

# Package ‘cooccur’

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**Type** Package

**Title** Probabilistic Species Co-Occurrence Analysis in R

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**Author** Daniel M. Griffith, Joseph A. Veech, and Charles J. Marsh

**Maintainer** Daniel M. Griffith <griffith.dan@gmail.com>

**Description** This R package applies the probabilistic model of species co-occurrence (Veech 2013) to a set of species distributed among a set of survey or sampling sites. The algorithm calculates the observed and expected frequencies of co-occurrence between each pair of species. The expected frequency is based on the distribution of each species being random and independent of the other species. The analysis returns the probabilities that a more extreme (either low or high) value of co-occurrence could have been obtained by chance. The package also includes functions for visualizing species co-occurrence results and preparing data for downstream analyses.

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cooccur-package	<i>cooccur: Probabilistic Species Co-occurrence Analysis in R</i>
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## Description

This R package applies the probabilistic model of species co-occurrence (Veech 2013) to a set of species distributed among a set of survey or sampling sites. The algorithm calculates the observed and expected frequencies of co-occurrence between each pair of species. The expected frequency is based on the distribution of each species being random and independent of the other species. The analysis returns the probabilities that a more extreme (either low or high) value of co-occurrence could have been obtained by chance. The package also includes functions for visualizing species co-occurrence results and preparing data for downstream analyses.

## Details

Package: cooccur  
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## Author(s)

Maintainer: Daniel M. Griffith <griffith.dan@gmail.com>

## References

Veech (2013). A probabilistic model for analysing species co-occurrence. *Global Ecology and Biogeography*, DOI: 10.1111/j.1466-8238.2012.00789.x

Griffith, Veech, and Marsh (2016). cooccur: Probabilistic Species Co-Occurrence Analysis in R. *Journal of Statistical Software*, 69(2), 1-17. doi:10.18637/jss.v069.c02

## Examples

```
#data(finches)
#cooccur.finches <- cooccur(mat=finches,
```

```
# type="spp_site",  
# thresh=TRUE,  
# spp_names=TRUE)  
#summary(cooccur.finch)
```

---

beetles	<i>Beetle occurrence data from (Ulrich and Zalewski 2006).</i>
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---

### Description

Occurrence data for 71 species from 17 sites. Columns are sites, rows are species. 1's are presences and 0's are absences.

### Usage

```
data(beetles)
```

### Format

A data frame with 71 observations on the following 17 variables.

### References

Ulrich W, Zalewski M (2006). Abundance and Co-occurrence Patterns of Core and Satellite Species of Ground Beetles on Small Lake Islands. *Oikos*, 114, 338-348.

### Examples

```
data(beetles)
```

---

cooccur	<i>A function to calculate pairwise co-occurrence patterns from a community dataset</i>
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---

### Description

This is the main function in the package `cooccur`. This R package applies the probabilistic model of species co-occurrence (Veech 2013) to a set of species distributed among a set of survey or sampling sites. The algorithm calculates the observed and expected frequencies of co-occurrence between each pair of species. The expected frequency is based on the distribution of each species being random and independent of the other species. The analysis returns the probabilities that a more extreme (either low or high) value of co-occurrence could have been obtained by chance. The package also includes functions for visualizing species co-occurrence results and preparing data for downstream analyses.

This function takes a community dataset (data frame or matrix) of species by site presence-absence data and classifies species pairs as having positive, negative, and random associations based on the probabilistic model of species co-occurrence from Veech (2013). It produces an object of class `cooccur`.

**Usage**

```
cooccur(mat, type = "spp_site", thresh = TRUE, spp_names = FALSE,
        true_rand_classifier = 0.1, prob = "hyper",
        site_mask = NULL, only_effects = FALSE,
        eff_standard = TRUE, eff_matrix = FALSE)
```

**Arguments**

<code>mat</code>	A species by site (r,c) data.frame or matrix of presence-absence (or abundance) data. Or, a site by species dataset with <code>type="site_spp"</code> .
<code>type</code>	Default is "spp_site" meaning <code>mat</code> specifies species by site (r,c) data. For site by species use "site_spp".
<code>thresh</code>	Logical. If TRUE then species pairs that are expected have less than 1 co-occurrences are filtered from the analysis. This will remove pairs from the results.
<code>spp_names</code>	Logical. Are there species names in either the column names or row names of the species matrix? If so then <code>spp_names</code> should be TRUE to use them.
<code>true_rand_classifier</code>	When a species pair is not classified as positive or negative, the species pair can be truly randomly distributed or they can be unclassifiable due to low statistical power. We classify truly random associations as those that do not deviate from their expected co-occurrences by more than 0.1 x the total number of sites. Therefore the default value is 0.1 but any proportion can be specified to be more or less strict.
<code>prob</code>	Should co-occurrence probabilities be calculated using the hypergeometric distribution ( <code>prob="hyper"</code> ) or the combinatorics approach from Veech 2013 ( <code>prob="comb"</code> ).
<code>site_mask</code>	A matrix with the same dimensions as <code>mat</code> , where each cell is a 1 or 0. 1 indicates sites that a species can exist and 0 indicates sites where the species cannot exist.
<code>only_effects</code>	Logical. Probability calculations can be time consuming; if only effect sizes are required from the analysis, then specific TRUE.
<code>eff_standard</code>	Logical. If <code>only_effects=TRUE</code> then should the effect sizes be standardized?
<code>eff_matrix</code>	Logical. If <code>only_effects=TRUE</code> then should the effect sizes be returned in a distance matrix? The alternative is a list of pairs.

**Value**

Returns a list of class `cooccur`.

<code>call</code>	Original function call.
<code>results</code>	Probability table containing all analyzed species pairs and their observed and expected co-occurrences and probabilities for classifying positive and negative associations.
<code>positive</code>	Number of positive pairs.

negative	Number of negative pairs.
co_occurrences	Sum of positive and negative pairs.
pairs	Number of analyzed species pairs.
random	Number of truly random species pairs.
unclassifiable	Number of unclassifiable species pairs.
sites	Number of sites.
species	Number of species.
percent_sig	Percent of pairs classified as either positive or negative.
true_rand_classifier	The proportion used to classify truly random pairs.
spp_key	A key relating the species numbers and names.
spp.names	Ordered list of species names.
omitted	Number of pairs removed due to the threshold filter.
pot_pairs	Number of pairs before application of the threshold.

### Author(s)

Daniel M Griffith

### References

Veech (2013). A probabilistic model for analysing species co-occurrence. *Global Ecology and Biogeography*, DOI: 10.1111/j.1466-8238.2012.00789.x

Griffith, Veech, and Marsh (2016). cooccur: Probabilistic Species Co-Occurrence Analysis in R. *Journal of Statistical Software*, 69(2), 1-17. doi:10.18637/jss.v069.c02

### Examples

```
#data(finches)
#cooccur.finches <- cooccur(mat=finches,
#   type="spp_site",
#   thresh=TRUE,
#   spp_names=TRUE)
#summary(cooccur.finches)
#plot(cooccur.finches)
```



---

effect.sizes	<i>Function to extract species pairwise effect sizes from an object of class cooccur.</i>
--------------	---

---

### Description

Calculate standardized and raw effect sizes from an object of class cooccur.

### Usage

```
effect.sizes(mod, standardized = TRUE, matrix = FALSE)
```

### Arguments

mod	Object of class cooccur.
standardized	Logical. Should the effect sizes be standardized?
matrix	Logical. Should the effect sizes be returned in a distance matrix? The alternative is a list of pairs.

### Value

Returns either a data.frame of species pairs and effects sizes or a distance matrix with the rows and columns ordered from the order of species in the original community data matrix.

### Author(s)

Daniel M Griffith

### Examples

```
#data(finches)
#cooccur.finches <- cooccur(mat=finches,
#   type="spp_site",
#   thresh=FALSE,
#   spp_names=TRUE)
#effect.sizes(cooccur.finches,matrix=TRUE)
```

---

finches

*Finch occurrence data from (Sanderson 2000).*

---

### Description

Occurrence data for 13 species from 17 sites. Columns are sites, rows are species. 1's are presences and 0's are absences.

### Usage

```
data(finches)
```

### Format

A data frame with 13 observations on the following 17 variables.

### References

Sanderson JG (2000). Testing Ecological Patterns: A Well-known Algorithm from Computer Science Aids the Evaluation of Species Distributions. *American Scientist*, 88, pp. 332-339.

### Examples

```
data(finches)
```

---

obs.v.exp

*Function to plot a visualization of the observed versus expected occurrences from an analysis stored in a cooccur object.*

---

### Description

Plot the observed number of co-occurrences versus the number expected from the probability analysis in a cooccur object.

### Usage

```
obs.v.exp(mod)
```

### Arguments

mod                      Object of class cooccur.

### Author(s)

Daniel M Griffith

**See Also**[pair.profile](#), [plot.cooccur](#)**Examples**

```
#data(finches)
#cooccur.finches <- cooccur(mat=finches,
#   type="spp_site",
#   thresh=TRUE,
#   spp_names=TRUE)
#obs.v.exp(cooccur.finches)
```

---

**pair***Function to examine co-occurrence patterns for an individual species.*

---

**Description**

Extracts results for a single species from a cooccur object.

**Usage**

```
pair(mod, spp, all = FALSE)
```

**Arguments**

mod	Object of class cooccur.
spp	Name of the species, or the number assigned to it.
all	Logical. If TRUE then all, not just significant, results are returned.

**Value**

Same as `prob.table()` but for only one species.

**Author(s)**

Daniel M Griffith

**See Also**[prob.table](#)**Examples**

```
#data(finches)
#cooccur.finches <- cooccur(mat=finches,
#   type="spp_site",
#   thresh=TRUE,
#   spp_names=TRUE)
#pair(cooccur.finches, "Geospiza fortis", all=TRUE)
```

pair.attributes      *Function to create a species-wise summary of co-occurrence patterns.*

---

**Description**

Summarizes the positive, negative, and random interactions for each species in an cooccur analysis.

**Usage**

```
pair.attributes(mod)
```

**Arguments**

mod                      Object of class cooccur.

**Value**

Returns a data.frame with the percentage of "pos", "neg", "rand" associations that each species ("spp") participates in. Columns with the prefix "num\_" are counts.

**Author(s)**

Daniel M. Griffith

**Examples**

```
#data(finches)
#cooccur.finches <- cooccur(mat=finches,
#   type="spp_site",
#   thresh=TRUE,
#   spp_names=TRUE)
#pair.attributes(cooccur.finches)
```

---

pair.profile      *Function to produce a visualization of species contributions to co-occurrence patterns.*

---

**Description**

Plots a bar plot for visualizing the associations of each individual species from a cooccur object.

**Usage**

```
pair.profile(mod)
```

**Arguments**

mod                    Object of class cooccur.

**Author(s)**

Daniel M Griffith

**See Also**

[obs.v.exp,plot.cooccur](#)

**Examples**

```
#data(finches)
#cooccur.finches <- cooccur(mat=finches,
#   type="spp_site",
#   thresh=TRUE,
#   spp_names=TRUE)
#pair.profile(cooccur.finches)
```

---

plot.cooccur

*Function for producing a heatmap co-occurrence visualization.*

---

**Description**

Heatmap visualization of the pairwise species associations revealed by a cooccur analysis.

**Usage**

```
## S3 method for class 'cooccur'
plot(x, ...)
```

**Arguments**

x                    Object of class cooccur.  
...                  Additional args

**Author(s)**

Daniel M Griffith

**See Also**

[obs.v.exp,pair.profile](#)

## Examples

```
#data(finches)
#cooccur.finches <- cooccur(mat=finches,
#   type="spp_site",
#   thresh=TRUE,
#   spp_names=TRUE)
#plot(cooccur.finches)
```

---

print.cooccur	<i>Print significant pairwise species results.</i>
---------------	--

---

## Description

Returns a table of analysis results for all significant pairwise interactions found in a cooccur object.

## Usage

```
## S3 method for class 'cooccur'
print(x, ...)
```

## Arguments

x	Object of class cooccur.
...	Additional args

## Author(s)

Daniel M Griffith

## Examples

```
#data(finches)
#cooccur.finches <- cooccur(mat=finches,
#   type="spp_site",
#   thresh=TRUE,
#   spp_names=TRUE)
#print(cooccur.finches)
```

---

prob.table	<i>Function to extract the probability table from an analysis of species co-occurrence.</i>
------------	---

---

**Description**

Returns a results table for all analyzed species pairs in a cooccur object.

**Usage**

```
prob.table(mod)
```

**Arguments**

mod	Object of class cooccur.
-----	--------------------------

**Value**

Returns a data.frame with the following columns.

sp1	Numeric label giving the identity of species 1, assigned based on the order in the input matrix
sp2	Numeric label for species 2
sp1_inc	Number of sites (or samples) that have species 1
sp2_inc	Number of sites that have species 2
obs	cooccur Observed number of sites having both species
prob	cooccur Probability that both species occur at a site
exp	cooccur Expected number of sites having both species
p_lt	Probability that the two species would co-occur at a frequency less than the observed number of co-occurrence sites if the two species were distributed randomly (independently) of one another
p_gt	Probability of co-occurrence at a frequency greater than the observed frequency
sp1_name	If species names were specified in the community data matrix this field will contain the supplied name of sp1
sp2_name	The supplied name of sp2

**Author(s)**

Daniel M Griffith

**See Also**

[pair](#), [pair.attributes](#)

**Examples**

```
#data(finches)
#cooccur.finches <- cooccur(mat=finches,
#   type="spp_site",
#   thresh=TRUE,
#   spp_names=TRUE)
#prob.table(cooccur.finches)
```

---

 rodents

*Rodent occurrence data from (Brown and Kurzius 1987).*


---

**Description**

Occurrence data for 16 species from 39 sites. Columns are sites, rows are species. 1's are presences and 0's are absences.

**Usage**

```
data(rodents)
```

**Format**

A data frame with 16 observations on the following 39 variables.

**References**

Brown JH, Kurzius MA (1987). Composition of Desert Rodent Faunas: Combinations of Coexisting Species. *Annales Zoologici Fennici*, 24, 227-237.

**Examples**

```
data(rodents)
```

---

 summary.cooccur

*Method to summarize co-occurrence patterns.*


---

**Description**

Presents a count of positive, negative, random, and unclassified pairwise comparisons from a cooccur object.

**Usage**

```
## S3 method for class 'cooccur'
summary(object, ...)
```

**Arguments**

object            Object of class cooccur.  
...                Additional args

**Author(s)**

Daniel M Griffith

**Examples**

```
#data(finches)
#cooccur.finches <- cooccur(mat=finches,
#   type="spp_site",
#   thresh=TRUE,
#   spp_names=TRUE)
#summary(cooccur.finches)
```

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