Package 'coenoflex'

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R topics documented:

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coenoflex   *Coenoflex - Flexible Coenospace Simulation*

Description

Coenoflex simulates complex vegetation data sets. Species have modal physiological response
curves along gradients, which can be either complex or direct environmental gradients, or resource
gradients sensu Austin and Smith 1989. The integrated response of species can be a nested response
of specific gradient response functions. Simulated samples can be placed at random or on a grid on
up to 10 dimensions; species modes can be placed at random or on a grid.

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Usage

```
coenoflex(numgrd,numplt,numspc,grdtyp,grdlen,width,variab,grdprd,
          alphad,pdist,sdist,skew,aacorr,cmpasy,cmpphy,
          maxtot,noise,slack,autlin)
```

Arguments

numgrd	number of gradients to simulate
numplt	number of sample plots
numspc	number of species to simuulate
grdtyp	a vector of gradient type equal in length to the number of gradients
grdlen	a vector of gradient length equal in length to the number of gradients
width	a vector of species ecological amplitude width equal in length to the number of gradients
variab	a vector of gradient variability equal in length to the number of gradients
grdprd	a vector of gradient productivity equal in length to the number of gradients
alphad	a vector of alpha-diversities equal in length to the number of gradients
pdist	sample plot distribution, 'r' for random, 'g' for grid
sdist	species distribution, 'r' for random, 'g' for grid
skew	the skewness in the pseudo-log normal distribution of species maximum abundances
aacorr	the correlation between maximum abundance and amplitude width
cmpasy	competition asymmetry
cmpphy	physiological competition coefficient, currently not used
maxtot	the maximum total species cover in sample plots
noise	simulated sample error on species abundance
slack	the probability of species absence in suitable sites
autlin	the autecological function specifying how to combine gradient-specific response functions

Details

Coenoflex is a complex function to simulate vegetation and environment data sets. It is somewhat unusual as an R function, in that it can be run in classical command line prompt and response mode by calling the coenoflex function with no arguments. Any prompt can be replied to with '?' to invoke user help for that parameter. Alternatively, it can be called in classical R mode by specifying all parameters in the function call. Surprisingly, there are no defaults for parameters, so if you fail to specify a value for a parameter you will still be prompted for a value, even if you specified most values in the function call.

Coenoflex has many parameters, many of which are vector-valued with lengths equal to the number of gradients simulated. Accordingly, calling coenoflex can be a long-winded affair. In more detail, the parameters are:

'numgrd' The number of gradients to simulate. 'Gradients' are central to modern vegetation theory, and are used to describe environmental variability in a stylized manner, similar to the role of fields in physics or vector calculus.

'numplt' The number of sample plots to simulate. Sample plots can be visualized as points in a high dimensional space defined by the gradients. Accordingly, as the number of gradients simulated goes up, the number of sample points should also go up exponentially to maintain a reasonable density of points.

'numspc' The number of species to simulate. The sample plot species richness is a function of the number of species simulated, their amplitude compared to gradient length, and the number of gradients simulated. As the mean species amplitude (or width) gets smaller relative to gradient length, the species richness goes down. As the number of gradients simulated goes up, fewer species will occcur in any given plot due to the curse of dimensionality. Again, as the number of gradients goes up the number of species should go up exponentially.

'grdtyp' Gradient type, with one value specified for each gradient. Gradient types can be either 'e' for 'environmental' or 'r' for 'resource'. On environmental gradients, species have modal distributions defined by a minimum, optimum, and maximum gradient values. None of these values need occur within the range of the gradient values simulated, but in general species exhibit such a modal curve. On resource gradients, all species have their maximim value at the end of the gradient, with grid-based or random minimum values. See Austin and Smith (1989) for details.

'grdlen' Gradient length, with one value specified for each gradient. Coenoflex calculates gradient lengths in arbitrary units. These units are used to compare gradient lengths in relative values, so that for example a gradient of 200 units is twice as long as a gradient of 100 units. In addition, species amplitudes are measured in the same units so that a species with an amplitude of 50 would extend about one half the length of a gradient of 100 units.

'width' Species mean ecological amplitude width, with one value specified for each gradient. Coenoflex calculates the ecological amplitude of species in gradient units. Thus, if the gradient length is 100, and a species amplitude is 50, it will extend about one half the length of the gradient. Species amplitude, along with the number of species, determines the number of species per plot and the rate of species turnover.

'variab' Species amplitude variability in percent, with one value for each gradient. Coenoflex varies individual species amplitudes according to the variance parameter. Previously you specified a mean species amplitude along each gradient. The variance parameter modifies that value for each species by +/- %. For example, if you specified a mean amplitude of 50 and a variance of 50%, species amplitudes would vary randomly from 25 units to 75 units.

'grdprd' Gradient productivity, with one value for each gradient. Coenoflex can vary the productivity along gradients systematically. To increase productivity along the gradient, enter the percent increase in productivity from the low to high end of the gradient. Resource gradients should have a significant increase associated with them; environmental gradients may or may not.

'alphad' Alpha diversity, with one value for each gradient. Coenoflex can systematically vary the alpha-diversity along gradients by modifying the location of species centroids. Values from 0.5 to 1.0 increase the alpha-diversity at the high end of the gradient, and values from 1.0 to 2.0 increase alpha-diversity at the low end of the gradient. Values near 1.0 have small effects; the farther from 1.0 the more dramatic the effect.

'pdist' Sample plot distribution. Coenoflex can establish plot centers randomly or along a grid. If you select randomly, plot centers will have random coordinates along each gradient with approximately constant density throughout the sample space. If you select a grid, Coenoflex will attempt

to space plots along the gradients in proportion to their length, again attempting to maintain approximately constant density. If necessary, Coenoflex will change the number of plots specified to achieve equal spacing.

'sdist' Species centroid distribution. Coenoflex can establish species modes randomly or along a grid. If you select randomly, species modes will have random coordinates along each gradient with approximately constant density throughout the sample space. Many species will have their centroid outside the sample space, depending on the ratio of species amplitude to gradient length. If you select a grid, Coenoflex will attempt to space species modes along the gradients in proportion to their length, again attempting to maintain approximately constant density. If necessary, Coenoflex will change the number of species specified to achieve equal spacing.

'skew' Species maximum abundance distribution skew. Coenoflex simulates the maximum abundance of organisms according an equation similar to a log-random distribution. The skew coefficient controls how skewed the distribution is toward low values. A skew of 1.0 results in a normal distribution with a mean of 50% cover. As the value increases, the mode moves left and the tail to the right grows longer.

'aacorr' Correlation of species amplitude and maximum abundance. Coenoflex allows species abundances to be correlated with their ecological amplitude as proposed in the Core-Satelite hypothesis and described in the Hierarchical Continuum Model (Collins et al. 1993). Values greater than 0.0 result in positive correlation between amplitude and abundance while 0.0 results in independence.

'cmpasy' Competition asymmetry. This is the primary mechanism to simulate competition. The competition asymmetry coefficient simulates a competitive advantage to larger plants intended to simulate asymmetric competition such as for light. The algorithm scales species abundance proportional to raw abundance raised to the competition asymmetry coefficient. Accordingly, a value of 1.0 confers no advantage, and increasingly larger values give large species more advantage.

'maxtot' Maximum total abundance in sample plots. The typical total abundance of sample plots is normally a simple sum of the abundances of species in that sample. It's possible to standardize the value to any specified total, including the commonly used 100%. The 'maxtot' parameter interacts with the competition asymmetry parameter by specifying the total abundance to be partitioned among species. If no total is specified, or a total of zero is specified, no competition occurs.

'noise' Noise from sample error. Coenoflex allows you to simulate noise in the species response model. Values are +/- in percent. For example, a response of 25 randomly adds plus or minus 25% of the actual value.

'slack' Probability of absence in suitable sites. Coenoflex includes a form of noise known as slack. In contrast to noise, slack causes a species to be absent in a favorable environment, due perhaps to poor dispersal (or incorrect identification in the field). The values are probabilities of absence in favorable conditions, for example a value of 0.1 means a species will be absent in 10% of favorble plots.

'autlin' Autecological response model. Coenoflex combines the physiological response of a species along each gradient into an autecological response using:

min(x,y,...)	= minimum response of gradients x,y,...
max(x,y,...)	= maximum response of gradients x,y,...
irm(x,y,...)	= integrated rate methodology response of gradients x,y,...
geo(x,y,...)	= geometric mean response of gradients x,y,...
ave(x,y,...)	= arithmetic mean response of gradients of gradients x,y,...

Functions can be nested as e.g. min(1,irm(2,3),geo(4,5)) takes the integrated rate methodology of gradients 2 and 3, the geometric mean of gradients 4 and 5, and then finally the minimum value of gradients 1 and those combinations.

Value

a list object with class 'coenoflex' with components:

params	a copy of all the parameters used to specify the model
site	the sample plot coordinates on each gradient
veg	the vegetation data matrix
spcamp	the parameters that describe the species amplitude response functions
maxabu	the list of maximum abundance for each species
pltprd	the plot productivity for each sample plot

Author(s)

David W. Roberts <droberts@montana.edu>

References

Austin, M.P. and T.M. Smith. 1989. A new model for the continuum concept. Vegetatio 83:35-47.

Collins, S.L., S. Glenn, and D.W. Roberts. 1993. The hierarchical continuum concept. J. Veg. Sci. 4:149-156.

Roberts, D.W. 2008. Statistical analysis of multidimensional fuzzy set ordination. Ecology 89:1246-1260.

Examples

```
example <- coenoflex(numgrd=3,numplt=100,numspc=100,grdtyp=c('e','e','e'),
            grdlen=c(300,200,100),width=c(100,75,50),variab=c(20,20,20),
            grdprd=c(0,0,0),alphad=c(1,1,1),pdist='r',sdist='r',
            skew=3.0,aacorr=0.0,cmpasy=3.0,cmpphy=0.0,maxtot=100,
            noise=20,slack=0.2,autlin='irm(1,2,3)')
```

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plot.coenoflex   *Plotting Coenoflex Results*

Description

Plots the various components of a coenoflex simulation results

Usage

```
## S3 method for class 'coenoflex'
plot(x,which='all',...)
```

Arguments

x	an object of class 'coenoflex'
which	a switch to control ploting just 'plots', 'species', 'amplitude', or 'all' attributes
...	ancillary arguments for the plot generic function

Details

coenoflex generates a complex object of class 'coenoflex' with simulated vegetation samples and species response curves. `plot.coenoflex` graphs the results in a series of panels depending on the argument 'which'.

Value

plot.coenoflex produces only graphical out and does not return anything.

Author(s)

David W. Roberts `<droberts@montana.edu>`

Examples

```
example <- coenoflex(numgrd=3,numplt=100,numspc=100,grdtyp=c('e','e','e'),
             grdlen=c(300,200,100),width=c(100,75,50),variab=c(20,20,20),
             grdprd=c(0,0,0),alphad=c(1,1,1),pdist='r',sdist='r',
             skew=3.0,aacorr=0.0,cmpasy=3.0,cmpphy=0.0,maxtot=100,
             noise=20,slack=0.2,autlin='irm(1,2,3)')
## Not run: plot(example,which='all')
```

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