Package 'spant'

May 21, 2026

Type Package

Title MR Spectroscopy Analysis Tools

Version 4.1.0

Date 2026-05-19

Description Tools for reading, visualising and processing Magnetic Resonance Spectroscopy data. The package includes methods for spectral fitting: Wilson (2021) <DOI:10.1002/mrm.28385>, Wilson (2025) <DOI:10.1002/mrm.30462> and spectral alignment: Wilson (2018) <DOI:10.1002/mrm.27605>.

BugReports https://github.com/martin3141/spant/issues/

License GPL-3

NeedsCompilation yes

Depends R (>= 4.1.0)

Imports abind, plyr, pbapply, pracma, stringr, expm (>= 1.0-0), signal, minpack.lm, utils, graphics, grDevices, ptw, mmand, RNifti, RNiftyReg, fields, numDeriv, nloptr, irlba, jsonlite

Suggests viridisLite, shiny, shinyFiles, ggplot2, miniUI, knitr, kableExtra, rmarkdown, testthat, ragg, doParallel, parallel, digest, readxl, fslr, car, divest, rpyANTs

VignetteBuilder knitr

Encoding UTF-8

Language en-GB

URL https://spantdoc.wilsonlab.co.uk/, https://martin3141.github.io/spant/, https://github.com/martin3141/spant/

Config/roxygen2/version 8.0.0

Author Martin Wilson [cre, aut] (ORCID: <https://orcid.org/0000-0002-2089-3956>), Yong Wang [ctb], John Muschelli [ctb]

Maintainer Martin Wilson <martin.wilson111@gmail.com>

Repository CRAN

Date/Publication 2026-05-21 13:30:02 UTC

Contents

`spant-package` *spant: spectroscopy analysis tools.*

Description

spant provides a set of tools for reading, visualising and processing Magnetic Resonance Spectroscopy (MRS) data.

Details

To get started with spant, take a look at the introduction vignette:

```
vignette("spant-intro", package="spant")
```

Full list of vignettes:

```
browseVignettes(package = "spant")
```

Full list of functions:

```
help(package = spant, help_type = "html")
```

An online version of the documentation is available from:

https://martin3141.github.io/spant/

Author(s)

Maintainer: Martin Wilson <martin.wilson111@gmail.com> (ORCID)

Authors:

- Martin Wilson <martin.wilson111@gmail.com> (ORCID)

Other contributors:

- Yong Wang [contributor]
- John Muschelli [contributor]

See Also

Useful links:

- https://spantdoc.wilsonlab.co.uk/
- https://martin3141.github.io/spant/
- https://github.com/martin3141/spant/
- Report bugs at https://github.com/martin3141/spant/issues/

`abfit_opts` *Return a list of options for an ABfit analysis.*

Description

Return a list of options for an ABfit analysis.

Usage

```
abfit_opts(
  init_damping = 5,
  maxiters = 1024,
  max_shift_pre = 0.078,
  max_shift_fine = NULL,
  max_damping = 15,
  max_phase = 360,
  lambda = NULL,
  ppm_left = 4,
  ppm_right = 0.2,
  zp = TRUE,
  bl_ed_pppm = 2,
  auto_bl_flex = TRUE,
  bl_comps_pppm = 15,
  adaptive_bl_comps_pppm = FALSE,
  export_sp_fit = FALSE,
  max_asym = 0.25,
```

```
  max_basis_shift = 0.0078,
  max_basis_damping = 2,
  maxiters_pre = 1000,
  algo_pre = "NLOPT_LN_NELDERMEAD",
  min_bl_ed_pppm = NULL,
  max_bl_ed_pppm = 7,
  auto_bl_flex_n = 20,
  pre_fit_bl_ed_pppm = 1,
  remove_lip_mm_prefit = FALSE,
  pre_align = TRUE,
  max_pre_align_shift = 0.1,
  pre_align_ref_freqs = c(2.01, 3.03, 3.22),
  noise_region = c(-0.5, -2.5),
  optimal_smooth_criterion = "maic",
  aic_smoothing_factor = 5,
  anal_jac = TRUE,
  pre_fit_ppm_left = 4,
  pre_fit_ppm_right = 1.8,
  phi1_optim = FALSE,
  phi1_init = 0,
  max_dphi1 = 0.2,
  max_basis_shift_broad = NULL,
  max_basis_damping_broad = NULL,
  ahat_calc_method = "lh_pnnls",
  prefit_phase_search = TRUE,
  freq_reg = NULL,
  freq_reg_naa = NULL,
  lb_reg = NULL,
  asym_reg = NULL,
  output_all_paras = FALSE,
  output_all_paras_raw = FALSE,
  input_paras_raw = NULL,
  optim_lw_only = FALSE,
  optim_lw_only_limit = 20,
  lb_init = 0.001,
  lb_init_approx_fit = FALSE,
  zf_offset = NULL
)
```

Arguments

`init_damping`	initial value of the Gaussian global damping parameter (Hz). Very poorly shimmed or high field data may benefit from a larger value.
`maxiters`	The maximum number of iterations to run for the detailed fit.
`max_shift_pre`	The maximum allowable global shift to be applied in the approximate (pre-fit) phases of analysis (ppm).
`max_shift_fine`	The maximum allowable global shift to be applied in the detailed fit phase of analysis (ppm).

`max_damping` maximum permitted value of the global damping parameter (Hz).

`max_phase` the maximum absolute permitted value of the global zero-order phase term (degrees). Note, the prefit_phase_search option is not constrained by this term.

`lambda` manually set the the baseline smoothness parameter.

`ppm_left` downfield frequency limit for the fitting range (ppm).

`ppm_right` upfield frequency limit for the fitting range (ppm).

`zp` zero pad the data to twice the original length before fitting.

`bl_ed_pppm` manually set the the baseline smoothness parameter (ED per ppm).

`auto_bl_flex` automatically determine the level of baseline smoothness.

`bl_comps_pppm` spline basis density (signals per ppm).

`adaptive_bl_comps_pppm` adjust the spline basis density in the detailed fit phase, based on the required level of smoothness, to reduce computation time.

`export_sp_fit` add the fitted spline functions to the fit result.

`max_asym` maximum allowable value of the asymmetry parameter.

`max_basis_shift` maximum allowable frequency shift for individual basis signals (ppm).

`max_basis_damping` maximum allowable Lorentzian damping factor for individual basis signals (Hz).

`maxiters_pre` maximum iterations for the coarse (pre-)fit.

`algo_pre` optimisation method for the coarse (pre-)fit.

`min_bl_ed_pppm` minimum value for the candidate baseline flexibility analyses (ED per ppm).

`max_bl_ed_pppm` minimum value for the candidate baseline flexibility analyses (ED per ppm).

`auto_bl_flex_n` number of candidate baseline analyses to perform.

`pre_fit_bl_ed_pppm` level of baseline flexibility to use in the coarse fitting stage of the algorithm (ED per ppm).

`remove_lip_mm_prefit` remove broad signals in the coarse fitting stage of the algorithm.

`pre_align` perform a pre-alignment step before coarse fitting.

`max_pre_align_shift` maximum allowable shift in the pre-alignment step (ppm).

`pre_align_ref_freqs` a vector of prominent spectral frequencies used in the pre-alignment step (ppm).

`noise_region` spectral region to estimate the noise level (ppm).

`optimal_smooth_criterion` method to determine the optimal smoothness.

`aic_smoothing_factor` modification factor for the AIC calculation. Larger values result in less flexible baselines.

`anal_jac` use a analytical approximation to the jacobian in the detailed fitting stage.

`pre_fit_ppm_left`
: downfield frequency limit for the fitting range in the coarse fitting stage of the algorithm (ppm).

`pre_fit_ppm_right`
: upfield frequency limit for the fitting range in the coarse fitting stage of the algorithm (ppm).

`phi1_optim`
: apply and optimise a frequency dependant phase term.

`phi1_init`
: initial value for the frequency dependant phase term (ms).

`max_dphi1`
: maximum allowable change from the initial frequency dependant phase term (ms).

`max_basis_shift_broad`
: maximum allowable shift for broad signals in the basis (ppm). Determined based on their name beginning with Lip or MM. The default value is set to max_basis_shift.

`max_basis_damping_broad`
: maximum allowable Lorentzian damping for broad signals in the basis (Hz). Determined based on their name beginning with Lip or MM. The default value is set to max_basis_damping.

`ahat_calc_method`
: method to calculate the metabolite amplitudes. May be one of: "lh_pnnls" or "ls".

`prefit_phase_search`
: perform a 1D search for the optimal phase in the prefit stage of the algorithm.

`freq_reg`
: frequency shift parameter.

`freq_reg_naa`
: frequency shift parameter for NAA and NAAG.

`lb_reg`
: individual line broadening parameter.

`asym_reg`
: lineshape asymmetry parameter.

`output_all_paras`
: include more fitting parameters in the fit table, e.g. individual shift and damping factors for each basis set element.

`output_all_paras_raw`
: include raw fitting parameters in the fit table. For advanced diagnostic use only.

`input_paras_raw`
: input raw fitting parameters. For advanced diagnostic use only.

`optim_lw_only`
: optimize the global line-broadening term only.

`optim_lw_only_limit`
: limits for the line-breading term as a percentage of the starting value when optim_lw_only is TRUE.

`lb_init`
: initial Lorentzian line broadening value (in Hz) for the individual basis signals. Setting to 0 will clash with the minimum allowable value (eg hard constraint) during the detailed fit.

`lb_init_approx_fit`
: apply lb_init to the basis during the approximate iterative fit.

`zf_offset`
: offset in number of data points from the end of the FID to zero-fill. Default is NULL and will automatically set this to 50 points when the FID distortion flag is set for the mrs_data.

Value

full list of options.

Examples

```
opts <- abfit_opts(ppm_left = 4.2, noise_region = c(-1, -3))
```

`abfit_opts_v1_9_0` *Return a list of options for an ABfit analysis to maintain comparability with analyses performed with version 1.9.0 (and earlier) of spant.*

Description

Return a list of options for an ABfit analysis to maintain comparability with analyses performed with version 1.9.0 (and earlier) of spant.

Usage

```
abfit_opts_v1_9_0(...)
```

Arguments

`...`	arguments passed to abfit_opts.

Value

full list of options.

`abfit_reg_opts` *Return a list of options for an ABfit analysis with regularision.*

Description

Return a list of options for an ABfit analysis with regularision.

Usage

```
abfit_reg_opts(
  init_damping = 5,
  maxiters = 128,
  max_shift_pre = 0.078,
  max_shift_fine = 0.05,
  max_damping = 15,
  max_phase = 360,
  lambda = NULL,
  ppm_left = 4,
```

```
  ppm_right = 0.2,
  zp = TRUE,
  bl_ed_pppm = 2,
  auto_bl_flex = TRUE,
  bl_comps_pppm = 15,
  adaptive_bl_comps_pppm = TRUE,
  export_sp_fit = FALSE,
  max_asym = Inf,
  max_basis_shift = Inf,
  max_basis_damping = Inf,
  maxiters_pre = 1000,
  algo_pre = "NLOPT_LN_NELDERMEAD",
  min_bl_ed_pppm = NULL,
  max_bl_ed_pppm = 7,
  auto_bl_flex_n = 20,
  pre_fit_bl_ed_pppm = 1,
  remove_lip_mm_prefit = FALSE,
  pre_align = TRUE,
  max_pre_align_shift = 0.1,
  pre_align_ref_freqs = c(2.01, 3.03, 3.22),
  noise_region = c(-0.5, -2.5),
  optimal_smooth_criterion = "maic",
  aic_smoothing_factor = 5,
  anal_jac = TRUE,
  pre_fit_ppm_left = 4,
  pre_fit_ppm_right = 1.8,
  phi1_optim = FALSE,
  phi1_init = 0,
  max_dphi1 = 0.2,
  max_basis_shift_broad = NULL,
  max_basis_damping_broad = NULL,
  ahat_calc_method = "lh_pnnls",
  prefit_phase_search = TRUE,
  freq_reg = 0.004,
  freq_reg_naa = NULL,
  lb_reg = "lcm_compat",
  asym_reg = 0.1,
  output_all_paras = FALSE,
  output_all_paras_raw = FALSE,
  input_paras_raw = NULL,
  optim_lw_only = FALSE,
  optim_lw_only_limit = 20,
  lb_init = "lcm_compat",
  lb_init_approx_fit = FALSE,
  zf_offset = NULL
)
```

Arguments

`init_damping`	initial value of the Gaussian global damping parameter (Hz). Very poorly shimmed or high field data may benefit from a larger value.
`maxiters`	The maximum number of iterations to run for the detailed fit.
`max_shift_pre`	The maximum allowable global shift to be applied in the approximate (pre-fit) phases of analysis (ppm).
`max_shift_fine`	The maximum allowable global shift to be applied in the detailed fit phase of analysis (ppm).
`max_damping`	maximum permitted value of the global damping parameter (Hz).
`max_phase`	the maximum absolute permitted value of the global zero-order phase term (degrees). Note, the prefit_phase_search option is not constrained by this term.
`lambda`	manually set the the baseline smoothness parameter.
`ppm_left`	downfield frequency limit for the fitting range (ppm).
`ppm_right`	upfield frequency limit for the fitting range (ppm).
`zp`	zero pad the data to twice the original length before fitting.
`bl_ed_pppm`	manually set the the baseline smoothness parameter (ED per ppm).
`auto_bl_flex`	automatically determine the level of baseline smoothness.
`bl_comps_pppm`	spline basis density (signals per ppm).
`adaptive_bl_comps_pppm`	adjust the spline basis density in the detailed fit phase, based on the required level of smoothness, to reduce computation time.
`export_sp_fit`	add the fitted spline functions to the fit result.
`max_asym`	maximum allowable value of the asymmetry parameter.
`max_basis_shift`	maximum allowable frequency shift for individual basis signals (ppm).
`max_basis_damping`	maximum allowable Lorentzian damping factor for individual basis signals (Hz).
`maxiters_pre`	maximum iterations for the coarse (pre-)fit.
`algo_pre`	optimisation method for the coarse (pre-)fit.
`min_bl_ed_pppm`	minimum value for the candidate baseline flexibility analyses (ED per ppm).
`max_bl_ed_pppm`	minimum value for the candidate baseline flexibility analyses (ED per ppm).
`auto_bl_flex_n`	number of candidate baseline analyses to perform.
`pre_fit_bl_ed_pppm`	level of baseline flexibility to use in the coarse fitting stage of the algorithm (ED per ppm).
`remove_lip_mm_prefit`	remove broad signals in the coarse fitting stage of the algorithm.
`pre_align`	perform a pre-alignment step before coarse fitting.
`max_pre_align_shift`	maximum allowable shift in the pre-alignment step (ppm).

`pre_align_ref_freqs`
: a vector of prominent spectral frequencies used in the pre-alignment step (ppm).

`noise_region`
: spectral region to estimate the noise level (ppm).

`optimal_smooth_criterion`
: method to determine the optimal smoothness.

`aic_smoothing_factor`
: modification factor for the AIC calculation. Larger values result in less flexible baselines.

`anal_jac`
: use a analytical approximation to the jacobian in the detailed fitting stage.

`pre_fit_ppm_left`
: downfield frequency limit for the fitting range in the coarse fitting stage of the algorithm (ppm).

`pre_fit_ppm_right`
: upfield frequency limit for the fitting range in the coarse fitting stage of the algorithm (ppm).

`phi1_optim`
: apply and optimise a frequency dependant phase term.

`phi1_init`
: initial value for the frequency dependant phase term (ms).

`max_dphi1`
: maximum allowable change from the initial frequency dependant phase term (ms).

`max_basis_shift_broad`
: maximum allowable shift for broad signals in the basis (ppm). Determined based on their name beginning with Lip or MM. The default value is set to max_basis_shift.

`max_basis_damping_broad`
: maximum allowable Lorentzian damping for broad signals in the basis (Hz). Determined based on their name beginning with Lip or MM. The default value is set to max_basis_damping.

`ahat_calc_method`
: method to calculate the metabolite amplitudes. May be one of: "lh_pnnls" or "ls".

`prefit_phase_search`
: perform a 1D search for the optimal phase in the prefit stage of the algorithm.

`freq_reg`
: frequency shift parameter.

`freq_reg_naa`
: frequency shift parameter for NAA and NAAG.

`lb_reg`
: individual line broadening parameter.

`asym_reg`
: lineshape asymmetry parameter.

`output_all_paras`
: include more fitting parameters in the fit table, e.g. individual shift and damping factors for each basis set element.

`output_all_paras_raw`
: include raw fitting parameters in the fit table. For advanced diagnostic use only.

`input_paras_raw`
: input raw fitting parameters. For advanced diagnostic use only.

`optim_lw_only`
: optimize the global line-broadening term only.

optim_lw_only_limit
: limits for the line-breading term as a percentage of the starting value when optim_lw_only is TRUE.

lb_init
: initial Lorentzian line broadening value (in Hz) for the individual basis signals. Setting to 0 will clash with the minimum allowable value (eg hard constraint) during the detailed fit.

lb_init_approx_fit
: apply lb_init to the basis during the approximate iterative fit.

zf_offset
: offset in number of data points from the end of the FID to zero-fill. Default is NULL and will automatically set this to 50 points when the FID distortion flag is set for the mrs_data.

Value

full list of options.

Examples

```
opts <- abfit_reg_opts(ppm_left = 4.2, noise_region = c(-1, -3))
```

---

acquire *Simulate pulse sequence acquisition.*

Description

Simulate pulse sequence acquisition.

Usage

```
acquire(sys, rec_phase = 0, tol = 1e-04, detect = NULL, amp_scale = 1)
```

Arguments

sys
: spin system object.

rec_phase
: receiver phase in degrees.

tol
: ignore resonance amplitudes below this threshold.

detect
: detection nuclei.

amp_scale
: scaling factor for the output amplitudes.

Value

a list of resonance amplitudes and frequencies.

add_noise *Add noise to an mrs_data object.*

Description

Add noise to an mrs_data object.

Usage

```
add_noise(mrs_data, sd = 0.1, fd = TRUE)
```

Arguments

mrs_data	data to add noise to.
sd	standard deviation of the noise.
fd	generate the noise samples in the frequency-domain (TRUE) or time-domain (FALSE). This is required since the absolute value of the standard deviation of noise samples changes when data is Fourier transformed.

Value

mrs_data object with additive normally distributed noise.

add_noise_spec_snr *Add noise to an mrs_data object to match a given SNR.*

Description

Add noise to an mrs_data object to match a given SNR.

Usage

```
add_noise_spec_snr(
  mrs_data,
  target_snr,
  sig_region = c(4, 0.5),
  ref_data = NULL,
  noise_free_input = TRUE
)
```

Arguments

mrs_data	data to add noise to.
target_snr	desired spectral SNR, note this assumes the input data is noise-free, eg simulated data (unless noise_free_input is set to FALSE). Note the SNR is estimated from the first scan in the dataset and the same noise level is added to all spectra.
sig_region	spectral limits to search for the strongest spectral data point.
ref_data	measure the signal from the first scan in this reference data and apply the same target noise level to mrs_data.
noise_free_input	accounts for the reference data already containing noise when set to FALSE. Defaults to TRUE.

Value

mrs_data object with additive normally distributed noise.

---

align *Align spectra to a reference frequency using a convolution based method.*

Description

Align spectra to a reference frequency using a convolution based method.

Usage

```
align(
  mrs_data,
  ref_freq = 4.65,
  ref_amp = 1,
  zf_factor = 2,
  lb = 2,
  max_shift = 20,
  ret_df = FALSE,
  mean_dyns = FALSE
)
```

Arguments

mrs_data	data to be aligned.
ref_freq	reference frequency in ppm units. More than one frequency may be specified.
ref_amp	amplitude value for the reference signal. More than one value may be specified to match the number of ref_freq signals.
zf_factor	zero filling factor to increase alignment resolution.
lb	line broadening to apply to the reference signal.

max_shift	maximum allowable shift in Hz.
ret_df	return frequency shifts in addition to aligned data (logical).
mean_dyns	align the mean spectrum and apply the same shift to each dynamic.

Value

aligned data object.

---

apodise_xy *Apodise MRSI data in the x-y direction with a k-space filter.*

Description

Apodise MRSI data in the x-y direction with a k-space filter.

Usage

```
apodise_xy(mrs_data, func = "hamming", w = 2.5)
```

Arguments

mrs_data	MRSI data.
func	must be "hamming", "hanning" or "gaussian".
w	the reciprocal of the standard deviation for the Gaussian function.

Value

apodised data.

---

append_basis *Combine a pair of basis set objects.*

Description

Combine a pair of basis set objects.

Usage

```
append_basis(basis_a, basis_b)
```

Arguments

basis_a	first basis.
basis_b	second basis.

Value

combined basis set object.

append_coils *Append MRS data across the coil dimension, assumes they matched across the other dimensions.*

Description

Append MRS data across the coil dimension, assumes they matched across the other dimensions.

Usage

```
append_coils(...)
```

Arguments

...	MRS data objects as arguments, or a list of MRS data objects.

Value

a single MRS data object with the input objects concatenated together.

append_dyns *Append MRS data across the dynamic dimension, assumes they matched across the other dimensions.*

Description

Append MRS data across the dynamic dimension, assumes they matched across the other dimensions.

Usage

```
append_dyns(...)
```

Arguments

...	MRS data objects as arguments, or a list of MRS data objects.

Value

a single MRS data object with the input objects concatenated together.

append_regs *Append multiple regressor data frames into a single data frame.*

Description

Append multiple regressor data frames into a single data frame.

Usage

```
append_regs(...)
```

Arguments

...	input regressor data frames.

Value

output regressor data frame.

apply_axes *Apply a function over specified array axes.*

Description

Apply a function over specified array axes.

Usage

```
apply_axes(x, axes, fun, ...)
```

Arguments

x	an array.
axes	a vector of axes to apply fun over.
fun	function to be applied.
...	optional arguments to fun.

Value

array.

Examples

```
z <- array(1:1000, dim = c(10, 10, 10))
a <- apply_axes(z, 3, fft)
a[1,1,] == fft(z[1,1,])
a <- apply_axes(z, 3, sum)
a[1,1,] == sum(z[1,1,])
```

apply_mrs *Apply a function across given dimensions of a MRS data object.*

Description

Apply a function across given dimensions of a MRS data object.

Usage

```
apply_mrs(mrs_data, dims, fun, ..., data_only = FALSE)
```

Arguments

mrs_data	MRS data.
dims	dimensions to apply the function.
fun	name of the function.
...	arguments to the function.
data_only	return an array rather than an MRS data object.

apply_pulse *Simulate an RF pulse on a single spin.*

Description

Simulate an RF pulse on a single spin.

Usage

```
apply_pulse(sys, rho, spin_n, angle, nuc, xy)
```

Arguments

sys	spin system object.
rho	density matrix.
spin_n	spin index.
angle	RF flip angle in degrees.
nuc	nucleus influenced by the pulse.
xy	x or y pulse.

Value

density matrix.

`Arg.mrs_data` *Apply Arg operator to an MRS dataset.*

Description

Apply Arg operator to an MRS dataset.

Usage

```
## S3 method for class 'mrs_data'
Arg(z)
```

Arguments

`z`	MRS data.

Value

MRS data following Arg operator.

`array2mrs_data` *Convert a 7 dimensional array in into a mrs_data object. The array dimensions should be ordered as : dummy, X, Y, Z, dynamic, coil, FID.*

Description

Convert a 7 dimensional array in into a mrs_data object. The array dimensions should be ordered as : dummy, X, Y, Z, dynamic, coil, FID.

Usage

```
array2mrs_data(
  data_array,
  mrs_data = NULL,
  fs = NULL,
  ft = NULL,
  ref = NULL,
  nuc = NULL,
  fd = FALSE
)
```

Arguments

data_array	7d data array.
mrs_data	example data to copy acquisition parameters from.
fs	sampling frequency in Hz.
ft	transmitter frequency in Hz.
ref	reference value for ppm scale.
nuc	nucleus that is resonant at the transmitter frequency.
fd	flag to indicate if the matrix is in the frequency domain (logical).

Value

mrs_data object.

---

assign_dyns *Overwrite a subset of dynamic scans.*

Description

Overwrite a subset of dynamic scans.

Usage

```
assign_dyns(mrs_data, subset, mrs_data_new)
```

Arguments

mrs_data	dynamic MRS data to be updated.
subset	vector containing indices to the dynamic scans to be assigned.
mrs_data_new	dynamic MRS data with new values.

Value

MRS data with updated dynamics.

`auto_phase` *Perform zeroth-order phase correction based on the minimisation of the squared difference between the real and magnitude components of the spectrum.*

Description

Perform zeroth-order phase correction based on the minimisation of the squared difference between the real and magnitude components of the spectrum.

Usage

```
auto_phase(mrs_data, xlim = c(4, 1.8), smo_ppm_sd = 0.05, ret_phase = FALSE)
```

Arguments

`mrs_data`	an object of class `mrs_data`.
`xlim`	frequency range (default units of PPM) to including in the phase.
`smo_ppm_sd`	Gaussian smoother sd in ppm units.
`ret_phase`	return phase values (logical).

Value

MRS data object and phase values (optional).

`auto_phase_bl` *Perform zeroth-order phase correction based on expected baseline regions.*

Description

Default arguments are appropriate for water suppressed 1H MRS of the brain. The following options are suitable for a water signal at 4.65 ppm: ppm_start = c(5.2, 4.0), ppm_end = c(5.3, 4.1), xlim = c(5.2, 4.1)

Usage

```
auto_phase_bl(
  mrs_data,
  ppm_start = c(0.5, 4),
  ppm_end = c(0, 4.2),
  xlim = c(1.8, 4),
  mean_dyns = FALSE,
  ret_phase = FALSE
)
```

Arguments

mrs_data	an object of class mrs_data.
ppm_start	a vector of ppm values designating baseline regions.
ppm_end	a vectors of ppm values designating baseline regions.
xlim	region containing signal of interest, eg strong metabolite resonances.
mean_dyns	phase the mean spectrum and apply the same value to each dynamic.
ret_phase	return phase values (logical).

Value

MRS data object with corrected phase.

---

back_extrap_ar *Back extrapolate time-domain data points using an autoregressive model.*

Description

Back extrapolate time-domain data points using an autoregressive model.

Usage

```
back_extrap_ar(
  mrs_data,
  extrap_pts,
  pred_pts = NULL,
  method = "burg",
  rem_add = TRUE,
  ...
)
```

Arguments

mrs_data	mrs_data object.
extrap_pts	number of points to extrapolate.
pred_pts	number of points to base the extrapolation on.
method	character string specifying the method to fit the model. Must be one of the strings in the default argument (the first few characters are sufficient). Defaults to "burg".
rem_add	remove additional points from the end of the FID to maintain the original length of the dataset. Default to TRUE.
...	additional arguments to specific methods, see ?ar.

Value

back extrapolated data.

basis2dyn_mrs_data *Convert a basis object to a dynamic mrs_data object.*

Description

Convert a basis object to a dynamic mrs_data object.

Usage

```
basis2dyn_mrs_data(basis, amps, tr)
```

Arguments

basis	basis set object.
amps	a data frame with each column corresponding to a basis element and each row corresponding to each dynamic scan.
tr	the dataset repetition time in seconds.

Value

a dynamic mrs_data object.

basis2mrs_data *Convert a basis object to an mrs_data object - where basis signals are spread across the dynamic dimension.*

Description

Convert a basis object to an mrs_data object - where basis signals are spread across the dynamic dimension.

Usage

```
basis2mrs_data(
  basis,
  sum_elements = FALSE,
  amps = NULL,
  shifts = NULL,
  lbs = NULL
)
```

Arguments

basis	basis set object.
sum_elements	return the sum of basis elements (logical)
amps	a vector of scaling factors to apply to each basis element.
shifts	a vector of frequency shifts (in ppm) to apply to each basis element.
lbs	a vector of Lorentzian line broadening terms (in Hz) to apply to each basis element.

Value

an mrs_data object with basis signals spread across the dynamic dimension or summed.

---

bbase *Generate a spline basis, slightly adapted from : "Splines, knots, and penalties", Eilers 2010.*

Description

Generate a spline basis, slightly adapted from : "Splines, knots, and penalties", Eilers 2010.

Usage

```
bbase(N, number, deg = 3)
```

Arguments

N	number of data points.
number	number of spline functions.
deg	spline degree : deg = 1 linear, deg = 2 quadratic, deg = 3 cubic.

Value

spline basis as a matrix.

bc_als — *Baseline correction using the ALS method.*

Description

Eilers P. H. C. and Boelens H. F. M. (2005) Baseline correction with asymmetric least squares smoothing. Leiden Univ. Medical Centre Report.

Usage

```
bc_als(mrs_data, lambda = 10000, p = 0.001, ret_bc_only = TRUE)
```

Arguments

mrs_data	mrs_data object.
lambda	controls the baseline flexibility.
p	controls the penalty for negative data points.
ret_bc_only	return the baseline corrected data only. When FALSE the baseline estimate and input data will be returned.

Value

baseline corrected data.

bc_constant — *Remove a constant baseline offset based on a reference spectral region.*

Description

Remove a constant baseline offset based on a reference spectral region.

Usage

```
bc_constant(mrs_data, xlim)
```

Arguments

mrs_data	MRS data.
xlim	spectral range containing a flat baseline region to measure the offset.

Value

baseline corrected data.

bc_gauss — *Apply and subtract a Gaussian smoother in the spectral domain.*

Description

Apply and subtract a Gaussian smoother in the spectral domain.

Usage

```
bc_gauss(mrs_data, smo_ppm_sd)
```

Arguments

mrs_data	mrs_data object.
smo_ppm_sd	Gaussian smoother sd in ppm units.

Value

smoother subtracted data.

bc_poly — *Fit and subtract a polynomial to each spectrum in a dataset.*

Description

Fit and subtract a polynomial to each spectrum in a dataset.

Usage

```
bc_poly(mrs_data, p_deg = 1)
```

Arguments

mrs_data	mrs_data object.
p_deg	polynomial degree.

Value

polynomial subtracted data.

`bc_spline` *Fit and subtract a smoothing spline to each spectrum in a dataset.*

Description

Fit and subtract a smoothing spline to each spectrum in a dataset.

Usage

```
bc_spline(mrs_data, spar = 0.5, nknots = 100)
```

Arguments

`mrs_data`	mrs_data object.
`spar`	smoothing parameter typically between 0 and 1.
`nknots`	number of spline knots.

Value

smoothing spline subtracted data.

`beta2lw` *Covert a beta value in the time-domain to an equivalent linewidth in Hz: x * exp(-i * t * t * beta).*

Description

Covert a beta value in the time-domain to an equivalent linewidth in Hz: x * exp(-i * t * t * beta).

Usage

```
beta2lw(beta)
```

Arguments

`beta`	beta damping value.

Value

linewidth value in Hz.

bin_spec *Bin equally spaced spectral regions.*

Description

Bin equally spaced spectral regions.

Usage

```
bin_spec(mrs_data, width = 0.05, unit = "ppm")
```

Arguments

mrs_data	data to be "binned".
width	bin width.
unit	bin width unit, can be "ppm" (default) or "pts".

Value

binned mrs_data object.

calc_basis_corr_mat *Estimate the correlation matrix for a basis set.*

Description

Estimate the correlation matrix for a basis set.

Usage

```
calc_basis_corr_mat(basis, xlim = c(4, 0.2), zf = TRUE)
```

Arguments

basis	basis_set object.
xlim	spectral range to use in ppm.
zf	zero-fill the basis set.

Value

correlation matrix.

calc_basis_crlbs *Estimate the CRLB for each element in a basis set.*

Description

Estimate the CRLB for each element in a basis set.

Usage

```
calc_basis_crlbs(
  basis,
  xlim = c(4, 0.2),
  zf = TRUE,
  sd = 1,
  bl_comp_pppm = NULL
)
```

Arguments

basis	basis_set object.
xlim	spectral range to use in ppm.
zf	zero-fill the basis set.
sd	standard deviation of the noise.
bl_comp_pppm	number spline baseline components to append per-ppm.

Value

a vector of predicted errors.

calc_coil_noise_cor *Calculate the noise correlation between coil elements.*

Description

Calculate the noise correlation between coil elements.

Usage

```
calc_coil_noise_cor(noise_data)
```

Arguments

noise_data	mrs_data object with one FID for each coil element.

Value

correlation matrix.

calc_coil_noise_sd *Calculate the noise standard deviation for each coil element.*

Description

Calculate the noise standard deviation for each coil element.

Usage

```
calc_coil_noise_sd(noise_data)
```

Arguments

noise_data	mrs_data object with one FID for each coil element.

Value

array of standard deviations.

calc_design_efficiency *Calculate the efficiency of a regressor data frame.*

Description

Calculate the efficiency of a regressor data frame.

Usage

```
calc_design_efficiency(regressor_df, contrasts)
```

Arguments

regressor_df	input regressor data frame.
contrasts	a vector of contrast values.

calc_ed_from_lambda *Calculate the effective dimensions of a spline smoother from lambda.*

Description

Calculate the effective dimensions of a spline smoother from lambda.

Usage

```
calc_ed_from_lambda(spline_basis, deriv_mat, lambda)
```

Arguments

spline_basis	spline basis.
deriv_mat	derivative matrix.
lambda	smoothing parameter.

Value

the effective dimension value.

calc_peak_info_vec *Calculate the FWHM of a peak from a vector of intensity values.*

Description

Calculate the FWHM of a peak from a vector of intensity values.

Usage

```
calc_peak_info_vec(data_pts, interp_f)
```

Arguments

data_pts	input vector.
interp_f	interpolation factor to improve the FWHM estimate.

Value

a vector of: x position of the highest data point, maximum peak value in the y axis, FWHM in the units of data points.

`calc_sd_poly` *Perform a polynomial fit, subtract and return the standard deviation of the residuals.*

Description

Perform a polynomial fit, subtract and return the standard deviation of the residuals.

Usage

```
calc_sd_poly(y, degree = 1)
```

Arguments

`y`	array.
`degree`	polynomial degree.

Value

standard deviation of the fit residuals.

`calc_spec_diff` *Calculate the sum of squares differences between two mrs_data objects.*

Description

Calculate the sum of squares differences between two mrs_data objects.

Usage

```
calc_spec_diff(mrs_data, ref = NULL, xlim = c(4, 0.5))
```

Arguments

`mrs_data`	mrs_data object.
`ref`	reference mrs_data object to calculate differences.
`xlim`	spectral limits to perform calculation.

Value

an array of the sum of squared difference values.

`calc_spec_snr` *Calculate the spectral SNR.*

Description

SNR is defined as the maximum signal value divided by the standard deviation of the noise.

Usage

```
calc_spec_snr(
  mrs_data,
  sig_region = c(4, 0.5),
  noise_region = c(-0.5, -2.5),
  p_order = 2,
  interp_f = 4,
  full_output = FALSE
)
```

Arguments

`mrs_data`	an object of class `mrs_data`.
`sig_region`	a ppm region to define where the maximum signal value should be estimated.
`noise_region`	a ppm region to defined where the noise level should be estimated.
`p_order`	polynomial order to fit to the noise region before estimating the standard deviation.
`interp_f`	interpolation factor to improve detection of the highest signal value.
`full_output`	output signal, noise and SNR values separately.

Details

The mean noise value is subtracted from the maximum signal value to reduce DC offset bias. A polynomial detrending fit (second order by default) is applied to the noise region before the noise standard deviation is estimated.

Value

an array of SNR values.

check_lcm *Check LCModel can be run*

Description

Check LCModel can be run

Usage

```
check_lcm()
```

check_tqn *Check the TARQUIN binary can be run*

Description

Check the TARQUIN binary can be run

Usage

```
check_tqn()
```

circ_mask *Create a logical circular mask spanning the full extent of an n x n matrix.*

Description

Create a logical circular mask spanning the full extent of an n x n matrix.

Usage

```
circ_mask(d, n, offset = 1)
```

Arguments

d	diameter of the mask.
n	number of matrix rows and columns.
offset	offset the mask centre in matrix dimension units.

Value

logical n x n mask matrix.

`coherence_filter` *Zero all coherence orders other than the one supplied as an argument.*

Description

Zero all coherence orders other than the one supplied as an argument.

Usage

```
coherence_filter(sys, rho, order = 0)
```

Arguments

`sys`	spin system object.
`rho`	density matrix.
`order`	coherence order to keep (default is 0).

Value

density matrix.

`collapse_to_dyns` *Collapse MRS data by concatenating spectra along the dynamic dimension.*

Description

Collapse MRS data by concatenating spectra along the dynamic dimension.

Usage

```
collapse_to_dyns(x, rm_masked = FALSE)

## S3 method for class 'mrs_data'
collapse_to_dyns(x, rm_masked = FALSE)

## S3 method for class 'fit_result'
collapse_to_dyns(x, rm_masked = FALSE)
```

Arguments

`x`	data object to be collapsed (mrs_data or fit_result object).
`rm_masked`	remove masked dynamics from the output.

Value

collapsed data with spectra or fits concatenated along the dynamic dimension.

comb_coils *Combine coil data based on the first data point of a reference signal.*

Description

By default, elements are phased and scaled prior to summation. Where a reference signal is not given, the mean dynamic signal will be used instead.

Usage

```
comb_coils(
  metab,
  ref = NULL,
  noise = NULL,
  scale = TRUE,
  scale_method = "sig_noise_sq",
  sum_coils = TRUE,
  noise_region = c(-0.5, -2.5),
  average_ref_dyns = TRUE,
  ref_pt_index = 1,
  ret_metab_only = FALSE
)
```

Arguments

metab	MRS data containing metabolite data.
ref	MRS data containing reference data (optional).
noise	MRS data from a noise scan (optional).
scale	option to rescale coil elements based on the first data point (logical).
scale_method	one of "sig_noise_sq", "sig_noise" or "sig".
sum_coils	sum the coil elements as a final step (logical).
noise_region	the spectral region (in ppm) to estimate the noise.
average_ref_dyns	take the mean of the reference scans in the dynamic dimension before use.
ref_pt_index	time-domain point to use for estimating phase and scaling values.
ret_metab_only	return the metabolite data only, even if reference data has been specified.

Value

MRS data.

comb_coils_mrsi_gls — *Combine MRSI coil data using the GLS method presented by An et al JMRI 37:1445-1450 (2013).*

Description

Combine MRSI coil data using the GLS method presented by An et al JMRI 37:1445-1450 (2013).

Usage

```
comb_coils_mrsi_gls(metab, noise_pts = 30, noise_mrs = NULL)
```

Arguments

metab	MRSI data containing metabolite data.
noise_pts	number of points from the end of the FIDs to use for noise covariance estimation.
noise_mrs	MRS data containing noise information for each coil.

Value

coil combined MRSI data.

comb_coils_svs_gls — *Combine SVS coil data using the GLS method presented by An et al JMRI 37:1445-1450 (2013).*

Description

Combine SVS coil data using the GLS method presented by An et al JMRI 37:1445-1450 (2013).

Usage

```
comb_coils_svs_gls(
  metab,
  ref = NULL,
  noise_pts = 256,
  noise_mrs = NULL,
  use_mean_sens = TRUE
)
```

Arguments

metab	MRS data containing metabolite data.
ref	MRS data containing reference data (optional).
noise_pts	number of points from the end of the FIDs to use for noise covariance estimation.
noise_mrs	MRS data containing noise information for each coil.
use_mean_sens	use the dynamic mean to estimate coil sensitivities.

Value

coil combined MRS data.

`comb_fit_list_dyns` *Combine a list of fit results into a single fit result object across the dynamic dimension.*

Description

Combine a list of fit results into a single fit result object across the dynamic dimension.

Usage

```
comb_fit_list_dyns(fit_list, dyn_basis_sets = FALSE)
```

Arguments

`fit_list`	a list of fit_result objects.
`dyn_basis_sets`	save all basis sets separately as a list, defaults to FALSE.

Value

fit result object.

`comb_fit_list_fit_tables` *Combine all fitting data points from a list of fits into a single data frame.*

Description

Combine all fitting data points from a list of fits into a single data frame.

Usage

```
comb_fit_list_fit_tables(
  fit_list,
  add_extra = TRUE,
  harmonise_ppm = TRUE,
  inc_basis_sigs = FALSE,
  inc_indices = TRUE,
  add_res_id = TRUE
)
```

Arguments

fit_list	list of fit_result objects.
add_extra	add variables in the extra data frame to the output (TRUE).
harmonise_ppm	ensure the ppm scale for each fit is identical to the first.
inc_basis_sigs	include the individual fitting basis signals in the output table, defaults to FALSE.
inc_indices	include indices such as X, Y and coil in the output, defaults to TRUE. These are generally not useful for SVS analysis.
add_res_id	add a res_id column to the output to distinguish between datasets.

Value

a data frame containing the fit data points.

---

comb_fit_list_result_tables

Combine the fit result tables from a list of fit results.

Description

Combine the fit result tables from a list of fit results.

Usage

```
comb_fit_list_result_tables(fit_list, add_extra = TRUE, add_res_id = TRUE)
```

Arguments

fit_list	a list of fit_result objects.
add_extra	add variables in the extra data frame to the output (TRUE).
add_res_id	add a res_id column to the output to distinguish between datasets.

Value

a data frame combine all fit result tables with an additional id column to differentiate between data sets. Any variables in the extra data frame may be optionally added to the result.

comb_fit_tables *Combine all fitting data points into a single data frame.*

Description

Combine all fitting data points into a single data frame.

Usage

```
comb_fit_tables(fit_res, inc_basis_sigs = FALSE, inc_indices = TRUE)
```

Arguments

fit_res	a single fit_result object.
inc_basis_sigs	include the individual fitting basis signals in the output table, defaults to FALSE.
inc_indices	include indices such as X, Y and coil in the output, defaults to TRUE. These are generally not useful for SVS analysis.

Value

a data frame containing the fit data points.

comb_metab_ref *Combine a reference and metabolite mrs_data object.*

Description

Combine a reference and metabolite mrs_data object.

Usage

```
comb_metab_ref(metab, ref)
```

Arguments

metab	metabolite mrs_data object.
ref	reference mrs_data object.

Value

combined metabolite and reference mrs_data object.

Conj.mrs_data *Apply Conj operator to an MRS dataset.*

Description

Apply Conj operator to an MRS dataset.

Usage

```
## S3 method for class 'mrs_data'
Conj(z)
```

Arguments

z	MRS data.

Value

MRS data following Conj operator.

conv_mrs *Convolve two MRS data objects.*

Description

Convolve two MRS data objects.

Usage

```
conv_mrs(mrs_data, conv)
```

Arguments

mrs_data	MRS data to be convolved.
conv	convolution data stored as an mrs_data object.

Value

convolved data.

crop_basis *Crop* basis_set *object based on a frequency range.*

Description

Crop basis_set object based on a frequency range.

Usage

```
crop_basis(basis, xlim = c(4, 0.2), scale = "ppm")
```

Arguments

basis	basis_set object to be cropped in the spectral dimension.
xlim	range of values to crop in the spectral dimension eg xlim = c(4, 0.2).
scale	the units to use for the frequency scale, can be one of: "ppm", "hz" or "points".

Value

cropped mrs_data object.

crop_spec *Crop* mrs_data *object based on a frequency range.*

Description

Crop mrs_data object based on a frequency range.

Usage

```
crop_spec(mrs_data, xlim = c(4, 0.2), scale = "ppm")
```

Arguments

mrs_data	MRS data.
xlim	range of values to crop in the spectral dimension eg xlim = c(4, 0.2).
scale	the units to use for the frequency scale, can be one of: "ppm", "hz" or "points".

Value

cropped mrs_data object.

crop_td_pts *Crop* mrs_data *object data points in the time-domain.*

Description

Crop mrs_data object data points in the time-domain.

Usage

```
crop_td_pts(mrs_data, start = NULL, end = NULL)
```

Arguments

mrs_data	MRS data.
start	starting data point (defaults to 1).
end	ending data point (defaults to the last saved point).

Value

cropped mrs_data object.

crop_td_pts_end *Crop* mrs_data *object data points at the end of the FID.*

Description

Crop mrs_data object data points at the end of the FID.

Usage

```
crop_td_pts_end(mrs_data, pts)
```

Arguments

mrs_data	MRS data.
pts	number of points to remove from the end of the FID.

Value

cropped mrs_data object.

crop_td_pts_pot *Crop* mrs_data *object data points in the time-domain rounding down to the next smallest power of two (pot). Data that already has a pot length will not be changed.*

Description

Crop mrs_data object data points in the time-domain rounding down to the next smallest power of two (pot). Data that already has a pot length will not be changed.

Usage

```
crop_td_pts_pot(mrs_data)
```

Arguments

mrs_data	MRS data.

Value

cropped mrs_data object.

crop_xy *Crop an MRSI dataset in the x-y direction*

Description

Crop an MRSI dataset in the x-y direction

Usage

```
crop_xy(mrs_data, x_dim, y_dim)
```

Arguments

mrs_data	MRS data object.
x_dim	x dimension output length.
y_dim	y dimension output length.

Value

selected subset of MRS data.

`crossprod_3d` *Compute the vector cross product between vectors x and y. Adapted from http://stackoverflow.com/questions/15162741/what-is-rs-crossproduct-function*

Description

Compute the vector cross product between vectors x and y. Adapted from http://stackoverflow.com/questions/15162741/what-is-rs-crossproduct-function

Usage

```
crossprod_3d(x, y)
```

Arguments

x	vector of length 3.
y	vector of length 3.

Value

vector cross product of x and y.

`decimate_mrs_fd` *Decimate an MRS signal to half the original sampling frequency by filtering in the frequency domain before down sampling.*

Description

Decimate an MRS signal to half the original sampling frequency by filtering in the frequency domain before down sampling.

Usage

```
decimate_mrs_fd(mrs_data)
```

Arguments

mrs_data	MRS data object.

Value

decimated data at half the original sampling frequency.

decimate_mrs_td — *Decimate an MRS signal by filtering in the time domain before downsampling.*

Description

Decimate an MRS signal by filtering in the time domain before downsampling.

Usage

```
decimate_mrs_td(mrs_data, q = 2, n = 4, ftype = "iir")
```

Arguments

mrs_data	MRS data object.
q	integer factor to downsample by (default = 2).
n	filter order used in the downsampling.
ftype	filter type, "iir" or "fir".

Value

decimated data.

deconv_mrs — *Deconvolve two MRS data objects.*

Description

Deconvolve two MRS data objects.

Usage

```
deconv_mrs(mrs_data_a, mrs_data_b)
```

Arguments

mrs_data_a	MRS data to be deconvolved.
mrs_data_b	MRS data to be deconvolved.

Value

deconvolved data.

`def_acq_paras` *Return (and optionally modify using the input arguments) a list of the default acquisition parameters.*

Description

Return (and optionally modify using the input arguments) a list of the default acquisition parameters.

Usage

```
def_acq_paras(
  ft = getOption("spant.def_ft"),
  fs = getOption("spant.def_fs"),
  N = getOption("spant.def_N"),
  ref = getOption("spant.def_ref"),
  nuc = getOption("spant.def_nuc")
)
```

Arguments

`ft`	specify the transmitter frequency in Hz.
`fs`	specify the sampling frequency in Hz.
`N`	specify the number of data points in the spectral dimension.
`ref`	specify the reference value for ppm scale.
`nuc`	specify the resonant nucleus.

Value

A list containing the following elements:

- ft transmitter frequency in Hz.
- fs sampling frequency in Hz.
- N number of data points in the spectral dimension.
- ref reference value for ppm scale.
- nuc resonant nucleus.

def_fs *Return the default sampling frequency in Hz.*

Description

Return the default sampling frequency in Hz.

Usage

```
def_fs()
```

Value

sampling frequency in Hz.

def_ft *Return the default transmitter frequency in Hz.*

Description

Return the default transmitter frequency in Hz.

Usage

```
def_ft()
```

Value

transmitter frequency in Hz.

def_N *Return the default number of data points in the spectral dimension.*

Description

Return the default number of data points in the spectral dimension.

Usage

```
def_N()
```

Value

number of data points in the spectral dimension.

def_nuc *Return the default nucleus.*

Description

Return the default nucleus.

Usage

```
def_nuc()
```

Value

number of data points in the spectral dimension.

def_ref *Return the default reference value for ppm scale.*

Description

Return the default reference value for ppm scale.

Usage

```
def_ref()
```

Value

reference value for ppm scale.

dicom_reader *A very simple DICOM reader.*

Description

Note this reader is very basic and does not use a DICOM dictionary or try to convert the data to the correct datatype. For a more robust and sophisticated reader use the oro.dicom package.

Usage

```
dicom_reader(
  input,
  tags = list(sop_class_uid = "0008,0016"),
  endian = "little",
  debug = FALSE
)
```

Arguments

input	either a file path or raw binary object.
tags	a named list of tags to be extracted from the file. eg tags <- list(spec_data = "7FE1,1010", pat_name = "0010,0010")
endian	can be "little" or "big".
debug	print out some debugging information, can be "little" or "big".

Value

a list with the same structure as the input, but with tag codes replaced with the corresponding data in a raw format.

---

diff_mrs *Apply the diff operator to an MRS dataset in the FID/spectral dimension.*

Description

Apply the diff operator to an MRS dataset in the FID/spectral dimension.

Usage

```
diff_mrs(mrs_data, ...)
```

Arguments

mrs_data	MRS data.
...	additional arguments to the diff function.

Value

MRS data following diff operator.

`downsample_mrs_fd` *Downsample an MRS signal by a factor of 2 using an FFT "brick-wall" filter.*

Description

Downsample an MRS signal by a factor of 2 using an FFT "brick-wall" filter.

Usage

```
downsample_mrs_fd(mrs_data)
```

Arguments

`mrs_data`	MRS data object.

Value

downsampled data.

`downsample_mrs_td` *Downsample an MRS signal by a factor of 2 by removing every other data point in the time-domain. Note, signals outside the new sampling frequency will be aliased.*

Description

Downsample an MRS signal by a factor of 2 by removing every other data point in the time-domain. Note, signals outside the new sampling frequency will be aliased.

Usage

```
downsample_mrs_td(mrs_data)
```

Arguments

`mrs_data`	MRS data object.

Value

downsampled data.

dyn_acq_times — *Return a time scale vector of acquisition times for a dynamic MRS scan. The first temporal scan is assigned a value of 0.*

Description

Return a time scale vector of acquisition times for a dynamic MRS scan. The first temporal scan is assigned a value of 0.

Usage

```
dyn_acq_times(mrs_data = NULL, tr = NULL, Ndyns = NULL, Ntrans = NULL)
```

Arguments

mrs_data	MRS data.
tr	repetition time.
Ndyns	number of dynamic scans stored, potentially less than Ntrans if block averaging has been performed.
Ntrans	number of dynamic scans acquired.

Value

time scale vector in units of seconds.

ecc — *Eddy current correction.*

Description

Apply eddy current correction using the Klose method.

Usage

```
ecc(metab, ref, rev = FALSE)
```

Arguments

metab	MRS data to be corrected.
ref	reference dataset.
rev	reverse the correction.

Details

In vivo proton spectroscopy in presence of eddy currents. Klose U. Magn Reson Med. 1990 Apr;14(1):26-30.

Value

corrected data in the time domain.

`elliptical_mask` *Create an elliptical mask stored as a matrix of logical values.*

Description

Create an elliptical mask stored as a matrix of logical values.

Usage

```
elliptical_mask(xN, yN, x0, y0, xr, yr, angle)
```

Arguments

`xN`	number of pixels in the x dimension.
`yN`	number of pixels in the y dimension.
`x0`	centre of ellipse in the x direction in units of pixels.
`y0`	centre of ellipse in the y direction in units of pixels.
`xr`	radius in the x direction in units of pixels.
`yr`	radius in the y direction in units of pixels.
`angle`	angle of rotation in degrees.

Value

logical mask matrix with dimensions fov_yN x fov_xN.

est_noise_sd

Estimate the standard deviation of the noise from a segment of an mrs_data object.

Description

Estimate the standard deviation of the noise from a segment of an mrs_data object.

Usage

```
est_noise_sd(mrs_data, n = 100, offset = 100, p_order = 2)
```

Arguments

mrs_data	MRS data object.
n	number of data points (taken from the end of array) to use in the estimation.
offset	number of final points to exclude from the calculation.
p_order	polynomial order to fit to the data before estimating the standard deviation.

Value

standard deviation array.

faceoff

Deface a T1 weighted head scan using the FaceOff method described in : https://github.com/srikash/FaceOff. Requires ANTs to be installed.

Description

Deface a T1 weighted head scan using the FaceOff method described in : https://github.com/srikash/FaceOff. Requires ANTs to be installed.

Usage

```
faceoff(mri_path, out_dir = NULL)
```

Arguments

mri_path	path to the volumetric T1 data.
out_dir	optional output directory. Defaults to the same directory as mri_path if not specified.

fd2td — *Transform frequency-domain data to the time-domain.*

Description

Transform frequency-domain data to the time-domain.

Usage

```
fd2td(mrs_data)
```

Arguments

mrs_data	MRS data in frequency-domain representation.

Value

MRS data in time-domain representation.

fd_conv_filt — *Frequency-domain convolution based filter.*

Description

Frequency-domain convolution based filter.

Usage

```
fd_conv_filt(mrs_data, K = 25, ext = 1)
```

Arguments

mrs_data	MRS data to be filtered.
K	window width in data points.
ext	point separation for linear extrapolation.

fd_gauss_smo *Apply a Gaussian smoother in the spectral domain.*

Description

Apply a Gaussian smoother in the spectral domain.

Usage

```
fd_gauss_smo(mrs_data, smo_ppm_sd)
```

Arguments

mrs_data	mrs_data object.
smo_ppm_sd	Gaussian smoother sd in ppm units.

Value

spectrally smoothed data.

find_bids_mrs *Search for MRS data files in a BIDS filesystem structure.*

Description

Search for MRS data files in a BIDS filesystem structure.

Usage

```
find_bids_mrs(path, output_full_path = FALSE)
```

Arguments

path	path to the directory containing the BIDS structure.
output_full_path	output the full normalised data paths.

Value

data frame containing full paths and information on each MRS file.

find_mrs_files *Find valid MRS data files recursively from a directory path.*

Description

Find valid MRS data files recursively from a directory path.

Usage

```
find_mrs_files(dir)
```

Arguments

dir	a directory path.

Value

a vector of valid MRS data files.

fit_amps *Extract the fit amplitudes from an object of class* fit_result.

Description

Extract the fit amplitudes from an object of class fit_result.

Usage

```
fit_amps(
  x,
  inc_index = FALSE,
  sort_names = FALSE,
  append_common_1h_comb = TRUE
)
```

Arguments

x	fit_result object.
inc_index	include columns for the voxel index.
sort_names	sort the basis set names alphabetically.
append_common_1h_comb	append commonly used 1H metabolite combinations eg tNAA = NAA + NAAG.

Value

a dataframe of amplitudes.

fit_asy_pvoigt — *Fit a single asymmetric pseudo-Voigt resonance in the frequency domain.*

Description

Fit a single asymmetric pseudo-Voigt resonance in the frequency domain.

Usage

```
fit_asy_pvoigt(
  mrs_data,
  freq_ppm = 4.65,
  xlim = c(5.2, 4.1),
  lg_limits = c(0, 1)
)
```

Arguments

mrs_data	data containing the resonance to be fit.
freq_ppm	frequency estimate (in ppm) for the resonance to be fitted.
xlim	spectral range (in ppm) where the fit will be evaluated.
lg_limits	lg lineshape parameter limits.

Value

list of fitting results and parameters.

fit_diags — *Calculate diagnostic information for object of class* fit_result.

Description

Calculate diagnostic information for object of class fit_result.

Usage

```
fit_diags(x, amps = NULL)
```

Arguments

x	fit_result object.
amps	known metabolite amplitudes.

Value

a dataframe of diagnostic information.

`fit_mrs` *Perform a fit based analysis of MRS data.*

Description

Note that TARQUIN and LCModel require these packages to be installed, and the functions set_tqn_cmd and set_lcm_cmd (respectively) need to be used to specify the location of these software packages.

Usage

```
fit_mrs(
  metab,
  basis = NULL,
  method = "ABFIT",
  w_ref = NULL,
  opts = NULL,
  parallel = FALSE,
  cl = NULL,
  time = TRUE,
  progress = "text",
  extra = NULL
)
```

Arguments

`metab`	metabolite data.
`basis`	basis class object or character vector to basis file in LCModel .basis format.
`method`	'ABFIT' (default), 'VARPRO', 'VARPRO_3P', 'TARQUIN' or 'LCMODEL'.
`w_ref`	water reference data for concentration scaling (optional).
`opts`	options to pass to the analysis method.
`parallel`	perform analyses in parallel (TRUE or FALSE).
`cl`	a parallel socket cluster required to run analyses in parallel. Eg, cl <- parallel::makeCluster(4).
`time`	measure the time taken for the analysis to complete (TRUE or FALSE).
`progress`	option is passed to plyr::alply function to display a progress bar during fitting. Default value is "text", set to "none" to disable.
`extra`	an optional data frame to provide additional variables for use in subsequent analysis steps, eg id or grouping variables.

Details

Fitting approaches described in the following references: ABfit Wilson, M. Adaptive baseline fitting for 1H MR spectroscopy analysis. Magn Reson Med 2012;85:13-29.

VARPRO van der Veen JW, de Beer R, Luyten PR, van Ormondt D. Accurate quantification of in vivo 31P NMR signals using the variable projection method and prior knowledge. Magn Reson Med 1988;6:92-98.

TARQUIN Wilson, M., Reynolds, G., Kauppinen, R. A., Arvanitis, T. N. & Peet, A. C. A constrained least-squares approach to the automated quantitation of in vivo 1H magnetic resonance spectroscopy data. Magn Reson Med 2011;65:1-12.

LCModel Provencher SW. Estimation of metabolite concentrations from localized in vivo proton NMR spectra. Magn Reson Med 1993;30:672-679.

Value

MRS analysis object.

Examples

```
fname <- system.file("extdata", "philips_spar_sdat_WS.SDAT", package =
"spant")
svs <- read_mrs(fname)
## Not run:
basis <- sim_basis_1h_brain_press(svs)
fit_result <- fit_mrs(svs, basis)

## End(Not run)
```

---

fit_res2csv *Write fit results table to a csv file.*

Description

Write fit results table to a csv file.

Usage

```
fit_res2csv(fit_res, fname, unscaled = FALSE)
```

Arguments

fit_res	fit result object.
fname	filename of csv file.
unscaled	output the unscaled result table (default = FALSE).

`fit_svs` *Standard SVS 1H brain analysis pipeline.*

Description

Note this function is under active development and liable to changes.

Usage

```
fit_svs(
  input,
  w_ref = NULL,
  output_dir = NULL,
  mri = NULL,
  mri_seg = NULL,
  deface = FALSE,
  segment_t1 = FALSE,
  segment_t1_method = "rpyants",
  external_basis = NULL,
  append_external_basis = FALSE,
  p_vols = NULL,
  format = NULL,
  pul_seq = NULL,
  TE = NULL,
  TR = NULL,
  TE1 = NULL,
  TE2 = NULL,
  TE3 = NULL,
  TM = NULL,
  append_basis = NULL,
  remove_basis = NULL,
  pre_align = TRUE,
  pre_align_max_shift = 40,
  pre_align_ref_freq = c(2.01, 3.03, 3.22),
  pre_align_ref_amp = 1,
  dfp_corr = TRUE,
  dfp_corr_ref_subset = NULL,
  output_ratio = NULL,
  ecc = FALSE,
  hsvd_width = NULL,
  decimate = FALSE,
  trunc_fid_pts = NULL,
  fit_method = NULL,
  fit_opts = NULL,
  fit_subset = NULL,
  w_ref_subset = NULL,
  legacy_ws = FALSE,
```

```
  w_att = 0.7,
  w_conc = 35880,
  use_basis_cache = "auto",
  summary_measures = NULL,
  dyn_av_block_size = NULL,
  dyn_av_scheme = NULL,
  dyn_av_scheme_file = NULL,
  dyn_basis_lb = NULL,
  dyn_basis_lg = NULL,
  lcm_bin_path = NULL,
  plot_ppm_xlim = NULL,
  extra_output = FALSE,
  verbose = FALSE,
  return_fit = FALSE,
  write_preproc_metab_path = NULL,
  overwrite = FALSE
)
```

Arguments

input	path or mrs_data object containing MRS data.
w_ref	path or mrs_data object containing MRS water reference data.
output_dir	directory path to output fitting results.
mri	filepath or nifti object containing anatomical MRI data.
mri_seg	filepath or nifti object containing segmented MRI data.
deface	option to apply faceoff to the mri input. Defaults to FALSE.
segment_t1	segment the t1 weighted mri file with ANTs and use the results to perform partial volume correction. Defaults to FALSE.
segment_t1_method	one of : "rpyants" (default), "ants" or "fslr".
external_basis	precompiled basis set object to use for analysis.
append_external_basis	append the external basis with the internally generated one. Useful for adding experimentally acquired baseline signals to internally simulated basis sets. Defaults to FALSE - meaning only signals from the external basis will be used in analysis.
p_vols	a numeric vector of partial volumes expressed as percentages. Defaults to 100% white matter. A voxel containing 100% gray matter tissue would use : p_vols = c(WM = 0, GM = 100, CSF = 0).
format	Override automatic data format detection. See format argument in read_mrs() for permitted values.
pul_seq	Pulse sequence to use for basis simulation. Can be one of the following values : "press", "press_ideal", "press_shaped", "steam" or "slaser". If "press" then "press_ideal" will be assumed unless the magnetic field is stronger that 2.8 Tesla, "press_shaped" will be assumed for 2.9 Tesla and above.

TE — metabolite mrs data echo time in seconds. If not supplied this will be guessed from the metab data file.

TR — metabolite mrs data repetition time in seconds. If not supplied this will be guessed from the metab data file.

TE1 — PRESS or sLASER sequence timing parameter in seconds.

TE2 — PRESS or sLASER sequence timing parameter in seconds.

TE3 — sLASER sequence timing parameter in seconds.

TM — STEAM mixing time parameter in seconds.

append_basis — names of extra signals to add to the default basis. Eg append_basis = c("peth", "cit"). Use get_mol_names() function to print all available signals. Cannot be used with precompiled basis sets.

remove_basis — grep expression to match names of signals to remove from the basis. For example: use "lac|ala" to remove lactate and alanine; "*" to remove all signals and "^mm|^lip" to remove all macromolecular and lipid signals. This operation is performed before signals are added with append_basis. Cannot be used with precompiled basis sets.

pre_align — perform simple frequency alignment to known reference peaks.

pre_align_max_shift — maximum allowable shift in Hz. Defaults to 40 Hz.

pre_align_ref_freq — reference frequency in ppm units. More than one frequency may be specified. Defaults to : c(2.01, 3.03, 3.22).

pre_align_ref_amp — reference frequency relative amplitudes. Defaults to 1, corresponding to equal amplitudes.

dfp_corr — perform dynamic frequency and phase correction using the RATS method.

dfp_corr_ref_subset — specify a subset of dynamics to use as reference scans for dynamic frequency and phase correction. For example, 1:16 would use the mean of the first 16 dynamic scans as a reference spectrum.

output_ratio — optional string to specify a metabolite ratio to output. Defaults to "tCr". Multiple metabolites may be specified for multiple outputs. Set to NA to omit.

ecc — option to perform water reference based eddy current correction, defaults to FALSE.

hsvd_width — set the width of the HSVD filter in Hz. Note the applied width is between -width and +width Hz, with 0 Hz being defined at the centre of the spectral width. Default is disabled (set to NULL), 30 Hz is a reasonable value.

decimate — option on decimate the data by a factor of 2 before analysis. Defaults to FALSE.

trunc_fid_pts — number of points to truncate the input data by in the time-domain. E.g. setting to 1024 will ensure data with more time-domain points will be truncated to a length of 1024. Defaults to NULL, where truncation is not performed.

fit_method — can be "ABFIT-REG" or "LCMODEL. Defaults to "ABFIT-REG".

fit_opts — options to pass to the fitting method.

`fit_subset` specify a subset of dynamics to analyse, for example 1:16 would only fit the first 16 dynamic scans.

`w_ref_subset` specify a subset of dynamics to use as water reference following rats alignment and averaging. For example c(1, 2) would only use the average of the first two dynamic water reference scans. Default value of NULL uses all available water reference scans.

`legacy_ws` perform and output legacy water scaling compatible with default LCModel and TARQUIN behaviour. See w_att and w_conc arguments to change the default assumptions. Default value is FALSE.

`w_att` water attenuation factor (default = 0.7) for legacy water scaling. Assumes water T2 of 80ms and a TE = 30 ms. exp(-30ms / 80ms) ~ 0.7.

`w_conc` assumed water concentration (default = 35880) for legacy water scaling. Default value corresponds to typical white matter. Set to 43300 for gray matter, and 55556 for phantom measurements.

`use_basis_cache`
Pre-cache basis sets to reduce analysis speed. Can be one of the following : "auto", "all" or "none". The default value of "auto" will only use the cache for 3T PRESS - which generally requires more detailed simulation due to high CSD.

`summary_measures`
output an additional table with a subset of metabolite levels, eg c("tNAA", "tNAA/tCr", "tNAA/tCho", "Lac/tNAA").

`dyn_av_block_size`
perform temporal averaging with the specified block size. Defaults to NULL, eg average across all dynamic scans.

`dyn_av_scheme` a numeric vector of sequential integers (starting at 1), with the same length as the number of dynamic scans in the metabolite data. For example: c(1, 1, 2, 1, 1, 3, 1, 1).

`dyn_av_scheme_file`
a file path containing a single column of sequential integers (starting at 1) with the same length as the number of dynamic scans in the metabolite data. File may be formatted as .xlsx, .xls, text or csv format.

`dyn_basis_lb` dynamic basis line-broadening to apply in Hz.

`dyn_basis_lg` dynamic basis Lorentz-Gauss lineshape factor between 0 and 1. Defaults to 0, pure Lorentzian.

`lcm_bin_path` set the path to LCModel binary.

`plot_ppm_xlim` plotting ppm axis limits in the html results. results.

`extra_output` write extra output files for generating custom plots. Defaults to FALSE.

`verbose` output potentially useful information.

`return_fit` return a fit object, defaults to FALSE.

`write_preproc_metab_path`
path to write the preprocessed metabolite data in NIfTI format.

`overwrite` overwrite existing fitting result files, defaults to FALSE.

Examples

```
metab <- system.file("extdata", "philips_spar_sdat_WS.SDAT",
                     package = "spant")
w_ref <- system.file("extdata", "philips_spar_sdat_W.SDAT",
                     package = "spant")
out_dir <- file.path("~", "fit_svs_result")
## Not run:
fit_result <- fit_svs(metab, w_ref, out_dir)

## End(Not run)
```

`fit_svs_edited` *Edited SVS 1H brain analysis pipeline.*

Description

Note this function is still under development and liable to changes.

Usage

```
fit_svs_edited(
  input,
  w_ref = NULL,
  output_dir = NULL,
  mri = NULL,
  mri_seg = NULL,
  deface = FALSE,
  segment_t1 = FALSE,
  segment_t1_method = "rpyants",
  external_basis = NULL,
  p_vols = NULL,
  format = NULL,
  editing_type = "gaba_1.9",
  editing_scheme = NULL,
  invert_edit_on = NULL,
  invert_edit_off = NULL,
  pul_seq = NULL,
  TE = NULL,
  TR = NULL,
  TE1 = NULL,
  TE2 = NULL,
  TE3 = NULL,
  TM = NULL,
  append_basis_ed_off = NULL,
  remove_basis_ed_off = NULL,
  pre_align = TRUE,
  dfp_corr = TRUE,
```

```
  output_ratio = NULL,
  ecc = FALSE,
  hsvd_width = NULL,
  decimate = FALSE,
  trunc_fid_pts = NULL,
  fit_opts_edited = NULL,
  fit_opts_ed_off = NULL,
  fit_subset = NULL,
  legacy_ws = FALSE,
  w_att = 0.7,
  w_conc = 35880,
  use_basis_cache = "auto",
  summary_measures = NULL,
  dyn_av_block_size = NULL,
  dyn_av_scheme = NULL,
  dyn_av_scheme_file = NULL,
  plot_ppm_xlim = NULL,
  extra_output = FALSE,
  verbose = FALSE,
  return_fit = FALSE,
  overwrite = FALSE
)
```

Arguments

input	path or mrs_data object containing MRS data.
w_ref	path or mrs_data object containing MRS water reference data.
output_dir	directory path to output fitting results.
mri	filepath or nifti object containing anatomical MRI data.
mri_seg	filepath or nifti object containing segmented MRI data.
deface	option to apply faceoff to the mri input. Defaults to FALSE.
segment_t1	segment the t1 weighted mri file with ANTs and use the results to perform partial volume correction. Defaults to FALSE.
segment_t1_method	one of : "rpyants" (default), "ants" or "fslr".
external_basis	precompiled basis set object to use for analysis.
p_vols	a numeric vector of partial volumes expressed as percentages. Defaults to 100% white matter. A voxel containing 100% gray matter tissue would use : p_vols = c(WM = 0, GM = 100, CSF = 0).
format	Override automatic data format detection. See format argument in read_mrs() for permitted values.
editing_type	can be one of : "gaba_1.9" or "gsh_4.54". Defaults to "gaba_1.9".
editing_scheme	describes the dynamic data ordering. Can be one of: 'on-off-blocks', 'on-off-interleaved', 'off-on-blocks' or 'off-on-interleaved'.
invert_edit_on	set to TRUE to invert the edit-on sub-spectra.

`invert_edit_off`
: set to TRUE to invert the edit-off sub-spectra.

`pul_seq`
: Pulse sequence to use for basis simulation. Can be one of the following values : "press", "press_ideal", "press_shaped", "steam" or "slaser". If "press" then "press_ideal" will be assumed unless the magnetic field is stronger that 2.8 Tesla, "press_shaped" will be assumed for 2.9 Tesla and above.

`TE`
: metabolite mrs data echo time in seconds. If not supplied this will be guessed from the metab data file.

`TR`
: metabolite mrs data repetition time in seconds. If not supplied this will be guessed from the metab data file.

`TE1`
: PRESS or sLASER sequence timing parameter in seconds.

`TE2`
: PRESS or sLASER sequence timing parameter in seconds.

`TE3`
: sLASER sequence timing parameter in seconds.

`TM`
: STEAM mixing time parameter in seconds.

`append_basis_ed_off`
: names of extra signals to add to the default basis. Eg append_basis = c("peth", "cit"). Use get_mol_names() function to print all available signals. Cannot be used with precompiled basis sets.

`remove_basis_ed_off`
: grep expression to match names of signals to remove from the basis. For example: use "lac|ala" to remove lactate and alanine; "*" to remove all signals and "^mm|^lip" to remove all macromolecular and lipid signals. This operation is performed before signals are added with append_basis_ed_off. Cannot be used with precompiled basis sets.

`pre_align`
: perform simple frequency alignment to known reference peaks.

`dfp_corr`
: perform dynamic frequency and phase correction using the RATS method.

`output_ratio`
: optional string to specify a metabolite ratio to output. Defaults to "tCr". Multiple metabolites may be specified for multiple outputs. Set to NA to omit.

`ecc`
: option to perform water reference based eddy current correction, defaults to FALSE.

`hsvd_width`
: set the width of the HSVD filter in Hz. Note the applied width is between -width and +width Hz, with 0 Hz being defined at the centre of the spectral width. Default is disabled (set to NULL), 30 Hz is a reasonable value.

`decimate`
: option on decimate the data by a factor of 2 before analysis. Defaults to FALSE.

`trunc_fid_pts`
: number of points to truncate the input data by in the time-domain. E.g. setting to 1024 will ensure data with more time-domain points will be truncated to a length of 1024. Defaults to NULL, where truncation is not performed.

`fit_opts_edited`
: options to pass to the fitting method for the edited spectrum.

`fit_opts_ed_off`
: options to pass to the fitting method for the edit-off spectrum.

`fit_subset`
: specify a subset of dynamics to analyse, for example 1:16 would only fit the first 16 dynamic scans.

`legacy_ws` perform and output legacy water scaling compatible with default LCModel and TARQUIN behaviour. See w_att and w_conc arguments to change the default assumptions. Default value is FALSE.

`w_att` water attenuation factor (default = 0.7) for legacy water scaling. Assumes water T2 of 80ms and a TE = 30 ms. exp(-30ms / 80ms) ~ 0.7.

`w_conc` assumed water concentration (default = 35880) for legacy water scaling. Default value corresponds to typical white matter. Set to 43300 for gray matter, and 55556 for phantom measurements.

`use_basis_cache`
Pre-cache basis sets to reduce analysis speed. Can be one of the following : "auto", "all" or "none". The default value of "auto" will only use the cache for 3T PRESS - which generally requires more detailed simulation due to high CSD.

`summary_measures`
output an additional table with a subset of metabolite levels, eg c("tNAA", "tNAA/tCr", "tNAA/tCho", "Lac/tNAA").

`dyn_av_block_size`
perform temporal averaging with the specified block size. Defaults to NULL, eg average across all dynamic scans.

`dyn_av_scheme` a numeric vector of sequential integers (starting at 1), with the same length as the number of dynamic scans in the metabolite data. For example: c(1, 1, 2, 1, 1, 3, 1, 1).

`dyn_av_scheme_file`
a file path containing a single column of sequential integers (starting at 1) with the same length as the number of dynamic scans in the metabolite data. File may be formatted as .xlsx, .xls, text or csv format.

`plot_ppm_xlim` plotting ppm axis limits in the html results. results.

`extra_output` write extra output files for generating custom plots. Defaults to FALSE.

`verbose` output potentially useful information.

`return_fit` return a fit object, defaults to FALSE.

`overwrite` overwrite existing fitting result files, defaults to FALSE.

Examples

```
metab <- system.file("extdata", "philips_spar_sdat_WS.SDAT",
                     package = "spant")
w_ref <- system.file("extdata", "philips_spar_sdat_W.SDAT",
                     package = "spant")
out_dir <- file.path("~", "fit_svs_result")
## Not run:
fit_result <- fit_svs(metab, w_ref, out_dir)

## End(Not run)
```

fit_svs_edited_group_results *Combine edited fitting results for group analysis.*

Description

Combine edited fitting results for group analysis.

Usage

```
fit_svs_edited_group_results(
  search_path = NULL,
  paths = NULL,
  output_dir = "fit_svs_edited_group_results",
  verbose = TRUE
)
```

Arguments

search_path	path to start recursive search for fitting results. Cannot be used together with the paths argument.
paths	a set of paths to spant output files, usually named : "spant_fit_svs_edited_data.rds". Cannot be used together with the search_path argument.
output_dir	directory path to store group results.
verbose	verbose, defaults to TRUE.

fit_svs_group_results *Combine fitting results for group analysis.*

Description

Combine fitting results for group analysis.

Usage

```
fit_svs_group_results(
  search_path = NULL,
  paths = NULL,
  output_dir = "fit_svs_group_results",
  verbose = TRUE
)
```

Arguments

search_path	path to start recursive search for fitting results. Cannot be used together with the paths argument.
paths	a set of paths to spant output files, usually named : "spant_fit_svs_data.rds". Cannot be used together with the search_path argument.
output_dir	directory path to store group results.
verbose	verbose, defaults to TRUE.

---

fit_svs_gui *GUI interface for the standard SVS 1H brain analysis pipeline, this is a work in progress, and not ready for serious use.*

Description

GUI interface for the standard SVS 1H brain analysis pipeline, this is a work in progress, and not ready for serious use.

Usage

```
fit_svs_gui()
```

---

fit_t1_ti_array *Fit a T1 recovery curve, from multiple TIs, to a set of amplitudes.*

Description

Fit a T1 recovery curve, from multiple TIs, to a set of amplitudes.

Usage

```
fit_t1_ti_array(
  ti_vec,
  amp_vec,
  lower = 0,
  upper = 10,
  output_fit_res = 0.01,
  ret_full = TRUE
)
```

Arguments

ti_vec	vector of TI values in seconds.
amp_vec	vector of amplitudes.
lower	minimum allowable T1 value.
upper	maximum allowable T1 value.
output_fit_res	temporal resolution (seconds) of the ideal output relaxation curve.
ret_full	return full fitting information including ideal relaxation curve.

Value

a list containing relaxation parameters and an ideal curve for fit evaluation.

---

fit_t1_tr_array *Fit a T1 recovery curve, from multiple TRs, to a set of amplitudes.*

Description

Fit a T1 recovery curve, from multiple TRs, to a set of amplitudes.

Usage

```
fit_t1_tr_array(
  tr_vec,
  amp_vec,
  lower = 0,
  upper = 10,
  output_fit_res = 0.01,
  ret_full = TRUE
)
```

Arguments

tr_vec	vector of TR values in seconds.
amp_vec	vector of amplitudes.
lower	minimum allowable T1 value.
upper	maximum allowable T1 value.
output_fit_res	temporal resolution (seconds) of the ideal output relaxation curve.
ret_full	return full fitting information including ideal relaxation curve.

Value

a list containing relaxation parameters and an ideal curve for fit evaluation.

fit_t2_te_array *Fit a T2 relaxation curve, from multiple TEs, to a set of amplitudes.*

Description

Fit a T2 relaxation curve, from multiple TEs, to a set of amplitudes.

Usage

```
fit_t2_te_array(
  te_vec,
  amp_vec,
  lower = 0,
  upper = 10,
  output_fit_res = 0.01,
  ret_full = TRUE
)
```

Arguments

te_vec	vector of TE values in seconds.
amp_vec	vector of amplitudes.
lower	minimum allowable T2 value.
upper	maximum allowable T2 value.
output_fit_res	temporal resolution (seconds) of the ideal output relaxation curve.
ret_full	return full fitting information including ideal relaxation curve.

Value

a list containing relaxation parameters and an ideal curve for fit evaluation.

fp_phase *Return the phase of the first data point in the time-domain.*

Description

Return the phase of the first data point in the time-domain.

Usage

```
fp_phase(mrs_data)
```

Arguments

mrs_data	MRS data.

Value

phase values in degrees.

`fp_phase_correct` *Perform a zeroth order phase correction based on the phase of the first data point in the time-domain.*

Description

Perform a zeroth order phase correction based on the phase of the first data point in the time-domain.

Usage

```
fp_phase_correct(mrs_data, ret_phase = FALSE)
```

Arguments

`mrs_data`	MRS data to be corrected.
`ret_phase`	return phase values (logical).

Value

corrected data or a list with corrected data and optional phase values.

`fp_scale` *Scale the first time-domain data point in an mrs_data object.*

Description

Scale the first time-domain data point in an mrs_data object.

Usage

```
fp_scale(mrs_data, scale = 0.5)
```

Arguments

`mrs_data`	MRS data.
`scale`	scaling value, defaults to 0.5.

Value

scaled mrs_data object.

fs — *Return the sampling frequency in Hz of an MRS dataset.*

Description

Return the sampling frequency in Hz of an MRS dataset.

Usage

```
fs(mrs_data)
```

Arguments

mrs_data	MRS data.

Value

sampling frequency in Hz.

ft_dyns — *Apply the Fourier transform over the dynamic dimension.*

Description

Apply the Fourier transform over the dynamic dimension.

Usage

```
ft_dyns(mrs_data, ft_shift = FALSE, ret_mod = FALSE, fd = TRUE)
```

Arguments

mrs_data	MRS data where the dynamic dimension is in the time-domain.
ft_shift	apply FT shift to the output, default is FALSE.
ret_mod	return the modulus out the transform, default is FALSE.
fd	transform the chemical shift axis to the frequency domain first, default is TRUE.

Value

transformed MRS data.

`ft_shift` *Perform a fft and ffshift on a vector.*

Description

Perform a fft and ffshift on a vector.

Usage

```
ft_shift(vec_in)
```

Arguments

`vec_in`	vector input.

Value

output vector.

`ft_shift_mat` *Perform a fft and fftshift on a matrix with each column replaced by its shifted fft.*

Description

Perform a fft and fftshift on a matrix with each column replaced by its shifted fft.

Usage

```
ft_shift_mat(mat_in)
```

Arguments

`mat_in`	matrix input.

Value

output matrix.

gausswin_2d *Create a two dimensional Gaussian window function stored as a matrix.*

Description

Create a two dimensional Gaussian window function stored as a matrix.

Usage

```
gausswin_2d(xN, yN, x0, y0, xw, yw)
```

Arguments

xN	number of pixels in the x dimension.
yN	number of pixels in the y dimension.
x0	centre of window function in the x direction in units of pixels. Note, only integer values are applied.
y0	centre of window function in the y direction in units of pixels. Note, only integer values are applied.
xw	the reciprocal of the standard deviation of the Gaussian window in x direction.
yw	the reciprocal of the standard deviation of the Gaussian window in y direction.

Value

matrix with dimensions fov_yN x fov_xN.

gen_baseline_reg *Generate baseline regressor.*

Description

Generate baseline regressor.

Usage

```
gen_baseline_reg(mrs_data = NULL, tr = NULL, Ndyns = NULL, Ntrans = NULL)
```

Arguments

mrs_data	mrs_data object for timing information.
tr	repetition time.
Ndyns	number of dynamic scans stored, potentially less than Ntrans if block averaging has been performed.
Ntrans	number of dynamic scans acquired.

Value

a single baseline regressor with value of 1.

`gen_bold_reg` *Generate BOLD regressors.*

Description

Generate BOLD regressors.

Usage

```
gen_bold_reg(
  onset,
  duration = NULL,
  trial_type = NULL,
  mrs_data = NULL,
  tr = NULL,
  Ndyns = NULL,
  Ntrans = NULL,
  match_tr = TRUE,
  dt = 0.1,
  normalise = FALSE
)
```

Arguments

`onset`	stimulus onset in seconds.
`duration`	stimulus duration in seconds.
`trial_type`	string label for the stimulus.
`mrs_data`	mrs_data object for timing information.
`tr`	repetition time.
`Ndyns`	number of dynamic scans stored, potentially less than Ntrans if block averaging has been performed.
`Ntrans`	number of dynamic scans acquired.
`match_tr`	match the output to the input mrs_data.
`dt`	timing resolution for internal calculations.
`normalise`	normalise the response function to have a maximum value of one.

Value

BOLD regressor data frame.

gen_conv_reg *Generate regressors by convolving a specified response function with a stimulus.*

Description

Generate regressors by convolving a specified response function with a stimulus.

Usage

```
gen_conv_reg(
  onset,
  duration = NULL,
  trial_type = NULL,
  mrs_data = NULL,
  tr = NULL,
  Ndyns = NULL,
  Ntrans = NULL,
  resp_fn,
  match_tr = TRUE,
  normalise = FALSE
)
```

Arguments

onset	stimulus onset in seconds.
duration	stimulus duration in seconds.
trial_type	string label for the stimulus.
mrs_data	mrs_data object for timing information.
tr	repetition time.
Ndyns	number of dynamic scans stored, potentially less than Ntrans if block averaging has been performed.
Ntrans	number of dynamic scans acquired.
resp_fn	a data frame specifying the response function to be convolved.
match_tr	match the output to the input mrs_data.
normalise	normalise the response function to have a maximum value of one.

Value

BOLD regressor data frame.

gen_F — *Generate the F product operator.*

Description

Generate the F product operator.

Usage

```
gen_F(sys, op, detect = NULL)
```

Arguments

sys	spin system object.
op	operator, one of "x", "y", "z", "p", "m".
detect	detection nuclei.

Value

F product operator matrix.

gen_F_xy — *Generate the Fxy product operator with a specified phase.*

Description

Generate the Fxy product operator with a specified phase.

Usage

```
gen_F_xy(sys, phase, detect = NULL)
```

Arguments

sys	spin system object.
phase	phase angle in degrees.
detect	detection nuclei.

Value

product operator matrix.

gen_group_reg *Expand a regressor matrix for a group analysis.*

Description

Expand a regressor matrix for a group analysis.

Usage

```
gen_group_reg(regressor_df, n)
```

Arguments

regressor_df	input regressor data frame.
n	number of datasets n the group.

gen_I *Generate the I product operator for a single spin.*

Description

Generate the I product operator for a single spin.

Usage

```
gen_I(n, spin_num, op)
```

Arguments

n	spin index number for the required operator.
spin_num	vector of spin numbers in the system.
op	operator, one of "x", "y", "z", "p", "m".

Value

I product operator matrix.

gen_impulse_reg *Generate impulse regressors.*

Description

Generate impulse regressors.

Usage

```
gen_impulse_reg(
  onset,
  trial_type = NULL,
  mrs_data = NULL,
  tr = NULL,
  Ndyns = NULL,
  Ntrans = NULL
)
```

Arguments

onset	stimulus onset in seconds.
trial_type	string label for the stimulus.
mrs_data	mrs_data object for timing information.
tr	repetition time.
Ndyns	number of dynamic scans stored, potentially less than Ntrans if block averaging has been performed.
Ntrans	number of dynamic scans acquired.

Value

impulse regressors data frame.

gen_numeric_reg *Generate a regressor from a numeric vector.*

Description

Generate a regressor from a numeric vector.

Usage

```
gen_numeric_reg(
  in_vec,
  name,
  mrs_data = NULL,
  tr = NULL,
  Ndyns = NULL,
  Ntrans = NULL
)
```

Arguments

in_vec	a numeric input vector the same length as the number of stored dynamic scans.
name	a character vector representing the regressor name.
mrs_data	mrs_data object for timing information.
tr	repetition time.
Ndyns	number of dynamic scans stored, potentially less than Ntrans if block averaging has been performed.
Ntrans	number of dynamic scans acquired.

Value

a single baseline regressor with value of 1.

---

gen_poly_reg *Generate polynomial regressors.*

Description

Generate polynomial regressors.

Usage

```
gen_poly_reg(degree, mrs_data = NULL, tr = NULL, Ndyns = NULL, Ntrans = NULL)
```

Arguments

degree	the degree of the polynomial.
mrs_data	mrs_data object for timing information.
tr	repetition time.
Ndyns	number of dynamic scans stored, potentially less than Ntrans if block averaging has been performed.
Ntrans	number of dynamic scans acquired.

Value

polynomial regressors.

gen_trap_reg *Generate trapezoidal regressors.*

Description

Generate trapezoidal regressors.

Usage

```
gen_trap_reg(
  onset,
  duration,
  trial_type = NULL,
  mrs_data = NULL,
  tr = NULL,
  Ndyns = NULL,
  Ntrans = NULL,
  rise_t = 0,
  fall_t = 0,
  exp_fall = FALSE,
  exp_fall_power = 1,
  smo_sigma = NULL,
  match_tr = TRUE,
  dt = 0.01,
  normalise = FALSE
)
```

Arguments

onset	stimulus onset in seconds.
duration	stimulus duration in seconds.
trial_type	string label for the stimulus.
mrs_data	mrs_data object for timing information.
tr	repetition time.
Ndyns	number of dynamic scans stored, potentially less than Ntrans if block averaging has been performed.
Ntrans	number of dynamic scans acquired.
rise_t	time to reach a plateau from baseline in seconds.
fall_t	time to fall from plateau level back to baseline in seconds.
exp_fall	model an exponential fall instead of linear.
exp_fall_power	exponential fall power.
smo_sigma	standard deviation of Gaussian smoothing kernel in seconds. Set to NULL to disable (default behavior).

match_tr	match the output to the input mrs_data.
dt	timing resolution for internal calculations.
normalise	normalise the response function to have a maximum value of one.

Value

trapezoidal regressor data frame.

`get_1h_braino_basis_names`

Return a character vector of molecules included in the GE BRAINO phantom.

Description

Return a character vector of molecules included in the GE BRAINO phantom.

Usage

```
get_1h_braino_basis_names()
```

Value

a character vector of molecule names.

`get_1h_brain_basis_names`

Return a character vector of common 1H molecules found in healthy human brain.

Description

Note, this is a basic set and it may be appropriate to also include Asc, Gly and PEth for high quality MRS data.

Usage

```
get_1h_brain_basis_names(add = NULL, remove = NULL, inc_lip_mm = TRUE)
```

Arguments

add	optional character vector of additional molecular names. Eg c("asc", "gly", "peth").
remove	optional character vector of molecular names to remove from the set. Eg c("m_cr_ch2").
inc_lip_mm	include Lipid and MM basis signals.

Value

a character vector of molecule names.

`get_1h_brain_basis_paras` *Return a list of* `mol_parameter` *objects suitable for 1H brain MRS analyses.*

Description

Return a list of `mol_parameter` objects suitable for 1H brain MRS analyses.

Usage

```
get_1h_brain_basis_paras(ft, metab_lw = NULL, lcm_compat = FALSE)
```

Arguments

`ft`	transmitter frequency in Hz.
`metab_lw`	linewidth of metabolite signals (Hz).
`lcm_compat`	when TRUE, lipid, MM and -CrCH molecules will be excluded from the output.

Value

list of `mol_parameter` objects.

`get_1h_brain_basis_paras_v1` *Return a list of* `mol_parameter` *objects suitable for 1H brain MRS analyses.*

Description

Return a list of `mol_parameter` objects suitable for 1H brain MRS analyses.

Usage

```
get_1h_brain_basis_paras_v1(ft, metab_lw = NULL, lcm_compat = FALSE)
```

Arguments

`ft`	transmitter frequency in Hz.
`metab_lw`	linewidth of metabolite signals (Hz).
`lcm_compat`	when TRUE, lipid, MM and -CrCH molecules will be excluded from the output.

Value

list of `mol_parameter` objects.

`get_1h_brain_basis_paras_v2`

Return a list of `mol_parameter` *objects suitable for 1H brain MRS analyses.*

Description

Return a list of `mol_parameter` objects suitable for 1H brain MRS analyses.

Usage

```
get_1h_brain_basis_paras_v2(ft, metab_lw = NULL, lcm_compat = FALSE)
```

Arguments

`ft`	transmitter frequency in Hz.
`metab_lw`	linewidth of metabolite signals (Hz).
`lcm_compat`	when TRUE, lipid, MM and -CrCH molecules will be excluded from the output.

Value

list of `mol_parameter` objects.

`get_1h_brain_basis_paras_v3`

Return a list of `mol_parameter` *objects suitable for 1H brain MRS analyses.*

Description

Return a list of `mol_parameter` objects suitable for 1H brain MRS analyses.

Usage

```
get_1h_brain_basis_paras_v3(ft, metab_lw = NULL, lcm_compat = FALSE)
```

Arguments

`ft`	transmitter frequency in Hz.
`metab_lw`	linewidth of metabolite signals (Hz).
`lcm_compat`	when TRUE, lipid, MM and -CrCH molecules will be excluded from the output.

Value

list of `mol_parameter` objects.

`get_1h_spectre_basis_names` *Return a character vector of molecules included in the Gold Star Phantoms SPECTRE phantom.*

Description

Return a character vector of molecules included in the Gold Star Phantoms SPECTRE phantom.

Usage

```
get_1h_spectre_basis_names()
```

Value

a character vector of molecule names.

`get_2d_psf` *Get the point spread function (PSF) for a 2D phase encoded MRSI scan.*

Description

Get the point spread function (PSF) for a 2D phase encoded MRSI scan.

Usage

```
get_2d_psf(
  FOV = 160,
  mat_size = 16,
  sampling = "circ",
  hamming = FALSE,
  ensure_odd = TRUE
)
```

Arguments

`FOV`	field of view in mm.
`mat_size`	acquisition matrix size (not interpolated).
`sampling`	can be either "circ" for circular or "rect" for rectangular.
`hamming`	should Hamming k-space weighting be applied (default FALSE).
`ensure_odd`	add 1mm to the FOV when required to ensure the output pdf has odd dimensions. Required when using get_mrsi2d_seg.

Value

A matrix of the PSF with 1mm resolution.

`get_acq_paras` *Return acquisition parameters from a MRS data object.*

Description

Return acquisition parameters from a MRS data object.

Usage

```
get_acq_paras(mrs_data)
```

Arguments

`mrs_data`	MRS data.

Value

list of acquisition parameters.

`get_ants_dir` *Return the ANTs installation directory, or throw an error if not found.*

Description

Will check and return the "spant.ants_dir" option set by set_ants_dir. If not set, will search the spant_resources directory for ANTs and return the most recent version if multiple are found.

Usage

```
get_ants_dir()
```

Value

ANTs installation directory.

get_basis_subset *Return a subset of the input basis.*

Description

Return a subset of the input basis.

Usage

```
get_basis_subset(basis, names, invert = FALSE)
```

Arguments

basis	input basis.
names	basis set elements to keep in the returned object.
invert	set to true to return all basis elements except those given in the names argument.

Value

a subset of the input basis.

get_dyns *Extract a subset of dynamic scans.*

Description

Extract a subset of dynamic scans.

Usage

```
get_dyns(mrs_data, subset)
```

Arguments

mrs_data	dynamic MRS data.
subset	vector containing indices to the dynamic scans to be returned.

Value

MRS data containing the subset of requested dynamics.

get_even_dyns *Return even numbered dynamic scans starting from 1 (2,4,6...).*

Description

Return even numbered dynamic scans starting from 1 (2,4,6...).

Usage

```
get_even_dyns(mrs_data)
```

Arguments

mrs_data	dynamic MRS data.

Value

dynamic MRS data containing even numbered scans.

get_fh_dyns *Return the first half of a dynamic series.*

Description

Return the first half of a dynamic series.

Usage

```
get_fh_dyns(mrs_data)
```

Arguments

mrs_data	dynamic MRS data.

Value

first half of the dynamic series.

get_fit_map *Get a data array from a fit result.*

Description

Get a data array from a fit result.

Usage

```
get_fit_map(fit_res, name)
```

Arguments

fit_res	fit_result object.
name	name of the quantity to plot, eg "tNAA".

get_fp *Return the first time-domain data point.*

Description

Return the first time-domain data point.

Usage

```
get_fp(mrs_data)
```

Arguments

mrs_data	MRS data.

Value

first time-domain data point.

get_guassian_pulse *Generate a gaussian pulse shape.*

Description

Generate a gaussian pulse shape.

Usage

```
get_guassian_pulse(angle, n, trunc = 1)
```

Arguments

angle	pulse angle in degrees.
n	number of points to generate.
trunc	percentage truncation factor.

get_head_dyns *Return the first scans of a dynamic series.*

Description

Return the first scans of a dynamic series.

Usage

```
get_head_dyns(mrs_data, n = 1)
```

Arguments

mrs_data	dynamic MRS data.
n	the number of dynamic scans to return.

Value

first scans of a dynamic series.

get_hrf *Generate a double gamma model of the HRF as used in SPM.*

Description

Generate a double gamma model of the HRF as used in SPM.

Usage

```
get_hrf(end_t = 30, res_t = 0.01)
```

Arguments

end_t	last time point to generate in seconds.
res_t	temporal resolution in seconds, defaults to 10ms.

Value

a data.frame of time and HRF vectors.

get_lcm_cmd *Print the command to run the LCModel command-line program.*

Description

Print the command to run the LCModel command-line program.

Usage

```
get_lcm_cmd()
```

get_metab *Extract the metabolite component from an mrs_data object.*

Description

Extract the metabolite component from an mrs_data object.

Usage

```
get_metab(mrs_data)
```

Arguments

mrs_data	MRS data.

Value

metabolite component.

---

get_mol_names *Return a character array of names that may be used with the* get_mol_paras *function.*

Description

Return a character array of names that may be used with the get_mol_paras function.

Usage

```
get_mol_names()
```

Value

a character array of names.

---

get_mol_paras *Get a* mol_parameters *object for a named molecule.*

Description

Get a mol_parameters object for a named molecule.

Usage

```
get_mol_paras(name, ...)
```

Arguments

name	the name of the molecule.
...	arguments to pass to molecule definition function.

get_mrsi2d_seg *Calculate the partial volume estimates for each voxel in a 2D MRSI dataset.*

Description

Localisation is assumed to be perfect in the z direction and determined by the ker input in the x-y direction.

Usage

```
get_mrsi2d_seg(mrs_data, mri_seg, ker)
```

Arguments

mrs_data	2D MRSI data with multiple voxels in the x-y dimension.
mri_seg	MRI data with values corresponding to the segmentation class. Must be 1mm isotropic resolution.
ker	MRSI PSF kernel in the x-y direction compatible with the mmand package, eg: mmand::shapeKernel(c(10, 10), type = "box").

Value

a data frame of partial volume estimates and individual segmentation maps.

get_mrsi_voi *Generate a MRSI VOI from an* mrs_data *object.*

Description

Generate a MRSI VOI from an mrs_data object.

Usage

```
get_mrsi_voi(mrs_data, target_mri = NULL, map = NULL, ker = mmand::boxKernel())
```

Arguments

mrs_data	MRS data.
target_mri	optional image data to match the intended volume space.
map	optional voi intensity map.
ker	kernel to rescale the map data to the target_mri. Default value is mmand::boxKernel(), use mmand::mnKernel() for a smoothed map.

Value

volume data as a nifti object.

get_mrsi_voxel *Generate a MRSI voxel from an* mrs_data *object.*

Description

Generate a MRSI voxel from an mrs_data object.

Usage

```
get_mrsi_voxel(mrs_data, target_mri, x_pos, y_pos, z_pos)
```

Arguments

mrs_data	MRS data.
target_mri	optional image data to match the intended volume space.
x_pos	x voxel coordinate.
y_pos	y voxel coordinate.
z_pos	z voxel coordinate.

Value

volume data as a nifti object.

get_mrsi_voxel_xy_psf *Generate a MRSI voxel PSF from an* mrs_data *object.*

Description

Generate a MRSI voxel PSF from an mrs_data object.

Usage

```
get_mrsi_voxel_xy_psf(mrs_data, target_mri, x_pos, y_pos, z_pos)
```

Arguments

mrs_data	MRS data.
target_mri	optional image data to match the intended volume space.
x_pos	x voxel coordinate.
y_pos	y voxel coordinate.
z_pos	z voxel coordinate.

Value

volume data as a nifti object.

get_mrs_affine *Generate an affine for nifti generation.*

Description

Generate an affine for nifti generation.

Usage

```
get_mrs_affine(mrs_data, x_pos = 1, y_pos = 1, z_pos = 1)
```

Arguments

mrs_data	input data.
x_pos	x_position coordinate.
y_pos	y_position coordinate.
z_pos	z_position coordinate.

Value

affine matrix.

get_odd_dyns *Return odd numbered dynamic scans starting from 1 (1,3,5...).*

Description

Return odd numbered dynamic scans starting from 1 (1,3,5...).

Usage

```
get_odd_dyns(mrs_data)
```

Arguments

mrs_data	dynamic MRS data.

Value

dynamic MRS data containing odd numbered scans.

get_ref — *Extract the reference component from an mrs_data object.*

Description

Extract the reference component from an mrs_data object.

Usage

```
get_ref(mrs_data)
```

Arguments

mrs_data	MRS data.

Value

reference component.

get_seg_ind — *Get the indices of data points lying between two values (end > x > start).*

Description

Get the indices of data points lying between two values (end > x > start).

Usage

```
get_seg_ind(scale, start, end)
```

Arguments

scale	full list of values.
start	smallest value in the subset.
end	largest value in the subset.

Value

set of indices.

get_sh_dyns *Return the second half of a dynamic series.*

Description

Return the second half of a dynamic series.

Usage

```
get_sh_dyns(mrs_data)
```

Arguments

mrs_data	dynamic MRS data.

Value

second half of the dynamic series.

get_slice *Return a single slice from a larger MRSI dataset.*

Description

Return a single slice from a larger MRSI dataset.

Usage

```
get_slice(mrs_data, z_pos)
```

Arguments

mrs_data	MRSI data.
z_pos	the z index to extract.

Value

MRS data.

get_spant_resources_dir *Return the spant resources directory.*

Description

Usually used to store additional software, datasets and templates. An attempt will be made to create the folder if not found. The default resources directory is "spant_resources" located in the users HOME directory.

Usage

```
get_spant_resources_dir()
```

Value

full path to the spant resources directory.

get_spin_num *Return the spin number for a given nucleus.*

Description

Return the spin number for a given nucleus.

Usage

```
get_spin_num(nucleus)
```

Arguments

nucleus	nucleus name, eg "1H".

Value

spin number.

`get_subset` *Extract a subset of MRS data.*

Description

Extract a subset of MRS data.

Usage

```
get_subset(
  mrs_data,
  x_set = NULL,
  y_set = NULL,
  z_set = NULL,
  dyn_set = NULL,
  coil_set = NULL,
  fd_set = NULL,
  td_set = NULL
)
```

Arguments

`mrs_data`	MRS data object.
`x_set`	x indices to include in the output (default all).
`y_set`	y indices to include in the output (default all).
`z_set`	z indices to include in the output (default all).
`dyn_set`	dynamic indices to include in the output (default all).
`coil_set`	coil indices to include in the output (default all).
`fd_set`	frequency domain data indices to include in the output (default all).
`td_set`	time-domain indices to include in the output (default all).

Value

selected subset of MRS data.

get_svs_voi *Generate a SVS acquisition volume from an* mrs_data *object.*

Description

Generate a SVS acquisition volume from an mrs_data object.

Usage

```
get_svs_voi(mrs_data, target_mri)
```

Arguments

mrs_data	MRS data.
target_mri	optional image data to match the intended volume space.

Value

volume data as a nifti object.

get_tail_dyns *Return the last scans of a dynamic series.*

Description

Return the last scans of a dynamic series.

Usage

```
get_tail_dyns(mrs_data, n = 1)
```

Arguments

mrs_data	dynamic MRS data.
n	the number of dynamic scans to return.

Value

last scans of a dynamic series.

get_td_amp *Return an array of amplitudes derived from fitting the initial points in the time domain and extrapolating back to t=0.*

Description

Return an array of amplitudes derived from fitting the initial points in the time domain and extrapolating back to t=0.

Usage

```
get_td_amp(mrs_data, nstart = 10, nend = 50, method = "poly")
```

Arguments

mrs_data	MRS data.
nstart	first data point to fit.
nend	last data point to fit.
method	method for measuring the amplitude, one of "poly", spline" or exp".

Value

array of amplitudes.

get_tqn_cmd *Print the command to run the TARQUIN command-line program.*

Description

Print the command to run the TARQUIN command-line program.

Usage

```
get_tqn_cmd()
```

get_uncoupled_mol *Generate a* mol_parameters *object for a simple spin system with one resonance.*

Description

Generate a mol_parameters object for a simple spin system with one resonance.

Usage

```
get_uncoupled_mol(
  name,
  chem_shift,
  nucleus,
  scale_factor,
  lw,
  lg,
  full_name = NULL
)
```

Arguments

name	abbreviated name of the molecule.
chem_shift	chemical shift of the resonance (PPM).
nucleus	nucleus (1H, 31P...).
scale_factor	multiplicative scaling factor. Note, this value can be made complex to adjust the phase of the resonance.
lw	linewidth in Hz.
lg	Lorentz-Gauss lineshape parameter (between 0 and 1).
full_name	long name of the molecule (optional).

Value

mol_parameters object.

get_voi_cog *Calculate the centre of gravity for an image containing 0 and 1's.*

Description

Calculate the centre of gravity for an image containing 0 and 1's.

Usage

```
get_voi_cog(voi)
```

Arguments

voi	nifti object.

Value

triplet of x,y,z coordinates.

---

get_voi_seg *Return the white matter, gray matter and CSF composition of a volume.*

Description

Return the white matter, gray matter and CSF composition of a volume.

Usage

```
get_voi_seg(voi, mri_seg)
```

Arguments

voi	volume data as a nifti object.
mri_seg	segmented brain volume as a nifti object.

Value

a vector of partial volumes expressed as percentages.

---

get_voi_seg_psf *Return the white matter, gray matter and CSF composition of a volume.*

Description

Return the white matter, gray matter and CSF composition of a volume.

Usage

```
get_voi_seg_psf(psf, mri_seg)
```

Arguments

psf	volume data as a nifti object.
mri_seg	segmented brain volume as a nifti object.

Value

a vector of partial volumes expressed as percentages.

get_voxel *Return a single voxel from a larger mrs dataset.*

Description

Return a single voxel from a larger mrs dataset.

Usage

```
get_voxel(mrs_data, x_pos = 1, y_pos = 1, z_pos = 1, dyn = 1, coil = 1)
```

Arguments

mrs_data	MRS data.
x_pos	the x index to plot.
y_pos	the y index to plot.
z_pos	the z index to plot.
dyn	the dynamic index to plot.
coil	the coil element number to plot.

Value

MRS data.

glm_spec *Perform a GLM analysis of dynamic MRS data in the spectral domain.*

Description

Perform a GLM analysis of dynamic MRS data in the spectral domain.

Usage

```
glm_spec(mrs_data, regressor_df, full_output = FALSE)
```

Arguments

mrs_data	single-voxel dynamics MRS data.
regressor_df	a data frame containing temporal regressors to be applied to each spectral datapoint.
full_output	append mrs_data and regressor_df to the output list.

Value

list of statistical results.

`glm_spec_fmrs_fl` *Perform first-level spectral GLM analysis of an fMRS dataset.*

Description

Perform first-level spectral GLM analysis of an fMRS dataset.

Usage

```
glm_spec_fmrs_fl(
  regressor_df,
  analysis_dir = "spant_analysis",
  output_dir = "spec_glm",
  exclude_labels = NULL,
  labels = NULL,
  xlim = c(4, 0.2),
  vline = c(1.35, 1.28, 2.35, 2.29),
  lb = 4,
  return_results = FALSE
)
```

Arguments

`regressor_df`	a data frame containing temporal regressors to be applied to each spectral datapoint.
`analysis_dir`	directory containing preprocessed data generated by the preproc_svs_dataset function.
`output_dir`	directory to save glm results.
`exclude_labels`	vector of labels of scans to exclude, eg poor quality data.
`labels`	labels to describe each data set.
`xlim`	spectral range to include in the analysis.
`vline`	vertical lines to add to the plot.
`lb`	linebroading to add in Hz before GLM analysis.
`return_results`	function will return key outputs, defaults to FALSE.

glm_spec_fmrs_group *Perform group-level spectral GLM analysis of an fMRS dataset.*

Description

Perform group-level spectral GLM analysis of an fMRS dataset.

Usage

```
glm_spec_fmrs_group(
  regressor_df,
  analysis_dir = "spant_analysis",
  exclude_labels = NULL,
  labels = NULL
)
```

Arguments

regressor_df	a data frame containing temporal regressors to be applied to each spectral datapoint.
analysis_dir	directory containing preprocessed data generated by the preproc_svs_dataset function.
exclude_labels	vector of labels of scans to exclude, eg poor quality data.
labels	labels to describe each data set.

glm_spec_group_linhyp *Test a group-level spectral GLM linear hypothesis.*

Description

Test a group-level spectral GLM linear hypothesis.

Usage

```
glm_spec_group_linhyp(hmat, analysis_dir = "spant_analysis")
```

Arguments

hmat	linear hypothesis matrix.
analysis_dir	directory containing preprocessed data generated by the preproc_svs_dataset function.

gridplot *Arrange spectral plots in a grid.*

Description

Arrange spectral plots in a grid.

Usage

```
gridplot(x, ...)
```

Arguments

x	object for plotting.
...	arguments to be passed to methods.

gridplot.mrs_data *Arrange spectral plots in a grid.*

Description

Arrange spectral plots in a grid.

Usage

```
## S3 method for class 'mrs_data'
gridplot(
  x,
  rows = NA,
  cols = NA,
  mar = c(0, 0, 0, 0),
  oma = c(3.5, 1, 1, 1),
  bty = "o",
  restore_def_par = TRUE,
  ...
)
```

Arguments

x	object of class mrs_data.
rows	number of grid rows.
cols	number of grid columns.
mar	option to adjust the plot margins. See ?par.
oma	outer margin area.

bty	option to draw a box around the plot. See ?par.
restore_def_par	restore default plotting par values after the plot has been made.
...	other arguments to pass to the plot method.

`grid_shift_xy` *Grid shift MRSI data in the x/y dimension.*

Description

Grid shift MRSI data in the x/y dimension.

Usage

```
grid_shift_xy(mrs_data, x_shift, y_shift)
```

Arguments

mrs_data	MRSI data in the spatial domain.
x_shift	shift to apply in the x-direction in units of voxels.
y_shift	shift to apply in the y-direction in units of voxels.

Value

shifted data.

`hsvd` *HSVD of an mrs_data object.*

Description

HSVD method as described in: Barkhuijsen H, de Beer R, van Ormondt D. Improved algorithm for noniterative and timedomain model fitting to exponentially damped magnetic resonance signals. J Magn Reson 1987;73:553-557.

Usage

```
hsvd(mrs_data, comps = 40, irlba = TRUE, max_damp = 10)
```

Arguments

mrs_data	mrs_data object to be decomposed.
comps	number of Lorentzian components to use for modelling.
irlba	option to use irlba SVD (logical).
max_damp	maximum allowable damping factor.

Value

basis matrix and signal table.

`hsvd_filt` *HSVD based signal filter.*

Description

HSVD based signal filter described in: Barkhuijsen H, de Beer R, van Ormondt D. Improved algorithm for noniterative and timedomain model fitting to exponentially damped magnetic resonance signals. J Magn Reson 1987;73:553-557.

Usage

```
hsvd_filt(
  mrs_data,
  xlim = c(-30, 30),
  comps = 40,
  irlba = TRUE,
  max_damp = 10,
  scale = "hz",
  return_model = FALSE
)
```

Arguments

`mrs_data`	MRS data to be filtered.
`xlim`	frequency range to filter, default units are Hz which can be changed to ppm using the "scale" argument.
`comps`	number of Lorentzian components to use for modelling.
`irlba`	option to use irlba SVD (logical).
`max_damp`	maximum allowable damping factor.
`scale`	either "hz" or "ppm" to set the frequency units of xlim.
`return_model`	by default the filtered spectrum is returned. Set return_model to TRUE to return the HSVD model of the data.

Value

filtered data or model depending on the return_model argument.

hsvd_vec *HSVD of a complex vector.*

Description

HSVD method as described in: Barkhuijsen H, de Beer R, van Ormondt D. Improved algorithm for noniterative and timedomain model fitting to exponentially damped magnetic resonance signals. J Magn Reson 1987;73:553-557.

Usage

```
hsvd_vec(y, fs, comps = 40, irlba = TRUE, max_damp = 0)
```

Arguments

y	time domain signal to be filtered as a vector.
fs	sampling frequency of y.
comps	number of Lorentzian components to use for modelling.
irlba	option to use irlba SVD (logical).
max_damp	maximum allowable damping factor. Default value of 0 ensures resultant model is damped.

Value

basis matrix and signal table.

hz *Return the frequency scale of an MRS dataset in Hz.*

Description

Return the frequency scale of an MRS dataset in Hz.

Usage

```
hz(mrs_data, fs = NULL, N = NULL)
```

Arguments

mrs_data	MRS data.
fs	sampling frequency in Hz.
N	number of data points in the spectral dimension.

Value

frequency scale.

ift_shift — *Perform an iffshift and ifft on a vector.*

Description

Perform an iffshift and ifft on a vector.

Usage

```
ift_shift(vec_in)
```

Arguments

vec_in	vector input.

Value

output vector.

ift_shift_mat — *Perform an ifft and ifftshift on a matrix with each column replaced by its shifted ifft.*

Description

Perform an ifft and ifftshift on a matrix with each column replaced by its shifted ifft.

Usage

```
ift_shift_mat(mat_in)
```

Arguments

mat_in	matrix input.

Value

output matrix.

Im.mrs_data *Apply Im operator to an MRS dataset.*

Description

Apply Im operator to an MRS dataset.

Usage

```
## S3 method for class 'mrs_data'
Im(z)
```

Arguments

z	MRS data.

Value

MRS data following Im operator.

image.mrs_data *Image plot method for objects of class mrs_data.*

Description

Image plot method for objects of class mrs_data.

Usage

```
## S3 method for class 'mrs_data'
image(
  x,
  xlim = NULL,
  mode = "re",
  col = NULL,
  plot_dim = NULL,
  x_pos = NULL,
  y_pos = NULL,
  z_pos = NULL,
  dyn = 1,
  coil = 1,
  restore_def_par = TRUE,
  y_ticks = NULL,
  hline = NULL,
  hline_lty = 2,
  hline_col = "white",
```

```
  vline = NULL,
  vline_lty = 2,
  vline_col = "white",
  legend = FALSE,
  ...
)
```

Arguments

x	object of class mrs_data.
xlim	the range of values to display on the x-axis, eg xlim = c(4,1).
mode	representation of the complex numbers to be plotted, can be one of: "re", "im", "mod" or "arg".
col	Colour map to use, defaults to viridis.
plot_dim	the dimension to display on the y-axis, can be one of: "dyn", "time_sec", x", "y", "z", "coil" or NULL. If NULL (the default) all spectra are collapsed into the dynamic dimension and displayed.
x_pos	the x index to plot.
y_pos	the y index to plot.
z_pos	the z index to plot.
dyn	the dynamic index to plot.
coil	the coil element number to plot.
restore_def_par	restore default plotting par values after the plot has been made.
y_ticks	a vector of indices specifying where to place additional red tick marks.
hline	add a horizontal line at the specified value.
hline_lty	linetype for the horizontal line.
hline_col	colour for the horizontal line.
vline	add a vertical line at the specified value.
vline_lty	linetype for the vertical line.
vline_col	colour for the vertical line.
legend	add a colour bar to the plot using the imagePlot function from the fields package.
...	other arguments to pass to the plot method.

img2kspace_xy *Transform 2D MRSI data to k-space in the x-y direction.*

Description

Transform 2D MRSI data to k-space in the x-y direction.

Usage

```
img2kspace_xy(mrs_data)
```

Arguments

mrs_data	2D MRSI data.

Value

k-space data.

Imzap *Complex rounding function taken from complexplus package to reduce the number of spant dependencies.*

Description

Complex rounding function taken from complexplus package to reduce the number of spant dependencies.

Usage

```
Imzap(x, tol = 1e-06)
```

Arguments

x	a scalar or vector, real or complex.
tol	a tolerance, 10^-6 by default. Prevents possible numerical problems. Can be set to 0 if desired.

install_ants *Install ANTs / ANTsX from : https://github.com/ANTsX/ANTs/releases*

Description

Install ANTs / ANTsX from : https://github.com/ANTsX/ANTs/releases

Usage

```
install_ants(platform, version = "2.6.5")
```

Arguments

platform	see the releases page for supported platforms. Common platforms include : "macos-14-ARM64-clang", "almalinux9-X64-gcc", "centos7-X64-gcc" or "ubuntu-24.04-X64-gcc". Note, It may be necessary to increase the timeout with "options(timeout = 1000)" on slower connections.
version	ANTs version to install, defaults to "2.6.5".

install_cli *Install the spant command-line interface scripts to a system path.*

Description

This should be run following each new install of spant to ensure consistency. Typical command line usage : sudo Rscript -e "spant::install_cli()"

Usage

```
install_cli(path = NULL)
```

Arguments

path	optional path to install the scripts. Defaults to : "/usr/local/bin".

install_faceoff *Install FaceOff from : https://github.com/srikash/FaceOff, requires ANTs to be installed to work.*

Description

Install FaceOff from : https://github.com/srikash/FaceOff, requires ANTs to be installed to work.

Usage

```
install_faceoff()
```

install_oasis_template *Install the Oasis brain template from : https://doi.org/10.6084/m9.figshare.915436.v2*

Description

Install the Oasis brain template from : https://doi.org/10.6084/m9.figshare.915436.v2

Usage

```
install_oasis_template()
```

interleave_dyns *Interleave the first and second half of a dynamic series.*

Description

Interleave the first and second half of a dynamic series.

Usage

```
interleave_dyns(mrs_data)
```

Arguments

mrs_data	dynamic MRS data.

Value

interleaved data.

int_spec *Integrate a spectral region.*

Description

See spec_op function for a more complete set of spectral operations.

Usage

```
int_spec(mrs_data, xlim = NULL, freq_scale = "ppm", mode = "re")
```

Arguments

mrs_data	MRS data.
xlim	spectral range to be integrated (defaults to full range).
freq_scale	units of xlim, can be : "ppm", "hz" or "points".
mode	spectral mode, can be : "re", "im", "mod" or "cplx".

Value

an array of integral values.

inv_even_dyns *Invert even numbered dynamic scans starting from 1 (2,4,6...).*

Description

Invert even numbered dynamic scans starting from 1 (2,4,6...).

Usage

```
inv_even_dyns(mrs_data)
```

Arguments

mrs_data	dynamic MRS data.

Value

dynamic MRS data with inverted even numbered scans.

inv_odd_dyns *Invert odd numbered dynamic scans starting from 1 (1,3,5...).*

Description

Invert odd numbered dynamic scans starting from 1 (1,3,5...).

Usage

```
inv_odd_dyns(mrs_data)
```

Arguments

mrs_data	dynamic MRS data.

Value

dynamic MRS data with inverted odd numbered scans.

is.def *Check if an object is defined, which is the same as being not NULL.*

Description

Check if an object is defined, which is the same as being not NULL.

Usage

```
is.def(x)
```

Arguments

x	object to test for being NULL.

Value

logical value.

is_fd

Check if the chemical shift dimension of an MRS data object is in the frequency domain.

Description

Check if the chemical shift dimension of an MRS data object is in the frequency domain.

Usage

```
is_fd(mrs_data)
```

Arguments

mrs_data	MRS data.

Value

logical value.

kspace2img_xy

Transform 2D MRSI data from k-space to image space in the x-y direction.

Description

Transform 2D MRSI data from k-space to image space in the x-y direction.

Usage

```
kspace2img_xy(mrs_data)
```

Arguments

mrs_data	2D MRSI data.

Value

MRSI data in image space.

`l2_reg` *Perform l2 regularisation artefact suppression.*

Description

Perform l2 regularisation artefact suppression using the method proposed by Bilgic et al. JMRI 40(1):181-91 2014.

Usage

```
l2_reg(
  mrs_data,
  thresh = 0.05,
  b = 1e-11,
  A = NA,
  xlim = NA,
  thresh_xlim = NULL,
  A_append = NULL,
  ret_norms = FALSE
)
```

Arguments

`mrs_data`	input data for artefact suppression.
`thresh`	threshold parameter to extract lipid signals from mrs_data based on the spectral integration of the thresh_xlim region in magnitude mode.
`b`	regularisation parameter.
`A`	set of spectra containing the artefact basis signals. The thresh parameter is ignored when A is specified.
`xlim`	spectral limits in ppm to restrict the reconstruction range. Defaults to the full spectral width.
`thresh_xlim`	spectral limits in ppm to integrate for the threshold map.
`A_append`	additional spectra to append to the A basis.
`ret_norms`	return the residual norm and solution norms.

Value

l2 reconstructed mrs_data object.

lb — *Apply line-broadening (apodisation) to MRS data or basis object.*

Description

Apply line-broadening (apodisation) to MRS data or basis object.

Usage

```
lb(x, lb, lg = 1)

## S3 method for class 'list'
lb(x, lb, lg = 1)

## S3 method for class 'mrs_data'
lb(x, lb, lg = 1)

## S3 method for class 'basis_set'
lb(x, lb, lg = 1)
```

Arguments

x	input mrs_data or basis_set object.
lb	amount of line-broadening in Hz.
lg	Lorentz-Gauss lineshape parameter (between 0 and 1).

Value

line-broadened data.

lb_renoise — *Apply line-broadening to dynamic MRS data and add normally distributed noise (renoise) to reverse any associated improvement in SNR.*

Description

This function mimics a strategy used by : "Bednařík P, Tkáč I, Giove F, DiNuzzo M, Deelchand DK, Emir UE, Eberly LE, Mangia S. Neurochemical and BOLD responses during neuronal activation measured in the human visual cortex at 7 Tesla. J Cereb Blood Flow Metab. 2015 Mar 31;35(4):601-10. doi: 10.1038/jcbfm.2014.233. PMID: 25564236; PMCID: PMC4420878." Note that set.seed(XX) should be used for reproducible analyses.

Usage

```
lb_renoise(
  mrs_data,
  lb,
  lg = NULL,
  sig_region = c(4, 0.5),
  noise_region = c(-0.5, -2.5),
  p_order = 2
)
```

Arguments

mrs_data	data to be broadened.
lb	amount of line-broadening in Hz, length should be equal to the number of dynamics in mrs_data.
lg	Lorentz-Gauss lineshape parameter (between 0 and 1). Defaults to a fully Lorentzian value of 0. If one value is given, will be recycled to match the number of dynamics in mrs_data.
sig_region	a ppm region to define where the maximum signal value should be estimated.
noise_region	a ppm region to defined where the noise level should be estimated.
p_order	polynomial order to fit to the noise region before estimating the standard deviation.

Value

line-broadened and renoised data.

---

lofdc *Correct linear frequency drift.*

Description

Correct linear frequency drift.

Usage

```
lofdc(
  mrs_data,
  max_hz_s = 0.1,
  tr = NULL,
  ret_corr_only = TRUE,
  outlier_thresh = 3,
  xlim = c(4, 0.5),
  order = 1
)
```

Arguments

mrs_data	MRS data to be corrected.
max_hz_s	the maximum drift rate to search over.
tr	mrs_data repetition time.
ret_corr_only	return the corrected mrs_data object only.
outlier_thresh	threshold to remove outliers.
xlim	spectral width (in ppm) to evaluate outliers.
order	correction order.

Value

drift corrected mrs_data object.

---

lw2alpha *Covert a linewidth in Hz to an equivalent alpha value in the time-domain ie: x * exp(-t * alpha).*

Description

Covert a linewidth in Hz to an equivalent alpha value in the time-domain ie: x * exp(-t * alpha).

Usage

```
lw2alpha(lw)
```

Arguments

lw	linewidth in Hz.

Value

beta damping value.

lw2beta — *Covert a linewidth in Hz to an equivalent beta value in the time-domain ie: x * exp(-t * t * beta).*

Description

Covert a linewidth in Hz to an equivalent beta value in the time-domain ie: x * exp(-t * t * beta).

Usage

```
lw2beta(lw)
```

Arguments

lw	linewidth in Hz.

Value

beta damping value.

make_basis_from_raw — *Make a basis-set object from a directory containing LCModel formatted RAW files.*

Description

Make a basis-set object from a directory containing LCModel formatted RAW files.

Usage

```
make_basis_from_raw(dir_path, ft, fs, ref)
```

Arguments

dir_path	path to the directory containing LCModel RAW files. One file per signal.
ft	transmitter frequency in Hz.
fs	sampling frequency in Hz.
ref	reference value for ppm scale.

Value

a basis-set object.

mask_dyns *Mask an MRS dataset in the dynamic dimension.*

Description

Mask an MRS dataset in the dynamic dimension.

Usage

```
mask_dyns(mrs_data, mask)
```

Arguments

mrs_data	MRS data object.
mask	vector of boolean values specifying the dynamics to mask, where a value of TRUE indicates the spectrum should be removed.

Value

masked dataset.

mask_fit_res *Mask fit result spectra depending on a vector of bool values.*

Description

Mask fit result spectra depending on a vector of bool values.

Usage

```
mask_fit_res(fit_result, mask_vec, amps_only = FALSE)
```

Arguments

fit_result	fit result object to be masked.
mask_vec	a Boolean vector with the same number of rows as there are rows in the results table.
amps_only	only mask the amplitude and associated error estimate columns.

Value

a masked fit result object.

mask_xy *Mask an MRSI dataset in the x-y direction*

Description

Mask an MRSI dataset in the x-y direction

Usage

```
mask_xy(mrs_data, x_dim, y_dim)
```

Arguments

mrs_data	MRS data object.
x_dim	x dimension output length.
y_dim	y dimension output length.

Value

masked MRS data.

mask_xy_corners *Mask the four corners of an MRSI dataset in the x-y plane.*

Description

Mask the four corners of an MRSI dataset in the x-y plane.

Usage

```
mask_xy_corners(mrs_data)
```

Arguments

mrs_data	MRS data object.

Value

masked MRS data.

mask_xy_ellipse *Mask the voxels outside an elliptical region spanning the MRSI dataset in the x-y plane.*

Description

Mask the voxels outside an elliptical region spanning the MRSI dataset in the x-y plane.

Usage

```
mask_xy_ellipse(mrs_data)
```

Arguments

mrs_data	MRS data object.

Value

masked MRS data.

mask_xy_mat *Mask a 2D MRSI dataset in the x-y dimension.*

Description

Mask a 2D MRSI dataset in the x-y dimension.

Usage

```
mask_xy_mat(mrs_data, mask, value = NA)
```

Arguments

mrs_data	MRS data object.
mask	matrix of boolean values specifying the voxels to mask, where a value of TRUE indicates the voxel should be removed.
value	the value to set masked data to (usually NA or 0).

Value

masked dataset.

mat2mrs_data — *Convert a matrix (with spectral points in the column dimension and dynamics in the row dimensions) into a mrs_data object.*

Description

Convert a matrix (with spectral points in the column dimension and dynamics in the row dimensions) into a mrs_data object.

Usage

```
mat2mrs_data(
  mat,
  mrs_data = NULL,
  fs = NULL,
  ft = NULL,
  ref = NULL,
  nuc = NULL,
  fd = FALSE
)
```

Arguments

mat	data matrix.
mrs_data	example data to copy acquisition parameters from.
fs	sampling frequency in Hz.
ft	transmitter frequency in Hz.
ref	reference value for ppm scale.
nuc	resonant nucleus.
fd	flag to indicate if the matrix is in the frequency domain (logical).

Value

mrs_data object.

match_files — *Match files based on a vector of input paths and a glob pattern. The glob pattern is appended to each path and should match one file only.*

Description

Match files based on a vector of input paths and a glob pattern. The glob pattern is appended to each path and should match one file only.

Usage

```
match_files(paths, glob)
```

Arguments

paths	vectors of filesystem paths.
glob	pattern to append to each path before passing to Sys.glob.

Value

matched files. NA values correspond to either no match or multiple matches.

---

match_lineshape *Apply Voigt line-broadening to match a reference spectrum.*

Description

Apply Voigt line-broadening to match a reference spectrum.

Usage

```
match_lineshape(
  mrs_data,
  ref,
  xlim,
  init_lb = 0.2,
  init_lg = 0.5,
  init_amp = 1,
  min_lb = 0,
  max_lb = Inf,
  min_lg = 0,
  max_lg = 1,
  min_amp = 0.1,
  max_amp = 2,
  amp_optim = TRUE
)
```

Arguments

mrs_data	data to be broadened, note the linewidth of this spectrum must be narrower than the ref spectrum.
ref	reference data to match.
xlim	spectral region to match, eg c(5.2, 4.1) could be used to match two water resonances.
init_lb	initial value for the amount of line-broadening to apply (Hz).

init_lg	initial value for the Lorentz-Gauss lineshape parameter.
init_amp	initial value for the amplitude parameter.
min_lb	minimum value for the amount of line-broadening to apply (Hz).
max_lb	maximum value for the amount of line-broadening to apply (Hz).
min_lg	minimum value for the Lorentz-Gauss lineshape parameter.
max_lg	maximum value for the Lorentz-Gauss lineshape parameter.
min_amp	minimum value for the amplitude parameter.
max_amp	maximum value for the amplitude parameter.
amp_optim	flag to include amplitude adjustment in the optimisation procedure. Defaults to TRUE.

Value

a list containing the matched mrs_data, difference spectra and optimisation results.

---

matexp *Matrix exponential function taken from complexplus package to reduce the number of spant dependencies.*

Description

Matrix exponential function taken from complexplus package to reduce the number of spant dependencies.

Usage

```
matexp(x)
```

Arguments

x	a square complex matrix.

Value

the matrix exponential of x.

max_mrs — *Apply the max operator to an MRS dataset.*

Description

Apply the max operator to an MRS dataset.

Usage

```
max_mrs(mrs_data)
```

Arguments

mrs_data	MRS data.

Value

MRS data following max operator.

max_mrs_interp — *Apply the max operator to an interpolated MRS dataset.*

Description

Apply the max operator to an interpolated MRS dataset.

Usage

```
max_mrs_interp(mrs_data, interp_f = 4)
```

Arguments

mrs_data	MRS data.
interp_f	interpolation factor.

Value

Array of maximum values (real only).

mean.list *Calculate the mean spectrum from an mrs_data object.*

Description

Calculate the mean spectrum from an mrs_data object.

Usage

```
## S3 method for class 'list'
mean(x, ...)
```

Arguments

x	object of class mrs_data.
...	other arguments to pass to the colMeans function.

Value

mean mrs_data object.

mean.mrs_data *Calculate the mean spectrum from an mrs_data object.*

Description

Calculate the mean spectrum from an mrs_data object.

Usage

```
## S3 method for class 'mrs_data'
mean(x, ...)
```

Arguments

x	object of class mrs_data.
...	other arguments to pass to the colMeans function.

Value

mean mrs_data object.

mean_dyns *Calculate the mean dynamic data.*

Description

Calculate the mean dynamic data.

Usage

```
mean_dyns(mrs_data, subset = NULL)
```

Arguments

mrs_data	dynamic MRS data.
subset	vector containing indices to the dynamic scans to be averaged.

Value

mean dynamic data.

mean_dyns_scheme *Average sets of dynamics according to a scheme vector.*

Description

Average sets of dynamics according to a scheme vector.

Usage

```
mean_dyns_scheme(mrs_data, av_scheme)
```

Arguments

mrs_data	dynamic MRS data.
av_scheme	vector containing consecutive integer values (starting at 1) representing sets of dynamics to average. This vector must have the same length as the number of dynamic scans in mrs_data. Any elements set to NA will not contribute to averaging.

Value

Dynamic MRS data set containing the averaged dynamic sets.

mean_dyn_blocks *Calculate the mean of adjacent dynamic scans.*

Description

Calculate the mean of adjacent dynamic scans.

Usage

```
mean_dyn_blocks(mrs_data, block_size)
```

Arguments

mrs_data	dynamic MRS data.
block_size	number of adjacent dynamics scans to average over.

Value

dynamic data averaged in blocks.

mean_dyn_pairs *Calculate the pairwise means across a dynamic data set.*

Description

Calculate the pairwise means across a dynamic data set.

Usage

```
mean_dyn_pairs(mrs_data)
```

Arguments

mrs_data	dynamic MRS data.

Value

mean dynamic data of adjacent dynamic pairs.

mean_mrs_list *Return the mean of a list of mrs_data objects.*

Description

Return the mean of a list of mrs_data objects.

Usage

```
mean_mrs_list(mrs_list)
```

Arguments

mrs_list	list of mrs_data objects.

Value

mean mrs_data object.

mean_vec_blocks *Calculate the mean of adjacent blocks in a vector.*

Description

Calculate the mean of adjacent blocks in a vector.

Usage

```
mean_vec_blocks(x, block_size)
```

Arguments

x	input vector.
block_size	number of adjacent elements to average over.

Value

vector data averaged in blocks.

median_dyns *Calculate the median dynamic data.*

Description

Calculate the median dynamic data.

Usage

```
median_dyns(mrs_data)
```

Arguments

mrs_data	dynamic MRS data.

Value

median dynamic data.

Mod.mrs_data *Apply Mod operator to an MRS dataset.*

Description

Apply Mod operator to an MRS dataset.

Usage

```
## S3 method for class 'mrs_data'
Mod(z)
```

Arguments

z	MRS data.

Value

MRS data following Mod operator.

mod_td — *Apply the Modulus operator to the time-domain MRS signal.*

Description

Apply the Modulus operator to the time-domain MRS signal.

Usage

```
mod_td(mrs_data)
```

Arguments

mrs_data	MRS data input.

Value

time-domain modulus of input.

mrs_data2basis — *Convert an mrs_data object to basis object - where basis signals are spread across the dynamic dimension in the MRS data.*

Description

Convert an mrs_data object to basis object - where basis signals are spread across the dynamic dimension in the MRS data.

Usage

```
mrs_data2basis(mrs_data, names)
```

Arguments

mrs_data	mrs_data object with basis signals spread across the dynamic dimension.
names	list of names corresponding to basis signals.

Value

basis set object.

`mrs_data2bids` *Create a BIDS file structure from a vector of MRS data paths or list of mrs_data objects.*

Description

Create a BIDS file structure from a vector of MRS data paths or list of mrs_data objects.

Usage

```
mrs_data2bids(
  mrs_data,
  output_dir,
  suffix = NULL,
  sub = NULL,
  ses = NULL,
  task = NULL,
  acq = NULL,
  nuc = NULL,
  voi = NULL,
  rec = NULL,
  run = NULL,
  echo = NULL,
  inv = NULL,
  skip_existing = TRUE
)
```

Arguments

`mrs_data`	vector of MRS data paths or list of mrs_data objects.
`output_dir`	the base directory to create the BIDS structure.
`suffix`	optional vector of file suffixes. Default behaviour is to automatically determine these from the input data, however it is recommended that they are specified to allow more efficient skipping of existing data.
`sub`	optional vector of subject labels. If not specified, these will be automatically generated as a series of increasing zero-padded integer values corresponding to the mrs_data input indices.
`ses`	optional vector of session labels.
`task`	optional vector of task labels.
`acq`	optional vector of acquisition labels.
`nuc`	optional vector of nucleus labels.
`voi`	optional vector of volume of interest labels.
`rec`	optional vector of reconstruction labels.
`run`	optional vector of run indices.

echo	optional vector of echo time indices.
inv	optional vector of inversion indices.
skip_existing	skip any data files that have already been converted. Defaults to TRUE, set to FALSE to force an overwrite of any existing data files.

`mrs_data2list` *Split MRS data containing multiple spectra into a list of single spectra datasets.*

Description

Split MRS data containing multiple spectra into a list of single spectra datasets.

Usage

```
mrs_data2list(mrs_data)
```

Arguments

mrs_data	input MRS dataset

Value

list of MRS datasets

`mrs_data2mat` *Convert mrs_data object to a matrix, with spectral points in the column dimension and dynamics in the row dimension.*

Description

Convert mrs_data object to a matrix, with spectral points in the column dimension and dynamics in the row dimension.

Usage

```
mrs_data2mat(mrs_data, collapse = TRUE)
```

Arguments

mrs_data	MRS data object or list of MRS data objects.
collapse	collapse all other dimensions along the dynamic dimension, eg a 16x16 MRSI grid would be first collapsed across 256 dynamic scans.

Value

MRS data matrix.

mrs_data2spec_mat *Convert mrs_data object to a matrix, with spectral points in the column dimension and dynamics in the row dimension.*

Description

Convert mrs_data object to a matrix, with spectral points in the column dimension and dynamics in the row dimension.

Usage

```
mrs_data2spec_mat(mrs_data, collapse = TRUE)
```

Arguments

mrs_data	MRS data object or list of MRS data objects.
collapse	collapse all other dimensions along the dynamic dimension, eg a 16x16 MRSI grid would be first collapsed across 256 dynamic scans.

Value

MRS data matrix.

mrs_data2vec *Convert mrs_data object to a vector.*

Description

Convert mrs_data object to a vector.

Usage

```
mrs_data2vec(mrs_data, dyn = 1, x_pos = 1, y_pos = 1, z_pos = 1, coil = 1)
```

Arguments

mrs_data	MRS data object.
dyn	dynamic index.
x_pos	x index.
y_pos	y index.
z_pos	z index.
coil	coil element index.

Value

MRS data vector.

mr_data2bids *Create a BIDS file structure from a vector of data paths or list of mri/mrs data objects.*

Description

Create a BIDS file structure from a vector of data paths or list of mri/mrs data objects.

Usage

```
mr_data2bids(
  mr_data,
  suffix,
  output_dir,
  sub = NULL,
  ses = NULL,
  task = NULL,
  acq = NULL,
  nuc = NULL,
  voi = NULL,
  rec = NULL,
  run = NULL,
  echo = NULL,
  inv = NULL,
  skip_existing = TRUE,
  mri_format = "nifti",
  deface_mri = FALSE
)
```

Arguments

mr_data	vector of data paths or list of mri/mrs objects.
suffix	vector of file suffixes, eg : c("svs", "mrsi", "T1w).
output_dir	the base directory to create the BIDS structure.
sub	optional vector of subject labels. If not specified, these will be automatically generated as a series of increasing zero-padded integer values corresponding to the mrs_data input indices.
ses	optional vector of session labels.
task	optional vector of task labels.
acq	optional vector of acquisition labels.
nuc	optional vector of nucleus labels.
voi	optional vector of volume of interest labels.
rec	optional vector of reconstruction labels.
run	optional vector of run indices.

echo	optional vector of echo time indices.
inv	optional vector of inversion indices.
skip_existing	skip any data files that have already been converted. Defaults to TRUE, set to FALSE to force an overwrite of any existing data files.
mri_format	defaults to "nifti", can also be "dicom" provided the divest package is installed.
deface_mri	option to apply fsl_deface to the mri as a preprocessing step. Defaults to FALSE, requires ANTs and faceoff to be installed when TRUE.

`mvfftshift` *Perform a fftshift on a matrix, with each column replaced by its shifted result.*

Description

Perform a fftshift on a matrix, with each column replaced by its shifted result.

Usage

```
mvfftshift(x)
```

Arguments

x	matrix input.

Value

output matrix.

`mvifftshift` *Perform an ifftshift on a matrix, with each column replaced by its shifted result.*

Description

Perform an ifftshift on a matrix, with each column replaced by its shifted result.

Usage

```
mvifftshift(x)
```

Arguments

x	matrix input.

Value

output matrix.

n2coord *Print fit coordinates from a single index.*

Description

Print fit coordinates from a single index.

Usage

```
n2coord(n, fit_res)
```

Arguments

n	fit index.
fit_res	fit_result object.

Ncoils *Return the total number of coil elements in an MRS dataset.*

Description

Return the total number of coil elements in an MRS dataset.

Usage

```
Ncoils(mrs_data)
```

Arguments

mrs_data	MRS data.

Ndyns *Return the total number of dynamic scans in an MRS dataset.*

Description

Return the total number of dynamic scans in an MRS dataset.

Usage

```
Ndyns(mrs_data)
```

Arguments

mrs_data	MRS data.

`nifti_flip_lr` *Flip the x data dimension order of a nifti image. This corresponds to flipping MRI data in the left-right direction, assuming the data in save in neurological format (can check with fslorient program).*

Description

Flip the x data dimension order of a nifti image. This corresponds to flipping MRI data in the left-right direction, assuming the data in save in neurological format (can check with fslorient program).

Usage

```
nifti_flip_lr(x)
```

Arguments

`x`	nifti object to be processed.

Value

nifti object with reversed x data direction.

`Npts` *Return the number of data points in an MRS dataset.*

Description

Return the number of data points in an MRS dataset.

Usage

```
Npts(mrs_data)
```

Arguments

`mrs_data`	MRS data.

Value

number of data points.

Nspec — *Return the total number of spectra in an MRS dataset.*

Description

Return the total number of spectra in an MRS dataset.

Usage

```
Nspec(mrs_data)
```

Arguments

mrs_data	MRS data.

Ntrans — *Return the total number of acquired transients for an MRS dataset.*

Description

Return the total number of acquired transients for an MRS dataset.

Usage

```
Ntrans(mrs_data)
```

Arguments

mrs_data	MRS data.

Nx — *Return the total number of x locations in an MRS dataset.*

Description

Return the total number of x locations in an MRS dataset.

Usage

```
Nx(mrs_data)
```

Arguments

mrs_data	MRS data.

Ny — *Return the total number of y locations in an MRS dataset.*

Description

Return the total number of y locations in an MRS dataset.

Usage

```
Ny(mrs_data)
```

Arguments

mrs_data	MRS data.

Nz — *Return the total number of z locations in an MRS dataset.*

Description

Return the total number of z locations in an MRS dataset.

Usage

```
Nz(mrs_data)
```

Arguments

mrs_data	MRS data.

one_page_pdf — *Export a one-page pdf of a single fit result*

Description

Export a one-page pdf of a single fit result

Usage

```
one_page_pdf(fit_res, pdf_out_path, title = NULL)
```

Arguments

fit_res	fit_result object.
pdf_out_path	path to the exported pdf file.
title	output title.

ortho3 *Display an orthographic projection plot of a nifti object.*

Description

Display an orthographic projection plot of a nifti object.

Usage

```
ortho3(
  underlay,
  overlay = NULL,
  xyz = NULL,
  zlim = NULL,
  zlim_ol = NULL,
  alpha = 0.7,
  col_ol = viridisLite::viridis(64),
  orient_lab = TRUE,
  rescale = 1,
  crosshairs = TRUE,
  ch_lwd = 1,
  colourbar = TRUE,
  bg = "black",
  mar = c(0, 0, 0, 0),
  smallplot = c(0.63, 0.65, 0.07, 0.42),
  legend_axis_cex = 0.75
)
```

Arguments

underlay	underlay image to be shown in grayscale.
overlay	optional overlay image.
xyz	x, y, z slice coordinates to display.
zlim	underlay intensity limits.
zlim_ol	overlay intensity limits.
alpha	transparency of overlay.
col_ol	colour palette of overlay.
orient_lab	display orientation labels (default TRUE).
rescale	rescale factor for the underlay and overlay images.
crosshairs	display the crosshairs (default TRUE).
ch_lwd	crosshair linewidth.
colourbar	display a colourbar for the overlay (default TRUE).
bg	plot background colour.

mar	plot margins.
smallplot	smallplot option for positioning the colourbar.
legend_axis_cex	font expansion factor for the legend axis text.

`ortho3_inter` *Display an interactive orthographic projection plot of a nifti object.*

Description

Display an interactive orthographic projection plot of a nifti object.

Usage

```
ortho3_inter(
  underlay,
  overlay = NULL,
  xyz = NULL,
  zlim = NULL,
  zlim_ol = NULL,
  alpha = 0.7,
  ...
)
```

Arguments

underlay	underlay image to be shown in grayscale.
overlay	optional overlay image.
xyz	x, y, z slice coordinates to display.
zlim	underlay intensity limits.
zlim_ol	overlay intensity limits.
alpha	transparency of overlay.
...	other options to be passed to the ortho3 function.

`paths2df` *Split paths into parts based on backslash, forwardslash and dot characters and return a data frame of these parts.*

Description

Split paths into parts based on backslash, forwardslash and dot characters and return a data frame of these parts.

Usage

```
paths2df(paths, col_num = NULL, extra_regex = NULL)
```

Arguments

`paths`	a vector of paths.
`col_num`	when set, only the specified column number of the data frame will be returned.
`extra_regex`	extra regular expression for splitting the paths. Example, "_|-" could be used to additionally split on underscores and hyphen characters.

Value

data.frame of separated path elements.

`peak_info` *Search for the highest peak in a spectral region and return the frequency, height and FWHM.*

Description

Search for the highest peak in a spectral region and return the frequency, height and FWHM.

Usage

```
peak_info(
  mrs_data,
  xlim = c(4, 0.5),
  interp_f = 4,
  scale = "ppm",
  mode = "real"
)
```

Arguments

mrs_data	an object of class mrs_data.
xlim	frequency range (default units of PPM) to search for the highest peak.
interp_f	interpolation factor, defaults to 4x.
scale	the units to use for the frequency scale, can be one of: "ppm", "hz" or "points".
mode	spectral mode, can be : "real", "imag" or "mod".

Value

list of arrays containing the highest peak frequency, height and FWHM in units of PPM and Hz.

---

pg_extrap_xy *Papoulis-Gerchberg (PG) algorithm method for k-space extrapolation.*

Description

PG method as described in: Haupt CI, Schuff N, Weiner MW, Maudsley AA. Removal of lipid artifacts in 1H spectroscopic imaging by data extrapolation. Magn Reson Med. 1996 May;35(5):678-87. Extrapolation is performed to expand k-space coverage by a factor of 2, with the aim to reduce Gibbs ringing.

Usage

```
pg_extrap_xy(
  mrs_data,
  img_mask = NULL,
  kspace_mask = NULL,
  intensity_thresh = 0.15,
  iters = 50
)
```

Arguments

mrs_data	MRS data object.
img_mask	a boolean matrix of voxels with strong signals to be extrapolated. Must be twice the dimensions of the input data.
kspace_mask	a boolean matrix of kspace points that have been sampled. Typically a circle for MRSI, but defaults to the full rectangular area of k-space covered by the input data. Must match the x-y dimensions of the input data.
intensity_thresh	used to define img_mask based on the strength of the signal in each voxel. Defaults to intensities greater than 15% of the maximum. Ignored if img_mask is specified as argument.
iters	number of iterations to perform.

Value

extrapolated `mrs_data` object.

`phase` *Apply phasing parameters to MRS data.*

Description

Apply phasing parameters to MRS data.

Usage

```
phase(mrs_data, zero_order, first_order = 0)
```

Arguments

`mrs_data`	MRS data.
`zero_order`	zero'th order phase term in degrees.
`first_order`	first order (frequency dependent) phase term in ms.

Value

MRS data with applied phase parameters.

`phase_ref_1h_brain` *Corrected zero order phase and chemical shift offset in 1H MRS data from the brain.*

Description

Corrected zero order phase and chemical shift offset in 1H MRS data from the brain.

Usage

```
phase_ref_1h_brain(
  mrs_data,
  mean_ref = FALSE,
  ret_corr_only = TRUE,
  xlim = c(4, 1.9),
  p_deg = 3,
  sp_N = 2,
  basis_type = "poly"
)
```

Arguments

mrs_data	MRS data to be corrected.
mean_ref	apply the phase and offset of the mean spectrum to all others. Default is FALSE.
ret_corr_only	return the corrected data only.
xlim	frequency range in ppm to consider.
p_deg	polynomial baseline order.
sp_N	number of spline functions, note the true number will be sp_N + sp_deg.
basis_type	may be one of "poly" or "spline".

Value

corrected MRS data.

---

plot.fit_result *Plot the fitting results of an object of class* fit_result.

Description

Plot the fitting results of an object of class fit_result.

Usage

```
## S3 method for class 'fit_result'
plot(
  x,
  dyn = 1,
  x_pos = 1,
  y_pos = 1,
  z_pos = 1,
  coil = 1,
  xlim = NULL,
  data_only = FALSE,
  label = NULL,
  plot_sigs = NULL,
  n = NULL,
  sub_bl = FALSE,
  mar = NULL,
  restore_def_par = TRUE,
  ylim = NULL,
  y_scale = FALSE,
  show_grid = TRUE,
  grid_nx = NULL,
  grid_ny = NA,
  invert_fit = FALSE,
  ...
)
```

Arguments

x	fit_result object.
dyn	the dynamic index to plot.
x_pos	the x index to plot.
y_pos	the y index to plot.
z_pos	the z index to plot.
coil	the coil element number to plot.
xlim	the range of values to display on the x-axis, eg xlim = c(4,1).
data_only	display only the processed data (logical).
label	character string to add to the top left of the plot window.
plot_sigs	a character vector of signal names to add to the plot.
n	single index element to plot (overrides other indices when given).
sub_bl	subtract the baseline from the data and fit (logical).
mar	option to adjust the plot margins. See ?par.
restore_def_par	restore default plotting par values after the plot has been made.
ylim	range of values to display on the y-axis, eg ylim = c(0,10).
y_scale	option to display the y-axis values (logical).
show_grid	plot gridlines behind the data (logical). Defaults to TRUE.
grid_nx	number of cells of the grid in x and y direction. When NULL the grid aligns with the tick marks on the corresponding default axis (i.e., tickmarks as computed by axTicks). When NA, no grid lines are drawn in the corresponding direction.
grid_ny	as above.
invert_fit	show the fit result "upside-down"/
...	further arguments to plot method.

`plot.mrs_data` *Plotting method for objects of class mrs_data.*

Description

Plotting method for objects of class mrs_data.

Usage

```
## S3 method for class 'mrs_data'
plot(
  x,
  dyn = 1,
  x_pos = 1,
  y_pos = 1,
  z_pos = 1,
  coil = 1,
  fd = TRUE,
  x_units = NULL,
  xlim = NULL,
  y_scale = FALSE,
  x_ax = TRUE,
  mode = "re",
  lwd = NULL,
  bty = NULL,
  label = "",
  restore_def_par = TRUE,
  mar = NULL,
  xaxis_lab = NULL,
  yaxis_lab = NULL,
  xat = NULL,
  xlabs = TRUE,
  yat = NULL,
  ylabs = TRUE,
  show_grid = TRUE,
  grid_nx = NULL,
  grid_ny = NA,
  col = NULL,
  alpha = NULL,
  bl_lty = NULL,
  hline = NULL,
  hline_lty = 2,
  hline_col = "red",
  vline = NULL,
  vline_lty = 2,
  vline_col = "red",
  ...
)
```

Arguments

x	object of class mrs_data.
dyn	the dynamic index to plot.
x_pos	the x index to plot.
y_pos	the y index to plot.

z_pos	the z index to plot.
coil	the coil element number to plot.
fd	display data in the frequency-domain (default), or time-domain (logical).
x_units	the units to use for the x-axis, can be one of: "ppm", "hz", "points", "seconds" or "ms".
xlim	the range of values to display on the x-axis, eg xlim = c(4,1).
y_scale	option to display the y-axis values (logical).
x_ax	option to display the x-axis values (logical).
mode	representation of the complex numbers to be plotted, can be one of: "re", "im", "mod" or "arg".
lwd	plot linewidth.
bty	option to draw a box around the plot. See ?par.
label	character string to add to the top left of the plot window.
restore_def_par	restore default plotting par values after the plot has been made.
mar	option to adjust the plot margins. See ?par.
xaxis_lab	x-axis label.
yaxis_lab	y-axis label.
xat	x-axis tick label values.
xlabs	x-axis tick labels.
yat	y-axis tick label values.
ylabs	y-axis tick labels.
show_grid	plot gridlines behind the data (logical). Defaults to TRUE.
grid_nx	number of cells of the grid in x and y direction. When NULL the grid aligns with the tick marks on the corresponding default axis (i.e., tickmarks as computed by axTicks). When NA, no grid lines are drawn in the corresponding direction.
grid_ny	as above.
col	set the line colour, eg col = rgb(0.5, 0.5, 0.5).
alpha	set the line transparency, eg alpha = 0.5 is 50% transparency. Overrides any transparency levels set by col.
bl_lty	linetype for the y = 0 baseline trace. A default value NULL results in no baseline being plotted.
hline	add a horizontal line at the specified value.
hline_lty	linetype for the horizontal line.
hline_col	colour for the horizontal line.
vline	add a vertical line at the specified value.
vline_lty	linetype for the vertical line.
vline_col	colour for the vertical line.
...	other arguments to pass to the plot method.

plot_bc — *Convenience function to plot a baseline estimate with the original data.*

Description

Convenience function to plot a baseline estimate with the original data.

Usage

```
plot_bc(orig_data, bc_data, ...)
```

Arguments

orig_data	the original data.
bc_data	the baseline corrected data.
...	other arguments to pass to the stackplot function.

plot_reg — *Plot regressors as an image.*

Description

Plot regressors as an image.

Usage

```
plot_reg(regressor_df)
```

Arguments

regressor_df	input regressor data frame.

plot_slice_fit *Plot a 2D slice from an MRSI fit result object.*

Description

Plot a 2D slice from an MRSI fit result object.

Usage

```
plot_slice_fit(
  fit_res,
  map,
  map_denom = NULL,
  slice = 1,
  zlim = NULL,
  interp = 1
)
```

Arguments

fit_res	fit_result object.
map	fit result values to display as a colour map. Can be specified as a character string or array of numeric values. Defaults to "tNAA".
map_denom	fit result values to divide the map argument by. Can be specified as a character string (eg "tCr") or array of numeric values.
slice	slice to plot in the z direction.
zlim	range of values to plot.
interp	interpolation factor.

plot_slice_fit_inter *Plot a 2D slice from an MRSI fit result object.*

Description

Plot a 2D slice from an MRSI fit result object.

Usage

```
plot_slice_fit_inter(
  fit_res,
  map = NULL,
  map_denom = NULL,
  slice = 1,
  zlim = NULL,
  interp = 1,
  xlim = NULL
)
```

Arguments

fit_res	fit_result object.
map	fit result values to display as a colour map. Can be specified as a character string or array of numeric values. Defaults to "tNAA".
map_denom	fit result values to divide the map argument by. Can be specified as a character string (eg "tCr") or array of numeric values.
slice	slice to plot in the z direction.
zlim	range of values to plot.
interp	interpolation factor.
xlim	spectral plot limits for the x axis.

---

plot_slice_map *Plot a slice from a 7 dimensional array.*

Description

Plot a slice from a 7 dimensional array.

Usage

```
plot_slice_map(
  data,
  zlim = NULL,
  mask_map = NULL,
  mask_cutoff = 20,
  interp = 1,
  slice = 1,
  dyn = 1,
  coil = 1,
  ref = 1,
  denom = NULL,
  horizontal = FALSE
)
```

Arguments

data	7d array of values to be plotted.
zlim	smallest and largest values to be plotted.
mask_map	matching map with logical values to indicate if the corresponding values should be plotted.
mask_cutoff	minimum values to plot (as a percentage of the maximum).
interp	map interpolation factor.
slice	the slice index to plot.

dyn	the dynamic index to plot.
coil	the coil element number to plot.
ref	reference index to plot.
denom	map to use as a denominator.
horizontal	display the colourbar horizontally (logical).

`plot_slice_map_inter` *Plot an interactive slice map from a data array where voxels can be selected to display a corresponding spectrum.*

Description

Plot an interactive slice map from a data array where voxels can be selected to display a corresponding spectrum.

Usage

```
plot_slice_map_inter(
  mrs_data,
  map = NULL,
  xlim = NULL,
  slice = 1,
  zlim = NULL,
  mask_map = NULL,
  denom = NULL,
  mask_cutoff = 20,
  interp = 1,
  mode = "re",
  y_scale = FALSE,
  ylim = NULL,
  coil = 1,
  fd = TRUE
)
```

Arguments

mrs_data	spectral data.
map	array of values to be plotted, defaults to the integration of the modulus of the full spectral width.
xlim	spectral region to plot.
slice	the slice index to plot.
zlim	smallest and largest values to be plotted.
mask_map	matching map with logical values to indicate if the corresponding values should be plotted.

denom	map to use as a denominator.
mask_cutoff	minimum values to plot (as a percentage of the maximum).
interp	map interpolation factor.
mode	representation of the complex spectrum to be plotted, can be one of: "re", "im", "mod" or "arg".
y_scale	option to display the y-axis values (logical).
ylim	intensity range to plot.
coil	coil element to plot.
fd	display data in the frequency-domain (default), or time-domain (logical).

---

plot_spec_sd *Plot the spectral standard deviation.*

Description

Plot the spectral standard deviation.

Usage

```
plot_spec_sd(mrs_data, xlim = NULL, scale_sd = 1.96, ...)
```

Arguments

mrs_data	MRS data to be plotted.
xlim	plotting limits in ppm.
scale_sd	scaling factor for the standard deviation trace.
...	other arguments passed to the stackplot function.

---

plot_voi_overlay *Plot a volume as an image overlay.*

Description

Plot a volume as an image overlay.

Usage

```
plot_voi_overlay(mri, voi, export_path = NULL, zlim = NULL, ...)
```

Arguments

mri	image data as a nifti object or path to data file.
voi	volume data as a nifti object or path to data file.
export_path	optional path to save the image in png format.
zlim	underlay intensity limits.
...	additional arguments to the ortho3 function.

plot_voi_overlay_seg *Plot a volume as an overlay on a segmented brain volume.*

Description

Plot a volume as an overlay on a segmented brain volume.

Usage

```
plot_voi_overlay_seg(mri_seg, voi, export_path = NULL, ...)
```

Arguments

mri_seg	segmented brain volume as a nifti object.
voi	volume data as a nifti object.
export_path	optional path to save the image in png format.
...	additional arguments to the ortho3 function.

ppm *Return the ppm scale of an MRS dataset or fit result.*

Description

Return the ppm scale of an MRS dataset or fit result.

Usage

```
ppm(x, ft = NULL, ref = NULL, fs = NULL, N = NULL)

## S3 method for class 'mrs_data'
ppm(x, ft = NULL, ref = NULL, fs = NULL, N = NULL)

## S3 method for class 'fit_result'
ppm(x, ft = NULL, ref = NULL, fs = NULL, N = NULL)
```

Arguments

x	MRS dataset of fit result.
ft	transmitter frequency in Hz, does not apply when the object is a fit result.
ref	reference value for ppm scale, does not apply when the object is a fit result.
fs	sampling frequency in Hz, does not apply when the object is a fit result.
N	number of data points in the spectral dimension, does not apply when the object is a fit result.

Value

ppm scale.

`precomp` *Save function results to file and load on subsequent calls to avoid repeat computation.*

Description

Save function results to file and load on subsequent calls to avoid repeat computation.

Usage

```
precomp(file, fun, ...)
```

Arguments

`file`	file name to write the results.
`fun`	function to run.
`...`	arguments to be passed to fun.

`preproc_svs` *Preprocess and perform quality assessment of a single SVS data set.*

Description

Preprocess and perform quality assessment of a single SVS data set.

Usage

```
preproc_svs(
  path,
  label = NULL,
  output_dir = NULL,
  ref_inds = NULL,
  dyn_water_ref_path = NULL,
  Ntrans = NULL,
  TR = NULL
)
```

Arguments

path	path to the MRS data file or IMA directory.
label	a label to describe the data set.
output_dir	output directory.
ref_inds	a vector of 1-based indices for any water reference dynamic scans.
dyn_water_ref_path	path to interleaved water reference data file or IMA directory.
Ntrans	override the number of transients set in the mrs_data file.
TR	override the TR (in seconds) set in the mrs_data file.

---

preproc_svs_dataset *Preprocess and perform quality assessment of one or more SVS data sets.*

Description

Preprocess and perform quality assessment of one or more SVS data sets.

Usage

```
preproc_svs_dataset(
  paths,
  labels = NULL,
  output_dir = "spant_analysis",
  exclude_labels = NULL,
  overwrite = FALSE,
  ref_inds = NULL,
  dyn_water_ref_paths = NULL,
  Ntrans = NULL,
  TR = NULL,
  return_results = FALSE
)
```

Arguments

paths	paths to the MRS data file or IMA directory.
labels	labels to describe each data set.
output_dir	output directory.
exclude_labels	vector of labels of scans to exclude, eg poor quality data.
overwrite	overwrite saved results, defaults to FALSE.
ref_inds	a vector of 1-based indices for any water reference dynamic scans.
dyn_water_ref_paths	paths to interleaved water reference scans.

Ntrans	override the number of transients set in the mrs_data file.
TR	override the TR (in seconds) set in the mrs_data file.
return_results	function will return key outputs, defaults to FALSE.

`print.fit_result` *Print a summary of an object of class* `fit_result`.

Description

Print a summary of an object of class `fit_result`.

Usage

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

Arguments

x	`fit_result` object.
...	further arguments.

`print.mrs_data` *Print a summary of mrs_data parameters.*

Description

Print a summary of mrs_data parameters.

Usage

```
## S3 method for class 'mrs_data'
print(x, full = FALSE, ...)
```

Arguments

x	mrs_data object.
full	print all parameters (default FALSE).
...	further arguments.

qn_states *Get the quantum coherence matrix for a spin system.*

Description

Get the quantum coherence matrix for a spin system.

Usage

```
qn_states(sys)
```

Arguments

sys	spin system object.

Value

quantum coherence number matrix.

rats *Robust Alignment to a Target Spectrum (RATS).*

Description

Robust Alignment to a Target Spectrum (RATS).

Usage

```
rats(
  mrs_data,
  ref = NULL,
  xlim = c(4, 0.5),
  max_shift = 20,
  p_deg = 2,
  sp_N = 2,
  sp_deg = 3,
  max_t = 0.2,
  basis_type = "poly",
  rescale_output = TRUE,
  phase_corr = TRUE,
  ret_corr_only = TRUE,
  zero_freq_shift_t0 = FALSE,
  list_mean_ref = TRUE,
  remove_freq_outliers = FALSE,
  freq_outlier_thresh = 3,
  remove_phase_outliers = FALSE,
```

```
  phase_outlier_thresh = 3,
  remove_amp_outliers = FALSE,
  amp_outlier_thresh = 3
)
```

Arguments

mrs_data	MRS data to be corrected.
ref	optional MRS data to use as a reference, the mean of all dynamics is used if this argument is not supplied.
xlim	optional frequency range to perform optimisation, set to NULL to use the full range.
max_shift	maximum allowable frequency shift in Hz.
p_deg	polynomial degree used for baseline modelling. Negative values disable baseline modelling.
sp_N	number of spline functions, note the true number will be sp_N + sp_deg.
sp_deg	degree of spline functions.
max_t	truncate the FID when longer than max_t to reduce time taken, set to NULL to use the entire FID.
basis_type	may be one of "poly" or "spline".
rescale_output	rescale the bl_matched_spec and bl output to improve consistency between dynamic scans.
phase_corr	apply phase correction (in addition to frequency). TRUE by default.
ret_corr_only	return the corrected mrs_data object only.
zero_freq_shift_t0	perform a linear fit to the frequency shifts and set the (linearly modeled) shift to be 0 Hz for the first dynamic scan.
list_mean_ref	is ref is not specified and a list is provided, use the list mean scan as reference. Otherwise use the mean of each list element as it's own reference.
remove_freq_outliers	remove dynamics based on their frequency shift.
freq_outlier_thresh	threshold to remove frequency outliers.
remove_phase_outliers	remove dynamics based on their phase shift.
phase_outlier_thresh	threshold to remove phase outliers.
remove_amp_outliers	remove dynamics based on their amplitude change.
amp_outlier_thresh	threshold to remove amplitude outliers.

Value

a list containing the corrected data; phase and shift values in units of degrees and Hz respectively.

Re.mrs_data *Apply Re operator to an MRS dataset.*

Description

Apply Re operator to an MRS dataset.

Usage

```
## S3 method for class 'mrs_data'
Re(z)
```

Arguments

z	MRS data.

Value

MRS data following Re operator.

read_basis *Read a basis file in LCModel .basis format.*

Description

Read a basis file in LCModel .basis format.

Usage

```
read_basis(basis_file, ref = def_ref(), sort_basis = TRUE)
```

Arguments

basis_file	path to basis file.
ref	assumed ppm reference value.
sort_basis	sort the basis set based on signal names.

Value

basis object.

read_basis_niidir *Read a basis folder containing one NIfTI MRS file for each basis element.*

Description

Read a basis folder containing one NIfTI MRS file for each basis element.

Usage

```
read_basis_niidir(basis_dir)
```

Arguments

basis_dir	directory of basis files.

Value

a basis_set object.

read_dkd_moco_log *Read the log from Dinesh's MoCo sLASER sequence.*

Description

Read the log from Dinesh's MoCo sLASER sequence.

Usage

```
read_dkd_moco_log(path, date, end_time)
```

Arguments

path	path to the log file.
date	scan date, eg "01-01-2025".
end_time	scan time, eg "14:00".

Value

data.frame of moco parameters.

`read_ima_coil_dir` *Read a directory containing Siemens MRS IMA files and combine along the coil dimension. Note that the coil ID is inferred from the sorted file name and should be checked when consistency is required between two directories.*

Description

Read a directory containing Siemens MRS IMA files and combine along the coil dimension. Note that the coil ID is inferred from the sorted file name and should be checked when consistency is required between two directories.

Usage

```
read_ima_coil_dir(dir, extra = NULL, verbose = FALSE)
```

Arguments

`dir`	data directory path.
`extra`	an optional data frame to provide additional variables for use in subsequent analysis steps, eg id or grouping variables.
`verbose`	output extra information to the console.

Value

mrs_data object.

`read_ima_dyn_dir` *Read a directory containing Siemens MRS IMA files and combine along the dynamic dimension. Note that the coil ID is inferred from the sorted file name and should be checked when consistency is required.*

Description

Read a directory containing Siemens MRS IMA files and combine along the dynamic dimension. Note that the coil ID is inferred from the sorted file name and should be checked when consistency is required.

Usage

```
read_ima_dyn_dir(dir, extra = NULL, verbose = FALSE)
```

Arguments

dir	data directory path.
extra	an optional data frame to provide additional variables for use in subsequent analysis steps, eg id or grouping variables.
verbose	output extra information to the console.

Value

mrs_data object.

---

read_lcm_coord *Read an LCModel formatted coord file containing fit information.*

Description

Read an LCModel formatted coord file containing fit information.

Usage

```
read_lcm_coord(coord_f)
```

Arguments

coord_f	path to the coord file.

Value

list containing a table of fit point and results structure containing signal amplitudes, errors and fitting diagnostics.

---

read_mrs *Read MRS data from the filesystem.*

Description

Read MRS data from the filesystem.

Usage

```
read_mrs(
  path,
  format = NULL,
  ft = NULL,
  fs = NULL,
  ref = NULL,
  n_ref_scans = NULL,
  full_fid = FALSE,
  omit_svs_ref_scans = TRUE,
  verbose = FALSE,
  extra = NULL,
  fid_filt_dist = NULL
)
```

Arguments

path	file name or directory containing the MRS data.
format	string describing the data format. Must be one of the following : "spar_sdat", "rda", "dicom", "twix", "pfile", "list_data", "paravis", "dpt", "lcm_raw", "rds", "nifti", "varian", "jmrui_txt". If not specified, the format will be guessed from the filename extension, or will be assumed to be a Siemens ima dynamic data if the path is a directory.
ft	transmitter frequency in Hz (required for list_data format).
fs	sampling frequency in Hz (required for list_data format).
ref	reference value for ppm scale (required for list_data format).
n_ref_scans	override the number of water reference scans detected in the file header (GE p-file only).
full_fid	export all data points, including those before the start of the FID (default = FALSE), TWIX format only.
omit_svs_ref_scans	remove any reference scans sometimes saved in SVS twix data (default = TRUE).
verbose	print data file information (default = FALSE).
extra	an optional data frame to provide additional variables for use in subsequent analysis steps, eg id or grouping variables.
fid_filt_dist	indicate if the data has a distorted FID due to a brick-wall filter being used to downsample the data. Default is to auto detect this from the data, but TRUE or FALSE options can be given to override detection.

Value

MRS data object.

Examples

```
fname <- system.file("extdata", "philips_spar_sdat_WS.SDAT", package = "spant")
mrs_data <- read_mrs(fname)
print(mrs_data)
```

`read_mrs_tqn` *Read MRS data using the TARQUIN software package.*

Description

Read MRS data using the TARQUIN software package.

Usage

```
read_mrs_tqn(fname, fname_ref = NA, format, id = NA, group = NA)
```

Arguments

`fname`	the filename containing the MRS data.
`fname_ref`	a second filename containing reference MRS data.
`format`	format of the MRS data. Can be one of the following: siemens, philips, ge, dcm, dpt, rda, lcm, varian, bruker, jmrui_txt.
`id`	optional ID string.
`group`	optional group string.

Value

MRS data object.

Examples

```
fname <- system.file("extdata","philips_spar_sdat_WS.SDAT",package="spant")
## Not run:
mrs_data <- read_mrs_tqn(fname, format="philips")

## End(Not run)
```

read_pulse_ascii *Read an ASCII formatted pulse file.*

Description

Read an ASCII formatted pulse file.

Usage

```
read_pulse_ascii(fname, deg2rad = TRUE)
```

Arguments

fname	ASCII formatted pulse file path.
deg2rad	convert phase values stored in degrees to radians.

Value

pulse waveform and header.

read_pulse_bruker *Read a Bruker formatted pulse file*

Description

Read a Bruker formatted pulse file

Usage

```
read_pulse_bruker(fname)
```

Arguments

fname	Bruker formatted pulse file path.

Value

pulse waveform and header.

read_pulse_pta *Read a .pta formatted pulse file compatible with Siemens PulseTool.*

Description

Read a .pta formatted pulse file compatible with Siemens PulseTool.

Usage

```
read_pulse_pta(fname)
```

Arguments

fname	pta formatted pulse file path.

Value

pulse waveform and header.

read_siemens_txt_hdr *Read the text format header found in Siemens IMA and TWIX data files.*

Description

Read the text format header found in Siemens IMA and TWIX data files.

Usage

```
read_siemens_txt_hdr(input, version = "vd", verbose = FALSE, offset = 0)
```

Arguments

input	file name to read or raw data.
version	software version, can be "vb" or "vd".
verbose	print information to the console.
offset	offset to begin searching for the text header.

Value

a list of parameter values

read_tqn_fit *Reader for csv fit results generated by TARQUIN.*

Description

Reader for csv fit results generated by TARQUIN.

Usage

```
read_tqn_fit(fit_f)
```

Arguments

fit_f	TARQUIN fit file.

Value

A data frame of the fit data points.

Examples

```
## Not run:
fit <- read_tqn_fit(system.file("extdata","fit.csv",package="spant"))

## End(Not run)
```

read_tqn_result *Reader for csv results generated by TARQUIN.*

Description

Reader for csv results generated by TARQUIN.

Usage

```
read_tqn_result(result_f, remove_rcs = TRUE)
```

Arguments

result_f	TARQUIN result file.
remove_rcs	omit row, column and slice ids from output.

Value

list of amplitudes, crlbs and diagnostics.

Examples

```
## Not run:
result <- read_tqn_result(system.file("extdata","result.csv",package="spant"))

## End(Not run)
```

`recon_imag` *Reconstruct complex time-domain data from the real part of frequency-domain data.*

Description

Reconstruct complex time-domain data from the real part of frequency-domain data.

Usage

```
recon_imag(mrs_data)
```

Arguments

`mrs_data`	MRS data.

Value

reconstructed MRS data.

`recon_imag_vec` *Reconstruct complex time-domain data from the real part of frequency-domain data.*

Description

Reconstruct complex time-domain data from the real part of frequency-domain data.

Usage

```
recon_imag_vec(data)
```

Arguments

`data`	data points in the frequency domain.

Value

reconstructed signal.

recon_twix_2d_mrsi *Reconstruct 2D MRSI data from a twix file loaded with read_mrs.*

Description

Reconstruct 2D MRSI data from a twix file loaded with read_mrs.

Usage

```
recon_twix_2d_mrsi(twix_mrs)
```

Arguments

twix_mrs	raw dynamic data.

Value

reconstructed data.

rectangular_mask *Create a rectangular mask stored as a matrix of logical values.*

Description

Create a rectangular mask stored as a matrix of logical values.

Usage

```
rectangular_mask(xN, yN, x0, y0, xw, yw, angle)
```

Arguments

xN	number of pixels in the x dimension.
yN	number of pixels in the y dimension.
x0	centre of rectangle in the x direction in units of pixels.
y0	centre of rectangle in the y direction in units of pixels.
xw	width in the x direction in units of pixels.
yw	width in the y direction in units of pixels.
angle	angle of rotation in degrees.

Value

logical mask matrix with dimensions fov_yN x fov_xN.

rep_array_dim *Repeat an array over a given dimension.*

Description

Repeat an array over a given dimension.

Usage

```
rep_array_dim(x, rep_dim, n)
```

Arguments

x	array.
rep_dim	dimension to extend.
n	number of times to repeat.

Value

extended array.

rep_dyn *Replicate a scan in the dynamic dimension.*

Description

Replicate a scan in the dynamic dimension.

Usage

```
rep_dyn(mrs_data, times)
```

Arguments

mrs_data	MRS data to be replicated.
times	number of times to replicate.

Value

replicated data object.

rep_mrs *Replicate a scan over a given dimension.*

Description

Replicate a scan over a given dimension.

Usage

```
rep_mrs(
  mrs_data,
  x_rep = 1,
  y_rep = 1,
  z_rep = 1,
  dyn_rep = 1,
  coil_rep = 1,
  warn = TRUE
)
```

Arguments

mrs_data	MRS data to be replicated.
x_rep	number of x replications.
y_rep	number of y replications.
z_rep	number of z replications.
dyn_rep	number of dynamic replications.
coil_rep	number of coil replications.
warn	print a warning when the data dimensions do not change.

Value

replicated data object.

resample_basis *Resample a basis-set to match a mrs_data acquisition.*

Description

Resample a basis-set to match a mrs_data acquisition.

Usage

```
resample_basis(basis, mrs_data, ref_freq_match = TRUE)
```

Arguments

basis	the basis to be resampled.
mrs_data	the mrs_data to match the number of data points and sampling frequency.
ref_freq_match	apply a frequency shift to the basis to match the reference frequency (usually 4.65 or 4.68) of the mrs_data.

Value

resampled basis set object.

---

resample_img *Resample an image to match a target image space.*

Description

Resample an image to match a target image space.

Usage

```
resample_img(source, target, interp = 3L)
```

Arguments

source	image data as a nifti object.
target	image data as a nifti object.
interp	interpolation parameter, see nifyreg.linear definition.

Value

resampled image data as a nifti object.

---

resample_voi *Resample a VOI to match a target image space using nearest-neighbour interpolation.*

Description

Resample a VOI to match a target image space using nearest-neighbour interpolation.

Usage

```
resample_voi(voi, mri)
```

Arguments

voi	volume data as a nifti object.
mri	image data as a nifti object.

Value

volume data as a nifti object.

---

reslice_to_mrs *Reslice a nifti object to match the orientation of mrs data.*

Description

Reslice a nifti object to match the orientation of mrs data.

Usage

```
reslice_to_mrs(mri, mrs, interp = 3L)
```

Arguments

mri	nifti object to be resliced.
mrs	mrs_data object for the target orientation.
interp	interpolation parameter, see nifyreg.linear definition.

Value

resliced imaging data.

---

reson_table2mrs_data *Generate mrs_data from a table of single Lorentzian resonances.*

Description

Generate mrs_data from a table of single Lorentzian resonances.

Usage

```
reson_table2mrs_data(
  reson_table,
  acq_paras = def_acq_paras(),
  back_extrap_pts = 0
)
```

Arguments

reson_table	as produced by the hsvd function.
acq_paras	list of acquisition parameters. See
back_extrap_pts	number of data points to back extrapolate def_acq_paras

Value

mrs_data object.

---

re_weighting *Apply a weighting to the FID to enhance spectral resolution.*

Description

Apply a weighting to the FID to enhance spectral resolution.

Usage

```
re_weighting(mrs_data, re, alpha)
```

Arguments

mrs_data	data to be enhanced.
re	resolution enhancement factor (rising exponential factor).
alpha	alpha factor (Gaussian decay)

Value

resolution enhanced mrs_data.

---

rm_dyns *Remove a subset of dynamic scans.*

Description

Remove a subset of dynamic scans.

Usage

```
rm_dyns(mrs_data, subset)
```

Arguments

mrs_data	dynamic MRS data.
subset	vector containing indices to the dynamic scans to be removed.

Value

MRS data without the specified dynamic scans.

---

scale_amp_legacy *Apply water reference scaling to a fitting results object to yield metabolite quantities in units of "mmol per Kg wet weight".*

Description

See the LCModel manual (section 10.2) on water-scaling for details on the assumptions and relevant references. Use this type of concentration scaling to compare fit results with LCModel and TARQUIN defaults. Otherwise scale_amp_molal_pvc is the preferred method. Note, the LCModel manual (section 1.3) states:

Usage

```
scale_amp_legacy(fit_result, ref_data, w_att = 0.7, w_conc = 35880, ...)
```

Arguments

fit_result	a result object generated from fitting.
ref_data	water reference MRS data object.
w_att	water attenuation factor (default = 0.7). Assumes water T2 of 80ms and a TE = 30 ms. exp(-30ms / 80ms) ~ 0.7.
w_conc	assumed water concentration (default = 35880). Default value corresponds to typical white matter. Set to 43300 for gray matter, and 55556 for phantom measurements.
...	additional arguments to get_td_amp function.

Details

"Concentrations should be labelled 'mmol per Kg wet weight'. We use the shorter (incorrect) abbreviation mM. The actual mM is the mmol per Kg wet weight multiplied by the specific gravity of the tissue, typically 1.04 in brain."

Value

a fit_result object with a rescaled results table.

`scale_amp_molal` *Apply water reference scaling to a fitting results object to yield metabolite quantities in millimolar (mM) units (mol / kg of tissue water).*

Description

Note, this function assumes the volume contains a homogeneous voxel, eg pure WM, GM or CSF. Also note that in the case of a homogeneous voxel the relative densities of MR-visible water (eg GM=0.78, WM=0.65, and CSF=0.97) cancel out and don't need to be considered. Use scale_amp_molal_pvc for volumes containing multiple compartments. Details of this method can be found in "Use of tissue water as a concentration reference for proton spectroscopic imaging" by Gasparovic et al MRM 2006 55(6):1219-26.

Usage

```
scale_amp_molal(
  fit_result,
  ref_data,
  te,
  tr,
  water_t1,
  water_t2,
  metab_t1,
  metab_t2,
  ...
)
```

Arguments

`fit_result`	result object generated from fitting.
`ref_data`	water reference MRS data object.
`te`	the MRS TE in seconds.
`tr`	the MRS TR in seconds.
`water_t1`	assumed water T1 value.
`water_t2`	assumed water T2 value.
`metab_t1`	assumed metabolite T1 value.
`metab_t2`	assumed metabolite T2 value.
`...`	additional arguments to get_td_amp function.

Value

A `fit_result` object with a rescaled results table.

scale_amp_molal_pvc *Apply water reference scaling to a fitting results object to yield metabolite quantities in millimolar (mM) units (mol / kg of tissue water).*

Description

Details of this method can be found in "Use of tissue water as a concentration reference for proton spectroscopic imaging" by Gasparovic et al MRM 2006 55(6):1219-26. 1.5 Tesla relaxation assumptions are taken from this paper. For 3 Tesla data, relaxation assumptions are taken from "NMR relaxation times in the human brain at 3.0 Tesla" by Wansapura et al J Magn Reson Imaging 1999 9(4):531-8.

Usage

```
scale_amp_molal_pvc(fit_result, ref_data, p_vols, te, tr, ...)
```

Arguments

fit_result	result object generated from fitting.
ref_data	water reference MRS data object.
p_vols	a numeric vector of partial volumes expressed as percentages. For example, a voxel containing 100% white matter tissue would use : p_vols = c(WM = 100, GM = 0, CSF = 0).
te	the MRS TE in seconds.
tr	the MRS TR in seconds.
...	additional arguments to get_td_amp function.

Value

A fit_result object with a rescaled results table.

scale_amp_molar *Apply water reference scaling to a fitting results object to yield metabolite quantities in millimolar (mM) units (mol / Litre of tissue). This function is depreciated, please use scale_amp_legacy instead.*

Description

See the LCModel manual (section 10.2) on water-scaling for details on the assumptions and relevant references. Use this type of concentration scaling to compare fit results with LCModel and TARQUIN defaults. Otherwise scale_amp_molal_pvc is generally the preferred method.

Usage

```
scale_amp_molar(fit_result, ref_data, w_att = 0.7, w_conc = 35880, ...)
```

Arguments

fit_result	a result object generated from fitting.
ref_data	water reference MRS data object.
w_att	water attenuation factor (default = 0.7). Assumes water T2 of 80ms and a TE = 30 ms. exp(-30ms / 80ms) ~ 0.7.
w_conc	assumed water concentration (default = 35880). Default value corresponds to typical white matter. Set to 43300 for gray matter, and 55556 for phantom measurements.
...	additional arguments to get_td_amp function.

Value

a fit_result object with a rescaled results table.

---

scale_amp_molar2molal_pvc

Convert default LCM/TARQUIN concentration scaling to molal units with partial volume correction.

Description

Convert default LCM/TARQUIN concentration scaling to molal units with partial volume correction.

Usage

```
scale_amp_molar2molal_pvc(fit_result, p_vols, te, tr)
```

Arguments

fit_result	a fit_result object to apply partial volume correction.
p_vols	a numeric vector of partial volumes expressed as percentages. For example, a voxel containing 100% white matter tissue would use : p_vols = c(WM = 100, GM = 0, CSF = 0).
te	the MRS TE.
tr	the MRS TR.

Value

a fit_result object with a rescaled results table.

scale_amp_ratio *Scale fitted amplitudes to a ratio of signal amplitude.*

Description

Scale fitted amplitudes to a ratio of signal amplitude.

Usage

```
scale_amp_ratio(fit_result, name, use_mean_value = FALSE)
```

Arguments

fit_result	a result object generated from fitting.
name	the signal name to use as a denominator (usually, "tCr" or "tNAA").
use_mean_value	scales the result by the mean of the signal when set to TRUE.

Value

a fit_result object with a rescaled results table.

scale_amp_ratio_value *Scale fitted amplitudes to a ratio of signal amplitude.*

Description

Scale fitted amplitudes to a ratio of signal amplitude.

Usage

```
scale_amp_ratio_value(fit_result, value)
```

Arguments

fit_result	a result object generated from fitting.
value	the number use as a denominator.

Value

a fit_result object with a rescaled results table.

scale_amp_water_ratio *Scale metabolite amplitudes as a ratio to the unsuppressed water amplitude.*

Description

Scale metabolite amplitudes as a ratio to the unsuppressed water amplitude.

Usage

```
scale_amp_water_ratio(fit_result, ref_data, ...)
```

Arguments

fit_result	a result object generated from fitting.
ref_data	a water reference MRS data object.
...	additional arguments to get_td_amp function.

Value

a fit_result object with a rescaled results table.

scale_basis_amp *Scale a basis object by a scalar.*

Description

Scale a basis object by a scalar.

Usage

```
scale_basis_amp(basis, amp)
```

Arguments

basis	basis_set object to be scaled.
amp	multiplicative factor with length 1.

Value

basis_set object multiplied by the amplitude scale factor.

scale_basis_from_singlet

Scale a basis-set to be consistent with spant assumptions for water scaling.

Description

For correct water scaling, spant assumes the time-domain amplitude (t = 0) for a single proton is 0.5. Internally simulated basis-sets will be correctly scaled, however imported basis-sets should be assumed to be un-scaled and this function should be used. Note that the singlet specified should only contain one resonance, and that any additional signals (eg TSP or residual water) will result in incorrect scaling. Therefore, only simulated basis sets are appropriate for use with this function.

Usage

```
scale_basis_from_singlet(basis, name, protons)
```

Arguments

basis	basis set to be scaled.
name	the name of the singlet to be used as a scaling reference.
protons	the number of MRS visible protons contributing to the singlet resonance.

Value

a scaled basis.

scale_mrs_amp

Scale an mrs_data object by a scalar or vector or amplitudes.

Description

Scale an mrs_data object by a scalar or vector or amplitudes.

Usage

```
scale_mrs_amp(mrs_data, amp)
```

Arguments

mrs_data	data to be scaled.
amp	multiplicative factor, must have length equal to 1 or Nspec(mrs_data).

Value

mrs_data object multiplied by the amplitude scale factor.

scale_spec *Scale mrs_data to a spectral region.*

Description

Scale mrs_data to a spectral region.

Usage

```
scale_spec(
  mrs_data,
  xlim = NULL,
  operator = "sum",
  freq_scale = "ppm",
  mode = "re",
  mean_dyns = NULL,
  ret_scale_factor = FALSE
)
```

Arguments

mrs_data	MRS data.
xlim	spectral range to be integrated (defaults to full range).
operator	can be "sum" (default), "mean", "l2", "max", "min" or "max-min".
freq_scale	units of xlim, can be : "ppm", "Hz" or "points".
mode	spectral mode, can be : "re", "im", "mod" or "cplx".
mean_dyns	mean the dynamic scans before applying the operator. The same scaling value will be applied to each individual dynamic.
ret_scale_factor	option to return the scaling factor in addition to the scaled data.

Value

normalised data.

sd.list *Calculate the standard deviation spectrum from an mrs_data object.*

Description

Calculate the standard deviation spectrum from an mrs_data object.

Usage

```
## S3 method for class 'list'
sd(x, na.rm = FALSE)

sd(x, na.rm)
```

Arguments

x	object of class mrs_data.
na.rm	remove NA values.

Value

sd mrs_data object.

---

sd.mrs_data *Calculate the standard deviation spectrum from an mrs_data object.*

Description

Calculate the standard deviation spectrum from an mrs_data object.

Usage

```
## S3 method for class 'mrs_data'
sd(x, na.rm = FALSE)
```

Arguments

x	object of class mrs_data.
na.rm	remove NA values.

Value

sd mrs_data object.

seconds — *Return a time scale vector to match the FID of an MRS data object.*

Description

Return a time scale vector to match the FID of an MRS data object.

Usage

```
seconds(mrs_data)
```

Arguments

mrs_data	MRS data.

Value

time scale vector in units of seconds.

segment_t1_ants — *Segment T1 weighted MRI data using the ANTs binaries and write to file.*

Description

Segment T1 weighted MRI data using the ANTs binaries and write to file.

Usage

```
segment_t1_ants(mri_path, out_dir = NULL)
```

Arguments

mri_path	path to the volumetric T1 data.
out_dir	optional output directory. Defaults to the same directory as mri_path if not specified.

`segment_t1_fsl` *Segment T1 weighted MRI data using FSL FAST and write to file. Runs bet as a preprocessing step by default.*

Description

This function requires a working installation of FSL and uses the fslr package. You may need to specify the fsl install directory, eg: 'options(fsl.path = "/path/to/fsl")'

Usage

```
segment_t1_fsl(mri_path, out_dir = NULL, deface = FALSE, bet_fit = 0.5)
```

Arguments

`mri_path`	path to the volumetric T1 data.
`out_dir`	optional output directory. Defaults to the same directory as mri_path if not specified.
`deface`	deface the input T1 data before analysis. Defaults to FALSE.
`bet_fit`	fractional intensity threshold for bet brain extraction. Values should be between 0 and 1. Defaults to 0.5 with smaller values giving larger brain estimates.

`segment_t1_rpyants` *Segment T1 weighted MRI data using the rpyANTs interface to ANTs and write to file.*

Description

Segment T1 weighted MRI data using the rpyANTs interface to ANTs and write to file.

Usage

```
segment_t1_rpyants(mri_path, out_dir = NULL)
```

Arguments

`mri_path`	path to the volumetric T1 data.
`out_dir`	optional output directory. Defaults to the same directory as mri_path if not specified.

seq_cpmg_ideal *CPMG style sequence with ideal pulses.*

Description

CPMG style sequence with ideal pulses.

Usage

```
seq_cpmg_ideal(spin_params, ft, ref, TE = 0.03, echoes = 4)
```

Arguments

spin_params	spin system definition.
ft	transmitter frequency in Hz.
ref	reference value for ppm scale.
TE	echo time in seconds.
echoes	number of echoes.

Value

list of resonance amplitudes and frequencies.

seq_mega_press_ideal *MEGA-PRESS sequence with ideal localisation pulses and Gaussian shaped editing pulse.*

Description

MEGA-PRESS sequence with ideal localisation pulses and Gaussian shaped editing pulse.

Usage

```
seq_mega_press_ideal(
  spin_params,
  ft,
  ref,
  ed_freq = 1.89,
  TE1 = 0.015,
  TE2 = 0.053,
  BW = 110,
  steps = 50
)
```

Arguments

spin_params	spin system definition.
ft	transmitter frequency in Hz.
ref	reference value for ppm scale.
ed_freq	editing pulse frequency in ppm.
TE1	TE1 sequence parameter in seconds (TE=TE1+TE2).
TE2	TE2 sequence parameter in seconds.
BW	editing pulse bandwidth in Hz.
steps	number of hard pulses used to approximate the editing pulse.

Value

list of resonance amplitudes and frequencies.

---

seq_press_2d_shaped *PRESS sequence with shaped refocusing pulses.*

Description

PRESS sequence with shaped refocusing pulses.

Usage

```
seq_press_2d_shaped(
  spin_params,
  ft,
  ref,
  TE1 = 0.01,
  TE2 = 0.02,
  pulse_file,
  pulse_dur,
  pulse_file_format,
  refoc_flip_angle = 180,
  xy_pulse_ppm = NULL,
  resamp = TRUE,
  fs_resamp = 1e-04
)
```

Arguments

spin_params	spin system definition.
ft	transmitter frequency in Hz.
ref	reference value for ppm scale.
TE1	TE1 sequence parameter in seconds (TE=TE1+TE2).

TE2	TE2 sequence parameter in seconds.
pulse_file	path to refocusing pulse file.
pulse_dur	refocusing pulse duration.
pulse_file_format	file format for the refocusing pulse.
refoc_flip_angle	refocusing pulse flip angle in degrees (defaults to 180).
xy_pulse_ppm	a vector of ppm values for the offset of each sub-simulation.
resamp	option to resample the pulse shape.
fs_resamp	sampling frequency (Hz) to resample.

Value

list of resonance amplitudes and frequencies.

`seq_press_ideal` *PRESS sequence with ideal pulses.*

Description

PRESS sequence with ideal pulses.

Usage

```
seq_press_ideal(spin_params, ft, ref, TE1 = 0.01, TE2 = 0.02)
```

Arguments

spin_params	spin system definition.
ft	transmitter frequency in Hz.
ref	reference value for ppm scale.
TE1	TE1 sequence parameter in seconds (TE=TE1+TE2).
TE2	TE2 sequence parameter in seconds.

Value

list of resonance amplitudes and frequencies.

seq_pulse_acquire *Simple pulse and acquire sequence with ideal pulses.*

Description

Simple pulse and acquire sequence with ideal pulses.

Usage

```
seq_pulse_acquire(spin_params, ft, ref, nuc = "1H", acq_delay = 0)
```

Arguments

spin_params	spin system definition.
ft	transmitter frequency in Hz.
ref	reference value for ppm scale.
nuc	acquisition nucleus.
acq_delay	delay between excitation and acquisition.

Value

list of resonance amplitudes and frequencies.

seq_slaser_ideal *sLASER sequence with ideal pulses.*

Description

sLASER sequence with ideal pulses.

Usage

```
seq_slaser_ideal(spin_params, ft, ref, TE1 = 0.008, TE2 = 0.011, TE3 = 0.009)
```

Arguments

spin_params	spin system definition.
ft	transmitter frequency in Hz.
ref	reference value for ppm scale.
TE1	first echo time (between exc. and 1st echo) in seconds.
TE2	second echo time (between 2nd echo and 4th echo) in seconds.
TE3	third echo time (between 4th echo and 5th echo) in seconds.

Value

list of resonance amplitudes and frequencies.

seq_spin_echo_ideal *Spin echo sequence with ideal pulses.*

Description

Spin echo sequence with ideal pulses.

Usage

```
seq_spin_echo_ideal(spin_params, ft, ref, nuc = "1H", TE = 0.03)
```

Arguments

spin_params	spin system definition.
ft	transmitter frequency in Hz.
ref	reference value for ppm scale.
nuc	acquisition nucleus.
TE	echo time in seconds.

Value

list of resonance amplitudes and frequencies.

seq_steam_ideal *STEAM sequence with ideal pulses.*

Description

STEAM sequence with ideal pulses.

Usage

```
seq_steam_ideal(spin_params, ft, ref, TE = 0.03, TM = 0.02, amp_scale = 2)
```

Arguments

spin_params	spin system definition.
ft	transmitter frequency in Hz.
ref	reference value for ppm scale.
TE	sequence parameter in seconds.
TM	sequence parameter in seconds.
amp_scale	amplitude scaling factor. Set to 2 (default) to ensure correct scaling for water reference scaling. Set to 1 to maintain the inherent loss of signal associated with STEAM.

Value

list of resonance amplitudes and frequencies.

`seq_steam_ideal_cof` *STEAM sequence with ideal pulses and coherence order filtering to simulate gradient crushers.*

Description

See Landheer et al NMR Biomed 2021 34(5):e4129 and Landheer et al MRM 2019 Apr;81(4):2209-2222 for more details on the coherence order filtering method.

Usage

```
seq_steam_ideal_cof(spin_params, ft, ref, TE = 0.03, TM = 0.02, amp_scale = 2)
```

Arguments

`spin_params`	spin system definition.
`ft`	transmitter frequency in Hz.
`ref`	reference value for ppm scale.
`TE`	sequence parameter in seconds.
`TM`	sequence parameter in seconds.
`amp_scale`	amplitude scaling factor. Set to 2 (default) to ensure correct scaling for water reference scaling. Set to 1 to maintain the inherent loss of signal associated with STEAM.

Value

list of resonance amplitudes and frequencies.

`seq_steam_ideal_young` *STEAM sequence with ideal pulses using the z-rotation gradient simulation method described by Young et al JMR 140, 146-152 (1999).*

Description

STEAM sequence with ideal pulses using the z-rotation gradient simulation method described by Young et al JMR 140, 146-152 (1999).

Usage

```
seq_steam_ideal_young(
  spin_params,
  ft,
  ref,
  TE = 0.03,
  TM = 0.02,
  amp_scale = 2
)
```

Arguments

spin_params	spin system definition.
ft	transmitter frequency in Hz.
ref	reference value for ppm scale.
TE	sequence parameter in seconds.
TM	sequence parameter in seconds.
amp_scale	amplitude scaling factor. Set to 2 (default) to ensure correct scaling for water reference scaling. Set to 1 to maintain the inherent loss of signal associated with STEAM.

Value

list of resonance amplitudes and frequencies.

---

set_ants_dir *Set the ANTs installation directory location.*

Description

Set the ANTs installation directory location.

Usage

```
set_ants_dir(dir)
```

Arguments

dir	ANTs installation directory.

set_def_acq_paras *Set the default acquisition parameters.*

Description

Set the default acquisition parameters.

Usage

```
set_def_acq_paras(
  ft = getOption("spant.def_ft"),
  fs = getOption("spant.def_fs"),
  N = getOption("spant.def_N"),
  ref = getOption("spant.def_ref"),
  nuc = getOption("spant.nuc")
)
```

Arguments

ft	transmitter frequency in Hz.
fs	sampling frequency in Hz.
N	number of data points in the spectral dimension.
ref	reference value for ppm scale.
nuc	resonant nucleus.

set_lcm_cmd *Set the command to run the LCModel command-line program.*

Description

Set the command to run the LCModel command-line program.

Usage

```
set_lcm_cmd(cmd)
```

Arguments

cmd	path to binary.

set_lw — *Apply line-broadening to an mrs_data object to achieve a specified linewidth.*

Description

Apply line-broadening to an mrs_data object to achieve a specified linewidth.

Usage

```
set_lw(mrs_data, lw, xlim = c(4, 0.5), lg = 1, mask_narrow = TRUE)
```

Arguments

mrs_data	data in.
lw	target linewidth in units of ppm.
xlim	region to search for peaks to obtain a linewidth estimate.
lg	Lorentz-Gauss lineshape parameter.
mask_narrow	masks spectra where the requested linewidth is too narrow, if set FALSE the spectra are not changed.

Value

line-broadened data.

set_mask_xy_mat — *Set the masked voxels in a 2D MRSI dataset to given spectrum.*

Description

Set the masked voxels in a 2D MRSI dataset to given spectrum.

Usage

```
set_mask_xy_mat(mrs_data, mask, mask_mrs_data)
```

Arguments

mrs_data	MRSI data object.
mask	matrix of boolean values specifying the voxels to set, where a value of TRUE indicates the voxel should be set to mask_mrs_data.
mask_mrs_data	the spectral data to be assigned to the masked voxels.

Value

updated dataset.

set_Ntrans *Set the number of transients for an mrs_data object.*

Description

Set the number of transients for an mrs_data object.

Usage

```
set_Ntrans(mrs_data, n_trans)
```

Arguments

mrs_data	MRS data.
n_trans	number of acquired transients.

set_precomp_mode *Set the precompute mode.*

Description

Set the precompute mode.

Usage

```
set_precomp_mode(mode = NA)
```

Arguments

mode	can be one of: "default", "overwrite", "clean" or "disabled".

set_precomp_verbose *Set the verbosity of the precompute function.*

Description

Set the verbosity of the precompute function.

Usage

```
set_precomp_verbose(verbose = NA)
```

Arguments

verbose	can be TRUE or FALSE.

set_ref — *Set the ppm reference value (eg ppm value at 0Hz).*

Description

Set the ppm reference value (eg ppm value at 0Hz).

Usage

```
set_ref(mrs_data, ref)
```

Arguments

mrs_data	MRS data.
ref	reference value for ppm scale.

set_td_pts — *Set the number of time-domain data points, truncating or zero-filling as appropriate.*

Description

Set the number of time-domain data points, truncating or zero-filling as appropriate.

Usage

```
set_td_pts(mrs_data, pts)
```

Arguments

mrs_data	MRS data.
pts	number of data points.

Value

MRS data with pts data points.

set_tqn_cmd *Set the command to run the TARQUIN command-line program.*

Description

Set the command to run the TARQUIN command-line program.

Usage

```
set_tqn_cmd(cmd)
```

Arguments

cmd	path to binary.

set_tr *Set the repetition time of an MRS dataset.*

Description

Set the repetition time of an MRS dataset.

Usage

```
set_tr(mrs_data, tr)
```

Arguments

mrs_data	MRS data.
tr	repetition time in seconds.

Value

updated mrs_data set.

shift *Apply a frequency shift to MRS data.*

Description

Apply a frequency shift to MRS data.

Usage

```
shift(mrs_data, shift, units = "ppm")
```

Arguments

mrs_data	MRS data.
shift	frequency shift (in ppm by default).
units	of the shift ("ppm" or "hz").

Value

frequency shifted MRS data.

shift_basis *Apply frequency shifts to basis set signals.*

Description

Apply frequency shifts to basis set signals.

Usage

```
shift_basis(basis, shifts)
```

Arguments

basis	the basis to apply the shift to.
shifts	a vector of frequency shifts to apply in ppm units. Must be the same length as there are basis elements, or one value to be applied to all elements.

Value

modified basis set object.

sim_asy_pvoigt — *Generate an asymmetric pseudo-Voigt resonance in the frequency domain.*

Description

Method is described in detail by Stancik AL and Brauns EB: "A simple asymmetric lineshape for fitting infrared absorption spectra." Vib Spectrosc. 2008; 47: 66-69.

Usage

```
sim_asy_pvoigt(
  freq = 0,
  fwhm = 0,
  lg = 0,
  asy = 0,
  acq_paras = def_acq_paras(),
  gen_im_pts = FALSE
)
```

Arguments

freq	resonance frequency in ppm.
fwhm	resonance FWHM in Hz.
lg	Lorentz-Gauss lineshape parameter (between 0 and 1).
asy	asymmetry parameter.
acq_paras	list of acquisition parameters. See def_acq_paras
gen_im_pts	option to generate imaginary data points, defaults to FALSE.

sim_basis — *Simulate a basis set object.*

Description

Simulate a basis set object.

Usage

```
sim_basis(
  mol_list,
  pul_seq = seq_pulse_acquire,
  acq_paras = def_acq_paras(),
  xlim = NULL,
  auto_scale = FALSE,
```

```
  use_basis_cache = FALSE,
  verbose = FALSE,
  ...
)
```

Arguments

mol_list	list of mol_parameter objects. Alternatively, a character vector matching molecules may also be provided. Use the get_mol_names function for a full list of molecules.
pul_seq	pulse sequence function to use.
acq_paras	list of acquisition parameters or an mrs_data object. See def_acq_paras
xlim	ppm range limiting signals to be simulated.
auto_scale	scale the basis based on the intensity of a singlet resonance. Needed for sequences with spatial simulation.
use_basis_cache	create and use a cache of simulated basis sets stored in the "basis_cache" folder in the spant resources directory. Defaults to FALSE.
verbose	output simulation progress and timings.
...	extra parameters to pass to the pulse sequence function.

Value

basis object.

---

sim_basis_1h_brain *Simulate a basis-set suitable for 1H brain MRS analysis acquired with a PRESS sequence. Note, ideal pulses are assumed.*

Description

Simulate a basis-set suitable for 1H brain MRS analysis acquired with a PRESS sequence. Note, ideal pulses are assumed.

Usage

```
sim_basis_1h_brain(
  pul_seq = seq_press_ideal,
  acq_paras = def_acq_paras(),
  xlim = c(0.5, 4.2),
  lcm_compat = FALSE,
  ...
)
```

Arguments

pul_seq	pulse sequence function to use.
acq_paras	list of acquisition parameters or an mrs_data object. See def_acq_paras.
xlim	range of frequencies to simulate in ppm.
lcm_compat	exclude lipid and MM signals for use with default LCModel options.
...	extra parameters to pass to the pulse sequence function.

Value

basis object.

---

sim_basis_1h_brain_press

Simulate a basis-set suitable for 1H brain MRS analysis acquired with a PRESS sequence. Note, ideal pulses are assumed.

Description

Simulate a basis-set suitable for 1H brain MRS analysis acquired with a PRESS sequence. Note, ideal pulses are assumed.

Usage

```
sim_basis_1h_brain_press(
  acq_paras = def_acq_paras(),
  xlim = c(0.5, 4.2),
  lcm_compat = FALSE,
  TE1 = 0.01,
  TE2 = 0.02
)
```

Arguments

acq_paras	list of acquisition parameters or an mrs_data object. See def_acq_paras
xlim	range of frequencies to simulate in ppm.
lcm_compat	exclude lipid and MM signals for use with default LCModel options.
TE1	TE1 of PRESS sequence (TE = TE1 + TE2).
TE2	TE2 of PRESS sequence.

Value

basis object.

sim_basis_mm_lip_lcm *Simulate a macromolecular and lipid basis-set suitable for 1H brain MRS analysis.*

Description

Simulate a macromolecular and lipid basis-set suitable for 1H brain MRS analysis.

Usage

```
sim_basis_mm_lip_lcm(acq_paras = def_acq_paras())
```

Arguments

acq_paras	list of acquisition parameters or an mrs_data object. See def_acq_paras

Value

basis object.

sim_basis_tqn *Simulate a basis file using TARQUIN.*

Description

Simulate a basis file using TARQUIN.

Usage

```
sim_basis_tqn(
  fs = def_fs(),
  ft = def_ft(),
  N = def_N(),
  ref = def_ref(),
  opts = NULL
)
```

Arguments

fs	sampling frequency
ft	transmitter frequency
N	number of data points
ref	chemical shift reference
opts	list of options to pass to TARQUIN.

Examples

```
## Not run:
write_basis_tqn('test.basis',mrs_data,c("--echo","0.04"))

## End(Not run)
```

`sim_brain_1h` *Simulate MRS data with a similar appearance to normal brain (by default).*

Description

Simulate MRS data with a similar appearance to normal brain (by default).

Usage

```
sim_brain_1h(
  acq_paras = def_acq_paras(),
  type = "normal_v2",
  pul_seq = seq_slaser_ideal,
  xlim = c(0.5, 4.2),
  full_output = FALSE,
  amps = NULL,
  basis_lb = NULL,
  zero_lip_mm = FALSE,
  remove_lip_mm = FALSE,
  ...
)
```

Arguments

`acq_paras`	list of acquisition parameters or an mrs_data object. See `def_acq_paras`.
`type`	type of spectrum, only "normal" is implemented currently.
`pul_seq`	pulse sequence function to use.
`xlim`	range of frequencies to simulate in ppm.
`full_output`	when FALSE (default) only output the simulated MRS data. When TRUE output a list containing the MRS data, basis set object and corresponding amplitudes.
`amps`	a vector of basis amplitudes may be specified to modify the output spectrum.
`basis_lb`	apply additional Gaussian line-broadening to the basis (Hz).
`zero_lip_mm`	zero the amplitudes of any lipid or macromolecular components based on their name starting with "MM" or "Lip".
`remove_lip_mm`	remove any lipid or macromolecular basis components based on their name starting with "MM" or "Lip".
`...`	extra parameters to pass to the pulse sequence function.

Value

see full_output option.

`sim_mol` *Simulate a* `mol_parameter` *object.*

Description

Simulate a `mol_parameter` object.

Usage

```
sim_mol(
  mol,
  pul_seq = seq_pulse_acquire,
  ft = def_ft(),
  ref = def_ref(),
  fs = def_fs(),
  N = def_N(),
  xlim = NULL,
  ...
)
```

Arguments

`mol`	`mol_parameter` object.
`pul_seq`	pulse sequence function to use.
`ft`	transmitter frequency in Hz.
`ref`	reference value for ppm scale.
`fs`	sampling frequency in Hz.
`N`	number of data points in the spectral dimension.
`xlim`	ppm range limiting signals to be simulated.
`...`	extra parameters to pass to the pulse sequence function.

Value

`mrs_data` object.

`sim_noise` *Simulate an mrs_data object containing simulated Gaussian noise.*

Description

Simulate an mrs_data object containing simulated Gaussian noise.

Usage

```
sim_noise(
  sd = 0.1,
  fs = def_fs(),
  ft = def_ft(),
  N = def_N(),
  ref = def_ref(),
  nuc = def_nuc(),
  dyns = 1,
  fd = TRUE
)
```

Arguments

`sd`	standard deviation of the noise.
`fs`	sampling frequency in Hz.
`ft`	transmitter frequency in Hz.
`N`	number of data points in the spectral dimension.
`ref`	reference value for ppm scale.
`nuc`	resonant nucleus.
`dyns`	number of dynamic scans to generate.
`fd`	return data in the frequency-domain (TRUE) or time-domain (FALSE)

Value

mrs_data object.

`sim_resonances` *Simulate a MRS data object containing a set of simulated resonances.*

Description

Simulate a MRS data object containing a set of simulated resonances.

Usage

```
sim_resonances(
  freq = 0,
  amp = 1,
  lw = 0,
  lg = 0,
  phase = 0,
  freq_ppm = TRUE,
  acq_paras = def_acq_paras(),
  fp_scale = TRUE,
  back_extrap_pts = 0,
  sum_resonances = TRUE
)
```

Arguments

`freq`	resonance frequency.
`amp`	resonance amplitude.
`lw`	line width in Hz.
`lg`	Lorentz-Gauss lineshape parameter (between 0 and 1).
`phase`	phase in degrees.
`freq_ppm`	frequencies are given in ppm units if set to TRUE, otherwise Hz are assumed.
`acq_paras`	list of acquisition parameters. See `def_acq_paras`
`fp_scale`	multiply the first data point by 0.5.
`back_extrap_pts`	number of data points to back extrapolate.
`sum_resonances`	sum all resonances (default is TRUE), otherwise return a dynamic mrs_data object.

Value

MRS data object.

Examples

```
sim_data <- sim_resonances(freq = 2, lw = 5)
```

sim_th_excit_profile *Simulate an ideal pulse excitation profile by smoothing a top-hat function with a Gaussian.*

Description

Simulate an ideal pulse excitation profile by smoothing a top-hat function with a Gaussian.

Usage

```
sim_th_excit_profile(bw = 1500, sigma = 50, fa = 180)
```

Arguments

bw	top-hat bandwidth (Hz).
sigma	Gaussian width smoothing parameter (Hz).
fa	intended flip angle of the pulse.

Value

data frame containing the frequency scale, excitation profile and corresponding flip-angles.

sim_zero *Simulate an mrs_data object containing complex zero valued samples.*

Description

Simulate an mrs_data object containing complex zero valued samples.

Usage

```
sim_zero(
  fs = def_fs(),
  ft = def_ft(),
  N = def_N(),
  ref = def_ref(),
  nuc = def_nuc(),
  dyns = 1
)
```

Arguments

fs	sampling frequency in Hz.
ft	transmitter frequency in Hz.
N	number of data points in the spectral dimension.
ref	reference value for ppm scale.
nuc	resonant nucleus.
dyns	number of dynamic scans to generate.

Value

mrs_data object.

---

smooth_dyns *Smooth data across the dynamic dimension with a Gaussian kernel.*

Description

Smooth data across the dynamic dimension with a Gaussian kernel.

Usage

```
smooth_dyns(mrs_data, sigma)
```

Arguments

mrs_data	data to be smoothed.
sigma	standard deviation of the underlying Gaussian kernel in seconds.

Value

smoothed mrs_data object.

sort_basis *Sort the basis-set elements alphabetically.*

Description

Sort the basis-set elements alphabetically.

Usage

```
sort_basis(basis)
```

Arguments

basis	input basis.

Value

sorted basis.

spant_abfit_benchmark *Simulate and fit some spectra with ABfit for benchmarking purposes. Basic timing and performance metrics will be printed.*

Description

Simulate and fit some spectra with ABfit for benchmarking purposes. Basic timing and performance metrics will be printed.

Usage

```
spant_abfit_benchmark(noise_reps = 10, return_res = FALSE, opts = abfit_opts())
```

Arguments

noise_reps	number of spectra to fit with differing noise samples.
return_res	return a list of fit_result objects.
opts	ABfit options structure.

`spant_simulation_benchmark` *Simulate a typical metabolite basis set for benchmarking. Timing metrics will be printed on completion.*

Description

Simulate a typical metabolite basis set for benchmarking. Timing metrics will be printed on completion.

Usage

```
spant_simulation_benchmark(sim_reps = 10, N = 1024)
```

Arguments

`sim_reps`	number of times to simulate the basis set.
`N`	number of FID data points to simulate.

`spant_sim_fmrs_dataset` *Simulate an example fMRS dataset for a block design fMRS experiment and export a BIDS structure.*

Description

Simulate an example fMRS dataset for a block design fMRS experiment and export a BIDS structure.

Usage

```
spant_sim_fmrs_dataset(output_dir = NULL)
```

Arguments

`output_dir`	output directory for the BIDS data. Defaults to : "HOME/sim_fmrs_dataset/data".

spec_decomp *Decompose an mrs_data object into white and gray matter spectra.*

Description

An implementation of the method published by Goryawala et al MRM 79(6) 2886-2895 (2018). "Spectral decomposition for resolving partial volume effects in MRSI".

Usage

```
spec_decomp(mrs_data, wm, gm, norm_fractions = TRUE)
```

Arguments

mrs_data	data to be decomposed into white and gray matter spectra.
wm	vector of white matter contributions to each voxel.
gm	vector of gray matter contributions to each voxel.
norm_fractions	option to normalise the wm, gm vectors for each voxel.

Value

a list of two mrs_data objects corresponding to the two tissue types.

spec_op *Perform a mathematical operation on a spectral region.*

Description

Perform a mathematical operation on a spectral region.

Usage

```
spec_op(
  mrs_data,
  xlim = NULL,
  operator = "sum",
  freq_scale = "ppm",
  mode = "re"
)
```

Arguments

mrs_data	MRS data.
xlim	spectral range to be integrated (defaults to full range).
operator	can be "sum" (default), "mean", "l2", "max", "max_cplx, "min" or "max-min".
freq_scale	units of xlim, can be : "ppm", "hz" or "points".
mode	spectral mode, can be : "re", "im", "mod" or "cplx".

Value

an array of integral values.

---

spin_sys *Create a spin system object for pulse sequence simulation.*

Description

Create a spin system object for pulse sequence simulation.

Usage

```
spin_sys(spin_params, ft, ref, precomp_jc_H = NULL, precomp_Iz = NULL)
```

Arguments

spin_params	an object describing the spin system properties.
ft	transmitter frequency in Hz.
ref	reference value for ppm scale.
precomp_jc_H	use a precomputed J-coupling H matrix to save time.
precomp_Iz	use precomputed Iz matrices to save time.

Value

spin system object.

spm_pve2categorical *Convert SPM style segmentation files to a single categorical image where the numerical values map as: 0) Other, 1) CSF, 2) GM and 3) WM.*

Description

Convert SPM style segmentation files to a single categorical image where the numerical values map as: 0) Other, 1) CSF, 2) GM and 3) WM.

Usage

```
spm_pve2categorical(fname)
```

Arguments

fname	any of the segmentation files (eg c1_MY_T1.nii).

Value

nifti object.

ssp *Signal space projection method for lipid suppression.*

Description

Signal space projection method as described in: Tsai SY, Lin YR, Lin HY, Lin FH. Reduction of lipid contamination in MR spectroscopy imaging using signal space projection. Magn Reson Med 2019 Mar;81(3):1486-1498.

Usage

```
ssp(mrs_data, comps = 5, xlim = c(1.5, 0.8))
```

Arguments

mrs_data	MRS data object.
comps	the number of spatial components to use.
xlim	spectral range (in ppm) covering the lipid signals.

Value

lipid suppressed mrs_data object.

stackplot *Produce a plot with multiple traces.*

Description

Produce a plot with multiple traces.

Usage

```
stackplot(x, ...)
```

Arguments

x	object for plotting.
...	arguments to be passed to methods.

stackplot.fit_result *Plot the fitting results of an object of class* fit_result *with individual basis set components shown.*

Description

Plot the fitting results of an object of class fit_result with individual basis set components shown.

Usage

```
## S3 method for class 'fit_result'
stackplot(
  x,
  xlim = NULL,
  y_offset = 0,
  dyn = 1,
  x_pos = 1,
  y_pos = 1,
  z_pos = 1,
  coil = 1,
  n = NULL,
  sub_bl = FALSE,
  labels = FALSE,
  label_names = NULL,
  sig_col = "black",
  restore_def_par = TRUE,
  omit_signals = NULL,
  combine_lipmm = FALSE,
  combine_metab = FALSE,
```

```
  mar = NULL,
  show_grid = TRUE,
  grid_nx = NULL,
  grid_ny = NA,
  invert_fit = FALSE,
  ...
)
```

Arguments

x	fit_result object.
xlim	the range of values to display on the x-axis, eg xlim = c(4,1).
y_offset	separate basis signals in the y-axis direction by this value.
dyn	the dynamic index to plot.
x_pos	the x index to plot.
y_pos	the y index to plot.
z_pos	the z index to plot.
coil	the coil element number to plot.
n	single index element to plot (overrides other indices when given).
sub_bl	subtract the baseline from the data and fit (logical).
labels	print signal labels at the right side of the plot.
label_names	provide a character vector of signal names to replace the defaults determined from the basis set.
sig_col	colour of individual signal components.
restore_def_par	restore default plotting par values after the plot has been made.
omit_signals	a character vector of basis signal names to be removed from the plot.
combine_lipmm	combine all basis signals with names starting with "Lip" or "MM".
combine_metab	combine all basis signals with names not starting with "Lip" or "MM".
mar	option to adjust the plot margins. See ?par.
show_grid	plot gridlines behind the data (logical). Defaults to TRUE.
grid_nx	number of cells of the grid in x and y direction. When NULL the grid aligns with the tick marks on the corresponding default axis (i.e., tickmarks as computed by axTicks). When NA, no grid lines are drawn in the corresponding direction.
grid_ny	as above.
invert_fit	show the fit result "upside-down"/
...	further arguments to plot method.

`stackplot.mrs_data` *Stackplot plotting method for objects of class mrs_data.*

Description

Stackplot plotting method for objects of class mrs_data.

Usage

```
## S3 method for class 'mrs_data'
stackplot(
  x,
  xlim = NULL,
  mode = "re",
  x_units = NULL,
  fd = TRUE,
  col = NULL,
  alpha = NULL,
  x_offset = 0,
  y_offset = 0,
  plot_dim = NULL,
  x_pos = NULL,
  y_pos = NULL,
  z_pos = NULL,
  dyn = 1,
  coil = 1,
  bty = NULL,
  labels = NULL,
  lab_cex = 1,
  bl_lty = NULL,
  bl_lwd = 0.5,
  restore_def_par = TRUE,
  show_grid = NULL,
  grid_nx = NULL,
  grid_ny = NA,
  lwd = NULL,
  vline = NULL,
  vline_lty = 2,
  vline_col = "red",
  mar = NULL,
  y_scale = FALSE,
  ...
)
```

Arguments

x	object of class mrs_data.

xlim	the range of values to display on the x-axis, eg xlim = c(4,1).
mode	representation of the complex numbers to be plotted, can be one of: "re", "im", "mod" or "arg".
x_units	the units to use for the x-axis, can be one of: "ppm", "hz", "points" or "seconds".
fd	display data in the frequency-domain (default), or time-domain (logical).
col	set the colour of the line, eg col = rgb(1, 0, 0, 0.5).
alpha	set the line transparency, eg alpha = 0.5 is 50% transparency. Overrides any transparency levels set by col.
x_offset	separate plots in the x-axis direction by this value. Default value is 0.
y_offset	separate plots in the y-axis direction by this value.
plot_dim	the dimension to display on the y-axis, can be one of: "dyn", "x", "y", "z", "coil" or NULL. If NULL (the default) all spectra will be collapsed into the dynamic dimension and displayed.
x_pos	the x index to plot.
y_pos	the y index to plot.
z_pos	the z index to plot.
dyn	the dynamic index to plot.
coil	the coil element number to plot.
bty	option to draw a box around the plot. See ?par.
labels	add labels to each data item.
lab_cex	label size.
bl_lty	linetype for the y = 0 baseline trace. A default value NULL results in no baseline being plotted.
bl_lwd	linewith for the y = 0 baseline trace. Defaults to 0.5.
restore_def_par	restore default plotting par values after the plot has been made.
show_grid	plot gridlines behind the data (logical). Defaults to TRUE.
grid_nx	number of cells of the grid in x and y direction. When NULL the grid aligns with the tick marks on the corresponding default axis (i.e., tickmarks as computed by axTicks). When NA, no grid lines are drawn in the corresponding direction.
grid_ny	as above.
lwd	plot linewidth.
vline	x-value to draw a vertical line.
vline_lty	linetype for the vertical line.
vline_col	colour for the vertical line.
mar	option to adjust the plot margins. See ?par.
y_scale	option to display the y-axis values (logical).
...	other arguments to pass to the matplot method.

`subtract_rest_task` *Subtract mean rest spectrum from mean task spectrum after applying optimal linebroadening to the mean task spectrum. Usually used to correct for the BOLD lineshape narrowing effect in 1H fMRS data.*

Description

Subtract mean rest spectrum from mean task spectrum after applying optimal linebroadening to the mean task spectrum. Usually used to correct for the BOLD lineshape narrowing effect in 1H fMRS data.

Usage

```
subtract_rest_task(mrs_data, task_vec, xlim = c(2.11, 1.91))
```

Arguments

`mrs_data`	dynamic MRS data.
`task_vec`	a logical vector with the same length and dynamic scans. Elements set to TRUE and FALSE will be assigned to task and rest respectively.
`xlim`	spectral region to match, eg c(2.11, 1.91) for tNAA region.

Value

a list containing the matched mrs_data, difference spectra and optimisation results.

`sub_even_from_odd_dyns` *Subtract the even dynamic scans from the odd dynamic scans.*

Description

Subtract the even dynamic scans from the odd dynamic scans.

Usage

```
sub_even_from_odd_dyns(mrs_data)
```

Arguments

`mrs_data`	dynamic MRS data.

Value

subtracted result.

sub_first_dyn *Subtract the first dynamic spectrum from a dynamic series.*

Description

Subtract the first dynamic spectrum from a dynamic series.

Usage

```
sub_first_dyn(mrs_data, scale = 1)
```

Arguments

mrs_data	dynamic MRS data.
scale	scale factor for the first spectrum.

Value

subtracted data.

sub_mean_dyns *Subtract the mean dynamic spectrum from a dynamic series.*

Description

Subtract the mean dynamic spectrum from a dynamic series.

Usage

```
sub_mean_dyns(mrs_data, scale = 1)
```

Arguments

mrs_data	dynamic MRS data.
scale	scale factor for the mean spectrum.

Value

subtracted data.

sub_median_dyns *Subtract the median dynamic spectrum from a dynamic series.*

Description

Subtract the median dynamic spectrum from a dynamic series.

Usage

```
sub_median_dyns(mrs_data, scale = 1)
```

Arguments

mrs_data	dynamic MRS data.
scale	scale factor for the medium spectrum.

Value

subtracted data.

sub_odd_from_even_dyns *Subtract the odd dynamic scans from the even dynamic scans.*

Description

Subtract the odd dynamic scans from the even dynamic scans.

Usage

```
sub_odd_from_even_dyns(mrs_data)
```

Arguments

mrs_data	dynamic MRS data.

Value

subtracted result.

sum_coils *Calculate the sum across receiver coil elements.*

Description

Calculate the sum across receiver coil elements.

Usage

```
sum_coils(mrs_data)
```

Arguments

mrs_data	MRS data split across receiver coil elements.

Value

sum across coil elements.

sum_dyns *Calculate the sum of data dynamics.*

Description

Calculate the sum of data dynamics.

Usage

```
sum_dyns(mrs_data)
```

Arguments

mrs_data	dynamic MRS data.

Value

sum of data dynamics.

sum_mrs *Sum two mrs_data objects.*

Description

Sum two mrs_data objects.

Usage

```
sum_mrs(a, b, force = FALSE)
```

Arguments

a	first mrs_data object to be summed.
b	second mrs_data object to be summed.
force	set to TRUE to force mrs_data objects to be summed, even if they are in different time/frequency domains.

Value

a + b

sum_mrs_list *Return the sum of a list of mrs_data objects.*

Description

Return the sum of a list of mrs_data objects.

Usage

```
sum_mrs_list(mrs_list)
```

Arguments

mrs_list	list of mrs_data objects.

Value

sum mrs_data object.

`svs_1h_brain_analysis` *Standard SVS 1H brain analysis pipeline.*

Description

Standard SVS 1H brain analysis pipeline.

Usage

```
svs_1h_brain_analysis(
  metab,
  basis = NULL,
  w_ref = NULL,
  mri_seg = NULL,
  mri = NULL,
  output_dir = NULL,
  extra = NULL,
  decimate = NULL,
  rats_corr = TRUE,
  ecc = FALSE,
  comb_dyns = TRUE,
  hsvd_filt = FALSE,
  scale_amps = TRUE,
  te = NULL,
  tr = NULL,
  preproc_only = FALSE,
  method = "ABFIT",
  opts = NULL
)
```

Arguments

`metab`	filepath or mrs_data object containing MRS metabolite data.
`basis`	basis set object to use for analysis.
`w_ref`	filepath or mrs_data object containing MRS water reference data.
`mri_seg`	filepath or nifti object containing segmented MRI data.
`mri`	filepath or nifti object containing anatomical MRI data.
`output_dir`	directory path to output fitting results.
`extra`	data.frame with one row containing additional information to be attached to the fit results table.
`decimate`	option to decimate the input data by a factor of two. The default value of NULL does not perform decimation unless the spectral width is greater than 20 PPM.
`rats_corr`	option to perform rats correction, defaults to TRUE.
`ecc`	option to perform water reference based eddy current correction, defaults to FALSE.

comb_dyns	option to combine dynamic scans, defaults to TRUE.
hsvd_filt	option to apply hsvd water removal, defaults to FALSE.
scale_amps	option to scale metabolite amplitude estimates, defaults to TRUE.
te	metabolite mrs data echo time in seconds.
tr	metabolite mrs data repetition time in seconds.
preproc_only	only perform the preprocessing steps and omit fitting. The preprocessed metabolite data will be returned in this case.
method	analysis method to use, see fit_mrs help.
opts	options to pass to the analysis method.

Value

a fit_result or mrs_data object depending on the preproc_only option.

`svs_1h_brain_analysis_dev` *Standard SVS 1H brain analysis pipeline.*

Description

Note this function is still under development and liable to changes.

Usage

```
svs_1h_brain_analysis_dev(
  metab,
  w_ref = NULL,
  output_dir = NULL,
  basis = NULL,
  p_vols = NULL,
  append_basis = NULL,
  remove_basis = NULL,
  dfp_corr = FALSE,
  omit_bad_dynamics = FALSE,
  te = NULL,
  tr = NULL,
  output_ratio = "tCr",
  ecc = FALSE,
  abfit_opts = NULL,
  verbose = FALSE
)
```

Arguments

metab	filepath or mrs_data object containing MRS metabolite data.
w_ref	filepath or mrs_data object containing MRS water reference data.
output_dir	directory path to output fitting results.
basis	precompiled basis set object to use for analysis.
p_vols	a numeric vector of partial volumes expressed as percentages. Defaults to 100% white matter. A voxel containing 100% gray matter tissue would use : p_vols = c(WM = 0, GM = 100, CSF = 0).
append_basis	names of extra signals to add to the default basis. Eg append_basis = c("peth", "cit"). Cannot be used with precompiled basis sets.
remove_basis	names of signals to remove from the basis. Cannot be used with precompiled basis sets.
dfp_corr	perform dynamic frequency and phase correction using the RATS method.
omit_bad_dynamics	detect and remove bad dynamics.
te	metabolite mrs data echo time in seconds. If not supplied this will be guessed from the metab data file.
tr	metabolite mrs data repetition time in seconds. If not supplied this will be guessed from the metab data file.
output_ratio	optional string to specify a metabolite ratio to output. Defaults to "tCr" and multiple metabolites may be specified for multiple outputs. Set as NULL to omit.
ecc	option to perform water reference based eddy current correction, defaults to FALSE.
abfit_opts	options to pass to ABfit.
verbose	output potentially useful information.

Examples

```
metab <- system.file("extdata", "philips_spar_sdat_WS.SDAT",
                     package = "spant")
w_ref <- system.file("extdata", "philips_spar_sdat_W.SDAT",
                     package = "spant")
## Not run:
fit_result <- svs_1h_brain_analysis(metab, w_ref, "fit_res_dir")

## End(Not run)
```

svs_1h_brain_batch_analysis *Batch interface to the standard SVS 1H brain analysis pipeline.*

Description

Batch interface to the standard SVS 1H brain analysis pipeline.

Usage

```
svs_1h_brain_batch_analysis(
  metab_list,
  w_ref_list = NULL,
  mri_seg_list = NULL,
  mri_list = NULL,
  output_dir_list = NULL,
  extra = NULL,
  ...
)
```

Arguments

metab_list	list of file paths or mrs_data objects containing MRS metabolite data.
w_ref_list	list of file paths or mrs_data objects containing MRS water reference data.
mri_seg_list	list of file paths or nifti objects containing segmented MRI data.
mri_list	list of file paths or nifti objects containing anatomical MRI data.
output_dir_list	list of directory paths to output fitting results.
extra	a data frame with the same number of rows as metab_list, containing additional information to be attached to the fit results table.
...	additional options to be passed to the svs_1h_brain_analysis function.

Value

a list of fit_result objects.

sv_res_table — *Output a table of fit amplitudes and error estimates for a single-voxel fit.*

Description

Output a table of fit amplitudes and error estimates for a single-voxel fit.

Usage

```
sv_res_table(fit_res, format_out = FALSE)
```

Arguments

fit_res	input vector.
format_out	reduce the accuracy of values to aid table formatting.

Value

data.frame of values.

td2fd — *Transform time-domain data to the frequency-domain.*

Description

Transform time-domain data to the frequency-domain.

Usage

```
td2fd(mrs_data)
```

Arguments

mrs_data	MRS data in time-domain representation.

Value

MRS data in frequency-domain representation.

tdsr *Time-domain spectral registration.*

Description

An implementation of the method published by Near et al MRM 73:44-50 (2015).

Usage

```
tdsr(mrs_data, ref = NULL, xlim = c(4, 0.5), max_t = 0.2)
```

Arguments

mrs_data	MRS data to be corrected.
ref	optional MRS data to use as a reference, the mean of all dynamics is used if this argument is not supplied.
xlim	optional frequency range to perform optimisation, set to NULL to use the full range.
max_t	truncate the FID when longer than max_t to reduce time taken.

Value

a list containing the corrected data; phase and shift values in units of degrees and Hz respectively.

td_conv_filt *Time-domain convolution based filter.*

Description

Time-domain convolution based filter described by: Marion D, Ikura M, Bax A. Improved solvent suppression in one-dimensional and twodimensional NMR spectra by convolution of time-domain data. J Magn Reson 1989;84:425-430.

Usage

```
td_conv_filt(mrs_data, K = 25, ext = 1)
```

Arguments

mrs_data	MRS data to be filtered.
K	window width in data points.
ext	point separation for linear extrapolation.

te *Return the echo time of an MRS dataset.*

Description

Return the echo time of an MRS dataset.

Usage

```
te(mrs_data)
```

Arguments

mrs_data	MRS data.

Value

echo time in seconds.

tr *Return the repetition time of an MRS dataset.*

Description

Return the repetition time of an MRS dataset.

Usage

```
tr(mrs_data)
```

Arguments

mrs_data	MRS data.

Value

repetition time in seconds.

trim_paths *Trim a vector of filesystem paths.*

Description

Trim a vector of filesystem paths.

Usage

```
trim_paths(paths, dir = 0, char = 0)
```

Arguments

paths	vectors of filesystem paths.
dir	number of times to apply the base dirname function.
char	number of characters to trim from the end of each path. Note this is performed after the dir based trimming.

Value

a vector of trimmed paths.

t_test_spec *Perform a t-test on spectral data points.*

Description

Perform a t-test on spectral data points.

Usage

```
t_test_spec(mrs_data, group)
```

Arguments

mrs_data	an mrs_data object with spectra in the dynamic dimension.
group	vector describing the group membership of each dynamic spectrum.

Value

a list of statistical results.

varpro_3_para_opts *Return a list of options for VARPRO based fitting with 3 free parameters.*

Description

Return a list of options for VARPRO based fitting with 3 free parameters.

Usage

```
varpro_3_para_opts(
  nstart = 20,
  init_damping = 2,
  maxiters = 200,
  max_shift = 5,
  max_damping = 5,
  anal_jac = FALSE,
  bl_smth_pts = 80
)
```

Arguments

nstart	position in the time-domain to start fitting, units of data points.
init_damping	starting value for the global Gaussian line-broadening term - measured in Hz.
maxiters	maximum number of levmar iterations to perform.
max_shift	maximum global shift allowed, measured in Hz.
max_damping	maximum damping allowed, FWHM measured in Hz.
anal_jac	option to use the analytic or numerical Jacobian (logical).
bl_smth_pts	number of data points to use in the baseline smoothing calculation.

Value

list of options.

varpro_basic_opts *Return a list of options for a basic VARPRO analysis.*

Description

Return a list of options for a basic VARPRO analysis.

Usage

```
varpro_basic_opts(method = "fd_re", nnls = TRUE, ppm_left = 4, ppm_right = 0.2)
```

Arguments

method	one of "td", "fd", "fd_re".
nnls	restrict basis amplitudes to non-negative values.
ppm_left	downfield frequency limit for the fitting range (ppm).
ppm_right	upfield frequency limit for the fitting range (ppm).

Value

full list of options.

---

varpro_opts *Return a list of options for VARPRO based fitting.*

Description

Return a list of options for VARPRO based fitting.

Usage

```
varpro_opts(
  nstart = 20,
  init_g_damping = 2,
  maxiters = 200,
  max_shift = 5,
  max_g_damping = 5,
  max_ind_damping = 5,
  anal_jac = TRUE,
  bl_smth_pts = 80
)
```

Arguments

nstart	position in the time-domain to start fitting, units of data points.
init_g_damping	starting value for the global Gaussian line-broadening term - measured in Hz.
maxiters	maximum number of levmar iterations to perform.
max_shift	maximum shift allowed to each element in the basis set, measured in Hz.
max_g_damping	maximum permitted global Gaussian line-broadening.
max_ind_damping	maximum permitted Lorentzian line-broadening for each element in the basis set, measured in Hz.
anal_jac	option to use the analytic or numerical Jacobian (logical).
bl_smth_pts	number of data points to use in the baseline smoothing calculation.

Value

list of options.

Examples

```
varpro_opts(nstart = 10)
```

`vec2mrs_data` *Convert a vector into a mrs_data object.*

Description

Convert a vector into a mrs_data object.

Usage

```
vec2mrs_data(
  vec,
  mrs_data = NULL,
  fs = NULL,
  ft = NULL,
  ref = NULL,
  nuc = NULL,
  dyns = 1,
  fd = FALSE
)
```

Arguments

`vec`	the data vector.
`mrs_data`	example data to copy acquisition parameters from.
`fs`	sampling frequency in Hz.
`ft`	transmitter frequency in Hz.
`ref`	reference value for ppm scale.
`nuc`	resonant nucleus.
`dyns`	replicate the data across the dynamic dimension.
`fd`	flag to indicate if the vector is in the frequency domain (logical).

Value

mrs_data object.

`write_basis` *Write a basis object to an LCModel .basis formatted file.*

Description

Write a basis object to an LCModel .basis formatted file.

Usage

```
write_basis(basis, basis_file, fwhmba = 0.1)
```

Arguments

`basis`	basis object to be exported.
`basis_file`	path to basis file to be generated.
`fwhmba`	parameter used by LCModel.

`write_basis_niidir` *Write a basis object to folder containing one NIfTI MRS file for each basis element.*

Description

Write a basis object to folder containing one NIfTI MRS file for each basis element.

Usage

```
write_basis_niidir(basis, basis_dir)
```

Arguments

`basis`	basis object to be exported.
`basis_dir`	directory for basis files to be written.

write_basis_tqn *Generate a basis file using TARQUIN.*

Description

Generate a basis file using TARQUIN.

Usage

```
write_basis_tqn(basis_file, metab_data, opts = NULL)
```

Arguments

basis_file	filename of the basis file to be generated.
metab_data	MRS data object to match the generated basis parameters.
opts	list of options to pass to TARQUIN.

Examples

```
## Not run:
write_basis_tqn('test.basis',mrs_data,c("--echo","0.04"))

## End(Not run)
```

write_mrs *Write MRS data object to file.*

Description

Write MRS data object to file.

Usage

```
write_mrs(mrs_data, fname, format = NULL, force = FALSE)
```

Arguments

mrs_data	object to be written to file, or list of mrs_data objects.
fname	one or more filenames to output.
format	string describing the data format. Must be one of the following : "nifti", "dpt", "lcm_raw", "rds". If not specified, the format will be guessed from the filename extension.
force	set to TRUE to overwrite any existing files.

write_mrs_nifti *Write MRS data object to file in NIFTI format.*

Description

Write MRS data object to file in NIFTI format.

Usage

```
write_mrs_nifti(mrs_data, fname)
```

Arguments

mrs_data	object to be written to file.
fname	the filename of the output NIFTI MRS data.

write_pulse_ascii *Write an ASCII formatted pulse file.*

Description

Write an ASCII formatted pulse file.

Usage

```
write_pulse_ascii(pulse, path)
```

Arguments

pulse	pulse data object.
path	file path for export.

`zero_fade_spec` *Fade a spectrum to zero by frequency domain multiplication with a tanh function. Note this operation distorts data points at the end of the FID.*

Description

Fade a spectrum to zero by frequency domain multiplication with a tanh function. Note this operation distorts data points at the end of the FID.

Usage

```
zero_fade_spec(mrs_data, start_ppm, end_ppm)
```

Arguments

`mrs_data`	data to be faded.
`start_ppm`	start point of the fade in ppm units.
`end_ppm`	end point of the fade in ppm units.

Value

modified mrs_data object.

`zero_higher_orders` *Zero all coherences including and above a given order.*

Description

Zero all coherences including and above a given order.

Usage

```
zero_higher_orders(sys, rho, order)
```

Arguments

`sys`	spin system object.
`rho`	density matrix.
`order`	states higher than or equal to this argument will be set to zero.

Value

density matrix.

zero_td_pts_end *Set* mrs_data *object data points at the end of the FID to zero.*

Description

Set mrs_data object data points at the end of the FID to zero.

Usage

```
zero_td_pts_end(mrs_data, pts)
```

Arguments

mrs_data	MRS data.
pts	number of end points to set to zero.

Value

modified mrs_data object.

zf *Zero-fill MRS data in the time domain.*

Description

Zero-fill MRS data in the time domain.

Usage

```
zf(x, factor = 2, offset = 0)

## S3 method for class 'list'
zf(x, factor = 2, offset = 0)

## S3 method for class 'mrs_data'
zf(x, factor = 2, offset = 0)

## S3 method for class 'basis_set'
zf(x, factor = 2, offset = 0)
```

Arguments

x	input mrs_data or basis_set object.
factor	zero-filling factor, factor of 2 returns a dataset with twice the original data points.
offset	number of points from the end of the FID to insert the zero values.

Value

zero-filled data.

`zf_xy` *Zero-fill MRSI data in the k-space x-y direction.*

Description

Zero-fill MRSI data in the k-space x-y direction.

Usage

```
zf_xy(mrs_data, factor = 2)
```

Arguments

`mrs_data`	MRSI data.
`factor`	zero-filling factor, a factor of 2 returns a dataset with twice the original points in the x-y directions. Factors smaller than one are permitted, such that a factor of 0.5 returns half the k-space points in the x-y directions.

Value

zero-filled data.

Index