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Author Alexandre Adalardo de Oliveira and Paulo Inacio Prado
<ecovirtualpackage@gmail.com>

Maintainer Alexandre Adalardo de Oliveira
<ecovirtualpackage@gmail.com>

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Contents

anima	2
animaColExt	3
archip	4
bioGeoIsl	6
comCompete	7
compLV	8
dynPop	9
extGame	12
metaComp	13

metaPop	14
randWalk	16
regNicho	17
rich	19
simHub	19
sucMatrix	21

Index	23
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anima	<i>Internal EcoVirtual Graphics and Animations</i>
-------	--

Description

Internal functions for graphics and animations of the simulations results.

Usage

```
grColExt(E, I, P, area)
```

Arguments

E	extinction rate
I	colonization rate
P	species available in mainland
area	islands sizes

Details

The list below relates each function graphical and its primary functions:

animaCena - regNicho
animaGame - extGame
animaHub - simHub1, simHub2, simHub3
animaIsl - archip
animaMeta2 - metaPop, metaCi, metaEr, metaCiEr
animaMetaComp - metaComp
animaRandWalk - randWalk
grColExt - animaColExt, bioGeoIsl
grFim - metaPop, metaCi, metaEr, metaCiEr

Value

Show simulation in a graphic device.

Author(s)

Alexandre Adalardo de Oliveira <ecovirtualpackage@gmail.com>

See Also

<http://ecovirtual.ib.usp.br>

Examples

```
## Not run:
grColExt(E = 0.5 , I = 0.5 , P = 100, area=1:10)

## End(Not run)
```

animaColExt	<i>Colonization and Extinction balance in the Island Biogeography Equilibrium model</i>
-------------	---

Description

Simulate the balance between extinction and colonization rates given the equilibrium number of species in a island, based on the Island Biogeography Equilibrium model.

Usage

```
animaColExt(min = 0.01, max = 1, cycles = 100, Ext = "crs",
            Col = "dcr")
```

Arguments

min	between 0-1. The minimum value of the extinction and colonization rates.
max	between 0-1. The maximum value of the extinction and colonization rates.
cycles	number of cycles in the simulation.
Ext	a string representing the extinction rate. This can be 'crs' for an increasing extinction rate, 'fix' for a fixed extinction rate in 0.5, or 'dcr' for a decreasing extinction rate.
Col	a string representing the colonization rate. This can be 'crs' for an increasing colonization rate, 'fix' for a fixed colonization rate in 0.5, or 'dcr' for a decreasing colonization rate.

Details

The number of species is the balance between extinction and colonization rates at the equilibrium.

Value

'animaColExt' returns a graph of the extinction and colonization rates varying one or both rates in relation with the number of species of an island.

Author(s)

Alexandre Adalardo de Oliveira <ecovirtualpackage@gmail.com>

References

Gotelli, N.J. 2008. A primer of Ecology. 4th ed. Sinauer Associates, 291pp.

See Also

[archip bioGeoIsl](http://archip.bioGeoIsl) <http://ecovirtual.ib.usp.br>

Examples

```
## Not run:
animaColExt(Ext='fix', Col="fix")

## End(Not run)
```

archip

Species Colonization and Species-Area Relationship in Archipelagos

Description

Simulate species colonization from mainland to islands with different sizes.

Usage

```
archip(n.isl, ar.min, ar.max, S, seed.rain, abund, tmax = 100, anima = TRUE)
```

Arguments

n.isl	numeric, number of islands.
ar.min	numeric, area of the smallest island.
ar.max	numeric, area of the biggest island.
S	numeric, number of species (species richness from mainland).
seed.rain	numeric, seed rain. Number of seeds colonizing islands on each time.
abund	numeric, abundance of each species in the seed rain.
tmax	numeric, maximum time for the simulations.
anima	logical; if TRUE, show simulation frames.

Details

The mainland has richness (S) and the evenness can be controlled argument `abund`. The 'abund' argument can be one of these 3 options:

1. a vector with the same length of the species richness, meaning the proportion of each species population;
2. a single value more than 1 representing equal abundance of each species (maximum evenness);
3. a single value between 0 and 1, meaning the model of geometric species rank-abundance distribution. The model is: $abund * (1 - abund)^{((1:S) - 1)}$, where S is the number of species.

Value

'archip' returns 3 graphics:

- The species-area relationship: number of species x island area at the end of the simulation. It also returns the coefficients c and z from species-area relationship $S = cA^z$.
- Colonization rate curves: colonization (number of species per cycle) x number of species for each island.
- Passive colonization: number of species x time for each island.

'archip' also returns an invisible array with the simulation results.

Author(s)

Alexandre Adalardo de Oliveira <ecovirtualpackage@gmail.com>

References

Gotelli, N.J. 2008. A primer of Ecology. 4th ed. Sinauer Associates, 291pp.

See Also

[animaColExt](#), [bioGeoIsl](#), <http://ecovirtual.ib.usp.br>

Examples

```
## Not run:
archip(n.isl=10,ar.min=10, ar.max=100, S=1000, seed.rain=100, abund=10, tmax=100, anima=TRUE)

archip(n.isl=10,ar.min=10, ar.max=100, S=1000, seed.rain=100, abund=0.5, tmax=100, anima=TRUE)

## End(Not run)
```

 bioGeoIsl

Island Biogeographical Model

Description

Simulates island biogeographical models, with rates of colonization and extinction for islands of different sizes and distances to the mainland.

Usage

```
bioGeoIsl(area, dist, P, weight.A = 0.5, a.e = 1, b.e = -0.01, c.i = 1,
  d.i = -0.01, e.i = 0, f.i = 0.01, g.e = 0, h.e = 0.01)
```

Arguments

area	a vector with the sizes of the island areas. It must have the same length as 'dist'
dist	a vector with the distances of the islands to the mainland. It must have the same length as 'areas'
P	the number of species in the mainland (species richness of the pool).
weight.A	ratio between the area and distance effects. Should be a number between 0 to 1. When the ration is 1 the extinction is only affected by size and colonization only by distance. The default ratio is 0.5, meaning that distance and size equally influence colonization and extinction.
a.e	basal extinction coefficient for area.
b.e	extinction/area coefficient.
c.i	basal colonization coefficient for distance.
d.i	numeric, colonization/distance coefficient.
e.i	basal colonization coefficient for area.
f.i	colonization/area coefficient.
g.e	basal extinction coefficient for distance.
h.e	extinction/distance coefficient.

Value

'bioGeoIsl' returns a graph with the rates of colonization and extinction in relation with the species richness for each island.

'bioGeoIsl' also returns a invisible data frame with the values for area, distance and species richness (S) for each island.

Author(s)

Alexandre Adalardo de Oliveira <ecovirtualpackage@gmail.com>

References

Gotelli, N.J. 2008. A primer of Ecology. 4th ed. Sinauer Associates, 291pp.

See Also

[animaCoLExt archip, http://ecovirtual.ib.usp.br](http://ecovirtual.ib.usp.br)

Examples

```
## Not run:
bioGeoIsl(area=c(5,10,50,80), dist=c(10,100,100,10), P=100, weight.A=.5, a=1,
b=-0.01, c=1, d=-0.01, e=0, f=.01, g=0, h=.01)

## End(Not run)
```

comCompete

Multispecies competition-colonization tradeoff

Description

Simulates the trade-off between colonization and competition abilities in a multispecies system.

Usage

```
comCompete(rw, cl, S, fi, fsp1, pe, fr = 0, int = 0, tmax)
```

Arguments

rw	number of rows for the simulated landscape.
cl	number of columns for the simulated landscape.
S	number of species.
fi	initial fraction of patches occupied
fsp1	superior competitor abundance.
pe	mortality rate.
fr	disturbance frequency.
int	disturbance intensity.
tmax	maximum simulation time.

Details

In the system, the competitive abilities are inversely proportional to the colonization abilities. The number of patches in the simulated landscape is defined by $rw \cdot cl$.

Value

'comCompete' returns a graph with the proportion of patches occupied in time by each species and the trade-off scale, the superior competitor in one side and the superior colonizator in the other.

Author(s)

Alexandre Adalardo de Oliveira <ecovirtualpackage@gmail.com>

References

Tilman. R. 1994. Competition and biodiversity in spatially structured habitats. *Ecology*,75:2-16.
Stevens, M.H.H. 2009. A primer in ecology with R. New York, Springer.

See Also

[metaComp](http://ecovirtual.ib.usp.br), <http://ecovirtual.ib.usp.br>

Examples

```
## Not run:
comCompete(tmax=1000, rw=100, cl=100, S=10, fi=1, fsp1=0.20, pe=0.01, fr=0, int=0)

## End(Not run)
```

compLV

Lotka-Volterra Competition Model

Description

Simulate the Lotka-Volterra competition model for two populations.

Usage

```
compLV(n01, n02, tmax, r1, r2, k1, k2, alfa, beta)
```

Arguments

n01	initial population for the superior competitor species.
n02	initial population for the inferior competitor species.
tmax	maximum simulation time.
r1	intrinsic growth rate for the superior competitor species.
r2	intrinsic growth rate for the inferior competitor species.
k1	carrying capacity for the superior competitor species.
k2	carrying capacity for the inferior competitor species.
alfa	alfa coefficient.
beta	beta coefficient

Details

The Lotka-Volterra competition model follows the equations:

- SP1:

$$\frac{dN_1}{dt} = r_1 N_1 \left(\frac{K_1 - N_1 - \alpha N_2}{K_1} \right)$$

- SP2:

$$\frac{dN_2}{dt} = r_2 N_2 \left(\frac{K_2 - N_2 - \beta N_1}{K_2} \right)$$

Value

'compLV' returns a graph of the population size in time, and a graph with the isoclines of the equilibrium for both species. 'compLV' also returns an invisible matrix with the population size of each species in time.

Author(s)

Alexandre Adalardo de Oliveira <ecovirtualpackage@gmail.com>

References

Gotelli, N.J. 2008. A primer of Ecology. 4th ed. Sinauer Associates, 291pp. Hastings, A. 1980. Disturbance, coexistence, history and competition for space. *Theoretical Population Biology*, 18:363-373. Stevens, M.H.H. 2009. A primer in ecology with R. New York, Springer.

See Also

<http://ecovirtual.ib.usp.br>

Examples

```
## Not run:
compLV(n01=10, n02=10, r1=0.05, r2=0.03, k1=80, k2=50, alfa=1.2, beta=0.5, tmax=200)

## End(Not run)
```

dynPop

Population Dynamic Models

Description

Functions to simulate population dynamic models.

Usage

```

popExp(N0, lamb, tmax, intt = 1)

estEnv(N0, lamb, tmax, varr, npop = 1, ext = FALSE)

BDM(tmax, nmax = 10000, b, d, migr = 0, N0, barpr = FALSE)

simpleBD(tmax = 10, nmax = 10000, b = 0.2, d = 0.2, N0 = 10,
  cycles = 1000, barpr = FALSE)

estDem(N0 = 10, tmax = 10, nmax = 10000, b = 0.2, d = 0.2, migr = 0,
  nsim = 20, cycles = 1000, type = c("simpleBD", "BDM"), barpr = FALSE)

popLog(N0, tmax, r, K, ext = FALSE)

popStr(tmax, p.sj, p.jj, p.ja, p.aa, fec, ns, nj, na, rw, cl)

logDiscr(N0, tmax, rd, K)

bifAttr(N0, K, tmax, nrd, maxrd = 3, minrd = 1)

```

Arguments

N0	number of individuals at start time.
lamb	finite rate of population growth.
tmax	maximum simulation time.
intt	interval time size.
varr	variance.
npop	number of simulated populations.
ext	extinction.
nmax	maximum population size.
b	birth rate.
d	death rate.
migr	migration. logical.
barpr	show progress bar.
cycles	number of cycles in simulation.
nsim	number of simulated populations.
type	type of stochastic algorithm.
r	intrinsic growth rate.
K	carrying capacity.
p.sj	probability of seed survival.
p.jj	probability of juvenile survival.

p.ja	probability of transition from juvenile to adult phase.
p.aa	probability of adult survival.
fec	mean number of propagules per adult each cycle.
ns	number of seeds at initial time.
nj	number of juveniles at initial time.
na	number of adults at initial time.
rw	number of rows for the simulated scene.
cl	number of columns for the simulated scene.
rd	discrete growth rate.
nrd	number of discrete population growth rate to simulate.
maxrd	maximum discrete population growth rate.
minrd	minimum discrete population growth rate.

Details

popExp simulates discrete and continuous exponential population growth.

estEnv simulates a geometric population growth with environmental stochasticity.

BDM simulates simple stochastic birth death and immigration dynamics of a population (Renshaw 1991). simpleBD another algorithm for simple birth dead dynamics. This is usually more efficient than BDM but not implemented migration.

estDem creates a graphic output based on BDM simulations.

Stochastic models uses lambda values taken from a normal distribution with mean lambda and variance var.

popLog simulates a logistic growth for continuous and discrete models.

popStr simulates a structured population dynamics, with Lefkovitch matrices.

In popStr the number of patches in the simulated scene is defined by $rw \cdot cl$.

logDiscr simulates a discrete logistic growth model.

bifAttr creates a bifurcation graphic for logistic discrete models.

Value

The functions return graphics with the simulation results, and a matrix with the population size for deterministic and stochastic models.

Author(s)

Alexandre Adalardo de Oliveira and Paulo Inacio Prado <ecovirtualpackage@gmail.com>

References

Gotelli, N.J. 2008. A primer of Ecology. 4th ed. Sinauer Associates, 291pp. Renshaw, E. 1991. Modelling biological populations in space and time Cambridge University Press. Stevens, M.H.H. 2009. A primer in ecology with R. New York, Springer.

See Also

[metaComp](http://ecovirtual.ib.usp.br), <http://ecovirtual.ib.usp.br>

Examples

```
## Not run:  
popStr(p.sj=0.4, p.jj=0.6, p.ja=0.2, p.aa=0.9, fec=0.8, ns=100,nj=40,na=20, rw=30, cl=30, tmax=20)  
  
## End(Not run)
```

extGame	<i>Zero-sum game</i>
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Description

Simulates a zero-sum game between two competitors with a fixed amount of resource.

Usage

```
extGame(bet = 1, total = 100, tmax = 2)
```

Arguments

bet	bet size of each competitor on each time.
total	total amount of resource.
tmax	maximum game time.

Details

A zero-sum game is a mathematical representation of a situation in which a participant's gain (or loss) of resource is exactly balanced by the losses (or gains) of the resource of the other participant(s). If the total gains of the participants are added up, and the total losses are subtracted, they will sum to zero.

Value

'extGame' returns a graphic with the amount of resource of each competitor on each time.

'extGame' also returns an invisible vector with the results of the loser on each time.

Author(s)

Alexandre Adalardo de Oliveira and Paulo Inacio Prado <ecovirtualpackage@gmail.com>

References

http://en.wikipedia.org/wiki/Zero-sum_game

See Also

[simHub](#), [randWalk](#), <http://ecovirtual.ib.usp.br>

Examples

```
## Not run:
extGame(bet=1, total=20)
extGame(bet=1, total=100)

## End(Not run)
```

 metaComp

Metapopulation Competition Model

Description

Simulate a metapopulation dynamics with two competing species, a superior and an inferior competitor. Includes the possibility of habitat destruction in the model.

Usage

```
metaComp(tmax, rw, cl, f01, f02, i1, i2, pe, D = 0, anima = TRUE)
```

Arguments

tmax	maximum simulation time.
rw	number of rows for the simulated landscape.
cl	number of columns for the simulated landscape.
f01	initial fraction of patches occupied by the superior competitor.
f02	initial fraction of patches occupied by the inferior competitor.
i1	colonization coefficient for the superior competitor.
i2	colonization coefficient for the inferior competitor.
pe	probability of extinction (equal for both species).
D	proportion of habitat destroyed.
anima	logical; if TRUE, show simulation frames.

Details

This function uses the metapopulation model with internal colonization (see function [metaCi](#) in [metapopulation](#)) for the superior competitor. The inferior competitor can only occupy empty patches and is displaced by the superior competitor if it occupies the same patch.

The argument 'D' inserts the influences of habitat destruction in the model.

The number of patches in the simulated landscape is defined by $rw \cdot cl$.

Value

'metaComp' returns a graphic with the simulated landscapes and the results of the proportion of patch occupied by both species.

This function also return an invisible array with the simulation results.

Author(s)

Alexandre Adalardo de Oliveira and Paulo Inacio Prado <ecovirtualpackage@gmail.com>

References

Stevens, M.H.H. 2009. A primer in ecology with R. New York, Springer.

Gotelli, N.J. 1991. Metapopulation models: the rescue effect, the propagule rain, and the core-satellite hypothesis. *The American Naturalist* 138:768-776.

See Also

comCompete, <http://ecovirtual.ib.usp.br>

Examples

```
## Not run:
metaComp(tmax=100, cl=20, rw=20, f01=0.1, f02=0.4, i1=0.4, i2=0.5, pe=0.25)
metaComp(tmax=100, cl=20, rw=20, f01=0.1, f02=0.4, i1=0.4, i2=0.5, pe=0.25, D=0.1)

## End(Not run)
```

metaPop

Metapopulation Models

Description

Simulate metapopulation dynamics with propagules seed rain, internal colonization and rescue effect.

Usage

```
metaPop(cl, rw, f0, pi, pe, tmax, anima = TRUE)

metaCi(cl, rw, f0, ci, pe, tmax, anima = TRUE)

metaEr(cl, rw, f0, pi, ce, tmax, anima = TRUE)

metaCiEr(cl, rw, f0, ci, ce, tmax, anima = TRUE)
```

Arguments

cl	number of columns for the simulated landscape.
rw	number of rows for the simulated landscape.
f0	initial proportion of occupied patches.
pi	probability of colonization.
pe	probability of extinction.
tmax	maximum simulation time.
anima	show animation frames.
ci	colonization coefficient, represents the maximum probability of colonization (when f=1) and should be a number between 0 and 1.
ce	coefficient of extinction, represents the maximum probability of extinction (when f=0) and should be a number between 0 and 1.

Details

'metaPop' is the seed rain metapopulation model, including only propagules seed rain from an external pool (no extinction).

'metaCi' is the Internal Colonization model, where number of propagules depends on number of occupied patches, there is no external pool.

'metaEr' is the Rescue Effect model, where extinction probability is negatively associated with number of occupied patches.

'metaCiEr' includes both effects: Rescue Effect and Internal Colonization.

The number of patches in the simulated landscape is defined by $rw \cdot cl$.

Value

Metapopulation functions return graphics with the simulation results. These functions also return an invisible array with the simulation data.

Author(s)

Alexandre Adalardo de Oliveira and Paulo Inacio Prado <ecovirtualpackage@gmail.com>

References

Gotelli, N.J. 1991. Metapopulation models: the rescue effect, the propagule rain, and the core-satellite hypothesis. *The American Naturalist* 138:768-776.

Gotelli, N.J. 2008. *A primer of Ecology*. 4th ed. Sinauer Associates, 291pp.

See Also

<http://ecovirtual.ib.usp.br>

Examples

```
## Not run:
metaPop(cl=10,rw=10,f0=0.5,pi=0.3,pe=0.15, tmax=100)
metaCi(cl=10,rw=10,f0=0.1,ci=1,pe=0.5, tmax=100)
metaEr(cl=10, rw=10, f0=0.2, pi=0.2, ce=0.15, tmax=100)
metaCiEr(cl=10, rw=10, f0=0.2, ci=0.2, ce=0.15, tmax=100)

## End(Not run)
```

randWalk

Random Walk Simulations

Description

Simulates random walk models.

Usage

```
randWalk(S = 1, step = 1, tmax = 1e+05, x1max = 200, alleq = FALSE)
```

Arguments

S	number of individuals.
step	step size (number of steps on each time)
tmax	maximum simulation time.
x1max	maximum initial distance from absorption surface.
alleq	logical; if TRUE, all initial distance are equal. if FALSE, initial distances for each individual is a sample between 1 and maximum initial distance(x1max).

Details

Random walk is a stochastic process of a succession of random steps.

Zero is the absorption surface. When an individual simulation reaches zero, it means that the individual is dead.

See http://en.wikipedia.org/wiki/Random_walk.

Value

'randWalk' returns a graphic with the simulated trajectories of each individual.

'randWalk' also returns an invisible matrix with the distance from de edge for each individual on each time.

Author(s)

Alexandre Adalardo de Oliveira and Paulo Inacio Prado <ecovirtualpackage@gmail.com>

References

http://en.wikipedia.org/wiki/Random_walk

See Also

[extGame](#), [simHub](#), <http://ecovirtual.ib.usp.br>

Examples

```
## Not run:
randWalk(S=100,step=2,tmax=2e5)
randWalk(S=10,step=1,tmax=1e4, x1max=300, alleq=TRUE)

## End(Not run)
```

regNicho

Successional Niche Model

Description

Simulates the process of niche succession by successional stages in a community with 2 species (a superior and an inferior competitor), following the model of Pacala and Rees (1998).

Usage

```
regNicho(tmax, rw, c1, c1, c2, ec, dst, er, sc, mx, rs, anima = TRUE)
```

Arguments

tmax	maximum simulation time.
rw	number of rows for the simulated landscape.
c1	number of columns for the simulated landscape.
c1	colonization rate for the late successional species (superior competitor).
c2	colonization rate for the early successional species (inferior competitor).
ec	rate of competitive exclusion.
dst	disturbance rate.
er	initial proportion of patches in early stage.
sc	initial proportion of patches in susceptible stage.
mx	initial proportion of patches in mixed stage.
rs	initial proportion of patches in resistant stage.
anima	show animation frames.

Details

There are five possible states of this model:

- *free* - open, unoccupied space;
- *early* - occupied by only the early successional species;
- *susceptible* - occupied by only the late successional species and susceptible to invasion by the early successional species;
- *mixed* - occupied by both species;
- *resistant* - occupied by only the late successional species.

The early successional species is the inferior competitor in the model, and the later successional species is the superior competitor.

The number of patches in the simulated landscape is defined by $rw \cdot cl$.

'dst' is the proportion of patches in any stage that turns empty, it represents a disturbance in the landscape.

'ec' is the probability of susceptible and mixed stages turns resistant stage.

Value

'regNicho' returns the simulation results of patch occupancy in time for each successional stage.

'regNicho' also returns an invisible array with the simulation results per time.

Author(s)

Alexandre Adalardo de Oliveira <ecovirtualpackage@gmail.com>

References

Pacala, S & Rees, M. 1998. Models suggesting field experiments to test two hypotheses explaining successional diversity. *The American Naturalist* 152(2): 729:737.

Stevens, MHH. 2009. *A primer in ecology with R*. New York, Springer.

See Also

comCompete, <http://ecovirtual.ib.usp.br>

Examples

```
## Not run:
regNicho(tmax=50, rw=100, cl=100, c1=0.2, c2=0.8, ec=0.5, dst=0.04, er=0.08, sc=0.02, mx=0, rs=0)

## End(Not run)
```

rich	<i>Number of Species</i>
------	--------------------------

Description

Count the number of species (species richness) from a vector with a species list.

Usage

```
rich(x)
```

Arguments

x a vector with names.

Details

This function is used internally in the functions 'simHub1', 'simHub2', and 'simHub3'.

Value

returns the number of species (species richness).

Author(s)

Alexandre Adalardo de Oliveira <ecovirtualpackage@gmail.com>

Examples

```
lsp <- sample(LETTERS,50,replace=TRUE)
lsp
rich(lsp)
```

simHub	<i>Neutral Theory of Biogeography</i>
--------	---------------------------------------

Description

Simulates Community Dynamics as in the Neutral Theory of Biogeography

Usage

```
simHub1(S = 100, j = 10, D = 1, cycles = 10000, m.weights = 1,
        anima = TRUE)
```

```
simHub2(S = 100, j = 10, D = 1, cycles = 10000, m = 0.01,
        anima = TRUE)
```

```
simHub3(Sm = 200, jm = 20, S = 100, j = 10, D = 1, cycles = 10000,
        m = 0.01, nu = 0.001, anima = TRUE)
```

Arguments

S	number of species in the community.
j	individuals per species in the metacommunity.
D	number of deaths per cycle.
cycles	number of cycles in the simulation.
m.weights	Mortality weights for each species. Mortality rates of individuals of each species is proportional to species' abundances multiplied by these weights as in Yu et al. (1998). In neutral dynamics all weights are equal. If $\text{length}(\text{m.weights}) < S$ then species are divided in groups of (approximately) $S/\text{length}(\text{m.weights})$ and species of each group have a value in m.weights. This allows to create groups of species with different mortality probabilities and compare to the neutral dynamics.
anima	logical; if TRUE, the simulation frames of the metacommunity are shown.
m	colonization/immigration rate.
Sm	number of species in the metacommunity.
jm	individuals per species in the metacommunity.
nu	speciation rate.

Details

'simHub1' is the model without immigration.

'simHub2' incorporates immigration rate from the metacommunity

'simHub3' incorporates immigration and speciation rates in the metacommunity.

Value

These functions returns a graph with the number of species in time (cycles) in the metacommunity.

They also return an invisible matrix with the results of species richness on each community per time.

Author(s)

Alexandre Adalardo de Oliveira and Paulo Inacio Prado <ecovirtualpackage@gmail.com>

References

- Hubbell, S.P. 2001. The Unified Neutral Theory of Biodiversity and Biogeography. Princeton University Pres, 448p.
- Yu, D. W., Terborgh, J. W., and Potts, M. D. 1998. Can high tree species richness be explained by Hubbell's null model?. Ecology Letters, 1(3): 193–199.

See Also

[extGame](#), [randWalk](#), <http://ecovirtual.ib.usp.br>

Examples

```
## Not run:
simHub1(S=10,j=10, D=1, cycles=5e3)
simHub2(j=2,cycles=2e4,m=0.1)
simHub3(Sm=200, jm=20, S= 10, j=100, D=1, cycles=1e4, m=0.01, nu=0.001, anima=TRUE)

## End(Not run)
```

sucMatrix

Successional Stages Matrix

Description

Simulates a successional model based on a transitional matrix of stages and its initial proportion of occurrence in the landscape.

Usage

```
sucMatrix(mat.trans, init.prop, rw, cl, tmax)
```

Arguments

<code>mat.trans</code>	a matrix of stage transition probabilities.
<code>init.prop</code>	a vector with the initial proportions of each stage.
<code>rw</code>	number of rows to build the simulated landscape.
<code>cl</code>	number of columns to build the simulated landscape.
<code>tmax</code>	maximum simulation time.

Details

The number of patches in the simulated landscape is defined by $rw \cdot cl$.

Value

'sucMatrix' return a simulation graphic with the proportions of stages in the landscape in time, and a stage distribution graphic with the results of the simulation with the number o patches in time for each stage.

'sucMatrix' also return an invisible array with the simulation results.

Author(s)

Alexandre Adalardo de Oliveira <ecovirtualpackage@gmail.com>

References

Gotelli, N.J. 2008. A primer of Ecology. 4th ed. Sinauer Associates, 291pp.

Examples

```
## Not run:  
sucMatrix(mat.trans=matrix(data=c(0.5,0.5,0.5,0.5), nrow=2),  
init.prop=c(0.5,0.5),rw=20,cl=20, tmax=100)  
  
## End(Not run)
```

Index

- * **Biogeography**
 - animaColExt, 3
 - * **Functions**
 - rich, 19
 - * **Internal**
 - rich, 19
 - * **Island**
 - animaColExt, 3
 - * **Neutral**
 - randWalk, 16
 - rich, 19
 - simHub, 19
 - * **Niche**
 - regNicho, 17
 - * **Species-area**
 - archip, 4
 - * **Theory**
 - randWalk, 16
 - rich, 19
 - simHub, 19
 - * **biogeography**
 - archip, 4
 - bioGeoIsl, 6
 - * **competition**
 - compLV, 8
 - * **dynamics**
 - dynPop, 9
 - * **ecological**
 - sucMatrix, 21
 - * **island**
 - archip, 4
 - bioGeoIsl, 6
 - * **metacompetition**
 - comCompete, 7
 - * **metapopulation**
 - metaComp, 13
 - metaPop, 14
 - * **neutral**
 - extGame, 12
 - * **population**
 - dynPop, 9
 - * **relationship**
 - archip, 4
 - * **simulation**
 - anima, 2
 - animaColExt, 3
 - archip, 4
 - bioGeoIsl, 6
 - comCompete, 7
 - compLV, 8
 - dynPop, 9
 - extGame, 12
 - metaComp, 13
 - metaPop, 14
 - randWalk, 16
 - regNicho, 17
 - rich, 19
 - simHub, 19
 - sucMatrix, 21
 - * **succession**
 - sucMatrix, 21
 - * **sucession**
 - regNicho, 17
 - * **theory**
 - extGame, 12
- anima, 2
- animaCena (anima), 2
- animaColExt, 3, 5, 7
- animaGame (anima), 2
- animaHub (anima), 2
- animaIsl (anima), 2
- animaMeta2 (anima), 2
- animaMetaComp (anima), 2
- animaRandWalk (anima), 2
- archip, 4, 4, 7
- BDM (dynPop), 9
- bifAttr (dynPop), 9

bioGeoIsl, [4](#), [5](#), [6](#)

comCompete, [7](#), [14](#), [18](#)
compLV, [8](#)

dynPop, [9](#)

estDem (dynPop), [9](#)
estEnv (dynPop), [9](#)
extGame, [12](#), [17](#), [21](#)

gr.toff (anima), [2](#)
grColExt (anima), [2](#)
grFim (anima), [2](#)

logDiscr (dynPop), [9](#)

metaCi (metaPop), [14](#)
metaCiEr (metaPop), [14](#)
metaComp, [8](#), [12](#), [13](#)
metaEr (metaPop), [14](#)
metaPop, [14](#)
metapopulation, [13](#)
metapopulation (metaPop), [14](#)

popExp (dynPop), [9](#)
popLog (dynPop), [9](#)
popStr (dynPop), [9](#)

randWalk, [13](#), [16](#), [21](#)
regNicho, [17](#)
rich, [19](#)

simHub, [13](#), [17](#), [19](#)
simHub1 (simHub), [19](#)
simHub2 (simHub), [19](#)
simHub3 (simHub), [19](#)
simpleBD (dynPop), [9](#)
sucMatrix, [21](#)