRUE)
res <- evaluateDimRed(sce, sce$cluster, covars=c("sum","detected"))
# average silhouette widths:
res$clust.avg.silwidth
# adjusted R2 of covariates:
res$covar.adjR2
```

`evaluateNorm` *evaluateNorm*

Description

evaluateNorm

Usage

```
evaluateNorm(x, clusters = NULL, covars)
```

Arguments

`x`	An object of class 'Seurat' or 'SingleCellExperiment' with normalized data
`clusters`	A vector of true cluster identities. If missing, will attempt to fetch it from the 'phenoid' colData.
`covars`	Covariates to include, either as data.frame or as colData columns of 'x'

Value

a data.frame.

Examples

```
# random data
library(scater)
sce <- logNormCounts(mockSCE(ngenes = 500))
sce <- addPerCellQC(sce)
# random population labels
sce$cluster <- sample(LETTERS[1:3], ncol(sce), replace=TRUE)
evaluateNorm(sce, sce$cluster, covars="detected")
```

exampleDEAresults *Example results from the DEA pipeline*

Description

Example benchmarking results from a DEA pipeline (see vignette 'pipeComp_dea').

Value

a list.

exampleResults *Example pipeline results*

Description

Example benchmarking results from a scRNAseq pipeline (see vignette 'pipeComp_scRNA').

Value

a list.

farthestPoint *farthestPoint*

Description

Identifies the point farthest from a line passing through by the first and last points. Used for automatization of the elbow method.

Usage

```
farthestPoint(y, x = NULL)
```

Arguments

y	Monotonically inscreasing or decreasing values
x	Optional x coordinates corresponding to 'y' (defaults to seq)

Value

The value of 'x' farthest from the diagonal.

Examples

```
y <- 2^(10:1)
plot(y)
x <- farthestPoint(y)
points(x,y[x],pch=16)
```

`getDimensionality` *getDimensionality*

Description

Returns the estimated intrinsic dimensionality of a dataset.

Usage

```
getDimensionality(dat, method, maxDims = NULL)
```

Arguments

`dat`	A Seurat or SCE object with a pca embedding.
`method`	The dimensionality method to use.
`maxDims`	Deprecated and ignored.

Value

An integer.

`getQualitativePalette` *getQualitativePalette*

Description

Returns a qualitative color palette of the given size. If less than 23 colors are required, the colors are based on Paul Tol's palettes. If more, the 'randomcoloR' package is used.

Usage

```
getQualitativePalette(nbcolors)
```

Arguments

`nbcolors`	A positive integer indicating the number of colors

Value

A vector of colors

Examples

```
getQualitativePalette(5)
```

match_evaluate_multiple *match_evaluate_multiple*

Description

Function to match cluster labels with 'true' clusters using the Hungarian algorithm, and return precision, recall, and F1 score. Written by Lukas Weber in August 2016 as part of his cytometry clustering comparison, with just slight modifications on initial handling of input arguments.

Usage

```
match_evaluate_multiple(clus_algorithm, clus_truth = NULL)
```

Arguments

clus_algorithm	cluster labels from algorithm
clus_truth	true cluster labels. If NULL, will attempt to read them from the names of 'clus_algorithm' (expecting the format 'clusterName.cellName')

Value

A list.

Examples

```
# random data
dat <- data.frame(
 cluster=rep(LETTERS[1:3], each=10),
 x=c(rnorm(20, 0), rnorm(10, 1)),
 y=c(rnorm(10, 1), rnorm(20, 0))
)
# clustering
dat$predicted <- kmeans(dist(dat[,-1]),3)$cluster
# evaluation
match_evaluate_multiple(dat$predicted, dat$cluster)
```

mergePipelineResults *mergePipelineResults*

Description

Merges the (non-aggregated) results of any number of runs of 'runPipeline' using the same PipelineDefinition (but on different datasets and/or using different parameters). First read the different sets of results using readPipelineResults, and pass them to this function.

Usage

```
mergePipelineResults(..., rr = NULL, verbose = TRUE)
```

Arguments

...	Any number of lists of pipeline results, each as produced by readPipelineResults
rr	Alternatively, the pipeline results can be passed as a list (in which case '...' is ignored)
verbose	Whether to print processing information

Value

A list of merged pipeline results.

Examples

```
# we produce 2 mock pipeline results:
pip <- mockPipeline()
datasets <- list( ds1=1:3, ds2=c(5,10,15) )
tmpdir1 <- paste0(tempdir(),'/')
res <- runPipeline(datasets, pipelineDef=pip, output.prefix=tmpdir1,
                   alternatives=list() )
alternatives <- list(meth1=c('log2','sqrt'), meth2='cumsum')
tmpdir2 <- paste0(tempdir(),'/')
res <- runPipeline(datasets, alternatives, pip, output.prefix=tmpdir2)
# we read the evaluation files:
res1 <- readPipelineResults(tmpdir1)
res2 <- readPipelineResults(tmpdir2)
# we merge them:
res <- mergePipelineResults(res1,res2)
# and we aggregate:
res <- aggregatePipelineResults(res)
```

---

mockPipeline *mockPipeline*

Description

A mock 'PipelineDefinition' for use in examples.

Usage

```
mockPipeline()
```

Value

a 'PipelineDefinition'

Examples

```
mockPipeline()
```

parsePipNames *parsePipNames*

Description

Parses the names of analyses performed through ‘runPipeline‘ to extract a data.frame of parameter values (with decent classes).

Usage

```
parsePipNames(x, setRowNames = FALSE, addcolumns = NULL)
```

Arguments

x	The names to parse, or a data.frame with the names to parse as row.names. All names are expected to contain the same parameters.
setRowNames	Logical; whether to set original names as row.names of the output data.frame (default FALSE)
addcolumns	An optional data.frame of ‘length(x)‘ rows to cbind to the output.

Value

A data.frame

Examples

```
my_names <- c("param1=A;param2=5","param1=B;param2=0")
parsePipNames(my_names)
```

PipelineDefinition *PipelineDefinition*

Description

Creates on object of class ‘PipelineDefinition‘ containing step functions, as well as optionally step evaluation and aggregation functions.

Usage

```
PipelineDefinition(
  functions,
  descriptions = NULL,
  evaluation = NULL,
  aggregation = NULL,
  initiation = identity,
  defaultArguments = list(),
  misc = list(),
  verbose = TRUE
)
```

Arguments

functions	A list of functions for each step
descriptions	A list of descriptions for each step
evaluation	A list of optional evaluation functions for each step
aggregation	A list of optional aggregation functions for each step
initiation	A function ran when initiating a dataset
defaultArguments	A lsit of optional default arguments
misc	A list of whatever.
verbose	Whether to output additional warnings (default TRUE).

Value

An object of class 'PipelineDefinition', with the slots functions, descriptions, evaluation, aggregation, defaultArguments, and misc.

See Also

PipelineDefinition-methods, addPipelineStep. For an example pipeline, see scrna_pipeline.

Examples

```
PipelineDefinition(
  list( step1=function(x, meth1){ get(meth1)(x) },
        step2=function(x, meth2){ get(meth2)(x) } )
)
```

PipelineDefinition-methods

Methods for PipelineDefinition *class*

Description

Methods for PipelineDefinition class

get names of PipelineDefinition steps

set names of PipelineDefinition steps

Usage

```
## S4 method for signature 'PipelineDefinition'
show(object)

## S4 method for signature 'PipelineDefinition'
names(x)

## S4 replacement method for signature 'PipelineDefinition'
names(x) <- value

## S4 method for signature 'PipelineDefinition'
```

```
x$name

## S4 method for signature 'PipelineDefinition'
length(x)

## S4 method for signature 'PipelineDefinition,ANY,ANY,ANY'
x[i]

## S4 method for signature 'PipelineDefinition'
as.list(x)

arguments(object)

## S4 method for signature 'PipelineDefinition'
arguments(object)

defaultArguments(object)

defaultArguments(object) <- value

## S4 method for signature 'PipelineDefinition'
defaultArguments(object)

## S4 replacement method for signature 'PipelineDefinition'
defaultArguments(object) <- value

stepFn(object, step = NULL, type)

## S4 method for signature 'PipelineDefinition'
stepFn(object, step = NULL, type)

stepFn(object, step, type) <- value

## S4 replacement method for signature 'PipelineDefinition'
stepFn(object, step, type) <- value
```

Arguments

object	An object of class PipelineDefinition
x	An object of class PipelineDefinition
value	Replacement values
name	The step name
i	The index(es) of the steps
step	The name of the step for which to set or get the function
type	The type of function to set/get, either ‘functions‘, ‘evaluation‘, ‘aggregation‘, ‘descriptions‘, or ‘initiation‘ (will parse partial matches)

Value

Depends on the method.

See Also

PipelineDefinition, addPipelineStep

Examples

```
pd <- mockPipeline()
length(pd)
names(pd)
pd$step1
pd[2:1]
```

---

plotElapsed *plotElapsed*

Description

Plot total elapsed time per run, split per step.

Usage

```
plotElapsed(
  res,
  steps = names(res$elapsed$stepwise),
  agg.by,
  agg.fn = mean,
  width = 0.9,
  split.datasets = TRUE,
  return.df = FALSE
)
```

Arguments

res	Aggregated pipeline results
steps	The step(s) to plot (default all)
agg.by	The parameters by which to aggregate (set to FALSE to disable aggregation)
agg.fn	Aggregation function
width	Width of the bar; default 0.9, use 1 to remove the gaps
split.datasets	Logical; whether to split the datasets into facets
return.df	Logical; whether to return the data.frame instead of plot

Value

A ggplot, or a data.frame if ‘return.df=TRUE‘

Examples

```
data("exampleResults", package="pipeComp")
plotElapsed(exampleResults, agg.by = "norm")
```

readPipelineResults *readPipelineResults*

Description

readPipelineResults

Usage

```
readPipelineResults(path = NULL, resfiles = NULL)
```

Arguments

path	The path (e.g. folder or prefix) to the results. Either ‘path‘ or ‘resfiles‘ should be given.
resfiles	A vector of paths to ‘*.evaluation.rds‘ files. Either ‘path‘ or ‘resfiles‘ should be given.

Value

A list of results.

Examples

```
# we produce mock pipeline results:
pip <- mockPipeline()
datasets <- list( ds1=1:3, ds2=c(5,10,15) )
tmpdir1 <- paste0(tempdir(),'/')
res <- runPipeline(datasets, pipelineDef=pip, output.prefix=tmpdir1,
                   alternatives=list() )
# we read the evaluation files:
res <- readPipelineResults(tmpdir1)
```

runPipeline *runPipeline*

Description

This function runs a pipeline with combinations of parameter variations on nested steps. The pipeline has to be defined as a list of functions applied consecutively on their respective outputs. See ’examples’ for more details.

Usage

```
runPipeline(
  datasets,
  alternatives,
  pipelineDef,
  comb = NULL,
  output.prefix = "",
```

```
  nthreads = 1,
  saveEndResults = TRUE,
  debug = FALSE,
  skipErrors = TRUE,
  ...
)
```

Arguments

datasets	A named vector of initial objects or paths to rds files.
alternatives	The (named) list of alternative values for each parameter.
pipelineDef	An object of class PipelineDefinition.
comb	An optional matrix of indexes indicating the combination to run. Each column should correspond to an element of 'alternatives', and contain indexes relative to this element. If omitted, all combinations will be performed.
output.prefix	An optional prefix for the output files.
nthreads	Number of threads, default 1. If the memory requirements are very high or the first steps very long to compute, consider setting this as the number of datasets or below.
saveEndResults	Logical; whether to save the output of the last step.
debug	Logical (default FALSE). When enabled, disables multithreading and prints extra information.
skipErrors	Logical. When enabled, 'runPipeline' will continue even when an error has been encountered, and report the list of steps/datasets in which errors were encountered.
...	passed to MulticoreParam. Can for instance be used to set 'makeCluster' arguments, or set 'threshold="TRACE"' when debugging in a multithreaded context.

Value

A SimpleList with elapsed time and the results of the evaluation functions defined by the given 'pipelineDef'.

The results are also stored in the output folder with:

- The clustering results for each dataset ('endOutputs.rds' files),
- A SimpletList of elapsed time and evaluations for each dataset ('evaluation.rds' files),
- A list of the 'pipelineDef', 'alternatives', 'sessionInfo()' and function call used to produce the results ('runPipelineInfo.rds' file),
- A copy of the SimpleList returned by the function ('aggregated.rds'file).

Examples

```
pip <- mockPipeline()
datasets <- list( ds1=1:3, ds2=c(5,10,15) )
tmpdir1 <- paste0(tempdir(),"/")
res <- runPipeline(datasets, pipelineDef=pip, output.prefix=tmpdir1,
                   alternatives=list() )
# See the `pipeComp_scRNA` vignette for a more complex example
```

scrna_describeDatasets *scrna_describeDatasets*

Description

Plots descriptive information about the datasets

Usage

```
scrna_describeDatasets(sces, pt.size = 0.3, ...)
```

Arguments

sces	A character vector of paths to SCE rds files, or a list of SCEs
pt.size	Point size (for reduced dims)
...	Passed to geom_point()

Value

A plot_grid output

scrna_evalPlot_filtering *scrna_evalPlot_filtering*

Description

scrna_evalPlot_filtering

Usage

```
scrna_evalPlot_filtering(
  res,
  steps = c("doublet", "filtering"),
  clustMetric = "mean_F1",
  filterExpr = TRUE,
  atNearestK = FALSE,
  returnTable = FALSE,
  point.size = 2.2,
  ...
)
```

Arguments

res	Aggregated pipeline results (i.e. the output of 'runPipeline' or 'aggregateResults')
steps	Steps to include (default 'doublet' and 'filtering'); other steps will be averaged.
clustMetric	Clustering accuracy metric to use (default 'mean_F1")
filterExpr	An optional filtering expression based on the columns of the clustering evaluation (e.g. 'filterExpr=param1=="value1"' or 'filterExpr=n_clus==true.nbClusts').
atNearestK	Logical; whether to restrict analyses to those giving the smallest deviation from the real number of clusters (default FALSE).
returnTable	Logical; whether to return the data rather than plot.
point.size	Size of the points
...	passed to 'geom_point'

Value

A ggplot, or a data.frame if 'returnTable=TRUE'

Examples

```
data("exampleResults", package="pipeComp")
scrna_evalPlot_filtering(exampleResults)
```

---

scrna_evalPlot_overall

scrna_evalPlot_overall

Description

Plots a multi-level summary heatmap of many analyses of the 'scrna_pipeline'.

Usage

```
scrna_evalPlot_overall(
  res,
  agg.by = NULL,
  width = NULL,
  datasets_as_columnNames = TRUE,
  rowAnnoColors = NULL,
  column_names_gp = gpar(fontsize = 10),
  column_title_gp = gpar(fontsize = 12),
  heatmap_legend_param = list(by_row = TRUE, direction = "horizontal", nrow = 1),
  ...
)
```

Arguments

res	Aggregated pipeline results (i.e. the output of 'runPipeline' or 'aggregateResults')
agg.by	The paramters by which to aggregate.
width	The width of individual heatmap bodies.
datasets_as_columnNames	Logical; whether dataset names should be printed below the columns (except for silhouette) rather than using a legend.
rowAnnoColors	Optional list of colors for the row annotation variables (passed to 'HeatmapAnnotation(col=...)')
column_names_gp	Passed to each calls to 'Heatmap'
column_title_gp	Passed to each calls to 'Heatmap'
heatmap_legend_param	Passed to each calls to 'Heatmap'
...	Passed to each calls to 'Heatmap'

Value

A HeatmapList

Examples

```
library(ComplexHeatmap)
data("exampleResults")
h <- scrna_evalPlot_overall(exampleResults)
draw(h, heatmap_legend_side="bottom")
```

---

scrna_evalPlot_silh *scrna_evalPlot_silh*

Description

Plot a min/max/mean/median silhouette width heatmap from aggregated evaluation results of the 'scrna_pipeline'.

Usage

```
scrna_evalPlot_silh(
  res,
  what = c("minSilWidth", "meanSilWidth"),
  step = "dimreduction",
  dims = 1,
  agg.by = NULL,
  agg.fn = mean,
  filterExpr = NULL,
  value_format = "",
  reorder_rows = FALSE,
```

```
  reorder_columns = TRUE,
  show_heatmap_legend = TRUE,
  show_column_names = FALSE,
  col = rev(RColorBrewer::brewer.pal(n = 11, "RdBu")),
  font_factor = 0.9,
  row_split = NULL,
  shortNames = TRUE,
  value_cols = c("white", "black"),
  title = NULL,
  anno_legend = TRUE,
  ...
)
```

Arguments

res	Aggregated pipeline results (i.e. the output of 'runPipeline' or 'aggregateResults')
what	What metric to plot, possible values are "minSilWidth", "meanSilWidth" (default), "medianSilWidth", or "maxSilWidth".
step	Name of the step for which to plot the evaluation results. Defaults to "dimreduction".
dims	If multiple sets of dimensions are available, which one to use (defaults to the first).
agg.by	Aggregate results by these columns (default no aggregation)
agg.fn	Function for aggregation (default mean)
filterExpr	An optional filtering expression based on the columns of the target dataframe, (e.g. 'filterExpr=param1=="value1"').
value_format	Format for displaying cells' values (no label by default)
reorder_rows	Whether to sort rows (default FALSE). The row names themselves can also be passed to specify an order, or a 'ComplexHeatmap'.
reorder_columns	Whether to sort columns (default TRUE).
show_heatmap_legend	Passed to 'Heatmap' (default FALSE)
show_column_names	Passed to 'Heatmap' (default FALSE)
col	Colors for the heatmap
font_factor	A scaling factor applied to fontsizes (default 1)
row_split	Optional column (included in 'agg.by') by which to split the rows. Alternatively, an expression using the columns (retained after aggregation) can be passed.
shortNames	Logical; whether to use short row names (with only the parameter values instead of the parameter name and value pairs), default TRUE.
value_cols	A vector of length 2 indicating the colors of the values (above and below the mean), if printed
title	Plot title
anno_legend	Logical; whether to plot the legend for the datasets
...	Passed to 'Heatmap'

Value

A Heatmap

Examples

```
data("exampleResults", package="pipeComp")
scrna_evalPlot_silh( exampleResults, agg.by=c("filt","norm"),
                     row_split="norm" )
```

`scrna_pipeline` *scrna_pipeline*

Description

The 'PipelineDefinition' for the default scRNAseq clustering pipeline, with steps for doublet identification, filtering, normalization, feature selection, dimensionality reduction, and clustering. Alternative arguments should be character, numeric or logical vectors of length 1 (e.g. the function name for a method, the number of dimensions, etc). The default pipeline has the following steps and arguments:

- doublet: 'doubletmethod' (name of the doublet removal function)
- filtering: 'filt' (name of the filtering function, or filter string)
- normalization: 'norm' (name of the normalization function)
- selection: 'sel' (name of the selection function, or variable of rowData on which to select) and 'selnb' (number of features to select)
- dimreduction: 'dr' (name of the dimensionality reduction function) and 'maxdim' (maximum number of components to compute)
- clustering: 'clustmethod' (name of the clustering function), 'dims' (number of dimensions to use), 'k' (number of nearest neighbors to use, if applicable), 'steps' (number of steps in the random walk, if applicable), 'resolution' (resolution, if applicable), 'min.size' (minimum cluster size, if applicable). If using the 'scrna_alternatives.R' wrappers, the dimensionality can be automatically estimated by specifying 'dims = "method_name"'.

Usage

```
scrna_pipeline(saveDimRed = FALSE, pipeClass = c("seurat", "sce"))
```

Arguments

`saveDimRed`	Logical; whether to save the dimensionality reduction for each analysis (default FALSE)
`pipeClass`	'sce' or 'seurat'; which object class to use throughout the pipeline. Note that the 'alternatives' functions have to be built around the chosen class. Given that, if running the 'scrna_alternatives', the class of whole pipeline is determined by the output of the filtering, only this step is affected by this option.

Value

A 'PipelineDefinition' object to be used with 'runPipeline'.

Examples

```
pip <- scrna_pipeline()
pip
```

`stableG` *Lists of stable genes*

Description

Genes were simply obtained by querying the respective GO terms

Value

a list.

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