

# 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).

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

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	AAACCTGCAAAGTGC.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
<input type="text" value="Cell name"/>	AAACCTGAGCGCTCCA-1, AA...	<input type="checkbox"/>	Categorical
<input type="text" value="Cell Type"/>	B cells, CD14 Monocytes, Cytot...	<input checked="" type="checkbox"/>	Categorical
<input type="text" value="Cluster"/>	1, 2, 3, 5, 6, 7, 8	<input checked="" type="checkbox"/>	<input type="text" value="Numeric"/> <ul style="list-style-type: none"> <li><input type="text" value="Numeric"/></li> <li style="background-color: #007bff; color: white;"><input type="text" value="Categorical"/></li> </ul>

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).

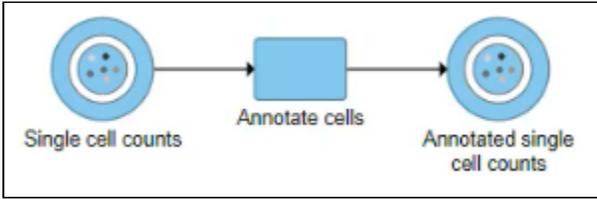


Figure 8. Output of annotate cells

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.



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Your Rating: ☆☆☆☆☆ Results: ★★★★★ 0 rates