# Package 'scCNAutils'

November 3, 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

**Suggests** testthat

**RoxygenNote** 6.1.0

## R topics documented:



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`convert_to_coord` *Convert gene symbols to coordinates*

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### 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

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

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### 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

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

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### 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

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