

# MetaboKit

October 28, 2020

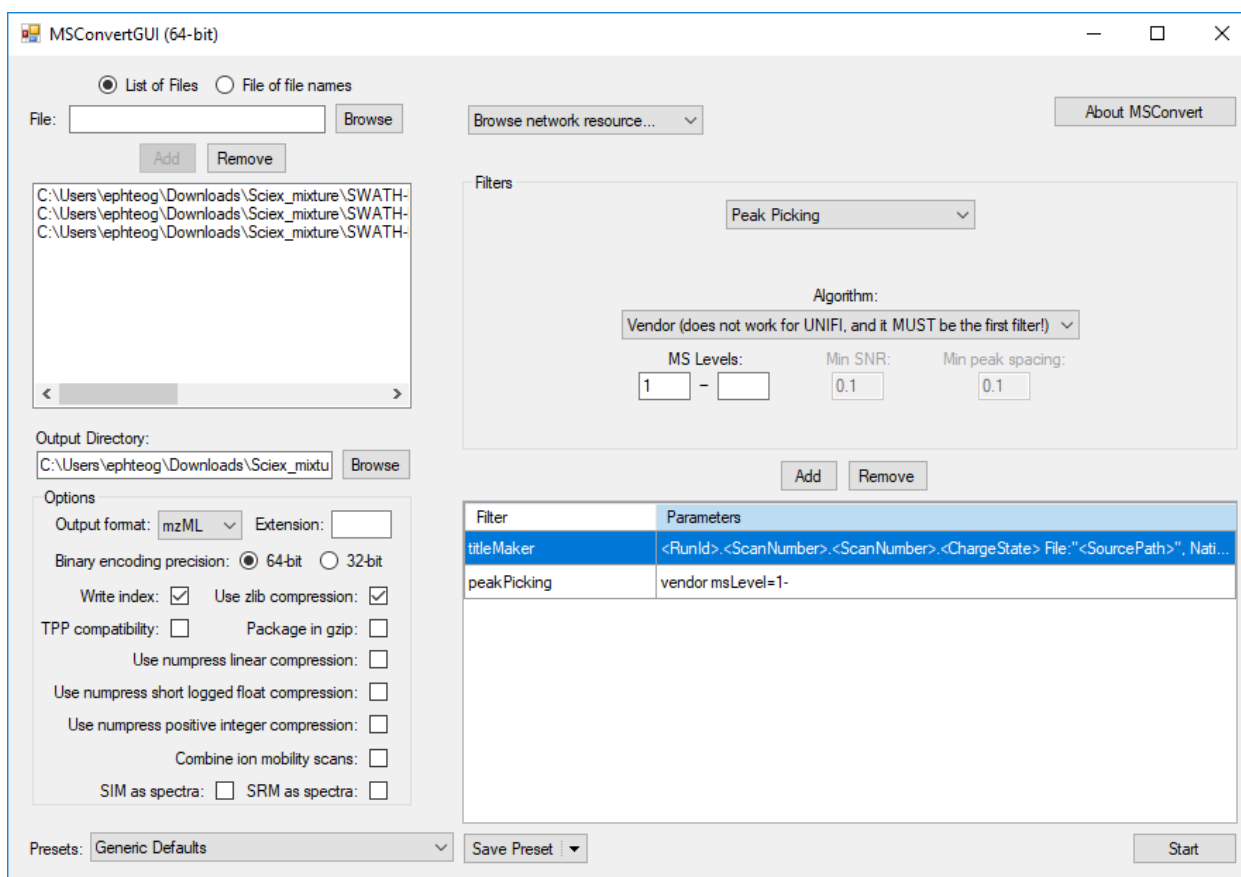
## 1 Installation

Executables for all three major platforms (OS X, Windows, linux) are included.

## 2 Raw Data Conversion into mzML

The input files need to be in mzML format for MetaboKit. MSConvert, provided through the ProteoWizard software suite, enables conversion of proprietary raw data files (.wiff for SCIEX, .raw files for Thermo Fisher instruments) into mzML.

1. Download and install a recent version ProteoWizard on a Windows computer.
2. Start the software by opening the Start Menu, type “MSConvert” in the search field and click on “MSConvert”.
3. In the MSConvert window, use the “Browse” button to select the raw files to be converted (the .wiff and .wiff.scan files need to be located in the same folder). Select “mzML” for “Output format”, “64-bit” for “Binary encoding precision”, check “Write index” and “Use zlib compression” checkbox. “Peak Picking” filter should be added (see figure below).



### 3 Input Parameters

Input parameters must be specified according to the user's preference for various aspects of the data processing. Input parameters are to be specified in the "param.txt" file.

MetaboKit requires that the user provide the following options for data processing:

- **mzML\_files**: Names of the centroided mzML files. Use "\*.mzML" to select all mzML files in the folder.
- **num\_threads**: Number of threads to use
- **length\_of\_ion\_chromatogram**: range of ion chromatogram of feature in seconds
- **MS2\_score**: Minimum dot product score for match between library spectra and experimental spectra
- **ms1\_ppm**: MS1 ppm tolerance (e.g. 15)
- **ms2\_ppm**: MS2 ppm tolerance (e.g. 30)
- **library**: External libraries to be used for analysis

- **ISF\_rt\_diff**: Retention time difference between parent and fragment
- **RT\_shift**: Maximum allowable RT shift
- **min\_peaks**(DDA only): Minimum number of matching peaks between library spectra and experimental spectra
- **ISF\_score**(DDA only): Minimum dot product score for match between parent spectra and fragment spectra
- **adduct**(DDA only): Adducts to be considered for identification in the data
- **pfcor**(DIA only): precursor-fragment ion chromatogram correlation threshold
- **rt\_diff**(DIA only): Retention time difference between library entry and feature in the DIA sample
- **topNfrag**(DIA only): Number of high intensity fragments in library entry to score against DIA sample
- **ms2\_auc\_w/o\_feature**(DIA only): Fragment-level quantitation if MS1 feature not detected
- **window\_setting**(DIA only): DIA MS/MS window setting

## 4 Analysis Output Table

- **quant\_...All.txt** A table of MS1-based or MS2-based quantification.
- **ann\_...All.txt**(DDA only) This file contains the information of compounds identified and corresponding spectra. This file will be used as rt-annotated library in SWATH DIA extraction
- **una\_...mzML.txt**(DDA only) This gives information of non-matched spectra

## 5 Example

The example datasets are located in the “example” folder.

## 5.1 Library generation from DDA and DDA quantitation

The data folder with all DDA mzML files and param.txt file.

```
C:\Users\ephteog\Downloads\standards_example>dir
Volume in drive C is WINDOWS
Volume Serial Number is 805C-0F96

Directory of C:\Users\ephteog\Downloads\standards_example

29/08/2019  12:51 PM    <DIR>          .
29/08/2019  12:51 PM    <DIR>          ..
31/07/2019  12:51 PM                886 param.txt
05/07/2019  03:12 PM    126,755,018 SWATH-POS-MODE-PathwayMetabolites_PosIDA-1.wiff.mzML
05/07/2019  03:12 PM    127,658,748 SWATH-POS-MODE-PathwayMetabolites_PosIDA-2.wiff.mzML
05/07/2019  03:13 PM    128,593,806 SWATH-POS-MODE-PathwayMetabolites_PosIDA-3.wiff.mzML
            4 File(s)      383,008,458 bytes
            2 Dir(s)  1,264,493,162,496 bytes free

C:\Users\ephteog\Downloads\standards_example>
```

First, run the feature detection executable.

```
C:\Users\ephteog\Downloads\standards_example>..\metabokit_dda\DDAfeature.exe_
```

Next, MS/MS spectra scoring.

```
C:\Users\ephteog\Downloads\standards_example>..\metabokit_dda\DDAscore.exe
```

Next, features and annotations are aligned between samples.

```
C:\Users\ephteog\Downloads\standards_example>..\metabokit_dda\DDAalign.exe
```

## 5.2 DIA

The data folder should contain all DIA mzML files and param.txt file, in addition copy “ann...All.txt” from DDA output to this folder.

First, run the feature detection executable.

```
C:\Users\ephteog\Downloads\calibration_example>..\metabokit_dia\DIAscore.exe_
```

Next, MS/MS spectra scoring.

```
C:\Users\ephteog\Downloads\calibration_example>..\metabokit_dia\DIAscore.exe
```

Next, features and annotations are aligned between samples.

```
C:\Users\ephteog\Downloads\calibration_example>..\metabokit_dia\DIAalign.exe_
```

## 6 Example “param.txt”

### 6.1 DDA

```
mzML_files
*.mzML

num_threads
3

length_of_ion_chromatogram
3 50

ISF_rt_diff
2

ISF_score
.5

MS2_score
.5

min_peaks
2

RT_shift
10

library
msdial
#hmdb
#nist
LipidBlast
LipidBlast-fork

adduct
M      0 1+
M+H    1.007825 1+
M+2H   2.014102 2+
M+Na   22.98977 1+
M+NH4  18.03437 1+
M+K    38.96371 1+
```

M+Li 7.016004 1+  
#M-H -1.007825 1-  
#M-2H -2.014102 2-  
#M+HCOO 44.99765 1-  
#M+Na-2H 20.97412 1-  
#M+Cl 34.96885 1-

ms1\_ppm  
15

ms2\_ppm  
30

## 6.2 DIA

mzML\_files  
\*.mzML

num\_threads  
3

length\_of\_ion\_chromatogram  
3 50

library  
metabokit

ms1\_ppm  
15

ms2\_ppm  
30

ISF\_rt\_diff  
2

rt\_diff  
10

topNfrag

6

MS2\_score

0.5

pfcor

0.5

ms2\_auc\_w/o\_feature

1

RT\_shift

10

#30

window\_setting

40 70

69 100

99 130

129 160

159 190

189 220

219 250

249 280

279 310

309 340

339 370

369 400

399 430

429 460

459 490

489 520

519 550

549 580

579 610

609 640

639 670

669 700

699 730

729 760

759 790

789 820

819 850  
849 880  
879 910  
909 940  
939 970  
969 1000

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