Sample creation vignette for using the PBMC dataset

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Introduction

This document provides an analysis of the **PBMC dataset** using `Seurat` package in R. We'll go through loading the dataset, initializing the `Seurat` object, performing quality control (QC) and visualization.

```
library(dplyr)
library(Seurat)
library(patchwork)
```

Load the PBMC Dataset

```
pbmc.data <- Read10X(data.dir = "C:\\Users\\richa\\Downloads\\filtered_gene_bc_matrices\\hg19")
knitr::kable(head(pbmc.data))
```

	AAACATACAACCAC-1	AAACATTGAGCTAC-1	AAACATTGATCAGC-1	AAACCGTGCTTCCG-1	AAACCGTGTATGCG-1	AAACGCACTGGTAC-1	AAACGC
MIR1302-10	0	0	0	0	0	0	
FAM138A	0	0	0	0	0	0	
OR4F5	0	0	0	0	0	0	
RP11-34P13.7	0	0	0	0	0	0	
RP11-34P13.8	0	0	0	0	0	0	
AL627309.1	0	0	0	0	0	0	

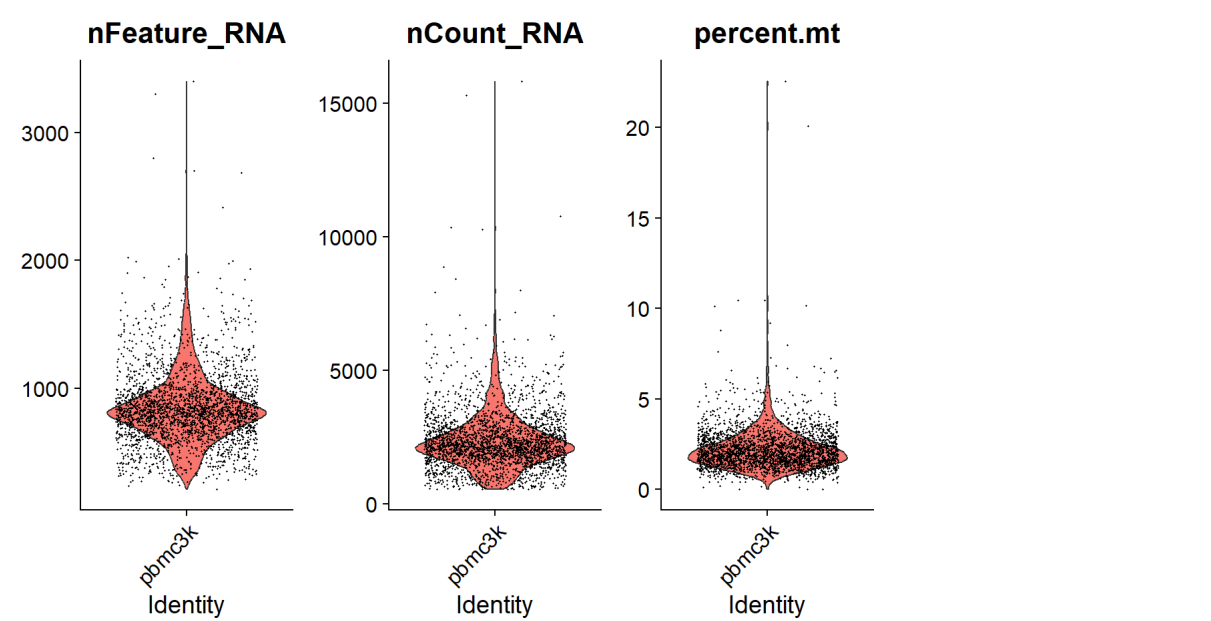## Initialize the Seurat Object with the raw data (non-normalized data)

```
pbmc <- CreateSeuratObject(counts = pbmc.data, project = "pbmc3k", min.cells = 3, min.features = 200)
```

Add QC Metrics to Metadata

```
pbmc[["percent.mt"]] <- PercentageFeatureSet(pbmc, pattern = "^MT-")
```
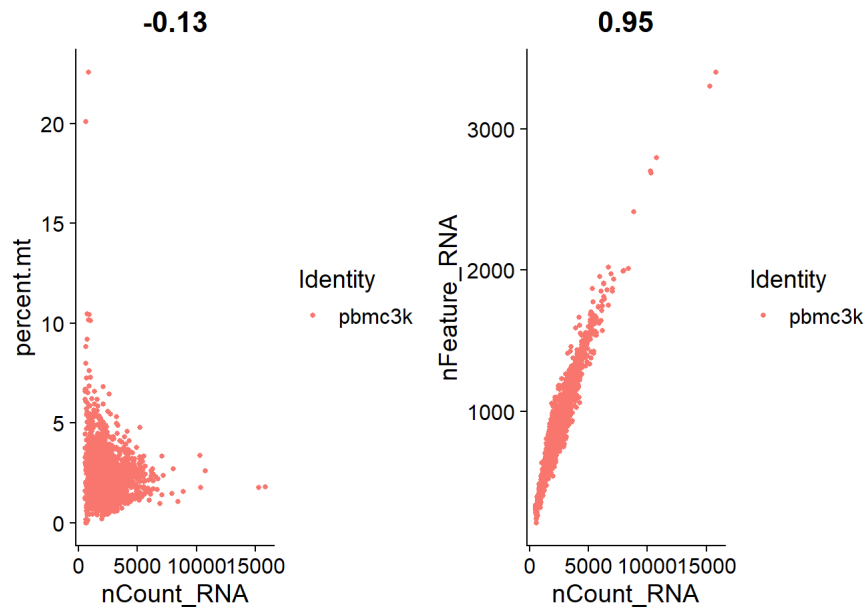
Visualize QC Metrics

```
VlnPlot(pbmc, features = c("nFeature_RNA", "nCount_RNA", "percent.mt"), ncol = 3)
```

Feature-Feature Relationships

```
plot1 <- FeatureScatter(pbmc, feature1 = "nCount_RNA", feature2 = "percent.mt")
plot2 <- FeatureScatter(pbmc, feature1 = "nCount_RNA", feature2 = "nFeature_RNA")
plot1 + plot2
```


Conclusion

This document presented an analysis of the **PBMC dataset** using `Seurat` in R, including data loading, initialization of Seurat object, QC analysis, and visualization of feature-feature relationships.