Package ‘STEPCAM’

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Title ABC-SMC inference of the STEPCAM model
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Depends R (>= 3.0.2), vcd, FD
Imports gtools, MASS
Description This package is an implementation of the process of stepwise community assembly through the inverse process of stepwise species deletion with Stepwise Community Assembly Models (STEPCAM)
License GPL-2
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R topics documented:

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Description

ABC-SMC inference of the relative contribution of stochasticity (random removal), filtering and competition (limiting similarity) through the use of stepwise community assembly.

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The function STEPCAM_ABC performs an ABC-SMC analysis of the STEPCAM model on user provided data, the functions plotSMC, plotSTEPCAM and TernPlot provide functions to plot the output generated by the ABC-SMC analysis.

Author(s)

Thijs Janzen & Fons van der Plas
Maintainer: Thijs Janzen <thijsjanzen@gmail.com>

References


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generate.Artificial.Data

Generate Artificial data that can be used by the STEPCAM model

Description

This function generates artificial data with a given number of species, traits and communities. The generated data can directly be used in STEPCAM-ABC inference.

Usage

generate.Artificial.Data(numSpecies, numTraits, numCommunities, occurrence_distribution, average_richness, SD_richness, random.Mechanism)
plotSMC

Arguments

numSpecies  The number of species in the species pool (so across all communities) of the desired dataset.
numTraits   The number of traits in the desired dataset.
numCommunities  The number of communities in the desired dataset.
occurrence_distribution  species occurrence distribution (analogous to species abundance distribution) in species pool. A lognormal distribution is assumed. The higher the value, the more uneven the occurrence distribution in the species pool
average_richness  average richness in local community as a proportion of richness in species pool
SD_richness  standard deviation in richness across communities
random.Mechanism  if TRUE, species are randomly drawn from from species pool. If FALSE, it is assumed that a certain trait combination is optimal in each community and species with traits similar to this optimum more likely end up in the local community. Therefore, random.mechanism = FALSE assumes filtering processes to be most dominant in community assembly

Value

traits  A matrix containing the traits for all species, rows are the different species, column correspond to the respective traits.
abundances A matrix containing the abundances of all species for all plots. Rows correspond to species, columns to plots.

Author(s)

Thijs Janzen & Fons van der Plas

Examples

Artificial.Data <- generate.Artificial.Data(numSpecies=40,numTraits=3,numCommunities=5,
occurrence_distribution=0.2,average_richness=0.5,SD_richness=0.2,
random.Mechanism=FALSE);

plotSMC  Plot the progression of the SMC algorithm.

Description

This function plots the progression over the several iterations of the ABC-SMC algorithm. It can be used to explore results obtained with the STEPCAM-ABC function.
plotSTEPCAM

Usage

plotSMC(path)

Arguments

path Working Directory

Author(s)

Thijs Janzen

Examples

artificial.data <M generate.artificial.data(numspecies=40,numTraits=3,numCommunities=5, occurrence_distribution=0.2,average_richness=0.5,SD_richness=0.2, random.Mechanism=FALSE);
o <M stepcam_abc(artificial.dataDabundancesLartificial.dataDtraitsL numparticles=1Ln_traits=3Lplot_number=1Lstoprate=0.8);
currentDir <- getwd(); plotSMC(paste(currentDir,"/",sep=""));

plotSTEPCAM

Plot the output generated by the STEPCAM_ABC function

Description

This function plots the posterior distribution inferred by the STEPCAM_ABC function for the three community assembly parameters stochasticity (i.e. random removal), filtering and competition (i.e. limiting similarity).

Usage

plotSTEPCAM(output)

Arguments

output The list generated by the function STEPCAM_ABC as output, this list contains the following elements:
- Stoch a vector containing the posterior distribution for the parameter stochasticity or random removal
- Filt a vector containing the posterior distribution for the parameter filtering
- Comp a vector containing the posterior distribution for the parameter competition or limiting similarity

Author(s)

Thijs Janzen
Examples

```r
Artificial.Data <- generate.Artificial.Data(numSpecies=40,numTraits=3,numCommunities=5, occurrence_distribution=0.2,average_richness=0.5,SD_richness=0.2, random.Mechanism=FALSE);
O <- STEPCAM_ABC(Artificial.Data$abundances,Artificial.Data$traits, numParticles=10,n_traits=3,plot_number=1,stopRate=0.8);
plotSTEPCAM(O);
```

Description

ABC-SMC inference of the relative contribution of stochasticity (or random removal), filtering and limiting similarity (e.g. of shared resources (competition) or predators) through the use of stepwise community assembly and fitting Functional Diversity patterns of simulated communities with those of observed communities. It takes quite a lot of computing time to run this function, so it is recommended to first run it for a very simple (species poor, artificial) dataset (see example).

Usage

```r
STEPCAM_ABC(data_abundances,data_species,numParticles,n_traits,plot_number,stopRate)
```

Arguments

data_abundances
data_abundances is a matrix containing the abundances of all species over all plots.
rows every row corresponds to a different plot or community
columns every column corresponds to a different species.
For an example of a suitable data_abundances matrix, run the generate.Artificial.Data function

data_species
data_species is a matrix containing the species’ specific traits.
rows every row corresponds to a different species
columns the first column contains the name of the species, every consecutive column corresponds to a different trait
For an example of a suitable data_species matrix, run the generate.Artificial.Data function

numParticles The number of particles to be used in the ABC-SMC analysis.
n_traits The number of traits used in the analysis.
plot_number Row number of the plot for which we want to infer the contributions of stochasticity, filtering and competition.
stopRate The SMC procedure stops as soon as the acceptance rate of newly proposed parameter combinations drops below this level. Beware that low values for this parameter might lead into long computation times.
Value

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<tr>
<td>stochasticity</td>
<td>Posterior distribution of the relative contribution of stochasticity (random removal steps) to community assembly</td>
</tr>
<tr>
<td>filtering</td>
<td>Posterior distribution of the relative contribution of filtering to community assembly</td>
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<tr>
<td>competition</td>
<td>Posterior distribution of the relative contribution of competition (or limiting similarity processes) to community assembly</td>
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Author(s)

Thijs Janzen & Fons van der Plas

References


Examples

```r
artificial.data <- generate.Artificial.Data(numSpecies=40,numTraits=3,numCommunities=5, occurrence_distribution=0.2,average_richness=0.5,SD_richness=0.2, random.Mechanism=FALSE);
O <- STEPCAM_ABC(Artificial.Data$abundances,Artificial.Data$traits,
numParticles=10,n_traits=3,plot_number=1,stopRate=0.8);
```

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**TernPlot**

Create a ternary plot from results of the STEPCAM_ABC function

Description

This function plots the obtained combinations of Stochasticity (random removal), Filtering and Competition (limiting similarity) of best fitting models in a Ternary plot, similar to Figure 1 in van der Plas et al. 2013

Usage

`TernPlot(output)`

Arguments

- `output` A list with the following elements:
  - `stoch` a vector containing the posterior distribution for the parameter stochasticity (random removal)
  - `filt` a vector containing the posterior distribution for the parameter filtering
  - `comp` a vector containing the posterior distribution for the parameter competition (limiting similarity)

This list is generated as output by the function STEPCAM_ABC
**Author(s)**

Fons van der Plas. Adapted from the ternaryplot function from the `vcd` package

**References**


**Examples**

```r
Artificial.Data <- generate.Artificial.Data(numSpecies=40,numTraits=3,numCommunities=5, occurrence_distribution=0.2,average_richness=0.5,SD_richness=0.2, random.Mechanism=FALSE);
O <- STEPCAM_ABC(Artificial.Data$abundances,Artificial.Data$traits,
    numParticles=10,n_traits=3,plot_number=1,stopRate=0.8);
TernPlot(O);
```
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