

Annotate cells

If you have attribute information about your cells, you can use the Annotate cells task in Partek Flow to apply this information to the data. Once applied, these can be used like any other attribute in Partek Flow, and thus can be used for cell selection, classification and differential analysis.

To run Annotate cells:

- Click a Single cell counts data node
- Click the **Annotation/Metadata** section in the toolbox
- Click **Annotate cells**

You will be prompted to specify annotation input options:

- Single file (all sample): it requires one .txt file for all your cells in all samples, each row in the file represents a barcode, at least one barcode column which will match the barcodes in your data. It also requires an column contains sample ID which will match the sample name in the data tab of your project.
- File per sample: it requires the format of all of the annotation files to be the same. Each file has barcodes on rows, it requires one barcode column that will match the barcodes in your data in that sample. All files have to have the same set of column, column headers are case sensitive.

You can pick the file for each sample from the Partek Flow server, you have to specify annotation files for all the samples in the dialog (Figure 1).

☒ Apply cell annotations from file

Specify annotation input as

☐ Single file (all samples) ☒ File per sample

Annotating with multiple files at once requires all files have the same column layout. If that is not the case, please annotate them in separate task runs.

Cell annotation files

<input checked="" type="checkbox"/>	Sample name	Annotation file	Browse
<input checked="" type="checkbox"/>	CT1_1		<div>Browse</div>
<input checked="" type="checkbox"/>	CT2_1		<div>Browse</div>
<input checked="" type="checkbox"/>	CT3_1		<div>Browse</div>
<input checked="" type="checkbox"/>	CT4_1		<div>Browse</div>
<input checked="" type="checkbox"/>	CT5_1		<div>Browse</div>
<input checked="" type="checkbox"/>	SC1_1		<div>Browse</div>
<input checked="" type="checkbox"/>	SC2_1		<div>Browse</div>
<input checked="" type="checkbox"/>	SC3_1		<div>Browse</div>
<input checked="" type="checkbox"/>	SC4_1		<div>Browse</div>
<input checked="" type="checkbox"/>	SC5_1		<div>Browse</div>
<input checked="" type="checkbox"/>	SC6_1		<div>Browse</div>
<input checked="" type="checkbox"/>	SC7_1		<div>Browse</div>

Figure 5. Selecting a cell annotation file

To view a preview of the files, click Show Preview (Figure 2).

<input checked="" type="checkbox"/>	SC6_1	SC6_1.txt		<input type="button" value="Browse"/>
<input checked="" type="checkbox"/>	SC7_1	SC7_1.txt		<input type="button" value="Browse"/>

Show/hide details

SC7_1.txt (594.46 KB)

	1	2	3	4	5	6
1	Cell name	Sample name	Age	Gender	Samples	4_CellTypes
2	AAACCTGAGAGCTATA.7	SC7_1	Supercentenarian	Female	SC7	NK cell
3	AAACCTGAGCTACCTA.7	SC7_1	Supercentenarian	Female	SC7	Monocyte
4	AAACCTGAGCTCCTCT.7	SC7_1	Supercentenarian	Female	SC7	NK cell
5	AAACCTGAGGATTCGG.7	SC7_1	Supercentenarian	Female	SC7	Monocyte
6	AAACCTGAGTTCGATC.7	SC7_1	Supercentenarian	Female	SC7	NK cell
7	AAACCTGCAACAACA.7	SC7_1	Supercentenarian	Female	SC7	NK cell
8	AAACCTGCAAGGTGC.7	SC7_1	Supercentenarian	Female	SC7	NK cell
9	AAACCTGCAGCCAATT.7	SC7_1	Supercentenarian	Female	SC7	T cell
10	AAACCTGCAGGTTTCA.7	SC7_1	Supercentenarian	Female	SC7	T cell
11	AAACCTGCATTAGCCA.7	SC7_1	Supercentenarian	Female	SC7	Monocyte

Figure 6. Annotation files should have cells on rows and cell attributes on columns

If you would like to annotate your matrix features with a gene annotation file, you can choose an annotation file at the bottom on the dialog. You can choose any gene/feature annotation available on the Partek Flow server. If a feature annotation is selected, the percentage of mitochondrial reads will be calculated using the selected annotation file.

- Click **Next** to continue

The next dialog page previews the attributes found in the annotations text file (Figure 3).

The attributes presented are the ones that are common to all files that were selected.

Imported attributes that do not currently exist will create new Project-specific attributes.

Attribute name	Terms	Import	Attribute type
Cell name	AAACCTGAGCGCTCCA-1, AA...	<input type="checkbox"/>	Categorical
Cell Type	B cells, CD14 Monocytes, Cytot...	<input checked="" type="checkbox"/>	Categorical
Cluster	1, 2, 3, 5, 6, 7, 8	<input checked="" type="checkbox"/>	<div>Numeric</div> <div>Numeric</div> <div>Categorical</div>

Show/hide file preview

Figure 7. Previewing attributes to import

You can choose which attributes to import using the check-boxes, change the names of attributes using the text fields, and indicate whether an attribute with numbers is categorical or numeric.

- Click **Finish** to import the attributes.

A new data node, Annotated single cell counts, will be generated (Figure 4).

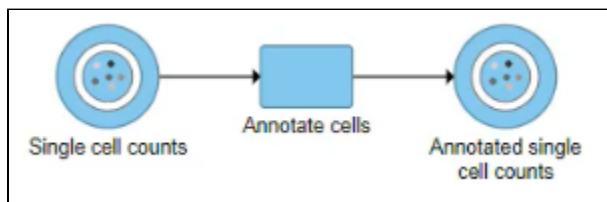


Figure 8. Output of *annotate cells*

You annotations will be available in downstream analysis tasks.

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: ★★★★★ 0 rates