On Finding putative PTM (pPTM) Marker Ion in HCD scans using `PTM_MarkerFinder`

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Abstract

Glycopeptides as well as acetylated, methylated and other modified peptides release specific fragment ions during CID (collision-induced dissociation) and HCD (higher energy collisional dissociation) fragmentation. These fragment ions can be used to validate the presence of the PTM (post translational modifications) on the peptides. `PTM_MarkerFinder`, an R function of the **protViz** package that takes advantage of such marker ions. `PTM_MarkerFinder` scans the MS/MS spectra in the output of a peptide spectrum match search, e.g., Mascot, for marker ions specific for selected PTMs.

While the software tool has been described by Nanni, Panse, Gehrig, Mueller, Grossmann, and Schlapbach (2013) here we provide a step-by-step guide on how the software can be used.

Keywords: MarkerFinder, putative post translational modifications, R.

1. Howto get the software and data

The method for finding the marker ions is contained in the R package **protViz** available through CRAN using https://cran.r-project.org/package=protViz. The package requires R (R Development Core Team 2008) installed.

The minimal data structure requirement for the `PTM_MarkerFinder` function looks as follow.

```
R> library(protViz)
R> data(HexNAc)
R> str(HexNAc[[1]], nchar.max = 30)

List of 12
 $ peptideSequence   : chr "STMQELNSR"
 $ mascotScore       : num 49.5
 $ modification      : chr "00000000000"
 $ MonoisotopicAAmass: num [1:9] 0 0 0 0 0 0 0 0 0
 $ proteinInformation: chr "zz|ZZ_FGCZCont0219|"
 $ title             : chr "NGlycoFASP_NH"| __truncated__
```

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```
$ pepmass           : num 533
$ charge            : num 2
$ scans             : num 2659
$ rtinseconds       : num 1846
$ mZ                : num [1:150] 101 104 105 110 112 ...
$ intensity         : num [1:150] 369.3 2860 37.3 103.8 190.7 ...
```

Here we have listed the `HexNAc` data which is included in **protViz**.

protViz also provides and perl script `protViz_mascotDat2RData.pl`[1] taking mascot server dat files as input and producing RData output.

```
$ /usr/local/lib/R/site-library/protViz/exec/protViz_mascotDat2RData.pl \
  -d=/usr/local/mascot/data/20130116/F178287.dat \
  -m=$HOME/mod_file
```

`mascotDat2RData.pl` requires the mascot server `mod_file` keeping all the configured modification of the mascot server.

In theory `PTM_MarkerFinder` can process the output of any search engine for peptide identification. It is up to the R user writing a wrapper script converting the output of any particular peptide identification search engine to the data structure listed above.

2. Finding the Marker Ions

2.1. HexNAc – Example

`PTM_MarkerFinder` can search for any Marker ion series. The next lines define the `HexNAc_MarkerIons`.

```
R> HexNAc_MarkerIons <- c(126.05495, 138.05495, 144.06552,
+     168.06552, 186.07608, 204.08665)
```

The lines below configure the modification information used by the search engine. The HexNAc modification below is described on unimod http://www.unimod.org/modifications_view.php?editid1=43.

```
R> ptm.0 <- cbind(AA = "-",
+          mono = 0.0, avg = 0.0, desc = "unmodified", unimodAccID = NA)
R> ptm.1 <- cbind(AA='N',
+          mono = 317.122300, avg = NA, desc = "HexNAc",
+          unimodAccID=2)
R> ptm.2 <- cbind(AA='M',
+          mono = 147.035400, avg = NA, desc = "Oxidation",
+          unimodAccID=1)
R> m <- as.data.frame(rbind(ptm.0, ptm.1, ptm.2))
```

[1] The prefix `protViz_` is used to benefit from the `bash` tab completion.

`PTM_MarkerFinder` is called.

```
R> S <- PTM_MarkerFinder(data = HexNAc,
+          modification = m$mono,
+          modificationName = m$desc,
+          minMarkerIntensityRatio = 3,
+          itol_ppm = 20,
+          mZmarkerIons = HexNAc_MarkerIons)
```

The content of `S` can be seen in the Table below.

scans	mZ	markerIonMZ	markerIonIntensity	markerIonMzError	markerIonPpmError	query	pepmass	peptideSequence	modification
3687	126.06	126.05	9945.00	-0.00	-0.642576494978 98	4	713.36	IMNVTTDSLTK	0001000000000
3687	138.06	138.05	1933.00	-0.00	-2.49175522390729	4	713.36	IMNVTTDSLTK	0001000000000
3687	144.07	144.07	412.30	-0.00	-1.59649326794302	4	713.36	IMNVTTDSLTK	0001000000000
3687	168.07	168.07	810.20	-0.00	-2.36811844277867	4	713.36	IMNVTTDSLTK	0001000000000
3687	204.09	204.09	3273.00	-0.00	-1.74435407225623	4	713.36	IMNVTTDSLTK	0001000000000
2540	126.06	126.05	2945.00	-0.00	-0.825036336847078	6	490.56	HSFNGNQSTFK	0000001000000
2540	138.06	138.05	759.20	-0.00	-10.3725737215287	6	490.56	HSFNGNQSTFK	0000001000000
2540	144.07	144.07	195.40	-0.00	-0.118001850879316	6	490.56	HSFNGNQSTFK	0000001000000
2540	168.07	168.07	262.90	-0.00	-0.916308466469431	6	490.56	HSFNGNQSTFK	0000001000000
2540	186.08	186.08	188.50	-0.00	-2.95577150125756	6	490.56	HSFNGNQSTFK	0000001000000
2540	204.09	204.09	998.40	-0.00	-1.5189603491234	6	490.56	HSFNGNQSTFK	0000001000000
4393	126.06	126.05	13620.00	-0.00	-1.03922824020165	9	891.41	EASGLSDNETEWLK	0000000010000000
4393	138.06	138.05	3798.00	-0.00	-0.420122390602973	9	891.41	EASGLSDNETEWLK	0000000010000000
4393	168.07	168.07	1526.00	-0.00	-0.642606113437682	9	891.41	EASGLSDNETEWLK	0000000010000000
4393	186.08	186.08	1014.00	-0.00	-0.983467730223809	9	891.41	EASGLSDNETEWLK	0000000010000000
4393	204.09	204.09	5041.00	-0.00	-1.06817259804309	9	891.41	EASGLSDNETEWLK	0000000010000000
2739	126.06	126.05	7327.00	-0.00	-0.690174721011021	10	665.59	NA	NA
2739	138.05	138.05	1963.00	-0.00	-0.311470082107949	10	665.59	NA	NA
2739	144.07	144.07	468.60	-0.00	-0.5344787486255	10	665.59	NA	NA
2739	168.07	168.07	624.30	-0.00	-0.642606113437682	10	665.59	NA	NA
2739	204.09	204.09	2496.00	-0.00	-0.622284313992652	10	665.59	NA	NA

Table 1: Result

```
R> summary(S)
```

```
 scans          mZ          markerIonMZ     markerIonIntensity
2540:6   Min.   :126.1   Min.   :126.1   Min.   :  188.5
2739:5   1st Qu.:138.1   1st Qu.:138.1   1st Qu.:  624.3
3687:5   Median :144.1   Median :144.1   Median : 1526.0
4393:5   Mean   :159.5   Mean   :159.5   Mean   : 2838.1
         3rd Qu.:186.1   3rd Qu.:186.1   3rd Qu.: 3273.0
         Max.   :204.1   Max.   :204.1   Max.   :13620.0

markerIonMzError              markerIonPpmError query
Min.   :-0.0014320   -0.642606113437682: 2      10:5
1st Qu.:-0.0003100   -0.118001850879316: 1      4 :5
Median :-0.0001310   -0.311470082107949: 1      6 :6
Mean   :-0.0002436   -0.420122390602973: 1      9 :5
3rd Qu.:-0.0000870   -0.5344787486255  : 1
Max.   :-0.0000170   -0.622284313992652: 1
                     (Other)           :14
   pepmass             peptideSequence           modification
Min.   :490.6   EASGLSDNETEWLK:5      0000000010000000:5
1st Qu.:490.6   HSFNGNQSTFK   :6      0000001000000   :6
Median :665.6   IMNVTTDSLTK   :5      0001000000000   :5
```

```
 Mean   :680.7   NA            :5      NA              :5
 3rd Qu.:713.4
 Max.   :891.4
```

Some overview graphics just an overview of the sample data set `HexNAc`.

```
R> op <- par(mfrow = c(2, 2), mar=c(4, 4, 4, 1))
R> dump <- lapply(split(S, S$query),
+      function(x){
+        plot(x$mZ, x$markerIonIntensity,
+          type = 'h',
+          col = 'lightblue',
+          cex = 2,
+          ylab = 'intensity', xlab='m/z',
+          xlim = range(c(HexNAc_MarkerIons,
+              max(HexNAc_MarkerIons)
+                  + 0.1 * (max(HexNAc_MarkerIons) - min(HexNAc_MarkerIons)),
+              min(HexNAc_MarkerIons)
+                  - 0.1 * (max(HexNAc_MarkerIons) - min(HexNAc_MarkerIons)))),
+          ylim = range(S$markerIonIntensity),
+              log = 'y',
+              main = paste("scan=", unique(x$scans),
+                  "/query=", unique(x$query), sep=''));
+              text(x$mZ, x$markerIonIntensity,
+                  round(x$mZ,2),col='red',cex=0.7)
+          }
+      )
R> par(op)
```

Figure 1 dislays the output of `PTM_MarkerFinder`.

2.2. Reshaping the output and export

The R method `reshape` transforms the data frame `S` from a long format to a wide format.

```
R> names(S)[4] <- "mII"
R> S.wide <- reshape(S[,c(1,7,3,4)],
+                    direction = 'wide',
+                    timevar = "markerIonMZ",
+                    idvar = c('scans','query'))
R>
```

export as comma separeted file

```
R> write.table(S.wide,
+          file = "HexNAc_PTM_markerFinder.csv",
```

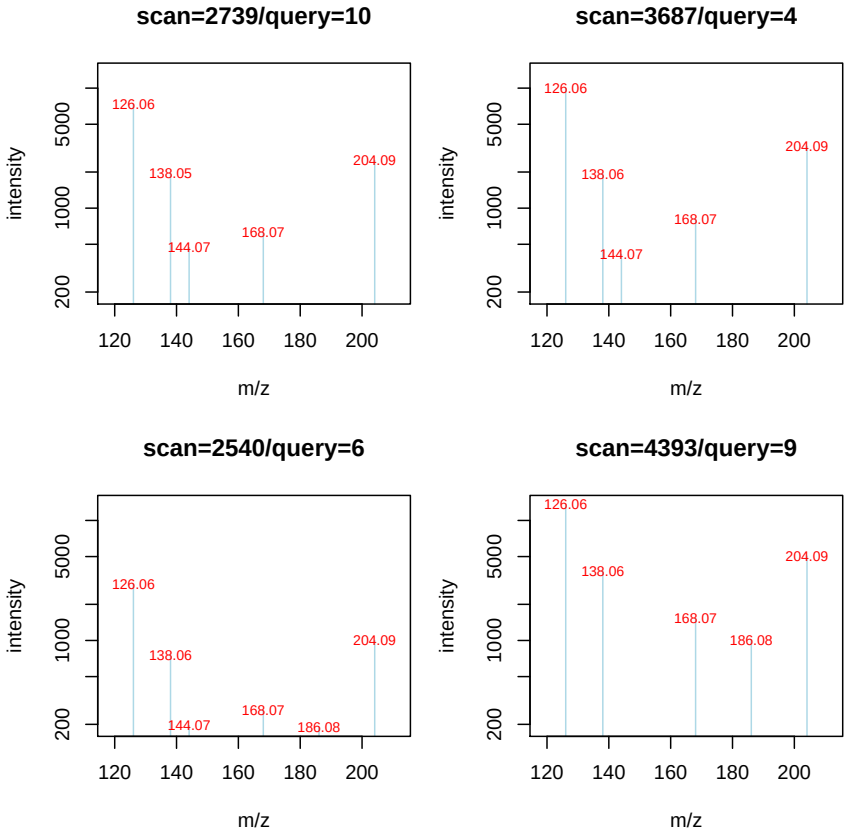

Figure 1: Overview of the marker ions.

scans	query	mII.126.05495	mII.138.05495	mII.144.06552	mII.168.06552	mII.204.08665	mII.186.07608
3687	4	9945.00	1933.00	412.30	810.20	3273.00	
2540	6	2945.00	759.20	195.40	262.90	998.40	188.50
4393	9	13620.00	3798.00		1526.00	5041.00	1014.00
2739	10	7327.00	1963.00	468.60	624.30	2496.00	

Table 2: Result

```
+             sep = ',',
+         row.names = FALSE,
+         col.names = TRUE,
+         quote = FALSE)
```

2.3. Visualization of the Result

```
R> # prepare the input
R> d <- list(); d[[1]] <- HexNAc[[3]]; d[[2]] <- HexNAc[[4]]; d[[3]] <- HexNAc[[5]]
R> S <- PTM_MarkerFinder(data = d, modification = m$mono,
+         modificationName = m$desc,
+         minMarkerIntensityRatio = 3,
```

```
+          itol_ppm = 20,
+          mZmarkerIons = HexNAc_MarkerIons)
```

The graphics can be seen in Figure 2.

3. Demonstartion

The user can call the demonstration with

```
R> demo(PTM_MarkerFinder)
```

3.1. Other examples

The following ADP-Ribose marker ions configuration was described by Bilan, Leutert, Nanni, Panse, and Hottiger (2017).

```
R> ADP_Ribose <- c(136.0618, 250.0935, 348.0704, 428.0367)
```

4. Session information

An overview of the package versions used to produce this document are shown below.

- R version 3.4.1 (2017-06-30), `x86_64-apple-darwin15.6.0`
- Locale: `C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8`
- Running under: `macOS Sierra 10.12.6`
- Matrix products: default
- BLAS: `/Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRblas.0.dylib`
- LAPACK: `/Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRlapack.dylib`
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Other packages: protViz 0.2.37, xtable 1.8-2
- Loaded via a namespace (and not attached): Rcpp 0.12.12, compiler 3.4.1, tools 3.4.1

References

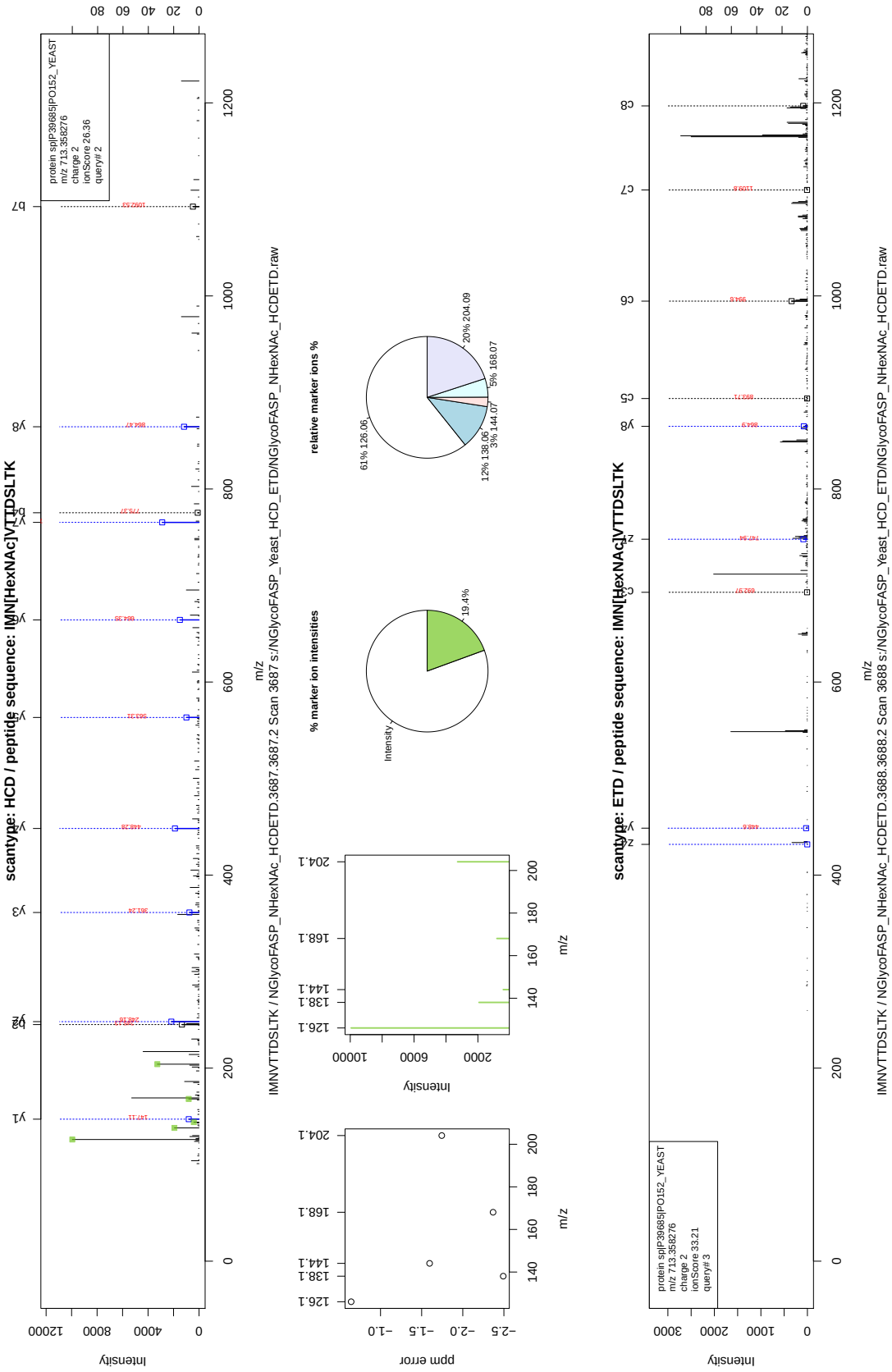

Figure 2: Graphical output of the method.

Bilan V, Leutert M, Nanni P, Panse C, Hottiger MO (2017). "Combining Higher-Energy Collision Dissociation and Electron-Transfer/Higher-Energy Collision Dissociation Fragmentation in a Product-Dependent Manner Confidently Assigns Proteomewide ADP-Ribose Acceptor Sites." *Anal. Chem.*, **89**(3), 1523–1530. doi:10.1021/acs.analchem.6b03365.

Nanni P, Panse C, Gehrig P, Mueller S, Grossmann J, Schlapbach R (2013). "PTM MarkerFinder, a software tool to detect and validate spectra from peptides carrying post-translational modifications." *Proteomics*, **13**(15), 2251–2255. doi:10.1002/pmic.201300036.

R Development Core Team (2008). *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL http://www.R-project.org.

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