ProteoIDViewer user guide

Version 1.2

21/06/2013

Contents

1 Basic instructions

1.1   To start the viewer and open files

Double-click "run.bat" (windows) or "run.sh" (linux)

File→Open:

Supported input files:

The ProteoIDViewer can be used to visualize mzIdentML format files which either have the extension

.mzid or .mzid.gz (gzipped). Files must be valid with respect to version 1.1 (see Common errors

section). The ProteoIDViewer can also display Omssa (omx format) and X!Tandem files (xml format), which are converted to mzid format internally using the MzidLib library (https://code.google.com/p/mzidentml-lib/).

An extra optional file can be used to load spectrum source file (with file extension .mgf or .mzML). If this is the file you searched, the ProteoIDViewer will be able to link the identification results to each spectrum in the spectrum and peptide panels.

1.2   Viewing data

The input file can be visualized using multiple tabs view. The first tab will visualize all protein groups identified, plus individual proteins within those groups and links to the supporting peptide evidence for each identification. The second tab visualizes ranked identifications for each input spectrum, including peptide fragmentation data. The third tab visualizes all peptides identified, and the possible protein mappings for each peptide. The fourth tab visualizes global statistics include the total count of PSMs and proteins identified, statistics such as false discovery rate (FDR) if a decoy database search has been performed and graphs showing various statistics. The fifth tab displays all protein sequence records contained within the file. The sixth tab displays the search parameters for the peptide and protein identification stages.

2 Common problems

2.1   Out of memory error

If you are trying to visualise large files, you may need to edit the amount of memory available to Java. Do this by editing the "run.bat" or "run.sh" in a plain text editor, such as Notepad++.

java -Xms1024m -jar ProteoIDViewer.jar

Change to (for example):

java –Xms3072m -jar ProteoIDViewer.jar

The upper-limit of this number is controlled by your operating system and memory available on your PC.

2.2 Incorrect file format

If you attempt to load a file that is not valid mzIdentML version 1.1, an error will result. If you suspect this may be the problem, please validate your file using the mzidValidator: http://code.google.com/p/psi-pi/downloads/list

2.3 Reporting errors and getting help

If you have ensured that your input files are valid and that you are not getting an out of memory error, please log a report on the issues list: http://code.google.com/p/mzidentml-viewer/issues/list, including a description of what you were trying to do and the zipped file you were viewing.