

# Package ‘AlpsNMR’

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**Type** Package

**Title** Automated spectral Processing System for NMR

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**Description** Reads Bruker NMR data directories both zipped and unzipped.

It provides automated and efficient signal processing for untargeted NMR metabolomics.

It is able to interpolate the samples, detect outliers, exclude regions, normalize, detect peaks, align the spectra, integrate peaks, manage metadata and visualize the spectra.

After spectra processing, it can apply multivariate analysis on extracted data.

Efficient plotting with 1-D data is also available.

Basic reading of 1D ACD/Labs exported JDX samples is also available.

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**URL** <https://sipss.github.io/AlpsNMR/>, <https://github.com/sipss/AlpsNMR>

**BugReports** <https://github.com/sipss/AlpsNMR/issues>

**LazyData** FALSE

**Depends** R (>= 4.2)

**Imports** utils, generics, graphics, stats, grDevices, cli, magrittr (>=

1.5), dplyr (>= 1.1.0), signal (>= 0.7-6), rlang (>= 0.3.0.1),

scales (>= 1.2.0), stringr (>= 1.3.1), tibble (>= 1.3.4), tidyr

(>= 1.0.0), tidyselect, readxl (>= 1.1.0), purrr (>= 0.2.5),

glue (>= 1.2.0), reshape2 (>= 1.4.3), mixOmics (>= 6.22.0),

matrixStats (>= 0.54.0), fs (>= 1.2.6), rmarkdown (>= 1.10),

speaq (>= 2.4.0), htmltools (>= 0.3.6), pcaPP (>= 1.9-73),

ggplot2 (>= 3.1.0), baseline (>= 1.2-1), vctrs (>= 0.3.0),

BiocParallel (>= 1.34.0)

**Suggests** ASICS, BiocStyle, ChemoSpec, cowplot, curl, DT (>= 0.5),

GGally (>= 1.4.0), ggrepel (>= 0.8.0), gridExtra, knitr,

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S4Vectors, testthat (>= 2.0.0), writexl (>= 1.0), zip (>=

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Autophase wrapper, ASICS export)

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| AlpsNMR-package | <i>AlpsNMR: Automated spectral Processing System for NMR</i> |
|-----------------|--|

---

## Description

AlpsNMR allows you to import NMR spectra into R and provides automated and efficient signal processing for untargeted NMR metabolomics.

## Details

The following functions can be combined with the pipe. They create or modify the `nmr_dataset` object.

- `nmr_read_samples_dir()` or `nmr_read_samples()`
- `nmr_interpolate_1D()`
- `nmr_exclude_region()`
- `nmr_normalize()`
- `plot()`

There are also functions to extract the metadata and submit the samples to irods, see the example below.

The `nmr_dataset` object is essentially a list, so it is easy to access its components for further analysis.

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### See Also

Useful links:

- <https://sipss.github.io/AlpsNMR/>
- <https://github.com/sipss/AlpsNMR>
- Report bugs at <https://github.com/sipss/AlpsNMR/issues>

### Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
my_nmr_dataset <- dataset %>%
  nmr_interpolate_1D(axis = c(0.4, 10)) %>%
  nmr_exclude_region(exclude = list(water = c(4.6, 5))) %>%
  nmr_normalize(method = "pqn") %>%
  plot()
```

---

bp\_kfold\_VIP\_analysis *K-fold bootstrap and permutation over PLS-VIP*

---

### Description

Bootstrap and permutation over PLS-VIP on AlpsNMR can be performed on both [nmr\\_dataset\\_1D](#) full spectra as well as [nmr\\_dataset\\_peak\\_table](#) peak tables.

### Usage

```
bp_kfold_VIP_analysis(dataset, y_column, k = 4, ncomp = 3, nbootstrap = 300)
```

### Arguments

|            |   |
|------------|---|
| dataset    | An <a href="#">nmr_dataset_family</a> object                                    |
| y_column   | A string with the name of the y column (present in the metadata of the dataset) |
| k          | Number of folds, recommended between 4 to 10                                    |
| ncomp      | number of components for the bootstrap models                                   |
| nbootstrap | number of bootstrap dataset   |

### Details

Use of the bootstrap and permutation methods for a more robust variable importance in the projection metric for partial least squares regression, in a k-fold cross validation

**Value**

A list with the following elements:

- `important_vips`: A list with the important vips selected
- `relevant_vips`: List of vips with some relevance
- `wilcoxon_vips`: List of vips that pass a wilcoxon test
- `vip_means`: Means of the vips scores
- `vip_score_plot`: plot of the vips scores
- `kfold_results`: results of the k `bp_VIP_analysis`
- `kfold_index`: list of index of partitions of the folds

**Examples**

```
# Data analysis for a table of integrated peaks
set.seed(42)
## Generate an artificial nmr_dataset_peak_table:
### Generate artificial metadata:
num_samples <- 64 # use an even number in this example
num_peaks <- 10
metadata <- data.frame(
  NMRExperiment = as.character(1:num_samples),
  Condition = sample(rep(c("A", "B"), times = num_samples / 2), num_samples)
)

### The matrix with peaks
peak_means <- runif(n = num_peaks, min = 300, max = 600)
peak_sd <- runif(n = num_peaks, min = 30, max = 60)
peak_matrix <- mapply(function(mu, sd) rnorm(num_samples, mu, sd),
  mu = peak_means, sd = peak_sd
)
colnames(peak_matrix) <- paste0("Peak", 1:num_peaks)
rownames(peak_matrix) <- paste0("Sample", 1:num_samples)

## Artificial differences depending on the condition:
peak_matrix[metadata$Condition == "A", "Peak2"] <-
  peak_matrix[metadata$Condition == "A", "Peak2"] + 70

peak_matrix[metadata$Condition == "A", "Peak6"] <-
  peak_matrix[metadata$Condition == "A", "Peak6"] - 60

### The nmr_dataset_peak_table
peak_table <- new_nmr_dataset_peak_table(
  peak_table = peak_matrix,
  metadata = list(external = metadata)
)

## We will use bootstrap and permutation method for VIPs selection
## in a k-fold cross validation
bp_results <- bp_kfold_VIP_analysis(peak_table, # Data to be analyzed
  y_column = "Condition", # Label
```

```

    k = 2,
    ncomp = 1,
    nbootstrap = 5
)

message("Selected VIPs are: ", bp_results$important_vips)

```

---

bp\_VIP\_analysis

*Bootstrap and permutation over PLS-VIP*


---

### Description

Bootstrap and permutation over PLS-VIP on AlpsNMR can be performed on both [nmr\\_dataset\\_1D](#) full spectra as well as [nmr\\_dataset\\_peak\\_table](#) peak tables.

### Usage

```
bp_VIP_analysis(dataset, train_index, y_column, ncomp, nbootstrap = 300)
```

### Arguments

|             |   |
|-------------|---|
| dataset     | An <a href="#">nmr_dataset_family</a> object                                    |
| train_index | set of index used to generate the bootstrap datasets                            |
| y_column    | A string with the name of the y column (present in the metadata of the dataset) |
| ncomp       | number of components used in the plsda models                                   |
| nbootstrap  | number of bootstrap dataset   |

### Details

Use of the bootstrap and permutation methods for a more robust variable importance in the projection metric for partial least squares regression

### Value

A list with the following elements:

- `important_vips`: A list with the important vips selected
- `relevant_vips`: List of vips with some relevance
- `pls_vip`: Pls-VIPs of every bootstrap
- `pls_vip_perm`: Pls-VIPs of every bootstrap with permuted variables
- `pls_vip_means`: Pls-VIPs normalized differences means
- `pls_vip_score_diff`: Differences of `pls_vip` and `pls_vip_perm`
- `pls_models`: pls models of the diferent bootstraps
- `pls_perm_models`: pls permuted models of the diferent bootstraps



- `classif_rate`: classification rate of the bootstrap models
- `general_model`: pls model trained with all train data
- `general_CR`: classification rate of the `general_model`
- `vips_model`: pls model trained with vips selection over all train data
- `vips_CR`: classification rate of the `vips_model`
- `error`: error spected in a t distribution
- `lower_bound`: lower bound of the confidence interval
- `upper_bound`: upper bound of the confidence interval

## Examples

```
# Data analysis for a table of integrated peaks

## Generate an artificial nmr_dataset_peak_table:
### Generate artificial metadata:
num_samples <- 32 # use an even number in this example
num_peaks <- 20
metadata <- data.frame(
  NMRExperiment = as.character(1:num_samples),
  Condition = rep(c("A", "B"), times = num_samples / 2)
)

### The matrix with peaks
peak_means <- runif(n = num_peaks, min = 300, max = 600)
peak_sd <- runif(n = num_peaks, min = 30, max = 60)
peak_matrix <- mapply(function(mu, sd) rnorm(num_samples, mu, sd),
  mu = peak_means, sd = peak_sd
)
colnames(peak_matrix) <- paste0("Peak", 1:num_peaks)

## Artificial differences depending on the condition:
peak_matrix[metadata$Condition == "A", "Peak2"] <-
  peak_matrix[metadata$Condition == "A", "Peak2"] + 70

peak_matrix[metadata$Condition == "A", "Peak6"] <-
  peak_matrix[metadata$Condition == "A", "Peak6"] - 60

### The nmr_dataset_peak_table
peak_table <- new_nmr_dataset_peak_table(
  peak_table = peak_matrix,
  metadata = list(external = metadata)
)

## We will use a double cross validation, splitting the samples with random
## subsampling both in the external and internal validation.
## The classification model will be a PLSDA, exploring at maximum 3 latent
## variables.
## The best model will be selected based on the area under the ROC curve
methodology <- plsda_auroc_vip_method(ncomp = 3)
model <- nmr_data_analysis(
```

```

    peak_table,
    y_column = "Condition",
    identity_column = NULL,
    external_val = list(iterations = 1, test_size = 0.25),
    internal_val = list(iterations = 3, test_size = 0.25),
    data_analysis_method = methodology
  )
  ## Area under ROC for each outer cross-validation iteration:
  model$outer_cv_results_digested$auROC

  ## The number of components for the bootstrap models is selected
  ncomps <- model$outer_cv_results$`1`$model$ncomp
  train_index <- model$train_test_partitions$outer$`1`$outer_train

  # Bootstrap and permutation for VIP selection
  bp_VIPS <- bp_VIP_analysis(peak_table, # Data to be analyzed
    train_index,
    y_column = "Condition",
    ncomp = ncomps,
    nbootstrap = 10
  )

```

---

 download\_MTBL242

*Download MTBL242*


---

## Description

Downloads the [MTBL242](#) dataset from Gralka et al., 2015. DOI: [doi:10.3945/ajcn.115.110536](#).

## Usage

```

download_MTBL242(
  dest_dir = "MTBL242",
  force = FALSE,
  keep_only_CPMG_1r = TRUE,
  keep_only_preop_and_3months = TRUE,
  keep_only_complete_time_points = TRUE
)

```

## Arguments

|                   |  |
|-------------------|--|
| dest_dir          | Directory where the dataset should be saved  |
| force             | Logical. If TRUE we do not re-download files if they exist. The function does not check whether cached versions were downloaded with different keep_only_* arguments, so please use force = TRUE if you change the keep_only_* settings. |
| keep_only_CPMG_1r | If TRUE, remove all other data beyond the CPMG real spectrum, which is enough for the tutorial   |

`keep_only_preop_and_3months`  
If TRUE, keep only the preoperative and the "three months after surgery" time points, enough for the tutorial

`keep_only_complete_time_points`  
If TRUE, remove samples that do not appear on all timepoints. Useful for the tutorial.

## Details

Besides the destination directory, this function includes three logical parameters to limit the amount of downloaded/saved data. To run the tutorial workflow:

- only the "preop" and "three months" timepoints are used,
- only subjects measured in *both* preop and three months time points are used
- only the CPMG samples are used.

If you want to run the tutorial, you can set those filters to TRUE. Then, roughly 800MB will be downloaded, and 77MB of disk space will be used, since for each downloaded sample we remove all the data but the CPMG.

If you set those filters to FALSE, roughly 1.8GB of data will be downloaded (since we have more timepoints to download) and 1.8GB of disk space will be used.

Note that we have experienced some sporadic timeouts from Metabolights, when downloading the dataset. If you get those timeouts simply re-run the download function and it will restart from where it stopped.

Note as well, that we observed several files to have incorrect data:

- Obs4\_0346s.zip is not present in the FTP server
- Obs0\_0110s.zip and Obs1\_0256s.zip incorrectly contain sample Obs1\_0010s

This function removes all three samples from the samples annotations and doesn't download their data.

## Value

Invisibly, the annotations. See the example for how to download the annotations and create a dataset from the downloaded files.

## Examples

```
## Not run:
download_MTBL242("./MTBL242")
annot <- readr::read_tsv(annotations_destfile)

dataset <- nmr_read_samples(annot$filename)
dataset <- nmr_meta_add(dataset, annot)
dataset

## End(Not run)
```

---

files\_to\_rDolphin      *Files to rDolphin*

---

### Description

The rDolphin family functions are introduced to perform automatic targeted metabolite profiling. Therefore, ensure that you interpolated from -0.1 ppm in order to consider the TSP/DSS signal at 0.0 ppm. The function generates a list with the files required by to\_rDolphin function. Then, it is required to save them with the save\_files\_to\_rDolphin. to\_rDolphin function will read the generated "parameters.csv" file. function.

### Usage

```
files_to_rDolphin(nmr_dataset, biological_origin)
```

### Arguments

nmr\_dataset      An [nmr\\_dataset](#) object  
biological\_origin  
                  String specify the type of sample (blood, urine, cell)

### Value

a list containing:

- meta\_rDolphin: metadata in rDolphin format,
- NMR\_spectra: spectra matrix
- ROI: ROI template
- Parameters: parameters file

### See Also

Other import/export functions: [Pipelines](#), [load\\_and\\_save\\_functions](#), [nmr\\_data\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_read\\_bruker\\_fid\(\)](#), [nmr\\_read\\_samples\(\)](#), [nmr\\_zip\\_bruker\\_samples\(\)](#), [save\\_files\\_to\\_rDolphin\(\)](#), [save\\_profiling\\_output\(\)](#), [to\\_ChemoSpec\(\)](#)

### Examples

```
## Not run:  
# Set the directory in which rDolphin files will be saved  
output_dir_10_rDolphin <- file.path(your_path, "10-rDolphin")  
fs::dir_create(output_dir_10_rDolphin)  
  
# Generate the files (for plasma/serum)  
files_rDolphin <- files_to_rDolphin(nmr_dataset_0_10_ppm, blood)  
  
# Save the files  
save_files_to_rDolphin(files_rDolphin, output_dir_10_rDolphin)
```

```
# Build the rDolphin object. Do not forget to set the directory
setwd(output_dir_10_rDolphin)
rDolphin_object <- to_rDolphin("Parameters.csv")

# Visualize your spectra
rDolphin_plot(rDolphin_object)

# Run the main profiling function (it takes a while)
targeted_profiling <- Automatic_targeted_profiling(rDolphin_object)

# Save results
save_profiling_output(targeted_profiling, output_dir_10_rDolphin)

save_profiling_plots(
  output_dir_10_rDolphin, targeted_profiling$final_output,
  targeted_profiling$reproducibility_data
)

# Additionally, you can run some stats
intensities <- targeted_profiling$final_output$intensity
group <- as.factor(rDolphin_object$Metadata$type)
model_PLS <- rdCV_PLS_RF(X = intensities, Y = group)

## End(Not run)
```

---

file\_lister

*NMR file lister*

---

## Description

The function lists samples from the chosen folder required to import and create a `nmr_dataset_1D` object. The function is based on the `fs::dir_ls()` function.

## Usage

```
file_lister(dataset_path_nmr, glob)
```

## Arguments

dataset\_path\_nmr

A character vector of the path where samples are.

glob

A wildcard or globbing pattern common for the samples to be read, for example ending with \*0 (spectra acquired by a NOESY sequence often end by 0: 10, 20, 30...) or \*s (for example, samples from the tutorial in this package) passed on to `grep()` to filter paths.

## Value

lists of samples from the chosen folder

## Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
lists_of_samples <- file_lister(dir_to_demo_dataset, "*0")
```

---

```
filter.nmr_dataset_family
```

*Keep samples based on metadata column criteria*

---

## Description

Keep samples based on metadata column criteria

## Usage

```
## S3 method for class 'nmr_dataset_family'
filter(.data, ...)
```

## Arguments

|                    |   |
|--------------------|---|
| <code>.data</code> | An <code>nmr_dataset_family</code> object |
| <code>...</code>   | conditions, as in <code>dplyr</code>      |

## Value

The same object, with the matching rows

## See Also

Other subsetting functions: [\[.nmr\\_dataset\(\)](#), [\[.nmr\\_dataset\\_1D\(\)](#), [\[.nmr\\_dataset\\_peak\\_table\(\)](#), [nmr\\_pca\\_outliers\\_filter\(\)](#)

## Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))

## example 1
sample_10 <- filter(dataset_1D, NMRExperiment == "10")

## example 2
# test_samples <- dataset_1D %>% filter(nmr_peak_table$metadata$external$Group == "placebo")
```

---

format.nmr\_dataset      *Format for nmr\_dataset*

---

### Description

Format for nmr\_dataset

### Usage

```
## S3 method for class 'nmr_dataset'  
format(x, ...)
```

### Arguments

x                      an [nmr\\_dataset](#) object  
...                    for future use

### Value

Format for nmr\_dataset

### See Also

Other class helper functions: [format.nmr\\_dataset\\_1D\(\)](#), [format.nmr\\_dataset\\_peak\\_table\(\)](#), [is.nmr\\_dataset\\_1D\(\)](#), [is.nmr\\_dataset\\_peak\\_table\(\)](#), [new\\_nmr\\_dataset\(\)](#), [new\\_nmr\\_dataset\\_1D\(\)](#), [new\\_nmr\\_dataset\\_peak\\_table\(\)](#), [print.nmr\\_dataset\(\)](#), [print.nmr\\_dataset\\_1D\(\)](#), [print.nmr\\_dataset\\_peak\\_table\(\)](#), [validate\\_nmr\\_dataset\(\)](#), [validate\\_nmr\\_dataset\\_family\(\)](#), [validate\\_nmr\\_dataset\\_peak\\_table\(\)](#)

### Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")  
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)  
format(dataset)
```

---

format.nmr\_dataset\_1D      *format for nmr\_dataset\_1D*

---

### Description

format for nmr\_dataset\_1D

### Usage

```
## S3 method for class 'nmr_dataset_1D'  
format(x, ...)
```

**Arguments**

x                    an `nmr_dataset_1D` object  
 ...                  for future use

**Value**

format for `nmr_dataset_1D`

**See Also**

Other class helper functions: `format.nmr_dataset()`, `format.nmr_dataset_peak_table()`, `is.nmr_dataset_1D()`, `is.nmr_dataset_peak_table()`, `new_nmr_dataset()`, `new_nmr_dataset_1D()`, `new_nmr_dataset_peak_table()`, `print.nmr_dataset()`, `print.nmr_dataset_1D()`, `print.nmr_dataset_peak_table()`, `validate_nmr_dataset()`, `validate_nmr_dataset_family()`, `validate_nmr_dataset_peak_table()`

Other `nmr_dataset_1D` functions: `[.nmr_dataset_1D()`, `get_integration_with_metadata()`, `is.nmr_dataset_1D()`, `nmr_integrate_peak_positions()`, `nmr_integrate_regions()`, `nmr_meta_add()`, `nmr_meta_export()`, `nmr_meta_get()`, `nmr_meta_get_column()`, `nmr_ppm_resolution()`, `print.nmr_dataset_1D()`

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
format(dataset_1D)
```

---

format.nmr\_dataset\_peak\_table

*Format for nmr\_dataset\_peak\_table*

---

**Description**

Format for `nmr_dataset_peak_table`

**Usage**

```
## S3 method for class 'nmr_dataset_peak_table'
format(x, ...)
```

**Arguments**

x                    an `nmr_dataset_peak_table` object  
 ...                  for future use

**Value**

Format for `nmr_dataset_peak_table`



## See Also

Other class helper functions: [format.nmr\\_dataset\(\)](#), [format.nmr\\_dataset\\_1D\(\)](#), [is.nmr\\_dataset\\_1D\(\)](#), [is.nmr\\_dataset\\_peak\\_table\(\)](#), [new\\_nmr\\_dataset\(\)](#), [new\\_nmr\\_dataset\\_1D\(\)](#), [new\\_nmr\\_dataset\\_peak\\_table\(\)](#), [print.nmr\\_dataset\(\)](#), [print.nmr\\_dataset\\_1D\(\)](#), [print.nmr\\_dataset\\_peak\\_table\(\)](#), [validate\\_nmr\\_dataset\(\)](#), [validate\\_nmr\\_dataset\\_family\(\)](#), [validate\\_nmr\\_dataset\\_peak\\_table\(\)](#)

## Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
meta <- file.path(dir_to_demo_dataset, "dummy_metadata.xlsx")
metadata <- readxl::read_excel(meta, sheet = 1)
dataset_1D <- nmr_meta_add(dataset_1D, metadata = metadata, by = "NMRExperiment")
metadata <- list(external = dataset_1D[["metadata"]][["external"]])
peak_table <- nmr_data(dataset_1D)
new <- new_nmr_dataset_peak_table(peak_table, metadata)
format(new)
```

---

get\_integration\_with\_metadata

*Get integrals with metadata from integrate peak positions*

---

## Description

Get integrals with metadata from integrate peak positions

## Usage

```
get_integration_with_metadata(integration_object)
```

## Arguments

integration\_object  
A [nmr\\_dataset](#) object

## Value

Get integrals with metadata from integrate peak positions  
integration dataframe

## See Also

Other peak integration functions: [Pipelines](#), [nmr\\_identify\\_regions\\_blood\(\)](#), [nmr\\_identify\\_regions\\_cell\(\)](#), [nmr\\_identify\\_regions\\_urine\(\)](#), [nmr\\_integrate\\_peak\\_positions\(\)](#), [nmr\\_integrate\\_regions\(\)](#)

Other [nmr\\_dataset\\_1D](#) functions: [\[.nmr\\_dataset\\_1D\(\)\]](#), [format.nmr\\_dataset\\_1D\(\)](#), [is.nmr\\_dataset\\_1D\(\)](#), [nmr\\_integrate\\_peak\\_positions\(\)](#), [nmr\\_integrate\\_regions\(\)](#), [nmr\\_meta\\_add\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_meta\\_get\(\)](#), [nmr\\_meta\\_get\\_column\(\)](#), [nmr\\_ppm\\_resolution\(\)](#), [print.nmr\\_dataset\\_1D\(\)](#)

**Examples**

```

peak_table <- matrix(1:6, nrow = 2, ncol = 3)
rownames(peak_table) <- c("10", "20")
colnames(peak_table) <- c("ppm_1.2", "ppm1.4", "ppm1.6")

dataset <- new_nmr_dataset_peak_table(
  peak_table = peak_table,
  metadata = list(external = data.frame(NMRExperiment = c("10", "20"), Condition = c("A", "B")))
)
get_integration_with_metadata(dataset)

```

---

hmdb

*The Human Metabolome DataBase multiplet table*


---

**Description**

The Human Metabolome DataBase multiplet table

**References**

<https://hmdb.ca/>

**Examples**

```

# Get all the 1-Methylhistidine peaks:
data("hmdb")
hmdb[hmdb$Metabolite == "1-Methylhistidine", ]

```

---

HMDB\_blood

*The Human Metabolome DataBase multiplet table: blood metabolites normally found in NMR-based metabolomics*


---

**Description**

The Human Metabolome DataBase multiplet table: blood metabolites normally found in NMR-based metabolomics

**References**

<https://hmdb.ca/>

**Examples**

```

data("HMDB_blood")
HMDB_blood[HMDB_blood$Metabolite == "1-Methylhistidine", ]

```

---

|           |   |
|-----------|---|
| HMDB_cell | <i>The Human Metabolome DataBase multiplet table: cell metabolites normally found in NMR-based metabolomics</i> |
|-----------|---|

---

**Description**

The Human Metabolome DataBase multiplet table: cell metabolites normally found in NMR-based metabolomics

**References**

<https://hmdb.ca/>

**Examples**

```
data("HMDB_cell")
HMDB_cell[HMDB_cell$Metabolite == "Acetone", ]
```

---

|            |  |
|------------|--|
| HMDB_urine | <i>The Human Metabolome DataBase multiplet table: urine metabolites normally found in NMR-based metabolomics</i> |
|------------|--|

---

**Description**

The Human Metabolome DataBase multiplet table: urine metabolites normally found in NMR-based metabolomics

**References**

<https://hmdb.ca/>

**Examples**

```
data("HMDB_urine")
HMDB_urine[HMDB_urine$Metabolite == "1-Methyladenosine", ]
```

is.nmr\_dataset      *Object is of [nmr\\_dataset](#) class*

---

**Description**

Object is of [nmr\\_dataset](#) class

**Usage**

```
is.nmr_dataset(x)
```

**Arguments**

x                      An object

**Value**

TRUE if the object is an [nmr\\_dataset](#), FALSE otherwise

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
is(dataset)
```

---

is.nmr\_dataset\_1D      *Object is of [nmr\\_dataset\\_1D](#) class*

---

**Description**

Object is of [nmr\\_dataset\\_1D](#) class

**Usage**

```
is.nmr_dataset_1D(x)
```

**Arguments**

x                      an [nmr\\_dataset\\_1D](#) object

**Value**

TRUE if the object is an [nmr\\_dataset\\_1D](#), FALSE otherwise

## See Also

Other class helper functions: `format.nmr_dataset()`, `format.nmr_dataset_1D()`, `format.nmr_dataset_peak_table()`, `is.nmr_dataset_peak_table()`, `new_nmr_dataset()`, `new_nmr_dataset_1D()`, `new_nmr_dataset_peak_table()`, `print.nmr_dataset()`, `print.nmr_dataset_1D()`, `print.nmr_dataset_peak_table()`, `validate_nmr_dataset()`, `validate_nmr_dataset_family()`, `validate_nmr_dataset_peak_table()`

Other `nmr_dataset_1D` functions: `[.nmr_dataset_1D()`, `format.nmr_dataset_1D()`, `get_integration_with_metadata`, `nmr_integrate_peak_positions()`, `nmr_integrate_regions()`, `nmr_meta_add()`, `nmr_meta_export()`, `nmr_meta_get()`, `nmr_meta_get_column()`, `nmr_ppm_resolution()`, `print.nmr_dataset_1D()`

## Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
result <- is(dataset_1D)
```

---

is.nmr\_dataset\_peak\_table

*Object is of `nmr_dataset_peak_table` class*

---

## Description

Object is of `nmr_dataset_peak_table` class

## Usage

```
is.nmr_dataset_peak_table(x)
```

## Arguments

x                    an `nmr_dataset_peak_table` object

## Value

TRUE if the object is an `nmr_dataset_peak_table`, FALSE otherwise

## See Also

Other class helper functions: `format.nmr_dataset()`, `format.nmr_dataset_1D()`, `format.nmr_dataset_peak_table()`, `is.nmr_dataset_1D()`, `new_nmr_dataset()`, `new_nmr_dataset_1D()`, `new_nmr_dataset_peak_table()`, `print.nmr_dataset()`, `print.nmr_dataset_1D()`, `print.nmr_dataset_peak_table()`, `validate_nmr_dataset()`, `validate_nmr_dataset_family()`, `validate_nmr_dataset_peak_table()`

## Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
meta <- file.path(dir_to_demo_dataset, "dummy_metadata.xlsx")
metadata <- readxl::read_excel(meta, sheet = 1)
dataset_1D <- nmr_meta_add(dataset_1D, metadata = metadata, by = "NMRExperiment")
metadata <- list(external = dataset_1D[["metadata"]][["external"]])
peak_table <- nmr_data(dataset_1D)
new <- new_nmr_dataset_peak_table(peak_table, metadata)
is(new)
```

---

load\_and\_save\_functions

*nmr\_dataset\_load*

---

## Description

nmr\_dataset\_load

nmr\_dataset\_save

## Usage

```
nmr_dataset_load(file_name)
```

```
nmr_dataset_save(nmr_dataset, file_name, ...)
```

## Arguments

|             |  |
|-------------|--|
| file_name   | The file name to load or save to                         |
| nmr_dataset | An object from the <a href="#">nmr_dataset_family</a>    |
| ...         | Additional arguments passed to <a href="#">saveRDS</a> . |

## Value

Functions to load and save nmr\_dataset objects

load nmr dataset

save nmr dataset

## See Also

Other import/export functions: [Pipelines](#), [files\\_to\\_rDolphin\(\)](#), [nmr\\_data\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_read\\_bruker\\_fid\(\)](#), [nmr\\_read\\_samples\(\)](#), [nmr\\_zip\\_bruker\\_samples\(\)](#), [save\\_files\\_to\\_rDolphin\(\)](#), [save\\_profiling\\_output\(\)](#), [to\\_ChemoSpec\(\)](#)

## Examples

```
# dataset <- nmr_dataset_load("test")
nmr_dataset <- nmr_dataset_load(system.file("extdata", "nmr_dataset.rds", package = "AlpsNMR"))

dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
# nmr_dataset_save(dataset, "test")
```

---

```
models_stability_plot_bootstrap
      Models stability plot
```

---

## Description

Plot stability among models of the external cross validation

## Usage

```
models_stability_plot_bootstrap(bp_results)
```

## Arguments

bp\_results      bp\_kfold\_VIP\_analysis results

## Value

A plot of models stability

## Examples

```
# Data analysis for a table of integrated peaks

## Generate an artificial nmr_dataset_peak_table:
### Generate artificial metadata:
num_samples <- 64 # use an even number in this example
num_peaks <- 20
metadata <- data.frame(
  NMRExperiment = as.character(1:num_samples),
  Condition = rep(c("A", "B"), times = num_samples / 2)
)

### The matrix with peaks
peak_means <- runif(n = num_peaks, min = 300, max = 600)
peak_sd <- runif(n = num_peaks, min = 30, max = 60)
peak_matrix <- mapply(function(mu, sd) rnorm(num_samples, mu, sd),
  mu = peak_means, sd = peak_sd
)
colnames(peak_matrix) <- paste0("Peak", 1:num_peaks)
```

```
## Artificial differences depending on the condition:
peak_matrix[metadata$Condition == "A", "Peak2"] <-
  peak_matrix[metadata$Condition == "A", "Peak2"] + 70

peak_matrix[metadata$Condition == "A", "Peak6"] <-
  peak_matrix[metadata$Condition == "A", "Peak6"] - 60

### The nmr_dataset_peak_table
peak_table <- new_nmr_dataset_peak_table(
  peak_table = peak_matrix,
  metadata = list(external = metadata)
)

## We will use bootstrap and permutation method for VIPs selection
## in a a k-fold cross validation
# bp_results <- bp_kfold_VIP_analysis(peak_table, # Data to be analyzed
#                                   y_column = "Condition", # Label
#                                   k = 3,
#                                   nbootstrap = 10)

# message("Selected VIPs are: ", bp_results$important_vips)

# models_stability_plot_bootstrap(bp_results)
```

---

models\_stability\_plot\_plsda

*Models stability plot*

---

## Description

Plot stability among models of the external cross validation

## Usage

```
models_stability_plot_plsda(model)
```

## Arguments

model            A nmr\_data\_analysis\_model

## Value

A plot of models stability



**Examples**

```

# Data analysis for a table of integrated peaks

## Generate an artificial nmr_dataset_peak_table:
### Generate artificial metadata:
num_samples <- 32 # use an even number in this example
num_peaks <- 20
metadata <- data.frame(
  NMRExperiment = as.character(1:num_samples),
  Condition = rep(c("A", "B"), times = num_samples / 2)
)

### The matrix with peaks
peak_means <- runif(n = num_peaks, min = 300, max = 600)
peak_sd <- runif(n = num_peaks, min = 30, max = 60)
peak_matrix <- mapply(function(mu, sd) rnorm(num_samples, mu, sd),
  mu = peak_means, sd = peak_sd
)
colnames(peak_matrix) <- paste0("Peak", 1:num_peaks)

## Artificial differences depending on the condition:
peak_matrix[metadata$Condition == "A", "Peak2"] <-
  peak_matrix[metadata$Condition == "A", "Peak2"] + 70

peak_matrix[metadata$Condition == "A", "Peak6"] <-
  peak_matrix[metadata$Condition == "A", "Peak6"] - 60

### The nmr_dataset_peak_table
peak_table <- new_nmr_dataset_peak_table(
  peak_table = peak_matrix,
  metadata = list(external = metadata)
)

methodology <- plsda_auroc_vip_method(ncomp = 3)
model <- nmr_data_analysis(
  peak_table,
  y_column = "Condition",
  identity_column = NULL,
  external_val = list(iterations = 3, test_size = 0.25),
  internal_val = list(iterations = 3, test_size = 0.25),
  data_analysis_method = methodology
)

# models_stability_plot_plsda(model)

```

**Description**

Create an `nmr_dataset` object

**Usage**

```
new_nmr_dataset(metadata, data_fields, axis)
```

**Arguments**

|                          |                                  |
|--------------------------|----------------------------------|
| <code>metadata</code>    | A named list of data frames      |
| <code>data_fields</code> | A named list. Check the examples |
| <code>axis</code>        | A list. Check the examples       |

**Value**

Create an `nmr_dataset` object

Create an `nmr_dataset` object

**See Also**

Other class helper functions: [format.nmr\\_dataset\(\)](#), [format.nmr\\_dataset\\_1D\(\)](#), [format.nmr\\_dataset\\_peak\\_table\(\)](#), [is.nmr\\_dataset\\_1D\(\)](#), [is.nmr\\_dataset\\_peak\\_table\(\)](#), [new\\_nmr\\_dataset\\_1D\(\)](#), [new\\_nmr\\_dataset\\_peak\\_table\(\)](#), [print.nmr\\_dataset\(\)](#), [print.nmr\\_dataset\\_1D\(\)](#), [print.nmr\\_dataset\\_peak\\_table\(\)](#), [validate\\_nmr\\_dataset\(\)](#), [validate\\_nmr\\_dataset\\_family\(\)](#), [validate\\_nmr\\_dataset\\_peak\\_table\(\)](#)

**Examples**

```
#
metadata_1D <- list(external = data.frame(NMRExperiment = c("10", "20")))
# Sample 10 and Sample 20 can have different lengths (due to different setups)
data_fields_1D <- list(data_1r = list(runif(16), runif(32)))
# Each sample has its own axis list, with one element (because this example is 1D)
axis_1D <- list(list(1:16), list(1:32))
my_1D_data <- new_nmr_dataset(metadata_1D, data_fields_1D, axis_1D)

# Example for 2D samples
metadata_2D <- list(external = data.frame(NMRExperiment = c("11", "21")))
data_fields_2D <- list(data_2rr = list(matrix(runif(16 * 3), nrow = 16, ncol = 3),
  runif(32 * 3),
  nrow = 32, ncol = 3
))
# Each sample has its own axis list, with one element (because this example is 1D)
axis_2D <- list(list(1:16, 1:3), list(1:32, 1:3))
my_2D_data <- new_nmr_dataset(metadata_2D, data_fields_2D, axis_2D)
```

---

new\_nmr\_dataset\_1D      *Creates a new 1D nmr\_dataset object from scratch*

---

### Description

Creates a new 1D nmr\_dataset object from scratch

### Usage

```
new_nmr_dataset_1D(ppm_axis, data_1r, metadata)
```

### Arguments

ppm\_axis            A numeric vector with the ppm values for the columns of data\_1r  
data\_1r            A numeric matrix with one NMR spectrum on each row  
metadata            A list of data frames with at least the NMRExperiment column

### Value

Creates a new 1D nmr\_dataset object from scratch

### See Also

Other class helper functions: [format.nmr\\_dataset\(\)](#), [format.nmr\\_dataset\\_1D\(\)](#), [format.nmr\\_dataset\\_peak\\_table\(\)](#), [is.nmr\\_dataset\\_1D\(\)](#), [is.nmr\\_dataset\\_peak\\_table\(\)](#), [new\\_nmr\\_dataset\(\)](#), [new\\_nmr\\_dataset\\_peak\\_table\(\)](#), [print.nmr\\_dataset\(\)](#), [print.nmr\\_dataset\\_1D\(\)](#), [print.nmr\\_dataset\\_peak\\_table\(\)](#), [validate\\_nmr\\_dataset\(\)](#), [validate\\_nmr\\_dataset\\_family\(\)](#), [validate\\_nmr\\_dataset\\_peak\\_table\(\)](#)

### Examples

```
# Create a random spectra matrix
nsamp <- 12
npoints <- 20
dummy_ppm_axis <- seq(from = 0.2, to = 10, length.out = npoints)
dummy_spectra_matrix <- matrix(runif(nsamp * npoints), nrow = nsamp, ncol = npoints)
metadata <- list(external = data.frame(
  NMRExperiment = paste0("Sample", 1:12),
  DummyClass = c("a", "b")
))
dummy_nmr_dataset_1D <- new_nmr_dataset_1D(
  ppm_axis = dummy_ppm_axis,
  data_1r = dummy_spectra_matrix,
  metadata = metadata
)
```

---

`new_nmr_dataset_peak_table`*Creates a new `nmr_dataset_peak_table` object from scratch*

---

### Description

Creates a new `nmr_dataset_peak_table` object from scratch

### Usage

```
new_nmr_dataset_peak_table(peak_table, metadata)
```

### Arguments

|                         |   |
|-------------------------|---|
| <code>peak_table</code> | A numeric matrix with one NMR spectrum on each row                        |
| <code>metadata</code>   | A list of data frames with at least the <code>NMRExperiment</code> column |

### Value

Creates a new `nmr_dataset_peak_table` object from scratch

### See Also

Other class helper functions: [format.nmr\\_dataset\(\)](#), [format.nmr\\_dataset\\_1D\(\)](#), [format.nmr\\_dataset\\_peak\\_table\(\)](#), [is.nmr\\_dataset\\_1D\(\)](#), [is.nmr\\_dataset\\_peak\\_table\(\)](#), [new\\_nmr\\_dataset\(\)](#), [new\\_nmr\\_dataset\\_1D\(\)](#), [print.nmr\\_dataset\(\)](#), [print.nmr\\_dataset\\_1D\(\)](#), [print.nmr\\_dataset\\_peak\\_table\(\)](#), [validate\\_nmr\\_dataset\(\)](#), [validate\\_nmr\\_dataset\\_family\(\)](#), [validate\\_nmr\\_dataset\\_peak\\_table\(\)](#)

### Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
meta <- file.path(dir_to_demo_dataset, "dummy_metadata.xlsx")
metadata <- readxl::read_excel(meta, sheet = 1)
dataset_1D <- nmr_meta_add(dataset_1D, metadata = metadata, by = "NMRExperiment")
metadata <- list(external = dataset_1D[["metadata"]][["external"]])
peak_table <- nmr_data(dataset_1D)
new <- new_nmr_dataset_peak_table(peak_table, metadata)
```

---

|           |                          |
|-----------|--------------------------|
| nmr_align | <i>Align NMR spectra</i> |
|-----------|--------------------------|

---

### Description

This function is based on [speaq::dohCluster](#).

### Usage

```
nmr_align(  
  nmr_dataset,  
  peak_data,  
  NMRExp_ref = NULL,  
  maxShift_ppm = 0.0015,  
  acceptLostPeak = FALSE  
)
```

### Arguments

|                |   |
|----------------|---|
| nmr_dataset    | An <a href="#">nmr_dataset_ID</a>   |
| peak_data      | The detected peak data given by <a href="#">nmr_detect_peaks</a> .  |
| NMRExp_ref     | NMRExperiment of the reference to use for alignment   |
| maxShift_ppm   | The maximum shift allowed, in ppm   |
| acceptLostPeak | This is an option for users, TRUE is the default value. If the users believe that all the peaks in the peak list are true positive, change it to FALSE. |

### Value

An [nmr\\_dataset\\_ID](#), with the spectra aligned

### See Also

Other alignment functions: [Pipelines](#), [nmr\\_align\\_find\\_ref\(\)](#)

Other peak alignment functions: [nmr\\_align\\_find\\_ref\(\)](#)

---

nmr\_align\_find\_ref      *Find alignment reference*

---

### Description

Find alignment reference

### Usage

```
nmr_align_find_ref(nmr_dataset, peak_data)
```

### Arguments

nmr\_dataset      An [nmr\\_dataset\\_ID](#)  
 peak\_data      The detected peak data given by [nmr\\_detect\\_peaks](#).

### Value

The NMRExperiment of the reference sample

### See Also

Other alignment functions: [Pipelines](#), [nmr\\_align\(\)](#)  
 Other peak alignment functions: [nmr\\_align\(\)](#)

---

nmr\_autophase      *Rephase 1D NMR data*

---

### Description

Use phasing algorithms to rephase data in the spectral domain.

This function may improve autophasing processing from instrument vendors. It wraps the [NMRphasing::NMRphasing\(\)](#) function, to automatically rephase spectra, allowing you to choose from a number of algorithms of which NLS, MPC\_DANM and SPC\_DANM are the most recent.

Rephasing should happen before any spectra interpolation.

Please use the `all_components = TRUE` when calling [nmr\\_read\\_samples\(\)](#) in order to load the complex spectra and fix NMR phasing correctly.

### Usage

```
nmr_autophase(  
  dataset,  
  method = c("NLS", "MPC_DANM", "MPC_EMP", "SPC_DANM", "SPC_EMP", "SPC_AAM", "SPC_DSM"),  
  withBC = FALSE,  
  ...  
)
```

**Arguments**

|         |  |
|---------|--|
| dataset | An <a href="#">nmr_dataset</a> object  |
| method  | The autophasing method. See <a href="#">NMRphasing::NMRphasing()</a> for details.  |
| withBC  | <a href="#">NMRphasing::NMRphasing</a> may perform a baseline correction using modified polynomial fitting. By default <a href="#">AlpsNMR</a> offers other baseline estimation methods and better visualization of its effect, so <a href="#">AlpsNMR</a> by default disables the baseline correction offered by <a href="#">NMRphasing</a> . |
| ...     | Other parameters passed on to <a href="#">NMRphasing::NMRphasing()</a> .   |

**Value**

A (hopefully better phased) [nmr\\_dataset](#) object, with updated real and imaginary parts.

**Examples**

```
if (requireNamespace("NMRphasing", quietly=TRUE)) {
  # Helpers to create a dataset:
  lorentzian <- function(x, x0, gamma, A) {
    A * (1 / (pi * gamma)) * ((gamma^2) / ((x - x0)^2 + gamma^2))
  }
  x <- seq(from=1, to=2, length.out = 300)
  y <- lorentzian(x, 1.3, 0.01, 1) + lorentzian(x, 1.6, 0.01, 1)
  dataset <- new_nmr_dataset(
    metadata = list(external = data.frame(NMRExperiment = "10")),
    data_fields = list(data_1r = list(y)),
    axis = list(list(x))
  )
  # Autophase, interpolate and plot:
  dataset <- nmr_autophase(dataset, method = "NLS")
  dataset <- nmr_interpolate_1D(dataset, axis = c(min = 1, max = 2, by = 0.01))
  plot(dataset)
}
```

---

nmr\_baseline\_estimation

*Estimate the baseline on an [nmr\\_dataset\\_1D](#) object, using [baseline::baseline.als](#).*

---

**Description**

Estimate the baseline on an [nmr\\_dataset\\_1D](#) object, using [baseline::baseline.als](#).

**Usage**

```
nmr_baseline_estimation(nmr_dataset, lambda = 9, p = 0.05, maxit = 20)
```

**Arguments**

|             |                                     |
|-------------|-------------------------------------|
| nmr_dataset | An <a href="#">nmr_dataset_1D</a> . |
| lambda      | 2nd derivative constraint           |
| p           | Weighting of positive residuals     |
| maxit       | Maximum number of iterations        |

**Value**

The same [nmr\\_dataset\\_1D](#) object with the data\_1r\_baseline element.

**See Also**

[baseline::baseline.als](#)

Other baseline removal functions: [nmr\\_baseline\\_removal\(\)](#)

**Examples**

```
dataset_1D <- nmr_dataset_load(system.file("extdata", "nmr_dataset.rds", package = "AlpsNMR"))
dataset_1D <- nmr_baseline_estimation(dataset_1D, lambda = 9, p = 0.01)
```

---

nmr\_baseline\_removal *Baseline Removal NMR*

---

**Description**

Removes the baseline on an [nmr\\_dataset\\_1D](#) object, using [baseline::baseline.als](#).

**Usage**

```
nmr_baseline_removal(nmr_dataset, lambda = 6, p = 0.05, maxit = 20)
```

**Arguments**

|             |                                     |
|-------------|-------------------------------------|
| nmr_dataset | An <a href="#">nmr_dataset_1D</a> . |
| lambda      | 2nd derivative constraint           |
| p           | Weighting of positive residuals     |
| maxit       | Maximum number of iterations        |

**Value**

The same [nmr\\_dataset\\_1D](#) object after baseline removal.

**See Also**

[baseline::baseline.als](#)

Other baseline removal functions: [nmr\\_baseline\\_estimation\(\)](#)



## Examples

```
dataset_1D <- nmr_dataset_load(system.file("extdata", "nmr_dataset.rds", package = "AlpsNMR"))
dataset_no_base_line <- nmr_baseline_removal(dataset_1D, lambda = 6, p = 0.01)
```

---

nmr\_baseline\_threshold

*Threshold estimation for peak detection*

---

## Description

Estimates the threshold value for peak detection on an [nmr\\_dataset\\_1D](#) object by examining a range without peaks, by default the 9.5 - 10 ppm range.

## Usage

```
nmr_baseline_threshold(  
  nmr_dataset,  
  range_without_peaks = c(9.5, 10),  
  method = c("mean3sd", "median3mad")  
)
```

## Arguments

|                     |  |
|---------------------|--|
| nmr_dataset         | An <a href="#">nmr_dataset_1D</a> .  |
| range_without_peaks | A vector with two doubles describing a range without peaks suitable for baseline detection |
| method              | Either "mean3sd" or the more robust "median3mad". See the details.                         |

## Details

Two methods can be used:

- "mean3sd": The mean3sd method computes the mean and the standard deviation of each spectrum in the 9.5 - 10 ppm range. The mean spectrum and the mean standard deviation are both vectors of length equal to the number of points in the given range. The mean of the mean spectrum the noise. The threshold is defined as center + 3 dispersion, and it is one single threshold for the whole dataset. This is the default for backwards compatibility.
- "median3mad": First we take the data matrix. If we have estimated a baseline already, subtract it. In the defined region without peaks, estimate the median of each sample and its median absolute deviation. Return a vector of length equal to the number of samples with the median+3mad for each sample. This is a new more robust method.

## Value

Numerical. A threshold value in intensity below that no peak is detected.

**See Also**

Other peak detection functions: [Pipelines](#), [nmr\\_detect\\_peaks\(\)](#), [nmr\\_detect\\_peaks\\_plot\(\)](#), [nmr\\_detect\\_peaks\\_plot\\_overview\(\)](#), [nmr\\_detect\\_peaks\\_tune\\_snr\(\)](#), [nmr\\_identify\\_regions\\_blood\(\)](#), [nmr\\_identify\\_regions\\_cell\(\)](#), [nmr\\_identify\\_regions\\_urine\(\)](#), [nmr\\_integrate\\_regions\(\)](#)

**Examples**

```
ppm_axis <- seq(from = 0, to = 10, length.out = 1000)
data_1r <- matrix(runif(1000, 0, 10), nrow = 1) + 100
dataset_1D <- new_nmr_dataset_1D(
  ppm_axis = ppm_axis,
  data_1r = data_1r,
  metadata = list(external=data.frame(NMRExperiment = "10"))
)
bl_threshold <- nmr_baseline_threshold(dataset_1D, range_without_peaks = c(9.5,10))
```

---

```
nmr_baseline_threshold_plot
      Plot the baseline thresholds
```

---

**Description**

If you have a lot of samples you can make the plot window bigger (or use "`````{r fig.height=10, fig.width=10}`" in notebooks), or choose some NMRExperiments.

**Usage**

```
nmr_baseline_threshold_plot(
  nmr_dataset,
  thresholds,
  NMRExperiment = "all",
  chemshift_range = c(9.5, 10),
  ...
)
```

**Arguments**

|                              |  |
|------------------------------|--|
| <code>nmr_dataset</code>     | An <a href="#">nmr_dataset_1D</a> object   |
| <code>thresholds</code>      | A named vector. The values are baseline thresholds. The names are NMRExperiments.  |
| <code>NMRExperiment</code>   | The NMRExperiments to plot (Use "all" to plot all of them)   |
| <code>chemshift_range</code> | The range to plot, as a first check use the <code>range_without_peaks</code> from <a href="#">nmr_baseline_threshold</a> |
| <code>...</code>             | arguments passed to <a href="#">ggplot2::aes</a> (or to <a href="#">ggplot2::aes_string</a> , being deprecated).         |

**Value**

A plot.

**Examples**

```
ppm_axis <- seq(from = 0, to = 10, length.out = 1000)
data_1r <- matrix(runif(1000, 0, 10), nrow = 1) + 100
dataset_1D <- new_nmr_dataset_1D(
  ppm_axis = ppm_axis,
  data_1r = data_1r,
  metadata = list(external=data.frame(NMRExperiment = "10"))
)
bl_threshold <- nmr_baseline_threshold(dataset_1D, range_without_peaks = c(9.5,10))
baselineThresh <- nmr_baseline_threshold(dataset_1D)
nmr_baseline_threshold_plot(dataset_1D, bl_threshold)
```

---

nmr\_batman

*Batman helpers*

---

**Description**

Batman helpers

**Usage**

```
nmr_batman_write_options(
  bopts,
  batman_dir = "BatmanInput",
  filename = "batmanOptions.txt"
)

nmr_batman_export_dataset(
  nmr_dataset,
  batman_dir = "BatmanInput",
  filename = "NMRdata.txt"
)

nmr_batman_multi_data_user_hmdb(
  batman_dir = "BatmanInput",
  filename = "multi_data_user.csv"
)

nmr_batman_multi_data_user(
  multiplet_table,
  batman_dir = "BatmanInput",
  filename = "multi_data_user.csv"
)
```

```
nmr_batman_metabolites_list(  
  metabolite_names,  
  batman_dir = "BatmanInput",  
  filename = "metabolitesList.csv"  
)
```

### Arguments

|                  |  |
|------------------|--|
| bopts            | Batman options   |
| batman_dir       | Batman input directorye                                |
| filename         | Filename to use, inside batman_dir                     |
| nmr_dataset      | An <a href="#">nmr_dataset_ID</a> object               |
| multiplet_table  | A data frame, like the <a href="#">hmdb</a> dataset    |
| metabolite_names | A character vector of the metabolite names to consider |

### Value

These are helper functions to make Batman tests easier

### See Also

Other batman functions: [nmr\\_batman\\_options\(\)](#)

### Examples

```
bopts <- nmr_batman_options()  
# nmr_batman_write_options(bopts)  
  
dataset_1D <- nmr_dataset_load(system.file("extdata", "nmr_dataset.rds", package = "AlpsNMR"))  
# nmr_batman_export_dataset(dataset_1D)  
  
message("Use of multi_data_user_hmdb")  
# multi_data_user_hmdb <- nmr_batman_multi_data_user_hmdb()  
hmdb <- NULL  
# utils::data("hmdb", package = "AlpsNMR", envir = environment())  
# hmdb <- nmr_batman_multi_data_user(hmdb)  
  
metabolite_names <- c("alanine", "glucose")  
# metabolite_names <- nmr_batman_metabolites_list(metabolite_names)
```

---

nmr\_batman\_options      *Batman Options helper*

---

## Description

Batman Options helper

## Usage

```
nmr_batman_options(  
  ppmRange = matrix(c(3, 3.1, 3.6, 3.7, 3.9, 4, 4, 4.1, 6.95, 7.05, 7.6, 7.7, 7.8, 7.9),  
    ncol = 2, byrow = TRUE),  
  specNo = "1",  
  paraProc = 4L,  
  negThresh = -0.5,  
  scaleFac = 1e+06,  
  downSamp = 1,  
  hiresFlag = 1,  
  randSeed = 100025L,  
  nItBurnin = 200L,  
  nItPostBurnin = 5000L,  
  multFile = 2L,  
  thinning = 50L,  
  cfeFlag = 0,  
  nItRerun = 5000L,  
  startTemp = 1000,  
  specFreq = 600,  
  a = 1e-05,  
  b = 1e-09,  
  muMean = 1.1,  
  muVar = 0.2,  
  muVar_prop = 0.002,  
  nuMVar = 0.0025,  
  nuMVarProp = 0.1,  
  tauMean = -0.05,  
  tauPrec = 2,  
  rdelta = 0.02,  
  csFlag = 0  
)
```

## Arguments

|           |   |
|-----------|---|
| ppmRange  | Range of ppm to process                       |
| specNo    | Index of spectra to process                   |
| paraProc  | Number of cores to use                        |
| negThresh | Truncation threshold for negative intensities |

|               |  |
|---------------|--|
| scaleFac      | Divide each spectrum by this number  |
| downSamp      | Decimate each spectrum by this factor  |
| hiresFlag     | Keep High Resolution deconvolved spectra   |
| randSeed      | A random seed  |
| nItBurnin     | Number of burn-in iterations   |
| nItPostBurnin | Number of iterations after burn-in   |
| multFile      | Multiplet file (integer)   |
| thinning      | Save MCMC state every thinning iterations  |
| cfeFlag       | Same concentration for all spectra (fixed effect)  |
| nItRerun      | Number of iterations for a batman rerun  |
| startTemp     | Start temperature  |
| specFreq      | NMR Spectrometer frequency   |
| a             | Shape parameter for the gamma distribution (used for lambda, the precision)                |
| b             | Rate distribution parameter for the gamma distribution (used for lambda, the precision)    |
| muMean        | Peak width mean in ln(Hz)  |
| muVar         | Peak width variance in ln(Hz)  |
| muVar_prop    | Peak width proposed variance in ln(Hz)   |
| nuMVar        | Peak width metabolite variance in ln(Hz)   |
| nuMVarProp    | Peak width metabolite proposed variance in ln(Hz)  |
| tauMean       | mean of the prior on tau   |
| tauPrec       | inverse of variance of prior on tau  |
| rdelta        | Truncation of the prior on peak shift (ppm)  |
| csFlag        | Specify chemical shift for each multiplet in each spectrum? (chemShiftperSpectra.csv file) |

**Value**

A batman\_options object with the Batman Options

**See Also**

Other batman functions: [nmr\\_batman](#)

**Examples**

```
bopts <- nmr_batman_options()
```

---

nmr\_build\_peak\_table    *Build a peak table from the clustered peak list*

---

### Description

Build a peak table from the clustered peak list

### Usage

```
nmr_build_peak_table(peak_data, dataset = NULL)
```

### Arguments

peak\_data        A peak list, with the cluster column  
dataset         A [nmr\\_dataset\\_1D](#) object, to get the metadata

### Value

An [nmr\\_dataset\\_peak\\_table](#), containing the peak table and the annotations

### Examples

```
peak_data <- data.frame(  
  NMRExperiment = c("10", "10", "20", "20"),  
  peak_id = paste0("Peak", 1:4),  
  ppm = c(1, 2, 1.1, 2.1),  
  area = c(10, 20, 12, 22)  
)  
clustering_result <- nmr_peak_clustering(peak_data, num_clusters = 2)  
peak_data <- clustering_result$peak_data  
peak_table <- nmr_build_peak_table(peak_data)  
stopifnot(ncol(peak_table) == 2)
```

---

nmr\_data                    *Set/Return the full spectra matrix*

---

### Description

Set/Return the full spectra matrix

## Usage

```
nmr_data(nmr_dataset, ...)  
  
## S3 method for class 'nmr_dataset_1D'  
nmr_data(nmr_dataset, what = "data_1r", ...)  
  
nmr_data(nmr_dataset, ...) <- value  
  
## S3 replacement method for class 'nmr_dataset_1D'  
nmr_data(nmr_dataset, what = "data_1r", ...) <- value
```

## Arguments

|             |  |
|-------------|--|
| nmr_dataset | An object from the <a href="#">nmr_dataset_family</a> to get the raw data from |
| ...         | Passed on to methods for compatibility   |
| what        | What data do we want to get (default: data_1r)                                 |
| value       | A matrix   |

## Value

a matrix  
The given nmr\_dataset

## See Also

Other import/export functions: [Pipelines](#), [files\\_to\\_rDolphin\(\)](#), [load\\_and\\_save\\_functions](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_read\\_bruker\\_fid\(\)](#), [nmr\\_read\\_samples\(\)](#), [nmr\\_zip\\_bruker\\_samples\(\)](#), [save\\_files\\_to\\_rDolphin\(\)](#), [save\\_profiling\\_output\(\)](#), [to\\_ChemoSpec\(\)](#)

## Examples

```
dataset_rds <- system.file("extdata", "nmr_dataset.rds", package = "AlpsNMR")  
dataset_1D <- nmr_dataset_load(dataset_rds)  
dataset_data <- nmr_data(dataset_1D)  
dataset_rds <- system.file("extdata", "nmr_dataset.rds", package = "AlpsNMR")  
dataset_1D <- nmr_dataset_load(dataset_rds)  
dataset_1D_data <- nmr_data(dataset_1D)
```

---

nmr\_dataset

*nmr\_dataset (S3 class)*

---

## Description

An `nmr_dataset` represents a set of NMR samples. It is defined as an S3 class, and it can be treated as a regular list.



## Details

It currently has the following elements:

- **metadata:** A list of data frames. Each data frame contains metadata of a given area (acquisition parameters, preprocessing parameters, general sample information...)
- **axis:** A list with length equal to the dimensionality of the data. For 1D spectra it is a list with a numeric vector
- **data\_\*:** Data arrays with the actual spectra. The first index represents the sample, the rest of the indices match the length of each **axis**. Typically **data\_1r** is a matrix with one sample on each row and the chemical shifts in the columns.
- **num\_samples:** The number of samples in the dataset

## See Also

[Functions to save and load these objects](#)

Other AlpsNMR dataset objects: [nmr\\_dataset\\_family](#)

## Examples

```
metadata_1D <- list(external = data.frame(NMRExperiment = c("10", "20")))
# Sample 10 and Sample 20 can have different lengths (due to different setups)
data_fields_1D <- list(data_1r = list(runif(16), runif(32)))
# Each sample has its own axis list, with one element (because this example is 1D)
axis_1D <- list(list(1:16), list(1:32))
my_1D_data <- new_nmr_dataset(metadata_1D, data_fields_1D, axis_1D)
```

---

|                |                                  |
|----------------|----------------------------------|
| nmr_dataset_1D | <i>nmr_dataset_1D (S3 class)</i> |
|----------------|----------------------------------|

---

## Description

An `nmr_dataset_1D` represents a set of 1D interpolated NMR samples. It is defined as an S3 class, and it can be treated as a regular list.

## Details

It currently has the following elements:

- **metadata:** A list of data frames. Each data frame contains metadata of a given area (acquisition parameters, preprocessing parameters, general sample information...)
- **axis:** A numeric vector with the chemical shift axis in ppm.
- **data\_1r:** A matrix with one sample on each row and the chemical shifts in the columns.

**Examples**

```
# Create a random spectra matrix
nsamp <- 12
npoints <- 20
dummy_ppm_axis <- seq(from = 0.2, to = 10, length.out = npoints)
dummy_spectra_matrix <- matrix(runif(nsamp * npoints), nrow = nsamp, ncol = npoints)
metadata <- list(external = data.frame(
  NMRExperiment = paste0("Sample", 1:12),
  DummyClass = c("a", "b")
))
dummy_nmr_dataset_1D <- new_nmr_dataset_1D(
  ppm_axis = dummy_ppm_axis,
  data_1r = dummy_spectra_matrix,
  metadata = metadata
)
```

---

nmr\_dataset\_family      *nmr\_dataset like objects (S3 classes)*

---

**Description**

The AlpsNMR package defines and uses several objects to manage NMR Data.

**Details**

These objects share some structure and functions, so it makes sense to have an abstract class to ensure that the shared structures are compatible

**See Also**

[Functions to save and load these objects](#)

Other AlpsNMR dataset objects: [nmr\\_dataset](#)

---

nmr\_dataset\_peak\_table  
*nmr\_dataset\_peak\_table (S3 class)*

---

**Description**

An `nmr_dataset_peak_table` represents a peak table with metadata. It is defined as an S3 class, and it can be treated as a regular list.

**Usage**

```
## S3 method for class 'nmr_dataset_peak_table'
as.data.frame(x, ...)
```

**Arguments**

x                    An nmr\_dataset\_peak\_table object,  
 ...                ignored

**Details**

- metadata: A list of data frames. Each data frame contains metadata. Usually the list only has one data frame named "external".
- peak\_table: A matrix with one sample on each row and the peaks in the columns

**Value**

A data frame with the sample metadata and the peak table

**Methods (by generic)**

- as.data.frame(nmr\_dataset\_peak\_table): Convert to a data frame

---

nmr\_dataset\_peak\_table\_to\_SummarizedExperiment

*Export nmr\_dataset\_peak\_table to SummarizedExperiment*

---

**Description**

Export nmr\_dataset\_peak\_table to SummarizedExperiment

**Usage**

```
nmr_dataset_peak_table_to_SummarizedExperiment(nmr_peak_table)
```

**Arguments**

nmr\_peak\_table    An [nmr\\_dataset\\_peak\\_table](#) object

**Value**

SummarizedExperiment object (unmodified)

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
meta <- file.path(dir_to_demo_dataset, "dummy_metadata.xlsx")
metadata <- readxl::read_excel(meta, sheet = 1)
dataset_1D <- nmr_meta_add(dataset_1D, metadata = metadata, by = "NMRExperiment")
metadata <- list(external = dataset_1D[["metadata"]][["external"]])
peak_table <- nmr_data(dataset_1D)
```

```
nmr_peak_table <- new_nmr_dataset_peak_table(peak_table, metadata)
se <- nmr_dataset_peak_table_to_SummarizedExperiment(nmr_peak_table)
```

---

```
nmr_data_1r_to_SummarizedExperiment
      Export 1D NMR data to SummarizedExperiment
```

---

### Description

Export 1D NMR data to SummarizedExperiment

### Usage

```
nmr_data_1r_to_SummarizedExperiment(nmr_dataset)
```

### Arguments

nmr\_dataset     An [nmr\\_dataset\\_1D](#) object

### Value

SummarizedExperiment An SummarizedExperiment object (unmodified)

### Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
se <- nmr_data_1r_to_SummarizedExperiment(dataset_1D)
```

---

```
nmr_data_analysis     Data analysis
```

---

### Description

Data analysis on AlpsNMR can be performed on both [nmr\\_dataset\\_1D](#) full spectra as well as [nmr\\_dataset\\_peak\\_table](#) peak tables.

### Usage

```
nmr_data_analysis(
  dataset,
  y_column,
  identity_column,
  external_val,
  internal_val,
  data_analysis_method,
  .enable_parallel = TRUE
)
```

**Arguments**

|                            |  |
|----------------------------|--|
| dataset                    | An <a href="#">nmr_dataset_family</a> object   |
| y_column                   | A string with the name of the y column (present in the metadata of the dataset)                                |
| identity_column            | NULL or a string with the name of the identity column (present in the metadata of the dataset).                |
| external_val, internal_val | A list with two elements: iterations and test_size. See <a href="#">random_subsampling</a> for further details |
| data_analysis_method       | An <a href="#">nmr_data_analysis_method</a> object   |
| .enable_parallel           | Set to FALSE to disable parallelization.   |

**Details**

The workflow consists of a double cross validation strategy using random subsampling for splitting into train and test sets. The classification model and the metric to choose the best model can be customized (see [new\\_nmr\\_data\\_analysis\\_method\(\)](#)), but for now only a PLSDA classification model with a best area under ROC curve metric is implemented (see the examples here and [plsda\\_auroc\\_vip\\_method](#))

**Value**

A list with the following elements:

- `train_test_partitions`: A list with the indices used in train and test on each of the cross-validation iterations
- `inner_cv_results`: The output returned by `train_evaluate_model` on each inner cross-validation
- `inner_cv_results_digested`: The output returned by `choose_best_inner`.
- `outer_cv_results`: The output returned by `train_evaluate_model` on each outer cross-validation
- `outer_cv_results_digested`: The output returned by `train_evaluate_model_digest_outer`.

**Examples**

```
# Data analysis for a table of integrated peaks

## Generate an artificial nmr_dataset_peak_table:
### Generate artificial metadata:
num_samples <- 32 # use an even number in this example
num_peaks <- 20
metadata <- data.frame(
  NMRExperiment = as.character(1:num_samples),
  Condition = rep(c("A", "B"), times = num_samples / 2)
)
```

```

### The matrix with peaks
peak_means <- runif(n = num_peaks, min = 300, max = 600)
peak_sd <- runif(n = num_peaks, min = 30, max = 60)
peak_matrix <- mapply(function(mu, sd) rnorm(num_samples, mu, sd),
  mu = peak_means, sd = peak_sd
)
colnames(peak_matrix) <- paste0("Peak", 1:num_peaks)

## Artificial differences depending on the condition:
peak_matrix[metadata$Condition == "A", "Peak2"] <-
  peak_matrix[metadata$Condition == "A", "Peak2"] + 70

peak_matrix[metadata$Condition == "A", "Peak6"] <-
  peak_matrix[metadata$Condition == "A", "Peak6"] - 60

### The nmr_dataset_peak_table
peak_table <- new_nmr_dataset_peak_table(
  peak_table = peak_matrix,
  metadata = list(external = metadata)
)

## We will use a double cross validation, splitting the samples with random
## subsampling both in the external and internal validation.
## The classification model will be a PLSDA, exploring at maximum 3 latent
## variables.
## The best model will be selected based on the area under the ROC curve
methodology <- plsda_auroc_vip_method(ncomp = 3)
model <- nmr_data_analysis(
  peak_table,
  y_column = "Condition",
  identity_column = NULL,
  external_val = list(iterations = 3, test_size = 0.25),
  internal_val = list(iterations = 3, test_size = 0.25),
  data_analysis_method = methodology
)
## Area under ROC for each outer cross-validation iteration:
model$outter_cv_results_digested$auroc
## Rank Product of the Variable Importance in the Projection
## (Lower means more important)
sort(model$outter_cv_results_digested$vip_rankproducts)

```

---

```
nmr_data_analysis_method
```

*Create method for NMR data analysis*

---

## Description

Create method for NMR data analysis

**Usage**

```
new_nmr_data_analysis_method(
  train_evaluate_model,
  train_evaluate_model_params_inner,
  choose_best_inner,
  train_evaluate_model_params_outer,
  train_evaluate_model_digest_outer
)
```

**Arguments**

`train_evaluate_model`

A function. The `train_evaluate_model` must have the following signature:

```
function(x_train, y_train, identity_train, x_test, y_test, identity_test, ...)
```

The `x_train` and `y_train` (and their test counterparts) are self-explanatory.

The `identity_` arguments are expected to be factors. They can be used for instance with a callback that uses [mixOmics::plsda](#) in a multilevel approach for longitudinal studies. In those studies the `identity` would be an identifier of the subject.

The `...` arguments are free to be defined for each `train_evaluate_model`.

`train_evaluate_model_params_inner`, `train_evaluate_model_params_outer`

A list with additional arguments to pass to `train_evaluate_model` either in the inner cv loop or in the outer cv loop.

`choose_best_inner`

A function with a single argument:

```
function(inner_cv_results)
```

The argument is a list of `train_evaluate_model` outputs. The return value of must be a list with at least an element named `train_evaluate_model_args`. `train_evaluate_model_args` must be a named list.

- Each element must be named as one of the `train_evaluate_model` arguments.
- Each element must be a vector as long as the number of outer cross-validations.
- The values of each vector must be the values that the `train_evaluate_model` argument must take on each outer cross-validation iteration. Additional list elements can be returned and will be given back to the user

`train_evaluate_model_digest_outer`

A function with a single argument:

```
function(outer_cv_results)
```

The argument is a list of `train_evaluate_model` outputs in outer cross-validation. The return value is returned by `nmr_data_analysis`

**Value**

An object encapsulating the method dependent functions that can be used with [nmr\\_data\\_analysis](#)

---

nmr\_detect\_peaks      *Peak detection for NMR*

---

### Description

The function detects peaks on an `nmr_dataset_1D` object, using `speaq::detectSpecPeaks`. `detectSpecPeaks` divides the whole spectra into smaller segments and uses `MassSpecWavelet::peakDetectionCWT` for peak detection.

### Usage

```
nmr_detect_peaks(
  nmr_dataset,
  nDivRange_ppm = 0.1,
  scales = seq(1, 16, 2),
  baselineThresh = NULL,
  SNR.Th = 3,
  range_without_peaks = c(9.5, 10),
  fit_lorentzians = FALSE,
  verbose = FALSE
)
```

### Arguments

|                                  |  |
|----------------------------------|--|
| <code>nmr_dataset</code>         | An <code>nmr_dataset_1D</code> .   |
| <code>nDivRange_ppm</code>       | Segment size, in ppms, to divide the spectra and search for peaks.   |
| <code>scales</code>              | The parameter of <code>peakDetectionCWT</code> function of <code>MassSpecWavelet</code> package, look it up in the original function.  |
| <code>baselineThresh</code>      | All peaks with intensities below the thresholds are excluded. Either: <ul style="list-style-type: none"> <li>• A numeric vector of length the number of samples. Each number is a threshold for that sample</li> <li>• A single number. All samples use this number as baseline threshold.</li> <li>• NULL. If that's the case, a default function is used (<code>nmr_baseline_threshold()</code>), which assumes that there is no signal in the region 9.5-10 ppm.</li> </ul> |
| <code>SNR.Th</code>              | The parameter of <code>peakDetectionCWT</code> function of <code>MassSpecWavelet</code> package, look it up in the original function. If you set -1, the function will itself recompute this value.  |
| <code>range_without_peaks</code> | A numeric vector of length two with a region without peaks, only used when <code>baselineThresh = NULL</code>  |
| <code>fit_lorentzians</code>     | If TRUE, fit a lorentzian to each detected peak, to infer its inflection points. For now disabled for backwards compatibility.   |
| <code>verbose</code>             | Logical (TRUE or FALSE). Show informational messages, such as the estimated baseline   |



**Details**

Optionally afterwards, the peak apex and the peak inflection points are used to efficiently adjust a lorentzian to each peak, and compute the peak area and width, as well as the error of the fit. These peak features can be used afterwards to reject false detections.

**Value**

A data frame with the NMRExperiment, the sample index, the position in ppm and index and the peak intensity

**See Also**

[nmr\\_align](#) for peak alignment with the detected peak table

Peak\_detection

Other peak detection functions: [Pipelines](#), [nmr\\_baseline\\_threshold\(\)](#), [nmr\\_detect\\_peaks\\_plot\(\)](#), [nmr\\_detect\\_peaks\\_plot\\_overview\(\)](#), [nmr\\_detect\\_peaks\\_tune\\_snr\(\)](#), [nmr\\_identify\\_regions\\_blood\(\)](#), [nmr\\_identify\\_regions\\_cell\(\)](#), [nmr\\_identify\\_regions\\_urine\(\)](#), [nmr\\_integrate\\_regions\(\)](#)

---

nmr\_detect\_peaks\_plot *Plot peak detection results*

---

**Description**

Plot peak detection results

**Usage**

```
nmr_detect_peaks_plot(
  nmr_dataset,
  peak_data,
  NMRExperiment = NULL,
  peak_id = NULL,
  accepted_only = NULL,
  ...
)
```

**Arguments**

|               |   |
|---------------|---|
| nmr_dataset   | An <a href="#">nmr_dataset_ID</a> .   |
| peak_data     | The peak table returned by <a href="#">nmr_detect_peaks</a>   |
| NMRExperiment | a single NMR experiment to plot   |
| peak_id       | A character vector. If given, plot only that peak id.   |
| accepted_only | If peak_data contains a logical column named accepted, only those with accepted=TRUE will be counted. By default, accepted_only = TRUE, unless a peak_id is given |
| ...           | Arguments passed to <a href="#">plot.nmr_dataset_ID</a> (chemshift_range, ...)  |

**Value**

Plot peak detection results

**See Also**

Peak\_detection nmr\_detect\_peaks

Other peak detection functions: [Pipelines](#), [nmr\\_baseline\\_threshold\(\)](#), [nmr\\_detect\\_peaks\(\)](#), [nmr\\_detect\\_peaks\\_plot\\_overview\(\)](#), [nmr\\_detect\\_peaks\\_tune\\_snr\(\)](#), [nmr\\_identify\\_regions\\_blood\(\)](#), [nmr\\_identify\\_regions\\_cell\(\)](#), [nmr\\_identify\\_regions\\_urine\(\)](#), [nmr\\_integrate\\_regions\(\)](#)

Other peak detection functions: [Pipelines](#), [nmr\\_baseline\\_threshold\(\)](#), [nmr\\_detect\\_peaks\(\)](#), [nmr\\_detect\\_peaks\\_plot\\_overview\(\)](#), [nmr\\_detect\\_peaks\\_tune\\_snr\(\)](#), [nmr\\_identify\\_regions\\_blood\(\)](#), [nmr\\_identify\\_regions\\_cell\(\)](#), [nmr\\_identify\\_regions\\_urine\(\)](#), [nmr\\_integrate\\_regions\(\)](#)

---

nmr\_detect\_peaks\_plot\_overview

*Overview of the peak detection results*

---

**Description**

This plot allows to explore the performance of the peak detection across all the samples, by summarizing how many peaks are detected on each sample at each chemical shift range.

**Usage**

```
nmr_detect_peaks_plot_overview(  
  peak_data,  
  ppm_breaks = pretty(range(peak_data$ppm), n = 20),  
  accepted_only = TRUE  
)
```

**Arguments**

|               |   |
|---------------|---|
| peak_data     | The output of <a href="#">nmr_detect_peaks()</a>  |
| ppm_breaks    | A numeric vector with the breaks that will be used to count the number of the detected peaks.         |
| accepted_only | If peak_data contains a logical column named accepted, only those with accepted=TRUE will be counted. |

**Details**

You can use this plot to find differences in the number of detected peaks across your dataset, and then use [nmr\\_detect\\_peaks\\_plot\(\)](#) to have a finer look at specific samples and chemical shifts, and assess graphically that the peak detection results that you have are correct.

**Value**

A scatter plot, with samples on one axis and chemical shift bins in the other axis. The size of each dot represents the number of peaks found on a sample within a chemical shift range.

**See Also**

Peak\_detection

Other peak detection functions: [Pipelines](#), [nmr\\_baseline\\_threshold\(\)](#), [nmr\\_detect\\_peaks\(\)](#), [nmr\\_detect\\_peaks\\_plot\(\)](#), [nmr\\_detect\\_peaks\\_tune\\_snr\(\)](#), [nmr\\_identify\\_regions\\_blood\(\)](#), [nmr\\_identify\\_regions\\_cell\(\)](#), [nmr\\_identify\\_regions\\_urine\(\)](#), [nmr\\_integrate\\_regions\(\)](#)

---

nmr\_detect\_peaks\_plot\_peaks

*Plot multiple peaks from a peak list*

---

**Description**

Plot multiple peaks from a peak list

**Usage**

```
nmr_detect_peaks_plot_peaks(
  nmr_dataset,
  peak_data,
  peak_ids,
  caption = paste("{peak_id}", "(NMRExp.\u00A0{NMRExperiment}",
    "\u003B3(ppb)\u00a0=\u00a0{gamma_ppb}", " \narea\u00a0=\u00a0{area}",
    "normse\u00a0=\u00a0{norm_rmse}")
)
```

**Arguments**

|             |  |
|-------------|--|
| nmr_dataset | The nmr_dataset_1D object with the spectra |
| peak_data   | A data frame, the peak list                |
| peak_ids    | The peak ids to plot                       |
| caption     | The caption for each subplot               |

**Value**

A plot object

---

 nmr\_detect\_peaks\_tune\_snr

*Diagnose SNR threshold in peak detection*


---

## Description

Diagnose SNR threshold in peak detection

## Usage

```
nmr_detect_peaks_tune_snr(
  ds,
  NMRExperiment = NULL,
  SNR_thresholds = seq(from = 2, to = 6, by = 0.1),
  ...
)
```

## Arguments

|                |  |
|----------------|--|
| ds             | An <a href="#">nmr_dataset_ID</a> dataset  |
| NMRExperiment  | A string with the single NMRExperiment used explore the SNR thresholds. If not given, use the first one.   |
| SNR_thresholds | A numeric vector with the SNR thresholds to explore  |
| ...            | Arguments passed on to <a href="#">nmr_detect_peaks</a>  |
|                | <a href="#">nmr_dataset</a> An <a href="#">nmr_dataset_ID</a> .  |
|                | nDivRange_ppm Segment size, in ppms, to divide the spectra and search for peaks.   |
|                | baselineThresh All peaks with intensities below the thresholds are excluded. Either: <ul style="list-style-type: none"> <li>• A numeric vector of length the number of samples. Each number is a threshold for that sample</li> <li>• A single number. All samples use this number as baseline threshold.</li> <li>• NULL. If that's the case, a default function is used (<a href="#">nmr_baseline_threshold()</a>), which assumes that there is no signal in the region 9.5-10 ppm.</li> </ul> |
|                | range_without_peaks A numeric vector of length two with a region without peaks, only used when baselineThresh = NULL   |
|                | fit_lorentzians If TRUE, fit a lorentzian to each detected peak, to infer its inflection points. For now disabled for backwards compatibility.   |
|                | verbose Logical (TRUE or FALSE). Show informational messages, such as the estimated baseline   |
|                | scales The parameter of peakDetectionCWT function of MassSpecWavelet package, look it up in the original function.   |
|                | SNR.Th The parameter of peakDetectionCWT function of MassSpecWavelet package, look it up in the original function. If you set -1, the function will itself re-compute this value.  |

**Value**

A list with the following elements:

- `peaks_detected`: A data frame with the columns from the [nmr\\_detect\\_peaks](#) output and an additional column `SNR_threshold` with the threshold used on each row.
- `num_peaks_per_region`: A summary of the `peaks_detected` table, with the number of peaks detected on each chemical shift region
- `plot_num_peaks_per_region`: A visual representation of `num_peaks_per_region`
- `plot_spectrum_and_detections`: A visual representation of the spectrum and the peaks detected with each SNR threshold. Use [plotly::ggplotly](#) or [plot\\_interactive](#) on this to zoom and explore the results.

**See Also**

`nmr_detect_peaks`

Other peak detection functions: [Pipelines](#), [nmr\\_baseline\\_threshold\(\)](#), [nmr\\_detect\\_peaks\(\)](#), [nmr\\_detect\\_peaks\\_plot\(\)](#), [nmr\\_detect\\_peaks\\_plot\\_overview\(\)](#), [nmr\\_identify\\_regions\\_blood\(\)](#), [nmr\\_identify\\_regions\\_cell\(\)](#), [nmr\\_identify\\_regions\\_urine\(\)](#), [nmr\\_integrate\\_regions\(\)](#)

---

|                                 |                                    |
|---------------------------------|------------------------------------|
| <code>nmr_exclude_region</code> | <i>Exclude region from samples</i> |
|---------------------------------|------------------------------------|

---

**Description**

Excludes a given region (for instance to remove the water peak)

**Usage**

```
nmr_exclude_region(samples, exclude = list(water = c(4.7, 5)))
```

```
## S3 method for class 'nmr_dataset_1D'
```

```
nmr_exclude_region(samples, exclude = list(water = c(4.7, 5)))
```

**Arguments**

|                      |   |
|----------------------|---|
| <code>samples</code> | An object   |
| <code>exclude</code> | A list with regions to be removed Typically: <code>exclude = list(water = c(4.7, 5.0))</code> |

**Value**

The same object, with the regions excluded

**See Also**

Other basic functions: [nmr\\_normalize\(\)](#)

## Examples

```
nmr_dataset <- nmr_dataset_load(system.file("extdata", "nmr_dataset.rds", package = "AlpsNMR"))
exclude_regions <- list(water = c(5.1, 4.5))
nmr_dataset <- nmr_exclude_region(nmr_dataset, exclude = exclude_regions)

nmr_dataset <- nmr_dataset_load(system.file("extdata", "nmr_dataset.rds", package = "AlpsNMR"))
exclude_regions <- list(water = c(5.1, 4.5))
nmr_dataset <- nmr_exclude_region(nmr_dataset, exclude = exclude_regions)
```

---

nmr\_export\_data\_1r      *Export 1D NMR data to a CSV file*

---

## Description

Export 1D NMR data to a CSV file

## Usage

```
nmr_export_data_1r(nmr_dataset, filename)
```

## Arguments

nmr\_dataset      An [nmr\\_dataset\\_1D](#) object  
filename          The csv filename

## Value

The nmr\_dataset object (unmodified)

## Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
# nmr_export_data_1r(dataset_1D, "exported_nmr_dataset")
```

---

`nmr_get_peak_distances`*Compute peak to peak distances*

---

**Description**

Compute peak to peak distances

**Usage**

```
nmr_get_peak_distances(peak_data, same_sample_dist_factor = 3)
```

**Arguments**

`peak_data`      A peak list

`same_sample_dist_factor`

The distance between two peaks from the same sample are set to this factor multiplied by the maximum of all the peak distances

**Value**

A dist object with the peak2peak distances

**Examples**

```
peak_data <- data.frame(
  NMRExperiment = c("10", "10", "20", "20"),
  peak_id = paste0("Peak", 1:4),
  ppm = c(1, 2, 1.1, 3)
)
peak2peak_dist <- nmr_get_peak_distances(peak_data)
stopifnot(abs(as.numeric(peak2peak_dist) - c(6, 0.1, 2, 0.9, 1, 6)) < 1E-8)
```

---

`nmr_identify_regions_blood`*NMR peak identification (plasma/serum samples)*

---

**Description**

Identify given regions and return a data frame with plausible assignments in human plasma/serum samples.

**Usage**

```
nmr_identify_regions_blood(  
  ppm_to_assign,  
  num_proposed_compounds = 3,  
  verbose = FALSE  
)
```

**Arguments**

ppm\_to\_assign A vector with the ppm regions to assign

num\_proposed\_compounds  
set the number of proposed metabolites sorted by the number times reported in the HMDB: HMDB\_blood.

verbose Logical value. Set it to TRUE to print additional information

**Value**

a data frame with plausible assignments.

**See Also**

Other peak detection functions: [Pipelines](#), [nmr\\_baseline\\_threshold\(\)](#), [nmr\\_detect\\_peaks\(\)](#), [nmr\\_detect\\_peaks\\_plot\(\)](#), [nmr\\_detect\\_peaks\\_plot\\_overview\(\)](#), [nmr\\_detect\\_peaks\\_tune\\_snr\(\)](#), [nmr\\_identify\\_regions\\_cell\(\)](#), [nmr\\_identify\\_regions\\_urine\(\)](#), [nmr\\_integrate\\_regions\(\)](#)

Other peak integration functions: [Pipelines](#), [get\\_integration\\_with\\_metadata\(\)](#), [nmr\\_identify\\_regions\\_cell\(\)](#), [nmr\\_identify\\_regions\\_urine\(\)](#), [nmr\\_integrate\\_peak\\_positions\(\)](#), [nmr\\_integrate\\_regions\(\)](#)

**Examples**

```
# We identify regions from from the corresponding ppm stored in a vector.  
ppm_to_assign <- c(  
  4.060960203, 3.048970634, 2.405935596,  
  3.24146865, 0.990616851, 1.002075066, 0.955325548  
)  
identification <- nmr_identify_regions_blood(ppm_to_assign)
```

---

```
nmr_identify_regions_cell  
  NMR peak identification (cell samples)
```

---

**Description**

Identify given regions and return a data frame with plausible assignments in cell samples.



## Usage

```
nmr_identify_regions_cell(  
  ppm_to_assign,  
  num_proposed_compounds = 3,  
  verbose = FALSE  
)
```

## Arguments

`ppm_to_assign` A vector with the ppm regions to assign

`num_proposed_compounds`  
set the number of proposed metabolites in HMDB\_cell.

`verbose` Logical value. Set it to TRUE to print additional information

## Value

a data frame with plausible assignments.

## See Also

Other peak detection functions: [Pipelines](#), [nmr\\_baseline\\_threshold\(\)](#), [nmr\\_detect\\_peaks\(\)](#), [nmr\\_detect\\_peaks\\_plot\(\)](#), [nmr\\_detect\\_peaks\\_plot\\_overview\(\)](#), [nmr\\_detect\\_peaks\\_tune\\_snr\(\)](#), [nmr\\_identify\\_regions\\_blood\(\)](#), [nmr\\_identify\\_regions\\_urine\(\)](#), [nmr\\_integrate\\_regions\(\)](#)

Other peak integration functions: [Pipelines](#), [get\\_integration\\_with\\_metadata\(\)](#), [nmr\\_identify\\_regions\\_blood\(\)](#), [nmr\\_identify\\_regions\\_urine\(\)](#), [nmr\\_integrate\\_peak\\_positions\(\)](#), [nmr\\_integrate\\_regions\(\)](#)

## Examples

```
# We identify regions from from the corresponding ppm stored in a vector.  
ppm_to_assign <- c(  
  4.060960203, 3.048970634, 2.405935596,  
  3.24146865, 0.990616851, 1.002075066, 0.955325548  
)  
identification <- nmr_identify_regions_cell(ppm_to_assign, num_proposed_compounds = 3)
```

---

`nmr_identify_regions_urine`

*NMR peak identification (urine samples)*

---

## Description

Identify given regions and return a data frame with plausible assignments in human urine samples. The data frame contains the column "Bouatra\_2013" showing if the proposed metabolite was reported in this publication as regular urinary metabolite.

**Usage**

```
nmr_identify_regions_urine(  
  ppm_to_assign,  
  num_proposed_compounds = 5,  
  verbose = FALSE  
)
```

**Arguments**

ppm\_to\_assign A vector with the ppm regions to assign

num\_proposed\_compounds  
set the number of proposed metabolites sorted by the number times reported in the HMDB: HMDB\_urine.

verbose Logical value. Set it to TRUE to print additional information

**Value**

a data frame with plausible assignments.

**See Also**

Other peak detection functions: [Pipelines](#), [nmr\\_baseline\\_threshold\(\)](#), [nmr\\_detect\\_peaks\(\)](#), [nmr\\_detect\\_peaks\\_plot\(\)](#), [nmr\\_detect\\_peaks\\_plot\\_overview\(\)](#), [nmr\\_detect\\_peaks\\_tune\\_snr\(\)](#), [nmr\\_identify\\_regions\\_blood\(\)](#), [nmr\\_identify\\_regions\\_cell\(\)](#), [nmr\\_integrate\\_regions\(\)](#)

Other peak integration functions: [Pipelines](#), [get\\_integration\\_with\\_metadata\(\)](#), [nmr\\_identify\\_regions\\_blood\(\)](#), [nmr\\_identify\\_regions\\_cell\(\)](#), [nmr\\_integrate\\_peak\\_positions\(\)](#), [nmr\\_integrate\\_regions\(\)](#)

**Examples**

```
# We identify regions from from the corresponding ppm stored in a vector.  
ppm_to_assign <- c(  
  4.060960203, 3.048970634, 2.405935596,  
  3.24146865, 0.990616851, 1.002075066, 0.955325548  
)  
identification <- nmr_identify_regions_urine(ppm_to_assign, num_proposed_compounds = 5)
```

---

nmr\_integrate\_peak\_positions  
*Integrate peak positions*

---

**Description**

The function allows the integration of a given ppm vector with a specific width.

**Usage**

```
nmr_integrate_peak_positions(
  samples,
  peak_pos_ppm,
  peak_width_ppm = 0.006,
  ...
)
```

**Arguments**

|                |  |
|----------------|--|
| samples        | A <a href="#">nmr_dataset</a> object   |
| peak_pos_ppm   | The peak positions, in ppm   |
| peak_width_ppm | The peak widths (or a single peak width for all peaks)   |
| ...            | Arguments passed on to <a href="#">nmr_integrate_regions</a>   |
| regions        | A named list. Each element of the list is a region, given as a named numeric vector of length two with the range to integrate. The name of the region will be the name of the column |

**Value**

Integrate peak positions

**See Also**

Other peak integration functions: [Pipelines](#), [get\\_integration\\_with\\_metadata\(\)](#), [nmr\\_identify\\_regions\\_blood\(\)](#), [nmr\\_identify\\_regions\\_cell\(\)](#), [nmr\\_identify\\_regions\\_urine\(\)](#), [nmr\\_integrate\\_regions\(\)](#)

Other `nmr_dataset_1D` functions: [\[.nmr\\_dataset\\_1D\(\)](#), [format.nmr\\_dataset\\_1D\(\)](#), [get\\_integration\\_with\\_metadata.is.nmr\\_dataset\\_1D\(\)](#), [nmr\\_integrate\\_regions\(\)](#), [nmr\\_meta\\_add\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_meta\\_get\(\)](#), [nmr\\_meta\\_get\\_column\(\)](#), [nmr\\_ppm\\_resolution\(\)](#), [print.nmr\\_dataset\\_1D\(\)](#)

---

nmr\_integrate\_regions *Integrate regions*

---

**Description**

Integrate given regions and return a data frame with them

**Usage**

```
nmr_integrate_regions(samples, regions, ...)

## S3 method for class 'nmr_dataset_1D'
nmr_integrate_regions(
  samples,
  regions,
```

```

    fix_baseline = FALSE,
    excluded_regions_as_zero = FALSE,
    set_negative_areas_to_zero = FALSE,
    ...
  )

```

## Arguments

|   |  |
|---|--|
| <code>samples</code>                    | A <a href="#">nmr_dataset</a> object   |
| <code>regions</code>                    | A named list. Each element of the list is a region, given as a named numeric vector of length two with the range to integrate. The name of the region will be the name of the column   |
| <code>...</code>                        | Keep for compatibility   |
| <code>fix_baseline</code>               | A logical. If TRUE it removes the baseline. See details below  |
| <code>excluded_regions_as_zero</code>   | A logical. It determines the behaviour of the integration when integrating regions that have been excluded. If TRUE, it will treat those regions as zero. If FALSE (the default) it will return NA values.<br>If <code>fix_baseline</code> is TRUE, then the region boundaries are used to estimate a baseline. The baseline is estimated "connecting the boundaries with a straight line". Only when the spectrum is above the baseline the area is integrated (negative contributions due to the baseline estimation are ignored). |
| <code>set_negative_areas_to_zero</code> | A logical. Ignored if <code>fix_baseline</code> is FALSE. When set to TRUE negative areas are set to zero.   |

## Value

An [nmr\\_dataset\\_peak\\_table](#) object

## See Also

Other peak detection functions: [Pipelines](#), [nmr\\_baseline\\_threshold\(\)](#), [nmr\\_detect\\_peaks\(\)](#), [nmr\\_detect\\_peaks\\_plot\(\)](#), [nmr\\_detect\\_peaks\\_plot\\_overview\(\)](#), [nmr\\_detect\\_peaks\\_tune\\_snr\(\)](#), [nmr\\_identify\\_regions\\_blood\(\)](#), [nmr\\_identify\\_regions\\_cell\(\)](#), [nmr\\_identify\\_regions\\_urine\(\)](#)

Other peak integration functions: [Pipelines](#), [get\\_integration\\_with\\_metadata\(\)](#), [nmr\\_identify\\_regions\\_blood\(\)](#), [nmr\\_identify\\_regions\\_cell\(\)](#), [nmr\\_identify\\_regions\\_urine\(\)](#), [nmr\\_integrate\\_peak\\_positions\(\)](#)

Other `nmr_dataset_1D` functions: [\[.nmr\\_dataset\\_1D\(\)](#), [format.nmr\\_dataset\\_1D\(\)](#), [get\\_integration\\_with\\_metadata.is.nmr\\_dataset\\_1D\(\)](#), [nmr\\_integrate\\_peak\\_positions\(\)](#), [nmr\\_meta\\_add\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_meta\\_get\(\)](#), [nmr\\_meta\\_get\\_column\(\)](#), [nmr\\_ppm\\_resolution\(\)](#), [print.nmr\\_dataset\\_1D\(\)](#)

## Examples

```

# Creating a dataset
dataset <- new_nmr_dataset_1D(
  ppm_axis = 1:10,
  data_1r = matrix(sample(0:99, replace = TRUE), nrow = 10),
  metadata = list(external = data.frame(NMRExperiment = c(

```

```

        "10",
        "20", "30", "40", "50", "60", "70", "80", "90", "100"
    )))
)

# Integrating selected regions
peak_table_integration <- nmr_integrate_regions(
  samples = dataset,
  regions = list(ppm = c(2, 5))
)

# Creating a dataset
dataset <- new_nmr_dataset_1D(
  ppm_axis = 1:10,
  data_1r = matrix(sample(0:99, replace = TRUE), nrow = 10),
  metadata = list(external = data.frame(NMRExperiment = c(
    "10",
    "20", "30", "40", "50", "60", "70", "80", "90", "100"
  )))
)

# Integrating selected regions
peak_table_integration <- nmr_integrate_regions(
  samples = dataset,
  regions = list(ppm = c(2, 5)),
  fix_baseline = FALSE
)

```

---

nmr\_interpolate\_1D      *Interpolate a set of 1D NMR Spectra*

---

## Description

Interpolate a set of 1D NMR Spectra

## Usage

```
nmr_interpolate_1D(samples, axis = c(min = 0.2, max = 10, by = 8e-04))
```

```
## S3 method for class 'nmr_dataset'
```

```
nmr_interpolate_1D(samples, axis = c(min = 0.2, max = 10, by = 8e-04))
```

## Arguments

|         |  |
|---------|--|
| samples | An NMR dataset   |
| axis    | The ppm axis range and optionally the ppm step. Set it to NULL for autodetection |

**Value**

Interpolate a set of 1D NMR Spectra

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))

dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
```

---

nmr\_meta\_add

*Add metadata to an nmr\_dataset object*


---

**Description**

This is useful to add metadata to datasets that can be later used for plotting spectra or further analysis (PCA...).

**Usage**

```
nmr_meta_add(nmr_data, metadata, by = "NMRExperiment")

nmr_meta_add_tidy_excel(nmr_data, excel_file)
```

**Arguments**

|            |  |
|------------|--|
| nmr_data   | an <a href="#">nmr_dataset_family</a> object   |
| metadata   | A data frame with metadata to add  |
| by         | A column name of both the <code>nmr_data\$metadata\$external</code> and the metadata data.frame. If you want to merge two columns with different headers you can use a named character vector <code>c("NMRExperiment" = "ExperimentNMR")</code> where the left side is the column name of the <code>nmr_data\$metadata\$external</code> and the right side is the column name of the metadata data frame.  |
| excel_file | Path to a tidy Excel file name. The Excel can consist of multiple sheets, that are added sequentially. The first column of the first sheet <b>MUST</b> be named as one of the metadata already present in the dataset, typically will be "NMRExperiment". The rest of the columns of the first sheet can be named at will. Similarly, the first column of the second sheet must be named as one of the metadata already present in the dataset, typically "NMRExperiment" or any of the columns of the first sheet. The rest of the columns of the second sheet can be named at will. See the package vignette for an example. |

**Value**

The `nmr_dataset_family` object with the added metadata

**See Also**

Other metadata functions: [Pipelines](#), `nmr_meta_export()`, `nmr_meta_get()`, `nmr_meta_get_column()`, `nmr_meta_groups()`

Other `nmr_dataset` functions: `nmr_meta_export()`, `nmr_meta_get()`, `nmr_meta_get_column()`

Other `nmr_dataset_1D` functions: `[.nmr_dataset_1D()`, `format.nmr_dataset_1D()`, `get_integration_with_metadata.is.nmr_dataset_1D()`, `nmr_integrate_peak_positions()`, `nmr_integrate_regions()`, `nmr_meta_export()`, `nmr_meta_get()`, `nmr_meta_get_column()`, `nmr_ppm_resolution()`, `print.nmr_dataset_1D()`

Other `nmr_dataset_peak_table` functions: `nmr_meta_export()`, `nmr_meta_get()`, `nmr_meta_get_column()`

**Examples**

```
# Load a demo dataset with four samples:
dataset <- system.file("dataset-demo", package = "AlpsNMR")
nmr_dataset <- nmr_read_samples_dir(dataset)

# At first we just have the NMRExperiment column
nmr_meta_get(nmr_dataset, groups = "external")
# Get a table with NMRExperiment -> SubjectID
dummy_metadata <- system.file("dataset-demo", "dummy_metadata.xlsx", package = "AlpsNMR")
NMRExp_SubjID <- readxl::read_excel(dummy_metadata, sheet = 1)

NMRExp_SubjID
# We can link the SubjectID column of the first excel into the dataset
nmr_dataset <- nmr_meta_add(nmr_dataset, NMRExp_SubjID, by = "NMRExperiment")
nmr_meta_get(nmr_dataset, groups = "external")
# The second excel can use the SubjectID:
SubjID_Age <- readxl::read_excel(dummy_metadata, sheet = 2)
SubjID_Age
# Add the metadata by its SubjectID:
nmr_dataset <- nmr_meta_add(nmr_dataset, SubjID_Age, by = "SubjectID")
# The final loaded metadata:
nmr_meta_get(nmr_dataset, groups = "external")

# Read a tidy excel file:

dataset <- system.file("dataset-demo", package = "AlpsNMR")
nmr_dataset <- nmr_read_samples_dir(dataset)

# At first we just have the NMRExperiment column
nmr_meta_get(nmr_dataset, groups = "external")
# Get a table with NMRExperiment -> SubjectID
dummy_metadata <- system.file("dataset-demo", "dummy_metadata.xlsx", package = "AlpsNMR")

nmr_dataset <- nmr_meta_add_tidy_excel(nmr_dataset, dummy_metadata)
# Updated Metadata:
nmr_meta_get(nmr_dataset, groups = "external")
```

---

|                 |   |
|-----------------|---|
| nmr_meta_export | <i>Export Metadata to an Excel file</i> |
|-----------------|---|

---

## Description

Export Metadata to an Excel file

## Usage

```
nmr_meta_export(  
  nmr_dataset,  
  xlsx_file,  
  groups = c("info", "orig", "title", "external")  
)
```

## Arguments

|             |   |
|-------------|---|
| nmr_dataset | An <a href="#">nmr_dataset_family</a> object  |
| xlsx_file   | "The .xlsx excel file"  |
| groups      | A character vector. Use "external" for the external metadata or the default for a more generic solution |

## Value

The Excel file name

## See Also

Other metadata functions: [Pipelines](#), [nmr\\_meta\\_add\(\)](#), [nmr\\_meta\\_get\(\)](#), [nmr\\_meta\\_get\\_column\(\)](#), [nmr\\_meta\\_groups\(\)](#)

Other nmr\_dataset functions: [nmr\\_meta\\_add\(\)](#), [nmr\\_meta\\_get\(\)](#), [nmr\\_meta\\_get\\_column\(\)](#)

Other nmr\_dataset\_1D functions: [\[.nmr\\_dataset\\_1D\(\)](#), [format.nmr\\_dataset\\_1D\(\)](#), [get\\_integration\\_with\\_metadata](#), [is.nmr\\_dataset\\_1D\(\)](#), [nmr\\_integrate\\_peak\\_positions\(\)](#), [nmr\\_integrate\\_regions\(\)](#), [nmr\\_meta\\_add\(\)](#), [nmr\\_meta\\_get\(\)](#), [nmr\\_meta\\_get\\_column\(\)](#), [nmr\\_ppm\\_resolution\(\)](#), [print.nmr\\_dataset\\_1D\(\)](#)

Other nmr\_dataset\_peak\_table functions: [nmr\\_meta\\_add\(\)](#), [nmr\\_meta\\_get\(\)](#), [nmr\\_meta\\_get\\_column\(\)](#)

Other import/export functions: [Pipelines](#), [files\\_to\\_rDolphin\(\)](#), [load\\_and\\_save\\_functions](#), [nmr\\_data\(\)](#), [nmr\\_read\\_bruker\\_fid\(\)](#), [nmr\\_read\\_samples\(\)](#), [nmr\\_zip\\_bruker\\_samples\(\)](#), [save\\_files\\_to\\_rDolphin](#), [save\\_profiling\\_output\(\)](#), [to\\_ChemoSpec\(\)](#)

## Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")  
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)  
# nmr_meta_export(dataset, "metadata.xlsx")
```



---

|              |                     |
|--------------|---------------------|
| nmr_meta_get | <i>Get metadata</i> |
|--------------|---------------------|

---

## Description

Get metadata

## Usage

```
nmr_meta_get(samples, columns = NULL, groups = NULL)
```

## Arguments

|         |  |
|---------|--|
| samples | a <a href="#">nmr_dataset_family</a> object  |
| columns | Columns to get. By default gets all the columns.   |
| groups  | Groups to get. Groups are predefined of columns. Typically "external" for metadata added with <a href="#">nmr_meta_add</a> . |

Both groups and columns can't be given simultaneously.

## Value

a data frame with the injection metadata

## See Also

Other metadata functions: [Pipelines](#), [nmr\\_meta\\_add\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_meta\\_get\\_column\(\)](#), [nmr\\_meta\\_groups\(\)](#)

Other nmr\_dataset functions: [nmr\\_meta\\_add\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_meta\\_get\\_column\(\)](#)

Other nmr\_dataset\_1D functions: [\[.nmr\\_dataset\\_1D\(\)](#), [format.nmr\\_dataset\\_1D\(\)](#), [get\\_integration\\_with\\_metadata](#), [is.nmr\\_dataset\\_1D\(\)](#), [nmr\\_integrate\\_peak\\_positions\(\)](#), [nmr\\_integrate\\_regions\(\)](#), [nmr\\_meta\\_add\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_meta\\_get\\_column\(\)](#), [nmr\\_ppm\\_resolution\(\)](#), [print.nmr\\_dataset\\_1D\(\)](#)

Other nmr\_dataset\_peak\_table functions: [nmr\\_meta\\_add\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_meta\\_get\\_column\(\)](#)

## Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
metadata <- nmr_meta_get(dataset)
```

---

nmr\_meta\_get\_column    *Get a single metadata column*

---

## Description

Get a single metadata column

## Usage

```
nmr_meta_get_column(samples, column = "NMRExperiment")
```

## Arguments

`samples`            a [nmr\\_dataset\\_family](#) object  
`column`             A column to get

## Value

A vector with the column

## See Also

Other metadata functions: [Pipelines](#), [nmr\\_meta\\_add\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_meta\\_get\(\)](#), [nmr\\_meta\\_groups\(\)](#)

Other `nmr_dataset` functions: [nmr\\_meta\\_add\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_meta\\_get\(\)](#)

Other `nmr_dataset_1D` functions: [\[.nmr\\_dataset\\_1D\(\)](#), [format.nmr\\_dataset\\_1D\(\)](#), [get\\_integration\\_with\\_metadata](#), [is.nmr\\_dataset\\_1D\(\)](#), [nmr\\_integrate\\_peak\\_positions\(\)](#), [nmr\\_integrate\\_regions\(\)](#), [nmr\\_meta\\_add\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_meta\\_get\(\)](#), [nmr\\_ppm\\_resolution\(\)](#), [print.nmr\\_dataset\\_1D\(\)](#)

Other `nmr_dataset_peak_table` functions: [nmr\\_meta\\_add\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_meta\\_get\(\)](#)

## Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")  
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)  
metadata_column <- nmr_meta_get_column(dataset)
```

---

|                 |   |
|-----------------|---|
| nmr_meta_groups | <i>Get the names of metadata groups</i> |
|-----------------|---|

---

**Description**

Get the names of metadata groups

**Usage**

```
nmr_meta_groups(samples)
```

**Arguments**

samples            a [nmr\\_dataset\\_family](#) object

**Value**

A character vector with group names

**See Also**

Other metadata functions: [Pipelines](#), [nmr\\_meta\\_add\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_meta\\_get\(\)](#), [nmr\\_meta\\_get\\_column\(\)](#)

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
metadata_column <- nmr_meta_get_column(dataset)
```

---

|               |   |
|---------------|---|
| nmr_normalize | <i>Normalize nmr_dataset_ID samples</i> |
|---------------|---|

---

**Description**

The `nmr_normalize` function is used to normalize all the samples according to a given criteria.

**Usage**

```
nmr_normalize(
  samples,
  method = c("area", "max", "value", "region", "pqn", "none"),
  ...
)

nmr_normalize_extra_info(samples)
```

## Arguments

|         |  |
|---------|--|
| samples | A <a href="#">nmr_dataset_1D</a> object  |
| method  | The criteria to be used for normalization - area: Normalize to the total area - max: Normalize to the maximum intensity - value: Normalize each sample to a user defined value - region: Integrate a region and normalize each sample to that region - pqn: Use Probabalistic Quotient Normalization for normalization - none: Do not normalize at all |
| ...     | Method dependent arguments: - method == "value": - value: A numeric vector with the normalization values to use - method == "region": - ppm_range: A chemical shift region to integrate - . . . : Other arguments passed on to <a href="#">nmr_integrate_regions</a>   |

## Details

The aim is to correct from changes between samples, so no matter the criteria used to normalize, once we get the factors (e.g. the areas), we divide them by the median normalization factor to avoid introducing global scaling factors.

The `nmr_normalize_extra_info` function is used to extract additional information after the normalization. Typically, we want to know what was the actual normalization factor applied to each sample. The extra information includes a plot, representing the dispersion of the normalization factor for each sample.

## Value

The [nmr\\_dataset\\_1D](#) object, with the samples normalized. Further information for diagnostic of the normalization process is also saved and can be extracted by calling `nmr_normalize_extra_info()` afterwards.

## See Also

Other basic functions: [nmr\\_exclude\\_region\(\)](#)

## Examples

```
nmr_dataset <- nmr_dataset_load(system.file("extdata", "nmr_dataset.rds", package = "AlpsNMR"))
nmr_dataset <- nmr_normalize(nmr_dataset, method = "area")
norm_dataset <- nmr_normalize(nmr_dataset)
norm_dataset$plot
nmr_dataset <- nmr_dataset_load(system.file("extdata", "nmr_dataset.rds", package = "AlpsNMR"))
nmr_dataset <- nmr_normalize(nmr_dataset, method = "area")
norm_extra_info <- nmr_normalize_extra_info(nmr_dataset)
norm_extra_info$plot
```

---

```
nmr_pca_build_model Build a PCA on for an nmr_dataset
```

---

### Description

This function builds a PCA model with all the NMR spectra. Regions with zero values (excluded regions) or near-zero variance regions are automatically excluded from the analysis.

### Usage

```
nmr_pca_build_model(
  nmr_dataset,
  ncomp = NULL,
  center = TRUE,
  scale = FALSE,
  ...
)

## S3 method for class 'nmr_dataset_1D'
nmr_pca_build_model(
  nmr_dataset,
  ncomp = NULL,
  center = TRUE,
  scale = FALSE,
  ...
)
```

### Arguments

|                          |  |
|--------------------------|--|
| <code>nmr_dataset</code> | a <a href="#">nmr_dataset_1D</a> object  |
| <code>ncomp</code>       | Integer, if data is complete <code>ncomp</code> decides the number of components and associated eigenvalues to display from the <code>pcasvd</code> algorithm and if the data has missing values, <code>ncomp</code> gives the number of components to keep to perform the reconstitution of the data using the NIPALS algorithm. If <code>NULL</code> , function sets <code>ncomp = min(nrow(X), ncol(X))</code>      |
| <code>center</code>      | (Default= <code>TRUE</code> ) Logical, whether the variables should be shifted to be zero centered. Only set to <code>FALSE</code> if data have already been centered. Alternatively, a vector of length equal the number of columns of <code>X</code> can be supplied. The value is passed to <code>scale</code> . If the data contain missing values, columns should be centered for reliable results.               |
| <code>scale</code>       | (Default= <code>FALSE</code> ) Logical indicating whether the variables should be scaled to have unit variance before the analysis takes place. The default is <code>FALSE</code> for consistency with <code>prcomp</code> function, but in general scaling is advisable. Alternatively, a vector of length equal the number of columns of <code>X</code> can be supplied. The value is passed to <code>scale</code> . |
| <code>...</code>         | Additional arguments passed on to <a href="#">mixOmics::pca</a>  |

**Value**

A PCA model as given by [mixOmics::pca](#) with two additional attributes:

- `nmr_data_axis` containing the full ppm axis
- `nmr_included` with the data points included in the model These attributes are used internally by AlpsNMR to create loading plots

**See Also**

Other PCA related functions: [nmr\\_pca\\_outliers\(\)](#), [nmr\\_pca\\_outliers\\_filter\(\)](#), [nmr\\_pca\\_outliers\\_plot\(\)](#), [nmr\\_pca\\_outliers\\_robust\(\)](#), [nmr\\_pca\\_plots](#)

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
model <- nmr_pca_build_model(dataset_1D)
```

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
model <- nmr_pca_build_model(dataset_1D)
```

---

|                               |   |
|-------------------------------|---|
| <code>nmr_pca_outliers</code> | <i>Compute PCA residuals and score distance for each sample</i> |
|-------------------------------|---|

---

**Description**

Compute PCA residuals and score distance for each sample

**Usage**

```
nmr_pca_outliers(
  nmr_dataset,
  pca_model,
  ncomp = NULL,
  quantile_critical = 0.975
)
```

**Arguments**

|                                |   |
|--------------------------------|---|
| <code>nmr_dataset</code>       | An <a href="#">nmr_dataset_1D</a> object                      |
| <code>pca_model</code>         | A pca model returned by <a href="#">nmr_pca_build_model</a>   |
| <code>ncomp</code>             | Number of components to use. Use NULL for 90% of the variance |
| <code>quantile_critical</code> | critical quantile   |

**Value**

A list with:

- outlier\_info: A data frame with the NMRExperiment, the Q residuals and T scores
- ncomp: Number of components used to compute Q and T
- Tscore\_critical, QResidual\_critical: Critical values, given a quantile, for both Q and T.

**See Also**

Other PCA related functions: [nmr\\_pca\\_build\\_model\(\)](#), [nmr\\_pca\\_outliers\\_filter\(\)](#), [nmr\\_pca\\_outliers\\_plot\(\)](#), [nmr\\_pca\\_outliers\\_robust\(\)](#), [nmr\\_pca\\_plots](#)

Other outlier detection functions: [Pipelines](#), [nmr\\_pca\\_outliers\\_filter\(\)](#), [nmr\\_pca\\_outliers\\_plot\(\)](#), [nmr\\_pca\\_outliers\\_robust\(\)](#)

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
model <- nmr_pca_build_model(dataset_1D)
outliers_info <- nmr_pca_outliers(dataset_1D, model)
```

---

nmr\_pca\_outliers\_filter

*Exclude outliers*

---

**Description**

Exclude outliers

**Usage**

```
nmr_pca_outliers_filter(nmr_dataset, pca_outliers)
```

**Arguments**

nmr\_dataset     An [nmr\\_dataset\\_1D](#) object  
pca\_outliers    The output from [nmr\\_pca\\_outliers\(\)](#)

**Value**

An [nmr\\_dataset\\_1D](#) without the detected outliers

**See Also**

Other PCA related functions: [nmr\\_pca\\_build\\_model\(\)](#), [nmr\\_pca\\_outliers\(\)](#), [nmr\\_pca\\_outliers\\_plot\(\)](#), [nmr\\_pca\\_outliers\\_robust\(\)](#), [nmr\\_pca\\_plots](#)

Other outlier detection functions: [Pipelines](#), [nmr\\_pca\\_outliers\(\)](#), [nmr\\_pca\\_outliers\\_plot\(\)](#), [nmr\\_pca\\_outliers\\_robust\(\)](#)

Other subsetting functions: [\[.nmr\\_dataset\(\)\]](#), [\[.nmr\\_dataset\\_1D\(\)\]](#), [\[.nmr\\_dataset\\_peak\\_table\(\)\]](#), [filter.nmr\\_dataset\\_family\(\)](#)

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
model <- nmr_pca_build_model(dataset_1D)
outliers_info <- nmr_pca_outliers(dataset_1D, model)
dataset_whitout_outliers <- nmr_pca_outliers_filter(dataset_1D, outliers_info)
```

---

`nmr_pca_outliers_plot` *Plot for outlier detection diagnostic*

---

**Description**

Plot for outlier detection diagnostic

**Usage**

```
nmr_pca_outliers_plot(nmr_dataset, pca_outliers, ...)
```

**Arguments**

|                           |   |
|---------------------------|---|
| <code>nmr_dataset</code>  | An <a href="#">nmr_dataset_1D</a> object  |
| <code>pca_outliers</code> | The output from <a href="#">nmr_pca_outliers()</a>  |
| <code>...</code>          | Additional parameters passed on to <a href="#">ggplot2::aes()</a> (or now deprecated to <a href="#">ggplot2::aes_string()</a> ) |

**Value**

A plot for the outlier detection

**See Also**

Other PCA related functions: [nmr\\_pca\\_build\\_model\(\)](#), [nmr\\_pca\\_outliers\(\)](#), [nmr\\_pca\\_outliers\\_filter\(\)](#), [nmr\\_pca\\_outliers\\_robust\(\)](#), [nmr\\_pca\\_plots](#)

Other outlier detection functions: [Pipelines](#), [nmr\\_pca\\_outliers\(\)](#), [nmr\\_pca\\_outliers\\_filter\(\)](#), [nmr\\_pca\\_outliers\\_robust\(\)](#)



## Examples

```
# dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
# dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
# dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
# model <- nmr_pca_build_model(dataset_1D)
# outliers_info <- nmr_pca_outliers(dataset_1D, model)
# nmr_pca_outliers_plot(dataset_1D, outliers_info)
```

---

nmr\_pca\_outliers\_robust

*Outlier detection through robust PCA*

---

## Description

Outlier detection through robust PCA

## Usage

```
nmr_pca_outliers_robust(nmr_dataset, ncomp = 5)
```

## Arguments

nmr\_dataset      An nmr\_dataset\_1D object

ncomp            Number of rPCA components to use

We have observed that the statistical test used as a threshold for outlier detection usually flags as outliers too many samples, due possibly to a lack of gaussianity. As a workaround, a heuristic method has been implemented: We know that in the Q residuals vs T scores plot from [nmr\\_pca\\_outliers\\_plot\(\)](#) outliers are on the right or on the top of the plot, and quite separated from non-outlier samples.

To determine the critical value, both for Q and T, we find the biggest gap between samples in the plot and use as critical value the center of the gap.

This approach seems to work well when there are outliers, but it fails when there isn't any outlier. For that case, the gap would be placed anywhere and that is not desirable as many samples would be incorrectly flagged. The second assumption that we use is that no more than 10% the samples may pass our critical value. If more than 10% pass the critical value, then we assume that our heuristics are not reasonable and we don't set any critical limit.

## Value

A list similar to [nmr\\_pca\\_outliers](#)

**See Also**

Other PCA related functions: [nmr\\_pca\\_build\\_model\(\)](#), [nmr\\_pca\\_outliers\(\)](#), [nmr\\_pca\\_outliers\\_filter\(\)](#), [nmr\\_pca\\_outliers\\_plot\(\)](#), [nmr\\_pca\\_plots](#)

Other outlier detection functions: [Pipelines](#), [nmr\\_pca\\_outliers\(\)](#), [nmr\\_pca\\_outliers\\_filter\(\)](#), [nmr\\_pca\\_outliers\\_plot\(\)](#)

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
outliers_info <- nmr_pca_outliers_robust(dataset_1D)
```

---

nmr\_pca\_plots

*Plotting functions for PCA*

---

**Description**

Plotting functions for PCA

**Usage**

```
nmr_pca_plot_variance(pca_model)
```

```
nmr_pca_scoreplot(nmr_dataset, pca_model, comp = seq_len(2), ...)
```

```
nmr_pca_loadingplot(pca_model, comp)
```

**Arguments**

|                          |   |
|--------------------------|---|
| <code>pca_model</code>   | A PCA model trained with <a href="#">nmr_pca_build_model</a>                              |
| <code>nmr_dataset</code> | an <a href="#">nmr_dataset_1D</a> object  |
| <code>comp</code>        | Components to represent   |
| <code>...</code>         | Additional aesthetics passed on to <a href="#">ggplot2::aes</a> (use bare unquoted names) |

**Value**

Plot of PCA

**See Also**

Other PCA related functions: [nmr\\_pca\\_build\\_model\(\)](#), [nmr\\_pca\\_outliers\(\)](#), [nmr\\_pca\\_outliers\\_filter\(\)](#), [nmr\\_pca\\_outliers\\_plot\(\)](#), [nmr\\_pca\\_outliers\\_robust\(\)](#)

## Examples

```
dataset_1D <- nmr_dataset_load(system.file("extdata", "nmr_dataset.rds", package = "AlpsNMR"))
model <- nmr_pca_build_model(dataset_1D)
nmr_pca_plot_variance(model)
nmr_pca_scoreplot(dataset_1D, model)
nmr_pca_loadingplot(model, 1)
```

---

nmr\_peak\_clustering    *Peak clustering*

---

## Description

Peak clustering

## Usage

```
nmr_peak_clustering(  
  peak_data,  
  peak2peak_dist = NULL,  
  num_clusters = NULL,  
  max_dist_thresh_ppb = NULL,  
  verbose = FALSE  
)
```

## Arguments

|                     |   |
|---------------------|---|
| peak_data           | The peak list   |
| peak2peak_dist      | The distances obtained with <a href="#">nmr_get_peak_distances</a> . If NULL it is computed from peak_data  |
| num_clusters        | If you want to fix the number of clusters. Leave NULL if you want to estimate it  |
| max_dist_thresh_ppb | To estimate the number of clusters, we enforce a limit on how far two peaks of the same cluster may be. By default this threshold will be computed as 3 times the median peak width (gamma), as given in the peak list. |
| verbose             | A logical vector to print additional information  |

## Value

A list including:

- The peak\_data with an additional "cluster" column
- cluster: the hierarchical cluster
- num\_clusters: an estimation of the number of clusters
- num\_cluster\_estimation: A list with tables and plots to justify the number of cluster estimation

**Examples**

```

peak_data <- data.frame(
  NMRExperiment = c("10", "10", "20", "20"),
  peak_id = paste0("Peak", 1:4),
  ppm = c(1, 2, 1.1, 2.2),
  gamma_ppb = 100
)
clustering_result <- nmr_peak_clustering(peak_data)
peak_data <- clustering_result$peak_data
stopifnot("cluster" %in% colnames(peak_data))

```

---

```
nmr_peak_clustering_plot
```

*Plot clustering results*

---

**Description**

Plot clustering results

**Usage**

```

nmr_peak_clustering_plot(
  dataset,
  peak_list_clustered,
  NMRExperiments,
  chemshift_range,
  baselineThresh = NULL
)

```

**Arguments**

**dataset** The `nmr_dataset_1D` object

**peak\_list\_clustered** A peak list table with a clustered column

**NMRExperiments** Two and only two experiments to compare in the plot

**chemshift\_range** A region, make it so it does not cover a huge range (maybe 1ppm or less)

**baselineThresh** If given (as returned from the `nmr_baseline_threshold()`) the baseline threshold will be plotted. This can be useful to diagnose whether a peak is missing due to this threshold or due to other parameters (e.g. SNR. Th). See `nmr_detect_peaks()`.

**Value**

A plot of the two experiments in the given chemshift range, with lines connecting peaks identified as the same and dots showing peaks without pairs

---

nmr\_ppm\_resolution      *PPM resolution of the spectra*

---

## Description

The function gets the ppm resolution of the dataset using the median of the difference of data points.

## Usage

```
nmr_ppm_resolution(nmr_dataset)

## S3 method for class 'nmr_dataset'
nmr_ppm_resolution(nmr_dataset)

## S3 method for class 'nmr_dataset_1D'
nmr_ppm_resolution(nmr_dataset)
```

## Arguments

nmr\_dataset      An object containing NMR samples

## Value

Numeric (the ppm resolution, measured in ppms)

## See Also

Other nmr\_dataset\_1D functions: [\[.nmr\\_dataset\\_1D\(\)](#), [format.nmr\\_dataset\\_1D\(\)](#), [get\\_integration\\_with\\_metadata.is.nmr\\_dataset\\_1D\(\)](#), [nmr\\_integrate\\_peak\\_positions\(\)](#), [nmr\\_integrate\\_regions\(\)](#), [nmr\\_meta\\_add\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_meta\\_get\(\)](#), [nmr\\_meta\\_get\\_column\(\)](#), [print.nmr\\_dataset\\_1D\(\)](#)

## Examples

```
nmr_dataset <- nmr_dataset_load(system.file("extdata", "nmr_dataset.rds", package = "AlpsNMR"))
nmr_ppm_resolution(nmr_dataset)
message("the ppm resolution of this dataset is ", nmr_ppm_resolution(nmr_dataset), " ppm")

nmr_dataset <- nmr_dataset_load(system.file("extdata", "nmr_dataset.rds", package = "AlpsNMR"))
nmr_ppm_resolution(nmr_dataset)
message("the ppm resolution of this dataset is ", nmr_ppm_resolution(nmr_dataset), " ppm")

nmr_dataset <- nmr_dataset_load(system.file("extdata", "nmr_dataset.rds", package = "AlpsNMR"))
nmr_ppm_resolution(nmr_dataset)
message("the ppm resolution of this dataset is ", nmr_ppm_resolution(nmr_dataset), " ppm")
```

---

nmr\_read Bruker FID     *Read Free Induction Decay file*

---

### Description

Reads an FID file. This is a very simple function.

### Usage

```
nmr_read Bruker FID(sample_name, endian = "little")
```

### Arguments

|             |  |
|-------------|--|
| sample_name | A single sample name   |
| endian      | Endianness of the fid file ("little" by default, use "big" if <code>acqus\$BYTORDA == 1</code> ) |

### Value

A numeric vector with the free induction decay values

### See Also

Other import/export functions: [Pipelines](#), [files\\_to\\_rDolphin\(\)](#), [load\\_and\\_save\\_functions](#), [nmr\\_data\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_read\\_samples\(\)](#), [nmr\\_zip Bruker samples\(\)](#), [save\\_files\\_to\\_rDolphin\(\)](#), [save\\_profiling\\_output\(\)](#), [to\\_ChemoSpec\(\)](#)

### Examples

```
fid <- nmr_read Bruker FID("sample.fid")
```

---

nmr\_read\_samples     *Read NMR samples*

---

### Description

These functions load samples from files and return a [nmr\\_dataset](#).

**Usage**

```

nmr_read_samples_dir(
  samples_dir,
  format = "bruker",
  pulse_sequence = NULL,
  metadata_only = FALSE,
  ...
)

nmr_read_samples(
  sample_names,
  format = "bruker",
  pulse_sequence = NULL,
  metadata_only = FALSE,
  ...
)

```

**Arguments**

|                               |   |
|-------------------------------|---|
| <code>samples_dir</code>      | A directory or directories that contain multiple samples  |
| <code>format</code>           | Either "bruker" or "jdx"  |
| <code>pulse_sequence</code>   | If it is set to a pulse sequence ("NOESY", "JRES", "CPMG"...) it will only load the samples that match that pulse sequence. |
| <code>metadata_only</code>    | A logical, to load only metadata (default: FALSE)   |
| <code>...</code>              | Arguments passed on to <a href="#">read_bruker_pdata</a>  |
| <code>pdata_file</code>       | File name of the binary NMR data to load. Usually "1r". If NULL, it is autodetected based on the dimension                  |
| <code>sample_path</code>      | A character path of the sample directory  |
| <code>pdata_path</code>       | Path from <code>sample_path</code> to the preprocessed data   |
| <code>all_components</code>   | If FALSE load only the real component. Otherwise load the real and imaginary components                                     |
| <code>read_pdata_title</code> | If TRUE also reads metadata from pdata title file.  |
| <code>sample_names</code>     | A character vector with file or directory names.  |

**Value**

a [nmr\\_dataset](#) object

**See Also**

[read\\_bruker\\_pdata\(\)](#)

Other import/export functions: [Pipelines](#), [files\\_to\\_rDolphin\(\)](#), [load\\_and\\_save\\_functions](#), [nmr\\_data\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_read\\_bruker\\_fid\(\)](#), [nmr\\_zip\\_bruker\\_samples\(\)](#), [save\\_files\\_to\\_rDolphin\(\)](#), [save\\_profiling\\_output\(\)](#), [to\\_ChemoSpec\(\)](#)

## Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
```

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
zip_files <- fs::dir_ls(dir_to_demo_dataset, glob = "*.zip")
dataset <- nmr_read_samples(sample_names = zip_files)
```

---

nmr\_zip\_bruker\_samples

*Create one zip file for each brucker sample path*

---

## Description

Create one zip file for each brucker sample path

## Usage

```
nmr_zip_bruker_samples(path, workdir, overwrite = FALSE, ...)
```

## Arguments

|           |   |
|-----------|---|
| path      | Character vector with sample directories  |
| workdir   | Directory to store zip files              |
| overwrite | Should existing zip files be overwritten? |
| ...       | Passed to <a href="#">utils::zip</a>      |

## Value

A character vector of the same length as path, with the zip file names

## See Also

Other import/export functions: [Pipelines](#), [files\\_to\\_rDolphin\(\)](#), [load\\_and\\_save\\_functions](#), [nmr\\_data\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_read\\_bruker\\_fid\(\)](#), [nmr\\_read\\_samples\(\)](#), [save\\_files\\_to\\_rDolphin\(\)](#), [save\\_profiling\\_output\(\)](#), [to\\_ChemoSpec\(\)](#)

## Examples

```
save_zip_files_to <- tempfile(pattern = "zip_file_storage_")
where_your_samples_are <- tempfile(pattern = "where_your_samples_are")
# prepare sample:
zip::unzip(
  system.file("dataset-demo", "10.zip", package = "AlpsNMR"),
  exdir = where_your_samples_are
)
```



```
outpaths <- nmr_zip_bruker_samples(  
  list.files(where_your_samples_are, full.names = TRUE),  
  workdir = save_zip_files_to  
)
```

---

Parameters\_blood      *to rDolphin*

---

### Description

Parameters for blood (plasma/serum) samples profiling

### Details

The template Parameters\_blood contains the chosen normalization approach (by default, PQN), the Spectrometer Frequency (by default, 600.04MHz), alignment (by default, TSP 0.00 ppm), bucket resolution (by default, 0.00023)

### References

[github.com/danielcanueto/rDolphin](https://github.com/danielcanueto/rDolphin)

### Examples

```
data("Parameters_blood")  
Parameters_blood
```

---

Parameters\_cell      *Parameters for cell samples profiling*

---

### Description

The template Parameters\_cell contains the chosen normalization approach (by default, PQN), the Spectrometer Frequency (by default, 600.04MHz), alignment (by default, TSP 0.00 ppm), bucket resolution (by default, 0.00023)

### References

[github.com/danielcanueto/rDolphin](https://github.com/danielcanueto/rDolphin)

### Examples

```
data("Parameters_cell")  
Parameters_cell
```

---

Parameters\_urine      *Parameters for urine samples profiling*

---

### Description

The template Parameters\_urine contains the chosen normalization approach (by default, PQN), the Spectrometer Frequency (by default, 600.04MHz), alignment (by default, TSP 0.00 ppm), bucket resolution (by default, 0.00023)

### References

[github.com/danielcanueto/rDolphin](https://github.com/danielcanueto/rDolphin)

### Examples

```
data("Parameters_urine")
Parameters_urine
```

---

peaklist\_accept\_peaks      *Peak list: Create an accepted column based on some criteria*

---

### Description

Peak list: Create an accepted column based on some criteria

### Usage

```
peaklist_accept_peaks(
  peak_data,
  nmr_dataset,
  nrmse_max = Inf,
  area_min = 0,
  area_max = Inf,
  ppm_min = -Inf,
  ppm_max = Inf,
  keep_rejected = TRUE,
  verbose = FALSE
)
```

### Arguments

|             |  |
|-------------|--|
| peak_data   | The peak list (a data frame)   |
| nmr_dataset | The nmr_dataset where the peak_data was computed from  |
| nrmse_max   | The normalized root mean squared error of the lorentzian peak fitting must be less than or equal to this value |

|               |   |
|---------------|---|
| area_min      | Peak areas must be larger or equal to this value  |
| area_max      | Peak areas must be smaller or equal to this value   |
| ppm_min       | The peak apex must be above this value  |
| ppm_max       | The peak apex must be below this value  |
| keep_rejected | If FALSE, removes those peaks that do not satisfy the criteria and remove the accepted column (since all would be accepted) |
| verbose       | Print informational message   |

**Value**

The peak\_data, with a new accepted column (or maybe some filtered rows)

**Examples**

```
# Fake data:
nmr_dataset <- new_nmr_dataset_1D(
  1:10,
  matrix(c(1:5, 4:2, 3, 0), nrow = 1),
  list(external = data.frame(NMRExperiment = "10"))
)
peak_data <- data.frame(
  peak_id = c("Peak1", "Peak2"),
  NMRExperiment = c("10", "10"),
  ppm = c(5, 9),
  pos = c(5, 9),
  intensity = c(5, 3),
  ppm_infl_min = c(3, 8),
  ppm_infl_max = c(7, 10),
  gamma_ppb = c(1, 1),
  area = c(25, 3),
  norm_rmse = c(0.01, 0.8)
)
# Create the accepted column:
peak_data <- peaklist_accept_peaks(peak_data, nmr_dataset, area_min = 10, keep_rejected = FALSE)
stopifnot(identical(peak_data$peak_id, "Peak1"))
```

---

peaklist\_fit\_lorentzians

*Fit lorentzians to each peak to estimate areas*

---

**Description**

The different methods are available for benchmarking while developing, we should pick one.

**Usage**

```
peaklist_fit_lorentzians(
  peak_data,
  nmr_dataset,
  amplitude_method = c("intensity", "2nd_derivative", "intensity_without_baseline"),
  refine_peak_model = c("none", "peak", "2nd_derivative")
)
```

**Arguments**

`peak_data`            The peak data

`nmr_dataset`        The `nmr_dataset` object with the data. This function for now assumes `nmr_dataset` is NOT be baseline corrected

`amplitude_method`    The method to estimate the amplitude. It may be:

- "intensity". The amplitude of the peak is proportional to the raw intensity at the apex. This is a bad estimation if the intensity includes a baseline, because the amplitude of the peak will be overestimated
- "2nd\_derivative": The amplitude of the peak is proportional to the second derivative of the raw intensity signal at the apex. This method aims to correct the "intensity" method, since it is expected that the baseline will be mostly removed when considering the 2nd derivative of the spectrum. The 2nd derivative is calculated with a 2nd order Savitzky-Golay filter of 21 points.
- "intensity\_without\_baseline": A baseline is estimated on the whole spectra and subtracted from it. Then the peak amplitude is proportional to the corrected intensity at the apex (as in the "intensity" method).

`refine_peak_model`    Whether a non linear least squares fitting should be used to refine the estimated parameters. It can be:

- "none": Do not refine using nls.
- "peak": Use a lorentzian peak model and the baseline corrected spectra.
- "2nd\_derivative":

**Details**

- $\gamma$  is estimated using the inflection points of the signal and fitting them to the lorentzian inflection points
- $\Delta A$  is estimated using the `amplitude_method` below
- The peak position ( $x_0$ ) is given in `peak_data`

Those estimations may be refined with non-linear least squares using `refine_peak_model`. If the nls does not converge, the initial estimations are kept. Convergence -and other nls errors- are saved for further reference and diagnostic. Use `attr(peak_data_fitted, "errors")` to retrieve the error messages, where `peak_data_fitted` is assumed to be the output of this function. The refining improves  $\gamma$ ,  $\Delta A$  and  $x_0$ .

The baseline estimation (when calculated, see the arguments) is set to Asymmetric Least Squares with  $\lambda = 6$ ,  $p=0.05$ ,  $\maxit=20$  and it is probably not optimal... yet.

**Value**

The given data frame `peak_data`, with added columns:

- inflection points,
- gamma
- area
- a `norm_rmse` fitting error

As well as some attributes

- "errors": A data frame with any error in the peak fitting
- "fit\_baseline": Whether the method used has any consideration for the baseline of the signal (maybe not very useful attribute)
- "method\_description": A textual description of what we did, to include it in plots

---

|                |                               |
|----------------|-------------------------------|
| Peak_detection | <i>Peak detection for NMR</i> |
|----------------|-------------------------------|

---

**Description**

Peak detection for NMR

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
nmr_dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
# Low resolution:
dataset_1D <- nmr_interpolate_1D(nmr_dataset, axis = c(min = -0.5, max = 10, by = 0.001))
dataset_1D <- nmr_exclude_region(dataset_1D, exclude = list(water = c(4.7, 5)))

# 1. Optimize peak detection parameters:
range_without_peaks <- c(9.5, 10)
# Choose a region without peaks:
plot(dataset_1D, chemshift_range = range_without_peaks)
baselineThresh <- nmr_baseline_threshold(dataset_1D, range_without_peaks = range_without_peaks)
# Plot to check the baseline estimations
nmr_baseline_threshold_plot(
  dataset_1D,
  baselineThresh,
  NMRExperiment = "all",
  chemshift_range = range_without_peaks
)

# 1. Peak detection in the dataset.
peak_data <- nmr_detect_peaks(
  dataset_1D,
  nDivRange_ppm = 0.1, # Size of detection segments
  scales = seq(1, 16, 2),
```

```

    baselineThresh = NULL, # Minimum peak intensity
    SNR.Th = 4, # Signal to noise ratio
    range_without_peaks = range_without_peaks, # To estimate
  )

sample_10 <- filter(dataset_1D, NMRExperiment == "10")
# nmr_detect_peaks_plot(sample_10, peak_data, "NMRExp_ref")

peaks_detected <- nmr_detect_peaks_tune_snr(
  sample_10,
  SNR_thresholds = seq(from = 2, to = 3, by = 0.5),
  nDivRange_ppm = 0.03,
  scales = seq(1, 16, 2),
  baselineThresh = 0
)

# 2.Find the reference spectrum to align with.
NMRExp_ref <- nmr_align_find_ref(dataset_1D, peak_data)

# 3.Spectra alignment using the ref spectrum and a maximum alignment shift
nmr_dataset <- nmr_align(dataset_1D, # the dataset
  peak_data, # detected peaks
  NMRExp_ref = NMRExp_ref, # ref spectrum
  maxShift_ppm = 0.0015, # max alignment shift
  acceptLostPeak = FALSE
) # lost peaks

# 4.PEAK INTEGRATION (please, consider previous normalization step).
# First we take the peak table from the reference spectrum
peak_data_ref <- filter(peak_data, NMRExperiment == NMRExp_ref)

# Then we integrate spectra considering the peaks from the ref spectrum
nmr_peak_table <- nmr_integrate_peak_positions(
  samples = nmr_dataset,
  peak_pos_ppm = peak_data_ref$ppm,
  peak_width_ppm = NULL
)

validate_nmr_dataset_peak_table(nmr_peak_table)

# If you wanted the final peak table before machine learning you can run
nmr_peak_table_completed <- get_integration_with_metadata(nmr_peak_table)

```

---

```
permutation_test_model
```

*Permutation test*

---

## Description

Make permutations with data and default settings from an `nmr_data_analysis_method`

**Usage**

```
permutation_test_model(
  dataset,
  y_column,
  identity_column,
  external_val,
  internal_val,
  data_analysis_method,
  nPerm = 50
)
```

**Arguments**

|                            |  |
|----------------------------|--|
| dataset                    | An <a href="#">nmr_dataset_family</a> object   |
| y_column                   | A string with the name of the y column (present in the metadata of the dataset)                                |
| identity_column            | NULL or a string with the name of the identity column (present in the metadata of the dataset).                |
| external_val, internal_val | A list with two elements: iterations and test_size. See <a href="#">random_subsampling</a> for further details |
| data_analysis_method       | An <a href="#">nmr_data_analysis_method</a> object   |
| nPerm                      | number of permutations   |

**Value**

A permutation matrix with permuted values

**Examples**

```
# Data analysis for a table of integrated peaks

## Generate an artificial nmr_dataset_peak_table:
### Generate artificial metadata:
num_samples <- 32 # use an even number in this example
num_peaks <- 20
metadata <- data.frame(
  NMRExperiment = as.character(1:num_samples),
  Condition = rep(c("A", "B"), times = num_samples / 2)
)

### The matrix with peaks
peak_means <- runif(n = num_peaks, min = 300, max = 600)
peak_sd <- runif(n = num_peaks, min = 30, max = 60)
peak_matrix <- mapply(function(mu, sd) rnorm(num_samples, mu, sd),
  mu = peak_means, sd = peak_sd
)
colnames(peak_matrix) <- paste0("Peak", 1:num_peaks)
```

```

## Artificial differences depending on the condition:
peak_matrix[metadata$Condition == "A", "Peak2"] <-
  peak_matrix[metadata$Condition == "A", "Peak2"] + 70

peak_matrix[metadata$Condition == "A", "Peak6"] <-
  peak_matrix[metadata$Condition == "A", "Peak6"] - 60

### The nmr_dataset_peak_table
peak_table <- new_nmr_dataset_peak_table(
  peak_table = peak_matrix,
  metadata = list(external = metadata)
)

methodology <- plsda_auroc_vip_method(ncomp = 3)
model <- nmr_data_analysis(
  peak_table,
  y_column = "Condition",
  identity_column = NULL,
  external_val = list(iterations = 3, test_size = 0.25),
  internal_val = list(iterations = 3, test_size = 0.25),
  data_analysis_method = methodology
)

p <- permutation_test_model(peak_table,
  y_column = "Condition",
  identity_column = NULL,
  external_val = list(iterations = 3, test_size = 0.25),
  internal_val = list(iterations = 3, test_size = 0.25),
  data_analysis_method = methodology,
  nPerm = 10
)

```

---

permutation\_test\_plot *Permutation test plot*

---

## Description

Plot permutation test using actual model and permuted models

## Usage

```

permutation_test_plot(
  nmr_data_analysis_model,
  permMatrix,
  xlab = "AUCs",
  xlim,
  ylim = NULL,
  breaks = "Sturges",

```



```

    main = "Permutation test"
  )

```

### Arguments

```

nmr_data_analysis_model      A nmr_data_analysis_model
permMatrix                   A permutation fitness outcome from permutation_test_model
xlab                          optional xlabel
xlim                          optional x-range
ylim                          optional y-range
breaks                        optional custom histogram breaks (defaults to 'sturges')
main                          optional plot title (or TRUE for autoname)

```

### Value

A plot with the comparison between the actual model versus the permuted models

### Examples

```

# Data analysis for a table of integrated peaks

## Generate an artificial nmr_dataset_peak_table:
### Generate artificial metadata:
num_samples <- 32 # use an even number in this example
num_peaks <- 20
metadata <- data.frame(
  NMRExperiment = as.character(1:num_samples),
  Condition = rep(c("A", "B"), times = num_samples / 2)
)

### The matrix with peaks
peak_means <- runif(n = num_peaks, min = 300, max = 600)
peak_sd <- runif(n = num_peaks, min = 30, max = 60)
peak_matrix <- mapply(function(mu, sd) rnorm(num_samples, mu, sd),
  mu = peak_means, sd = peak_sd
)
colnames(peak_matrix) <- paste0("Peak", 1:num_peaks)

## Artificial differences depending on the condition:
peak_matrix[metadata$Condition == "A", "Peak2"] <-
  peak_matrix[metadata$Condition == "A", "Peak2"] + 70

peak_matrix[metadata$Condition == "A", "Peak6"] <-
  peak_matrix[metadata$Condition == "A", "Peak6"] - 60

### The nmr_dataset_peak_table
peak_table <- new_nmr_dataset_peak_table(
  peak_table = peak_matrix,
  metadata = list(external = metadata)
)

```

```

)

methodology <- plsda_auroc_vip_method(ncomp = 3)
model <- nmr_data_analysis(
  peak_table,
  y_column = "Condition",
  identity_column = NULL,
  external_val = list(iterations = 3, test_size = 0.25),
  internal_val = list(iterations = 3, test_size = 0.25),
  data_analysis_method = methodology
)

p <- permutation_test_model(peak_table,
  y_column = "Condition",
  identity_column = NULL,
  external_val = list(iterations = 3, test_size = 0.25),
  internal_val = list(iterations = 3, test_size = 0.25),
  data_analysis_method = methodology,
  nPerm = 10
)

permutation_test_plot(model, p)

```

---

Pipelines

*Pipelines*


---

### Description

Uses [nmr\\_pca\\_outliers\\_robust](#) to perform the detection of outliers

Normalize the full spectra to the internal calibrant region, then exclude that region and finally perform PQN normalization.

### Usage

```

pipe_load_samples(samples_dir, glob = "*0", output_dir = NULL)

pipe_add_metadata(nmr_dataset_rds, excel_file, output_dir)

pipe_interpolate_1D(nmr_dataset_rds, axis, output_dir)

pipe_exclude_regions(nmr_dataset_rds, exclude, output_dir)

pipe_outlier_detection(nmr_dataset_rds, output_dir)

pipe_filter_samples(nmr_dataset_rds, conditions, output_dir)

pipe_peakdet_align(

```

```

    nmr_dataset_rds,
    nDivRange_ppm = 0.1,
    scales = seq(1, 16, 2),
    baselineThresh = 0.01,
    SNR.Th = -1,
    maxShift_ppm = 0.0015,
    acceptLostPeak = FALSE,
    output_dir = NULL
)

pipe_peak_integration(
  nmr_dataset_rds,
  peak_det_align_dir,
  peak_width_ppm,
  output_dir
)

pipe_normalization(
  nmr_dataset_rds,
  internal_calibrant = NULL,
  output_dir = NULL
)

```

### Arguments

|                              |  |
|------------------------------|--|
| <code>samples_dir</code>     | The directory where the samples are  |
| <code>glob</code>            | A wildcard aka globbing pattern (e.g. *.csv) passed on to <code>grep()</code> to filter paths.   |
| <code>output_dir</code>      | The output directory for this pipe element   |
| <code>nmr_dataset_rds</code> | The <code>nmr_dataset.rds</code> file name coming from previous nodes  |
| <code>excel_file</code>      | <p>An excel file name. See details for the requirements</p> <p>The excel file can have one or more sheets. The excel sheets need to be as simple as possible: One header column on the first row and values below.</p> <p>Each of the sheets contain metadata that has to be integrated. The merge (technically a left join) is done using the first column of each sheet as key.</p> <p>In practical terms this means that the first sheet of the excel file <b>MUST</b> start with an "NMRExperiment" column, and as many additional columns to add (e.g. FluidXBarcode, SampleCollectionDate, TimePoint and SubjectID).</p> <p>The second sheet can have as the first column any of the already added columns, for instance the "SubjectID", and any additional columns (e.g. Gender, Age).</p> <p>The first column on each sheet, named the key column, <b>MUST</b> have unique values. For instance, a sheet starting with "SubjectID" <b>MUST</b> specify each subject ID only once (without repetitions).</p> |
| <code>axis</code>            | The ppm axis range and optionally the ppm step. Set it to NULL for autodetection   |
| <code>exclude</code>         | A list with regions to be removed Typically: <code>exclude = list(water = c(4.7, 5.0))</code>  |

|                    |   |
|--------------------|---|
| conditions         | <p>A character vector with conditions to filter metadata. The conditions parameter should be a character vector of valid R logical conditions. Some examples:</p> <ul style="list-style-type: none"> <li>• <code>conditions &lt;- 'Gender == "Female"'</code></li> <li>• <code>conditions &lt;- 'Cohort == "Chuv"'</code></li> <li>• <code>conditions &lt;- 'TimePoint %in% c("T0", "T31")'</code></li> <li>• <code>conditions &lt;- c(Cohort == "Chuv", 'TimePoint %in% c("T0", "T31")')</code></li> </ul> <p>Only samples fulfilling all the given conditions are kept in further analysis.</p> |
| nDivRange_ppm      | Segment size, in ppms, to divide the spectra and search for peaks.  |
| scales             | The parameter of peakDetectionCWT function of MassSpecWavelet package, look it up in the original function.   |
| baselineThresh     | <p>All peaks with intensities below the thresholds are excluded. Either:</p> <ul style="list-style-type: none"> <li>• A numeric vector of length the number of samples. Each number is a threshold for that sample</li> <li>• A single number. All samples use this number as baseline threshold.</li> <li>• NULL. If that's the case, a default function is used (<code>nmr_baseline_threshold()</code>), which assumes that there is no signal in the region 9.5-10 ppm.</li> </ul>   |
| SNR.Th             | The parameter of peakDetectionCWT function of MassSpecWavelet package, look it up in the original function. If you set -1, the function will itself recompute this value.   |
| maxShift_ppm       | The maximum shift allowed, in ppm   |
| acceptLostPeak     | This is an option for users, TRUE is the default value. If the users believe that all the peaks in the peak list are true positive, change it to FALSE.   |
| peak_det_align_dir | Output directory from <a href="#">pipe_peakdet_align</a>  |
| peak_width_ppm     | A peak width in ppm   |
| internal_calibrant | A ppm range where the internal calibrant is, or NULL.   |

### Details

If there is no internal calibrant, only the PQN normalization is done.

### Value

This function saves the result to the output directory

This function saves the result to the output directory

This function saves the result to the output directory

This function saves the result to the output directory

This function saves the result to the output directory

Pipeline: Filter samples according to metadata conditions

Pipeline: Peak detection and Alignment

Pipeline: Peak integration

Pipe: Full spectra normalization

**See Also**

Other import/export functions: `files_to_rDolphin()`, `load_and_save_functions`, `nmr_data()`, `nmr_meta_export()`, `nmr_read_bruker_fid()`, `nmr_read_samples()`, `nmr_zip_bruker_samples()`, `save_files_to_rDolphin()`, `save_profiling_output()`, `to_ChemoSpec()`

Other metadata functions: `nmr_meta_add()`, `nmr_meta_export()`, `nmr_meta_get()`, `nmr_meta_get_column()`, `nmr_meta_groups()`

Other outlier detection functions: `nmr_pca_outliers()`, `nmr_pca_outliers_filter()`, `nmr_pca_outliers_plot()`, `nmr_pca_outliers_robust()`

Other peak detection functions: `nmr_baseline_threshold()`, `nmr_detect_peaks()`, `nmr_detect_peaks_plot()`, `nmr_detect_peaks_plot_overview()`, `nmr_detect_peaks_tune_snr()`, `nmr_identify_regions_blood()`, `nmr_identify_regions_cell()`, `nmr_identify_regions_urine()`, `nmr_integrate_regions()`

Other alignment functions: `nmr_align()`, `nmr_align_find_ref()`

Other peak integration functions: `get_integration_with_metadata()`, `nmr_identify_regions_blood()`, `nmr_identify_regions_cell()`, `nmr_identify_regions_urine()`, `nmr_integrate_peak_positions()`, `nmr_integrate_regions()`

**Examples**

```
## Example of pipeline usage
## There are differet ways of load the dataset
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
# excel_file <- system.file("dataset-demo",
#                           "dummy_metadata.xlsx",
#                           package = "AlpsNMR")
# output_dir <- tempdir()

## Load samples with pipes
# pipe_load_samples(dir_to_demo_dataset,
#                  glob = "*.zip",
#                  output_dir = "../pipe_output")

## Another way to load it
# nmr_dataset <- nmr_read_samples_dir(dir_to_demo_dataset)

## Saving the dataset in a .rds file
# nmr_dataset_rds <- tempfile(fileext = ".rds")
# nmr_dataset_save(nmr_dataset, nmr_dataset_rds)

## Interpolation
# pipe_interpolate_1D(nmr_dataset_rds,
#                    axis = c(min = -0.5, max = 10, by = 2.3E-4),
#                    output_dir)

## Get the new path, based in output_dir
# nmr_dataset_rds <- paste(output_dir, "\", "nmr_dataset.rds", sep = "", collapse = NULL)

## Adding metadata to samples
# pipe_add_metadata(nmr_dataset_rds = nmr_dataset_rds, output_dir = output_dir,
#                  excel_file = excel_file)
```

```
## Filtering samples
# conditions <- 'SubjectID == "Ana"'
# pipe_filter_samples(nmr_dataset_rds, conditions, output_dir)

## Outlier detection
# pipe_outlier_detection(nmr_dataset_rds, output_dir)

## Exclude regions
# exclude_regions <- list(water = c(5.1, 4.5))
# pipe_exclude_regions(nmr_dataset_rds, exclude_regions, output_dir)

## peak aling
# pipe_peakdet_align(nmr_dataset_rds, output_dir = output_dir)

## peak integration
# pipe_peak_integration(nmr_dataset_rds,
#                       peak_det_align_dir = output_dir,
#                       peak_width_ppm = 0.006, output_dir)

## Normalization
# pipe_normalization(nmr_dataset_rds, output_dir = output_dir)
```

---

plot.nmr\_dataset\_1D    *Plot an nmr\_dataset\_1D*

---

## Description

Plot an nmr\_dataset\_1D

## Usage

```
## S3 method for class 'nmr_dataset_1D'
plot(
  x,
  NMRExperiment = NULL,
  chemshift_range = NULL,
  interactive = FALSE,
  quantile_plot = NULL,
  quantile_colors = NULL,
  ...
)
```

## Arguments

**x**                    a [nmr\\_dataset\\_1D](#) object

**NMRExperiment**    A character vector with the NMRExperiments to include. Use "all" to include all experiments.

|                 |  |
|-----------------|--|
| chemshift_range | range of the chemical shifts to be included. Can be of length 3 to include the resolution in the third element (e.g. <code>c(0.2, 0.8, 0.005)</code> ) |
| interactive     | if TRUE return an interactive plotly plot, otherwise return a ggplot one.  |
| quantile_plot   | If TRUE plot the 10\ If two numbers between 0 and 1 are given then a custom percentile can be plotted  |
| quantile_colors | A vector with the colors for each of the quantiles   |
| ...             | arguments passed to <code>ggplot2::aes</code> (or to <code>ggplot2::aes_string</code> , being deprecated).   |

**Value**

The plot

**See Also**

Other plotting functions: `plot_interactive()`

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
# dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
# dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
# plot(dataset_1D)
```

---

plot\_bootstrap\_multimodel

*Bootstrap plot predictions*

---

**Description**

Bootstrap plot predictions

**Usage**

```
plot_bootstrap_multimodel(bp_results, dataset, y_column, plot = TRUE)
```

**Arguments**

|            |   |
|------------|---|
| bp_results | bp_kfold_VIP_analysis results   |
| dataset    | An <code>nmr_dataset_family</code> object                                       |
| y_column   | A string with the name of the y column (present in the metadata of the dataset) |
| plot       | A boolean that indicate if results are plotted or not                           |

**Value**

A plot of the results or a ggplot object

**Examples**

```
# Data analysis for a table of integrated peaks

## Generate an artificial nmr_dataset_peak_table:
### Generate artificial metadata:
num_samples <- 64 # use an even number in this example
num_peaks <- 20
metadata <- data.frame(
  NMRExperiment = as.character(1:num_samples),
  Condition = rep(c("A", "B"), times = num_samples / 2)
)

### The matrix with peaks
peak_means <- runif(n = num_peaks, min = 300, max = 600)
peak_sd <- runif(n = num_peaks, min = 30, max = 60)
peak_matrix <- mapply(function(mu, sd) rnorm(num_samples, mu, sd),
  mu = peak_means, sd = peak_sd
)
colnames(peak_matrix) <- paste0("Peak", 1:num_peaks)

## Artificial differences depending on the condition:
peak_matrix[metadata$Condition == "A", "Peak2"] <-
  peak_matrix[metadata$Condition == "A", "Peak2"] + 70

peak_matrix[metadata$Condition == "A", "Peak6"] <-
  peak_matrix[metadata$Condition == "A", "Peak6"] - 60

### The nmr_dataset_peak_table
peak_table <- new_nmr_dataset_peak_table(
  peak_table = peak_matrix,
  metadata = list(external = metadata)
)

## We will use bootstrap and permutation method for VIPs selection
## in a k-fold cross validation
# bp_results <- bp_kfold_VIP_analysis(peak_table, # Data to be analyzed
#                                     y_column = "Condition", # Label
#                                     k = 3,
#                                     nbootstrap = 10)

# message("Selected VIPs are: ", bp_results$important_vips)

# plot_bootstrap_multimodel(bp_results, peak_table, "Condition")
```



---

plot\_interactive      *Plots in WebGL*

---

**Description**

Plots in WebGL

**Usage**

```
plot_interactive(plt, html_filename, overwrite = NULL)
```

**Arguments**

plt                    A plot created with plotly or ggplot2  
html\_filename        The file name where the plot will be saved  
overwrite            Overwrite the lib/ directory (use NULL to prompt the user)

**Value**

The html\_filename

**See Also**

Other plotting functions: [plot.nmr\\_dataset\\_1D\(\)](#)

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")  
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)  
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))  
# plot <- plot(dataset_1D)  
# html_plot_interactive <- plot_interactive(plot, "html_plot_interactive.html")
```

---

plot\_plsda\_multimodel      *Multi PLDSA model plot predictions*

---

**Description**

Multi PLDSA model plot predictions

**Usage**

```
plot_plsda_multimodel(model, plot = TRUE)
```

**Arguments**

model            A nmr\_data\_analysis\_model  
 plot            A boolean that indicate if results are plotted or not

**Value**

A plot of the results or a ggplot object

**Examples**

```
#' # Data analysis for a table of integrated peaks

## Generate an artificial nmr_dataset_peak_table:
### Generate artificial metadata:
num_samples <- 32 # use an even number in this example
num_peaks <- 20
metadata <- data.frame(
  NMRExperiment = as.character(1:num_samples),
  Condition = rep(c("A", "B"), times = num_samples / 2)
)

### The matrix with peaks
peak_means <- runif(n = num_peaks, min = 300, max = 600)
peak_sd <- runif(n = num_peaks, min = 30, max = 60)
peak_matrix <- mapply(function(mu, sd) rnorm(num_samples, mu, sd),
  mu = peak_means, sd = peak_sd
)
colnames(peak_matrix) <- paste0("Peak", 1:num_peaks)

## Artificial differences depending on the condition:
peak_matrix[metadata$Condition == "A", "Peak2"] <-
  peak_matrix[metadata$Condition == "A", "Peak2"] + 70

peak_matrix[metadata$Condition == "A", "Peak6"] <-
  peak_matrix[metadata$Condition == "A", "Peak6"] - 60

### The nmr_dataset_peak_table
peak_table <- new_nmr_dataset_peak_table(
  peak_table = peak_matrix,
  metadata = list(external = metadata)
)

## We will use a double cross validation, splitting the samples with random
## subsampling both in the external and internal validation.
## The classification model will be a PLSDA, exploring at maximum 3 latent
## variables.
## The best model will be selected based on the area under the ROC curve
methodology <- plsda_auroc_vip_method(ncomp = 1)
model <- nmr_data_analysis(
  peak_table,
  y_column = "Condition",
  identity_column = NULL,
```

```

    external_val = list(iterations = 2, test_size = 0.25),
    internal_val = list(iterations = 2, test_size = 0.25),
    data_analysis_method = methodology
  )

  # plot_plsda_multimodel(model)

```

---

plot\_plsda\_samples      *Plot PLSDA predictions*

---

### Description

Plot PLSDA predictions

### Usage

```
plot_plsda_samples(model, newdata = NULL, plot = TRUE)
```

### Arguments

|         |  |
|---------|--|
| model   | A plsda model  |
| newdata | newdata to predict, if not included model\$X_test will be used |
| plot    | A boolean that indicate if results are plotted or not          |

### Value

A plot of the samples or a ggplot object

### Examples

```

#' # Data analysis for a table of integrated peaks

## Generate an artificial nmr_dataset_peak_table:
### Generate artificial metadata:
num_samples <- 32 # use an even number in this example
num_peaks <- 20
metadata <- data.frame(
  NMRExperiment = as.character(1:num_samples),
  Condition = rep(c("A", "B"), times = num_samples / 2)
)

### The matrix with peaks
peak_means <- runif(n = num_peaks, min = 300, max = 600)
peak_sd <- runif(n = num_peaks, min = 30, max = 60)
peak_matrix <- mapply(function(mu, sd) rnorm(num_samples, mu, sd),
  mu = peak_means, sd = peak_sd
)
colnames(peak_matrix) <- paste0("Peak", 1:num_peaks)

```

```

## Artificial differences depending on the condition:
peak_matrix[metadata$Condition == "A", "Peak2"] <-
  peak_matrix[metadata$Condition == "A", "Peak2"] + 70

peak_matrix[metadata$Condition == "A", "Peak6"] <-
  peak_matrix[metadata$Condition == "A", "Peak6"] - 60

### The nmr_dataset_peak_table
peak_table <- new_nmr_dataset_peak_table(
  peak_table = peak_matrix,
  metadata = list(external = metadata)
)

## We will use a double cross validation, splitting the samples with random
## subsampling both in the external and internal validation.
## The classification model will be a PLSDA, exploring at maximum 3 latent
## variables.
## The best model will be selected based on the area under the ROC curve
methodology <- plsda_auroc_vip_method(ncomp = 1)
model <- nmr_data_analysis(
  peak_table,
  y_column = "Condition",
  identity_column = NULL,
  external_val = list(iterations = 1, test_size = 0.25),
  internal_val = list(iterations = 1, test_size = 0.25),
  data_analysis_method = methodology
)

# plot_plsda_samples(model$outer_cv_results[[1]]$model)

```

---

plot\_vip\_scores

*Plot vip scores of bootstrap*


---

## Description

Plot vip scores of bootstrap

## Usage

```
plot_vip_scores(vip_means, error, nbootstrap, plot = TRUE)
```

## Arguments

|            |   |
|------------|---|
| vip_means  | vips means values of bootstraps                       |
| error      | error tolerated, calculated in the bootstrap          |
| nbootstrap | number of bootstraps realized                         |
| plot       | A boolean that indicate if results are plotted or not |

**Value**

A plot of the results or a ggplot object

**Examples**

```
# Data analysis for a table of integrated peaks

## Generate an artificial nmr_dataset_peak_table:
### Generate artificial metadata:
num_samples <- 64 # use an even number in this example
num_peaks <- 20
metadata <- data.frame(
  NMRExperiment = as.character(1:num_samples),
  Condition = rep(c("A", "B"), times = num_samples / 2)
)

### The matrix with peaks
peak_means <- runif(n = num_peaks, min = 300, max = 600)
peak_sd <- runif(n = num_peaks, min = 30, max = 60)
peak_matrix <- mapply(function(mu, sd) rnorm(num_samples, mu, sd),
  mu = peak_means, sd = peak_sd
)
colnames(peak_matrix) <- paste0("Peak", 1:num_peaks)

## Artificial differences depending on the condition:
peak_matrix[metadata$Condition == "A", "Peak2"] <-
  peak_matrix[metadata$Condition == "A", "Peak2"] + 70

peak_matrix[metadata$Condition == "A", "Peak6"] <-
  peak_matrix[metadata$Condition == "A", "Peak6"] - 60

### The nmr_dataset_peak_table
peak_table <- new_nmr_dataset_peak_table(
  peak_table = peak_matrix,
  metadata = list(external = metadata)
)

## We will use bootstrap and permutation method for VIPs selection
## in a k-fold cross validation
# bp_results <- bp_kfold_VIP_analysis(peak_table, # Data to be analyzed
#   y_column = "Condition", # Label
#   k = 3,
#   ncomp = 1,
#   nbootstrap = 10)

# message("Selected VIPs are: ", bp_results$important_vips)

# plot_vip_scores(bp_results$kfold_results[[1]]$vip_means,
#   bp_results$kfold_results[[1]]$error[1],
#   nbootstrap = 10)
```

---

plot\_webgl *Plot a dataset into a HTML file*

---

### Description

Uses WebGL for performance

### Usage

```
plot_webgl(nmr_dataset, html_filename, overwrite = NULL, ...)
```

### Arguments

|               |  |
|---------------|--|
| nmr_dataset   | An <a href="#">nmr_dataset_1D</a>  |
| html_filename | The output HTML filename to be created   |
| overwrite     | Overwrite the lib/ directory (use NULL to prompt the user)   |
| ...           | Arguments passed on to <a href="#">plot.nmr_dataset_1D</a>   |
|               | x a <a href="#">nmr_dataset_1D</a> object  |
|               | chemshift_range range of the chemical shifts to be included. Can be of length 3 to include the resolution in the third element (e.g. c(0.2, 0.8, 0.005)) |
|               | NMRExperiment A character vector with the NMRExperiments to include. Use "all" to include all experiments.   |
|               | quantile_plot If TRUE plot the 10\ If two numbers between 0 and 1 are given then a custom percentile can be plotted                                      |
|               | quantile_colors A vector with the colors for each of the quantiles   |
|               | interactive if TRUE return an interactive plotly plot, otherwise return a ggplot one.  |

### Value

the html filename created

### Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
# dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
# dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
# html_plot <- plot_webgl(dataset_1D, "html_plot.html")
```

---

`plsda_auroc_vip_compare`*Compare PLSDA auroc VIP results*

---

**Description**

Compare PLSDA auroc VIP results

**Usage**

```
plsda_auroc_vip_compare(...)
```

**Arguments**

... Results of [nmr\\_data\\_analysis](#) to be combined. Give each result a name.

**Value**

A plot of the AUC for each method

**Examples**

```
# Data analysis for a table of integrated peaks

## Generate an artificial nmr_dataset_peak_table:
### Generate artificial metadata:
num_samples <- 32 # use an even number in this example
num_peaks <- 20
metadata <- data.frame(
  NMRExperiment = as.character(1:num_samples),
  Condition = rep(c("A", "B"), times = num_samples / 2)
)

### The matrix with peaks
peak_means <- runif(n = num_peaks, min = 300, max = 600)
peak_sd <- runif(n = num_peaks, min = 30, max = 60)
peak_matrix <- mapply(function(mu, sd) rnorm(num_samples, mu, sd),
  mu = peak_means, sd = peak_sd
)
colnames(peak_matrix) <- paste0("Peak", 1:num_peaks)

## Artificial differences depending on the condition:
peak_matrix[metadata$Condition == "A", "Peak2"] <-
  peak_matrix[metadata$Condition == "A", "Peak2"] + 70

peak_matrix[metadata$Condition == "A", "Peak6"] <-
  peak_matrix[metadata$Condition == "A", "Peak6"] - 60

### The nmr_dataset_peak_table
peak_table <- new_nmr_dataset_peak_table(
```

```

    peak_table = peak_matrix,
    metadata = list(external = metadata)
  )

  ## We will use a double cross validation, splitting the samples with random
  ## subsampling both in the external and internal validation.
  ## The classification model will be a PLSDA, exploring at maximum 3 latent
  ## variables.
  ## The best model will be selected based on the area under the ROC curve
  methodology <- plsda_auroc_vip_method(ncomp = 1)
  model1 <- nmr_data_analysis(
    peak_table,
    y_column = "Condition",
    identity_column = NULL,
    external_val = list(iterations = 1, test_size = 0.25),
    internal_val = list(iterations = 1, test_size = 0.25),
    data_analysis_method = methodology
  )

  methodology2 <- plsda_auroc_vip_method(ncomp = 2)
  model2 <- nmr_data_analysis(
    peak_table,
    y_column = "Condition",
    identity_column = NULL,
    external_val = list(iterations = 1, test_size = 0.25),
    internal_val = list(iterations = 1, test_size = 0.25),
    data_analysis_method = methodology2
  )

  plsda_auroc_vip_compare(model1 = model1, model2 = model2)

```

---

plsda\_auroc\_vip\_method

*Method for nmr\_data\_analysis (PLSDA model with AUROC and VIP outputs)*

---

## Description

Method for nmr\_data\_analysis (PLSDA model with AUROC and VIP outputs)

## Usage

```
plsda_auroc_vip_method(ncomp, auc_increment_threshold = 0.05)
```

## Arguments

**ncomp**                    Max. number of latent variables to explore in the PLSDA analysis

**auc\_increment\_threshold**  
Choose the number of latent variables when the AUC does not increment more than this threshold.



**Value**

Returns an object to be used with [nmr\\_data\\_analysis](#) to perform a (optionally multilevel) PLS-DA model, using the area under the ROC curve as figure of merit to determine the optimum number of latent variables.

**Examples**

```
method <- plsda_auroc_vip_method(3)
```

---

|                |                                |
|----------------|--------------------------------|
| ppm_resolution | <i>Unlisted PPM resolution</i> |
|----------------|--------------------------------|

---

**Description**

A wrapper to unlist the output from the function `nmr_ppm_resolution(nmr_dataset)` when no interpolation has been applied.

**Usage**

```
ppm_resolution(nmr_dataset)
```

**Arguments**

`nmr_dataset` An object containing NMR samples

**Value**

A number (the ppm resolution, measured in ppms)

Numeric (the ppm resolution, measured in ppms)

**Examples**

```
nmr_dataset <- nmr_dataset_load(system.file("extdata", "nmr_dataset.rds", package = "AlpsNMR"))  
nmr_ppm_resolution(nmr_dataset)
```

print.nmr\_dataset      *Print for nmr\_dataset*

---

### Description

Print for nmr\_dataset

### Usage

```
## S3 method for class 'nmr_dataset'  
print(x, ...)
```

### Arguments

x                      an [nmr\\_dataset](#) object  
...                     for future use

### Value

Print for nmr\_dataset

### See Also

Other class helper functions: [format.nmr\\_dataset\(\)](#), [format.nmr\\_dataset\\_1D\(\)](#), [format.nmr\\_dataset\\_peak\\_table\(\)](#), [is.nmr\\_dataset\\_1D\(\)](#), [is.nmr\\_dataset\\_peak\\_table\(\)](#), [new\\_nmr\\_dataset\(\)](#), [new\\_nmr\\_dataset\\_1D\(\)](#), [new\\_nmr\\_dataset\\_peak\\_table\(\)](#), [print.nmr\\_dataset\\_1D\(\)](#), [print.nmr\\_dataset\\_peak\\_table\(\)](#), [validate\\_nmr\\_dataset\(\)](#), [validate\\_nmr\\_dataset\\_family\(\)](#), [validate\\_nmr\\_dataset\\_peak\\_table\(\)](#)

### Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")  
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)  
print(dataset)
```

---

print.nmr\_dataset\_1D      *print for nmr\_dataset\_1D*

---

### Description

print for nmr\_dataset\_1D

### Usage

```
## S3 method for class 'nmr_dataset_1D'  
print(x, ...)
```

**Arguments**

x                    an `nmr_dataset_1D` object  
...                    for future use

**Value**

print for `nmr_dataset_1D`

**See Also**

Other class helper functions: `format.nmr_dataset()`, `format.nmr_dataset_1D()`, `format.nmr_dataset_peak_table()`, `is.nmr_dataset_1D()`, `is.nmr_dataset_peak_table()`, `new_nmr_dataset()`, `new_nmr_dataset_1D()`, `new_nmr_dataset_peak_table()`, `print.nmr_dataset()`, `print.nmr_dataset_peak_table()`, `validate_nmr_dataset()`, `validate_nmr_dataset_family()`, `validate_nmr_dataset_peak_table()`

Other `nmr_dataset_1D` functions: `[.nmr_dataset_1D()`, `format.nmr_dataset_1D()`, `get_integration_with_metadata`, `is.nmr_dataset_1D()`, `nmr_integrate_peak_positions()`, `nmr_integrate_regions()`, `nmr_meta_add()`, `nmr_meta_export()`, `nmr_meta_get()`, `nmr_meta_get_column()`, `nmr_ppm_resolution()`

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
print(dataset_1D)
```

---

```
print.nmr_dataset_peak_table
      print for nmr_dataset_peak_table
```

---

**Description**

print for `nmr_dataset_peak_table`

**Usage**

```
## S3 method for class 'nmr_dataset_peak_table'
print(x, ...)
```

**Arguments**

x                    an `nmr_dataset_peak_table` object  
...                    for future use

**Value**

print for `nmr_dataset_peak_table`

**See Also**

Other class helper functions: `format.nmr_dataset()`, `format.nmr_dataset_1D()`, `format.nmr_dataset_peak_table()`, `is.nmr_dataset_1D()`, `is.nmr_dataset_peak_table()`, `new_nmr_dataset()`, `new_nmr_dataset_1D()`, `new_nmr_dataset_peak_table()`, `print.nmr_dataset()`, `print.nmr_dataset_1D()`, `validate_nmr_dataset()`, `validate_nmr_dataset_family()`, `validate_nmr_dataset_peak_table()`

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
meta <- file.path(dir_to_demo_dataset, "dummy_metadata.xlsx")
metadata <- readxl::read_excel(meta, sheet = 1)
dataset_1D <- nmr_meta_add(dataset_1D, metadata = metadata, by = "NMRExperiment")
metadata <- list(external = dataset_1D[["metadata"]][["external"]])
peak_table <- nmr_data(dataset_1D)
new <- new_nmr_dataset_peak_table(peak_table, metadata)
new
```

---

random\_subsampling      *Random subsampling*

---

**Description**

Random subsampling

**Usage**

```
random_subsampling(
  sample_idx,
  iterations = 10L,
  test_size = 0.25,
  keep_together = NULL,
  balance_in_train = NULL
)
```

**Arguments**

|               |   |
|---------------|---|
| sample_idx    | Typically a numeric vector with sample index to be separated. A character vector with sample IDs could also be used   |
| iterations    | An integer, the number of iterations in the random subsampling  |
| test_size     | A number between 0 and 1. The samples to be included in the test set on each iteration.   |
| keep_together | Either NULL or a factor with the same length as sample_idx. keep_together can be used to ensure that groups of samples are kept in together in all iterations (either on training or on test, but never split). A typical use case for this is when you have sample replicates and you want to keep all replicates together |

to prevent overoptimistic results (having one sample on the train subset and its replicate on the test subset would make the prediction easier to guess). Another use case for this is when you have a longitudinal study and you want to keep some subjects in the same train or test group, because you want to use some information in a longitudinal way (e.g. a multilevel plsda model).

#### balance\_in\_train

Either NULL or a factor with the same length as `sample_idx`. `balance_in_train` can be used to force that on each iteration, the train partition contains the same number of samples of the given factor levels. For instance, if we have a dataset with 40 samples of class "A" and 20 samples of class "B", using a `test_size = 0.25`, we can force to always have 16 samples of class "A" and 16 samples of class "B" in the training subset. This is beneficial to those algorithms that require that the training groups are balanced.

#### Value

A list of length equal to `iterations`. Each element of the list is a list with two entries (training and test) containing the `sample_idx` values that will belong to each subset.

#### Examples

```
random_subsampling(1:100, iterations = 4, test_size = 0.25)
```

```
subject_id <- c("Alice", "Bob", "Charlie", "Eve")
random_subsampling(1:4, iterations = 2, test_size = 0.25, keep_together = subject_id)
```

---

|                   |                                       |
|-------------------|---------------------------------------|
| read Bruker pdata | <i>Read processed Bruker NMR data</i> |
|-------------------|---------------------------------------|

---

#### Description

Read processed Bruker NMR data

#### Usage

```
read Bruker pdata(  
  sample_path,  
  pdata_file = NULL,  
  pdata_path = "pdata/1",  
  all_components = FALSE,  
  read_pdata_title = TRUE  
)
```

**Arguments**

|                  |   |
|------------------|---|
| sample_path      | A character path of the sample directory  |
| pdata_file       | File name of the binary NMR data to load. Usually "1r". If NULL, it is autode-<br>tected based on the dimension |
| pdata_path       | Path from sample_path to the preprocessed data  |
| all_components   | If FALSE load only the real component. Otherwise load the real and imaginary<br>components                      |
| read_pdata_title | If TRUE also reads metadata from pdata title file.  |

**Value**

A list with Bruker NMR processed data

---

|           |   |
|-----------|---|
| reexports | <i>Objects exported from other packages</i> |
|-----------|---|

---

**Description**

These objects are imported from other packages. Follow the links below to see their documentation.

**dplyr** [filter](#), [rename](#)

**generics** [tidy](#)

**magrittr** [%>%](#)

**utils** [.DollarNames](#)

---

|           |  |
|-----------|--|
| ROI_blood | <i>ROIs for blood (plasma/serum) samples</i> |
|-----------|--|

---

**Description**

The template ROI\_blood contains the targeted list of metabolites to be quantified (blood samples)

**References**

[github.com/danielcanueto/rDolphin](https://github.com/danielcanueto/rDolphin)

**Examples**

```
data("ROI_blood")
ROI_blood[ROI_blood$Metabolite == "Valine", ]
```

---

|          |                              |
|----------|------------------------------|
| ROI_cell | <i>ROIs for cell samples</i> |
|----------|------------------------------|

---

**Description**

The template ROI\_cell contains the targeted list of metabolites to be quantified (cell samples)

**References**

[github.com/danielcanueto/rDolphin](https://github.com/danielcanueto/rDolphin)

**Examples**

```
data("ROI_cell")
ROI_cell[ROI_cell$Metabolite == "Valine", ]
```

---

|           |                               |
|-----------|-------------------------------|
| ROI_urine | <i>ROIs for urine samples</i> |
|-----------|-------------------------------|

---

**Description**

The template ROI\_urine contains the targeted list of metabolites to be quantified (urine samples)

**References**

[github.com/danielcanueto/rDolphin](https://github.com/danielcanueto/rDolphin)

**Examples**

```
data("ROI_urine")
ROI_urine[ROI_urine$Metabolite == "Valine", ]
```

---

`save_files_to_rDolphin`*Save files to rDolphin*

---

## Description

The function saves the CSV files required by `to_rDolphin` and `Automatic_targeted_profiling` functions for metabolite profiling.

## Usage

```
save_files_to_rDolphin(files_rDolphin, output_directory)
```

## Arguments

`files_rDolphin` a list containing 4 elements from `files_to_rDolphin`

- `meta_rDolphin`: metadata in rDolphin format,
- `NMR_spectra`: spectra matrix
- `ROI`: ROI template
- `Parameters_blood`: parameters file

`output_directory`

a directory in which the CSV files are saved

## Value

CSV files containing:

## See Also

Other import/export functions: [Pipelines](#), [files\\_to\\_rDolphin\(\)](#), [load\\_and\\_save\\_functions](#), [nmr\\_data\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_read\\_bruker\\_fid\(\)](#), [nmr\\_read\\_samples\(\)](#), [nmr\\_zip\\_bruker\\_samples\(\)](#), [save\\_profiling\\_output\(\)](#), [to\\_ChemoSpec\(\)](#)

## Examples

```
## Not run:
dataset <- system.file("dataset-demo", package = "AlpsNMR")
excel_file <- system.file("dataset-demo", "dummy_metadata.xlsx", package = "AlpsNMR")
nmr_dataset <- nmr_read_samples_dir(dataset)
files_rDolphin <- files_to_rDolphin_blood(nmr_dataset)
save_files_to_rDolphin(files_rDolphin, output_directory = ".")

## End(Not run)
```



---

save\_profiling\_output *Save rDolphin output*

---

### Description

The function saves the output from Automatic\_targeted\_profiling function in CSV format.

### Usage

```
save_profiling_output(targeted_profiling, output_directory)
```

### Arguments

targeted\_profiling  
A list from Automatic\_targeted\_profiling function

output\_directory  
a directory in which the CSV files are saved

### Value

rDolphin output from Automatic\_targeted\_profiling function:

- metabolites\_intensity
- metabolites\_quantification
- ROI\_profiles\_used
- chemical\_shift
- fitting\_error
- half\_bandwidth
- signal\_area\_ratio

### See Also

Other import/export functions: [Pipelines](#), [files\\_to\\_rDolphin\(\)](#), [load\\_and\\_save\\_functions](#), [nmr\\_data\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_read\\_bruker\\_fid\(\)](#), [nmr\\_read\\_samples\(\)](#), [nmr\\_zip\\_bruker\\_samples\(\)](#), [save\\_files\\_to\\_rDolphin\(\)](#), [to\\_ChemoSpec\(\)](#)

### Examples

```
## Not run:  
rDolphin_object <- to_rDolphin(parameters)  
targeted_profiling <- Automatic_targeted_profiling(rDolphin)  
save_profiling_output(targeted_profiling, output_directory)  
  
## End(Not run)
```

---

SummarizedExperiment\_to\_nmr\_dataset\_peak\_table

*Import SummarizedExperiment as mr\_dataset\_peak\_table*

---

### Description

Import SummarizedExperiment as mr\_dataset\_peak\_table

### Usage

```
SummarizedExperiment_to_nmr_dataset_peak_table(se)
```

### Arguments

se                    An SummarizedExperiment object

### Value

nmr\_dataset\_peak\_table An [nmr\\_dataset\\_peak\\_table](#) object (unmodified)

### Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
meta <- file.path(dir_to_demo_dataset, "dummy_metadata.xlsx")
metadata <- readxl::read_excel(meta, sheet = 1)
dataset_1D <- nmr_meta_add(dataset_1D, metadata = metadata, by = "NMRExperiment")
metadata <- list(external = dataset_1D[["metadata"]][["external"]])
peak_table <- nmr_data(dataset_1D)
nmr_peak_table <- new_nmr_dataset_peak_table(peak_table, metadata)
se <- nmr_dataset_peak_table_to_SummarizedExperiment(nmr_peak_table)
nmr_peak_table <- SummarizedExperiment_to_nmr_dataset_peak_table(se)
```

---

SummarizedExperiment\_to\_nmr\_data\_1r

*Import SummarizedExperiment as 1D NMR data*

---

### Description

Import SummarizedExperiment as 1D NMR data

### Usage

```
SummarizedExperiment_to_nmr_data_1r(se)
```

**Arguments**

se An SummarizedExperiment object

**Value**

nmr\_dataset An [nmr\\_dataset\\_1D](#) object (unmodified)

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
se <- nmr_data_1r_to_SummarizedExperiment(dataset_1D)
dataset_1D <- SummarizedExperiment_to_nmr_data_1r(se)
```

---

tidy.nmr\_dataset\_1D *Get a tidy data frame from nmr\_data object*

---

**Description**

This dataframe is useful for plotting with ggplot, although it may be very long and therefore use a lot of RAM.

**Usage**

```
## S3 method for class 'nmr_dataset_1D'
tidy(
  x,
  NMRExperiment = NULL,
  chemshift_range = NULL,
  columns = character(0L),
  matrix_name = "data_1r",
  axis_name = "axis",
  ...
)
```

**Arguments**

x an [nmr\\_dataset\\_1D](#) object

NMRExperiment A character vector with the NMRExperiments to include. NULL means all.

chemshift\_range range of the chemical shifts to be included. Can be of length 3 to include the resolution in the third element (e.g. c(0.2, 0.8, 0.005))

columns A character vector with the metadata columns to get, use NULL to get all of them.

matrix\_name A string with the matrix name, typically "data\_1r"

axis\_name A string with the axis name, for now "axis" is the only valid option

... Ignored

**Value**

A data frame with NMRExperiment, chemshift, intensity and any additional column requested

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -1.0, max = 1.6, by = 2.3E-4))
dummy_metadata <- system.file("dataset-demo", "dummy_metadata.xlsx", package = "AlpsNMR")
NMRExp_SubjID <- readxl::read_excel(dummy_metadata, sheet = 1)
dataset_1D <- nmr_meta_add(dataset_1D, NMRExp_SubjID)
df_for_ggplot <- tidy(dataset_1D, chemshift_range = c(1.2, 1.4), columns = "SubjectID")
head(df_for_ggplot)
```

to\_ASICS

*Export data for the ASICS spectral quantification library***Description**

Exports the spectra matrix, sample names and chemical shift axis into an ASICS Spectra object.

**Usage**

```
to_ASICS(dataset, ...)
```

**Arguments**

|             |   |
|-------------|---|
| dataset     | An <a href="#">nmr_dataset_1D</a> object  |
| ...         | Arguments passed on to <a href="#">ASICS::createSpectra</a>   |
| norm.method | Character specifying the normalisation method to use on spectra ONLY if the <a href="#">importSpectra</a> function was not used.                              |
| norm.params | List containing normalisation parameteres (see <a href="#">normaliseSpectra</a> for details) ONLY if the <a href="#">importSpectra</a> function was not used. |

**Value**

An [ASICS::Spectra](#) object

**Examples**

```
if (requireNamespace("ASICS", quietly=TRUE)) {
  nsamp <- 3
  npoints <- 300
  metadata <- list(external = data.frame(
    NMRExperiment = paste0("Sample", seq_len(nsamp))
  ))
  dataset <- new_nmr_dataset_1D(
    ppm_axis = seq(from = 0.2, to = 10, length.out = npoints),
```

```
    data_1r = matrix(runif(nsamp * npoints), nrow = nsamp, ncol = npoints),
    metadata = metadata
  )
  forAsics <- to_ASICS(dataset)
  #ASICS::ASICS(forAsics)
}
```

---

|              |   |
|--------------|---|
| to_ChemoSpec | <i>Convert to ChemoSpec Spectra class</i> |
|--------------|---|

---

## Description

Convert to ChemoSpec Spectra class

## Usage

```
to_ChemoSpec(nmr_dataset, desc = "A nmr_dataset", group = NULL)
```

## Arguments

|             |   |
|-------------|---|
| nmr_dataset | An <a href="#">nmr_dataset_1D</a> object                                      |
| desc        | a description for the dataset   |
| group       | A string with the column name from the metadata that has grouping information |

## Value

A Spectra object from the ChemoSpec package

## See Also

Other import/export functions: [Pipelines](#), [files\\_to\\_rDolphin\(\)](#), [load\\_and\\_save\\_functions](#), [nmr\\_data\(\)](#), [nmr\\_meta\\_export\(\)](#), [nmr\\_read\\_bruker\\_fid\(\)](#), [nmr\\_read\\_samples\(\)](#), [nmr\\_zip\\_bruker\\_samples\(\)](#), [save\\_files\\_to\\_rDolphin\(\)](#), [save\\_profiling\\_output\(\)](#)

## Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
chemo_spectra <- to_ChemoSpec(dataset_1D)
```

---

validate\_nmr\_dataset    *Validate nmr\_dataset objects*

---

### Description

Validate nmr\_dataset objects

Validate 1D nmr datasets

### Usage

```
validate_nmr_dataset(samples)
```

```
validate_nmr_dataset_1D(nmr_dataset_1D)
```

### Arguments

samples            An nmr\_dataset object

nmr\_dataset\_1D    An [nmr\\_dataset\\_1D](#) object

### Value

Validate nmr\_dataset objects

The [nmr\\_dataset\\_1D](#) unchanged

This function is useful for its side-effects. Stopping in case of error

### See Also

Other class helper functions: [format.nmr\\_dataset\(\)](#), [format.nmr\\_dataset\\_1D\(\)](#), [format.nmr\\_dataset\\_peak\\_table\(\)](#), [is.nmr\\_dataset\\_1D\(\)](#), [is.nmr\\_dataset\\_peak\\_table\(\)](#), [new\\_nmr\\_dataset\(\)](#), [new\\_nmr\\_dataset\\_1D\(\)](#), [new\\_nmr\\_dataset\\_peak\\_table\(\)](#), [print.nmr\\_dataset\(\)](#), [print.nmr\\_dataset\\_1D\(\)](#), [print.nmr\\_dataset\\_peak\\_table\(\)](#), [validate\\_nmr\\_dataset\\_family\(\)](#), [validate\\_nmr\\_dataset\\_peak\\_table\(\)](#)

Other class helper functions: [format.nmr\\_dataset\(\)](#), [format.nmr\\_dataset\\_1D\(\)](#), [format.nmr\\_dataset\\_peak\\_table\(\)](#), [is.nmr\\_dataset\\_1D\(\)](#), [is.nmr\\_dataset\\_peak\\_table\(\)](#), [new\\_nmr\\_dataset\(\)](#), [new\\_nmr\\_dataset\\_1D\(\)](#), [new\\_nmr\\_dataset\\_peak\\_table\(\)](#), [print.nmr\\_dataset\(\)](#), [print.nmr\\_dataset\\_1D\(\)](#), [print.nmr\\_dataset\\_peak\\_table\(\)](#), [validate\\_nmr\\_dataset\\_family\(\)](#), [validate\\_nmr\\_dataset\\_peak\\_table\(\)](#)

### Examples

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
validate_nmr_dataset(dataset)
```

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
dataset_1D_validated <- validate_nmr_dataset_1D(dataset_1D)
```

---

validate\_nmr\_dataset\_family  
*Validate nmr\_dataset\_family objects*

---

**Description**

Validate nmr\_dataset\_family objects

**Usage**

```
validate_nmr_dataset_family(nmr_dataset_family)
```

**Arguments**

nmr\_dataset\_family  
An [nmr\\_dataset\\_family](#) object

**Value**

The [nmr\\_dataset\\_family](#) unchanged

This function is useful for its side-effects: Stopping in case of error

**See Also**

Other class helper functions: [format.nmr\\_dataset\(\)](#), [format.nmr\\_dataset\\_1D\(\)](#), [format.nmr\\_dataset\\_peak\\_table\(\)](#), [is.nmr\\_dataset\\_1D\(\)](#), [is.nmr\\_dataset\\_peak\\_table\(\)](#), [new\\_nmr\\_dataset\(\)](#), [new\\_nmr\\_dataset\\_1D\(\)](#), [new\\_nmr\\_dataset\\_peak\\_table\(\)](#), [print.nmr\\_dataset\(\)](#), [print.nmr\\_dataset\\_1D\(\)](#), [print.nmr\\_dataset\\_peak\\_table\(\)](#), [validate\\_nmr\\_dataset\(\)](#), [validate\\_nmr\\_dataset\\_peak\\_table\(\)](#)

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
validate_nmr_dataset_family(dataset_1D)
```

---

validate\_nmr\_dataset\_peak\_table  
*Validate nmr\_dataset\_peak\_table objects*

---

**Description**

Validate nmr\_dataset\_peak\_table objects

**Usage**

```
validate_nmr_dataset_peak_table(nmr_dataset_peak_table)
```

**Arguments**

nmr\_dataset\_peak\_table  
 An [nmr\\_dataset\\_peak\\_table](#) object

**Value**

The [nmr\\_dataset\\_peak\\_table](#) unchanged

**See Also**

Other class helper functions: [format.nmr\\_dataset\(\)](#), [format.nmr\\_dataset\\_1D\(\)](#), [format.nmr\\_dataset\\_peak\\_table\(\)](#), [is.nmr\\_dataset\\_1D\(\)](#), [is.nmr\\_dataset\\_peak\\_table\(\)](#), [new\\_nmr\\_dataset\(\)](#), [new\\_nmr\\_dataset\\_1D\(\)](#), [new\\_nmr\\_dataset\\_peak\\_table\(\)](#), [print.nmr\\_dataset\(\)](#), [print.nmr\\_dataset\\_1D\(\)](#), [print.nmr\\_dataset\\_peak\\_table\(\)](#), [validate\\_nmr\\_dataset\(\)](#), [validate\\_nmr\\_dataset\\_family\(\)](#)

**Examples**

```
pt <- new_nmr_dataset_peak_table(
  peak_table = matrix(c(1, 2), nrow = 1, dimnames = list("10", c("ppm_1.4", "ppm_1.6"))),
  metadata = list(external = data.frame(NMRExperiment = "10"))
)
pt_validated <- validate_nmr_dataset_peak_table(pt)
```

---

```
zzz
```

```
zzz
```

---

**Description**

```
zzz
```

**Examples**

```
# Workaround a bug in R CMD check
Sys.sleep(2)
```

---

```
[.nmr_dataset
```

```
Extract parts of an nmr_dataset
```

---

**Description**

Extract parts of an `nmr_dataset`

**Usage**

```
## S3 method for class 'nmr_dataset'
x[i]
```



**Arguments**

x            an `nmr_dataset` object  
i            indices of the samples to keep

**Value**

an `nmr_dataset` with the extracted samples

**See Also**

Other subsetting functions: `[.nmr_dataset_1D()`, `[.nmr_dataset_peak_table()`, `filter.nmr_dataset_family()`, `nmr_pca_outliers_filter()`

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset2 <- dataset[1:3] # get the first 3 samples
```

---

[.nmr\_dataset\_1D            *Extract parts of an nmr\_dataset\_1D*

---

**Description**

Extract parts of an `nmr_dataset_1D`

**Usage**

```
## S3 method for class 'nmr_dataset_1D'
x[i]
```

**Arguments**

x            an `nmr_dataset_1D` object  
i            indices of the samples to keep

**Value**

an `nmr_dataset_1D` with the extracted samples

**See Also**

Other subsetting functions: `[.nmr_dataset()`, `[.nmr_dataset_peak_table()`, `filter.nmr_dataset_family()`, `nmr_pca_outliers_filter()`

Other `nmr_dataset_1D` functions: `format.nmr_dataset_1D()`, `get_integration_with_metadata()`, `is.nmr_dataset_1D()`, `nmr_integrate_peak_positions()`, `nmr_integrate_regions()`, `nmr_meta_add()`, `nmr_meta_export()`, `nmr_meta_get()`, `nmr_meta_get_column()`, `nmr_ppm_resolution()`, `print.nmr_dataset_1D()`

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
dataset_1D[0]
```

---

```
[.nmr_dataset_peak_table
```

*Extract parts of an nmr\_dataset\_peak\_table*

---

**Description**

Extract parts of an `nmr_dataset_peak_table`

**Usage**

```
## S3 method for class 'nmr_dataset_peak_table'
x[i]
```

**Arguments**

`x` an `nmr_dataset_peak_table` object  
`i` indices of the samples to keep

**Value**

an `nmr_dataset_peak_table` with the extracted samples

**See Also**

Other subsetting functions: [\[.nmr\\_dataset\(\)\]](#), [\[.nmr\\_dataset\\_1D\(\)\]](#), [filter.nmr\\_dataset\\_family\(\)](#), [nmr\\_pca\\_outliers\\_filter\(\)](#)

**Examples**

```
dir_to_demo_dataset <- system.file("dataset-demo", package = "AlpsNMR")
dataset <- nmr_read_samples_dir(dir_to_demo_dataset)
dataset_1D <- nmr_interpolate_1D(dataset, axis = c(min = -0.5, max = 10, by = 2.3E-4))
meta <- file.path(dir_to_demo_dataset, "dummy_metadata.xlsx")
metadata <- readxl::read_excel(meta, sheet = 1)
dataset_1D <- nmr_meta_add(dataset_1D, metadata = metadata, by = "NMRExperiment")
metadata <- list(external = dataset_1D[["metadata"]][["external"]])
peak_table <- nmr_data(dataset_1D)
new <- new_nmr_dataset_peak_table(peak_table, metadata)
new[0]
```

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