

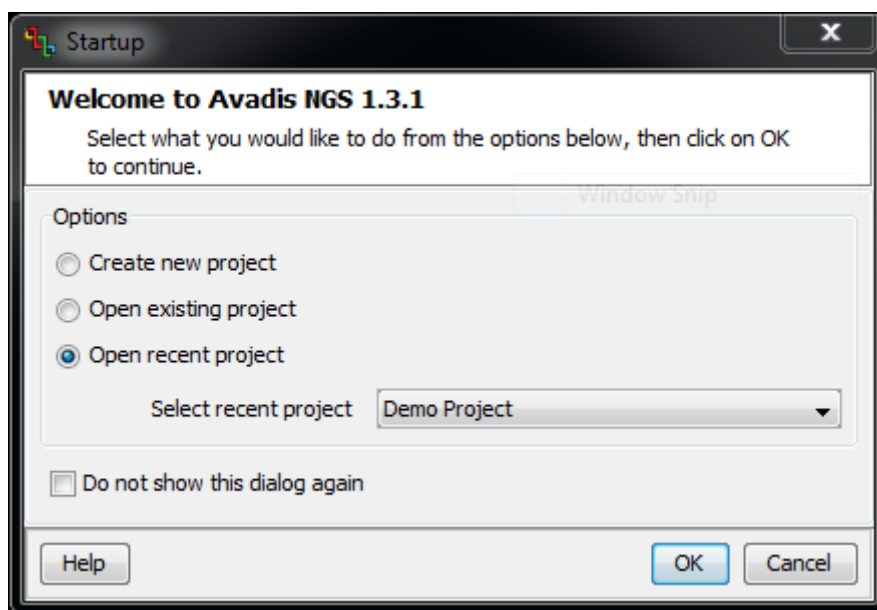
Getting Started

Aim

In this document, we will learn about the steps that precede the analysis of data in Avadis NGS. We will look at how data and analysis results are organized in Avadis and also download annotations that are needed for the analysis.

Demo Project

After launching Avadis NGS and entering the license key, a start-up window appears giving an option for creating or opening a project.

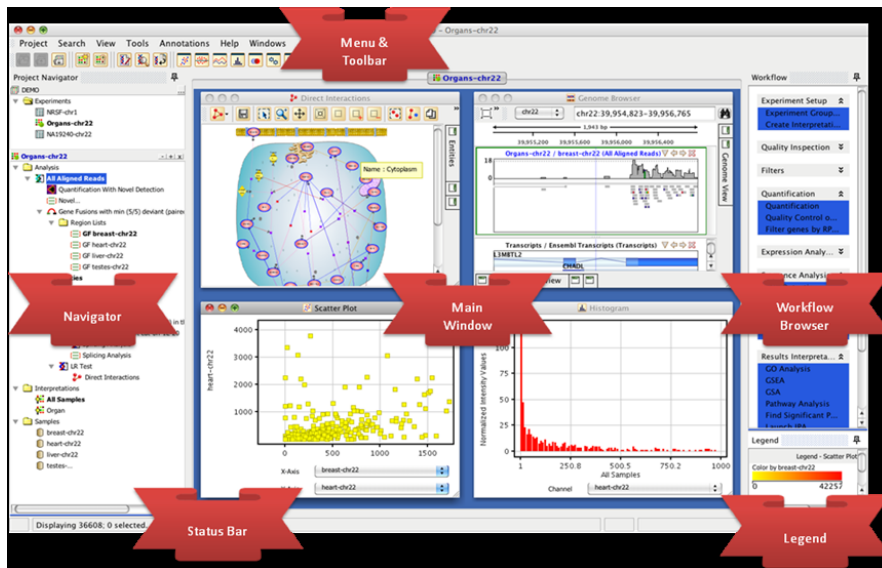


In this instance, we can go with the default option of opening the demo project. This would open the project and the demo experiment packaged in it. It would look similar to the below image which also has the organisational elements of the Avadis NGS user interface.

The left side of the UI has the project and experiment navigators. The project navigator shows the experiments that are part of it. 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.

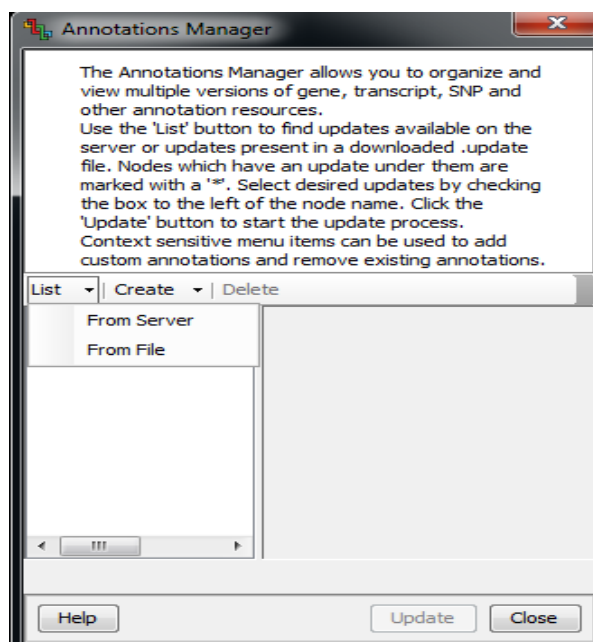
The workflow browser is customized to the particular kind of analysis being performed – for e.g., the small RNA analysis workflow browser is different from the RNA-Seq workflow browser. Most analysis are triggered from the workflow steps in the workflow browser. The rest of the elements of the UI include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

At this stage, it would be a good idea to explore the demo project. It contains RNA-Seq data from chr21 of an Alzhiemer's study.

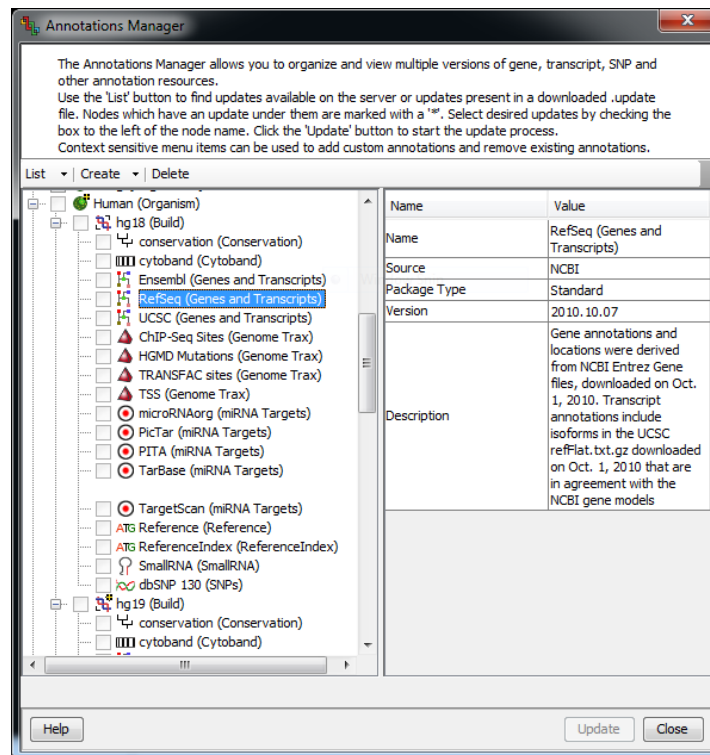


Downloading Annotations

Before starting any analysis, it is necessary to get the annotations for the organism under consideration. In Avadis NGS, the time consuming task of gathering annotations for data analysis is solved by the 'Annotations Manager'. This contains a list of standard organisms with many having multiple builds containing extensive annotations gathered from various public databases. Before proceeding to experiment creation, we need to download certain annotation packages (using the Annotations → Annotations Manager menu). Once the 'Annotations Manager' wizard opens, choose the List → From Server option.



This would open a list of all organisms, their corresponding builds with various annotation packages.



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

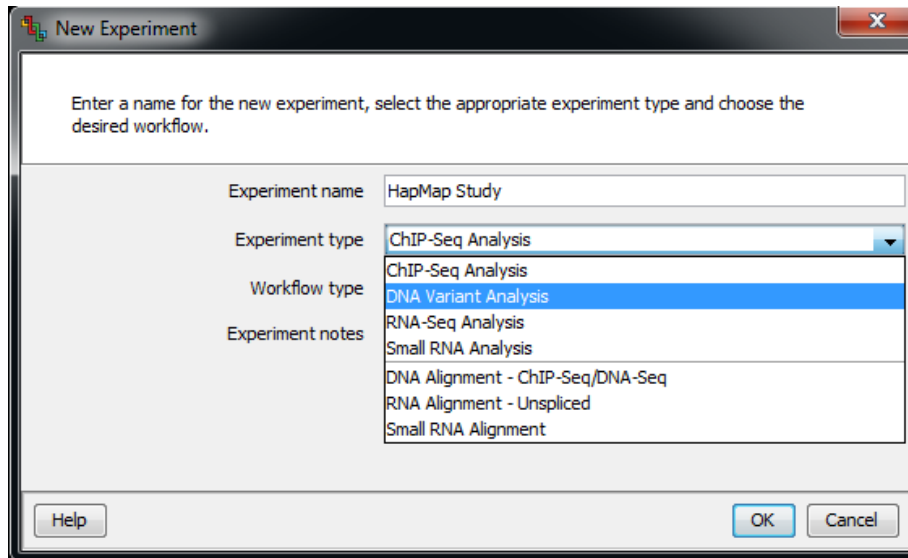
1. Cytoband
2. Ensembl (Genes and Transcripts)
3. RefSeq (Genes and Transcripts)
4. UCSC (Genes and Transcripts)
5. Reference
6. Reference Index
7. Small RNA (for hg19 build)
8. TargetScan (for hg19 build)

Note that these annotations are hosted on an amazon machine and some of them like the Reference, etc are large. So they may take a little while to download and load into Avadis.

Project and Experiment Creation

For the tutorials, new projects and experiments need to be created. You can create a single project called “Tutorials”, that will contain all the tutorial experiments. An experiment is a collection of related samples. Many experiments can be open, although there is only one active experiment at any time. Each experiment is of a unique Experiment Type – like small RNA, RNA-Seq, etc. The experiment type determines what kinds of analysis steps are available for this experiment. The workflow browser will change, based on the currently active experiment and its type.

A new experiment can be created either from the Project menu or from the icon in the tool bar (fourth from the left). This would launch the new experiment wizard.



Based on the tutorial, the appropriate experiment type needs to be selected for each experiment in the tutorials. More details about the downstream part of experiment creation will be present in each tutorial's document.