

Package ‘QCR’

May 3, 2022

Title What the Package Does (One Line, Title Case)

Version 0.1

Description QCR is a workflow for adding several Quality Control (QC) flags to scRNA-seq cells or nuclei which can be used for downstream processing.

License use_mit_license()

Depends data.table,
Rdpack,
Seurat,
tidyr,
scales,
dplyr,
tibble,
feather

Suggests knitr,
rmarkdown,
testthat

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

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QCR	<i>QCR</i>
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Description

This function computes various QC flags for a seurat object

Usage

```
QCR(
  rnaseq.data,
  class.col,
  class.cutoff,
  neuron.class.id,
  neuron.cutoff,
  non.neuron.class.id,
  non.neuron.cutoff,
  class.col.score,
  subclass.col.score,
  label.confidence.threshold = 0.7,
  resolution.value = 10
)
```

Arguments

rnaseq.data	Seurat object
class.col	Column of seurat object that contains class annotations
class.cutoff	Clusters with less than class.cutoff homogeneity are flagged
neuron.class.id	Name of neuronal cells within the class annotations
neuron.cutoff	Proportion of top/bottom clusters to flag for neuron clusters
non.neuron.class.id	Name of non-neuronal cells within the class annotations
non.neuron.cutoff	Proportion of top/bottom clusters to flag for non-neuron clusters
class.col.score	Confidence value per cell for class annotation
subclass.col.score	Confidence value per cell for subclass annotation
label.confidence.threshold	Threshold to determine low confidence and acceptable annotations
resolution.value	Seurat clustering resolution parameter if seurat_clusters is not defined in rnaseq.data

Value

data.frame with QCR flags

QC_cluster_class	<i>Checks each cluster for homogeneity of class level annotations. (Prev: QC2)</i>
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Description

Checks each cluster for homogeneity of class level annotations. (Prev: QC2)

Usage

```
QC_cluster_class(rnaseq.data, class.col, class.cutoff = 0.75)
```

Arguments

```
rnaseq.data    Seurat object
class.col      Column of seurat object that contains class annotations
class.cutoff   Clusters with less than class.cutoff homogeneity are flagged
```

Value

```
cluster.class.flag
```

QC_gene_umi	<i>Checks for min/max genes and umi in each cell (Prev: QC4)</i>
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Description

Flags the top and bottom clusters for both neuron and non-neurons to be removed based on median umi and expressed genes. Careful with this flag as cells within gene/umi tolerances could be flagged.

Usage

```
QC_gene_umi(
  rnaseq.data,
  class.col,
  non.neuron.class.id = "Non-neuron",
  non.neuron.cutoff = 0.05,
  neuron.class.id = "Neuron",
  neuron.cutoff = 0.05
)
```

Arguments

```
rnaseq.data    Seurat object
class.col      Column of seurat object that contains class annotations
non.neuron.class.id  Name of non-neuronal cells within the class annotations
non.neuron.cutoff  Proportion of top/bottom clusters to flag for non-neuron clusters
neuron.class.id  Name of neuronal cells within the class annotations
neuron.cutoff    Proportion of top/bottom clusters to flag for neuron clusters
```

Value

```
gene.umi.flag
```

QC_label_conf	<i>Check for confidence in cell annotation</i>
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Description

Check for confidence in cell annotation

Usage

```
QC_label_conf(rnaseq.data, label.confidence, label.confidence.threshold)
```

Arguments

rnaseq.data	Seurat object
label.confidence	Confidence value per cell
label.confidence.threshold	Threshold to determine low confidence and acceptable annotations

Value

label.conf.flag

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