

1.Question: What is min.features? Describe it and min.features = 100.

min.features is a parameter used in the creation of Seurat objects in single-cell RNA-seq analysis. It defines the minimum number of features (genes) that a cell must express to be included in the analysis. In other words, cells with fewer expressed features than this threshold will be filtered out from further analysis.

Setting min.features = 100 means that only cells expressing at least 100 genes will be retained in the analysis. This threshold is often used to filter out low-quality cells or potential contaminants that may not be biologically relevant.

2.Question: Report nCount\_RNA and nFeature\_RNA for AAACATACATTTC-1 (2nd item) from the ctrl\_raw\_feature\_bc\_matrix

```
[1] "nCount_RNA for AAACATACATTTC-1: 3125"
```

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[1] "nFeature_RNA for AAACATACATTTC-1: 896"
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For the cell with barcode AAACATACATTTC-1 from the ctrl\_raw\_feature\_bc\_matrix:

nCount\_RNA: 3125

nFeature\_RNA: 896

These values indicate that this particular cell has a total RNA count of 3125 and has 896 detected features .

The github link mentioned below

<https://github.com/anuhoshalli25/BCB5250>