

# Package ‘synchrony’

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**Type** Package

**Title** Methods for Computing Spatial, Temporal, and Spatiotemporal Statistics

**Version** 0.3.8

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**Description** Methods for computing spatial, temporal, and spatiotemporal statistics as described in Gouhier and Guichard (2014) <doi:10.1111/2041-210X.12188>. These methods include empirical univariate, bivariate and multivariate variograms; fitting variogram models; phase locking and synchrony analysis; generating autocorrelated and cross-correlated matrices.

**License** GPL (>= 2)

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synchrony-package	<i>Methods for Computing Spatial, Temporal, and Spatiotemporal Statistics</i>
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## Description

Methods for computing spatial, temporal, and spatiotemporal statistics as described in Gouhier and Guichard (2014) <doi:10.1111/2041-210X.12188>. These methods include empirical univariate, bivariate and multivariate variograms; fitting variogram models; phase locking and synchrony analysis; generating autocorrelated and cross-correlated matrices.

## Details

Package:	synchrony
Type:	Package
Version:	0.3.8
Date:	2019-12-05
License:	GPL (>=2)
URL:	<a href="https://github.com/tgouhier/synchrony">https://github.com/tgouhier/synchrony</a>
LazyLoad:	yes

## Author(s)

Tarik C. Gouhier (tarik.gouhier@gmail.com)

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## References

Bjornstad, O. N., and W. Falck. 2001. Nonparametric spatial covariance functions: Estimation and testing. *Environmental and Ecological Statistics* 8:53-70.

- Bjornstad, O. N., R. A. Ims, and X. Lambin. 1999. Spatial population dynamics: analyzing patterns and processes of population synchrony. *Trends in Ecology & Evolution* 14:427-432.
- Buonaccorsi, J. P., J. S. Elkinton, S. R. Evans, and A. M. Liebhold. 2001. Measuring and testing for spatial synchrony. *Ecology* 82:1668-1679.
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- Gouhier, T. C., F. Guichard, and A. Gonzalez. 2010. Synchrony and stability of food webs in metacommunities. *The American Naturalist* 175:E16-E34.
- Gouhier, T. C., F. Guichard, and B. A. Menge. 2010. Ecological processes can synchronize marine population dynamics over continental scales. *Proceedings of the National Academy of Sciences* 107:8281-8286.
- Loreau, M., and C. de Mazancourt. 2008. Species synchrony and its drivers: Neutral and nonneutral community dynamics in fluctuating environments. *The American Naturalist* 172:E48-E66.
- Purves, D. W., and R. Law. 2002. Fine-scale spatial structure in a grassland community: quantifying the plant's eye view. *Journal of Ecology* 90:121-129.
- Vasseur, D. A. 2007. Environmental colour intensifies the Moran effect when population dynamics are spatially heterogeneous. *Oikos* 116:1726-1736.
- Zar, J. H. 1999. *Biostatistical Analysis*, Fourth edition. Prentice-Hall, Inc., Upper Saddle River, NJ.

## Examples

```
# Compute phase synchrony
t1=runif(100)
t2=runif(100)
sync=phase.sync(t1, t2)
# Distribution of phase difference
hist(sync$deltaphase$mod_phase_diff_2pi)

# Compute concordant peaks
p=peaks(t1, t2, nrands=100)
# Find proportion of time steps where both time series peak together
p$peaks
# Plot (null) distribution of proportion of time steps where both time
# series peak together
hist(p$rand)
# p-value of observed value
p$pval

# Compute Kendall's W
data(bird.traits)
(w=kendall.w(bird.traits))

# Community matrix for 20 species undergoing random fluctuations
```

```
comm.rand=matrix(runif(100), nrow=5, ncol=20)
community.sync(comm.rand, nrands=10)
# Community matrix for 20 species undergoing synchronized fluctuations
comm.corr=matrix(rep(comm.rand[,1], 20), nrow=5, ncol=20)
community.sync(comm.corr, nrands=10)
```

---

bird.traits

*bird trait dataset*

---

### Description

Contains the wing length, tail length, and bill length from 12 birds

### Usage

```
data(bird.traits)
```

### Format

A data frame with 12 observations (birds) on the following 3 variables.

wing.length a numeric vector containing wing length in cm

tail.length a numeric vector containing tail length in cm

bill.length a numeric vector containing bill length in cm

### Details

Dataset from Zar (1999; page 444)

### Source

Zar, J. H. 1999. Biostatistical Analysis, Fourth edition. Prentice-Hall, Inc., Upper Saddle River, NJ.

### Examples

```
data(bird.traits)
(w=kendall.w(bird.traits))
```

---

community.sync	<i>Compute community-wide synchrony and its significance via Monte Carlo randomizations</i>
----------------	---

---

### Description

Compute community-wide synchrony and its the significance via Monte Carlo randomizations. If all species fluctuate in perfect unison, the community-wide synchrony will be 1. If species undergo uncorrelated fluctuations, the community-wide synchrony will be 1/S. The Monte Carlo randomizations are performed by shuffling the columns of the community matrix independently. This function also returns the mean correlation between the columns of the matrix.

### Usage

```
community.sync (data, nrands = 0, method = c("pearson", "kendall", "spearman"),
               alternative = c("greater", "less"), type = 1, quiet = FALSE, ...)
```

### Arguments

data	community matrix in wide format where each row contains the abundance at each time step and each column corresponds to a different species.
nrands	number of randomizations to perform (default is 0)
method	Method to compute mean correlation between columns? Options include pearson, kendall, and spearman. Default is pearson
alternative	Alternative hypothesis. Options are less and greater. Default is greater
type	Randomization method. The type=1 method randomly shuffles each column of the data matrix, thus destroying both the autocorrelation structure of each column and the cross-correlation between columns. The type=2 method shifts each column of the data matrix by a random amount, thus preserving the autocorrelation structure of each column but destroying the cross-correlation between columns (Purves and Law 2002). Default is type=1
quiet	Suppress progress bar when set to TRUE. Default is FALSE
...	Other parameters to <a href="#">cor</a> function.

### Details

Loreau and de Mazancourt (2008) show that community-wide synchrony  $\varphi$  can be quantified by computing the temporal variance  $\sigma_{x_T}^2$  of the community time series  $x_T(t) = \sum x_i(t)$  and the sum of the temporal standard deviation of the time series across all species  $(\sum \sigma_{x_i})^2$  such that:

$$\varphi = \frac{\sigma_{x_T}^2}{(\sum \sigma_{x_i})^2}$$

**Value**

Returns a named list containing:

obs	the observed community synchrony
meancorr	the mean correlation between the columns of the matrix
rands	the community synchrony value the randomizations. This variable is only returned if nrands > 0.
pval	p-value of observed community synchrony. This variable is only returned if nrands > 0.
alternative	Alternative hypothesis. This variable is only returned if nrands > 0.

**Author(s)**

Tarik C. Gouhier (tarik.gouhier@gmail.com)

**References**

Loreau, M., and C. de Mazancourt. 2008. Species synchrony and its drivers: Neutral and nonneutral community dynamics in fluctuating environments. *The American Naturalist* 172:E48-E66.

Purves, D. W., and R. Law. 2002. Fine-scale spatial structure in a grassland community: quantifying the plant's eye view. *Journal of Ecology* 90:121-129.

**Examples**

```
# Community matrix for 20 species undergoing random fluctuations
comm.rand=matrix(runif(100), nrow=5, ncol=20)
community.sync(comm.rand, nrands=20)$pval
# Community matrix for 20 species undergoing synchronized fluctuations
comm.corr=matrix(rep(comm.rand[,1], 20), nrow=5, ncol=20)
community.sync(comm.corr, nrands=20)$pval
# On "real" data
data(bird.traits)
community.sync(bird.traits, nrands=20)$pval
```

---

coord2dist

*coord2dist*

---

**Description**

Calculate distance between all pairs of sites

**Usage**

```
coord2dist (coords, is.latlon = TRUE, lower.tri = TRUE)
```

**Arguments**

coords	n x 4 matrix of coordinates consisting of lat or y, lon or x pairs for each each site
is.latlon	are coordinates latitudes/longitudes? Default is TRUE
lower.tri	Return lower triangular part of the distance matrix? Default is TRUE

**Value**

Returns the distance between all pairs of sites

**Author(s)**

Tarik C. Gouhier (tarik.gouhier@gmail.com)

**Examples**

```
coords=rbind(c(32, -125), c(43, -130))
# Compute great circle distance
coord2dist(coords)
```

---

correlated.matrix      *correlated.matrix*

---

**Description**

Create an ntimes x nspecies matrix with correlation rho, standard deviation sigma, and mean mu

**Usage**

```
correlated.matrix (rho = 0, sigma = 1, mu = 0, ntimes = 200, nspecies = 10)
```

**Arguments**

rho	Correlation between the columns of the matrix. This can be a single number describing the correlation between all columns, or the upper triangular portion of a correlation matrix describing the correlation between all pairs of columns. Default is 0
sigma	Standard deviation of the columns. Default is 1
mu	Mean of the columns. Default is 0
ntimes	Number of rows in the matrix. Default is 200
nspecies	Number of columns in the matrix. Default is 10

**Details**

This function is based on the Cholesky factorization method described by Legendre (2000).

**Value**

Returns a named list containing the following:

rho	Correlation(s) between the columns
sigma	Standard deviation of the columns
mu	Mean of the columns
community	ntimes x nspecies matrix

**Author(s)**

Tarik C. Gouhier (tarik.gouhier@gmail.com)

**References**

Gouhier, T. C., F. Guichard, and A. Gonzalez. 2010. Synchrony and stability of food webs in metacommunities. *The American Naturalist* 175:E16-E34.

Legendre, P. 2000. Comparison of permutation methods for the partial correlation and partial mantel tests. *Journal of Statistical Computation and Simulation* 67:37-73.

**Examples**

```
mat=correlated.matrix(rho=0.85, sigma=30, mu=10, nspecies=10)
# Check sd of each column
apply(mat$community, 2, sd)
# Check mean of each column
apply(mat$community, 2, mean)
# Check correlation of matrix
community.sync(mat$community)
```

---

find.minmax

*Find min/max of a time series*

---

**Description**

Find local minima and maxima of a time series

**Usage**

```
find.minmax (timeseries)
```

**Arguments**

timeseries time series in matrix format (n rows x 2 columns). The first column should contain the time steps and the second column should contain the values. If timeseries is a column vector instead of a matrix, then it will be automatically converted to a matrix with column 1 corresponding to a time index ranging from 1 to the length of timeseries



**Value**

Returns a named list containing:

mins	n x 3 matrix containing the index, time steps, and the local min values
maxs	n x 3 matrix containing the index, time steps, and the local max values

**Author(s)**

Tarik C. Gouhier (tarik.gouhier@gmail.com)

**Examples**

```
t1=runif(100)
min.max=find.minmax(t1)
min.max$maxs
plot (t1, t="l")
points (min.max$mins, col="blue", bg="blue", pch=19)
points (min.max$maxs, col="red", bg="red", pch=19)
```

---

kendall.w

*Kendall's W*

---

**Description**

Compute Kendall's coefficient of concordance (W)

**Usage**

```
kendall.w (data, nrand = 0, type = 1, quiet = FALSE)
```

**Arguments**

data	matrix in wide format where each row represents a different sample and each column represents a different variable.
nrand	Number of randomizations to perform to determine significance. Default is 0.
type	Randomization method. The type=1 method randomly shuffles each column of the data matrix, thus destroying both the autocorrelation structure of each column and the cross-correlation between columns. The type=2 method shifts each column of the data matrix by a random amount, thus preserving the autocorrelation structure of each column but destroying the cross-correlation between columns (Purves and Law 2002). Default is type=1
quiet	Suppress progress bar when set to TRUE. Default is FALSE

## Details

Kendall's W is a non-parametric statistic that ranges from 0 to 1 and measures the level of agreement between multiple variables. When the number of observations  $n > 10$ , its significance can be determined by using a  $\chi^2$  distribution with  $df = n - 1$ . Legendre (2005) shows that the  $\chi^2$  test is always too conservative (low power) compared to the randomization test. Hence, both tests have been made available in this function. The Monte Carlo randomizations are performed by shuffling the columns of the community matrix independently (Legendre 2005).

## Value

Returns a named list containing:

w.uncorrected	Kendall's W uncorrected for tied ranks
w.corrected	Kendall's W corrected for tied ranks
pval	p-value of Kendall's W
spearman.corr	Spearman's ranked correlation
pval.rand	p-value of Kendall's W based on randomization test. This variable is only returned if nrand > 0
rands	randomizations. This variable is only returned if nrand > 0

## Author(s)

Tarik C. Gouhier (tarik.gouhier@gmail.com)

## References

- Buonaccorsi, J. P., J. S. Elkinton, S. R. Evans, and A. M. Liebhold. 2001. Measuring and testing for spatial synchrony. *Ecology* 82:1668-1679.
- Gouhier, T. C., and F. Guichard. 2007. Local disturbance cycles and the maintenance of spatial heterogeneity across scales in marine metapopulations. *Ecology* 88:647-657.
- Gouhier, T. C., F. Guichard, and A. Gonzalez. 2010. Synchrony and stability of food webs in metacommunities. *The American Naturalist* 175:E16-E34.
- Legendre, P. 2005. Species associations: the Kendall coefficient of concordance revisited. *Journal of Agricultural, Biological, and Environmental Statistics* 10:226-245.
- Purves, D. W., and R. Law. 2002. Fine-scale spatial structure in a grassland community: quantifying the plant's eye view. *Journal of Ecology* 90:121-129.
- Zar, J. H. 1999. Biostatistical Analysis, Fourth edition. Prentice-Hall, Inc., Upper Saddle River, NJ.

## Examples

```
data(bird.traits)
(w=kendall.w(bird.traits))
```

---

latlon2dist	<i>latlon2dist</i>
-------------	--------------------

---

**Description**

Calculate distance between a pair of coordinates

**Usage**

```
latlon2dist (coords)
```

**Arguments**

coords            4-element vector of coordinates with format: (lat1, lon1, lat2, lon2)

**Value**

Returns the great circle distance between the pair of coordinates

**Author(s)**

Tarik C. Gouhier (tarik.gouhier@gmail.com)

**See Also**

[coord2dist](#)

**Examples**

```
coords=c(32, -125, 43, -130)
# Compute great circle distance
latlon2dist(coords)
```

---

meancorr	<i>Compute mean column-wise correlation and determine its significance via Monte Carlo randomizations</i>
----------	---

---

**Description**

Compute mean column-wise correlation and determine its significance via Monte Carlo randomizations. The Monte Carlo randomizations are performed by shuffling the columns of the community matrix independently.

**Usage**

```
meancorr (data, nrands = 0, alternative = c("two.tailed", "greater", "less"),
          method = c("pearson", "kendall", "spearman"),
          type = 1, quiet = FALSE, ...)
```

**Arguments**

data	community matrix in wide format where each row contains the abundance at each time step and each column corresponds to a different species.
nrand	number of randomizations to perform (default is 0)
alternative	Alternative hypothesis. Options include <code>greater</code> and <code>less</code> for the one-tailed test and <code>two.tailed</code> . Default is <code>two.tailed</code> .
method	Method to compute correlation? Options include <code>pearson</code> , <code>kendall</code> , and <code>spearman</code> . Default is <code>pearson</code>
type	Randomization method. The <code>type=1</code> method randomly shuffles each column of the data matrix, thus destroying both the autocorrelation structure of each column and the cross-correlation between columns. The <code>type=2</code> method shifts each column of the data matrix by a random amount, thus preserving the autocorrelation structure of each column but destroying the cross-correlation between columns (Purves and Law 2002). Default is <code>type=1</code>
quiet	Suppress progress bar when set to <code>TRUE</code> . Default is <code>FALSE</code>
...	Other parameters to <code>cor</code> function.

**Value**

Returns a named list containing:

obs	the observed mean correlation
rands	the mean correlation for each randomization. This variable is only returned if <code>nrand &gt; 0</code> .
pval	p-value of observed mean correlation. This variable is only returned if <code>nrand &gt; 0</code> .
alternative	Alternative hypothesis. This variable is only returned if <code>nrand &gt; 0</code> .
method	Method used to compute the mean correlation.

**Author(s)**

Tarik C. Gouhier (tarik.gouhier@gmail.com)

**References**

Purves, D. W., and R. Law. 2002. Fine-scale spatial structure in a grassland community: quantifying the plant's eye view. *Journal of Ecology* 90:121-129.

**Examples**

```
# Community matrix for 20 species undergoing random fluctuations
comm.rand=matrix(runif(100), nrow=5, ncol=20)
meancorr(comm.rand, nrand=20)$pval
# Community matrix for 20 species undergoing synchronized fluctuations
comm.corr=matrix(rep(comm.rand[,1], 20), nrow=5, ncol=20)
meancorr(comm.corr, nrand=20)$pval
```

```
# On "real" data
data(bird.traits)
meancorr(bird.traits, nrands=20)$pval
```

---

peaks	<i>Find the proportion of local minima/maxima common to both time series and compute its significance via Monte Carlo randomizations</i>
-------	--

---

### Description

Find the proportion of local minima/maxima common to both time series and compute its significance via Monte Carlo randomizations

### Usage

```
peaks (t1, t2, nrands = 0, type = 1, quiet = FALSE)
```

### Arguments

t1	time series 1 in matrix format (n rows x 2 columns). The first column should contain the time steps and the second column should contain the values. If t1 is a column vector instead of a matrix, then it will be automatically converted to a matrix with column 1 corresponding to a time index ranging from 1 to the length of t1
t2	time series 2 in matrix format (n rows x 2 columns). The first column should contain the time steps and the second column should contain the values. If t2 is a column vector instead of a matrix, then it will be automatically converted to matrix with column 1 corresponding to a time index ranging from 1 to the length of t2.
nrands	number of randomizations. Default is 0.
type	Randomization method. The type=1 method randomly shuffles each time series, thus destroying both the autocorrelation structure of each time series and their cross-correlation. The type=2 method shifts each time series by a random amount, thus preserving the autocorrelation structure but destroying the cross-correlation between the time series (Purves and Law 2002). Default is type=1
quiet	Suppress progress bar when set to TRUE. Default is FALSE

### Value

Returns a named list containing:

pval	p-value computed by randomly shuffling both time series nrands times
rands	proportion of local minima/maxima common to both time series for each randomization
obs	proportion of local minima/maxima common to both time series in the observed dataset
index	indices of local minima/maxima common to both time series in the observed dataset

**Author(s)**

Tarik C. Gouhier (tarik.gouhier@gmail.com)

**References**

Buonaccorsi, J. P., J. S. Elkinton, S. R. Evans, and A. M. Liebhold. 2001. Measuring and testing for spatial synchrony. *Ecology* 82:1668-1679.

Purves, D. W., and R. Law. 2002. Fine-scale spatial structure in a grassland community: quantifying the plant's eye view. *Journal of Ecology* 90:121-129.

**Examples**

```
t1=runif(100)
t2=runif(100)
(p=peaks(t1, t2))
```

---

phase.partnered	<i>Phase partnered time series</i>
-----------------	------------------------------------

---

**Description**

Create two time series with specific autocorrelation  $\gamma$ , cross-correlation  $\rho$ , mean `ts.mean`, and standard deviation `ts.sd` using the phase partnered algorithm described by Vasseur (2007)

**Usage**

```
phase.partnered (n = 2000, rho = 1, gamma = 1, sigma = 0.1, mu = 0)
```

**Arguments**

n	number of time steps in time series. Default is 2000.
rho	cross-correlation between the two time series ( $-1 \leq \rho \leq 1$ ). Default is 1.
gamma	autocorrelation of each time series. Gamma ( $\gamma$ ) describes the relationship between frequency $f$ and power $P$ : $P(f) = 1/f^\gamma$ . If $-2 \leq \gamma \leq 0$ : blue noise and $0 \leq \gamma \leq 2$ : red noise. Default is 1.
sigma	standard deviation of both time series. Default is 0.1.
mu	mean of both time series. Default is 0.

**Value**

Returns a named list containing the following:

rho	Cross-correlation of the time series
gamma	Autocorrelation of the time series
sigma	Standard deviation of the time series
mu	Mean of the time series
timeseries	n x 2 matrix containing the time series

**Author(s)**

Tarik C. Gouhier (tarik.gouhier@gmail.com)

**References**

Gouhier, T. C., F. Guichard, and A. Gonzalez. 2010. Synchrony and stability of food webs in metacommunities. *The American Naturalist* 175:E16-E34.

Vasseur, D. A. 2007. Environmental colour intensifies the Moran effect when population dynamics are spatially heterogeneous. *Oikos* 116:1726-1736.

**Examples**

```
# Positively cross-correlated white noise
pos.corr=phase.partnered(n = 100, rho = 0.7, gamma = 0)
# Negatively cross-correlated white noise
neg.corr=phase.partnered(n = 100, rho = -1, gamma = 0)
par(mfrow=c(2,1))
matplot (pos.corr$timeseries, t="l", lty=1)
matplot (neg.corr$timeseries, t="l", lty=1)
```

---

phase.sync

*Phase synchrony of quasi-periodic time series*

---

**Description**

Compute the phase synchrony between two quasi-periodic time series by quantifying their phase difference at each time step

**Usage**

```
phase.sync (t1, t2, nrand = 0, mod = 1, method = c("markov", "fft"),
           nbreaks = 10, mins = FALSE, quiet = FALSE)
```

**Arguments**

t1	time series 1 in matrix format (n rows x 2 columns). The first column should contain the time steps and the second column should contain the values. If t1 is a column vector instead of a matrix, then it will be automatically converted to a matrix with column 1 corresponding to a time index ranging from 1 to the length of t1.
t2	time series 2 in matrix format (n rows x 2 columns). The first column should contain the time steps and the second column should contain the values. If t2 is a column vector instead of a matrix, then it will be automatically converted to matrix with column 1 corresponding to a time index ranging from 1 to the length of t2.
nrand	number of randomizations to perform (default is 0)

mod	flag to indicate whether to compute phase difference modulus $2\pi$ between 0 and $2\pi$ (mod=1) or phase difference modulus $2\pi$ between $-\pi$ and $\pi$ (mod=2). Default is mod=1.
method	method to generate surrogate time series for Monte Carlo simulations. This can be set to markov to use the Markov process described in Cazelles and Stone (2004) or fft to use the FFT approach described in Theiler et al. (1992). Default is method=markov.
nbreaks	number of bins to use to group the values in the time series. Default is 10.
quiet	Suppress progress bar when set to TRUE. Default is FALSE
mins	use local minima instead of local maxima to compute and the interpolate the phase. Default is FALSE.

### Details

Two time series are phase-locked if the relationship between their phases remains constant over time. This function computes the phase of successive local maxima or minima for each time series and then uses linear interpolation to find the phase at time steps that fall between local maxima/minima. A histogram can be used to determine if the distribution of the phase difference at each time step is uniform (indicating no phase locking) or has a clear peak (indicating phase locking).

### Value

Returns a list containing Q.obs, pval, rands, phases1, phases2, deltapphase, and icdf:

Q.obs	Phase synchrony ranging from 0 (no phase synchrony) to 1 (full phase synchrony)
pval	p-value of observed phase synchrony based on randomization test
rands	Monte Carlo randomizations
phases1	n x 3 matrix containing the timestep, value, and phase of the first time series
phases2	n x 3 matrix containing the timestep, value, and phase of the second time series
deltaphase	n x 4 matrix containing the timestep, raw phase difference, phase difference modulus $2\pi$ between 0 and $2\pi$ , phase difference modulus $2\pi$ between $-\pi$ and $\pi$
icdf	Inverse cumulative distribution of Q values obtained from Monte Carlo randomizations

### Author(s)

Tarik C. Gouhier (tarik.gouhier@gmail.com)

### References

- Cazelles, B., and L. Stone. 2003. Detection of imperfect population synchrony in an uncertain world. *Journal of Animal Ecology* 72:953–968.
- Theiler, J., S. Eubank, A. Longtin, B. Galdrikian, and J. Doynne Farmer. 1992. Testing for nonlinearity in time series: the method of surrogate data. *Physica D: Nonlinear Phenomena* 58:77–94.



**Examples**

```
t1=runif(100)
t2=runif(100)
# Compute and interpolate phases using successive local minima
sync.mins=phase.sync(t1, t2, mins=TRUE)
# Compute and interpolate phases using successive local maxima
sync.maxs=phase.sync(t1, t2)
# Plot distribution of phase difference
hist(sync.mins$deltaphase$mod_phase_diff_2pi)
```

---

pisco.data	<i>PISCO multi-year and spatially-explicit mussel and environmental dataset</i>
------------	---

---

**Description**

Contains the mean annual chl-a concentration, sea surface temperature, upwelling currents, and mussel abundance at 48 intertidal sites along the West Coast of the United States from 2000-2003.

**Usage**

```
data(pisco.data)
```

**Format**

A data frame with 192 observations on the following 7 variables.

```
latitude latitude (degrees North)
longitude longitude (degrees West)
chl mean annual remote sensed chlorophyll-a concentration
sst mean annual remote sensed sea surface temperature
upwelling mean annual remote sensed upwelling currents
mussel_abund mean annual mussel cover (Mytilus californianus)
year sampling year
```

**References**

Gouhier, T. C., F. Guichard, and B. A. Menge. 2010. Ecological processes can synchronize marine population dynamics over continental scales. *Proceedings of the National Academy of Sciences* 107:8281-8286.

**Examples**

```
data(pisco.data)
```

---

plot.synchrony      *Plot synchrony objects*

---

### Description

Plot synchrony objects

### Usage

```
## S3 method for class 'synchrony'  
plot(x, main = "", xlab = "Values from randomizations",  
      ylab = "Frequency", line.col = "red", lty = 2,  
      lwd = 1, col = "grey", ...)
```

### Arguments

x	synchrony object
main	main title of the figure
xlab	xlabel of the figure. Default is "Values from randomizations"
ylab	ylabel of the figure. Default is "Frequency"
line.col	color of the vertical line indicating the value observed in the data. Default is "red"
lty	line type. Default is 2 or dashed
lwd	line width. Default is 1
col	color of the bars. Default is grey
...	other graphical parameters.

### Author(s)

Tarik C. Gouhier (tarik.gouhier@gmail.com)

### Examples

```
comm.rand=matrix(runif(100), nrow=5, ncol=20)  
comm.rand.sync=community.sync(comm.rand, nrands=20)  
plot(comm.rand.sync)
```

---

plot.vario

*Plot vario objects*


---

**Description**

Plot vario objects

**Usage**

```
## S3 method for class 'vario'
plot(x, xlab = "Lag distance", ylab = NULL, ylim = NULL,
      xtype = c("mean.bin.dist", "bins"), rug = FALSE, ci = FALSE,
      pch = 21, col.sig="black", col.nonsig="black", bg.sig="black",
      bg.nonsig = "white", alpha = 0.05, ...)
```

**Arguments**

x	vario object generated by vario function.
xlab	xlabel of the figure. Default is "Lag distance"
ylab	ylabel of the figure. Default is NULL and will automatically generate the right label
ylim	y-range. Default is NULL and will automatically generate the best range based on the metric
xtype	Use either the discrete bin classes (bins) or the mean distance of the points within each bin (mean.bin.dist) on the x-axis. Default is mean.bin.dist
rug	Plot rug indicating the density of data points? Default is FALSE
ci	Plot two-tailed (1- $\alpha$ )% confidence intervals? Default is FALSE
pch	Type of points to use when plotting the variogram. Default is 21
col.sig	Border color of points for significant values. Default is black
col.nonsig	Border color of points for non-significant values. Default is black
bg.sig	Background color of points for significant values. Default is black
bg.nonsig	Background color of points for non-significant values. Default is black
alpha	Significance level. Default is 0.05
...	other graphical parameters.

**Author(s)**

Tarik C. Gouhier (tarik.gouhier@gmail.com)

**Examples**

```

data(pisco.data)
d=subset(pisco.data, subset=year==2000, select=c("latitude", "longitude", "sst"))
semiv=vario(data=d)
moran=vario(data=d, type="moran", nrand=100)
geary=vario(data=d, type="geary", nrand=100)

par(mfrow=c(3,1))
plot(semiv)
plot(moran, bg.sig="blue")
plot(geary, bg.sig="red")

```

---

plot.variofit

*Plot variofit objects*


---

**Description**

Plot variofit objects

**Usage**

```

## S3 method for class 'variofit'
plot(x, xlab = "Lag distance", ylab = "Variogram",
      col.pts = "black", col.line = "red",
      pch = 21, ...)

```

**Arguments**

x	variofit object generated by vario.fit function
xlab	xlabel of the figure. Default is "Lag distance"
ylab	ylabel of the figure. Default is "Variogram"
col.pts	Border color of the points. Default is black
col.line	Color of the fitted variogram. Default is red
pch	Type of points to use when plotting the variogram. Default is 21
...	other graphical parameters.

**Author(s)**

Tarik C. Gouhier (tarik.gouhier@gmail.com)

**Examples**

```

# Environmental variogram
data(pisco.data)
d=subset(pisco.data, subset=year==2000, select=c("latitude", "longitude", "upwelling"))
semiv=vario(data=d)
mod.sph=vario.fit(semiv$vario, semiv$mean.bin.dist)
plot(mod.sph)

```

---

surrogate.ts                      *Create surrogate time series via Markov process*

---

### Description

Create surrogate time series with the same short-term time correlation and overall temporal pattern as the original time series using the Markov process described by Cazelles and Stones (2003)

### Usage

```
surrogate.ts (ts, distr.ts = NULL, trans.ts = NULL, nbreaks = 10)
```

### Arguments

ts	time series in matrix format (n rows x 2 columns). The first column should contain the time steps and the second column should contain the values. If ts is a column vector instead of a matrix, then it will be automatically converted to a matrix with column 1 corresponding to a time index ranging from 1 to the length of ts
distr.ts	binning of time series values. This parameter must be specified if trans.ts is not set to NULL. Default is NULL.
trans.ts	transition matrix from bin $i$ to bin $j$ . Default is NULL.
nbreaks	number of bins to use to group the time series values. Default is 10.

### Details

The values of the time series  $x_n$  are grouped into nbreak equally-sized bins. The transition matrix  $M_{ij}$  describing the probability of  $x_{n+1}$  belonging to bin  $j$  based on  $x_n$  belonging to bin  $i$  is defined using the relative frequencies of the data such that:  $M_{ij} = Pr(x_{n+1} \in b_j | x_n \in b_i)$ . The surrogate time series is then constructed by randomly selecting a starting value and randomly selecting the next value from the proper bin based on the transition matrix. This process is repeated until the surrogate time series has the same length as the original time series.

### Value

Returns a named list containing:

surr.ts	surrogate time series in matrix format
trans	transition matrix $M_{ij}$
distr	binning of time series values

### Author(s)

Tarik C. Gouhier (tarik.gouhier@gmail.com)

## References

Cazelles, B., and L. Stone. 2003. Detection of imperfect population synchrony in an uncertain world. *Journal of Animal Ecology* 72:953-968.

## See Also

[phase.sync](#)

## Examples

```
t1=runif(100)
surr.t1=surrogate.ts(ts=t1)
plot(t1, t="l")
lines(surr.t1$surr.ts, col="red")
```

---

vario

*vario*

---

## Description

Compute the empirical variogram and determine its significance via Monte Carlo randomizations

## Usage

```
vario (n.bins = 20, size.bins = NULL, extent = 0.5, data, data2 = NULL,
      is.latlon = TRUE, is.centered = FALSE, nrand = 0,
      type = c("semivar", "cov", "pearson",
              "spearman", "kendall", "moran", "geary"),
      alternative = c("one.tailed", "two.tailed"),
      mult.test.corr = c("none", "holm", "hochberg", "bonferroni"),
      regional = c("all", "extent"),
      quiet = FALSE)
```

## Arguments

n.bins	Number of bins or lag distances. This argument is only used when size.bins=NULL
size.bins	Size of bins in units of distance (e.g., km). When specified, this argument overrides n.bins. Default is NULL
extent	Proportion of the spatial extent of the data over which to compute the variogram. Default is 0.5 to limit potentially spurious results due to the limited number of data points at large lag distances.
data	n x m matrix containing y-coordinates (or latitude), x-coordinates (or longitude), and values. The values can either be a single column of observations at each site for univariate variograms or a matrix of observations at each site for multivariate variograms (e.g., to compute spatial synchrony).

<code>data2</code>	<code>n x m</code> matrix containing y-coordinates (or latitude), x-coordinates (or longitude), and values for second variable. The values can either be a single column of observations at each site for univariate variograms or a matrix of observations at each site for multivariate variograms (e.g., to compute spatial synchrony).
<code>is.latlon</code>	Are coordinates latitudes/longitudes? Default is TRUE
<code>is.centered</code>	Should the variogram be centered by subtracting the regional mean from each value? If so, the zero-line represents the regional mean. Default is FALSE
<code>nrand</code>	Number of randomizations to determine statistical significance of variogram. Default is 0.
<code>type</code>	Type of variogram to compute. Default is <code>semivar</code> for semivariance. Other options include <code>cov</code> for covariance, <code>pearson</code> for Pearson correlation, <code>spearman</code> for Spearman correlation, <code>kendall</code> for Kendall correlation, <code>moran</code> for Moran's I, and <code>geary</code> for Geary's C
<code>alternative</code>	Conduct a one-tailed or a two-tailed test? Note that the statistical test is to determine whether the local value within each lag distance is different from the regional mean. If the variogram is centered, the null hypothesis is that the local values are equal to zero. If the variogram is not centered, the null hypothesis is that the local values are equal to the regional mean. Default is <code>one.tailed</code>
<code>mult.test.corr</code>	Correct for multiple tests? Default is "none". Other options include <code>holm</code> , <code>hochberg</code> and <code>bonferroni</code>
<code>regional</code>	Should the regional average be computed for the entire dataset ( <code>all</code> ) or just the extent specified ( <code>extent</code> ). Default is the entire dataset ( <code>all</code> )
<code>quiet</code>	Suppress progress bar when set to TRUE. Default is FALSE

### Details

This function can be used to compute univariate correlograms using Moran's I, Geary's C, and the covariance function or variograms using the semivariance function. Multivariate (Mantel) correlograms can also be computed using the covariance function, Pearson's, Spearman's or Kendall's correlation coefficients. Cross-correlograms/variograms between `data1` and `data2` can be computed with the covariance function, Pearson's, Spearman's or Kendall's correlation coefficients for multivariate variograms and Moran's I, Geary's C, the covariance function, or semivariance for univariate variograms.

### Value

Returns a named list containing the following variables:

<code>bins</code>	Center of each lag/bin
<code>mean.bin.dist</code>	Mean distance of each lag/bin
<code>vario</code>	Variogram values in each lag/bin
<code>npoints</code>	Number of pairs of points in each lag/bin
<code>metric</code>	Type of variogram computed
<code>is.centered</code>	Is the variogram centered?
<code>regional.mean</code>	Regional mean value

pvals	p-value for each lag/bin. This variable is only returned if nrand > 0.
rands	nrand x n.bins matrix of randomizations. This variable is only returned if nrand > 0.
alternative	One-tailed or two-tailed test? This variable is only returned if nrand > 0.
mult.test.corr	Correct for multiple tests? This variable is only returned if nrand > 0.
is.multivar	Was the analysis performed on multivariate data?

### Author(s)

Tarik C. Gouhier (tarik.gouhier@gmail.com)

### References

- Bjornstad, O. N., and W. Falck. 2001. Nonparametric spatial covariance functions: Estimation and testing. *Environmental and Ecological Statistics* 8:53-70.
- Bjornstad, O. N., R. A. Ims, and X. Lambin. 1999. Spatial population dynamics: analyzing patterns and processes of population synchrony. *Trends in Ecology & Evolution* 14:427-432.
- Fortin, M. J., and M. R. T. Dale. 2005. *Spatial Analysis: A Guide for Ecologists*. Cambridge University Press.

### See Also

[vario.func](#)

### Examples

```
data(pisco.data)
d=subset(pisco.data, subset=year==2000, select=c("latitude", "longitude", "sst"))
semiv=vario(data=d)
moran=vario(data=d, type="moran", nrand=100)
par(mfrow=c(2,1), mar=c(4.2, 4, 1, 1))
plot(semiv$mean.bin.dist, semiv$vario, xlab="Lag distance (km)", ylab="Semivariance")
plot(moran$mean.bin.dist, moran$vario, xlab="Lag distance (km)", ylab="Moran's I", t="1")
points(moran$mean.bin.dist[moran$pvals >= 0.05], moran$vario[moran$pvals >= 0.05],
       bg="white", pch=21)
points(moran$mean.bin.dist[moran$pvals < 0.05], moran$vario[moran$pvals < 0.05],
       bg="black", pch=21)
abline(h=0, lty=2)

# Compute spatial synchrony
d.upw=subset(pisco.data, select=c("latitude", "longitude", "year", "upwelling"))
d.cov=subset(pisco.data, select=c("latitude", "longitude", "year", "mussel_abund"))
# Reshape the data
d.upw.wide=reshape(data=d.upw, idvar=c("latitude", "longitude"), timevar=c("year"),
                  direction="wide")
d.cov.wide=reshape(data=d.cov, idvar=c("latitude", "longitude"), timevar=c("year"),
                  direction="wide")
# Generate variograms
v.upw=vario(n.bins=12, data=d.upw.wide, type="pearson", extent=1, nrand=999)
```



```

v.cov=vario(n.bins=12, data=d.cov.wide, type="pearson", extent=1, nrands=999)
## Fit variograms
v.cov.per=vario.fit(v.cov$vario, v.cov$mean.bin.dist, type="period",
                   start.vals=list(a=1, b=3, c=0))
v.upw.lin=vario.fit(v.upw$vario, v.upw$mean.bin.dist, type="linear")

par(mfrow=c(2,1))
plot(v.cov, xlab="Lag distance (km)", bg.sig="red", col.nonsig="red",
     main="Mussel cover",
     rug=TRUE, ylim=c(-0.3, 0.3))
lines(v.cov$mean.bin.dist, v.cov.per$fit, col="red")
plot(v.upw, xlab="Lag distance (km)", bg.sig="blue", col.nonsig="blue",
     main="Upwelling", rug=TRUE)
lines(v.upw$mean.bin.dist, v.upw.lin$fit, col="blue")

```

---

vario.fit

*vario.fit*


---

## Description

Fit model to the empirical variogram

## Usage

```

vario.fit (vario, bins, weights = rep(1, length(vario)),
          type = c("spherical", "gaussian", "nugget", "linear",
                  "exponential", "sill", "periodic", "hole"),
          start.vals = list(c0 = 0, c1 = max(vario),
                           a = max(bins)/4, b=0.1, c=0.1),
          control = list(maxit=10000))

```

## Arguments

vario	Empirical variogram from emp.vario function
bins	Bins or lag distances from emp.vario function
weights	Vector of weights of the same length as vario. If weights is a vector containing the number of points in each distance bin, the model will be fit via weighted least squares with the weights corresponding to the proportion of points within each bin (i.e., weights sum to 1). Default is a vector of weights equal to 1
type	Type of variogram model to fit to the data. Default is spherical. Other options are gaussian, nugget, linear, exponential, sill, periodic, and hole
start.vals	Named list containing the start values for the variogram model: c0: nugget, c1: sill, a: spatial range; b: slope; c: frequency
control	optional parameter for the optim function. See ?optim for details

**Value**

Return a named list containing the following variables:

vario	Empirical variogram values
bins	Empirical variogram bins/lag distances
AIC	AIC score of the model fit: $AIC = n \log \left( \frac{SSE}{n} \right) + 2p$ where $n$ is the number of points in the variogram, $SSE = \sum (\hat{x}_i - x_i)^2$ , and $p$ is the number of parameters
RMSE	Root Mean Square Error of the model fit: $\sqrt{\frac{SSE}{n}}$
params	Named list containing the best model parameter estimates
fit	Predicted variogram values from the model fit
nls.success	did nls succeed?
convergence	did nls or optim converge?

**Note**

Selecting proper initial values is critical for fitting a reasonable model to the empirical variogram. If these values are off, nls will fail and fall-back functions will be used to determine the best parameter values that minimize the Root Mean Square Error (RMSE).

**Author(s)**

Tarik C. Gouhier (tarik.gouhier@gmail.com)

**See Also**

[vario](#), [vario.func](#)

**Examples**

```
# Load data
data(pisco.data)
# Environmental variogram
d=subset(pisco.data, subset=year==2000, select=c("latitude", "longitude", "upwelling"))
semiv=vario(data=d)
plot(semiv, xlab="Lag distance (km)")
mod.sph=vario.fit(semiv$vario, semiv$mean.bin.dist)
# Weighted least squares fit based on the number of points
mod.exp=vario.fit(semiv$vario, semiv$mean.bin.dist,
                 weights=semiv$npoints/sum(semiv$npoints),
                 type="expo")
mod.gau=vario.fit(semiv$vario, semiv$mean.bin.dist, type="gauss")
mod.lin=vario.fit(semiv$vario, semiv$mean.bin.dist, type="lin")
lines(semiv$mean.bin.dist, mod.sph$fit, col="red")
lines(semiv$mean.bin.dist, mod.exp$fit, col="black")
lines(semiv$mean.bin.dist, mod.gau$fit, col="blue")
lines(semiv$mean.bin.dist, mod.lin$fit, col="green")
legend(x="topleft", legend=paste(c("Spherical AIC:", "Exponential AIC:"),
```

```

                                "Gaussian AIC:", "Linear AIC:"),
                                c(format(mod.sph$AIC, dig=2),
                                  format(mod.exp$AIC, dig=2),
                                  format(mod.gau$AIC, dig=2),
                                  format(mod.lin$AIC, dig=2))), lty=1, col=c("red", "black", "blue", "green"),
                                bty="n")

# Correlogram
cover=subset(pisco.data, subset=year==2000,
             select=c("latitude", "longitude", "mussel_abund"))
moran=vario(data=cover, type="moran")
mod.hol=vario.fit(moran$vario, moran$mean.bin.dist,
                 type="hole", start.vals=list(c0=0.6, a=25, c1=0.01))
mod.per=vario.fit(moran$vario, moran$mean.bin.dist, type="period",
                 start.vals=list(a=1, b=3, c=0))
mod.lin=vario.fit(moran$vario, moran$mean.bin.dist, type="linear")
plot(moran, xlab="Lag distance (km)", ylim=c(-0.6, 0.8))
lines(moran$mean.bin.dist, mod.per$fit, col="red")
lines(moran$mean.bin.dist, mod.hol$fit, col="black")
lines(moran$mean.bin.dist, mod.lin$fit, col="blue")
legend(x="topleft", legend=paste(c("Periodic AIC:", "Hole AIC:",
                                  "Linear AIC:"),
                                c(format(mod.per$AIC, dig=2),
                                  format(mod.hol$AIC, dig=2),
                                  format(mod.lin$AIC, dig=2))),
                                lty=1, col=c("red", "black", "blue"), bty="n")

```

---

vario.func

*vario.func*


---

## Description

Compute the empirical variogram values for each bin

## Usage

```

vario.func (x, y, glob.mean, glob.sd, glob.N, is.multivar = FALSE,
           type = c("semivar", "cov", "pearson",
                   "spearman", "kendall", "moran", "geary"))

```

## Arguments

x	First set of sites within bin/lag distance
y	Second set of sites within bin/lag distance
glob.mean	Global mean
glob.sd	Global standard deviation
glob.N	Global number of points
is.multivar	Is the data multivariate? Default is FALSE

**type** Type of variogram to compute. Default is `semivar` for semivariance. Other options include `cov` for covariance, `pearson` for Pearson correlation, `spearman` for Spearman correlation, `kendall` for Kendall correlation, `moran` for Moran's I, and `geary` for Geary's C

**Value**

Return the value.

**Author(s)**

Tarik C. Gouhier ([tarik.gouhier@gmail.com](mailto:tarik.gouhier@gmail.com))

**See Also**

[vario](#)

**Examples**

```
# Internal function used by vario
```

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