

NMR-based metabolomic analysis of the dataset MTBLS242: serum samples

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This is an example of using AlpsNMR package on the MTBLS242 dataset structured as a pipeline so that inputs are needed and outputs are obtained in the selected folders. Edit “inputs” to match your parameters and just run the “code to run” for the pipeline execution. However, you can see the vignettes and use the functions as you wish. You can download the MTBLS242 dataset from MetaboLights database: <https://www.ebi.ac.uk/metabolights/MTBLS242>

```
library(AlpsNMR)
```

```
## Warning: replacing previous import 'ggplot2::last_plot' by  
## 'plotly::last_plot' when loading 'rDolphin'
```

```
##
```

```
## Attaching package: 'AlpsNMR'
```

```
## The following object is masked from 'package:stats':
```

```
##
```

```
##      filter
```

Pipeline preparation

To work as in a pipeline manner we need to set an output directory. We can set the number of cores of your computer for parallelization.

```
# Set a folder to keep results  
output_dir <- "C:/Users/fmadrid/MTBLS242/results"  
  
# How many cores to use for parallelization  
num_workers <- 12
```

Node 1: Load samples

Loads samples from a specified directory into a `nmr_dataset` object. Then we can save the loaded data into the output directory.

Input parameters

```
# Path of NMR samples downloaded from https://www.ebi.ac.uk/metabolights/MTBLS242:
dataset_path_nmr <- "C:/Users/fmadrid/MTBLS242/MTBLS242"

# Files/directories ending in "s" corresponding to the spectra in the dataset:
filename_glob <- "*.s"
```

Code to run

```
NMRExperiments <- as.character(fs::dir_ls(dataset_path_nmr, glob = filename_glob))
plan(multiprocess, workers = num_workers)
nmr_dataset <- nmr_read_samples(NMRExperiments)
plan(sequential)
```

Node 2: Append metadata

We now merge the metadata. To do that, you need an Excel file containing a first column called “NMRExperiments” with the name of the imported spectra (it does not have to be the name of the individuals).

Input parameters

```
# Path where metadata is contained
excel_file <- "C:/Users/fmadrid/MTBLS242/nmr_dataset_metadata_tidy.xlsx"
```

Code to run

```
nmr_dataset <- nmr_meta_add_tidy_excel(nmr_dataset, excel_file)
```

Node 3: Interpolation

Interpolation is used to unify the ppm axis from all spectra. However, you also can set a range for next steps avoiding noise regions from here. Note that ppm resolution is automatically calculated with the function `nmr_ppm_resolution` in “Code to run”.

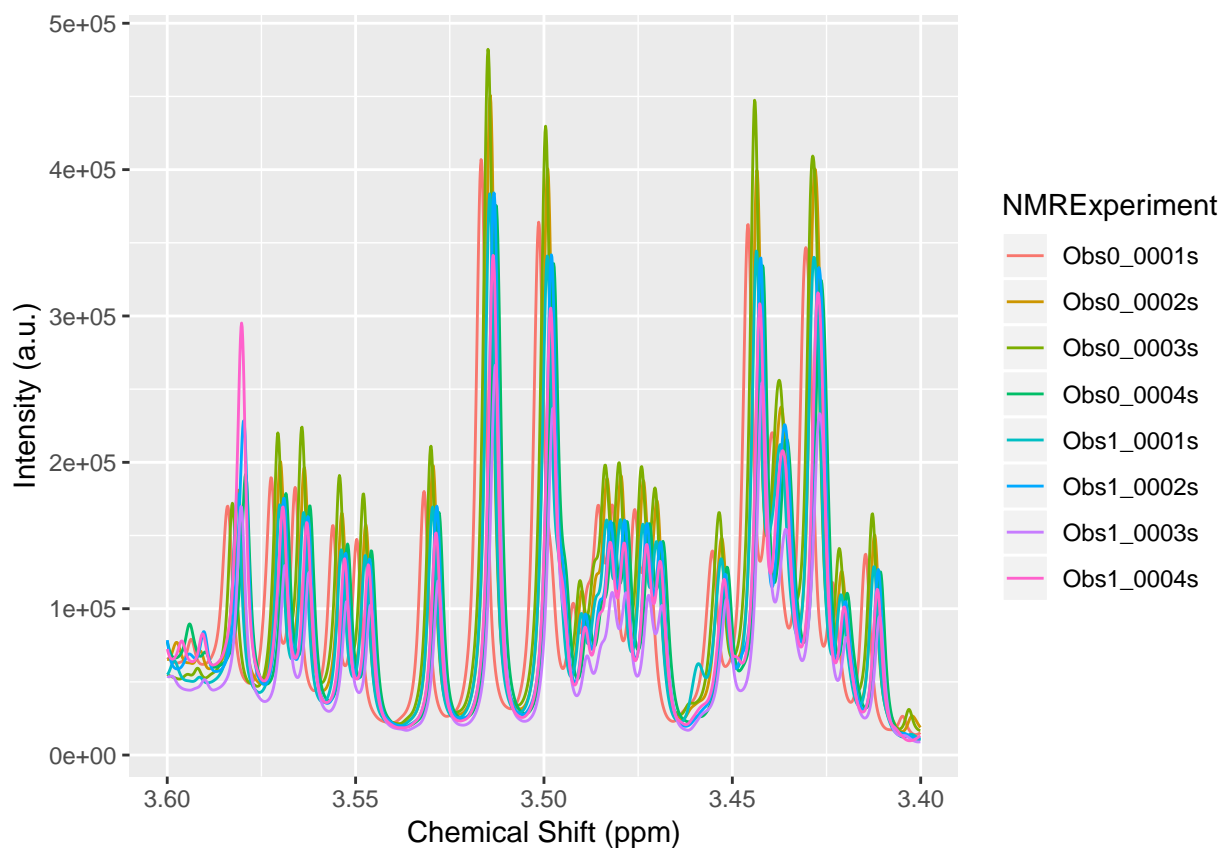
Input parameters

```
ppm_range_start <- 0.7
ppm_range_end <- 9.5
```

Code to run

```
ppm_resolution <- unlist(nmr_ppm_resolution(nmr_dataset[1]))
axis <- c(min = ppm_range_start, max = ppm_range_end, by = ppm_resolution)
nmr_dataset <- nmr_interpolate_1D(nmr_dataset, axis = axis)

plot(nmr_dataset,
     NMRExperiment = c(
       "Obs0_0001s",
       "Obs0_0002s",
       "Obs0_0003s",
       "Obs0_0004s",
       "Obs1_0001s",
       "Obs1_0002s",
       "Obs1_0003s",
       "Obs1_0004s"),
     chemshift_range = c(3.40, 3.60))
```



Node 4: Region Exclusion

Here it is important to know what type of signals can mask the results due to their intensity or what type of solvent has been used in sample processing since this can create artifacts in the spectra and should be removed. In this case, the biological samples correspond to serum, which contains a lot of water and its signal should be removed from further steps. To do this, we define a vector containing the range (min ppm

value, max ppm value) of the water signal, but other signals can be eliminated, for example: `exclude_regions <- list(water = c(4.5, 5.1), methanol = c(3.33, 3.34))`

Input parameters

```
exclude_regions <- list(water = c(4.5, 5.1))
```

Code to run

```
nmr_dataset <- nmr_exclude_region(nmr_dataset, exclude = exclude_regions)
```

Node 5: Initial Outlier Rejection

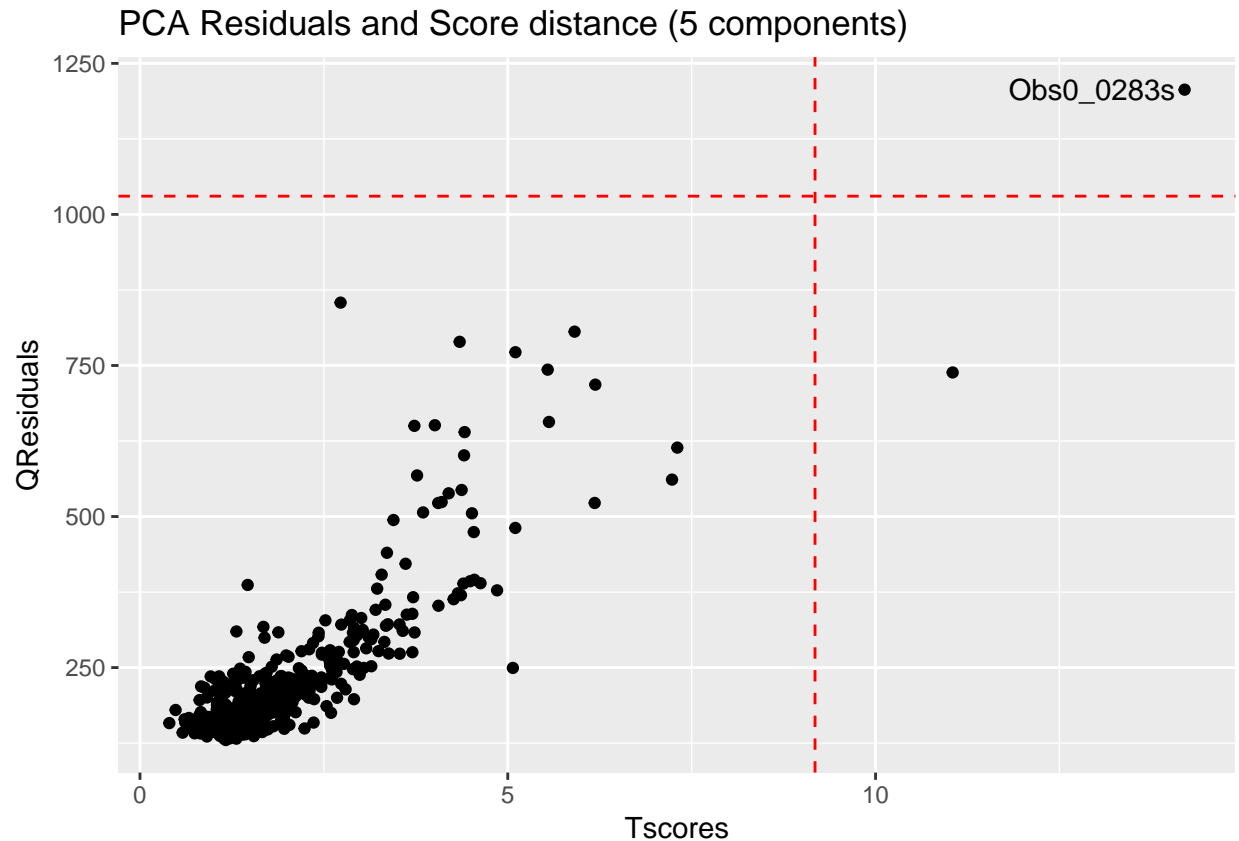
The robust principal component analysis (rPCA) for outlier detection gives an idea of potential outliers. A proposed threshold, based on quantiles, for Q residual and T2 score values, results less sensitive to extreme intensities. Then you choose if any sample should be excluded. The plot below indicated that a sample “Obs0_0283s” is extremely different than the other samples. The function is prepared to annotated samples that are in the top-right corner, exhibiting high differences.

Input parameters

```
# Nothing
```

Code to run

```
pca_outliers <- nmr_pca_outliers_robust(nmr_dataset)
nmr_pca_outliers_plot(nmr_dataset, pca_outliers)
```



Then, if we decide to discard this sample, we just run the function below. Otherwise, just ignore this:

```
nmr_dataset_with_outliers <- nmr_dataset
nmr_dataset <- nmr_pca_outliers_filter(nmr_dataset, pca_outliers)
```

Node 6: Filter samples

Input parameters

The filter node takes care of keeping only some samples. In this case, we want to compare two time points of the MTBLS242 dataset to compare them: “preop” and “3 months after surgery”. However, you can filter to keep other conditions kept in the metadata. Some examples: - `Cohort == "A"`: Keeps the A cohort - `TimePoint %in% c("preop", "3 months after surgery")`: Keeps timepoints “preop” and “3 months after surgery” - `Gender == "Female"`: Keeps Female samples - others

```
samples_to_keep_conditions <- 'Timepoint %in% c("preop", "3 months after surgery")'
```

Code to run

```
conditions_expr <- rlang::parse_exprs(samples_to_keep_conditions)
nmr_dataset <- AlpsNMR::filter(nmr_dataset, !!!conditions_expr)
```

Node 7: Peak detection and Alignment

Peak detection is based on a combination of an automated baseline threshold, signal to noise ratio and maximum tolerance. Alignment is based on hierarchical cluster-based peak alignment (CluPA) (Vu et al., 2011).

Input parameters

```
# Leave those as default/recommended for serum.
# Size of peak detection segments
nDivRange_ppm <- 0.1

# Baseline threshold
baselineThresh <- NULL

# Signal to noise ratio
SNR.Th <- 3

# Maximum alignment shift
maxShift_ppm <- 0.0015
```

Code to run

```
scales <- seq(1, 16, 2)
acceptLostPeak <- FALSE

# For parallelization
plan(multiprocess, workers = num_workers)

# Step 1: Peak detection
message("Detecting peaks...")

## Detecting peaks...

peak_data <- nmr_detect_peaks(nmr_dataset,
                             nDivRange_ppm = nDivRange_ppm,
                             scales = scales,
                             baselineThresh = baselineThresh,
                             SNR.Th = SNR.Th)

# Step 2: Finding the reference spectrum for alignment
message("Choosing alignment reference...")

## Choosing alignment reference...

NMRExp_ref <- nmr_align_find_ref(nmr_dataset, peak_data)

# Step 3: Alignment
message("Starting alignment...")
```

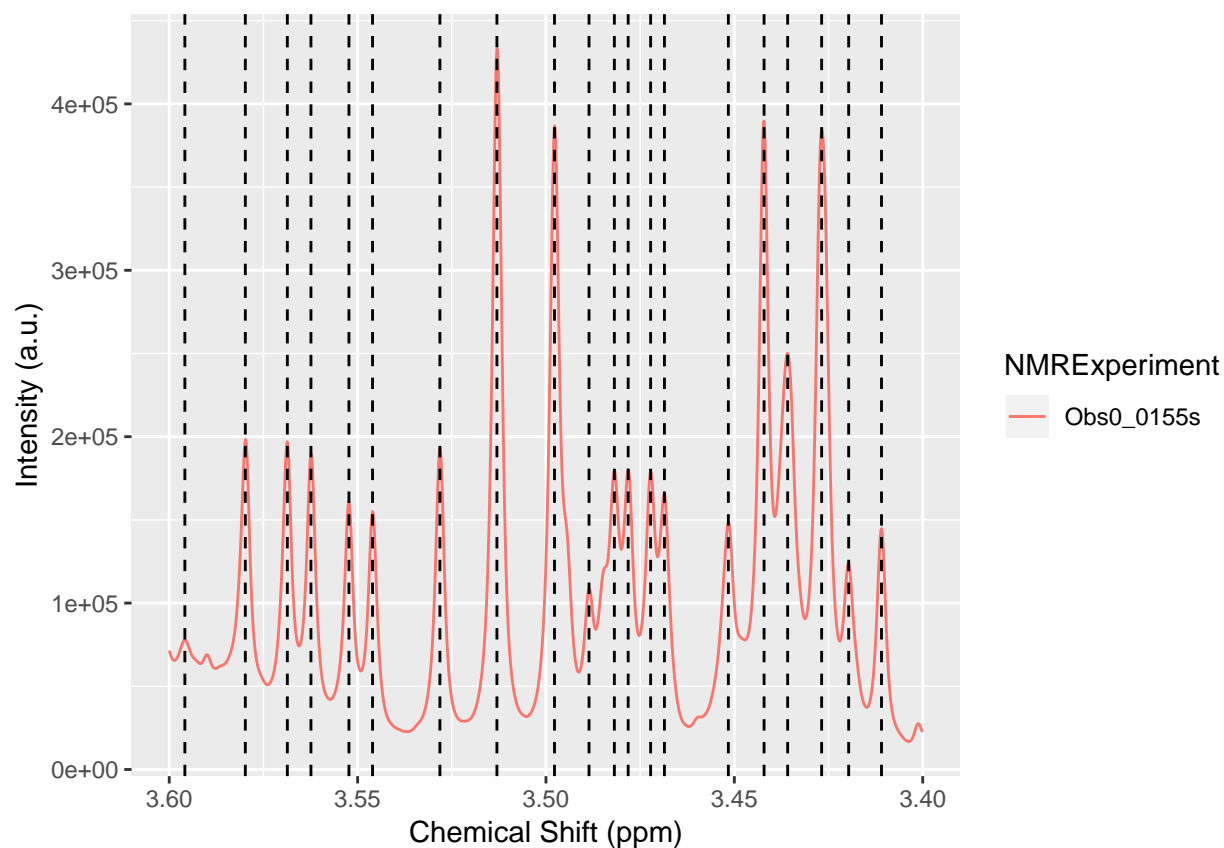
```
## Starting alignment...
```

```
nmr_dataset <- nmr_align(nmr_dataset, peak_data,  
  NMRExp_ref = NMRExp_ref,  
  maxShift_ppm = maxShift_ppm,  
  acceptLostPeak = acceptLostPeak)
```

```
plan(sequential)
```

```
# Plotting results
```

```
nmr_detect_peaks_plot(  
  nmr_dataset,  
  peak_data,  
  NMRExperiment = NMRExp_ref,  
  chemshift_range = c(3.40, 3.60)  
)
```



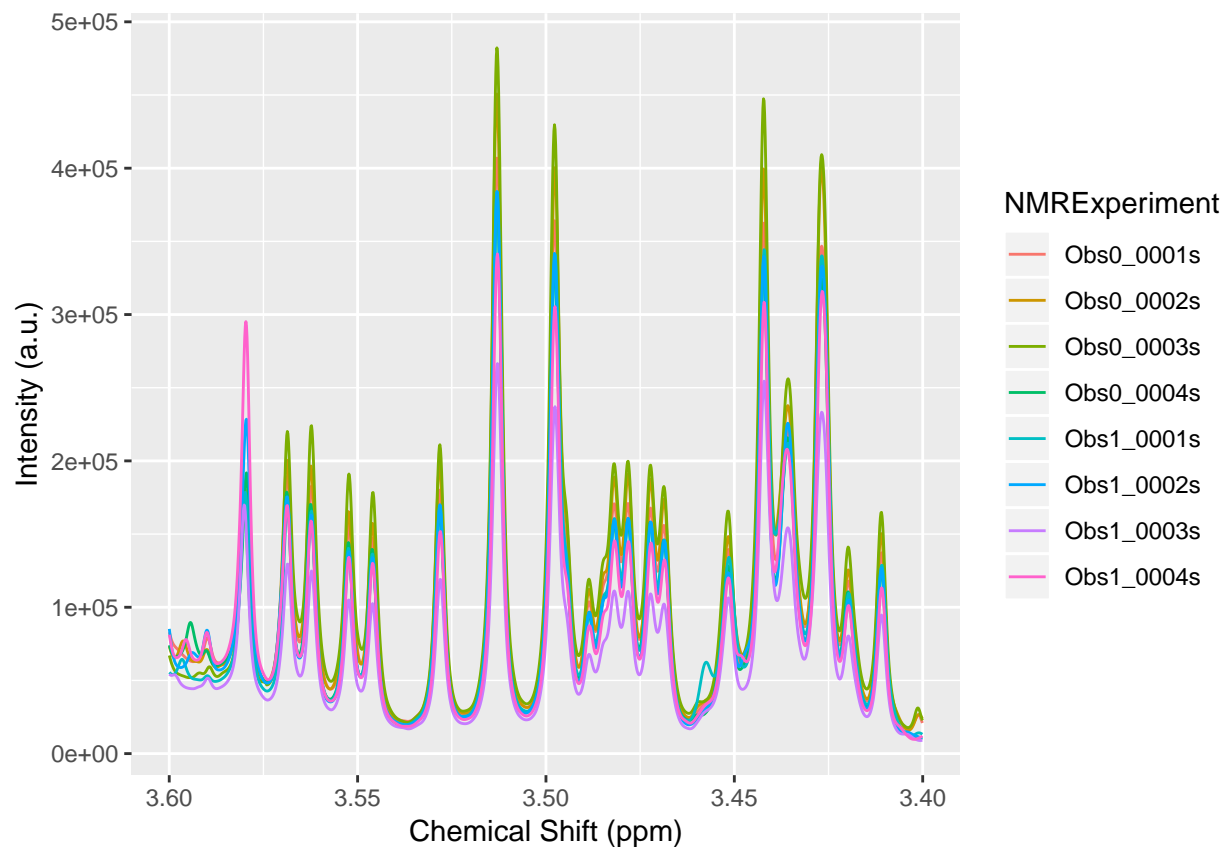
we can take a look into the detected peaks. The interactive plot allows you to zoom in in HTML files.

```
plot(nmr_dataset,  
  NMRExperiment = c(  
    "Obs0_0001s",  
    "Obs0_0002s",  
    "Obs0_0003s",  
    "Obs0_0004s",  
    "Obs1_0001s",
```

```

"Obs1_0002s",
"Obs1_0003s",
"Obs1_0004s"),
chemshift_range = c(3.40, 3.60))

```



Node 8: Normalization

We can normalize the dataset. This is recommended for biosamples, controlling for dilution factors, irregular pipetting, etc. Probabilistic quotient normalization is one of the most used model-based techniques NMR-based metabolomics.

Input parameters

```
# nothing
```

Code to run

```

nmr_dataset <- nmr_normalize(nmr_dataset, method = "pqn")
norm_pqn_diagnostic <- nmr_diagnose(nmr_dataset)
gplt_norm_factor_pqn <- norm_pqn_diagnostic$plot

```


Node 9: Integration

For peak integration, calculation of peak width may be performed automatically (set `peak_width_ppm = NULL`), from the detected peaks in the reference spectrum (if you wish, you can combine detected peaks other than the reference spectrum, see help), or manually, in which users can select a specific peak width for integrating the detected peaks. This differs than the bucketing approach in which spectra are equally divided into buckets (for example of 0.01 ppm) and this normally leads to a higher number of total variables. this has the inconvenient that several peaks might be split into several parts, lowering the statistical power, and vice-versa, certain overlapping tails might result in false positives because of this noisy parts. However, a good match between them is expected.

Input parameters

```
peak_width_ppm <- NULL
```

Code to run

```
# be carefull, you integrate based on peaks from a unique ref sample
peak_data_integ <- dplyr::filter(peak_data, NMRExperiment == !!NMRExp_ref)

nmr_peak_table <- nmr_integrate_peak_positions(
  samples = nmr_dataset,
  peak_pos_ppm = peak_data_integ$ppm,
  peak_width_ppm = peak_width_ppm)

## calculated width for integration is 0.00427905515639537 ppm

nmr_peak_table_completed <- get_integration_with_metadata(nmr_peak_table)
```

Node 10: Machine learning

Pairwise multilevel approach takes into consideration variability within the same individual. Therefore, we use the function “`rdCV_PLS_RF_ML`” to perform a multilevel repeated double cross-validation optimized for unbiased variable selection (MUVr algorithm, see Shi et al., 2018). The double cross-validation procedure comprises an inner “tuning” loop nested within an outer loop aimed at reducing bias resulting from overfitting models to experimental data. Then, autoselected variables are ranked according to their VIP value.

Modeling through the multivariate modelling with minimally biased variable selection (MUVr) algorithm

```
model <- rdCV_PLS_RF(nmr_data(nmr_peak_table),
  Y = nmr_peak_table_completed$Timepoint)
```

```
## Warning: package 'pROC' was built under R version 3.5.3
```

```
## Type 'citation("pROC")' for a citation.

##
## Attaching package: 'pROC'

## The following objects are masked from 'package:stats':
##
##      cov, smooth, var

##
## Missing ID -> Assume all unique (i.e. sample independence)
## Y is factor -> Classification (2 classes)
## Elapsed time 0.077 mins

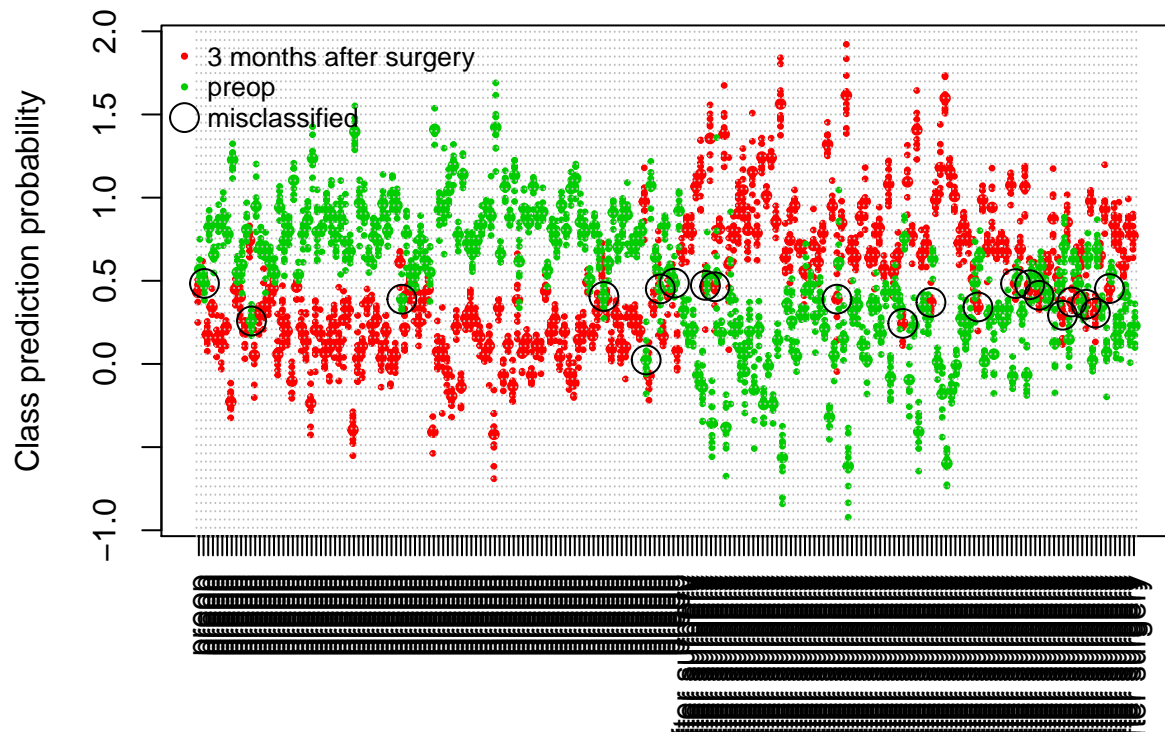
message("AUC model is ", model$auc[[2]])

## AUC model is 0.960264237814033
```

This is the misclassification plot from multilevel PLS-DA model between “preop” and “3 months after surgery”. Misclassification plot shows each sample predicted as “preop” and “3 months after surgery”. The first half of the horizontal axis represents “preop” actual samples, while the second half represents actual “3 months after surgery” samples. Bold points are the average predicted samples, while grey points display predictions from each iteration. To see the misclassification plot, which gives the information about the actual class and predicted class, run:

Model performance

```
MUVR_model_plot(model)
```



Permutation test

The function `permutation_test_model` performs the permutation test. Set the number of permutation at “nPerm”.

```
permutations = permutation_test_model(model, nPerm = 20)
```

```
##
## "MVObj" permutation 1 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.076 mins
##
## Estimated time left: 1.444 mins
##
##
## "MVObj" permutation 2 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.063 mins
##
## Estimated time left: 1.251 mins
##
##
```

```

## "MVObj" permutation 3 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.06383333 mins
##
## Estimated time left: 1.149389 mins
##
##
## "MVObj" permutation 4 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.06133333 mins
##
## Estimated time left: 1.056667 mins
##
##
## "MVObj" permutation 5 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.06233333 mins
##
## Estimated time left: 0.9795 mins
##
##
## "MVObj" permutation 6 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.06333333 mins
##
## Estimated time left: 0.9096111 mins
##
##
## "MVObj" permutation 7 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.06483333 mins
##
## Estimated time left: 0.844381 mins
##
##
## "MVObj" permutation 8 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.06116667 mins
##
## Estimated time left: 0.774 mins
##
##
## "MVObj" permutation 9 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.0655 mins
##
## Estimated time left: 0.7107222 mins

```

```

##
##
## "MVObj" permutation 10 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.0595 mins
##
## Estimated time left: 0.641 mins
##
##
## "MVObj" permutation 11 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.06333333 mins
##
## Estimated time left: 0.5762727 mins
##
##
## "MVObj" permutation 12 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.06483333 mins
##
## Estimated time left: 0.5127778 mins
##
##
## "MVObj" permutation 13 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.062 mins
##
## Estimated time left: 0.4475513 mins
##
##
## "MVObj" permutation 14 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.06166667 mins
##
## Estimated time left: 0.3826429 mins
##
##
## "MVObj" permutation 15 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.06383333 mins
##
## Estimated time left: 0.3188889 mins
##
##
## "MVObj" permutation 16 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.061 mins

```

```

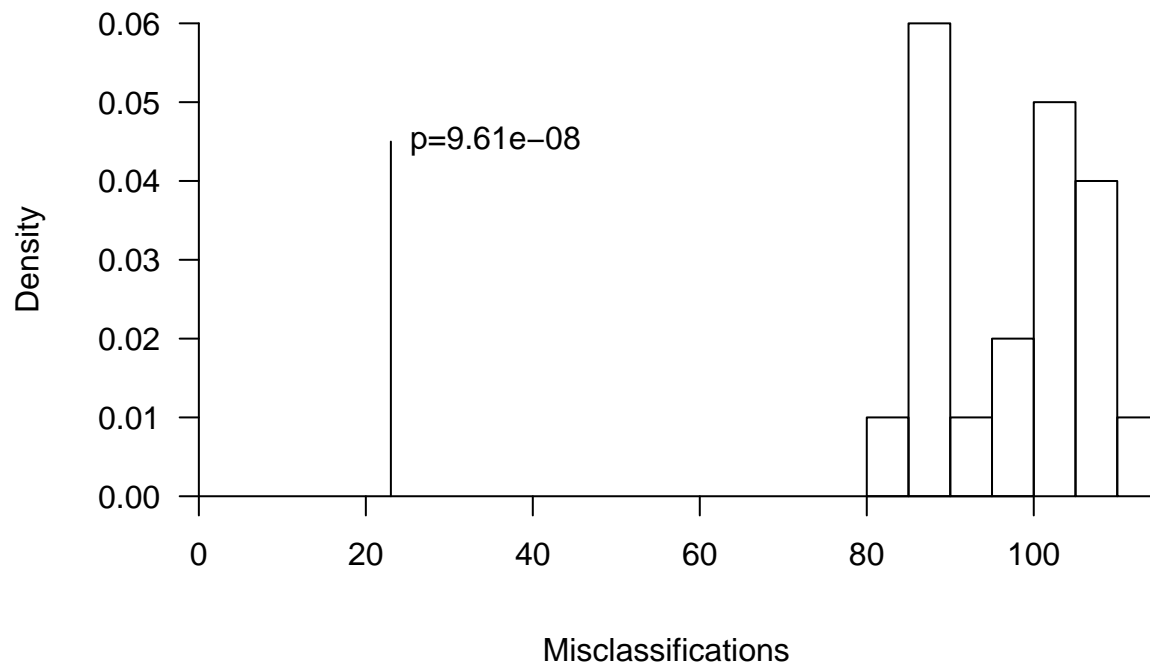
##
## Estimated time left: 0.2544167 mins
##
##
## "MVObj" permutation 17 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.06433333 mins
##
## Estimated time left: 0.1909412 mins
##
##
## "MVObj" permutation 18 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.0635 mins
##
## Estimated time left: 0.1272778 mins
##
##
## "MVObj" permutation 19 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.06333333 mins
##
## Estimated time left: 0.06362281 mins
##
##
## "MVObj" permutation 20 of 20
##
## Y is factor -> Classification (2 classes)
## Elapsed time 0.06583333 mins
##
## Estimated time left: 0 mins

```

Permutation test plot

Permutation test plot for multilevel PLS-DA model gives a p-value for the model performance. The actual misclassification departs from the null hypothesis distribution.

```
permutation_test_plot(model, permutations)
```



Autoselected features

Then, we can extract VIP values from the autoselected features.

```
VIPs= model_VIP(model)
VIPs
```

```
##          order      name    rank
## ppm_3.5798      1 ppm_3.5798  1.515
## ppm_1.2120      2 ppm_1.2120  4.125
## ppm_1.3515      3 ppm_1.3515  5.740
## ppm_1.0136      4 ppm_1.0136  5.905
## ppm_1.0639      5 ppm_1.0639  6.410
## ppm_4.1352      6 ppm_4.1352  6.465
## ppm_2.2463      7 ppm_2.2463  7.855
## ppm_4.1235      8 ppm_4.1235  9.780
## ppm_1.0521      9 ppm_1.0521 10.155
## ppm_1.0018     10 ppm_1.0018 11.850
## ppm_4.1119     11 ppm_4.1119 14.605
## ppm_1.2217     12 ppm_1.2217 15.185
## ppm_1.3399     13 ppm_1.3399 15.715
## ppm_1.1835     14 ppm_1.1835 17.175
## ppm_1.1938     15 ppm_1.1938 18.250
## ppm_3.0602     16 ppm_3.0602 19.810
## ppm_4.1468     17 ppm_4.1468 20.075
```

## ppm_1.2002	18 ppm_1.2002	24.385
## ppm_0.9881	19 ppm_0.9881	27.215
## ppm_3.6628	20 ppm_3.6628	27.565
## ppm_0.8461	21 ppm_0.8461	28.165
## ppm_1.2926	22 ppm_1.2926	31.175
## ppm_2.1518	23 ppm_2.1518	35.625
## ppm_2.2501	24 ppm_2.2501	36.240
## ppm_3.2311	25 ppm_3.2311	36.515
## ppm_5.2826	26 ppm_5.2826	36.690
## ppm_0.9775	27 ppm_0.9775	41.075
## ppm_1.2653	28 ppm_1.2653	43.485
## ppm_3.8940	29 ppm_3.8940	43.510
## ppm_1.5908	30 ppm_1.5908	45.005
## ppm_0.9670	31 ppm_0.9670	45.310
## ppm_1.5995	32 ppm_1.5995	46.975
## ppm_1.3199	33 ppm_1.3199	48.280
## ppm_2.0632	34 ppm_2.0632	50.705
## ppm_5.3228	35 ppm_5.3228	54.490
## ppm_3.3799	36 ppm_3.3799	54.795
## ppm_0.9422	37 ppm_0.9422	55.490
## ppm_1.5039	38 ppm_1.5039	56.265
## ppm_2.2611	39 ppm_2.2611	56.405
## ppm_2.2353	40 ppm_2.2353	57.250
## ppm_2.2324	41 ppm_2.2324	57.365
## ppm_1.5792	42 ppm_1.5792	58.470
## ppm_2.0569	43 ppm_2.0569	59.215
## ppm_2.0970	44 ppm_2.0970	63.265
## ppm_3.4782	45 ppm_3.4782	65.565
## ppm_0.9546	46 ppm_0.9546	65.665
## ppm_3.2807	47 ppm_3.2807	73.330
## ppm_2.2350	48 ppm_2.2350	74.530
## ppm_3.8118	49 ppm_3.8118	74.625
## ppm_3.2673	50 ppm_3.2673	79.705
## ppm_3.4722	51 ppm_3.4722	82.270
## ppm_0.8955	52 ppm_0.8955	87.950
## ppm_1.9937	53 ppm_1.9937	88.220
## ppm_3.6894	54 ppm_3.6894	89.375
## ppm_2.7630	55 ppm_2.7630	89.515
## ppm_1.4916	56 ppm_1.4916	89.545
## ppm_2.0172	57 ppm_2.0172	90.060
## ppm_3.9276	58 ppm_3.9276	90.490
## ppm_2.0045	59 ppm_2.0045	92.685
## ppm_3.4109	60 ppm_3.4109	93.815
## ppm_2.0858	61 ppm_2.0858	95.940
## ppm_3.4977	62 ppm_3.4977	96.325
## ppm_0.9071	63 ppm_0.9071	96.795
## ppm_3.4268	64 ppm_3.4268	97.070
## ppm_3.2520	65 ppm_3.2520	97.885
## ppm_0.8621	66 ppm_0.8621	98.745
## ppm_3.9072	67 ppm_3.9072	98.900
## ppm_3.5130	68 ppm_3.5130	102.005
## ppm_3.7528	69 ppm_3.7528	102.595

Node 11: Identification

Finally, AlpsNMR allows an identification step, in which we can select between plasma/serum, urine and cell functions giving a ranked dataframe with ppm and proposed candidates by the Human Metabolome Database (<http://www.hmdb.ca>). However, this needs to be double-checked, as there is overlap between several potential compounds for a given ppm value and different specific metabolite-shifts, this should be carefully taken as a first step in the identification. First, we extract a vector with significant ppm values. Then, we run “nmr_identify_regions_blood”. You can set the number of proposed candidates, but in this particular case, we set to 3. Even though, several NAs in the identification corresponded to Supplemental Table 1 in Supplemental Material.

Autoselected features (blood samples)

```
ppm_to_assign <- VIPs %>%
  tidyr::separate(col = name,
                  into = c("x1", "ppms"),
                  sep = "_")

ppm_to_assign <- as.numeric(ppm_to_assign$ppms)
assignation <-
  dplyr::select(nmr_identify_regions_blood(ppm_to_assign,
                                           num_proposed_compounds = 3),
                -Height,
                -n_reported_in_Blood,
                -J_Hz)
```

```
## [1] 3.5798
```

```
## your peak at 3.5798 probably corresponds to D-Mannose, Glycerol or L-Threonine
```

```
##
```

```
## [1] 1.212
```

```
## your peak at 1.212 probably corresponds to 3-Hydroxybutyric acid, Isobutyric acid or NA
```

```
## [1] 1.3515
```

```
## your peak at 1.3515 probably corresponds to NA, NA or NA
```

```
## [1] 1.0136
```

```
## your peak at 1.0136 probably corresponds to L-Isoleucine, NA or NA
```

```
## [1] 1.0639
```

```
## your peak at 1.0639 probably corresponds to NA, NA or NA
```

```
## [1] 4.1352
```

your peak at 4.1352 probably corresponds to L-Proline, Uridine or NA

[1] 2.2463

your peak at 2.2463 probably corresponds to Acetone, NA or NA

[1] 4.1235

your peak at 4.1235 probably corresponds to L-Lactic acid, L-Proline or Uridine

[1] 1.0521

your peak at 1.0521 probably corresponds to L-Valine, NA or NA

[1] 1.0018

your peak at 1.0018 probably corresponds to L-Alpha-aminobutyric acid, L-Isoleucine or L-Valine

[1] 4.1119

your peak at 4.1119 probably corresponds to L-Lactic acid, NA or NA

[1] 1.2217

your peak at 1.2217 probably corresponds to 3-Hydroxybutyric acid, Isobutyric acid or NA

[1] 1.3399

your peak at 1.3399 probably corresponds to L-Lactic acid, L-Threonine or NA

[1] 1.1835

your peak at 1.1835 probably corresponds to Ethanol, Isopropyl alcohol or NA

[1] 1.1938

your peak at 1.1938 probably corresponds to Ethanol, NA or NA

[1] 3.0602

your peak at 3.0602 probably corresponds to Ornithine, NA or NA

[1] 4.1468

your peak at 4.1468 probably corresponds to L-Proline, Uridine or NA

[1] 1.2002

your peak at 1.2002 probably corresponds to NA, NA or NA

[1] 0.9881

your peak at 0.9881 probably corresponds to L-Alpha-aminobutyric acid, L-Valine or NA

[1] 3.6628

your peak at 3.6628 probably corresponds to D-Mannose, Ethanol or Glycerol

[1] 0.8461

your peak at 0.8461 probably corresponds to 2-Hydroxy-3-methylbutyric acid, NA or NA

[1] 1.2926

your peak at 1.2926 probably corresponds to NA, NA or NA

[1] 2.1518

your peak at 2.1518 probably corresponds to L-Acetylcarnitine, L-Glutamine or NA

[1] 2.2501

your peak at 2.2501 probably corresponds to NA, NA or NA

[1] 3.2311

your peak at 3.2311 probably corresponds to L-Arginine, L-Histidine or NA

[1] 5.2826

your peak at 5.2826 probably corresponds to NA, NA or NA

[1] 0.9775

your peak at 0.9775 probably corresponds to 2-Hydroxy-3-methylbutyric acid, L-Leucine or L-Valine

[1] 1.2653

your peak at 1.2653 probably corresponds to 3-Hydroxyisovaleric acid, L-Isoleucine or NA

[1] 3.894

your peak at 3.894 probably corresponds to Betaine, D-Glucose or D-Mannose

[1] 1.5908

your peak at 1.5908 probably corresponds to NA, NA or NA

[1] 0.967

your peak at 0.967 probably corresponds to 2-Hydroxy-3-methylbutyric acid, L-Leucine or NA

[1] 1.5995

your peak at 1.5995 probably corresponds to NA, NA or NA

[1] 1.3199

your peak at 1.3199 probably corresponds to L-Threonine, NA or NA

[1] 2.0632

your peak at 2.0632 probably corresponds to Acetylglycine, Isovaleric acid or L-Glutamic acid

[1] 5.3228

your peak at 5.3228 probably corresponds to NA, NA or NA

[1] 3.3799

your peak at 3.3799 probably corresponds to D-Mannose, NA or NA

[1] 0.9422

your peak at 0.9422 probably corresponds to Ketoleucine, L-Isoleucine or NA

[1] 1.5039

your peak at 1.5039 probably corresponds to NA, NA or NA

[1] 2.2611

your peak at 2.2611 probably corresponds to L-Valine, NA or NA

[1] 2.2353

your peak at 2.2353 probably corresponds to Acetone, NA or NA

[1] 2.2324

your peak at 2.2324 probably corresponds to Acetone, NA or NA

[1] 1.5792

your peak at 1.5792 probably corresponds to NA, NA or NA

[1] 2.0569

your peak at 2.0569 probably corresponds to Acetylglycine, Isovaleric acid or L-Glutamic acid

[1] 2.097

your peak at 2.097 probably corresponds to Ketoleucine, NA or NA

[1] 3.4782

your peak at 3.4782 probably corresponds to D-Glucose, Sucrose or NA

[1] 0.9546

your peak at 0.9546 probably corresponds to 2-Hydroxy-3-methylbutyric acid, Ketoleucine or L-Isoleucine

[1] 3.2807

your peak at 3.2807 probably corresponds to Myoinositol, NA or NA

[1] 2.235

your peak at 2.235 probably corresponds to Acetone, NA or NA

[1] 3.8118

your peak at 3.8118 probably corresponds to D-Mannose, Uridine or NA

[1] 3.2673

your peak at 3.2673 probably corresponds to 3-Methylhistidine, Betaine or NA

[1] 3.4722

your peak at 3.4722 probably corresponds to D-Glucose, Sucrose or NA

[1] 0.8955

your peak at 0.8955 probably corresponds to NA, NA or NA

[1] 1.9937

your peak at 1.9937 probably corresponds to L-Isoleucine, L-Proline or NA

[1] 3.6894

your peak at 3.6894 probably corresponds to 1-Methylhistidine, L-Isoleucine or Sucrose

[1] 2.763

your peak at 2.763 probably corresponds to NA, NA or NA

[1] 1.4916

your peak at 1.4916 probably corresponds to L-Alanine, NA or NA

[1] 2.0172

your peak at 2.0172 probably corresponds to 2-Hydroxy-3-methylbutyric acid, L-Proline or NA

[1] 3.9276

your peak at 3.9276 probably corresponds to Creatine, D-Mannose or Uridine

[1] 2.0045

your peak at 2.0045 probably corresponds to L-Proline, NA or NA

[1] 3.4109

your peak at 3.4109 probably corresponds to D-Glucose, L-Carnitine or L-Proline

[1] 2.0858

your peak at 2.0858 probably corresponds to L-Proline, NA or NA

[1] 3.4977

your peak at 3.4977 probably corresponds to NA, NA or NA

[1] 0.9071

your peak at 0.9071 probably corresponds to 3-Methyl-2-oxovaleric acid, Isovaleric acid or NA

[1] 3.4268

your peak at 3.4268 probably corresponds to D-Glucose, L-Carnitine or L-Proline

[1] 3.252

your peak at 3.252 probably corresponds to 3-Methylhistidine, Betaine or D-Glucose

[1] 0.8621

your peak at 0.8621 probably corresponds to NA, NA or NA

[1] 3.9072

your peak at 3.9072 probably corresponds to Betaine, D-Glucose or D-Mannose

[1] 3.513

your peak at 3.513 probably corresponds to Choline, NA or NA

[1] 3.7528

your peak at 3.7528 probably corresponds to D-Glucose, D-Mannose or L-Glutamic acid

```
assignation_NArm <- na.omit(assignation)
assignation
```

##		Metabolite	HMDB_code	Shift_ppm	Type
## 7	2-Hydroxy-3-methylbutyric acid		HMDB00407	0.835	d
## NA16		<NA>	<NA>	NA	<NA>
## NA.19		<NA>	<NA>	NA	<NA>
## NA51		<NA>	<NA>	NA	<NA>
## NA.132		<NA>	<NA>	NA	<NA>
## NA.214		<NA>	<NA>	NA	<NA>
## NA42		<NA>	<NA>	NA	<NA>
## NA.126		<NA>	<NA>	NA	<NA>
## NA.211		<NA>	<NA>	NA	<NA>
## 17	3-Methyl-2-oxovaleric acid		HMDB00491	0.915	t
## 88	Isovaleric acid		HMDB00718	0.915	d
## NA50		<NA>	<NA>	NA	<NA>
## 135	L-Isoleucine		HMDB00172	0.941	t
## 92	Ketoleucine		HMDB00695	0.945	d
## NA29		<NA>	<NA>	NA	<NA>
## 1351	L-Isoleucine		HMDB00172	0.941	t
## 921	Ketoleucine		HMDB00695	0.945	d
## 102	2-Hydroxy-3-methylbutyric acid		HMDB00407	0.965	d
## 1421	L-Leucine		HMDB00687	0.963	t
## 101	2-Hydroxy-3-methylbutyric acid		HMDB00407	0.965	d
## NA24		<NA>	<NA>	NA	<NA>
## 1782	L-Valine		HMDB00883	0.991	d
## 142	L-Leucine		HMDB00687	0.963	t
## 10	2-Hydroxy-3-methylbutyric acid		HMDB00407	0.965	d
## 1781	L-Valine		HMDB00883	0.991	d
## 1031	L-Alpha-aminobutyric acid		HMDB00452	0.997	t
## NA15		<NA>	<NA>	NA	<NA>
## 178	L-Valine		HMDB00883	0.991	d
## 1371	L-Isoleucine		HMDB00172	1.012	d
## 103	L-Alpha-aminobutyric acid		HMDB00452	0.997	t
## 137	L-Isoleucine		HMDB00172	1.012	d
## NA2		<NA>	<NA>	NA	<NA>
## NA.11		<NA>	<NA>	NA	<NA>
## 179	L-Valine		HMDB00883	1.044	d

## NA6	<NA>	<NA>	NA <NA>
## NA.14	<NA>	<NA>	NA <NA>
## NA3	<NA>	<NA>	NA <NA>
## NA.12	<NA>	<NA>	NA <NA>
## NA.21	<NA>	<NA>	NA <NA>
## 86	Isopropyl alcohol	HMDB00863	1.177 d
## 70	Ethanol	HMDB00108	1.185 t
## NA10	<NA>	<NA>	NA <NA>
## 701	Ethanol	HMDB00108	1.185 t
## NA11	<NA>	<NA>	NA <NA>
## NA.16	<NA>	<NA>	NA <NA>
## NA14	<NA>	<NA>	NA <NA>
## NA.18	<NA>	<NA>	NA <NA>
## NA.22	<NA>	<NA>	NA <NA>
## 12	3-Hydroxybutyric acid	HMDB00357	1.219 d
## 84	Isobutyric acid	HMDB01873	1.225 d
## NA	<NA>	<NA>	NA <NA>
## 121	3-Hydroxybutyric acid	HMDB00357	1.219 d
## 841	Isobutyric acid	HMDB01873	1.225 d
## NA8	<NA>	<NA>	NA <NA>
## 139	L-Isoleucine	HMDB00172	1.263 m
## 16	3-Hydroxyisovaleric acid	HMDB00754	1.275 s
## NA22	<NA>	<NA>	NA <NA>
## NA17	<NA>	<NA>	NA <NA>
## NA.110	<NA>	<NA>	NA <NA>
## NA.23	<NA>	<NA>	NA <NA>
## 1671	L-Threonine	HMDB00167	1.331 d
## NA26	<NA>	<NA>	NA <NA>
## NA.115	<NA>	<NA>	NA <NA>
## 141	L-Lactic acid	HMDB00190	1.335 d
## 167	L-Threonine	HMDB00167	1.331 d
## NA9	<NA>	<NA>	NA <NA>
## NA1	<NA>	<NA>	NA <NA>
## NA.1	<NA>	<NA>	NA <NA>
## NA.2	<NA>	<NA>	NA <NA>
## 1011	L-Alanine	HMDB00161	1.485 d
## NA45	<NA>	<NA>	NA <NA>
## NA.128	<NA>	<NA>	NA <NA>
## NA30	<NA>	<NA>	NA <NA>
## NA.118	<NA>	<NA>	NA <NA>
## NA.29	<NA>	<NA>	NA <NA>
## NA34	<NA>	<NA>	NA <NA>
## NA.122	<NA>	<NA>	NA <NA>
## NA.210	<NA>	<NA>	NA <NA>
## NA23	<NA>	<NA>	NA <NA>
## NA.113	<NA>	<NA>	NA <NA>
## NA.26	<NA>	<NA>	NA <NA>
## NA25	<NA>	<NA>	NA <NA>
## NA.114	<NA>	<NA>	NA <NA>
## NA.27	<NA>	<NA>	NA <NA>
## 161	L-Proline	HMDB00162	2.005 m
## 134	L-Isoleucine	HMDB00172	1.983 m
## NA43	<NA>	<NA>	NA <NA>
## 1612	L-Proline	HMDB00162	2.005 m

## NA47	<NA>	<NA>	NA <NA>
## NA.129	<NA>	<NA>	NA <NA>
## 1611	L-Proline	HMDB00162	2.005 m
## 9	2-Hydroxy-3-methylbutyric acid	HMDB00407	2.025 m
## NA46	<NA>	<NA>	NA <NA>
## 301	Acetylglycine	HMDB00532	2.065 s
## 1251	L-Glutamic acid	HMDB00148	2.055 m
## 891	Isovaleric acid	HMDB00718	2.065 d
## 30	Acetylglycine	HMDB00532	2.065 s
## 125	L-Glutamic acid	HMDB00148	2.055 m
## 89	Isovaleric acid	HMDB00718	2.065 d
## 163	L-Proline	HMDB00162	2.075 m
## NA48	<NA>	<NA>	NA <NA>
## NA.130	<NA>	<NA>	NA <NA>
## 91	Ketoleucine	HMDB00695	2.105 m
## NA35	<NA>	<NA>	NA <NA>
## NA.123	<NA>	<NA>	NA <NA>
## 127	L-Glutamine	HMDB00641	2.140 m
## 97	L-Acetylcarnitine	HMDB00201	2.145 s
## NA18	<NA>	<NA>	NA <NA>
## 282	Acetone	HMDB01659	2.235 s
## NA33	<NA>	<NA>	NA <NA>
## NA.121	<NA>	<NA>	NA <NA>
## 283	Acetone	HMDB01659	2.235 s
## NA38	<NA>	<NA>	NA <NA>
## NA.125	<NA>	<NA>	NA <NA>
## 281	Acetone	HMDB01659	2.235 s
## NA32	<NA>	<NA>	NA <NA>
## NA.120	<NA>	<NA>	NA <NA>
## 28	Acetone	HMDB01659	2.235 s
## NA5	<NA>	<NA>	NA <NA>
## NA.13	<NA>	<NA>	NA <NA>
## NA19	<NA>	<NA>	NA <NA>
## NA.111	<NA>	<NA>	NA <NA>
## NA.24	<NA>	<NA>	NA <NA>
## 180	L-Valine	HMDB00883	2.276 m
## NA31	<NA>	<NA>	NA <NA>
## NA.119	<NA>	<NA>	NA <NA>
## NA44	<NA>	<NA>	NA <NA>
## NA.127	<NA>	<NA>	NA <NA>
## NA.212	<NA>	<NA>	NA <NA>
## 187	Ornithine	HMDB00214	3.061 t
## NA12	<NA>	<NA>	NA <NA>
## NA.17	<NA>	<NA>	NA <NA>
## 107	L-Arginine	HMDB00517	3.245 t
## 133	L-Histidine	HMDB00177	3.245 dd
## NA20	<NA>	<NA>	NA <NA>
## 54	D-Glucose	HMDB00122	3.248 dd
## 381	Betaine	HMDB00043	3.265 s
## 261	3-Methylhistidine	HMDB00479	3.255 m
## 38	Betaine	HMDB00043	3.265 s
## 26	3-Methylhistidine	HMDB00479	3.255 m
## NA40	<NA>	<NA>	NA <NA>
## 183	Myoinositol	HMDB00211	3.283 t

## NA37	<NA>	<NA>	NA	<NA>
## NA.124	<NA>	<NA>	NA	<NA>
## 60	D-Mannose	HMDB00169	3.385	ddd
## NA28	<NA>	<NA>	NA	<NA>
## NA.117	<NA>	<NA>	NA	<NA>
## 50	D-Glucose	HMDB00122	3.413	m
## 164	L-Proline	HMDB00162	3.425	dt
## 1211	L-Carnitine	HMDB0000062	3.419	m
## 501	D-Glucose	HMDB00122	3.413	m
## 1641	L-Proline	HMDB00162	3.425	dt
## 1212	L-Carnitine	HMDB0000062	3.419	m
## 491	D-Glucose	HMDB00122	3.473	m
## 2071	Sucrose	HMDB00258	3.475	t
## NA41	<NA>	<NA>	NA	<NA>
## 49	D-Glucose	HMDB00122	3.473	m
## 207	Sucrose	HMDB00258	3.475	t
## NA36	<NA>	<NA>	NA	<NA>
## NA49	<NA>	<NA>	NA	<NA>
## NA.131	<NA>	<NA>	NA	<NA>
## NA.213	<NA>	<NA>	NA	<NA>
## 41	Choline	HMDB00097	3.522	dd
## NA52	<NA>	<NA>	NA	<NA>
## NA.133	<NA>	<NA>	NA	<NA>
## 168	L-Threonine	HMDB00167	3.590	d
## 73	Glycerol	HMDB00131	3.566	m
## 57	D-Mannose	HMDB00169	3.579	t
## 75	Glycerol	HMDB00131	3.659	m
## 61	D-Mannose	HMDB00169	3.664	m
## 69	Ethanol	HMDB00108	3.665	q
## 138	L-Isoleucine	HMDB00172	3.676	d
## 1	1-Methylhistidine	HMDB00001	3.695	s
## 211	Sucrose	HMDB00258	3.685	s
## 55	D-Glucose	HMDB00122	3.743	m
## 63	D-Mannose	HMDB00169	3.754	m
## 122	L-Glutamic acid	HMDB00148	3.763	dd
## 59	D-Mannose	HMDB00169	3.814	m
## 217	Uridine	HMDB00296	3.816	dd
## NA39	<NA>	<NA>	NA	<NA>
## 51	D-Glucose	HMDB00122	3.904	dd
## 37	Betaine	HMDB00043	3.905	s
## 64	D-Mannose	HMDB00169	3.898	dd
## 511	D-Glucose	HMDB00122	3.904	dd
## 371	Betaine	HMDB00043	3.905	s
## 641	D-Mannose	HMDB00169	3.898	dd
## 58	D-Mannose	HMDB00169	3.938	m
## 45	Creatine	HMDB00064	3.935	s
## 221	Uridine	HMDB00296	3.922	dd
## 1401	L-Lactic acid	HMDB00190	4.115	q
## NA7	<NA>	<NA>	NA	<NA>
## NA.15	<NA>	<NA>	NA	<NA>
## 140	L-Lactic acid	HMDB00190	4.115	q
## 1621	L-Proline	HMDB00162	4.135	dd
## 2221	Uridine	HMDB00296	4.136	m
## 162	L-Proline	HMDB00162	4.135	dd

## 222	Uridine	HMDB00296	4.136	m
## NA4	<NA>	<NA>	NA	<NA>
## 1622	L-Proline	HMDB00162	4.135	dd
## 2222	Uridine	HMDB00296	4.136	m
## NA13	<NA>	<NA>	NA	<NA>
## NA21	<NA>	<NA>	NA	<NA>
## NA.112	<NA>	<NA>	NA	<NA>
## NA.25	<NA>	<NA>	NA	<NA>
## NA27	<NA>	<NA>	NA	<NA>
## NA.116	<NA>	<NA>	NA	<NA>
## NA.28	<NA>	<NA>	NA	<NA>
##	Blood_concentration	ppm_to_assign		
## 7	6.10000	0.8461		
## NA16	NA	0.8461		
## NA.19	NA	0.8461		
## NA51	NA	0.8621		
## NA.132	NA	0.8621		
## NA.214	NA	0.8621		
## NA42	NA	0.8955		
## NA.126	NA	0.8955		
## NA.211	NA	0.8955		
## 17	20.35000	0.9071		
## 88	1.60000	0.9071		
## NA50	NA	0.9071		
## 135	52.44667	0.9422		
## 92	30.75000	0.9422		
## NA29	NA	0.9422		
## 1351	52.44667	0.9546		
## 921	30.75000	0.9546		
## 102	6.10000	0.9546		
## 1421	112.74615	0.9670		
## 101	6.10000	0.9670		
## NA24	NA	0.9670		
## 1782	179.04615	0.9775		
## 142	112.74615	0.9775		
## 10	6.10000	0.9775		
## 1781	179.04615	0.9881		
## 1031	22.80000	0.9881		
## NA15	NA	0.9881		
## 178	179.04615	1.0018		
## 1371	52.44667	1.0018		
## 103	22.80000	1.0018		
## 137	52.44667	1.0136		
## NA2	NA	1.0136		
## NA.11	NA	1.0136		
## 179	179.04615	1.0521		
## NA6	NA	1.0521		
## NA.14	NA	1.0521		
## NA3	NA	1.0639		
## NA.12	NA	1.0639		
## NA.21	NA	1.0639		
## 86	83.30000	1.1835		
## 70	27.50000	1.1835		
## NA10	NA	1.1835		

## 701	27.50000	1.1938
## NA11	NA	1.1938
## NA.16	NA	1.1938
## NA14	NA	1.2002
## NA.18	NA	1.2002
## NA.22	NA	1.2002
## 12	147.74000	1.2120
## 84	2.30000	1.2120
## NA	NA	1.2120
## 121	147.74000	1.2217
## 841	2.30000	1.2217
## NA8	NA	1.2217
## 139	52.44667	1.2653
## 16	4.00000	1.2653
## NA22	NA	1.2653
## NA17	NA	1.2926
## NA.110	NA	1.2926
## NA.23	NA	1.2926
## 1671	124.23077	1.3199
## NA26	NA	1.3199
## NA.115	NA	1.3199
## 141	2235.17500	1.3399
## 167	124.23077	1.3399
## NA9	NA	1.3399
## NA1	NA	1.3515
## NA.1	NA	1.3515
## NA.2	NA	1.3515
## 1011	298.12000	1.4916
## NA45	NA	1.4916
## NA.128	NA	1.4916
## NA30	NA	1.5039
## NA.118	NA	1.5039
## NA.29	NA	1.5039
## NA34	NA	1.5792
## NA.122	NA	1.5792
## NA.210	NA	1.5792
## NA23	NA	1.5908
## NA.113	NA	1.5908
## NA.26	NA	1.5908
## NA25	NA	1.5995
## NA.114	NA	1.5995
## NA.27	NA	1.5995
## 161	151.34545	1.9937
## 134	52.44667	1.9937
## NA43	NA	1.9937
## 1612	151.34545	2.0045
## NA47	NA	2.0045
## NA.129	NA	2.0045
## 1611	151.34545	2.0172
## 9	6.10000	2.0172
## NA46	NA	2.0172
## 301	89.57000	2.0569
## 1251	45.47267	2.0569
## 891	1.60000	2.0569

## 30	89.57000	2.0632
## 125	45.47267	2.0632
## 89	1.60000	2.0632
## 163	151.34545	2.0858
## NA48	NA	2.0858
## NA.130	NA	2.0858
## 91	30.75000	2.0970
## NA35	NA	2.0970
## NA.123	NA	2.0970
## 127	539.32857	2.1518
## 97	5.57000	2.1518
## NA18	NA	2.1518
## 282	57.54000	2.2324
## NA33	NA	2.2324
## NA.121	NA	2.2324
## 283	57.54000	2.2350
## NA38	NA	2.2350
## NA.125	NA	2.2350
## 281	57.54000	2.2353
## NA32	NA	2.2353
## NA.120	NA	2.2353
## 28	57.54000	2.2463
## NA5	NA	2.2463
## NA.13	NA	2.2463
## NA19	NA	2.2501
## NA.111	NA	2.2501
## NA.24	NA	2.2501
## 180	179.04615	2.2611
## NA31	NA	2.2611
## NA.119	NA	2.2611
## NA44	NA	2.7630
## NA.127	NA	2.7630
## NA.212	NA	2.7630
## 187	55.76923	3.0602
## NA12	NA	3.0602
## NA.17	NA	3.0602
## 107	82.44688	3.2311
## 133	74.94615	3.2311
## NA20	NA	3.2311
## 54	4976.01765	3.2520
## 381	61.14750	3.2520
## 261	2.85000	3.2520
## 38	61.14750	3.2673
## 26	2.85000	3.2673
## NA40	NA	3.2673
## 183	23.52500	3.2807
## NA37	NA	3.2807
## NA.124	NA	3.2807
## 60	51.50000	3.3799
## NA28	NA	3.3799
## NA.117	NA	3.3799
## 50	4976.01765	3.4109
## 164	151.34545	3.4109
## 1211	28.50000	3.4109

## 501	4976.01765	3.4268
## 1641	151.34545	3.4268
## 1212	28.50000	3.4268
## 491	4976.01765	3.4722
## 2071	1.80000	3.4722
## NA41	NA	3.4722
## 49	4976.01765	3.4782
## 207	1.80000	3.4782
## NA36	NA	3.4782
## NA49	NA	3.4977
## NA.131	NA	3.4977
## NA.213	NA	3.4977
## 41	13.08000	3.5130
## NA52	NA	3.5130
## NA.133	NA	3.5130
## 168	124.23077	3.5798
## 73	103.51429	3.5798
## 57	51.50000	3.5798
## 75	103.51429	3.6628
## 61	51.50000	3.6628
## 69	27.50000	3.6628
## 138	52.44667	3.6894
## 1	12.52857	3.6894
## 211	1.80000	3.6894
## 55	4976.01765	3.7528
## 63	51.50000	3.7528
## 122	45.47267	3.7528
## 59	51.50000	3.8118
## 217	3.11000	3.8118
## NA39	NA	3.8118
## 51	4976.01765	3.8940
## 37	61.14750	3.8940
## 64	51.50000	3.8940
## 511	4976.01765	3.9072
## 371	61.14750	3.9072
## 641	51.50000	3.9072
## 58	51.50000	3.9276
## 45	48.47000	3.9276
## 221	3.11000	3.9276
## 1401	2235.17500	4.1119
## NA7	NA	4.1119
## NA.15	NA	4.1119
## 140	2235.17500	4.1235
## 1621	151.34545	4.1235
## 2221	3.11000	4.1235
## 162	151.34545	4.1352
## 222	3.11000	4.1352
## NA4	NA	4.1352
## 1622	151.34545	4.1468
## 2222	3.11000	4.1468
## NA13	NA	4.1468
## NA21	NA	5.2826
## NA.112	NA	5.2826
## NA.25	NA	5.2826

## NA27	NA	5.3228
## NA.116	NA	5.3228
## NA.28	NA	5.3228

assignment_NArm

##	Metabolite	HMDB_code	Shift_ppm	Type
## 7	2-Hydroxy-3-methylbutyric acid	HMDB00407	0.835	d
## 17	3-Methyl-2-oxovaleric acid	HMDB00491	0.915	t
## 88	Isovaleric acid	HMDB00718	0.915	d
## 135	L-Isoleucine	HMDB00172	0.941	t
## 92	Ketoleucine	HMDB00695	0.945	d
## 1351	L-Isoleucine	HMDB00172	0.941	t
## 921	Ketoleucine	HMDB00695	0.945	d
## 102	2-Hydroxy-3-methylbutyric acid	HMDB00407	0.965	d
## 1421	L-Leucine	HMDB00687	0.963	t
## 101	2-Hydroxy-3-methylbutyric acid	HMDB00407	0.965	d
## 1782	L-Valine	HMDB00883	0.991	d
## 142	L-Leucine	HMDB00687	0.963	t
## 10	2-Hydroxy-3-methylbutyric acid	HMDB00407	0.965	d
## 1781	L-Valine	HMDB00883	0.991	d
## 1031	L-Alpha-aminobutyric acid	HMDB00452	0.997	t
## 178	L-Valine	HMDB00883	0.991	d
## 1371	L-Isoleucine	HMDB00172	1.012	d
## 103	L-Alpha-aminobutyric acid	HMDB00452	0.997	t
## 137	L-Isoleucine	HMDB00172	1.012	d
## 179	L-Valine	HMDB00883	1.044	d
## 86	Isopropyl alcohol	HMDB00863	1.177	d
## 70	Ethanol	HMDB00108	1.185	t
## 701	Ethanol	HMDB00108	1.185	t
## 12	3-Hydroxybutyric acid	HMDB00357	1.219	d
## 84	Isobutyric acid	HMDB01873	1.225	d
## 121	3-Hydroxybutyric acid	HMDB00357	1.219	d
## 841	Isobutyric acid	HMDB01873	1.225	d
## 139	L-Isoleucine	HMDB00172	1.263	m
## 16	3-Hydroxyisovaleric acid	HMDB00754	1.275	s
## 1671	L-Threonine	HMDB00167	1.331	d
## 141	L-Lactic acid	HMDB00190	1.335	d
## 167	L-Threonine	HMDB00167	1.331	d
## 1011	L-Alanine	HMDB00161	1.485	d
## 161	L-Proline	HMDB00162	2.005	m
## 134	L-Isoleucine	HMDB00172	1.983	m
## 1612	L-Proline	HMDB00162	2.005	m
## 1611	L-Proline	HMDB00162	2.005	m
## 9	2-Hydroxy-3-methylbutyric acid	HMDB00407	2.025	m
## 301	Acetylglycine	HMDB00532	2.065	s
## 1251	L-Glutamic acid	HMDB00148	2.055	m
## 891	Isovaleric acid	HMDB00718	2.065	d
## 30	Acetylglycine	HMDB00532	2.065	s
## 125	L-Glutamic acid	HMDB00148	2.055	m
## 89	Isovaleric acid	HMDB00718	2.065	d
## 163	L-Proline	HMDB00162	2.075	m
## 91	Ketoleucine	HMDB00695	2.105	m
## 127	L-Glutamine	HMDB00641	2.140	m

## 97	L-Acetylcarnitine	HMDB00201	2.145	s
## 282	Acetone	HMDB01659	2.235	s
## 283	Acetone	HMDB01659	2.235	s
## 281	Acetone	HMDB01659	2.235	s
## 28	Acetone	HMDB01659	2.235	s
## 180	L-Valine	HMDB00883	2.276	m
## 187	Ornithine	HMDB00214	3.061	t
## 107	L-Arginine	HMDB00517	3.245	t
## 133	L-Histidine	HMDB00177	3.245	dd
## 54	D-Glucose	HMDB00122	3.248	dd
## 381	Betaine	HMDB00043	3.265	s
## 261	3-Methylhistidine	HMDB00479	3.255	m
## 38	Betaine	HMDB00043	3.265	s
## 26	3-Methylhistidine	HMDB00479	3.255	m
## 183	Myoinositol	HMDB00211	3.283	t
## 60	D-Mannose	HMDB00169	3.385	ddd
## 50	D-Glucose	HMDB00122	3.413	m
## 164	L-Proline	HMDB00162	3.425	dt
## 1211	L-Carnitine	HMDB0000062	3.419	m
## 501	D-Glucose	HMDB00122	3.413	m
## 1641	L-Proline	HMDB00162	3.425	dt
## 1212	L-Carnitine	HMDB0000062	3.419	m
## 491	D-Glucose	HMDB00122	3.473	m
## 2071	Sucrose	HMDB00258	3.475	t
## 49	D-Glucose	HMDB00122	3.473	m
## 207	Sucrose	HMDB00258	3.475	t
## 41	Choline	HMDB00097	3.522	dd
## 168	L-Threonine	HMDB00167	3.590	d
## 73	Glycerol	HMDB00131	3.566	m
## 57	D-Mannose	HMDB00169	3.579	t
## 75	Glycerol	HMDB00131	3.659	m
## 61	D-Mannose	HMDB00169	3.664	m
## 69	Ethanol	HMDB00108	3.665	q
## 138	L-Isoleucine	HMDB00172	3.676	d
## 1	1-Methylhistidine	HMDB00001	3.695	s
## 211	Sucrose	HMDB00258	3.685	s
## 55	D-Glucose	HMDB00122	3.743	m
## 63	D-Mannose	HMDB00169	3.754	m
## 122	L-Glutamic acid	HMDB00148	3.763	dd
## 59	D-Mannose	HMDB00169	3.814	m
## 217	Uridine	HMDB00296	3.816	dd
## 51	D-Glucose	HMDB00122	3.904	dd
## 37	Betaine	HMDB00043	3.905	s
## 64	D-Mannose	HMDB00169	3.898	dd
## 511	D-Glucose	HMDB00122	3.904	dd
## 371	Betaine	HMDB00043	3.905	s
## 641	D-Mannose	HMDB00169	3.898	dd
## 58	D-Mannose	HMDB00169	3.938	m
## 45	Creatine	HMDB00064	3.935	s
## 221	Uridine	HMDB00296	3.922	dd
## 1401	L-Lactic acid	HMDB00190	4.115	q
## 140	L-Lactic acid	HMDB00190	4.115	q
## 1621	L-Proline	HMDB00162	4.135	dd
## 2221	Uridine	HMDB00296	4.136	m

## 162	L-Proline	HMDB00162	4.135	dd
## 222	Uridine	HMDB00296	4.136	m
## 1622	L-Proline	HMDB00162	4.135	dd
## 2222	Uridine	HMDB00296	4.136	m
##	Blood_concentration	ppm_to_assign		
## 7	6.10000	0.8461		
## 17	20.35000	0.9071		
## 88	1.60000	0.9071		
## 135	52.44667	0.9422		
## 92	30.75000	0.9422		
## 1351	52.44667	0.9546		
## 921	30.75000	0.9546		
## 102	6.10000	0.9546		
## 1421	112.74615	0.9670		
## 101	6.10000	0.9670		
## 1782	179.04615	0.9775		
## 142	112.74615	0.9775		
## 10	6.10000	0.9775		
## 1781	179.04615	0.9881		
## 1031	22.80000	0.9881		
## 178	179.04615	1.0018		
## 1371	52.44667	1.0018		
## 103	22.80000	1.0018		
## 137	52.44667	1.0136		
## 179	179.04615	1.0521		
## 86	83.30000	1.1835		
## 70	27.50000	1.1835		
## 701	27.50000	1.1938		
## 12	147.74000	1.2120		
## 84	2.30000	1.2120		
## 121	147.74000	1.2217		
## 841	2.30000	1.2217		
## 139	52.44667	1.2653		
## 16	4.00000	1.2653		
## 1671	124.23077	1.3199		
## 141	2235.17500	1.3399		
## 167	124.23077	1.3399		
## 1011	298.12000	1.4916		
## 161	151.34545	1.9937		
## 134	52.44667	1.9937		
## 1612	151.34545	2.0045		
## 1611	151.34545	2.0172		
## 9	6.10000	2.0172		
## 301	89.57000	2.0569		
## 1251	45.47267	2.0569		
## 891	1.60000	2.0569		
## 30	89.57000	2.0632		
## 125	45.47267	2.0632		
## 89	1.60000	2.0632		
## 163	151.34545	2.0858		
## 91	30.75000	2.0970		
## 127	539.32857	2.1518		
## 97	5.57000	2.1518		
## 282	57.54000	2.2324		

## 283	57.54000	2.2350
## 281	57.54000	2.2353
## 28	57.54000	2.2463
## 180	179.04615	2.2611
## 187	55.76923	3.0602
## 107	82.44688	3.2311
## 133	74.94615	3.2311
## 54	4976.01765	3.2520
## 381	61.14750	3.2520
## 261	2.85000	3.2520
## 38	61.14750	3.2673
## 26	2.85000	3.2673
## 183	23.52500	3.2807
## 60	51.50000	3.3799
## 50	4976.01765	3.4109
## 164	151.34545	3.4109
## 1211	28.50000	3.4109
## 501	4976.01765	3.4268
## 1641	151.34545	3.4268
## 1212	28.50000	3.4268
## 491	4976.01765	3.4722
## 2071	1.80000	3.4722
## 49	4976.01765	3.4782
## 207	1.80000	3.4782
## 41	13.08000	3.5130
## 168	124.23077	3.5798
## 73	103.51429	3.5798
## 57	51.50000	3.5798
## 75	103.51429	3.6628
## 61	51.50000	3.6628
## 69	27.50000	3.6628
## 138	52.44667	3.6894
## 1	12.52857	3.6894
## 211	1.80000	3.6894
## 55	4976.01765	3.7528
## 63	51.50000	3.7528
## 122	45.47267	3.7528
## 59	51.50000	3.8118
## 217	3.11000	3.8118
## 51	4976.01765	3.8940
## 37	61.14750	3.8940
## 64	51.50000	3.8940
## 511	4976.01765	3.9072
## 371	61.14750	3.9072
## 641	51.50000	3.9072
## 58	51.50000	3.9276
## 45	48.47000	3.9276
## 221	3.11000	3.9276
## 1401	2235.17500	4.1119
## 140	2235.17500	4.1235
## 1621	151.34545	4.1235
## 2221	3.11000	4.1235
## 162	151.34545	4.1352
## 222	3.11000	4.1352

## 1622	151.34545	4.1468
## 2222	3.11000	4.1468