

Package ‘NullSens’

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Title Partitioning Abiotic and Biotic Contributions to Community Variation

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Description NullSens is a method for verifying hypotheses on species interactions when environmental gradients are present

Depends R (>= 2.15.0), MASS, censReg

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URL <http://www.github.com/sessinger/NullSens/>

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NullSens-package

NullSens: Partitioning Abiotic and Biotic Contributions to Community Variation

Description

NullSens is a method that employs a null model based on existing species covariation models to assess community-wide biotic covariation after removing individual species responses to environmental gradients. Analytical output from NullSens provides the percentages of the variation that can be explained due to abiotic, biotic and unexplained factors. Within the biotic variation results, the algorithm also outputs if it detects positive, negative, or mixed community covariation. NullSens can be used to verify hypotheses on species interactions when environmental gradients are present.

Author(s)

Steven D. Essinger <sde22@drexel.edu>, Christopher B. Blackwood, Gail L. Rosen

References

S.D. Essinger, "Partitioning Abiotic and Biotic Contributions to Community Variation," Ph.D. dissertation, Dept. Elect. Eng., Drexel Univ., Philadelphia, PA, 2013

coeffDet

Compute the coefficient of determination

Description

NullSens internal function: Computes the coefficient of determination for each species and the overall community.

Usage

```
coeffDet(CDM, X, Yhat)
```

Arguments

CDM	Community Data Matrix (sites x species)
X	Abiotic Factors (sites x # of abiotic factors + 1 (intercept))
Yhat	Predicted (fitted) responses

Details

Avg_Adj_R2 is the environmentally explained variation

Value

R2	Coefficient of Multiple Determination, per species
Adj_R2	Adjusted R2, per species
Avg_R2	Community R2
Avg_Adj_R2	Community Adjusted R2

Author(s)

Steve Essinger

covStatistic

*Test for significant positive/negative community covariation.***Description**

Covariation test statistic (species pair-wise) for significant community positive/negative covariance hypothesis testing

Usage

```
covStatistic(matrix, sites_sel, mutual_reject)
```

Arguments

matrix	Data matrix for computing test statistic
sites_sel	Nested list of booleans for including/excluding sites per species
mutual_reject	Threshold for excluding species pairs from test statistic

Details

mutual_reject (default 8): Any species pair having less than mutual_reject sites in common will be excluded from the test statistic calculation.

Value

index	Covariation type test statistic computed on input matrix
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Author(s)

Steve Essinger

mvrRobust

*Robust Regression using bisquare estimator objective function***Description**

Multivariate regression using iteratively reweighted least-squares bisquare estimator

Usage

```
mvrRobust(CDM, X, sites_sel)
```

Arguments

CDM	Community Data Matrix (sites x species)
X	Abiotic Factors (sites x factors) + vector of ones for intercept
sites_sel	Nested list of booleans for including/excluding sites per species

Value

Yhat	Predicted (fitted) responses
Yres	Residual responses
B_est	Model coefficient estimates

Note

Requires MASS package

Author(s)

Steve Essinger

References

Robust Statistics, Peter. J. Huber, Wiley, 1981 (republished in paperback, 2004)

mvrStandard

OLS Linear Regression

Description

Ordinary Least Squares Linear Regression

Usage

```
mvrStandard(CDM, X, sites_sel)
```

Arguments

CDM	Community Data Matrix (sites x species)
X	Abiotic Factors (sites x factors) + vector of ones for intercept
sites_sel	Nested list of booleans for including/excluding sites per species

Value

Yhat	Predicted (fitted) responses
Yres	Residual responses
B_est	Model coefficient estimates

Author(s)

Steve Essinger

References

Rao, C.R. (1973). Linear statistical inference and its applications (2nd ed.). New York: John Wiley & Sons.

mvrTobit	<i>Censored Regression (Tobit) Model</i>
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Description

Fitting a linear model with a censored dependent variable

Usage

```
mvrTobit(CDM, X, sites_sel)
```

Arguments

CDM	Community Data Matrix (sites x species)
X	Abiotic Factors (sites x factors) + vector of ones for intercept
sites_sel	Nested list of booleans for including/excluding sites per species

Value

Yhat	Predicted (fitted) responses
Yres	Residual responses
B_est	Model coefficient estimates

Note

Requires censReg package

Author(s)

Steve Essinger

References

Greene, W.H. (2008): Econometric Analysis, Sixth Edition, Prentice Hall, p. 871-875.

Kleiber, C. and Zeileis, A. (2008): Applied Econometrics with R, Springer, p. 141-143.

Tobin, J. (1958): Estimation of Relationships for Limited Dependent Variables. *Econometrica* 26, p. 24-36.

nullModel	<i>Null model</i>
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Description

Randomize matrix using null model

Usage

```
nullModel(matrix, sites_sel)
```

Arguments

matrix	Data matrix for randomization
sites_sel	Nested list of booleans for including/excluding sites per species

Details

This null model randomly permutes species abundance using the respective sites selected in sites_sel. Each species is randomized independently of the other species.

Value

rand_matrix	Return matrix randomized by null model
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Author(s)

Steve Essinger

NullSens	<i>Partitioning Abiotic and Biotic Contributions to Community Variation</i>
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Description

NullSens is a method that employs a nullmodel based on existing species covariation models to assess community-wide biotic covariation after removing individual species responses to environmental gradients. Analytical output from NullSens provides the percentages of the variation that can be explained due to abiotic, biotic and unexplained factors. Within the biotic variation results, the algorithm also outputs if it detects positive, negative, or mixed community covariation. NullSens can be used to verify hypotheses on species interactions when environmental gradients are present.

Usage

```
NullSens(CDM, X, select = TRUE, reg_method = "robust", null_reps = 200,
test_stat = c(1, 1), mutual_reject = 8, alpha = 0.05)
```

Arguments

CDM	Community Data Matrix (sites x species) *Must be a matrix
X	Abiotic Factors (sites x factors) *Must be a matrix (i.e. use as.matrix())
select	Enable site selection procedure – TRUE (default)
reg_method	Regression method – "robust" (default), "tobit", "standard"
null_reps	Number of random matrices to generate for null distribution – 200 (default)
test_stat	Test statistic employed for computing indices
mutual_reject	Ignore species pairs with less than m mutual sites in testStatistic – 8 (default)
alpha	Significance level – 0.05 (default)

Details

Test Statistic Options: test_stat[1] -> Statistic, test_stat[2] -> Weight

test_stat[1] = 1 -> abs(cvar), = 2 -> cvar^2, = 3 -> abs(ccorr), = 4 -> ccorr^2

test_stat[2] = 1 -> abs(cvar), = 2 -> abs(ccorr), = 3 -> sum(mutsel), = 4 -> 1

Value

CDM	Community Data Matrix
X	Abiotic Factors, vector of ones appended if missing
Yhat	Predicted (fitted) responses
Yres	Residual Responses
B_est	Estimated Regression Parameters
sites_sel	List Sites Selected for Analysis, per Species
p_value	P-Value of Covariation Significance Test
index	List of index values for random and test matrices (test is last element)
CR	Pairwise Residual (Yres) Correlation Matrix from testStatistic
CV	Pairwise Residual (Yres) Covariation Matrix from testStatistic
R2	Coefficient of Multiple Determination, per species
Adj_R2	Adjusted R2, per species
Avg_R2	Community Averaged R2
Avg_Adj_R2	Community Averaged Adjusted R2
IND_summary	abiotic, biotic, unexplained variation, per species
COM_summary	abiotic, biotic, unexplained variation, community
COM_var_type	[avg_covar, p-value_pos, p_value_neg]

Author(s)

Steve Essinger

References

S.D. Essinger, "Partitioning Abiotic and Biotic Contributions to Community Variation," Ph.D. dissertation, Dept. Elect. Eng., Drexel Univ., Philadelphia, PA, 2013

NullSens_Simulation *Evaluating NullSens on Simulated Community Data*

Description

This function is useful for performing sensitivity analyses on NullSens using simulated communities (see SpeciesResponseModel.R)

Usage

```
NullSens_Simulation(n, p, q, N, M, CD, Type, num_exp = 100, select = TRUE,
  reg_method = "robust", null_reps = 200, test_stat = c(1, 1), mutual_reject = 7, alpha = 0.05)
```

Arguments

n	Number of Sites to Include in Simulation
p	Number of Species to Include in Simulation
q	Number of Abiotic Factors to Include in Simulation
N	Noise Parameter Selection (integer 1 thru 12)
M	Covariation Magnitude Selection (integer 1 thru 5)
CD	Number of Covarying Species Pairs to Include in Simulation
Type	Type of Species Covariation in Simulation (see details)
num_exp	Number of Experiments to Include in Simulation
select	Enable site selection procedure – TRUE (default)
reg_method	Regression method – "robust" (default), "tobit", "standard"
null_reps	Number of random matrices to generate for null distribution – 200 (default)
test_stat	Test statistic employed for computing indices
mutual_reject	Ignore species pairs with less than m mutual sites in testStatistic – 8 (default)
alpha	Significance level – 0.05 (default)

Details

Type:

0 -> All negatively covarying pairs

1 -> All positively covarying pairs

2 -> Mixed type covarying pairs (randomly selected)

Value

Parameters	List of parameters used in function call
COM_summary	Community variation partitioning, for each experiment
p_values	Detection p-value for each experiment
avg_det_rate	Number of communities showing significant interaction over total experiments
avg_det_type	Number of communities with significant [positive,negative] interactions
run_time	Run-time of entire simulation (in seconds)

Author(s)

Steve Essinger

References

S.D. Essinger, "Partitioning Abiotic and Biotic Contributions to Community Variation," Ph.D. dissertation, Dept. Elect. Eng., Drexel Univ., Philadelphia, PA, 2013

sitesSelect	Site Selection Procedure
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Description

Procedure used to select sites for inclusion in analysis, per species.

Usage

sitesSelect(CDM, X)

Arguments

CDM	Community Data Matrix (sites x species)
X	Abiotic Factors (sites x factors) + vector of ones for intercept

Value

sites_sel	Nested list of booleans for including/excluding sites per species
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Author(s)

Steve Essinger

SpeciesResponseModel	Species Response Model - for use with simulations
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Description

This function generates a community data matrix (CDM) with n sites and p species to q environmental factors (X), using a linear model. The number (CD) of species pairs will covary within the community. The type of covariation for each pair depends on Type (0 negative, 1 positive, 2 mixed). The magnitude of covariation depends on Magnitude(M), while the noise depends on Noise(N). Both the noise and the covariation magnitude are added to the environmental species responses.

Usage

SpeciesResponseModel(n, p, q, N, M, CD, Type, Noise, Magnitude)

Arguments

n	Number of Sites to Include in Simulation
p	Number of Species to Include in Simulation
q	Number of Abiotic Factors to Include in Simulation
N	Noise Parameter Selection (integer 1 thru 12)
M	Covariation Magnitude Selection (integer 1 thru 5)
CD	Number of Covarying Species Pairs to Include in Simulation
Type	Type of Species Covariation in Simulation (see details)
Noise	Vector of Noise Parameters
Magnitude	Vector of Covariation Magnitude Parameters

Value

CDM	Community Data Matrix (Sites x Species)
X	Environmental Data (Explanatory Variables) (Includes 1's intercept)
Y	Environmental Species Responses
YN	Noise (Normal and Additive)
Mag	Magnitude of Species Covariation
CDMB	Community Data Matrix prior to Zero Censoring
B	Species Response Parameters
cvid	Type of species covariation for each pair (mixed dynamics only)

Author(s)

Steve Essinger

testStatistic	<i>Test Statistic for Significant Covariation Test</i>
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Description

Test Statistic employed to generate null distribution

Usage

```
testStatistic(matrix, sites_sel, test_stat, mutual_reject)
```

Arguments

matrix	Data matrix for computing test statistic
sites_sel	Nested list of booleans for including/excluding sites per species
test_stat	Selection of test statistic employed for computing indices for null distribution
mutual_reject	Threshold for excluding species pairs from test statistic

Details

test_stat (default c(1,1))

test_stat[1] = 1: absolute-covariance = 2: squared-covariance = 3: absolute-correlation = 4: squared-correlation

test_stat[2] = 1: absolute-covariance = 2: absolute-correlation = 3: sum of sites included per species pair = 4: 1 (constant)

mutual_reject (default 8): Any species pair having less than mutual_reject sites in common will be excluded from the test statistic calculation.

Value

index	Covariation test statistic computed on input matrix
CR	Pair-wise species correlation matrix
CV	Pair-wise species covariation matrix

Author(s)

Steve Essinger

tic	<i>Start of Stopwatch</i>
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Description

Helper function for computing elapsed run-time

Usage

tic()

References

<http://stackoverflow.com/questions/1716012/stopwatch-function-in-r>

toc	<i>Stopwatch Stop</i>
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Description

Helper function for computing elapsed run-time. Returns tic-toc.

Usage

toc()

References

<http://stackoverflow.com/questions/1716012/stopwatch-function-in-r>

varExplained	<i>Partitioning Abiotic and Biotic Variation</i>
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Description

Partitions community variation attributed to abiotic and biotic factors

Usage

```
varExplained(CDM,p_value,sites_sel,CR, Avg_Adj_R2,Adj_R2,alpha)
```

Arguments

CDM	Community Data Matrix (sites x species)
p_value	p-value from species interaction significance test
sites_sel	Nested list of booleans for including/excluding sites per species
CR	Pair-wise species correlation matrix
Avg_Adj_R2	Community Adjusted R2
Adj_R2	Adjusted R2, per species
alpha	Significance level for hypothesis test

Value

IND_summary	Abiotic, Biotic and Unexplained Variation (per species)
COM_summary	Abiotic, Biotic and Unexplained Variation (community)

Author(s)

Steve Essinger

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