

# Seurat R package

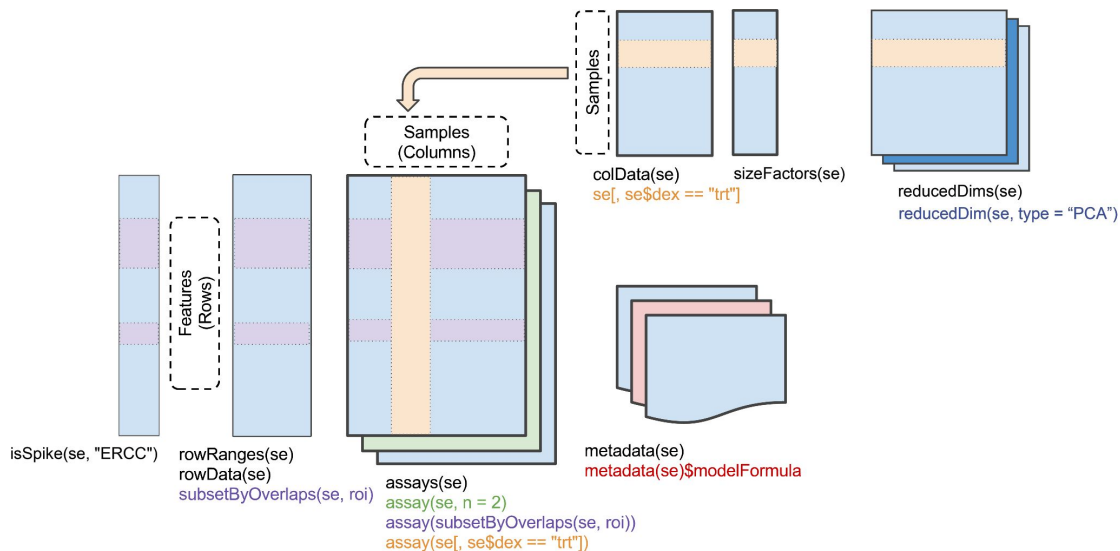
*Seurat is an R package designed for QC, analysis, and exploration of single-cell RNA-seq data.*

*Seurat aims to enable users to identify and interpret sources of heterogeneity from single-cell transcriptomic measurements, and to integrate diverse types of single-cell data.*

	Cell1	Cell2	...	CellN
Gene1	3	2	.	13
Gene2	2	3	.	1
Gene3	1	14	.	18
...	.	.	.	.
...	.	.	.	.
...	.	.	.	.
GeneM	25	0	.	0

# Seurat Object

	Cell1	Cell2	...	CellN
Gene1	3	2	.	13
Gene2	2	3	.	1
Gene3	1	14	.	18
...	.	.	.	.
...	.	.	.	.
...	.	.	.	.
GeneM	25	0	.	0



# Seurat Object

An object of class Seurat

33234 features across 59572 samples within 1 assay

Active assay: RNA (33234 features, 0 variable features)

1 layer present: data

1 dimensional reduction calculated: tsne

Name	Type	Value
se	S4 [33234 x 59572] (SeuratObject::Seurat)	S4 object of class Seurat
assays	list [1]	List of length 1
meta.data	list [59572 x 46] (S3: data.frame)	A data.frame with 59572 rows and 46 columns
active.assay	character [1]	'RNA'
active.ident	factor	Factor with 1 level: "local"
graphs	list [0]	List of length 0
neighbors	list [0]	List of length 0
reductions	list [1]	List of length 1
images	list [0]	List of length 0
project.name	character [1]	'local'
misc	list [6]	List of length 6
version	list [1] (S3: package_version, numeric_version)	List of length 1
commands	list [0]	List of length 0
tools	list [0]	List of length 0

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**Thank You!**