

# Quick Start Guide

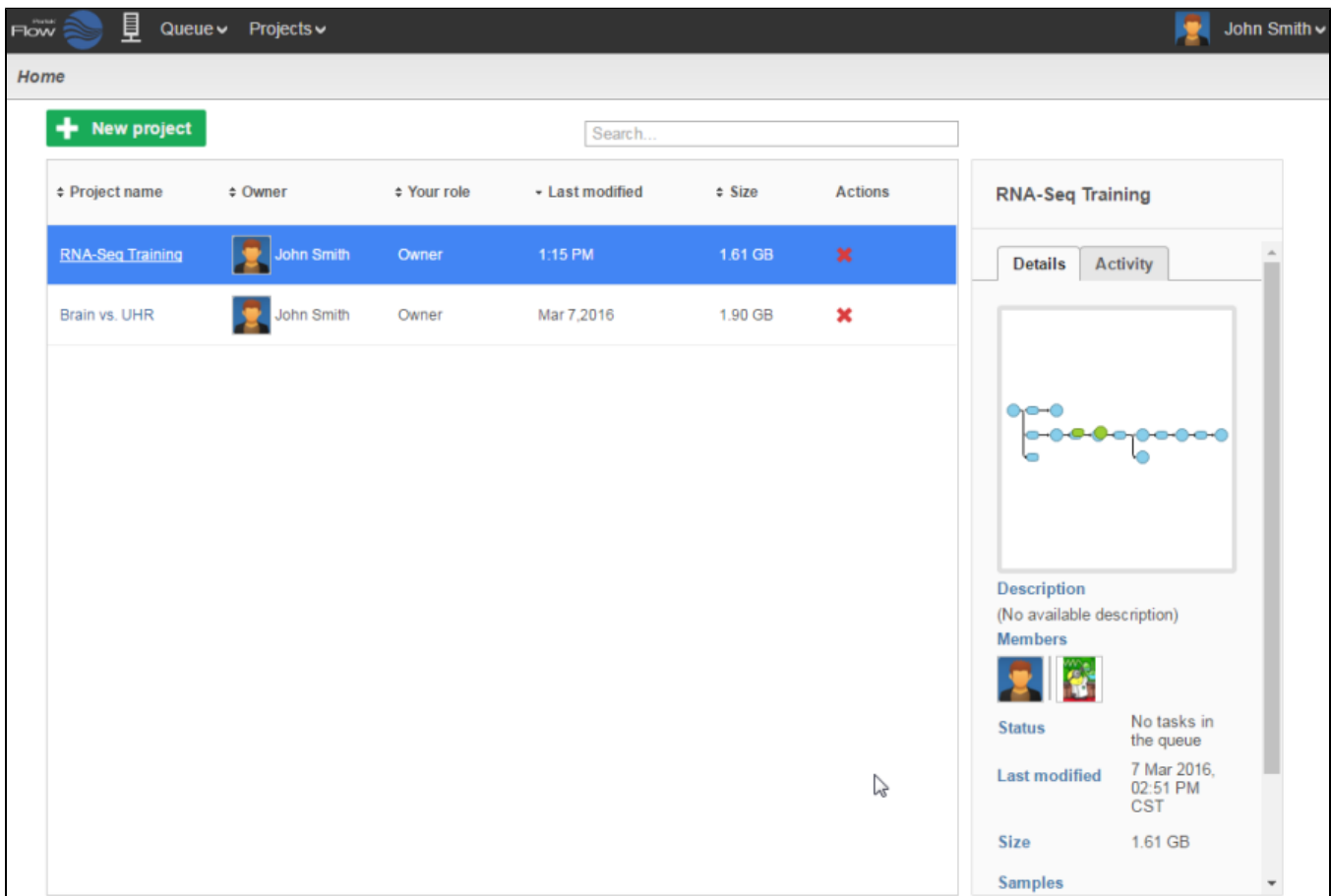
## Overview

This guide gives the basics of Partek® Flow® usage. Partek Flow can be installed in either a server, computer cluster or on the cloud. Regardless of where it's installed, it can be viewed using any web browser. We recommend using Google Chrome.

This guide covers:

- [Overview](#)
- [Starting a new project](#)
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- [Saving visualizations](#)
- [Downloading your data](#)
- [Partek Flow in action](#)

Logging in to your Partek Flow account will bring up the *Home page* (Figure 1). This page will show recent activities you've performed, recent projects you've worked on and pertinent details about each project.



Project name	Owner	Your role	Last modified	Size	Actions
RNA-Seq Training	John Smith	Owner	1:15 PM	1.61 GB	✖
Brain vs. UHR	John Smith	Owner	Mar 7, 2016	1.90 GB	✖

**RNA-Seq Training**

Details Activity

Description  
(No available description)

Members

Status: No tasks in the queue

Last modified: 7 Mar 2016, 02:51 PM CST

Size: 1.61 GB

Samples

Figure 9. Partek Flow Home page

## Starting a new project

From the *Home Page*, click the **New project** button. Assign a name to the project and click the **Create project** button

## Uploading your dataset

Upon creation of a new project, the *Data* tab will appear, prompting you to add samples to your project. Click the **Add samples** button. Selecting **Automatically create samples from files** is the fastest way to create a sample. Partek Flow accepts various data types including unaligned and aligned Next Generation Sequencing (NGS) reads, and microarray data. There are three ways you can upload data (*Figure 2*):

1. From your Partek Flow server
2. Directly from My computer (i.e. the computer you are currently using to access Partek Flow)
3. From a URL

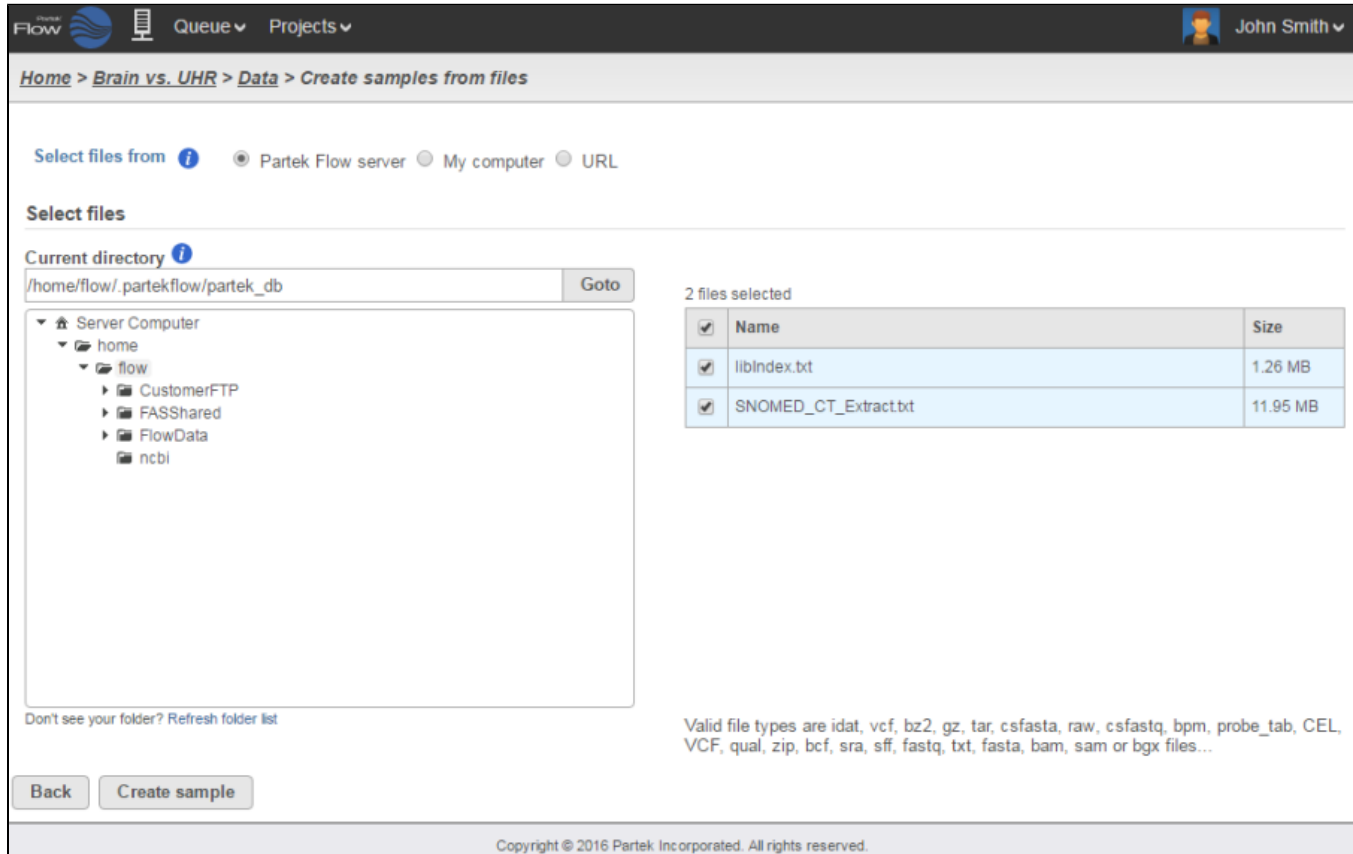


Figure 10. Uploading data into Partek Flow

Because genomics datasets are generally large, it is ideal to have the data copied in a folder directly accessible to the Partek Flow server. Make sure that the directory has the appropriate permissions for Partek Flow to read and write files in that folder. You may wish to seek assistance from your system administrator in uploading your data directly.

Select the files you would like to create samples from. Once they've been created, assign the corresponding sample attributes for each sample. The most efficient way to assign sample attributes is by clicking **Assign sample attributes from a file** and uploading a tab delimited text file. The file should contain a table with the following:

- The first row lists the attribute names (e.g. Treatment, Exposure) and
- The first column of the table lists the sample names (the sample names in the file must be identical to the ones listed in the *Sample name* column in the *Data* tab)
- List the corresponding attributes for each sample in the succeeding columns

## Basic Partek Flow layout

### The Analysis Tab

After samples have been added and associated with valid data files, a data node will appear in the *Analysis* tab (*Figure 3*). The *Analysis* tab is where you can invoke tasks and view the results of your analysis.

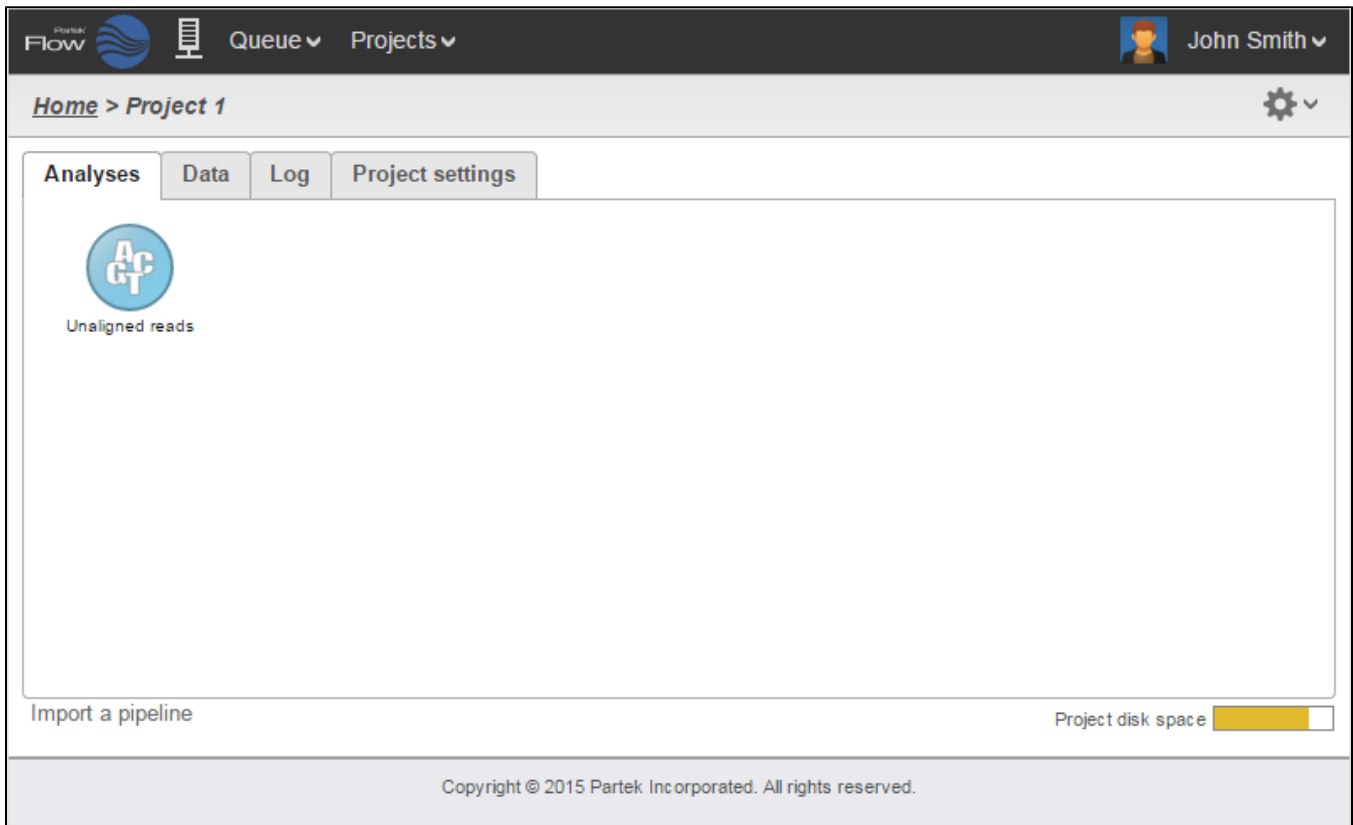


Figure 11. The Analyses tab showing a data node of unaligned reads

## Data and task nodes

The Analyses tab contains two elements: data nodes (circles) and task nodes (rounded rectangles) connected by lines and arrows. Collectively, they represent a data analysis pipeline (Figure 4).

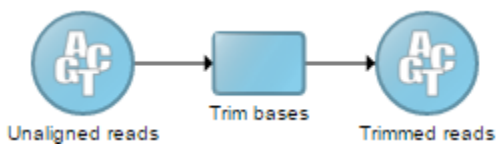


Figure 12. Example of a data analysis pipeline

## Performing tasks

Clicking a data node brings up a context sensitive menu on the right (Figure 5). This menu changes depending on the type of data node. It will only present tasks which can be performed on that specific data type.

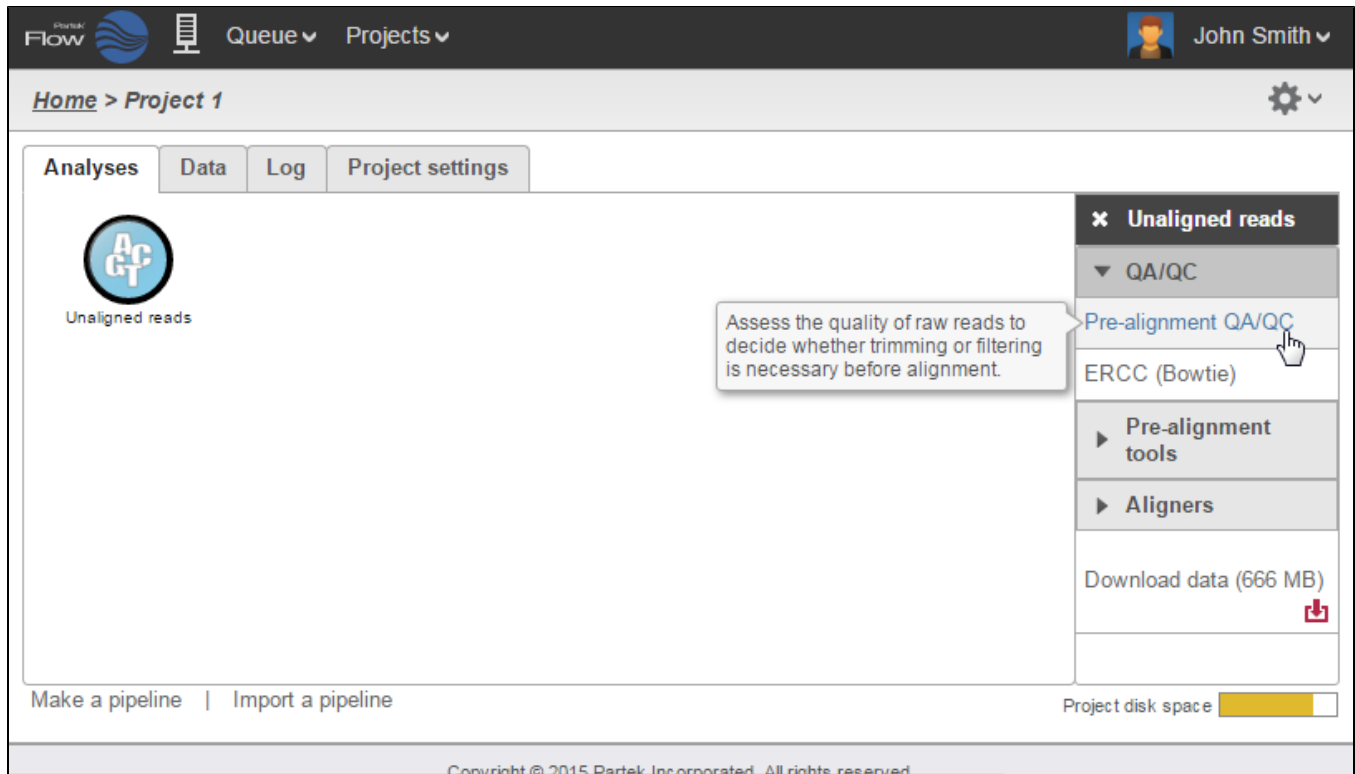



Figure 13. Context sensitive menu for unaligned reads data node

Select the task you wish to perform from the menu. When configuring task options, hover over the  tab to obtain additional information regarding each option (Figure 6). Click **Finish** to perform the task.

Partek Flow Queue Projects John Smith

Home > Project 1 > Trim bases

**Trim based on**

- Quality score *i*
- From 3' end *i*
- From 5' end *i*
- Both ends *i*

**Quality trimming**

End min quality level (Phred)

Trim from end

**Advanced options**

Min read length *i*

Max N *i*   %

Quality encoding *i*

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Figure 14. Obtaining additional information about a task option

Depending on the task, a new data node may automatically be created and connected to the original data node. This contains the data resulting from the task. Tasks that do not produce new data types, such as *Pre-alignment QA/QC*, will not produce an additional data node.

To view the results of a task, click the task node and choose the **Task report** option on the menu.

## Saving visualizations

Click the **Save** button on any visualization to export a publication-quality image (Figure 7).

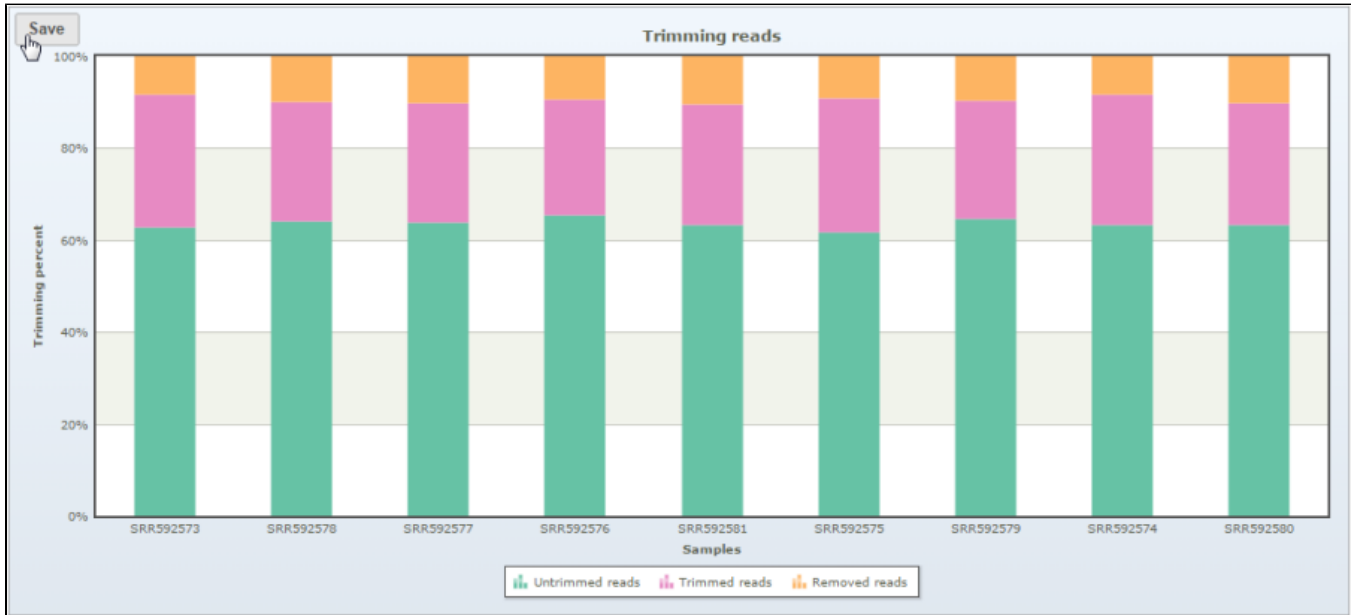


Figure 15. Saving visualizations

## Downloading your data

Data associated with any data node can be downloaded by clicking the node and choosing **Download data** (Figure 8). Compressed files will be downloaded to the local computer where the user is accessing the Partek Flow server. Note that bigger files (such as unaligned reads) would take longer to download. For guidance, a file size estimate is provided for each data node. Downloaded files can be seamlessly imported in Partek® Genomics Suite®.

Download the file(s) in the selected data node.

**Note:** The file size provided here is only an estimate, as the files themselves may be zipped before download.

Download data (600 MB)

Figure 16. Downloading data

# Partek Flow in action

Watch a webinar of [how to set-up a simple RNA-Seq project](#).

## 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: ★★★★★ 38 rates

