strandngs

Streamlining NGS Data Management & Analysis

Getting Started

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strand
New Generation Healthcare

Contents

Getting Started with Strand NGS

Aim

With this document, you will learn how to get started with the Strand NGS data analysis tool. We will discuss the steps that come before the analysis of data in Strand NGS. We will also look at how data and analysis results are organized, and how to download annotations that are needed for analysis.

Demo Project and User Interface

After launching Strand NGS and entering the license key, a start-up window appears with an option to create or open a project.
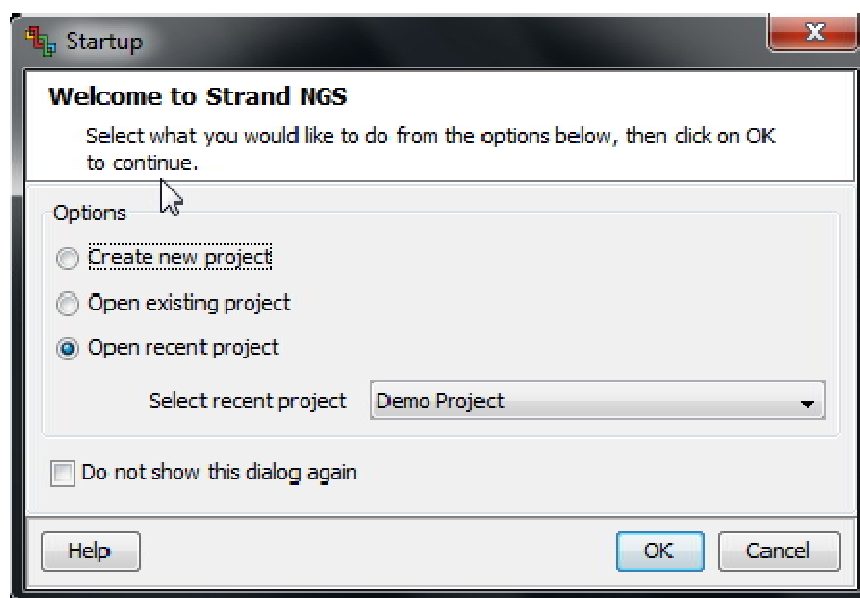

Figure 1: Startup Dialogue

If you are using the product for the first time, we recommend following the default option of opening the demo project. This project is packaged with the installation and allows you to browse through the various elements of the software and get a feel for its organisation. The demo project contains one experiment that opens in the Genome Browser and the initial view will look similar to what you can see in Figure 2, which defines the organisational elements of the Strand NGS user interface (UI).

The left side of the UI has the project and experiment navigators. The project navigator shows the experiments that are part of each project. The experiment navigator shows the samples and the analysis results in an intuitive hierarchical fashion. The right side of the UI has the workflow browser.

The workflow browser is customized to the particular kind of analysis being performed – for e.g., the small RNA analysis workflow browser is different from the RNA-Seq workflow browser. Most analyses are trigged from the workflow steps in the workflow browser. The rest of the elements of the UI include the Menu Bars and Toolbars at the top, the Status Bar at the bottom and the Legend at the bottom right corner.
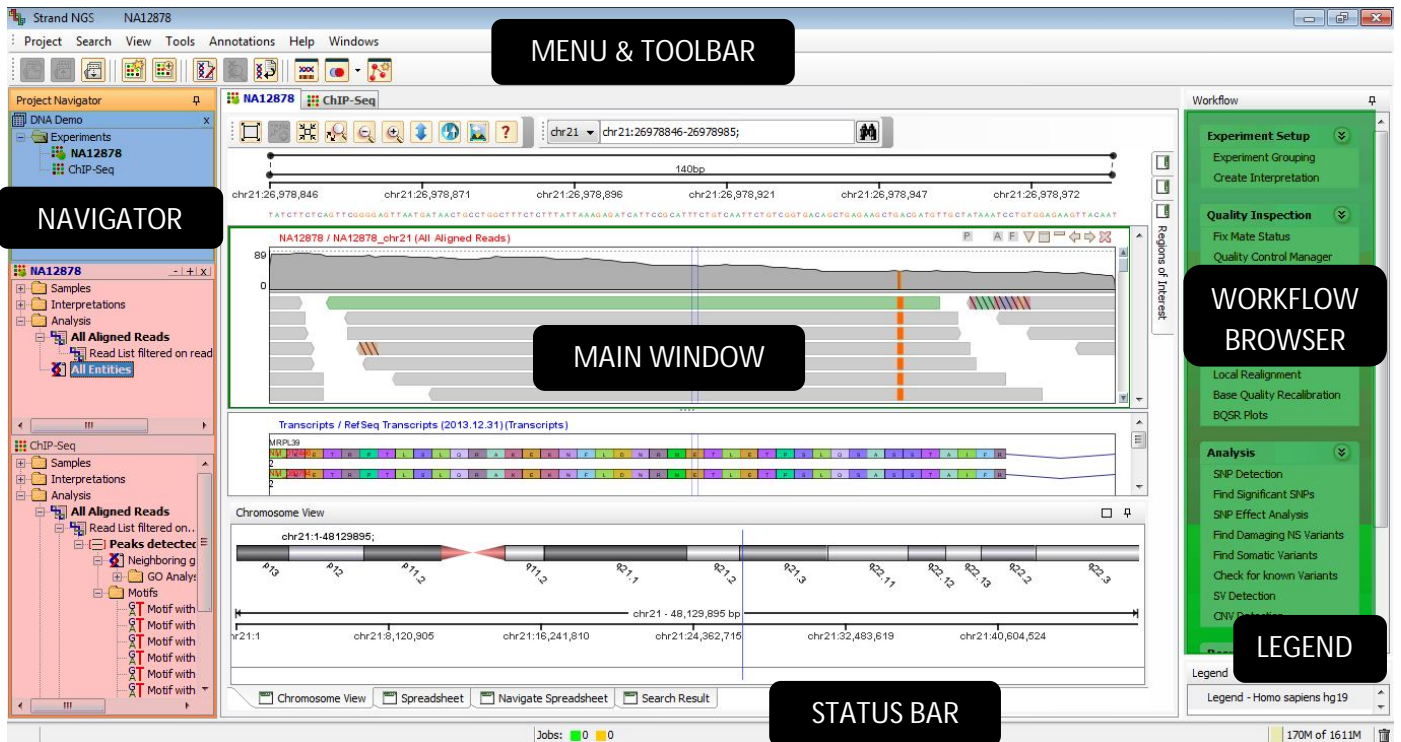
Figure 2: Strand NGS UI

With this basic information, you can explore the demo project. It contains RNA-Seq data from chr21 and a series of analysis results of an Alzheimer's study.

Downloading Annotations

Before starting any analysis, you should download the annotations for the organism you are working with. In Strand NGS, the time consuming task of gathering annotations for data analysis is solved by our 'Annotations Manager'. This contains an extensive list of annotations for standard organisms, some with multiple builds, gathered from various public databases. So before proceeding to the experiment creation step, download the required annotation packages (using the Annotations → Annotations Manager menu). Once the 'Annotations Manager' wizard opens, choose the List→ From Server option. (see Figure 3).
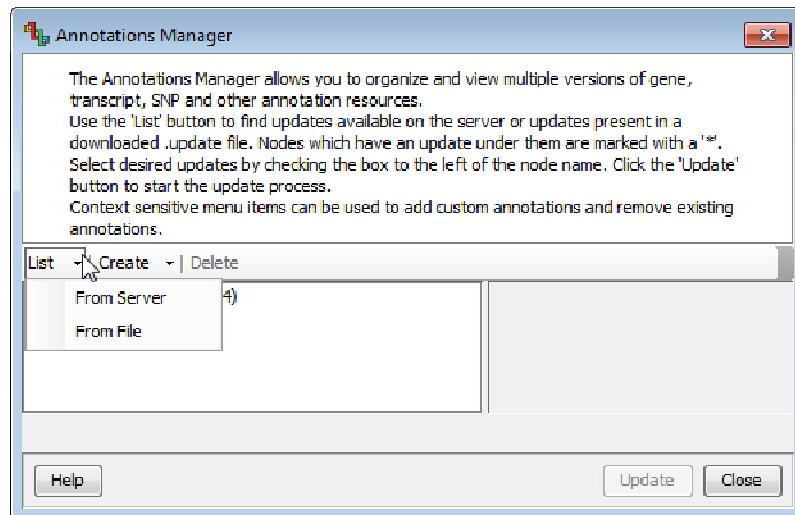
Figure 3: Annotations Download from Server

This opens a list of all organisms and their corresponding builds with various annotation packages as shown in Figure 4.
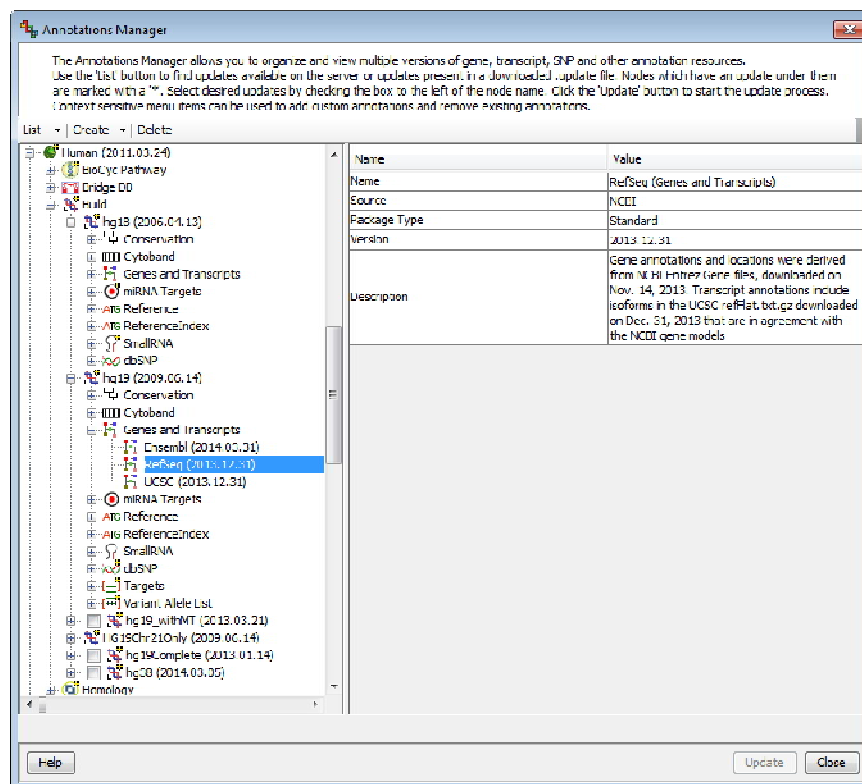

Figure 4: Pre-packaged annotations for hg19

For the purpose of experiment creation for the tutorial datasets, please download ONLY the following annotation packages from the human hg18 and hg19 builds:

1. Cytoband
2. Ensembl (Genes and Transcripts)
3. RefSeq (Genes and Transcripts)

4. UCSC (Genes and Transcripts)
5. Reference
6. Reference Index
7. dbSNP 137 (for DNA Variant Analysis demo)
8. Small RNA (for hg19 build)
9. TargetScan (for hg19 build)

Note that these annotations are hosted on an amazon machine and some of these, like the 'Reference', are large. So they may take a little while to download and load onto Strand NGS.

Project and Experiment Creation

As you go through each Strand NGS tutorial, in order to learn how data analysis is performed, you will create new projects and experiments. You could create a single project called "Tutorials" that will contain all these tutorial experiments or create separate projects for each tutorial. Further, each experiment can interrogate several samples. Each experiment has to be of a specific Experiment Type –you may only use one of these workflows- DNA Variant Analysis, or Small RNA Analysis, etc. while doing an experiment (see Figure 5). Additionally, many experiments can be open, but there can only be one active experiment at any given moment. The experiment type determines the kind of analysis steps available for that experiment. The workflow browser will therefore change to accommodate the experiment type.

To open a new experiment, click on the "Project" menu or on the New Experiment icon in the tool bar. This launches the New Experiment wizard.
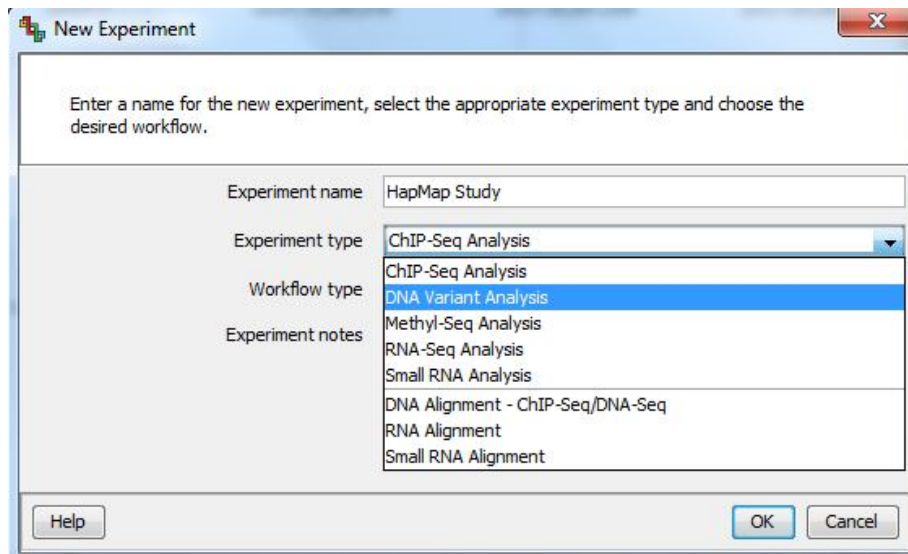

Figure 5: Available types of experiments

Choose the appropriate experiment type corresponding to the experiment described in the tutorial/s you have chose to follow. For further instructions on how to run DNA-Seq, RNA-Seq, ChIP-Seq or small RNA-Seq experiments, please look up the details in the corresponding tutorial document.