Avadis NGS

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.

₽, Startup	x			
Welcome to Avadis NGS 1.3.1				
Select what you would like to do from the options below, then click on OK to continue.				
Options Window Ship				
Create new project				
Open existing project				
Open recent project				
Select recent project Demo Project	•			
Do not show this dialog again				
Нер ОК С	ancel			

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 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.

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.



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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 \rightarrow Annotations Manager menu). Once the 'Annotations Manager' wizard opens, choose the List \rightarrow From Server option.

🖡 Annotations Manager					
The Annotations Manager allows you to organize and view multiple versions of gene, transcript, SNP and other annotation resources. Use the 'List' button to find updates available on the server or updates present in a downloaded .update file. Nodes which have an update under them are marked with a '*'. Select desired updates by checking the box to the left of the node name. Click the 'Update' button to start the update process. Context sensitive menu items can be used to add custom annotations and remove existing annotations.					
List	-	Create 🛛 - Dele	te		
	F	rom Server			
	F	rom File			
< <u> </u>					
н	elp		Update Close		





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.



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New Experiment					
Enter a name for the new experiment, select the appropriate experiment type and choose the desired workflow.					
Experiment name	HapMap Study				
Experiment type	ChIP-Seq Analysis				
Workflow type	ChIP-Seq Analysis DNA Variant Analysis				
Experiment notes	RNA-Seq Analysis Small RNA Analysis				
	DNA Alignment - ChIP-Seq/DNA-Seq				
	RNA Alignment - Unspliced Small RNA Alignment				
Help	OK Cancel				

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.

