

Package ‘ravetools’

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Type Package

Title Signal Processing Toolbox for Analyzing 'Electrophysiology' Data

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Language en-US

Description Implemented fast and memory-efficient 'Notch'-filter, 'Welch-periodogram', and discrete wavelet transform algorithm for hours of high-resolution signals; providing fundamental toolbox for 'iEEG' preprocess pipelines. Documentation and examples about 'RAVE' project are provided at <https://openwetware.org/wiki/RAVE>, and the paper by John F. Magnotti, Zhengjia Wang, Michael S. Beauchamp (2020) [doi:10.1016/j.neuroimage.2020.117341](https://doi.org/10.1016/j.neuroimage.2020.117341); see 'citation(`ravetools`)' for details.

BugReports <https://github.com/dipterix/ravetools/issues>

URL <http://dipterix.org/ravetools/>

License GPL-3

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| | |
|----------------|---|
| baseline_array | <i>Calculate Contrasts of Arrays in Different Methods</i> |
|----------------|---|

Description

Provides five methods to baseline an array and calculate contrast.

Usage

```
baseline_array(x, along_dim, unit_dims = seq_along(dim(x))[-along_dim], ...)
```

```
## S3 method for class 'array'
baseline_array(
  x,
  along_dim,
  unit_dims = seq_along(dim(x))[-along_dim],
  method = c("percentage", "sqrt_percentage", "decibel", "zscore", "sqrt_zscore"),
  baseline_indexpoints = NULL,
  baseline_subarray = NULL,
  ...
)
```

Arguments

| | |
|-----------------------------------|--|
| <code>x</code> | array (tensor) to calculate contrast |
| <code>along_dim</code> | integer range from 1 to the maximum dimension of <code>x</code> . baseline along this dimension, this is usually the time dimension. |
| <code>unit_dims</code> | integer vector, baseline unit: see Details. |
| <code>...</code> | passed to other methods |
| <code>method</code> | character, baseline method options are: "percentage", "sqrt_percentage", "decibel", "zscore", and "sqrt_zscore" |
| <code>baseline_indexpoints</code> | integer vector, which index points are counted into baseline window? Each index ranges from 1 to <code>dim(x)[[along_dim]]</code> . See Details. |
| <code>baseline_subarray</code> | sub-arrays that should be used to calculate baseline; default is NULL (automatically determined by <code>baseline_indexpoints</code>). |

Details

Consider a scenario where we want to baseline a bunch of signals recorded from different locations. For each location, we record n sessions. For each session, the signal is further decomposed into frequency-time domain. In this case, we have the input x in the following form:

$$session \times frequency \times time \times location$$

Now we want to calibrate signals for each session, frequency and location using the first 100 time points as baseline points, then the code will be

$$baseline_array(x, along_dim = 3, baseline_window = 1 : 100, unit_dims = c(1, 2, 4))$$

`along_dim=3` is dimension of time, in this case, it's the third dimension of x . `baseline_indexpoints=1:100`, meaning the first 100 time points are used to calculate baseline. `unit_dims` defines the unit signal. Its value `c(1, 2, 4)` means the unit signal is per session (first dimension), per frequency (second) and per location (fourth).

In some other cases, we might want to calculate baseline across frequencies then the unit signal is *frequency*time*, i.e. signals that share the same session and location also share the same baseline. In this case, we assign `unit_dims=c(1, 4)`.

There are five baseline methods. They fit for different types of data. Denote z is a unit signal, z_0 is its baseline slice. Then these baseline methods are:

"percentage"

$$\frac{z - \bar{z}_0}{\bar{z}_0} \times 100\%$$

"sqrt_percentage"

$$\frac{\sqrt{z} - \sqrt{\bar{z}_0}}{\sqrt{\bar{z}_0}} \times 100\%$$

"decibel"

$$10 \times (\log_{10}(z) - \log_{10}(\bar{z}_0))$$

"zscore"

$$\frac{z - \bar{z}_0}{sd(\bar{z}_0)}$$

"sqrt_zscore"

$$\frac{\sqrt{z} - \sqrt{\bar{z}_0}}{sd(\sqrt{\bar{z}_0})}$$

Value

Contrast array with the same dimension as x.

Examples

```
# Set ncores = 2 to comply to CRAN policy. Please don't run this line
ravetools_threads(n_threads = 2L)

library(ravetools)
set.seed(1)

# Generate sample data
dims = c(10,20,30,2)
x = array(rnorm(prod(dims))^2, dims)

# Set baseline window to be arbitrary 10 timepoints
baseline_window = sample(30, 10)

# ----- baseline percentage change -----

# Using base functions
re1 <- aperm(apply(x, c(1,2,4), function(y){
  m <- mean(y[baseline_window])
  (y/m - 1) * 100
}), c(2,3,1,4))

# Using ravetools
re2 <- baseline_array(x, 3, c(1,2,4),
  baseline_indexpoints = baseline_window,
  method = 'percentage')

# Check different, should be very tiny (double precisions)
range(re2 - re1)

# Check speed for large dataset
if(interactive()){
```

```

ravetools_threads(n_threads = -1)

dims <- c(200,20,300,2)
x <- array(rnorm(prod(dims))^2, dims)
# Set baseline window to be arbitrary 10 timepoints
baseline_window <- seq_len(100)
f1 <- function(){
  aperm(apply(x, c(1,2,4), function(y){
    m <- mean(y[baseline_window])
    (y/m - 1) * 100
  }), c(2,3,1,4))
}
f2 <- function(){
  # equivalent as bl = x[, ,baseline_window, ]
  #
  baseline_array(x, along_dim = 3,
                 baseline_indexpoints = baseline_window,
                 unit_dims = c(1,2,4), method = 'percentage')
}
range(f1() - f2())
microbenchmark::microbenchmark(f1(), f2(), times = 10L)

}

```

collapse

Collapse array

Description

Collapse array

Usage

```

collapse(x, keep, ...)

## S3 method for class 'array'
collapse(
  x,
  keep,
  average = TRUE,
  transform = c("asis", "10log10", "square", "sqrt"),
  ...
)

```

Arguments

| | |
|------------------------|--|
| <code>x</code> | A numeric multi-mode tensor (array), without NA |
| <code>keep</code> | Which dimension to keep |
| <code>...</code> | passed to other methods |
| <code>average</code> | collapse to sum or mean |
| <code>transform</code> | transform on the data before applying collapsing; choices are 'asis' (no change), '10log10' (used to calculate decibel), 'square' (sum-squared), 'sqrt' (square-root and collapse) |

Value

a collapsed array with values to be mean or summation along collapsing dimensions

Examples

```
# Set ncores = 2 to comply to CRAN policy. Please don't run this line
ravetools_threads(n_threads = 2L)

# Example 1
x = matrix(1:16, 4)

# Keep the first dimension and calculate sums along the rest
collapse(x, keep = 1)
rowMeans(x) # Should yield the same result

# Example 2
x = array(1:120, dim = c(2,3,4,5))
result = collapse(x, keep = c(3,2))
compare = apply(x, c(3,2), mean)
sum(abs(result - compare)) # The same, yield 0 or very small number (1e-10)

if(interactive()){
  ravetools_threads(n_threads = -1)
}

# Example 3 (performance)

# Small data, no big difference
x = array(rnorm(240), dim = c(4,5,6,2))
microbenchmark::microbenchmark(
  result = collapse(x, keep = c(3,2)),
  compare = apply(x, c(3,2), mean),
  times = 1L, check = function(v){
    max(abs(range(do.call('-', v)))) < 1e-10
  }
)

# large data big difference
x = array(rnorm(prod(300,200,105)), c(300,200,105,1))
```

```

microbenchmark::microbenchmark(
  result = collapse(x, keep = c(3,2)),
  compare = apply(x, c(3,2), mean),
  times = 1L, check = function(v){
    max(abs(range(do.call('-', v)))) < 1e-10
  })
}

```

decimate

Decimate with 'FIR' or 'IIR' filter

Description

Decimate with 'FIR' or 'IIR' filter

Usage

```
decimate(x, q, n = if (ftype == "iir") 8 else 30, ftype = "fir")
```

Arguments

| | |
|-------|---|
| x | signal to be decimated |
| q | integer factor to down-sample by |
| n | filter order used in the down-sampling; default is 30 if ftype='fir', or 8 if ftype='iir' |
| ftype | filter type, choices are 'fir' (default) and 'iir' |

Details

This function is migrated from signal package, but with bugs fixed on 'FIR' filters. The result agrees with 'Matlab' decimate function with 'FIR' filters. Under 'IIR' filters, the function is identical with signal::decimate, and is slightly different with 'Matlab' version.

Value

Decimated signal

Examples

```

x <- 1:100
y <- decimate(x, 2, ftype = "fir")
y

# compare with signal package
z <- signal::decimate(x, 2, ftype = "fir")

```

```
# Compare decimated results
plot(x, type = 'l')
points(seq(1,100, 2), y, col = "green")
points(seq(1,100, 2), z, col = "red")
```

detrend

Remove the trend for one or more signals

Description

'Detrending' is often used before the signal power calculation.

Usage

```
detrend(x, trend = c("constant", "linear"), break_points = NULL)
```

Arguments

| | |
|--------------|--|
| x | numerical or complex, a vector or a matrix |
| trend | the trend of the signal; choices are 'constant' and 'linear' |
| break_points | integer vector, or NULL; only used when trend is 'linear' to remove piecewise linear trend; will throw warnings if trend is 'constant' |

Value

The signals with trend removed in matrix form; the number of columns is the number of signals, and number of rows is length of the signals

Examples

```
x <- rnorm(100, mean = 1) + c(
  seq(0, 5, length.out = 50),
  seq(5, 3, length.out = 50))
plot(x)

plot(detrend(x, 'constant'))
plot(detrend(x, 'linear'))
plot(detrend(x, 'linear', 50))
```

| | |
|------------------|---|
| diagnose_channel | <i>Show channel signals with diagnostic plots</i> |
|------------------|---|

Description

The diagnostic plots include 'Welch Periodogram' ([pwelch](#)) and histogram ([hist](#))

Usage

```
diagnose_channel(
  s1,
  s2 = NULL,
  sc = NULL,
  srate,
  name = "",
  try_compress = TRUE,
  max_freq = 300,
  window = ceiling(srate * 2),
  noverlap = window/2,
  std = 3,
  cex = 1.5,
  lwd = 0.5,
  plim = NULL,
  nclass = 100,
  main = "Channel Inspection",
  col = c("black", "red"),
  which = NULL,
  start_time = 0,
  boundary = NULL,
  mar = c(5.2, 5.1, 4.1, 2.1),
  mai = c(0.6, 0.54, 0.4, 0.1),
  ...
)
```

Arguments

| | |
|--------------|---|
| s1 | the main signal to draw |
| s2 | the comparing signal to draw; usually s1 after some filters; must be in the same sampling rate with s1; can be NULL |
| sc | decimated s1 to show if srate is too high; will be automatically generated if NULL |
| srate | sampling rate |
| name | name of s1, or a vector of two names of s1 and s2 if s2 is provided |
| try_compress | whether try to compress (decimate) s1 if srate is too high for performance concerns |

max_freq the maximum frequency to display in 'Welch Periodograms'
 window, noverlap see [pwelch](#)
 std the standard deviation of the channel signals used to determine boundary; default is plus-minus 3 standard deviation
 cex, lwd, mar, mai, ... graphical parameters; see [par](#)
 plim the y-axis limit to draw in 'Welch Periodograms'
 nclass number of classes to show in histogram ([hist](#))
 main the title of the signal plot
 col colors of s1 and s2
 which NULL or integer from 1 to 4; if NULL, all plots will be displayed; otherwise only the subplot will be displayed
 start_time the starting time of channel (will only be used to draw signals)
 boundary a red boundary to show in channel plot; default is to be automatically determined by std

Value

A list of boundary and y-axis limit used to draw the channel

Examples

```

library(ravetools)

# Generate 20 second data at 2000 Hz
time <- seq(0, 20, by = 1 / 2000)
signal <- sin( 120 * pi * time) +
  sin(time * 20*pi) +
  exp(-time^2) *
  cos(time * 10*pi) +
  rnorm(length(time))

signal2 <- notch_filter(signal, 2000)

diagnose_channel(signal, signal2, srate = 2000,
  name = c("Raw", "Filtered"), cex = 1)

```

fast_cov

Calculate massive covariance matrix in parallel

Description

Speed up covariance calculation for large matrices. The default behavior is the same as [cov](#) ('pearson', no NA handling).

Usage

```
fast_cov(x, y = NULL, col_x = NULL, col_y = NULL, df = NA)
```

Arguments

| | |
|-------|--|
| x | a numeric vector, matrix or data frame; a matrix is highly recommended to maximize the performance |
| y | NULL (default) or a vector, matrix or data frame with compatible dimensions to x; the default is equivalent to y = x |
| col_x | integers indicating the subset indices (columns) of x to calculate the covariance, or NULL to include all the columns; default is NULL |
| col_y | integers indicating the subset indices (columns) of y to calculate the covariance, or NULL to include all the columns; default is NULL |
| df | a scalar indicating the degrees of freedom; default is nrow(x)-1 |

Value

A covariance matrix of x and y. Note that there is no NA handling. Any missing values will lead to NA in the resulting covariance matrices.

Examples

```
# Set ncores = 2 to comply to CRAN policy. Please don't run this line
ravetools_threads(n_threads = 2L)

x <- matrix(rnorm(400), nrow = 100)

# Call `cov(x)` to compare
fast_cov(x)

# Calculate covariance of subsets
fast_cov(x, col_x = 1, col_y = 1:2)

if(interactive()){

# Speed comparison, better to use multiple cores (4, 8, or more)
# to show the differences.

ravetools_threads(n_threads = -1)
x <- matrix(rnorm(100000), nrow = 1000)
microbenchmark::microbenchmark(
  fast_cov = {
    fast_cov(x, col_x = 1:50, col_y = 51:100)
  },
  cov = {
    cov(x[,1:50], x[,51:100])
  },
  unit = 'ms', times = 10
)
```

```
}

```

| | |
|----------------|---------------------------------------|
| matlab_palette | <i>'Matlab' heat-map plot palette</i> |
|----------------|---------------------------------------|

Description

'Matlab' heat-map plot palette

Usage

```
matlab_palette()
```

Value

vector of 64 colors

| | |
|------------|--|
| multitaper | <i>Compute 'multitaper' spectral densities of time-series data</i> |
|------------|--|

Description

Compute 'multitaper' spectral densities of time-series data

Usage

```
multitaper_config(
  data_length,
  fs,
  frequency_range = NULL,
  time_bandwidth = 5,
  num_tapers = NULL,
  window_params = c(5, 1),
  nfft = NA,
  detrend_opt = "linear"
)
```

```
multitaper(
  data,
  fs,
  frequency_range = NULL,
  time_bandwidth = 5,
  num_tapers = NULL,
```

```

    window_params = c(5, 1),
    nfft = NA,
    detrend_opt = "linear"
  )

```

Arguments

| | |
|-----------------|--|
| data_length | length of data |
| fs | sampling frequency in 'Hz' |
| frequency_range | frequency range to look at; length of two |
| time_bandwidth | a number indicating time-half bandwidth product; i.e. the window duration times the half bandwidth of main lobe; default is 5 |
| num_tapers | number of 'DPSS' tapers to use; default is NULL and will be automatically computed from $\text{floor}(2 * \text{time_bandwidth} - 1)$ |
| window_params | vector of two numbers; the first number is the window size in seconds; the second number is the step size; default is $c(5, 1)$ |
| nfft | 'NFFT' size, positive; see 'Details' |
| detrend_opt | how you want to remove the trend from data window; options are 'linear' (default), 'constant', and 'off' |
| data | numerical vector, signal traces |

Details

The original source code comes from 'Prerau' Lab (see 'Github' repository 'multitaper_toolbox' under user 'preraulab'). The results tend to agree with their 'Python' implementation with precision on the order of at $1E-7$ with standard deviation at most $1E-5$. The original copy was licensed under a Creative Commons Attribution 'NC'-'SA' 4.0 International License (<https://creativecommons.org/licenses/by-nc-sa/4.0/>).

This package ('ravetools') redistributes the multitaper function under minor modifications on nfft. In the original copy there is no parameter to control the exact numbers of nfft, and the nfft is always the power of 2. While choosing nfft to be the power of 2 is always recommended, the modified code allows other choices.

Value

multitaper_config returns a list of configuration parameters for the filters; multitaper also returns the time, frequency and corresponding spectral power.

Examples

```

time <- seq(0, 3, by = 0.001)
x <- sin(time * 20*pi) + exp(-time^2) * cos(time * 10*pi)

res <- multitaper(
  x, 1000, frequency_range = c(0,15),

```

```

time_bandwidth=1.5,
window_params=c(2,0.01)
)

image(
  x = res$time,
  y = res$frequency,
  z = 10 * log10(res$spec),
  xlab = "Time (s)",
  ylab = 'Frequency (Hz)',
  col = matlab_palette()
)

```

notch_filter

Apply 'Notch' filter

Description

Apply 'Notch' filter

Usage

```

notch_filter(
  s,
  sample_rate,
  lb = c(59, 118, 178),
  ub = c(61, 122, 182),
  domain = 1
)

```

Arguments

| | |
|-------------|---|
| s | numerical vector if domain=1 (voltage signals), or complex vector if domain=0 |
| sample_rate | sample rate |
| lb | filter lower bound of the frequencies to remove |
| ub | filter upper bound of the frequencies to remove; shares the same length as lb |
| domain | 1 if the input signal is in the time domain, 0 if it is in the frequency domain |

Details

Mainly used to remove electrical line frequencies at 60, 120, and 180 Hz.

Value

filtered signal in time domain (real numerical vector)

Examples

```
time <- seq(0, 3, 0.005)
s <- sin(120 * pi * time) + rnorm(length(time))

# Welch periodogram shows a peak at 60Hz
pwelch(s, 200, plot = 1, log = "y")

# notch filter to remove 60Hz
s1 <- notch_filter(s, 200, lb = 59, ub = 61)
pwelch(s1, 200, plot = 2, log = "y", col = "red")
```

| | |
|------------------|----------------------------------|
| parallel-options | <i>Set or get thread options</i> |
|------------------|----------------------------------|

Description

Set or get thread options

Usage

```
detect_threads()

ravetools_threads(n_threads = "auto", stack_size = "auto")
```

Arguments

| | |
|------------|--|
| n_threads | number of threads to set |
| stack_size | Stack size (in bytes) to use for worker threads. The default used for "auto" is 2MB on 32-bit systems and 4MB on 64-bit systems. |

Value

detect_threads returns an integer of default threads that is determined by the number of CPU cores; ravetools_threads returns nothing.

Examples

```
if(interactive()){
  detect_threads()
  ravetools_threads(n_threads = 2)
}
```

pwelch

Calculate 'Welch Periodogram'

Description

pwelch is for single signal trace only; mv_pwelch is for multiple traces. Currently mv_pwelch is experimental and should not be called directly.

Usage

```
pwelch(  
  x,  
  fs,  
  window = 64,  
  noverlap = 8,  
  nfft = 256,  
  col = "black",  
  xlim = NULL,  
  ylim = NULL,  
  main = "Welch periodogram",  
  plot = 0,  
  log = c("xy", "", "x", "y"),  
  ...  
)  
  
## S3 method for class 'pwelch'  
print(x, ...)  
  
## S3 method for class 'pwelch'  
plot(  
  x,  
  log = c("xy", "x", "y", ""),  
  type = "l",  
  add = FALSE,  
  col = 1,  
  cex = 1,  
  cex.main = cex,  
  cex.sub = cex,  
  cex.lab = cex * 0.8,  
  cex.axis = cex * 0.7,  
  las = 1,  
  main = "Welch periodogram",  
  xlab,  
  ylab,  
  xlim = NULL,  
  ylim = NULL,  
  ...  
)
```



```
)
mv_pwelch(x, margin, fs, nfft)
```

Arguments

| | |
|--|--|
| <code>x</code> | 'pwelch' instance returned by pwelch function |
| <code>fs</code> | sample rate, average number of time points per second |
| <code>window</code> | window length in time points, default size is 64 |
| <code>noverlap</code> | overlap between two adjacent windows, measured in time points; default is 8 |
| <code>nfft</code> | number of basis functions to apply |
| <code>col, xlim, ylim, main, type, cex, cex.main, cex.sub, cex.lab, cex.axis, las, xlab, ylab</code> | parameters passed to plot.default |
| <code>plot</code> | integer, whether to plot the result or not; choices are 0, no plot; 1 plot on a new canvas; 2 add to existing canvas |
| <code>log</code> | indicates which axis should be log ₁₀ -transformed, used by the plot function. For 'x' axis, it's log ₁₀ -transform; for 'y' axis, it's 10log ₁₀ -transform (decibel unit). Choices are "xy", "x", "y", and "". |
| <code>...</code> | will be passed to <code>plot.pwelch</code> or ignored |
| <code>add</code> | logical, whether the plot should be added to existing canvas |
| <code>margin</code> | the margin in which pwelch should be applied to |

Value

A list with class 'ravetools-pwelch' that contains the following items:

| | |
|-----------------------|--|
| <code>freq</code> | frequencies used to calculate the 'periodogram' |
| <code>spec</code> | resulting spectral power for each frequency |
| <code>window</code> | window function (in numerical vector) used |
| <code>noverlap</code> | number of overlapping time-points between two adjacent windows |
| <code>nfft</code> | number of basis functions |
| <code>fs</code> | sample rate |
| <code>x_len</code> | input signal length |
| <code>method</code> | a character string 'Welch' |

Examples

```
x <- rnorm(1000)
pwel <- pwelch(x, 100)
pwel

plot(pwel, log = "xy")
```

| | |
|-------------|-----------------------------|
| shift_array | <i>Shift array by index</i> |
|-------------|-----------------------------|

Description

Re-arrange arrays in parallel

Usage

```
shift_array(x, along_margin, unit_margin, shift_amount)
```

Arguments

| | |
|--------------|--------------------------------------|
| x | array, must have at least matrix |
| along_margin | which index is to be shifted |
| unit_margin | which dimension decides shift_amount |
| shift_amount | shift amount along along_margin |

Details

A simple use-case for this function is to think of a matrix where each row is a signal and columns stand for time. The objective is to align (time-lock) each signal according to certain events. For each signal, we want to shift the time points by certain amount.

In this case, the shift amount is defined by `shift_amount`, whose length equals to number of signals. `along_margin=2` as we want to shift time points (column, the second dimension) for each signal. `unit_margin=1` because the shift amount is depend on the signal number.

Value

An array with same dimensions as the input `x`, but with index shifted. The missing elements will be filled with NA.

Examples

```
# Set ncores = 2 to comply to CRAN policy. Please don't run this line
ravetools_threads(n_threads = 2L)
```

```
x <- matrix(1:10, nrow = 2, byrow = TRUE)
z <- shift_array(x, 2, 1, c(1,2))
```

```
y <- NA * x
y[1,1:4] = x[1,2:5]
y[2,1:3] = x[2,3:5]
```

```

# Check if z and y are the same
z - y

# array case
# x is Trial x Frequency x Time
x <- array(1:27, c(3,3,3))

# Shift time for each trial, amount is 1, -1, 0
shift_amount <- c(1,-1,0)
z <- shift_array(x, 3, 1, shift_amount)

if(interactive()){
  par(mfrow = c(3, 2), mai = c(0.8, 0.6, 0.4, 0.1))
  for( ii in 1:3 ){
    image(t(x[ii, ,]), ylab = 'Frequency', xlab = 'Time',
          main = paste('Trial', ii))
    image(t(z[ii, ,]), ylab = 'Frequency', xlab = 'Time',
          main = paste('Shifted amount:', shift_amount[ii]))
  }
}

```

wavelet

'Morlet' wavelet transform (Discrete)

Description

Transform analog voltage signals with 'Morlet' wavelets: complex wavelet kernels with $\pi/2$ phase differences.

Usage

```

wavelet_kernels(freqs, srate, wave_num)

morlet_wavelet(
  data,
  freqs,
  srate,
  wave_num,
  precision = c("float", "double"),
  trend = c("constant", "linear", "none"),
  ...
)

```

Arguments

| | |
|-----------|---|
| freqs | frequency in which data will be projected on |
| srate | sample rate, number of time points per second |
| wave_num | desired number of cycles in wavelet kernels to balance the precision in time and amplitude (control the smoothness); positive integers are strongly suggested |
| data | numerical vector such as analog voltage signals |
| precision | the precision of computation; choices are 'float' (default) and 'double'. |
| trend | choices are 'constant': center the signal at zero; 'linear': remove the linear trend; 'none' do nothing |
| ... | further passed to <code>detrend</code> ; |

Value

`wavelet_kernels` returns wavelet kernels to be used for wavelet function; `morlet_wavelet` returns a file-based array if precision is 'float', or a list of real and imaginary arrays if precision is 'double'

Examples

```
# generate sine waves
time <- seq(0, 3, by = 0.01)
x <- sin(time * 20*pi) + exp(-time^2) * cos(time * 10*pi)

plot(time, x, type = 'l')

# freq from 1 - 15 Hz; wavelet using float precision
freq <- seq(1, 15, 0.2)
coef <- morlet_wavelet(x, freq, 100, c(2,3))

# to get coefficients in complex number from 1-10 time points
coef[1:10, ]

# power
power <- Mod(coef[])^2

# Power peaks at 5Hz and 10Hz at early stages
# After 1.0 second, 5Hz component fade away
image(power, x = time, y = freq, ylab = "frequency")

# wavelet using double precision
coef2 <- morlet_wavelet(x, freq, 100, c(2,3), precision = "double")
power2 <- (coef2$real[])^2 + (coef2$imag[])^2

image(power2, x = time, y = freq, ylab = "frequency")

# The maximum relative change of power with different precisions
max(abs(power/power2 - 1))
```

```
# display kernels
freq <- seq(1, 15, 1)
kern <- wavelet_kernels(freq, 100, c(2,3))
print(kern)

plot(kern)
```

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