

Package: pbmc3k (via r-universe)

September 16, 2024

Title Raw and Processed Matrices of the PBMC 3k Dataset

Version 0.1.0

Description What the package does (one paragraph).

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Encoding UTF-8

Roxygen `list(rd_family_title = list(seurat = ``Seurat-processed
matrices:" , sce = ``Bioconductor-processed matrices:" , raw =
``Raw, filtered matrices:" , norm = ``Log-normalized matrices:")
)`

RoxygenNote 7.3.1

Depends Matrix

Suggests rprojroot, stats

Enhances scuttle, Seurat, SeuratObject, SingleCellExperiment

URL <https://mojaveazure.github.io/pbmc3k/>

Repository <https://mojaveazure.r-universe.dev>

RemoteUrl <https://github.com/mojaveazure/pbmc3k>

RemoteRef HEAD

RemoteSha d3edca829774ce4dcd4735114c1414b74cd8f852

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pbmc3k

PBMC 3k

Description

2,700 peripheral blood mononuclear cells (PBMC) from 10X genomics; this is effectively what one would get with `Seurat::Read10X()`

Usage

pbmc3k

Format

A `dgMatrix` with the raw, unfiltered PBMC 3k counts

Source

<https://support.10xgenomics.com/single-cell-gene-expression/datasets/1.1.0/pbmc3k>

pbmc3k.sce.logcounts

Log-Normalized PBMC 3k: SingleCellExperiment Edition

Description

Log-Normalized PBMC 3k: **SingleCellExperiment** Edition

Usage

pbmc3k.sce.logcounts

Format

A `dgMatrix` with the log-normalized PBMC 3k counts

Note

There is not a raw, filtered matrix following a Bioconductor workflow as **scuttle** does not filter the raw counts matrix in the same way that `SeuratObject::CreateSeuratObject()` does

Source

<https://support.10xgenomics.com/single-cell-gene-expression/datasets/1.1.0/pbmc3k>

References

Orchestrating Single-Cell Analysis with Bioconductor version 1.8.0

See Also

[scuttle::perCellQCMetrics\(\)](#), [scuttle::quickPerCellQC\(\)](#), [scuttle::perCellQCFilters\(\)](#),
[scuttle::isOutlier\(\)](#)

Log-normalized matrices: [pbmc3k.seurat.norm](#)

pbmc3k.seurat.counts *Raw PBMC 3k Counts:* [Rhrefhttps://CRAN.R-project.org/package=Seurat](https://CRAN.R-project.org/package=Seurat) **Seurat Edition**

Description

Raw PBMC 3k Counts: **Seurat** Edition

Usage

```
pbmc3k.seurat.counts
```

Format

A [dgMatrix](#) with the raw, filtered PBMC 3k counts

Source

<https://support.10xgenomics.com/single-cell-gene-expression/datasets/1.1.0/pbmc3k>

References

[Seurat PBMC 3k Guided Clustering Tutorial](#)

See Also

[SeuratObject::CreateSeuratObject\(\)](#), [SeuratObject::CreateAssayObject\(\)](#)

Seurat-processed matrices: [pbmc3k.seurat.norm](#)

pbmc3k.seurat.norm	<i>Log-Normalized</i>	<i>PBMC</i>	<i>3k:</i>	R hrefhttps://CRAN.R-
				project.org/package=Seurat Seurat Edition

Description

Log-Normalized PBMC 3k: **Seurat** Edition

Usage

```
pbmc3k.seurat.norm
```

Format

A [dgCMatrx](#) with the log-normalized PBMC 3k counts

Source

<https://support.10xgenomics.com/single-cell-gene-expression/datasets/1.1.0/pbmc3k>

References

[Seurat PBMC 3k Guided Clustering Tutorial](#)

See Also

[Seurat::NormalizeData\(\)](#)

Seurat-processed matrices: [pbmc3k.seurat.counts](#)

Log-normalized matrices: [pbmc3k.sce.logcounts](#)

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