CYTOGNOMIX

Accessing the Shannon Human Splicing Pipeline Trial Server

The trial version of the server does not report all of the results that the fully licensed version does:
-Any number of variants may be submitted.
-The set of variants shown is underline randomly selected from a larger set of results.
-Up to 20% of all possible results are shown.
-Only a few inactivating or leaky variants are returned.
-No more than 500 variants with changes in information content are displayed.
-User access is anonymous, but IP addresses are tracked.
-The only Server function that is enabled is the Shannon pipeline plugin.
-The full version of the plugin contains none these limitations.

*Please Note: The server may be accessed without completing steps 1 and 2 below. The server contains results generated from the full version of the plugin which can be viewed without installation of the trial. However, if you would like to examine your own variants (or analyze the sample variants in the _SAMPLE-VARIANTS folder) on the trial server, all of the following steps are required:

1. Uninstall any previously installed Shannon Human Splicing Pipeline plugins.

2. Installation of the CLC bio Workbench Client Plugin into to the workbench is required to allow the workbench to connect to any CLC bio server.

   - From within the Genomics Workbench, click the plugins button in the top toolbar

   - Select "Download Plugins"

   - Install the plugin named "CLC Workbench Client Plugin"

3. We will now install the Cytognomix client plugin used to submit and retrieve Shannon pipeline data from the Cytognomix trial server.

   - From within the Genomics Workbench, click the plugins button in the top toolbar

   - Select "Download Plugins"

   - Install the plugin named "Cytognomix Shannon Pipeline Client"

4. Connect to the server
   - From within the Genomics Workbench, select file->CLC Server Login
   - If necessary, expand the advanced option to uncover 'Server host' and 'Server port'
   - Login using the following credentials.

- o   User name: trial
- o   Password: Cytognomix
- o   Server host: 208.75.74.35
- o   Server port: 7777
- o   Click login

4. If desired, you can view some results generated by the full version of the plugin in the folder _SAMPLE-RESULTS-FROM-FULL-VERSION.

5. Your own data may be imported at this time. For instructions regarding the import process, please consult the Shannon Human Splicing Pipeline documentation on how to import either VCF or Shannon pipeline basic variant. For simplicity, the steps given below will use pre-imported data that are already resident on the Trial Server.

6. In the Genomics Workbench toolbox, expand Shannon Human Splicing Pipeline and double click 'Launch Pipeline'.

7. A wizard will pop up. Select CLC Server and click next.

8. Expand the folder _SAMPLE-VARIANTS to view its contents. Select 'Pre-Imported-hg19-Variants-Ready-to-be-examined-by-the-Shannon-Pipeline' and move it to the 'Selected Elements' region of the wizard. Click next.

9. The pre-imported variants are hg19, so ensure hg19 is selected in 'Genome Build' and click next. The trial server does not recognize filtering options under the 'Types' or 'Output Format' subheadings.

10. The results of the pipeline should be saved, this will be selected by default so click next on the Result handling wizard screen.

11. Create a folder to store your results. To do this, highlight the Trial_Server_Data folder and press the +folder button. Name the folder whatever you would like. Highlight your newly created folder and click finish to begin your run.

12. With this data (approximately 5000 variants on 3 different chromosomes), the run will take approximately 10 minutes to complete (if using the pre-imported variants), so be sure to check back to review your results.

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