

Getting Help

Partek Flow includes a number of tools to guide you through your analyses, answer your questions, and assist with possible problems. Those tools include:

- [On-line Documentation](#)
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On-line Documentation

To access the Partek on-line repository of user guides, tutorials, and whitepapers, go to your avatar and select **Help**. A new tab will be opened in your browser, showing the home page of the repository (Figure 1).



Figure 9. Online repository of user guides, tutorials, and whitepapers

Sample Data Sets

Two sample data sets can be downloaded directly to Partek Flow and you can use them to get familiar with the Partek Flow interface, tools, and pipelines. The download links are on the System information page (you can open it by selecting your avatar and then selecting the Settings option) (Figure 2).



Figure 10. Downloading sample data sets

Depending on your preference, choose one of the sets. A new project will be automatically created (iDEA Challenge or [Brain vs UHR](#)) and Partek Flow will take you to a *Data* tab of that project (Figure 3). Since this is a tutorial project, there is no need to click on **Import data** as it will be done automatically.

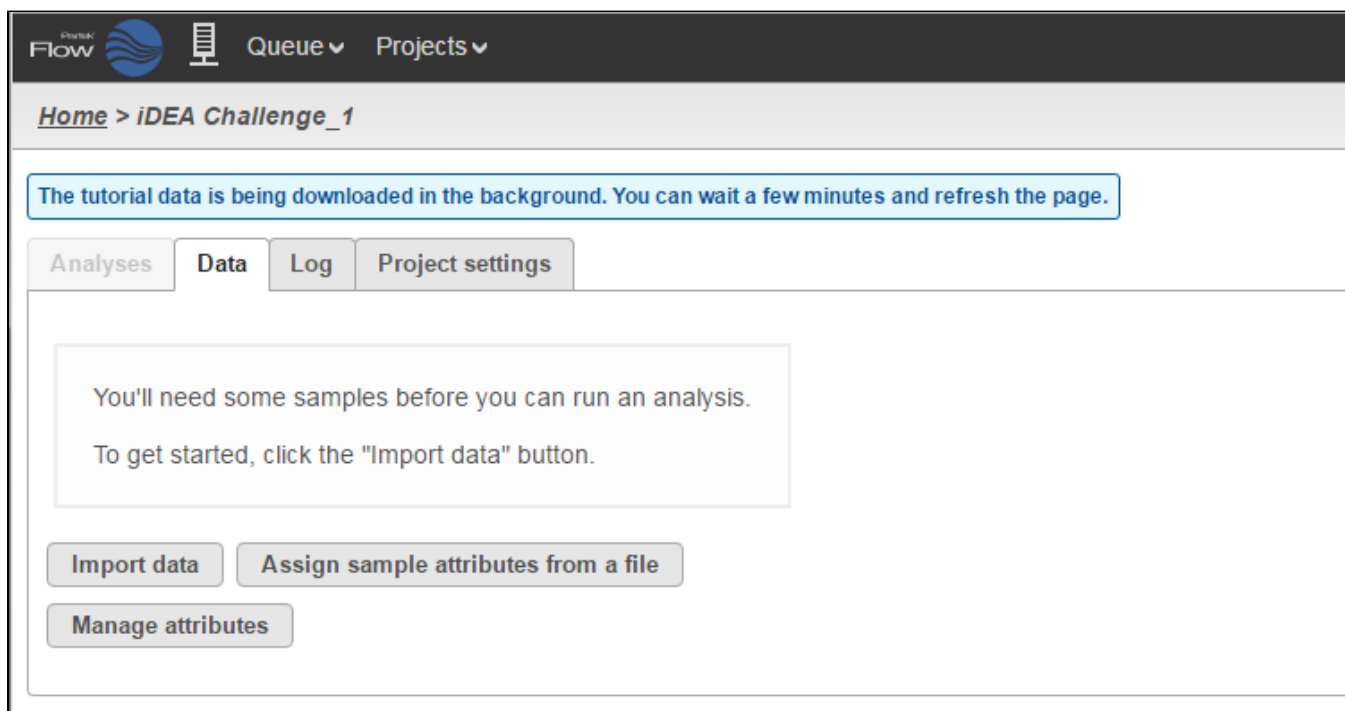


Figure 11. Creating a new project based on a sample data set. The project will be populated with samples automatically

At first the project is empty, but the file download will start automatically in the background. You can wait a few minutes and refresh the page or you can monitor the download progress in the *Queue* (Figure 4). You can access the *Queue* from the menu at the top of the page.

There is 1 task in the queue and Flow is set to run up to 100 project(s) simultaneously. (Anonymous tasks are not being displayed)

Status	Task	Project	User	Submitted	End	Cancel	
	Download Tutorial Data	iDEA Challenge	Administrator	23 Mar 2016, 06:11 AM CDT	23 Mar 2016, 06:24 AM CDT		View recent activity

T - Waiting for upstream tasks to complete R - Waiting for system resources P - Limited by number of running projects ⚠ - Cannot run with current system configuration

Time estimates are being continuously updated and will become more accurate.

Figure 12. Downloading tutorial data task in the queue (note that any user can download sample data set)

iDEA Challenge project is based on RNA-seq experiment performed using Illumina paired-end reads. The samples are eight commonly used breast cancer cell lines; therefore, the sample set consists of 16 fastq files (total size of 790 MB). For downstream steps you may want to divide the samples into two groups, based on expression of estrogen receptor (ER). ER-positive cell lines are: BT474, MCF7, T47D, and ZR751; the remaining cell lines are ER-negative.

Brain vs. UHR project is also an RNA-seq experiment, but based on Ion Torrent sequencing (single-end chemistry). Two sets of samples are included: human brain samples (HBR) and universal human reference (UHR) samples. The project consists of 10 fastq files with the combined size of 1.4 GB.

Tool Tips

Hovering over a task in the context sensitive menu (Figure 5) or the information icon in the different task dialog (Figure 6) brings up a balloon with short description of the task / option.

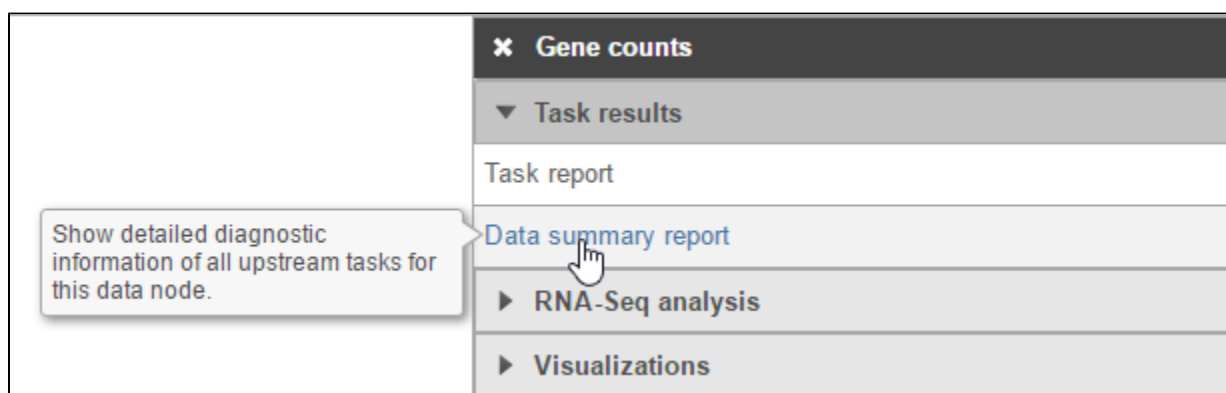


Figure 13. Hover over a task in the context sensitive menu to get a balloon with a short description

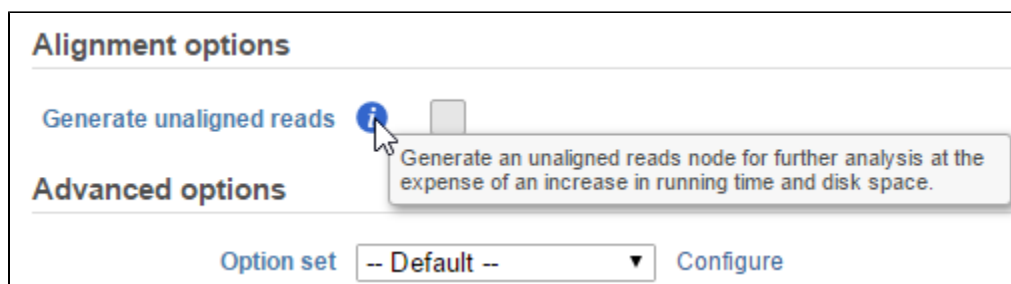


Figure 14. Hover over a tooltip icon to get a balloon with a short description

Reporting a Problem

In an unlikely case of an error occurring during the analysis, the failed task will be highlighted by an exclamation mark (Figure 7). However, if the task does not fail altogether (there is no exclamation mark, and the task report is produced), the results can still be missing or questionable for some features. In that case, the issue might be resolved by following the directions in [Differential Analysis Troubleshooting](#) section.

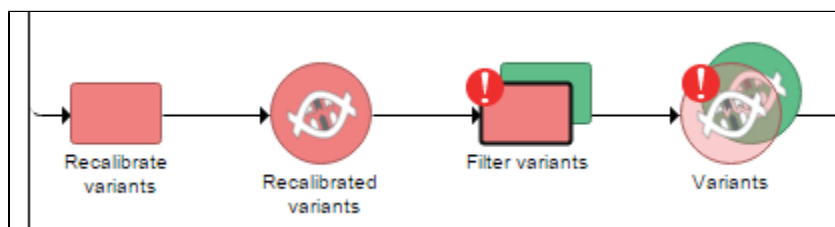


Figure 15. Failed task (in this example: Filter variants) highlighted by an exclamation mark. Note the the downstream task, i.e. Variants data node, is depicted as translucent to indicate that no result was produced

In case of failure, the task node's *Task details* page will contain *Warning information* section (optional) and the Error message section (Figure 8). In addition, you can download log files to your local computer (Download logs) or directly send them to Partek's technical support team (Send logs to Partek), who will get back to you shortly.

Warning information

- Failed validation: /home/flow/FlowData/Project_File10/SampleFileDownloadResult-1458571185844/GSM9
- Error: Line error near /home/flow/FlowData/Project_File10/SampleFileDownloadResult-1458571185844/G
- Reason: Quality String name is missing.

Error message

Unknown errors occurred, please send the logs to Partek or download logs.

Send logs to Partek

Download logs

Figure 16. Task details page of a failed task. Warning information section is optional, the content of the Error message section depends on the type of error. Send logs to Partek sends the log files to Partek's technical support team

Using the flowstatus.sh diagnostic script

Partek Flow version 5 and later come with a script that allow you to diagnose the status of the software even if you cannot access the Partek Flow user interface. Please refer to the [Diagnosing Issues](#) section for usage.

Contacting Support

If you wish to submit a support ticket directly, fill out a support ticket online. Go to your **avatar** and select **Contact us**. A new tab will be opened in your browser, and you will be presented with the support request form.

Phone numbers and support hours are also presented in the page if you wish to call us directly. There are also instructions on how to share screens if the support agent requests you during an online support call.

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: 39 rates

