

The TargetSearch Package

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October 18, 2010

This document describes how to use *TargetSearch* to preprocess GC-MS data.

1 Supplied Files

This section describes the files that have to be prepared before running *TargetSearch*. These comprise a sample definition file, a reference library file and a retention marker definition file. Throughout this manual, we will use the example files provided by the package *TargetSearchData*.

1.1 NetCDF Files and Sample File

TargetSearch can currently read only NetCDF files. Many GC-MS software packages are able to convert raw chromatograms to NetCDF. Although some baseline correction functionality is included in *TargetSearch*, it is recommended to baseline correct your chromatograms before exporting to NetCDF to increase processing speed. Please refer to your software documentation for further details.

Export the NetCDF files into a convenient location. Then prepare a tab-delimited text file describing your samples. It must contain (at least) the two columns entitled: “CDF_FILE” and “MEASUREMENT_DAY”. Other columns such as sample name, sample group, treatment, etc. may be additionally included to aid sample sub-setting and downstream analyses. An example is shown in table 1.

To import the sample list into R, use the function `ImportSamples()` specifying the options *CDFpath* (directory containing the NetCDF files) and *RIpath* (directory where the transformed cdf files, containing the retention index corrected apex data, also called RI-files, will be saved).

CDF_FILE	MEASUREMENT_DAY	TIME_POINT
7235eg08.cdf	7235	1
7235eg11.cdf	7235	1
7235eg26.cdf	7235	1
7235eg04.cdf	7235	3
7235eg30.cdf	7235	3
7235eg32.cdf	7235	3
...		

Table 1: Sample file example, “samples.txt”

```
> library(TargetSearchData)
> library(TargetSearch)
> cdf.path <- system.file("gc-ms-data", package = "TargetSearchData")
> sample.file <- file.path(cdf.path, "samples.txt")
> samples <- ImportSamples(sample.file, CDFpath = cdf.path, RIpath = ".")
```

Alternatively, you could create a `tsSample` object by using the sample class methods.

```
> cdffiles <- dir(cdf.path, pattern="cdf$")
> # define the RI file names
> rfiles <- paste("RI_", sub("cdf","txt", cdffiles), sep = "")
> # take the measurement day info from the cdf file names.
> days <- sub("^([[[:digit:]]+).*$", "\\1", cdffiles)
> # sample names
> smp_names <- sub("\\.cdf", "", cdffiles)
> # add some sample info
> smp_data <- data.frame(CDF_FILE =cdffiles, GROUP = gl(5,3))
> # create the sample object
> samples <- new("tsSample", Names = smp_names, CDFfiles = cdffiles,
+             CDFpath = cdf.path, RIpath = ".", days = days,
+             Rfiles = rfiles, data = smp_data)
```

1.2 Retention Time (RI) Markers

To align different chromatograms using RI markers, a tab-delimited definition file for these markers has to be provided. At a minimum it should contain three columns specifying the search window (lower and upper threshold) and the fixed standard value for each marker (table 2). Further, a characteristic ion mass (m/z) has to be provided either in an additional column or as an argument *mass* to function `ImportFameSettings()`.

```
> rim.file <- file.path(cdf.path, "rimLimits.txt")
> rimLimits <- ImportFameSettings(rim.file, mass = 87)
```

LowerLimit	UpperLimit	RIstandard
230	280	262320
290	340	323120
350	400	381020

Table 2: Retention time definition file example, “rimLimits.txt”

This will import the limits in “rimLimits.txt” file and set the marker mass to 87 for all markers.

If you do not use RI markers, you can skip this part by setting the parameter *rimLimits* to NULL in `RIcorrect` function. Please note that in this case, no retention time correction will be performed.

2 Baseline correction, peak identification and RI correction

Initially, *TargetSearch* identifies the local apex intensities in all chromatograms, finds the retention time (RT) of the RI markers and converts RT to RI using linear interpolation (Van den Dool and Kratz, 1963). This is done by the function `RIcorrect()`. Parameter to this function are sample and retention time limits objects, the mass range to extract (*MassRange* = *c(85,500)*), the intensity threshold (*IntThreshold* = 10), the peak picking method (*pp.method*) and a *Window* parameter that will be used by said method. The function will return a matrix with the retention times of all RI markers and create a tab-delimited file (RI file) for each chromatogram in the specified directory. These files contain the extracted peak list of the respective NetCDF file.

```
> RImatrix <- RIcorrect(samples, rimLimits, massRange = c(85,500),
+                       IntThreshold = 10, pp.method = "smoothing", Window = 7)
```

There are two peak picking methods available: “smoothing” implements the algorithm used by Tagfinder Luedemann et al. (2008), while the “ppc” algorithm is a adapted based on the function `ppc.peaks` from the package *ppc*. `ppc.peaks` searches for local maxima within a given time window. Therefore the *Window* parameter sets the window size of the chosen peak picking method.

In case the chromatograms were not baseline corrected by the platform specific GC-MS software, it is possible to achieve that in *TargetSearch* by setting *baseline* to TRUE in function `RIcorrect()` which calls the function `baselineCorrection()`. This algorithm is based on the work of Chang et al. (2007) and a description is found in the `baselineCorrection()` documentation. Some options can be passed to `baselineCorrection()` via *baseline.opts*.

After that, it is possible to check for outliers in the samples by using the function `FAMEoutliers()`. It creates a PDF report of the RI markers including information

about possible outliers that the user can remove or not. Alternatively, RI markers can be checked manually using the function `plotFAME` (Figure 1).

```
> outliers <- FAMEoutliers(samples, RImatrix, threshold = 3)
```

```
Outliers Report:
```

```
=====
```

```
No outliers were found.
```

Here, *threshold* sets the number of standard deviations a value has to be away from the mean before it will be considered an outlier. In this example, however, no outliers were detected.

```
> plotFAME(samples, RImatrix, 1)
```

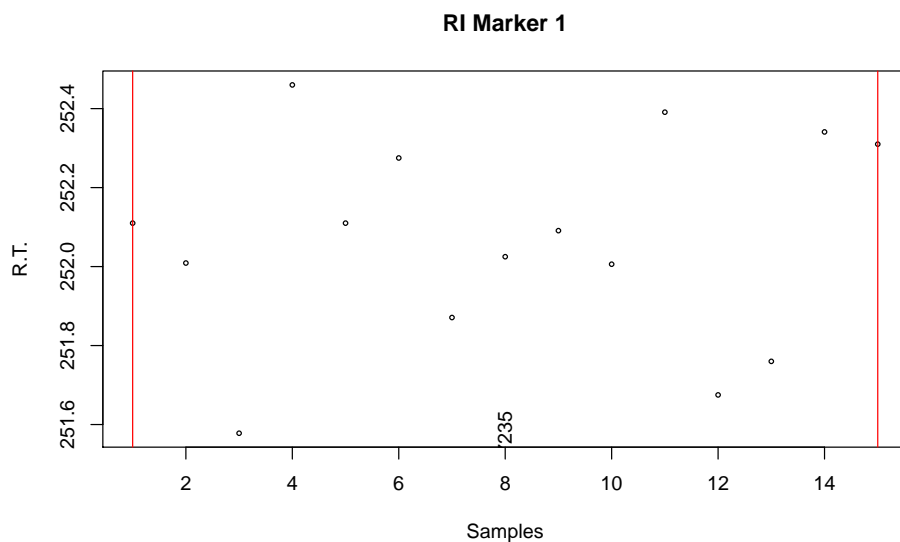


Figure 1: Retention Index Marker 1.

3 Library Search

3.1 Reference Library File

The “reference library” file contains the information of the metabolites or mass spectral tags (MSTs) that will be searched for in the chromatograms. A public spectra database

could be found here <http://csbdb.mpimp-golm.mpg.de/csbdb/gmd/gmd.html> at *The Golm Metabolome Database* (Kopka et al., 2005).

Required information is the metabolite name (“Name”), expected retention time index (“RI”), selective masses (“SEL_MASS”), most abundant masses (“TOP_MASS”), spectrum (“SPECTRUM”) and RI deviations (“Win_1”, “Win_2”, “Win_3”). See example in table 3. The columns “Name” and “RI” are mandatory and you have at least to include one of the columns “SEL_MASS”, “TOP_MASS” or “SPECTRUM” in the file (see below). The RI deviation columns are optional.

Name	RI	Win_1	SEL_MASS	SPECTRUM
Pyruvic acid	222767	4000	89;115;158;174;189	85:7 86:14 87:7 88:5 8...
Glycine (2TMS)	228554	4000	86;102;147;176;204	86:26 87:19 88:8 89:4...
Valine	271500	2000	100;144;156;218;246	85:8 86:14 87:6 88:5 8...
Glycerol (3TMS)	292183	2000	103;117;205;293	85:14 86:2 87:16 88:13...
Leucine	306800	1500	102;158;232;260	158:999 159:148 160:45...
Isoleucine	319900	1500	102;103;158;163;218	90:11 91:2 92:1 93:1 9...
Glycine	325000	2000	86;100;174;248;276	85:6 86:245 87:24 88:12...

Table 3: Reference Library example, “library.txt”

In this file, masses and intensities must be positive integers. RIs and RI deviations can be any positive real number. The selective and most abundant masses list must be delimited by semicolon (;). The spectrum is described by a list of mass and intensity pair. Every mass-intensity pair is separated by colon (:) and different pairs are separated by spaces.

The function `ImportLibrary()` imports the reference file.

```
> lib.file <- file.path(cdf.path, "library.txt")
> lib      <- ImportLibrary(lib.file, RI_dev = c(2000,1000,200),
+                          TopMasses = 15, ExcludeMasses = c(147, 148, 149))
```

Here we set the RI window deviations to 2000, 1000 and 200 RI units. Since “Win_1” column is already in the file, the first value (2000) is ignored. Also, the 15th most abundant masses are taken but excluding the masses 147, 148 and 149 (common confounding masses)

3.2 Library Search Algorithm

The library search is performed in three steps. First, for every metabolite, selective masses are searched in a given time window around the expected RI. This is done by the function `medianRILib()`. This function calculates the median RI of the selective masses and return new library object with the updated RI. The time deviation is given either in the library file (column “Win_1”) or when the library is imported (see `ImportLibrary()`).

```
> lib <- medianRILib(samples, lib)
```

It is also possible to examine visually the RI deviation of the metabolites by setting the parameter `makeReport=TRUE`, which creates a pdf report like the one shown in figure 2. This may help to set or update the expected RI deviation.

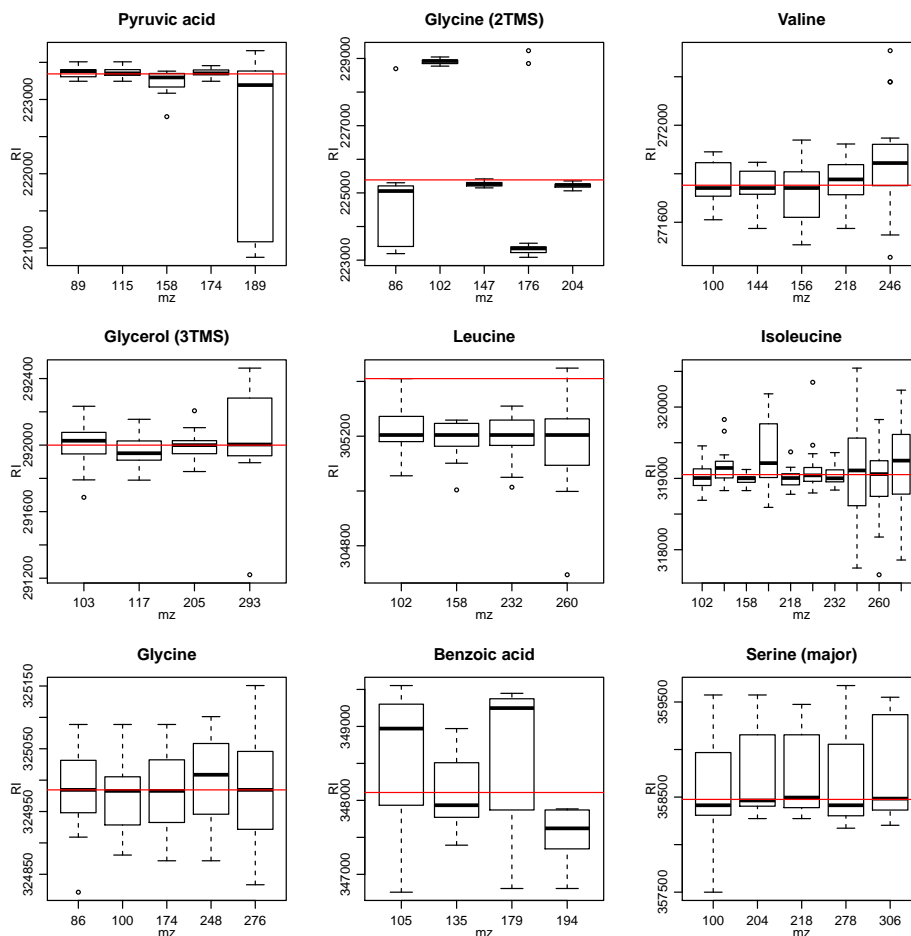


Figure 2: RI deviation of first 9 metabolites in the library.

In the second step, the function `sampleRI()` searches the selective masses again, but using the updated RI and the RI deviation defined in the library object (“Win_2”). After that, the intensities of the selected masses are normalised to the median of the day, and then used to extract other masses with correlated apex profiles. The masses for which the Pearson correlation coefficient is above `r_thres` are taken as metabolite markers and their RIs are averaged on a per sample basis. This average RI represents the exact position where the metabolite elutes in the respective sample, which is returned in a matrix form.

```
> cor_RI <- sampleRI(samples, lib, r_thres = 0.95,
+                     method = "dayNorm")
```

The third step will look up for all the masses (selective and most abundant masses) in all the samples. This is done by the function `peakFind()`. It returns a *tsMSdata* object with the intensities and RI of every mass (rows) and every sample (columns) that were search for.

```
> peakData <- peakFind(samples, lib, cor_RI)
```

The intensity and RI slots can be accessed by using the *Intensity* and *retIndex* methods. Each slot is a list, where every component of the list is a matrix, which is related to a metabolite in the library. There should be as many components as metabolites in the library. In every matrix, columns are samples and rows are masses.

```
> met.RI <- retIndex(peakData)
> met.Intensity <- Intensity(peakData)
> # show the intensity values of the first metabolite.
> met.Intensity[[1]]
```

	7235eg04	7235eg06	7235eg07	7235eg08	7235eg09	7235eg11
89	3185	7974	3211	3544	9475	2172
115	1811	4279	1652	1924	5138	1081
158	NA	1162	400	458	1139	288
174	5840	14031	5690	6414	16970	3928
189	NA	200	NA	101	250	NA
99	1131	3034	1191	1260	3658	753
100	1021	2672	1037	1046	3074	630
175	762	1828	731	795	2307	467
117	359	957	342	380	1208	225
90	NA	729	NA	301	855	170
176	239	547	234	232	729	149
116	271	1305	NA	NA	1012	155
114	153	338	133	150	455	96
101	130	NA	158	182	469	83
91	178	411	172	168	503	103
	7235eg12	7235eg15	7235eg20	7235eg21	7235eg22	7235eg25
89	9373	9873	11701	3245	10407	2738
115	5112	5460	6384	1819	5662	1488
158	1122	1214	1451	410	1229	NA
174	16852	17885	20963	5826	18655	5135
189	237	248	292	88	293	65
99	3621	3793	4471	1193	3945	1027
100	3136	3269	3876	1058	3408	NA
175	2265	2443	2831	725	2501	661
117	1214	1259	1451	NA	1350	303
90	865	977	1111	252	961	241
176	729	758	926	237	780	NA
116	1185	1262	1451	NA	1193	322

114	413	439	520	135	483	NA
101	507	528	666	153	516	130
91	490	592	624	213	525	103
	7235eg26	7235eg30	7235eg32			
89	1577	2330	460			
115	822	1311	253			
158	NA	325	NA			
174	2971	4425	909			
189	31	44	NA			
99	580	867	183			
100	446	696	170			
175	354	528	122			
117	138	264	39			
90	NA	215	56			
176	100	192	NA			
116	121	194	44			
114	NA	115	31			
101	NA	118	43			
91	121	134	44			

4 Metabolite Profile

The function `Profile` makes a profile of the MS data by averaging all the normalised mass intensities whose Pearson coefficient is greater than r_thresh .

```
> MetabProfile <- Profile(samples, lib, peakData, r_thres = 0.95,
+                          method = "dayNorm")
```

A *msProfile* object is returned. The averaged intensities and RI matrices that can be obtained by *Intensity* and *retIndex* methods. The profile information is represented by a *data.frame* in the *info* slot (accessible by *profileInfo* method). The columns are:

Name The metabolite/analyte name.

Lib_RI The expected RI (library RI).

Mass_count The number of correlating masses.

Non_consecutive_Mass_count Same as above, but not counting the consecutive masses.

Sample_Count_per_Mass The number of samples in which a correlating mass was found. The numbers are separated by semi-colon (;) and each number corresponds to one correlating masses (same order). If all the numbers are the same, only that unique number is shown.

Masses The correlating masses.

RI The average RI.

Score_all_masses The similarity score calculated using the average intensity of all the masses that were searched for, regardless of whether they are correlating masses.

Score_cor_masses Same as above, but only correlating masses are considered.

As metabolites with similar selective masses and RIs can be present in metabolite libraries, it is necessary to reduce redundancy. This is performed by the function `ProfileCleanUp` which selects peaks for which the RI gap is smaller than `timeSplit` and computes the Pearson correlation between them. When two metabolites within such a time-group are tightly correlated (given by `r_thres`) only the one with more correlated masses is retained.

```
> finalProfile <- ProfileCleanUp(MetabProfile, timeSplit = 500,  
+                               r_thres = 0.95)
```

The function returns a `msProfile` object. The `info` slot is similar as described above, but extra columns with a “Cor_” prefix (e.g., “Cor_Name”) are included. They provide information about metabolite redundancy.

5 Peaks and Spectra Visualisation

Finally, it may be of interest to check the chromatographic peak of selected metabolites and compare the median spectra of the metabolites, i.e., the median intensities of the selected masses across all the samples, with the reference spectra of the library. There are two functions to do so: `plotPeak` and `plotSpectra`.

For example, we can compare the median spectrum of “Valine” against its spectrum reference. Here we look for the library index of “Valine” and plot the spectra comparison in a “head-tail” plot (figure 3).

To look at the chromatographic peak of “Valine” in a given sample, we use the functions `peakCDFextraction` to extract the raw chromatogram and `plotPeak` to plot the peak (figure 4).

Refer to the documentation of the functions `plotPeak` and `plotSpectra` for further options not covered here.

6 TargetSearch GUI

We provide a graphical user interface intended to facilitate the use of `TargetSearch` for users unfamiliar with R. Many parameters that would be set calling the individual `TargetSearch` functions as described in this document can be set here “in one go” before running the complete analysis. A screenshot of the GUI is shown in figure 5.

```
> grep("Valine", libName(lib))  
[1] 3  
> plotSpectra(lib, peakData, libId = 3, type = "ht")
```

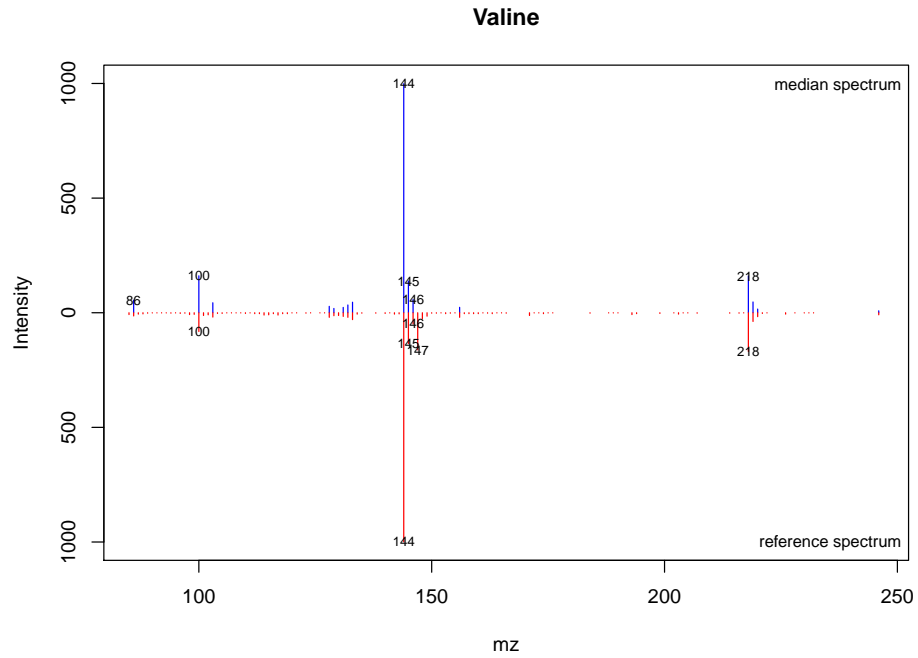


Figure 3: Spectra comparison of “Valine”

```

> top.masses <- topMass(lib)[[3]]
> # we select the first sample
> sample.id <- 1
> cdf.file <- file.path(cdf.path, cdffiles[sample.id])
> rawpeaks <- peakCDFextraction(cdf.file, massRange = c(85,500))
> plotPeak(rawpeaks, time.range = libRI(lib)[3] + c(-2000,2000),
+ masses = top.masses, userRI = TRUE, rimTime = RImatrix[,sample.id],
+ standard = rimStandard(rimLimits), massRange = c(85, 500),
+ main = "Valine")

```

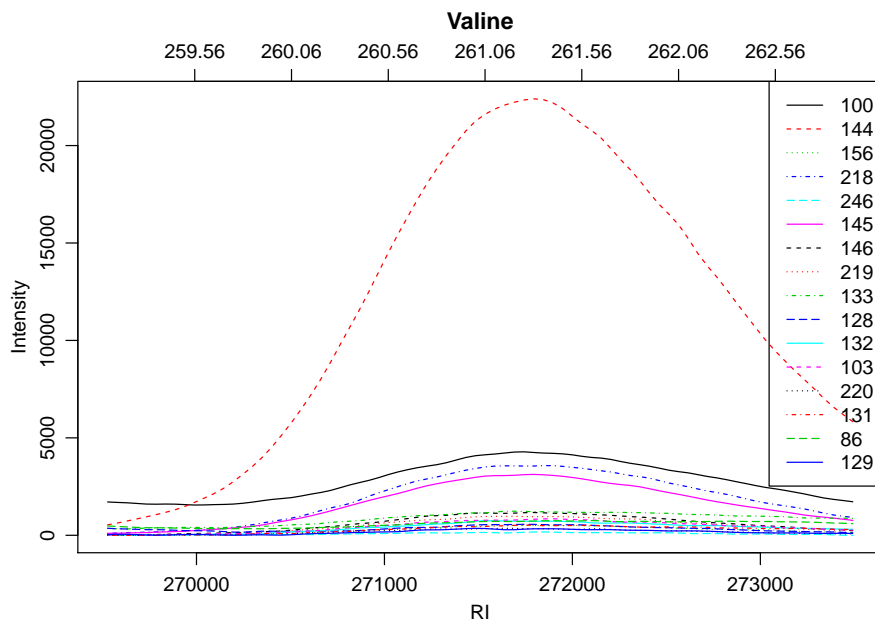


Figure 4: Chromatographic peak of Valine.

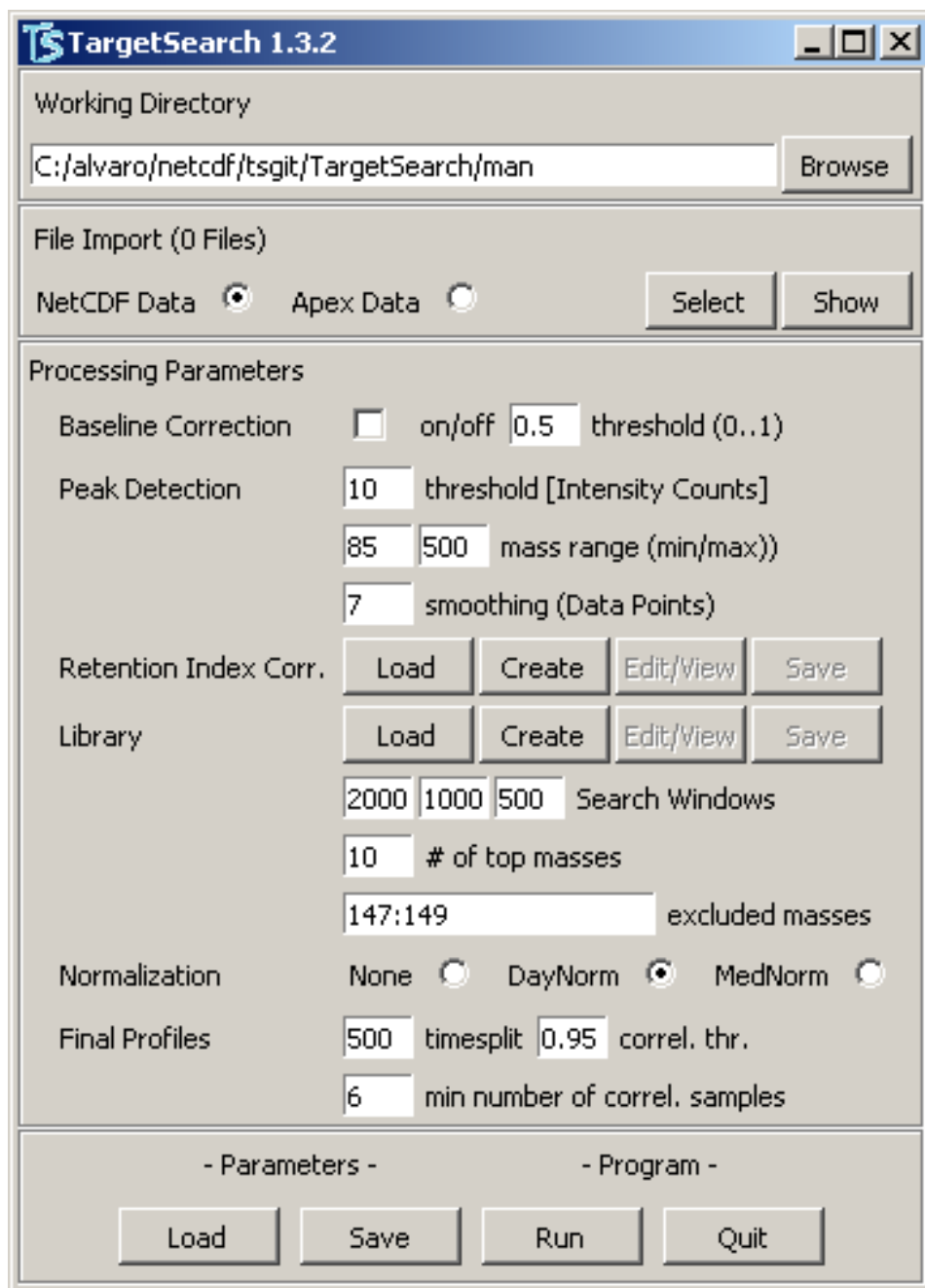


Figure 5: The *TargetSearch* GUI.

This is a description of all the GUI options.

Working Directory : Use the *Browse*-button to select the folder on your hard drive containing all your GC-MS data files. The output of *TargetSearch* will be written to this folder too.

File Import : Clicking *NetCDF Data* or *Apex Data* radio buttons will open a file select dialog. Choose the files you would like to be processed. You may check your selection pressing the *Show*-button.

Baseline Correction : Clicking *on/off* button will perform baseline correction before peak detection. If selected, the *threshold* parameter is a numeric value between 0 and 1. A value of one returns a baseline above the noise, 0.5 in the middle of the noise and 0 below the noise. See `baselineCorrection` documentation for further details.

Peak Detection : *Intensity Counts threshold* defines the minimum apex intensity incorporated in the analysis. A value of 1 would include all peaks. *Mass Range* allows to limit the mass values (m/z) to be included in the analysis. *Smoothing* averages raw data to eliminate some inherent noise leading to multiple peaks otherwise.

Retention Index Correction : Retention Index Correction is necessary and applied only if you supply NetCDF Data (Apex Data contain already Retention Indices). You may *Load* or *Create* the search windows for your RI-Markers here.

Library : A Library (to detect metabolites) usable by *TargetSearch* contains at least information about the metabolite 'Name', its expected 'RI' and the selective masses in its spectrum 'SEL_MASS'. You may *Load* or *Create* one yourself using the respective buttons. A more detailed description of the file formats can be found in `ImportLibrary`. *Search Windows* refers to the allowed RI deviation of your metabolites which are narrowed in 3 consecutive searches. *No. of top masses* is the number of most abundant masses that will be selected from the spectra, besides the selected masses. *ExcludeMasses* is only used when masses are obtained from the spectra. For example, "126,147:149,160" means that the masses 126, 147, 148, 149, and 160 will be excluded from the analysis (unless they are used as selected masses).

Normalization : This selects how the data will be normalized during the metabolite search. Options are *dayNorm*, a day based median normalization, *medianNorm*, normalization using the median of all the intensities of a given mass, and *none*, no normalization at all.

Final Profiles : Here you may set the parameters used by the functions `Profile` and `ProfileCleanUp`. *timesplit* sets an RI window that will be used to look

for metabolites that could have been redundantly identified. *correl. thr.* is the correlation threshold and *min. number of correlation samples* is a threshold used to make sure that correlations are computed with at least said number of observations.

Parameters : You may *Save* the current parameters as an *.RData file or *Load* previously saved parameters to compare the outcome of different settings or just repeat the analysis.

Program : *Run* starts to process all currently selected files using the current parameters and saving output to *Working Directory*. *Quit* closes the GUI.

7 Untargeted search

Although *TargetSearch* was designed to be targeted oriented, it is possible to perform untargeted searches. The basic idea is to create a library that contains evenly distributed “metabolites” in time and every “metabolite” uses the whole range of possible masses as selective masses. An example:

```
> metRI    <- seq(200000, 300000, by = 5000)
> metMZ    <- 85:250
> metNames <- paste("Metab",format(metRI,digits=6), sep = "_")
```

Here we define a set of metabolites located every 5000 RI units from each other in the RI range 200000-300000, with selective masses in the range of 85-300, and assign them a name. After that, we create an `tsLib` object.

```
> metLib   <- new("tsLib", Name = metNames, RI = metRI,
+               selMass = rep(list(metMZ), length(metRI)), RIdev = c(3000, 1500, 500))
```

Now we can use this library object to perform a targetive search with this library on the *E. coli* samples as we did before.

```
> metLib <- medianRILib(samples, metLib)
> metCorRI <- sampleRI(samples, metLib)
> metPeakData <- peakFind(samples, metLib, metCorRI)
> metProfile <- Profile(samples, metLib, metPeakData)
> metFinProf <- ProfileCleanUp(metProfile, timeSplit = 500)
```

The `metFinProf` object can be used to create a new library by taking only the metabolites that have, for example, more than 5 correlating masses and using the correlating masses as selective ones.

```
> sum( profileInfo(metFinProf)$Mass_count > 5)
[1] 12
```

```

> tmp <- profileInfo(metFinProf)$Mass_count > 5
> metRI <- profileInfo(metFinProf)$RI[tmp]
> metNames <- as.character( profileInfo(metFinProf)$Name[tmp] )
> metMZ <- sapply(profileInfo(metFinProf)$Masses[tmp],
+               function(x) as.numeric(unlist(strsplit(x,";")))) )
> metLib <- new("tsLib", Name = metNames, RI = metRI,
+             selMass = metMZ, RIddev = c(1500, 750, 250))

```

After the new library object is created, the process can be repeated as shown above.

Finally, by using the function `writeMSP`, it is possible to export the spectrum of the unknown metabolites to MSP format used by NIST mass spectra search (<http://www.nist.gov/srd/mslist.htm>), so the unknown spectra can be search against known metabolite spectra databases.

References

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