Package 'scCNAutils'

November 4, 2018

Title Functions to analyze copy number aberrations in single-cell data

Version 0.0.0.9000

Description Functions to analyze copy number aberrations in single-cell data. A bunch of scripts and workflows to read and analyze scRNA-seq data and look at CNA-oriented signal.

Depends R (¿= 3.4.4)

License MIT License + file LICENSE

Encoding UTF-8

LazyData true

Imports Matrix,
dplyr,
magrittr,
tidyr,
rlang,
parallel,
ggplot2,
data.table

Suggests testthat

RoxygenNote 6.1.0

R topics documented:

bin_genes *Merge consecutive genes into expressed bins*

Description

Merge consecutive genes into expressed bins

Usage

```
bin_genes(ge_df, mean_exp = 3, nb_cores = 1)
```

Arguments

ge_df	the input gene expression with coordinate columns (chr, start, end) and then one column per cell.
mean_exp	the desired minimum mean expression in the bin.
nb_cores	the number of processors to use.

Value

a data.frame with bin expression.

Author(s)

Jean Monlong

convert_to_coord *Convert gene symbols to coordinates*

Description

If genes_coord is a filename, the file is expected to be a tab-delimited file with four columns: 'chr', 'start', 'end', 'symbol'. The order of the columns is not important.

Usage

```
convert_to_coord(ge_df, genes_coord, chrs = c(1:22, "X", "Y"),
  rm_dup = TRUE)
```

Arguments

ge_df	the data.frame with gene expression and one column 'symbol' with gene names.
genes_coord	either a file name or a data.frame with coordinates and gene names.
chrs	the chromosome names to keep. NULL to include all the chromosomes.
rm_dup	remove duplicated coordinates? Default is TRUE.

Details

The gene names in column 'symbol' should match the gene names in the input ge_df.

Value

a data.frame with columns 'chr', 'start', 'end' columns with genes coordinates (and still one column per barcode).

Author(s)

Jean Monlong

`norm_ge` *Normalize gene expression*

Description

Normalize gene expression

Usage

```
norm_ge(ge_df, method = c("tmm", "total"), nb_cores = 1)
```

Arguments

`ge_df`	the input gene expression
`method`	the normalization method
`nb_cores`	the number of processors to use.

Value

a data.frame with the normalized expression.

Author(s)

Jean Monlong

`plot_qc_cells` *QC graphs*

Description

QC graphs

Usage

```
plot_qc_cells(qc_df)
```

Arguments

`qc_df`	the output data.frame from qc_cells

Value

a list of ggplots

Author(s)

Jean Monlong

`qc_cells` *Compute quality control metrics for each cell*

Description

If cell_cycle is provided it should be a data.frame (or a tsv file) with two columns: 'symbol' with gene names, and 'phase' with the cell cycle phase (e.g. either 'G1.S' or 'G2.M').

Usage

```
qc_cells(ge_df, cell_cycle = NULL)
```

Arguments

`ge_df`	the input gene expression with a 'symbol' column and then one column per cell.
`cell_cycle`	if non-null, either a file or data.frame to compute cell cycle scores. See details.

Value

a data.frame with qc metrics per cell.

Author(s)

Jean Monlong

`qc_filter` *Filter cells based from QC results*

Description

Filter cells based from QC results

Usage

```
qc_filter(ge_df, qc_df, max_mito_prop = 0.2, min_total_exp = 0)
```

Arguments

`ge_df`	the input gene expression with a 'symbol' column and then one column per cell.
`qc_df`	the output data.frame from qc_cells
`max_mito_prop`	the maximum proportion of mitochondrial RNA.
`min_total_exp`	the minimum total cell expression

Value

ge_df with only the cells that passed the filters

Author(s)

Jean Monlong

`read_mtx` *Read a trio of genes, barcodes and mtx files.*

Description

Read a trio of genes, barcodes and mtx files.

Usage

```
read_mtx(mtx_file = "matrix.mtx", genes_file = "genes.tsv",
  barcodes_file = "barcodes.tsv", path = ".", rm_dup = TRUE,
  genes_col = 2)
```

Arguments

mtx_file	the path to the mtx file
genes_file	the path to the genes file.
barcodes_file	the path to the barcodes file
path	the path to the folder containing the files
rm_dup	remove duplicated gene names? Default is TRUE.
genes_col	the column to use in genes_file. Default is 2.

Value

a data.frame with a 'symbol' column with gene names and one column per barcode.

Author(s)

Jean Monlong

---

run_pca *Run PCA*

Description

Cells in core_cells are used to build the principal components to which all cells are then projected to. Usually used to reduce the effect of cell cycle in the PCA, by using only cells that don't cycle (see qc_cells) as core_cells.

Usage

```
run_pca(z_df, core_cells = NULL, out_pcs = 100)
```

Arguments

z_df	a data.frame with z-scores for each cell
core_cells	if non-NULL, a vector with the names of the cells to use as core cells. See details. Default is NULL.
out_pcs	the number of top PCs to report. Default is 100.

Details

The graph (sdev.graph) shows the standard deviation for the top 50 PCs. To show more/less PCs, add "xlim(1,N)" to the sdev.graph. See examples.

Value

a list with

x	the PC matrix
sdev	the standard deviations of the PCs
sdev.graph	a ggplot graph of the sdev

Author(s)

Jean Monlong

Examples

```
## Not run:
pca.o = run_pca(z)

## Zoom in to the top 20 PCs
pca.o$sdev.graph + xlim(1,20)

## End(Not run)
```

---

smooth_movingw *Moving-window smoothin*

Description

Moving-window smoothin

Usage

```
smooth_movingw(df, wsize = 3, nb_cores = 1, FUN = stats::median)
```

Arguments

df	the input data.frame with coordinate columns (chr, start, end) and then one column per cell
wsize	the window size. Default is 3.
nb_cores	the number of processors to use.
FUN	the function to apply to each window. Default is median.

Value

a data.frame with smoothed signal.

Author(s)

Jean Monlong

zscore *Compute Z-score*

Description

Compute Z-score

Usage

```
zscore(ge_df, wins.th = 3, method = c("norm", "z"), normals = NULL)
```

Arguments

ge_df	the inpue expression data.frame
wins.th	the threshold to winsorize Z-score. Default is 3
method	the normalization method. Either norm or z.
normals	the cells to use as normals. If NULL (default) all cells are used as normals

Value

a data.frame with Z-scores.

Author(s)

Jean Monlong

Index