

Package ‘AlpsNMR’

November 21, 2024

Type Package

Title Automated spectral Processing System for NMR

Version 4.9.0

Date 2024-08-10

Encoding UTF-8

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.

License MIT + file LICENSE

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,

NMRphasing, plotly (>= 4.7.1), progressr, SummarizedExperiment,

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

2.0.4)

biocViews Software, Preprocessing, Visualization, Classification,
Cheminformatics, Metabolomics, DataImport

RoxygenNote 7.3.1

Roxygen list(markdown = TRUE)

VignetteBuilder knitr

git_url <https://git.bioconductor.org/packages/AlpsNMR>

git_branch devel

git_last_commit f8b70f5

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2024-11-21

Author Ivan Montoliu Roura [aut],
Sergio Oller Moreno [aut, cre] (ORCID:
<<https://orcid.org/0000-0002-8994-1549>>),
Francisco Madrid Gambin [aut] (ORCID:
<<https://orcid.org/0000-0001-9333-0014>>),
Luis Fernandez [aut] (ORCID: <<https://orcid.org/0000-0001-9790-6287>>),
Laura López Sánchez [ctb],
Héctor Gracia Cabrera [aut],
Santiago Marco Colás [aut] (ORCID:
<<https://orcid.org/0000-0003-2663-2965>>),
Nestlé Institute of Health Sciences [cph],
Institute for Bioengineering of Catalonia [cph],
Miller Jack [ctb] (ORCID: <<https://orcid.org/0000-0002-6258-1299>>),
Autophase wrapper, ASICS export)

Maintainer Sergio Oller Moreno <sergioller@gmail.com>

Contents

AlpsNMR-package	5
bp_kfold_VIP_analysis	6
bp_VIP_analysis	8
download_MTBL242	10
files_to_rDolphin	12
file_lister	13
filter.nmr_dataset_family	14
format.nmr_dataset	15
format.nmr_dataset_ID	15
format.nmr_dataset_peak_table	16
get_integration_with_metadata	17
hmdb	18
HMDB_blood	18
HMDB_cell	19
HMDB_urine	19

is.nmr_dataset	20
is.nmr_dataset_1D	20
is.nmr_dataset_peak_table	21
load_and_save_functions	22
models_stability_plot_bootstrap	23
models_stability_plot_plsda	24
new_nmr_dataset	25
new_nmr_dataset_1D	27
new_nmr_dataset_peak_table	28
nmr_align	29
nmr_align_find_ref	30
nmr_autophase	30
nmr_baseline_estimation	31
nmr_baseline_removal	32
nmr_baseline_threshold	33
nmr_baseline_threshold_plot	34
nmr_batman	35
nmr_batman_options	37
nmr_build_peak_table	39
nmr_data	39
nmr_dataset	40
nmr_dataset_1D	41
nmr_dataset_family	42
nmr_dataset_peak_table	42
nmr_dataset_peak_table_to_SummarizedExperiment	43
nmr_data_1r_to_SummarizedExperiment	44
nmr_data_analysis	44
nmr_data_analysis_method	46
nmr_detect_peaks	48
nmr_detect_peaks_plot	49
nmr_detect_peaks_plot_overview	50
nmr_detect_peaks_plot_peaks	51
nmr_detect_peaks_tune_snr	52
nmr_exclude_region	53
nmr_export_data_1r	54
nmr_get_peak_distances	55
nmr_identify_regions_blood	55
nmr_identify_regions_cell	56
nmr_identify_regions_urine	57
nmr_integrate_peak_positions	58
nmr_integrate_regions	59
nmr_interpolate_1D	61
nmr_meta_add	62
nmr_meta_export	64
nmr_meta_get	65
nmr_meta_get_column	66
nmr_meta_groups	67
nmr_normalize	67

nmr_pca_build_model	69
nmr_pca_outliers	70
nmr_pca_outliers_filter	71
nmr_pca_outliers_plot	72
nmr_pca_outliers_robust	73
nmr_pca_plots	74
nmr_peak_clustering	75
nmr_peak_clustering_plot	76
nmr_ppm_resolution	77
nmr_read_bruker_fid	78
nmr_read_samples	78
nmr_zip_bruker_samples	80
Parameters_blood	81
Parameters_cell	81
Parameters_urine	82
peaklist_accept_peaks	82
peaklist_fit_lorentzians	83
Peak_detection	85
permutation_test_model	86
permutation_test_plot	88
Pipelines	90
plot.nmr_dataset_1D	94
plot_bootstrap_multimodel	95
plot_interactive	97
plot_plsda_multimodel	97
plot_plsda_samples	99
plot_vip_scores	100
plot_webgl	102
plsda_auroc_vip_compare	103
plsda_auroc_vip_method	104
ppm_resolution	105
print.nmr_dataset	106
print.nmr_dataset_1D	106
print.nmr_dataset_peak_table	107
random_subsampling	108
read_bruker_pdata	109
reexports	110
ROI_blood	110
ROI_cell	111
ROI_urine	111
save_files_to_rDolphin	112
save_profiling_output	113
SummarizedExperiment_to_nmr_dataset_peak_table	114
SummarizedExperiment_to_nmr_data_1r	114
tidy.nmr_dataset_1D	115
to_ASICS	116
to_ChemoSpec	117
validate_nmr_dataset	118

validate_nmr_dataset_family	119
validate_nmr_dataset_peak_table	119
ZZZ	120
[.nmr_dataset	120
[.nmr_dataset_ID	121
[.nmr_dataset_peak_table	122

Index	123
--------------	------------

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.

Author(s)

Maintainer: Sergio Oller Moreno <sergioller@gmail.com> ([ORCID](#))

Authors:

- Ivan Montoliu Roura <Ivan.MontoliuRoura@rd.nestle.com>
- Francisco Madrid Gambin <fmadrid@ibecbarcelona.eu> ([ORCID](#))
- Luis Fernandez <lfernandez@ibecbarcelona.eu> ([ORCID](#))
- Héctor Gracia Cabrera <hgracia@ibecbarcelona.eu>
- Santiago Marco Colás <smarco@ibecbarcelona.eu> ([ORCID](#))

Other contributors:

- Laura López Sánchez [contributor]

- Nestlé Institute of Health Sciences [copyright holder]
- Institute for Bioengineering of Catalonia [copyright holder]
- Miller Jack <jack.miller@physics.org> ([ORCID](#)) (Autophase wrapper, ASICS export) [contributor]

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 nmr_dataset_family 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 nmr_dataset_family 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

<code>dest_dir</code>	Directory where the dataset should be saved
<code>force</code>	Logical. If TRUE we do not re-download files if they exist. The function does not check whether cached versions were downloaded with different <code>keep_only_*</code> arguments, so please use <code>force = TRUE</code> if you change the <code>keep_only_*</code> settings.
<code>keep_only_CPMG_1r</code>	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 nmr_dataset_family
...	Additional arguments passed to saveRDS .

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 nmr_dataset_ID
peak_data	The detected peak data given by nmr_detect_peaks .
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 nmr_dataset object
method	The autophasing method. See NMRphasing::NMRphasing() for details.
withBC	NMRphasing::NMRphasing may perform a baseline correction using modified polynomial fitting. By default AlpsNMR offers other baseline estimation methods and better visualization of its effect, so AlpsNMR by default disables the baseline correction offered by NMRphasing .
...	Other parameters passed on to NMRphasing::NMRphasing() .

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 nmr_dataset_1D .
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 nmr_dataset_1D .
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 nmr_dataset_1D .
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 nmr_dataset_1D 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 nmr_baseline_threshold
<code>...</code>	arguments passed to ggplot2::aes (or to ggplot2::aes_string , 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 directory
filename	Filename to use, inside batman_dir
nmr_dataset	An nmr_dataset_ID object
multiplet_table	A data frame, like the hmdb 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 nmr_dataset_family 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 nmr_dataset_family 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 random_subsampling for further details
data_analysis_method	An nmr_data_analysis_method 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$outer_cv_results_digested$auroc
## Rank Product of the Variable Importance in the Projection
## (Lower means more important)
sort(model$outer_cv_results_digested$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"> • A numeric vector of length the number of samples. Each number is a threshold for that sample • A single number. All samples use this number as baseline threshold. • 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.
<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 nmr_dataset_ID .
peak_data	The peak table returned by nmr_detect_peaks
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 plot.nmr_dataset_ID (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 nmr_detect_peaks()
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}",
    "\u03B3(ppb)\u00a0=\u00a0{gamma_ppb}", " \narea\u00a0=\u00a0{area}",
    "nrmse\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 nmr_dataset_ID 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 nmr_detect_peaks
	nmr_dataset An nmr_dataset_ID .
	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"> • A numeric vector of length the number of samples. Each number is a threshold for that sample • A single number. All samples use this number as baseline threshold. • NULL. If that's the case, a default function is used (nmr_baseline_threshold()), which assumes that there is no signal in the region 9.5-10 ppm.
	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 nmr_dataset 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 nmr_integrate_regions
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 nmr_dataset 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. 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 nmr_dataset_family 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 MUST 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 nmr_dataset_family 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`*Get metadata*

Description

Get metadata

Usage

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

Arguments

<code>samples</code>	a nmr_dataset_family object
<code>columns</code>	Columns to get. By default gets all the columns.
<code>groups</code>	Groups to get. Groups are predefined of columns. Typically "external" for metadata added with nmr_meta_add . 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 nmr_dataset_1D 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 nmr_integrate_regions

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

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

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 nmr_dataset_1D object
<code>pca_model</code>	A pca model returned by nmr_pca_build_model
<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 nmr_dataset_1D object
<code>pca_outliers</code>	The output from nmr_pca_outliers()
<code>...</code>	Additional parameters passed on to ggplot2::aes() (or now deprecated to ggplot2::aes_string())

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 nmr_pca_build_model
<code>nmr_dataset</code>	an nmr_dataset_1D object
<code>comp</code>	Components to represent
<code>...</code>	Additional aesthetics passed on to ggplot2::aes (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 nmr_get_peak_distances . 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 read_bruker_pdata
<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 utils::zip

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

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

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

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

- γ is estimated using the inflection points of the signal and fitting them to the lorentzian inflection points
- ΔA 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 γ , ΔA and x_0 .

The baseline estimation (when calculated, see the arguments) is set to Asymmetric Least Squares with $\lambda = 6$, $p=0.05$, $\text{maxit}=20$ 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 nmr_dataset_family 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 random_subsampling for further details
data_analysis_method	An nmr_data_analysis_method 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. <code>*.csv</code>) 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 MUST 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, MUST have unique values. For instance, a sheet starting with "SubjectID" MUST 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"> • <code>conditions <- 'Gender == "Female"'</code> • <code>conditions <- 'Cohort == "Chuv"'</code> • <code>conditions <- 'TimePoint %in% c("T0", "T31")'</code> • <code>conditions <- c(Cohort == "Chuv", 'TimePoint %in% c("T0", "T31")')</code> <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"> • A numeric vector of length the number of samples. Each number is a threshold for that sample • A single number. All samples use this number as baseline threshold. • 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.
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 pipe_peakdet_align
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 nmr_dataset_1D
html_filename	The output HTML filename to be created
overwrite	Overwrite the lib/ directory (use NULL to prompt the user)
...	Arguments passed on to plot.nmr_dataset_1D
	x a nmr_dataset_1D 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 *Read processed Bruker NMR data*

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- 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 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

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

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

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 nmr_dataset_1D object
...	Arguments passed on to ASICS::createSpectra
norm.method	Character specifying the normalisation method to use on spectra ONLY if the importSpectra function was not used.
norm.params	List containing normalisation parameteres (see normaliseSpectra for details) ONLY if the importSpectra 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 nmr_dataset_1D 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]
```

Index

- * **AlpsNMR dataset objects**
 - nmr_dataset, 40
 - nmr_dataset_family, 42
- * **PCA related functions**
 - nmr_pca_build_model, 69
 - nmr_pca_outliers, 70
 - nmr_pca_outliers_filter, 71
 - nmr_pca_outliers_plot, 72
 - nmr_pca_outliers_robust, 73
 - nmr_pca_plots, 74
- * **alignment functions**
 - nmr_align, 29
 - nmr_align_find_ref, 30
 - Pipelines, 90
- * **baseline removal functions**
 - nmr_baseline_estimation, 31
 - nmr_baseline_removal, 32
- * **basic functions**
 - nmr_exclude_region, 53
 - nmr_normalize, 67
- * **batman functions**
 - nmr_batman, 35
 - nmr_batman_options, 37
- * **class helper functions**
 - format.nmr_dataset, 15
 - format.nmr_dataset_1D, 15
 - format.nmr_dataset_peak_table, 16
 - is.nmr_dataset_1D, 20
 - is.nmr_dataset_peak_table, 21
 - new_nmr_dataset, 25
 - new_nmr_dataset_1D, 27
 - new_nmr_dataset_peak_table, 28
 - print.nmr_dataset, 106
 - print.nmr_dataset_1D, 106
 - print.nmr_dataset_peak_table, 107
 - validate_nmr_dataset, 118
 - validate_nmr_dataset_family, 119
 - validate_nmr_dataset_peak_table, 119
- * **data**
 - hmdb, 18
 - HMDB_blood, 18
 - HMDB_cell, 19
 - HMDB_urine, 19
 - Parameters_blood, 81
 - Parameters_cell, 81
 - Parameters_urine, 82
 - ROI_blood, 110
 - ROI_cell, 111
 - ROI_urine, 111
- * **import/export functions**
 - files_to_rDolphin, 12
 - load_and_save_functions, 22
 - nmr_data, 39
 - nmr_meta_export, 64
 - nmr_read_bruker_fid, 78
 - nmr_read_samples, 78
 - nmr_zip_bruker_samples, 80
 - Pipelines, 90
 - save_files_to_rDolphin, 112
 - save_profiling_output, 113
 - to_ChemoSpec, 117
- * **internal**
 - read_bruker_pdata, 109
 - reexports, 110
 - zzz, 120
- * **metadata functions**
 - nmr_meta_add, 62
 - nmr_meta_export, 64
 - nmr_meta_get, 65
 - nmr_meta_get_column, 66
 - nmr_meta_groups, 67
 - Pipelines, 90
- * **nmr_dataset functions**
 - nmr_meta_add, 62
 - nmr_meta_export, 64
 - nmr_meta_get, 65
 - nmr_meta_get_column, 66

- * **nmr_dataset_1D functions**
 - [.nmr_dataset_1D, 121
 - format.nmr_dataset_1D, 15
 - get_integration_with_metadata, 17
 - is.nmr_dataset_1D, 20
 - nmr_integrate_peak_positions, 58
 - nmr_integrate_regions, 59
 - nmr_meta_add, 62
 - nmr_meta_export, 64
 - nmr_meta_get, 65
 - nmr_meta_get_column, 66
 - nmr_ppm_resolution, 77
 - print.nmr_dataset_1D, 106
- * **nmr_dataset_peak_table functions**
 - nmr_meta_add, 62
 - nmr_meta_export, 64
 - nmr_meta_get, 65
 - nmr_meta_get_column, 66
- * **outlier detection functions**
 - nmr_pca_outliers, 70
 - nmr_pca_outliers_filter, 71
 - nmr_pca_outliers_plot, 72
 - nmr_pca_outliers_robust, 73
 - Pipelines, 90
- * **peak alignment functions**
 - nmr_align, 29
 - nmr_align_find_ref, 30
- * **peak detection functions**
 - nmr_baseline_threshold, 33
 - nmr_detect_peaks, 48
 - nmr_detect_peaks_plot, 49
 - nmr_detect_peaks_plot_overview, 50
 - nmr_detect_peaks_tune_snr, 52
 - nmr_identify_regions_blood, 55
 - nmr_identify_regions_cell, 56
 - nmr_identify_regions_urine, 57
 - nmr_integrate_regions, 59
 - Pipelines, 90
- * **peak integration functions**
 - get_integration_with_metadata, 17
 - nmr_identify_regions_blood, 55
 - nmr_identify_regions_cell, 56
 - nmr_identify_regions_urine, 57
 - nmr_integrate_peak_positions, 58
 - nmr_integrate_regions, 59
 - Pipelines, 90
- * **pipeline functions**
 - Pipelines, 90
- * **plotting functions**
 - plot.nmr_dataset_1D, 94
 - plot_interactive, 97
- * **plotting nmr datasets**
 - plot_webgl, 102
- * **subsetting functions**
 - [.nmr_dataset, 120
 - [.nmr_dataset_1D, 121
 - [.nmr_dataset_peak_table, 122
 - filter.nmr_dataset_family, 14
 - nmr_pca_outliers_filter, 71
 - .DollarNames, 110
 - .DollarNames (reexports), 110
 - [.nmr_dataset, 14, 72, 120, 121, 122
 - [.nmr_dataset_1D, 14, 16, 17, 21, 59, 60, 63–66, 72, 77, 107, 121, 121, 122
 - [.nmr_dataset_peak_table, 14, 72, 121, 122
 - %>% (reexports), 110
 - %>%, 110
- AlpsNMR (AlpsNMR-package), 5
- AlpsNMR-package, 5
- as.data.frame.nmr_dataset_peak_table (nmr_dataset_peak_table), 42
- ASICS::createSpectra, 116
- ASICS::Spectra, 116
- baseline::baseline.als, 31, 32
- bp_kfold_VIP_analysis, 6
- bp_VIP_analysis, 7, 8
- download_MTBLS242, 10
- dplyr, 14
- file_lister, 13
- files_to_rDolphin, 12, 22, 40, 64, 78–80, 93, 112, 113, 117
- filter, 110
- filter (reexports), 110
- filter.nmr_dataset_family, 14, 72, 121, 122
- format.nmr_dataset, 15, 16, 17, 21, 26–28, 106–108, 118–120
- format.nmr_dataset_1D, 15, 15, 17, 21, 26–28, 59, 60, 63–66, 77, 106–108, 118–121
- format.nmr_dataset_peak_table, 15, 16, 16, 21, 26–28, 106–108, 118–120

- `fs::dir_ls()`, 13
- Functions to save and load these objects, 41, 42
- `get_integration_with_metadata`, 16, 17, 21, 56–60, 63–66, 77, 93, 107, 121
- `ggplot2::aes`, 34, 74, 95
- `ggplot2::aes()`, 72
- `ggplot2::aes_string`, 34, 95
- `ggplot2::aes_string()`, 72
- `grep()`, 91
- `hmdb`, 18, 36
- `HMDB_blood`, 18
- `HMDB_cell`, 19
- `HMDB_urine`, 19
- `importSpectra`, 116
- `is.nmr_dataset`, 20
- `is.nmr_dataset_1D`, 15–17, 20, 21, 26–28, 59, 60, 63–66, 77, 106–108, 118–121
- `is.nmr_dataset_peak_table`, 15–17, 21, 21, 26–28, 106–108, 118–120
- `load_and_save_functions`, 12, 22, 40, 64, 78–80, 93, 112, 113, 117
- `MassSpecWavelet::peakDetectionCWT`, 48
- `mixOmics::pca`, 69, 70
- `mixOmics::plsda`, 47
- `models_stability_plot_bootstrap`, 23
- `models_stability_plot_plsda`, 24
- `new_nmr_data_analysis_method` (`nmr_data_analysis_method`), 46
- `new_nmr_data_analysis_method()`, 45
- `new_nmr_dataset`, 15–17, 21, 25, 27, 28, 106–108, 118–120
- `new_nmr_dataset_1D`, 15–17, 21, 26, 27, 28, 106–108, 118–120
- `new_nmr_dataset_peak_table`, 15–17, 21, 26, 27, 28, 106–108, 118–120
- `nmr_align`, 29, 30, 49, 93
- `nmr_align_find_ref`, 29, 30, 93
- `nmr_autophase`, 30
- `nmr_baseline_estimation`, 31, 32
- `nmr_baseline_removal`, 32, 32
- `nmr_baseline_threshold`, 33, 34, 49–51, 53, 56–58, 60, 93
- `nmr_baseline_threshold()`, 48, 52, 92
- `nmr_baseline_threshold_plot`, 34
- `nmr_batman`, 35, 38
- `nmr_batman_export_dataset` (`nmr_batman`), 35
- `nmr_batman_metabolites_list` (`nmr_batman`), 35
- `nmr_batman_multi_data_user` (`nmr_batman`), 35
- `nmr_batman_multi_data_user_hmdb` (`nmr_batman`), 35
- `nmr_batman_options`, 36, 37
- `nmr_batman_write_options` (`nmr_batman`), 35
- `nmr_build_peak_table`, 39
- `nmr_data`, 12, 22, 39, 64, 78–80, 93, 112, 113, 117
- `nmr_data<-` (`nmr_data`), 39
- `nmr_data_1r_to_SummarizedExperiment`, 44
- `nmr_data_analysis`, 44, 47, 103, 105
- `nmr_data_analysis_method`, 45, 46, 87
- `nmr_dataset`, 5, 12, 15, 17, 20, 31, 40, 42, 59, 60, 78, 79, 106, 121
- `nmr_dataset_1D`, 6, 8, 13, 16, 20, 29–34, 36, 39, 41, 44, 48, 49, 52, 54, 68–72, 74, 76, 94, 102, 107, 115–118, 121
- `nmr_dataset_family`, 6, 8, 14, 22, 40, 41, 42, 45, 62, 64–67, 87, 95, 119
- `nmr_dataset_load` (`load_and_save_functions`), 22
- `nmr_dataset_peak_table`, 6, 8, 16, 21, 39, 42, 43, 44, 60, 107, 114, 120, 122
- `nmr_dataset_peak_table_to_SummarizedExperiment`, 43
- `nmr_dataset_save` (`load_and_save_functions`), 22
- `nmr_detect_peaks`, 29, 30, 34, 48, 49–53, 56–58, 60, 93
- `nmr_detect_peaks()`, 50
- `nmr_detect_peaks_plot`, 34, 49, 49, 51, 53, 56–58, 60, 93
- `nmr_detect_peaks_plot()`, 50
- `nmr_detect_peaks_plot_overview`, 34, 49, 50, 50, 53, 56–58, 60, 93
- `nmr_detect_peaks_plot_peaks`, 51
- `nmr_detect_peaks_tune_snr`, 34, 49–51, 52, 56–58, 60, 93

- nmr_exclude_region, 53, 68
- nmr_exclude_region(), 5
- nmr_export_data_1r, 54
- nmr_get_peak_distances, 55, 75
- nmr_identify_regions_blood, 17, 34, 49–51, 53, 55, 57–60, 93
- nmr_identify_regions_cell, 17, 34, 49–51, 53, 56, 58–60, 93
- nmr_identify_regions_urine, 17, 34, 49–51, 53, 56, 57, 59, 60, 93
- nmr_integrate_peak_positions, 16, 17, 21, 56–58, 58, 60, 63–66, 77, 93, 107, 121
- nmr_integrate_regions, 16, 17, 21, 34, 49–51, 53, 56–59, 59, 63–66, 68, 77, 93, 107, 121
- nmr_interpolate_1D, 61
- nmr_interpolate_1D(), 5
- nmr_meta_add, 16, 17, 21, 59, 60, 62, 64–67, 77, 93, 107, 121
- nmr_meta_add_tidy_excel (nmr_meta_add), 62
- nmr_meta_export, 12, 16, 17, 21, 22, 40, 59, 60, 63, 64, 65–67, 77–80, 93, 107, 112, 113, 117, 121
- nmr_meta_get, 16, 17, 21, 59, 60, 63, 64, 65, 66, 67, 77, 93, 107, 121
- nmr_meta_get_column, 16, 17, 21, 59, 60, 63–65, 66, 67, 77, 93, 107, 121
- nmr_meta_groups, 63–66, 67, 93
- nmr_normalize, 53, 67
- nmr_normalize(), 5
- nmr_normalize_extra_info (nmr_normalize), 67
- nmr_pca_build_model, 69, 70–72, 74
- nmr_pca_loadingplot (nmr_pca_plots), 74
- nmr_pca_outliers, 70, 70, 72–74, 93
- nmr_pca_outliers(), 71, 72
- nmr_pca_outliers_filter, 14, 70, 71, 71, 72, 74, 93, 121, 122
- nmr_pca_outliers_plot, 70–72, 72, 74, 93
- nmr_pca_outliers_plot(), 73
- nmr_pca_outliers_robust, 70–72, 73, 74, 90, 93
- nmr_pca_plot_variance (nmr_pca_plots), 74
- nmr_pca_plots, 70–72, 74, 74
- nmr_pca_scoreplot (nmr_pca_plots), 74
- nmr_peak_clustering, 75
- nmr_peak_clustering_plot, 76
- nmr_ppm_resolution, 16, 17, 21, 59, 60, 63–66, 77, 107, 121
- nmr_read_bruker_fid, 12, 22, 40, 64, 78, 79, 80, 93, 112, 113, 117
- nmr_read_samples, 12, 22, 40, 64, 78, 78, 80, 93, 112, 113, 117
- nmr_read_samples(), 5, 30
- nmr_read_samples_dir (nmr_read_samples), 78
- nmr_read_samples_dir(), 5
- nmr_zip_bruker_samples, 12, 22, 40, 64, 78, 79, 80, 93, 112, 113, 117
- NMRphasing::NMRphasing(), 30, 31
- normaliseSpectra, 116
- Parameters_blood, 81
- Parameters_cell, 81
- Parameters_urine, 82
- Peak_detection, 85
- peaklist_accept_peaks, 82
- peaklist_fit_lorentzians, 83
- permutation_test_model, 86
- permutation_test_plot, 88
- pipe_add_metadata (Pipelines), 90
- pipe_exclude_regions (Pipelines), 90
- pipe_filter_samples (Pipelines), 90
- pipe_interpolate_1D (Pipelines), 90
- pipe_load_samples (Pipelines), 90
- Pipe_normalization (Pipelines), 90
- pipe_normalization (Pipelines), 90
- pipe_outlier_detection (Pipelines), 90
- pipe_pakdet_align (Pipelines), 90
- pipe_peak_integration (Pipelines), 90
- pipe_peakdet_align, 92
- pipe_peakdet_align (Pipelines), 90
- Pipelines, 12, 17, 22, 29, 30, 34, 40, 49–51, 53, 56–60, 63–67, 71, 72, 74, 78–80, 90, 112, 113, 117
- plot(), 5
- plot.nmr_dataset_1D, 49, 94, 97, 102
- plot_bootstrap_multimodel, 95
- plot_interactive, 53, 95, 97
- plot_plsda_multimodel, 97
- plot_plsda_samples, 99
- plot_vip_scores, 100
- plot_webgl, 102
- plotly::ggplotly, 53

- plsda_auroc_vip_compare, 103
- plsda_auroc_vip_method, 45, 104
- ppm_resolution, 105
- print.nmr_dataset, 15–17, 21, 26–28, 106, 107, 108, 118–120
- print.nmr_dataset_1D, 15–17, 21, 26–28, 59, 60, 63–66, 77, 106, 106, 108, 118–121
- print.nmr_dataset_peak_table, 15–17, 21, 26–28, 106, 107, 107, 118–120

- random_subsampling, 45, 87, 108
- read_bruker_pdata, 79, 109
- read_bruker_pdata(), 79
- reexports, 110
- rename, 110
- rename (reexports), 110
- ROI_blood, 110
- ROI_cell, 111
- ROI_urine, 111

- save_files_to_rDolphin, 12, 22, 40, 64, 78–80, 93, 112, 113, 117
- save_profiling_output, 12, 22, 40, 64, 78–80, 93, 112, 113, 117
- saveRDS, 22
- scale, 69
- speaq::detectSpecPeaks, 48
- speaq::dohCluster, 29
- SummarizedExperiment_to_nmr_data_1r, 114
- SummarizedExperiment_to_nmr_dataset_peak_table, 114

- tidy, 110
- tidy (reexports), 110
- tidy.nmr_dataset_1D, 115
- to_ASICS, 116
- to_ChemoSpec, 12, 22, 40, 64, 78–80, 93, 112, 113, 117

- utils::zip, 80

- validate_nmr_dataset, 15–17, 21, 26–28, 106–108, 118, 119, 120
- validate_nmr_dataset_1D (validate_nmr_dataset), 118
- validate_nmr_dataset_family, 15–17, 21, 26–28, 106–108, 118, 119, 120

- validate_nmr_dataset_peak_table, 15–17, 21, 26–28, 106–108, 118, 119, 119

- zzz, 120