Quick-start Guide

- 1. Download & install Python2.7: https://www.python.org/ftp/python/2.7.9/python-2.7.9.msi
- 2. Download & install isobarQuant https://github.com/protcode/isob/archive/master.zip, following given installation instructions
- 3. Place all .raw files to be analyzed into a local directory (for quickest results). It will work over a network but will be slower as data is transferred across the network.
- 4. Set the number of threads to desired value (preMascot.cfg & postMascot.cfg)
- 5. Run preMascot workflow (default values are given for TMT, iTRAQ, 8TRAQ, SILAC [up to three colours], dimethyl & hyperdimethyl are preconfigured in the file QuantMethod.cfg)

for TMT10 rawfiles in c:\vehicle_1 folder:

C:\isobarQuant>python preMascot.py --datadir c:\vehicle_1 --quant TMT10

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for SILAC rawfiles in c:\vehicle_1 folder:

C:\isobarQuant>python preMascot.py --datadir c:\vehicle_1 --quant SILAC3

6. Open Mascot Daemon, set up search parameters, edit 'External processes', in 'After each search' section. Add the following (on one line), replacing 'mymascotserver' with the URL to your Mascot server. Keep <resultfilepath> and <resultfilename> exactly as given below.

python C:\isobarQuant\CommonUtils\getDatFiles.py <resultfilepath> <resultfilename> http://mymascotserver/mascot/cgi/ c:\vehicle_1

Start Mascot Daemon running; once complete, all results files should be in the folder 'c:\vehicle_1'

7. Run the post-Mascot workflow:

for all files (.dat / .hdf5 files) in c:\vehicle_1 folder:

C:\isobarQuant>python postMascot.py --datadir c:\vehicle 1 --mergeresults yes