

# Package: pipeComp (via r-universe)

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**Type** Package

**Title** pipeComp pipeline benchmarking framework

**Version** 1.22.1

**Depends** R (>= 4.1)

**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 step-wise 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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## See Also

Useful links:

- [doi:10.1186/s13059020021367](https://doi.org/10.1186/s13059020021367)
- Report bugs at <https://github.com/plger/pipeComp>

addPipelineStep      *addPipelineStep*

## Description

Add a step to an existing [PipelineDefinition](#)

## Usage

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

## Arguments

object	A <a href="#">PipelineDefinition</a>
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 <a href="#">readPipelineResults</a> (or ‘mergePipelineResults’).
pipDef	An optional <a href="#">PipelineDefinition</a> 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	<i>Correlations across clustering evaluation metrics</i>
------------------	--

---

**Description**

A list of two matrices containing, respectively, the Pearson and Spearman pairwise correlations between various clustering evaluation 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	<i>colCenterScale</i>
----------------	-----------------------

---

**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	<i>Lists of control genes</i>
-----------	-------------------------------

---

**Description**

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

**Value**

a list.

---

dea_evalPlot_curve	<i>dea_evalPlot_curve</i>
--------------------	---------------------------

---

**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	<i>dea_pipeline</i>
--------------	---------------------

---

**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

<code>res</code>	Aggregated pipeline results (i.e. the output of <code>'runPipeline'</code> or <code>'aggregateResults'</code> )
<code>step</code>	Name of the step for which to plot the evaluation results. If unspecified, will use the latest step that has evaluation results.
<code>what</code>	What metric to plot.
<code>what2</code>	If the step has more than one benchmark data.frame, which one to use. The function will attempt to guess that automatically based on <code>'what'</code> , and will notify in case of ambiguity.
<code>agg.by</code>	Aggregate results by these columns (default no aggregation)
<code>agg.fn</code>	Function for aggregation (default mean)
<code>filterExpr</code>	An optional filtering expression based on the columns of the target dataframe, (e.g. <code>'filterExpr=param1=="value1"'</code> ).
<code>scale</code>	Controls the scaling of the columns for the color mapping. Can either be a logical ( <code>TRUE</code> will use NA-safe column z-scores, <code>FALSE</code> will not scale) or a function performing the scaling. The default uses the <code>'colCenterScale'</code> function (per-column centering, but per-matrix variance scaling).
<code>value_format</code>	Format for displaying cells' values (use <code>'value_format=""</code> to disable)
<code>reorder_rows</code>	Logical; whether to sort rows (default <code>FALSE</code> ). The row names themselves can also be passed to specify an order, or a <code>'ComplexHeatmap'</code> .
<code>show_heatmap_legend</code>	Passed to <code>'Heatmap'</code> (default <code>FALSE</code> )
<code>show_column_names</code>	Passed to <code>'Heatmap'</code> (default <code>FALSE</code> )
<code>col</code>	Colors for the heatmap, or a color-mapping function as produced by <code>'colorRamp2'</code> . 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 <code>'viridisLite::inferno'</code> palette.
<code>font_factor</code>	A scaling factor applied to font sizes (default 1)
<code>row_split</code>	Optional column (included in <code>'agg.by'</code> ) 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 'evaluateClustering' 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	<i>evaluateDimRed</i>
----------------	-----------------------

---

### Description

Gathers evaluation statistics on a reduced space using known cell labels. If using ‘evaluateDimRed’ 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 indicating 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 ‘col-Data’) to track during evaluation. 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	<i>evaluateNorm</i>
--------------	---------------------

---

**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	<i>Example results from the DEA pipeline</i>
-------------------	--

---

**Description**

Example benchmarking results from a DEA pipeline (see vignette 'pipeComp\_dea').

**Value**

a list.

---

exampleResults	<i>Example pipeline results</i>
----------------	---------------------------------

---

**Description**

Example benchmarking results from a scRNAseq pipeline (see vignette ‘pipeComp\_scRNA’).

**Value**

a list.

---

farthestPoint	<i>farthestPoint</i>
---------------	----------------------

---

**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 increasing 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**

<code>dat</code>	A Seurat or SCE object with a pca embedding.
<code>method</code>	The dimensionality method to use.
<code>maxDims</code>	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(nbc colors)
```

**Arguments**

<code>nbc colors</code>	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 an 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 list 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 <a href="#">PipelineDefinition</a>
x	An object of class <a href="#">PipelineDefinition</a>
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 <code>PipelineDefinition</code> .
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 <code>MulticoreParam</code> . 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 `SimpleList` 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**

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

**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**

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

**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**

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

---

**Description**

Genes were simply obtained by querying the respective GO terms

**Value**

a list.

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