Package 'rhosa'

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Title Higher-Order Spectral Analysis

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Version 0.2.0

Description Higher-order spectra or polyspectra of time series, such as bispectrum and bicoherence, have been investigated in abundant literature and applied to problems of signal detection in a wide range of fields. This package aims to provide a simple API to estimate and analyze them. The current implementation is based on Brillinger and Irizarry (1998) <doi:10.1016/S0165-1684(97)00217-X> for estimating bispectrum or bicoherence, Lii and Helland (1981) <doi:10.1145/355958.355961> for cross-bispectrum, and Kim and Powers (1979) <doi:10.1109/TPS.1979.4317207> for cross-bicoherence.

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Encoding UTF-8

URL `https://tabe.github.io/rhosa/`

BugReports `https://github.com/tabe/rhosa/issues`

RoxygenNote 7.1.2

Imports parallel

Suggests ggplot2, knitr, rmarkdown, testthat (>= 2.1.0)

VignetteBuilder knitr

NeedsCompilation no

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R topics documented:

`bicoherence` *Estimate bicoherence from given time series data.*

Description

Estimate magnitude-squared bicoherence from given real- or complex-valued time series data.

Usage

```
bicoherence(
  data,
  window_function = NULL,
  mc = FALSE,
  mc_cores = getOption("mc.cores", 2L),
  alpha = 0.05,
  p_adjust_method = "BH"
)
```

Arguments

`data`	Given time series, as a data frame or matrix with which columns correspond to sampled stretches.
`window_function`	A window function's name for tapering. Defaults to `NULL` ("no tapering"). Currently the following window functions are available: Hamming window ("hamming"), Hann window ("hann"), and Blackman window ("blackman").
`mc`	If `TRUE`, calculation is done in parallel computation. Defaults to `FALSE`.
`mc_cores`	The number of cores in use for parallel computation, passed `parallel::mcmapply()` etc. as `mc.cores`.
`alpha`	The alpha level of the hypotesis test. Defaults to 0.05.
`p_adjust_method`	The correction method for p-values, given to `p.adjust()`. Defaults to "BH" (Benjamini and Hochberg). No correction if a non-character is given.

Value

A data frame including the following columns:

f1: The first elements of frequency pairs.

f2: The second elements of frequency pairs.

value: The estimate of magnitude-squared bicoherence at the respective frequency pair.

p_value: The (corrected, if requested) p-value for hypothesis testing under null hypothesis that bicoherence is 0.

significance: TRUE if the null hypothesis of the above hypothesis test is rejected with given `alpha` level.

References

Brillinger, D.R. and Irizarry, R.A. "An investigation of the second- and higher-order spectra of music." Signal Processing, Volume 65, Issue 2, 30 March 1998, Pages 161-179.

Examples

```
f <- function(x) {
    sin(2 * x) + sin(3 * x + 1) + sin(2 * x) * sin(3 * x + 1)
}
v <- sapply(seq_len(1280), f) + rnorm(1280)
m <- matrix(v, nrow = 128)
bc1 <- bicoherence(m)
bc2 <- bicoherence(m, "hamming")
bc3 <- bicoherence(m, "hann", mc = TRUE, mc_cores = 1L)
```

`bispectrum` *Estimate bispectrum from time series data.*

Description

Estimate bispectrum from real- or complex-valued time series data.

Usage

```
bispectrum(
  data,
  window_function = NULL,
  mc = FALSE,
  mc_cores = getOption("mc.cores", 2L)
)
```

Arguments

`data`	Given time series, as a data frame or matrix with which columns correspond to sampled stretches.
`window_function`	A window function's name for tapering. Defaults to `NULL` ("no tapering"). Currently the following window functions are available: Hamming window ("hamming"), Hann window ("hann"), and Blackman window ("blackman").
`mc`	If `TRUE`, calculation is done in parallel computation. Defaults to `FALSE`.
`mc_cores`	The number of cores in use for parallel computation, passed `parallel::mcmapply()` etc. as `mc.cores`.

Value

A data frame including the following columns:

f1: The first elements of frequency pairs.

f2: The second elements of frequency pairs.

value: The estimated bispectrum at each frequency pair.

References

Brillinger, D.R. and Irizarry, R.A. "An investigation of the second- and higher-order spectra of music." Signal Processing, Volume 65, Issue 2, 30 March 1998, Pages 161-179.

Examples

```
f <- function(x) {
    sin(2 * x) + sin(3 * x + 1) + sin(2 * x) * sin(3 * x + 1)
}
v <- sapply(seq_len(1280), f) + rnorm(1280)
m <- matrix(v, nrow = 128)
bs1 <- bispectrum(m)
bs2 <- bispectrum(m, "hamming")
bs3 <- bispectrum(m, "blackman", mc = TRUE, mc_cores = 1L)
```

`cross_bicoherence` *Estimate cross-bicoherence from time series data.*

Description

Estimate cross-bicoherence from three real-valued time series data.

Usage

```
cross_bicoherence(
  x,
  y,
  z = y,
  dft_given = FALSE,
  mc = FALSE,
  mc_cores = getOption("mc.cores", 2L)
)
```

Arguments

`x`	Given 1st time series, as a data frame or matrix with which columns correspond to sampled stretches.
`y`	Given 2nd time series, with the same dimension as x.
`z`	Optional 3rd time series, with the same dimension as x (and thus as y). If omitted, y is used instead.
`dft_given`	If TRUE, suppose that DFTs is given instead of time series data and skip the fast fourier transform. Default: FALSE.
`mc`	If `TRUE`, calculation is done in parallel computation. Defaults to `FALSE`.
`mc_cores`	The number of cores in use for parallel computation, passed `parallel::mclapply()` etc. as `mc.cores`.

Value

A data frame including the following columns:

f1: The first elements of frequency pairs.

f2: The second elements of frequency pairs.

value: The estimated value of magnitude-squared cross-bicoherence at the respective frequency pair.

References

Kim, Y.C., Powers, E.J., 1979. Digital Bispectral Analysis and Its Applications to Nonlinear Wave Interactions. IEEE Trans. Plasma Sci. 7, 120–131. https://doi.org/10.1109/TPS.1979.4317207

Examples

```
x <- seq_len(1280)
v1 <- sapply(x, function(x) {sin(2 * x)}) + rnorm(1280)
v2 <- sapply(x, function(x) {sin(3 * x + 1)}) + rnorm(1280)
v3 <- sapply(x, function(x) {cos(2 * x) * cos(3 * x + 1)}) + rnorm(1280)
m1 <- matrix(v1, nrow = 128)
m2 <- matrix(v2, nrow = 128)
m3 <- matrix(v3, nrow = 128)
xbc1 <- cross_bicoherence(m1, m2, m3)

d1 <- stats::mvfft(m1)
d2 <- stats::mvfft(m2)
d3 <- stats::mvfft(m3)
xbc2 <- cross_bicoherence(d1, d2, d3, dft_given = TRUE)

xbc3 <- cross_bicoherence(d1, d2, d3, dft_given = TRUE, mc = TRUE, mc_cores = 1L)
```

`cross_bispectrum` *Estimate cross-bispectrum from time series data.*

Description

Estimate cross-bispectrum from three real-valued time series data.

Usage

```
cross_bispectrum(
  x,
  y,
  z = y,
  dft_given = FALSE,
  mc = FALSE,
  mc_cores = getOption("mc.cores", 2L)
)
```

Arguments

`x`	Given 1st time series, as a data frame or matrix with which columns correspond to sampled stretches.
`y`	Given 2nd time series, with the same dimension as x.
`z`	Optional 3rd time series, with the same dimension as x (and thus as y). If omitted, `y` is used instead.
`dft_given`	If TRUE, suppose that DFTs is given instead of time series data and skip the fast fourier transform. Default: FALSE.
`mc`	If `TRUE`, calculation is done in parallel computation. Defaults to `FALSE`.
`mc_cores`	The number of cores in use for parallel computation, passed `parallel::mclapply()` etc. as `mc.cores`.

Value

A data frame including the following columns:

f1: The first elements of frequency pairs.

f2: The second elements of frequency pairs.

value: The estimated cross-bispectrum at each frequency pair.

References

K. S. Lii and K. N. Helland. 1981. Cross-Bispectrum Computation and Variance Estimation. ACM Trans. Math. Softw. 7, 3 (September 1981), 284–294. DOI:https://doi.org/10.1145/355958.355961

Examples

```
x <- seq_len(1280)
v1 <- sapply(x, function(x) {sin(2 * x)}) + rnorm(1280)
v2 <- sapply(x, function(x) {sin(3 * x + 1)}) + rnorm(1280)
v3 <- sapply(x, function(x) {cos(2 * x) * cos(3 * x + 1)}) + rnorm(1280)
m1 <- matrix(v1, nrow = 128)
m2 <- matrix(v2, nrow = 128)
m3 <- matrix(v3, nrow = 128)
xbs1 <- cross_bispectrum(m1, m2, m3)

d1 <- stats::mvfft(m1)
d2 <- stats::mvfft(m2)
d3 <- stats::mvfft(m3)
xbs2 <- cross_bispectrum(d1, d2, d3, dft_given = TRUE)

xbs3 <- cross_bispectrum(d1, d2, d3, dft_given = TRUE, mc = TRUE, mc_cores = 1L)
```

`mode_matching` *Estimate cross-bicoherence's empirical null distribution by a mode matching method*

Description

Estimate false discovery rate by fitting scaled chi-squared distribution as an empirical null of cross-bicoherence with Schwartzman's mode matching method.

Usage

```
mode_matching(xbc, t_max = NULL, d = 0.001)
```

Arguments

`xbc`	cross-bicoherence, returned from `cross_bicoherence`.
`t_max`	the upper limit of interval $$S_0$$, see the reference.
`d`	the bin width of the tuning parameter.

References

Schwartzman, Armin. “Empirical Null and False Discovery Rate Inference for Exponential Families.” Annals of Applied Statistics 2, no. 4 (December 2008): 1332–59. https://doi.org/10.1214/08-AOAS184.

three_channel_model *A three-channel model of quadratic phase coupling*

Description

Simulate observations by a three-channel model of quadratic phase coupling.

Usage

```
three_channel_model(
  f1,
  f2,
  f3,
  num_samples = 256,
  num_observations = 100,
  input_freq = c(1.2, 0.7, 0.8),
  noise_sd = 1
)
```

Arguments

`f1`	A function of period 2π for the first channel.
`f2`	A function of period 2π for the second channel.
`f3`	A function of period 2π for the third channel.
`num_samples`	The number of sampling points in an observation.
`num_observations`	The number of observations.
`input_freq`	The scaling factor for the frequencies of input periodic functions. It can be a scalar or a vector of length three. If a scalar is given, the same frequency is used for all of inputs.
`noise_sd`	The standard deviation of a Gaussian noise perturbing samples. It can be a scalar or a vector of length three. If a scalar is given, the same value is used for all of noises. Giving 0 is possible and specifies no noise.

Details

Given three periodic functions, this function generate a list of three data frames in which each column represents a simulated observation at a channel. The phase is chosen at random from $[0, 2\pi]$ for each observation and each channel.

Value

A list of six data frames: `i1`, `i2`, `i3`, `o1`, `o2`, and `o3`. Each element has `num_observations` columns and `num_samples` rows. `i1`, `i2`, and `i3` are observations of input signals; `o1`, `o2`, and `o3` are of output.

Examples

```
sawtooth <- function(r) {
    x <- r/(2*pi)
    x - floor(x) - 0.5
}
data <- three_channel_model(cos, sin, sawtooth,
                            input_freq = c(0.2, 0.3, 0.4),
                            noise_sd = 0.9)
```

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