

Torrent Scout Experiment Explorer

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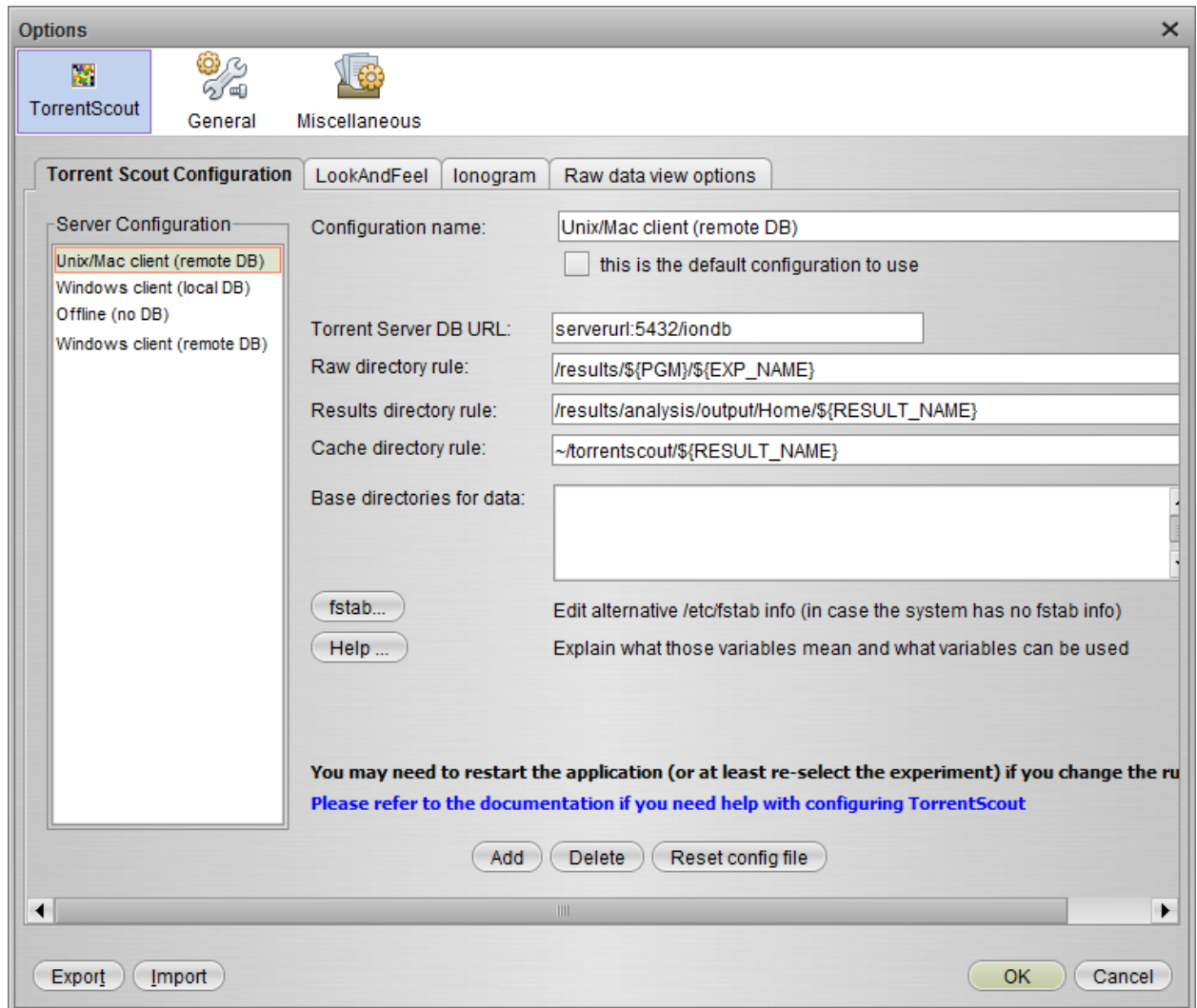
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Summary

The experiment explorer allows you to navigate your pgms, experiments and runs and shows detailed information about them that is obtained from a Torrent Server database (the iondb database used for the Torrent Browser). It has filtering options to narrow down the runs you might want to look at. You can select a run and view the associated data (as an alternative to the Offline component)

Configuring the Experiment Explorer

- Select menu Tools/Options

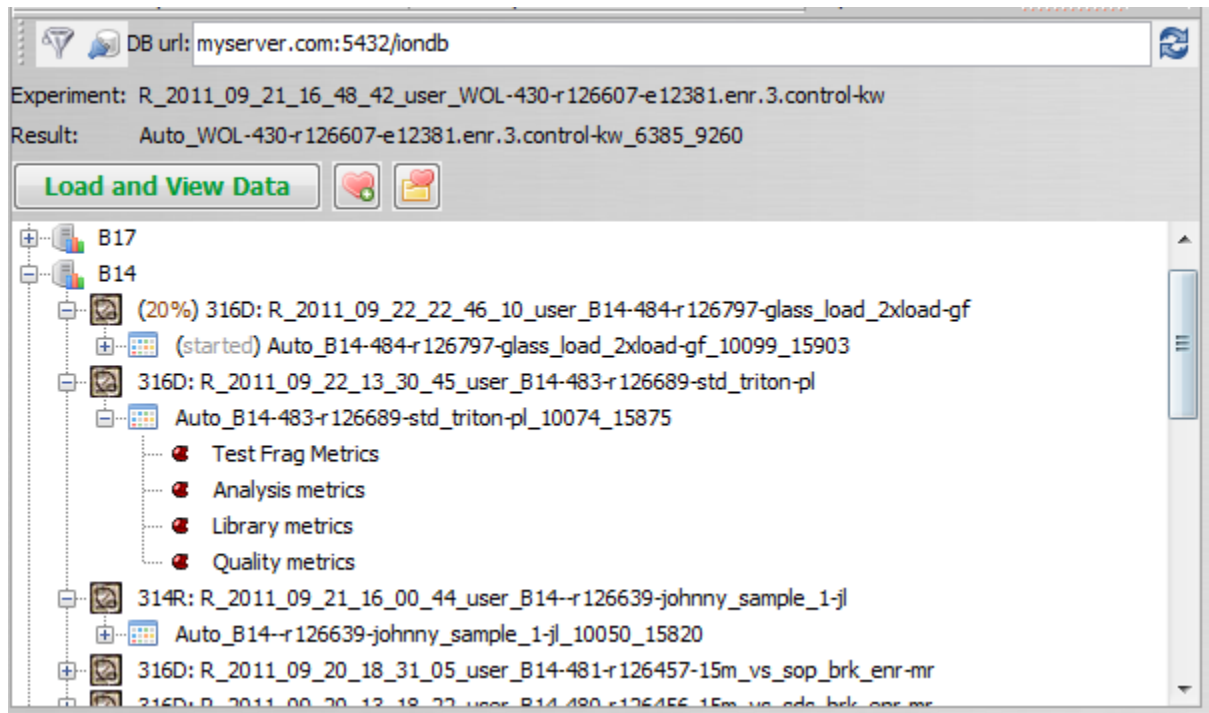


- Enter the URL of the torrent server
- The port is usually 5432, and the name of the database is iondb. So the entire URL typically has the form: some.server.url:5432/iondb

Please refer to the [Torrent Scout Configuration manual](#) for more details on how to set up the paths to the files!

Using the Experiment Explorer

- Start it by selecting Menu Windows/Experiment Browser
- Make sure the URL is correct that is displayed in the top text box
- If there is a problem, you can change the URL there for testing and hit the refresh button on the right

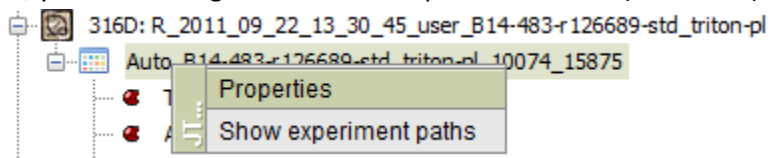


- The display shows first the PGM names, then the experiments names with chip type up front, and within the experiments are the runs for this experiment
- Each individual run contains the Analysis, Library and Quality metrics
- If an experiment is not completed yet, a percentage indicator is shown (such as (20%) in the example above)
- If a run was aborted or is not completed yet, the status is printed (such as 'started' in the example above)
- If you move your mouse over any item, a tool tip text will show a bit more information about the element

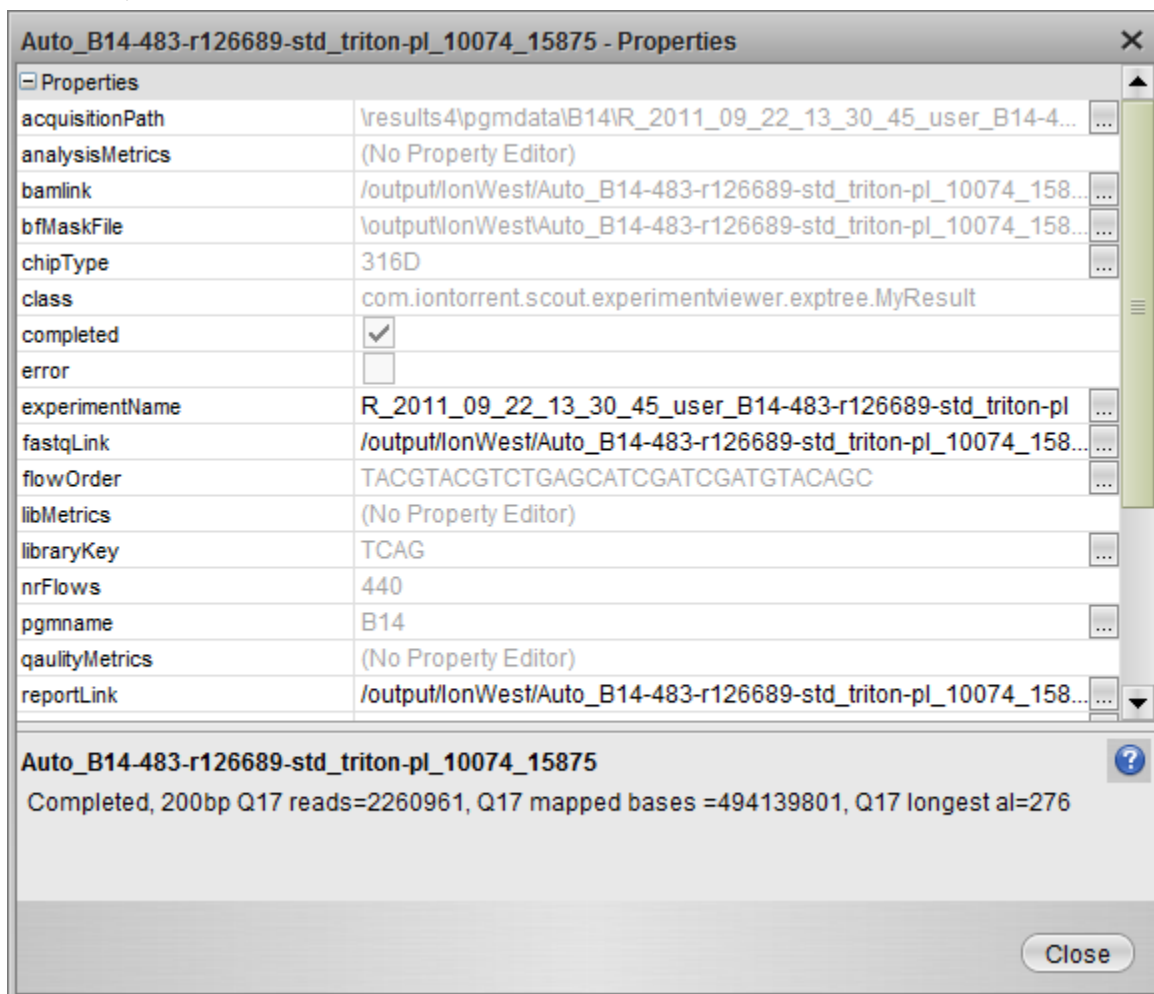
Viewing Details of Experiments and Runs

- You can either double click on an experiment or run to open the properties window
- Or you can select Menu Windows/Properties to turn it on

- Or, you can also right click on the experiment or run (or metrics) and select properties



- Here you can see the properties of this particular run, including the chip type, the nr of flows, the status, links to the files etc



- Similarly you can view the properties of experiments:

316D: R_2011_09_22_13_30_45_user_B14-483-r126689-std_triton-pl - Properties

Properties	
autoAnalyze	<input checked="" type="checkbox"/>
baselineRun	<input type="checkbox"/> true
chipBarcode	AA0066930
chipType	316D
class	com.iontorrent.dbaccess.RundbExperiment
cycles	110
date	22.09.2011 19:30:45
expComplInfo	
expDir	/results4/pgmdata/B14/R_2011_09_22_13_30_45_user_B14-483-r126689-std_trito...
expName	R_2011_09_22_13_30_45_user_B14-483-r126689-std_triton-pl
flows	440
flowsInOrder	TACGTACGTCTGAGCATCGATCGATGTACAGC

316D: R_2011_09_22_13_30_45_user_B14-483-r126689-std_triton-pl

Complete, project triton_test_0922, 440 flows,
dir=/results4/pgmdata/B14/R_2011_09_22_13_30_45_user_B14-483-r126689-std_triton-pl

Close

- And also of the various metrics:

Library metrics - Properties	
q20MappedBases	425908417
q20MeanAlignmentLength	180
q20QscoreBases	0
q47Alignments	2239763
q47CoveragePercentage	100.0
q47LongestAlignment	273
q47MappedBases	292469907
q47MeanAlignmentLength	131
q47QscoreBases	0
q7Alignments	2578474
q7CoveragePercentage	100.0
q7LongestAlignment	276
q7MappedBases	565042695

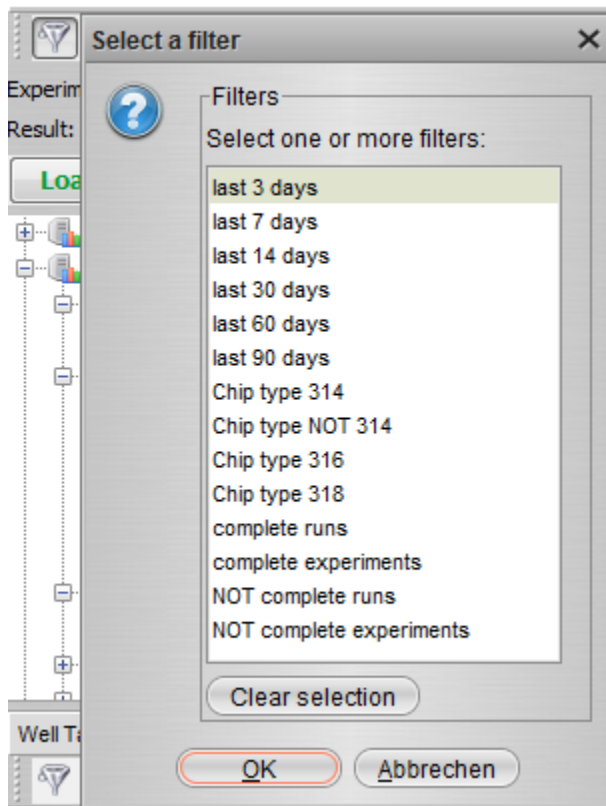
Library metrics	
2595027 total nr reads, genome E. coli DH10B	

Close

Filtering

- If your database has lots of experiments, you may want to filter by chip type or date. By default, the experiments of the last 14 days are shown
- To change the filter, select the filter icon on the top left

- You can combine filters by selecting Shift/Control



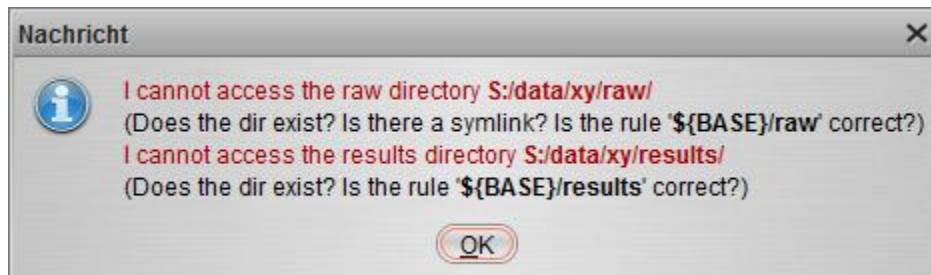
- For instance you can chose to only see runs for the last 3 days and chip type 314, or only runs that were completed and are not chip type 314
- To see all experiments in the database, use the clear selection button

Loading an Experiment

- Select a run
- Click on the “Load and View Data” button

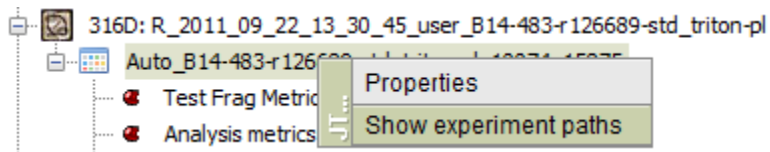
Problem: can't find data

- If you load an experiment and you get an error message similar to this:

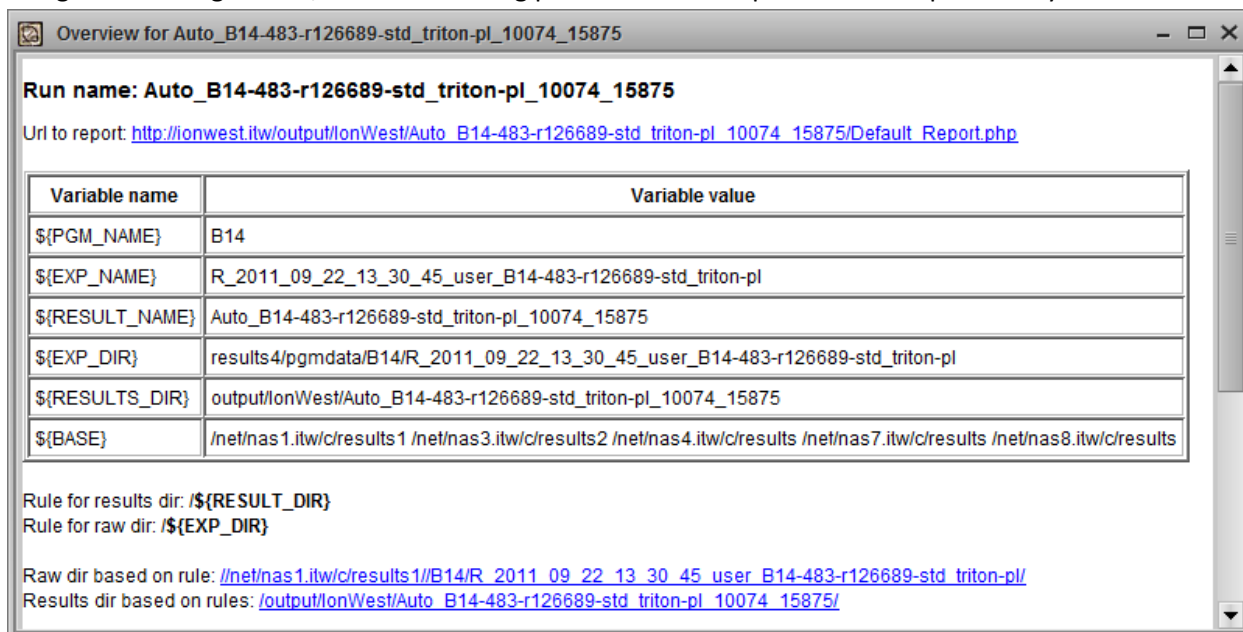


Then this indicates that either the rule for locating the data is not correct, or else that for some reason the drive/folder is not accessible.

- In that case, you may want to go back to the Tools/Options/Configuration panel to enter the correct rules/paths
- To help you with finding out what to put in there, you can right click on a run and select “Show experiment paths”:



- This will open a window and show you the current variable (name and value) that you can use in the config panel, such as \${PGM_NAME} and so on. It also shows you the current rule you are using in the configuration, and the resulting path that the rule plus current experiment yields:

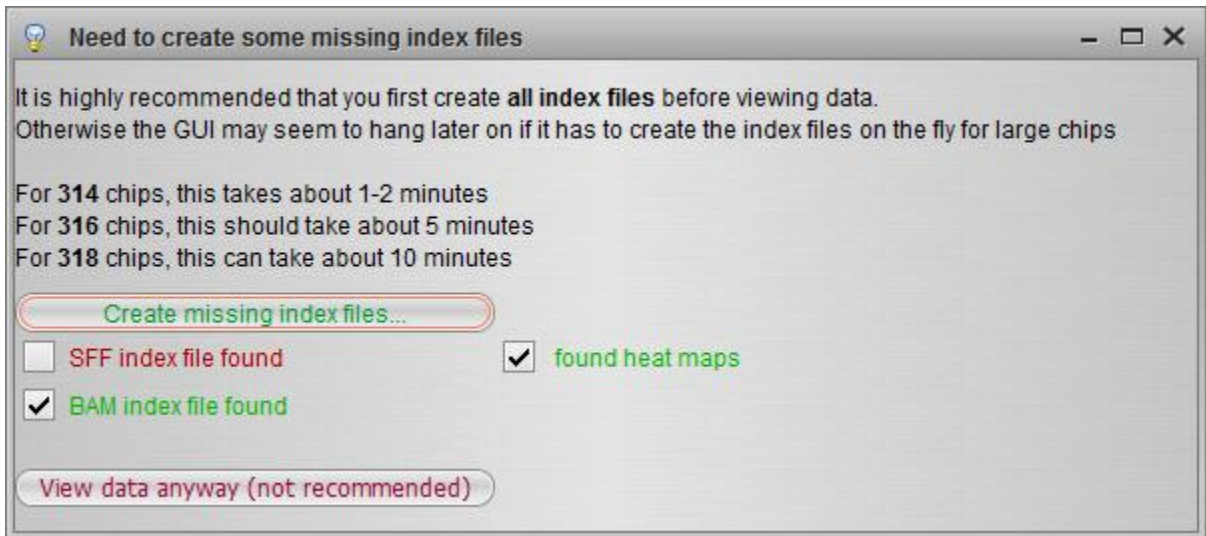


- There is also a URL on top that links back to the Torrent Browser report page

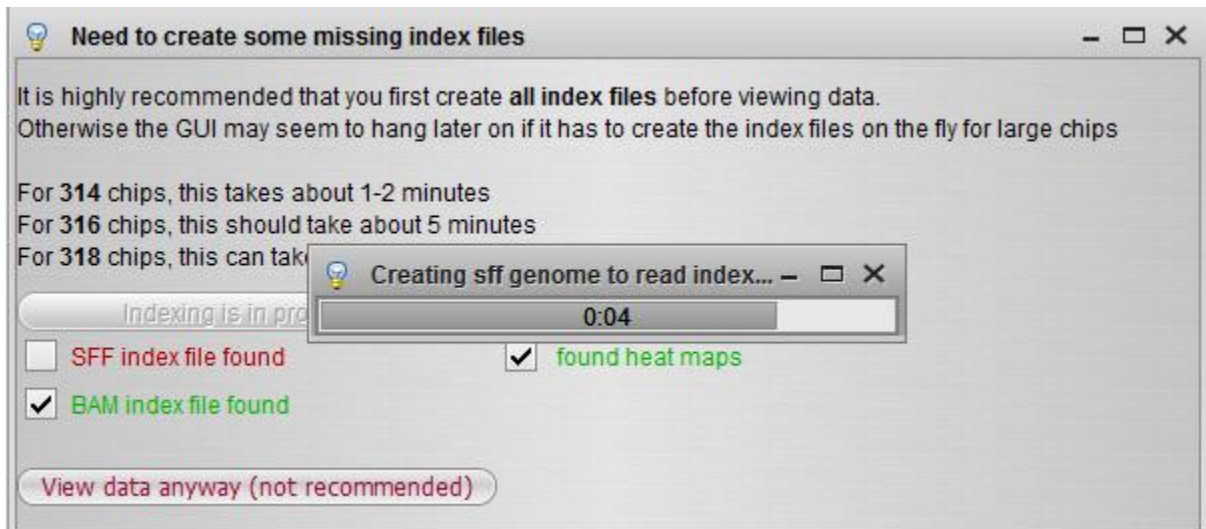
Problem: missing index files

- If you are not using the torrent scout plugin (or if it failed or was turned off), and you try to load an experiment, it might show you a message similar to this indicating that one or more index

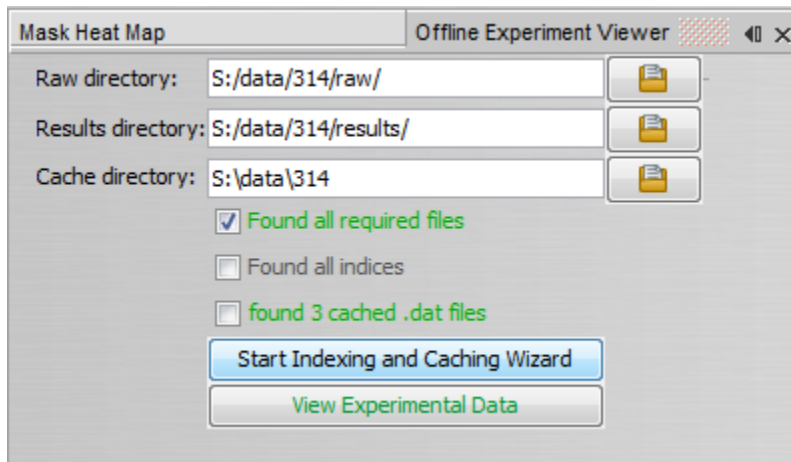
files are not there yet:



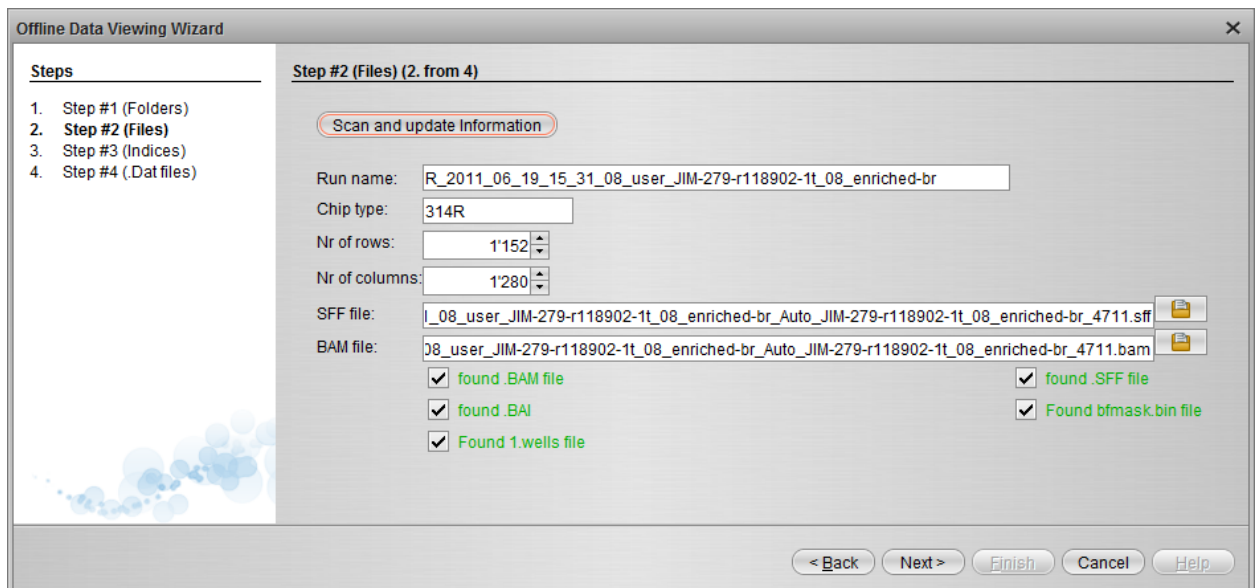
- It is highly recommended that you chose "Create missing index files" so that the tool runs smoothly afterwards
- If you choose to view the data anyway, the GUI might appear to hang later on if it has to create the index files on the fly. This is usually very fast for 314 chip data, but for larger chips and depending on your machine this can take several minutes or more
- When you select "Create missing index files" it will do all the indexing, and load the experiment automatically when it is done



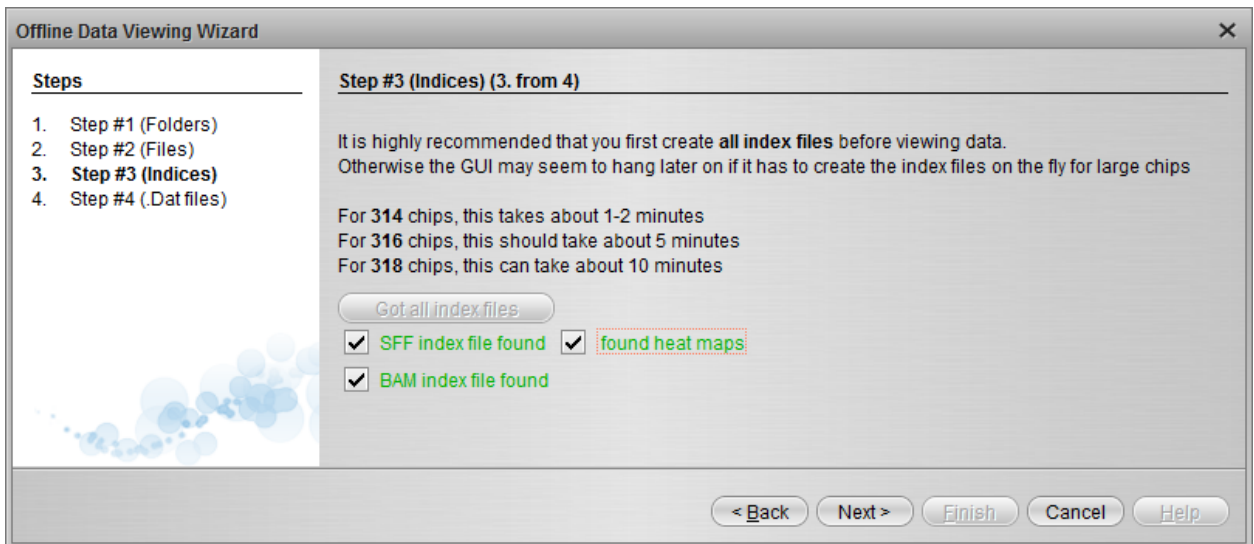
- You may also go to the Offline component (Windows/Offline) to get more information about what files may be missing and to create the index files:



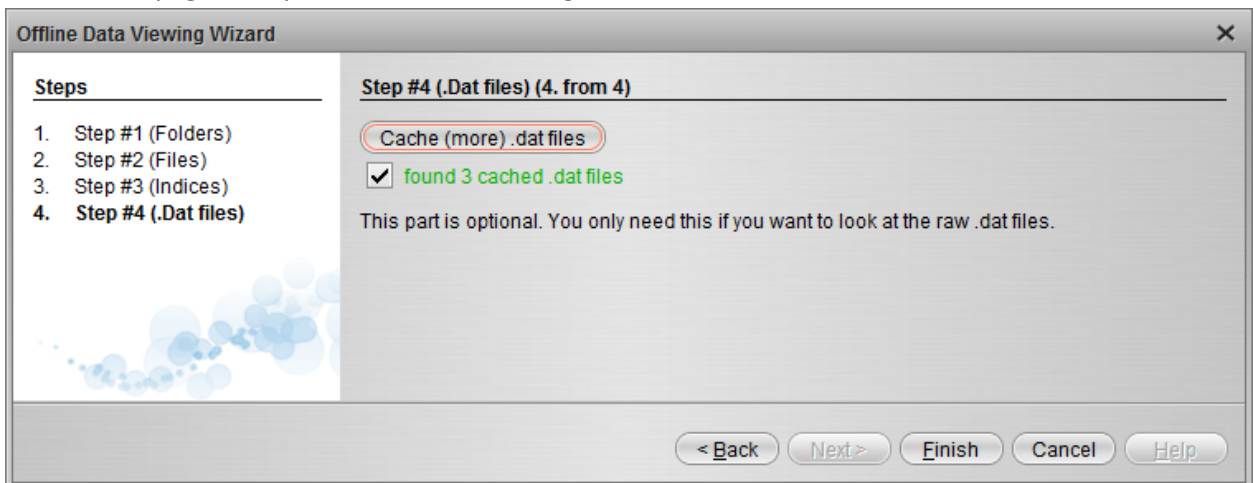
- It will automatically use the latest experiment context information and fill in the paths it has computed based on the rules (you can also use it to check your rules!)
- Start the indexing and caching wizard to see more details: on page 2 you can see if it has all required files:



- Page 3 shows you if you have all indices:

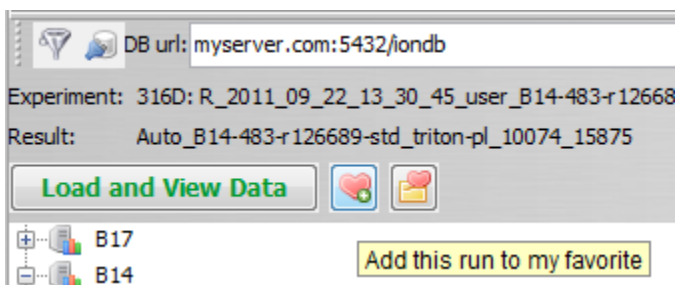


- And the last page is only needed for old non region base .dat file formats



Favorite Run

- If you have a particular run that you often want to look at, you can use the add favorite button to remember this one run:



- The button on the right loads the favorite run