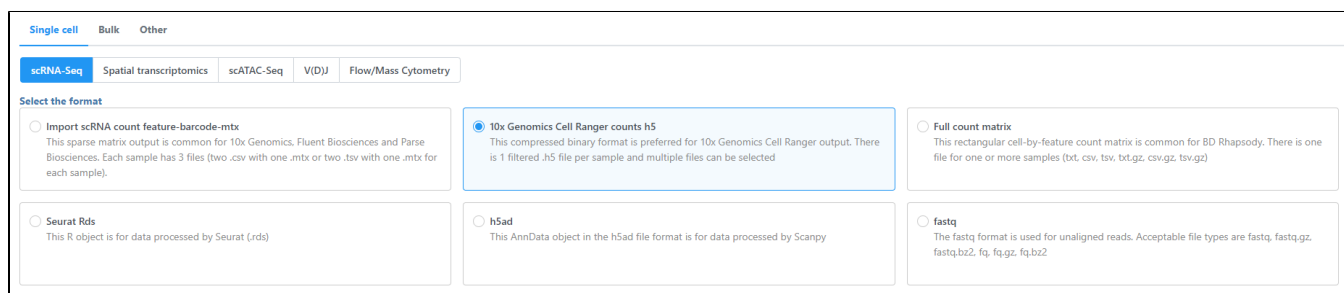


Import single cell data

- [Import single cell data for different assay types and formats](#)
- [Import single cell data from count matrix text file\(s\) using Full count matrix as the data format](#)

Import single cell data for different assay types and formats

Select **Single cell**, choose the **assay** type (scRNA-Seq, Spatial transcriptomics, scATAC-Seq, V(D)J, Flow/Mass cytometry), and select the data **format** (Figure 1). Use the **Next** button to proceed with import.



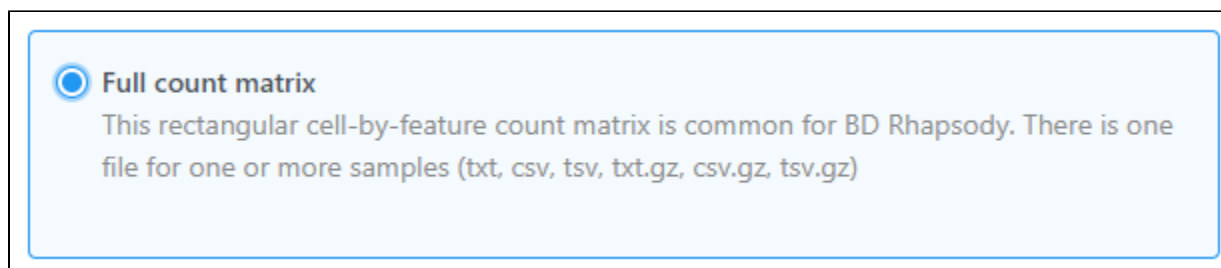
The screenshot shows a web interface for importing single cell data. At the top, there are tabs for 'Single cell', 'Bulk', and 'Other'. Below these, there are buttons for different assay types: 'scRNA-Seq', 'Spatial transcriptomics', 'scATAC-Seq', 'V(D)J', and 'Flow/Mass Cytometry'. The 'scRNA-Seq' button is selected. Below the assay type selection, there is a section titled 'Select the format' with six radio button options: 'Import scRNA count feature-barcode-mtx', '10x Genomics Cell Ranger counts h5' (which is selected), 'Full count matrix', 'Seurat Rds', 'h5ad', and 'fastq'. Each option has a brief description of the format.

Figure 3. Choose import single cell data option

Import single cell data from count matrix text file(s) using Full count matrix as the data format

Partek Flow supports single cell data analysis in count matrix text format using the Full count matrix data format (Figure 2). Each matrix text file is assumed to represent one sample, each value in the matrix represents expression value of a feature (e.g. a gene, or a transcript) in a cell. The expression value can be raw count, or normalized count. The requirement of the format of each text file should be the same as [count matrix data](#).

Specify text file location, only one text file (in other words one sample) can be imported at once, preview of the file will be displayed, configuration of the file format is the same as [Import count matrix data](#). In addition, you need to specify the details about this file.



The screenshot shows a single selection option for 'Full count matrix'. It is highlighted with a blue border and a blue radio button. The text describes it as a rectangular cell-by-feature count matrix common for BD Rhapsody, with one file per sample. Supported file formats listed are txt, csv, tsv, txt.gz, csv.gz, and tsv.gz.

Figure 4. Choose Full count matrix as the data format

Click **Finish**, the sample will be imported, on the data tab, number of cells in the sample will be displayed.

To import multiple samples, repeat the above steps by clicking **Import data** on the *Metadata* tab or within the task menu (toolbox) on the *Analyses* tab. Make the same previous selections using the cascading menu.

Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.



Your Rating:      Results:      2 rates