Adding Library Files from Within a Project

Missing library files can be added when setting up tasks within a project, without having to navigate to the library file management page. The user interface will vary depending on the task and which library files already exist on your system. Below are two examples scenarios.

Adding a missing whole genome aligner index (Bowtie 2 in this example)

1. Under the *Analyses* tab of a project, select an **Unaligned reads** data node
2. From the context sensitive menu on the right, choose **Aligners** followed by **Bowtie 2.** On the alignment task setup page, Partek Flow will display all assemblies that have a Bowtie 2 index (whole genome and transcriptome) in the *Assembly* drop-down list. If the assembly you want is missing, choose **New assembly…** from the drop-down list (Figure 1)

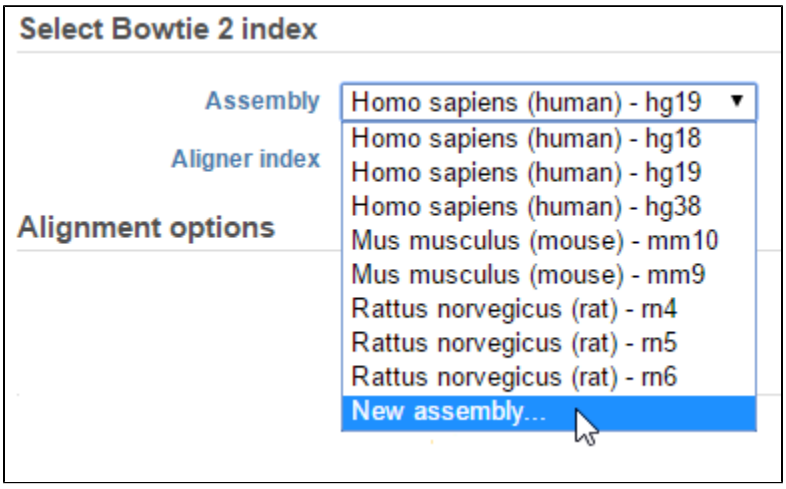


Figure 1. The drop-down list will show all assemblies that have a Bowtie 2 index associated with them. Choose New assembly... to add a Bowtie 2 index to another assembly

3. Choose the species and assembly in the *Add Bowtie 2 index* dialog. If the species and assembly you want do not appear in the drop-down lists, choose **Other** and manually type the names (Figure 2)
4. Choose **Whole genome** from the *Index* drop-down list (Figure 2)
5. Select the **Build index** radio button (Figure 2)
6. Click **Create** (Figure 2)

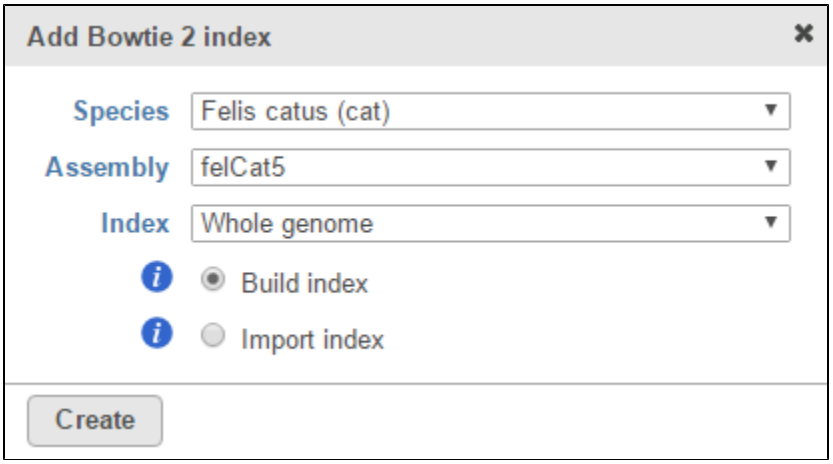


Figure 2. Add Bowtie 2 index to another assembly not listed in Figure 1.

Once the new Bowtie 2 index has been specified, you are able to queue the alignment task and it will execute once the Bowtie 2 index has been built.

Add a missing gene set file for enrichment analysis

1. Under the *Analyses* tab of a project, select a **Feature list** data node
2. Choose **Biological interpretation** from the menu on the right, followed by **Enrichment analysis**

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3. If there are no gene set files associated with the relevant assembly, click **Create gene set** (Figure 3)



Figure 3. If no gene sets are associated with the assembly, click the button to add one.

4. If you are working with an assembly/species supported by Partek (e.g. human), choose a gene set from the *Create gene set* drop-down list (Figure 4), select the **Download gene set** radio button and select **Create.** Alternatively, choose **Add gene ontology source** from the *Create gene set* drop-down list, manually type the custom gene set name and click **Create** to import your own gene set from the *Partek Flow server*, *My computer* or *URL* (Figure 5). Characters such as $ * | \ : " < > ? / % cannot be used in custom names. If you are working with a custom species /assembly (e.g. for a non-model organism), only the *Add gene ontology source* option is available.

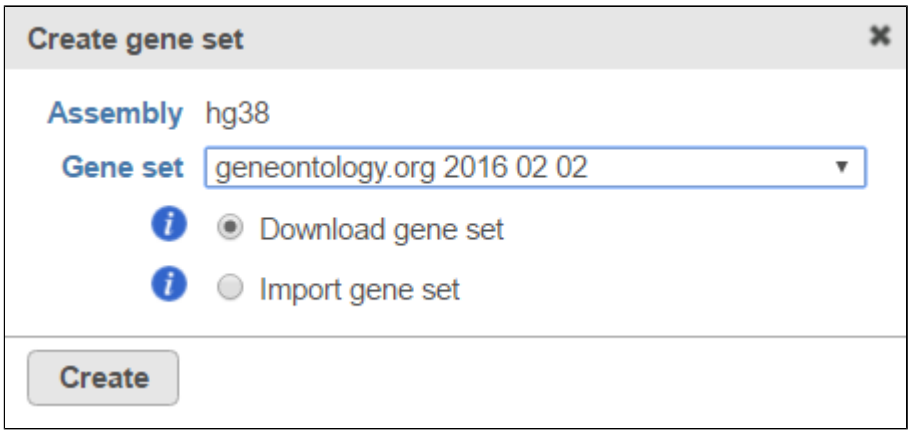


Figure 4. Download a gene set using the Create gene set dialog from within a project

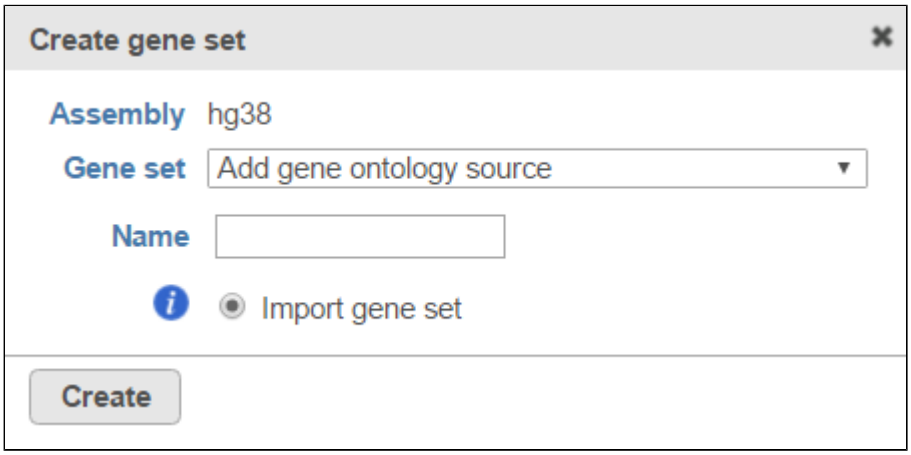


Figure 5. Import a gene set using the Create gene set dialog from within a project

Additional Assistance

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« Adding Aligner Indexes Based on an Annotation Model Microarray Library Files »







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