



BIODINAMICA



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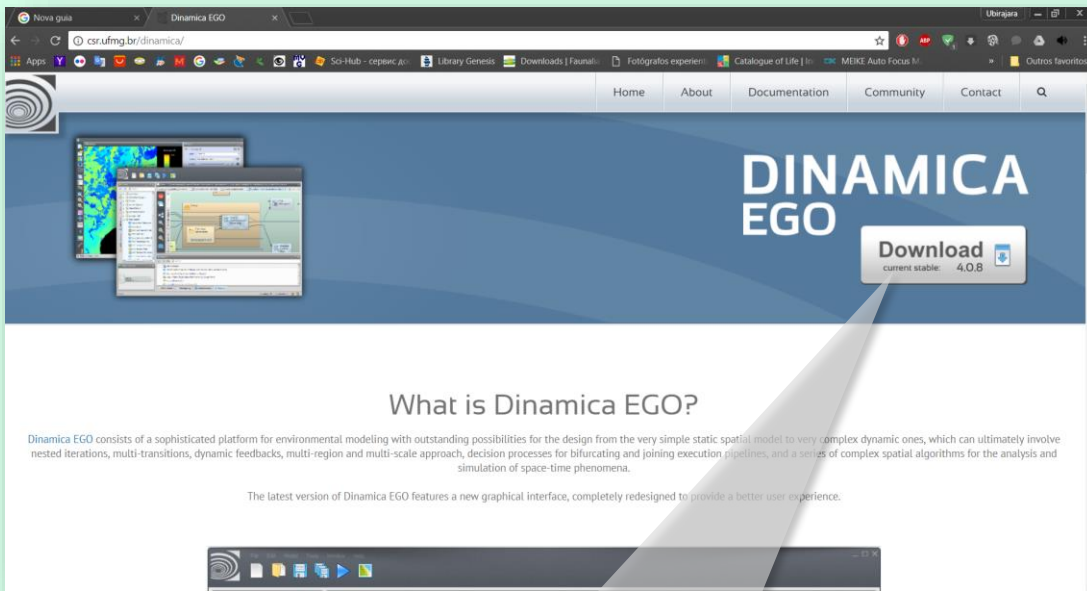


BIODINAMICA

Análise espacial de biodiversidade e biogeografia
na plataforma de modelagem Dinamica-EGO

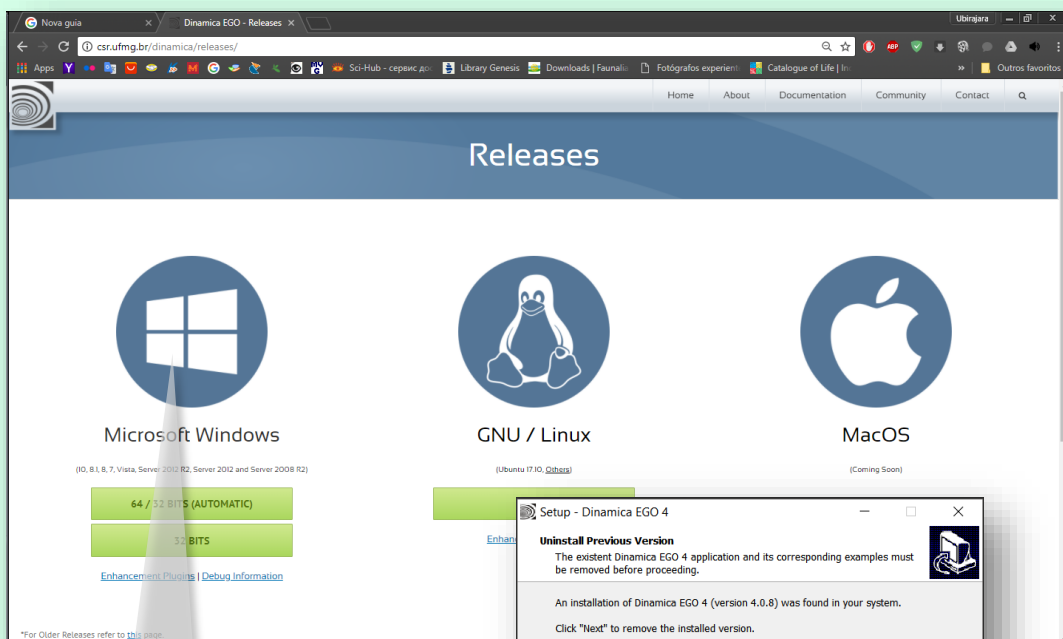
BIODINAMICA INSTALATION

BIODINAMICA INSTALATION



1

In webpage: <http://csr.ufmg.br/dinamica/> Click on download button



2

Click on download button and install the Dinamica-EGO

BIODINAMICA INSTALATION



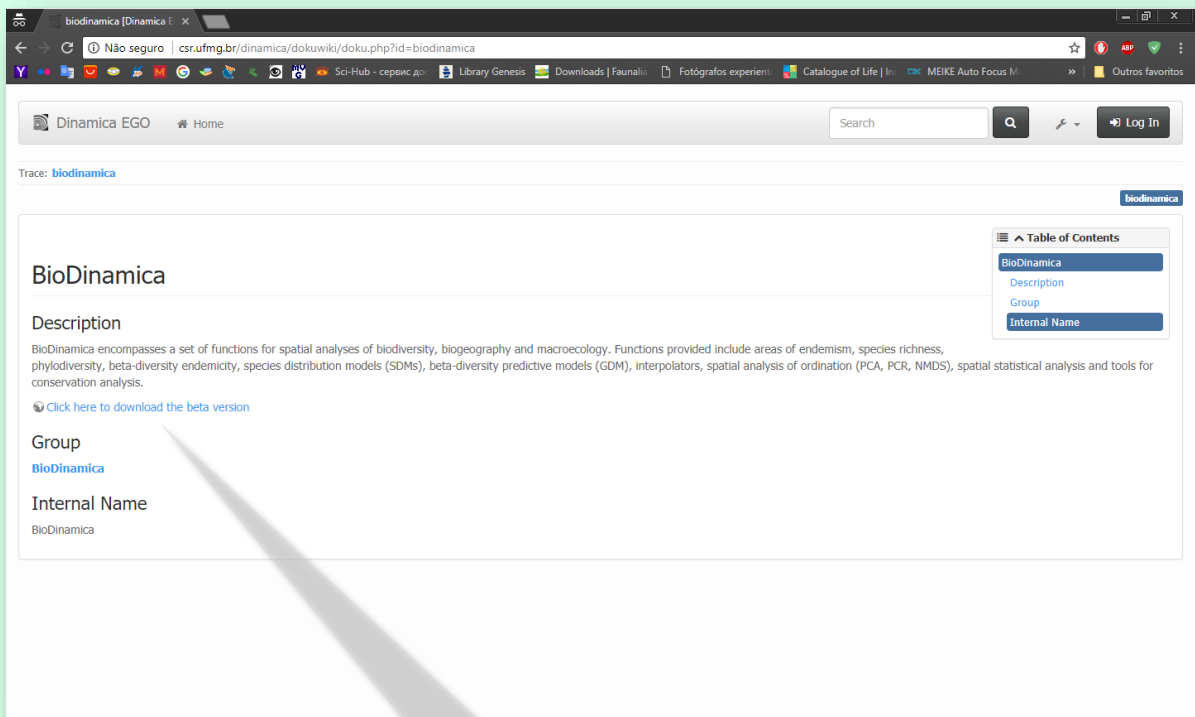
3

Click on Enhancement Plugins and install the program

http://csr.ufmg.br/dinamica/nui_download/926/

BIODINAMICA INSTALATION

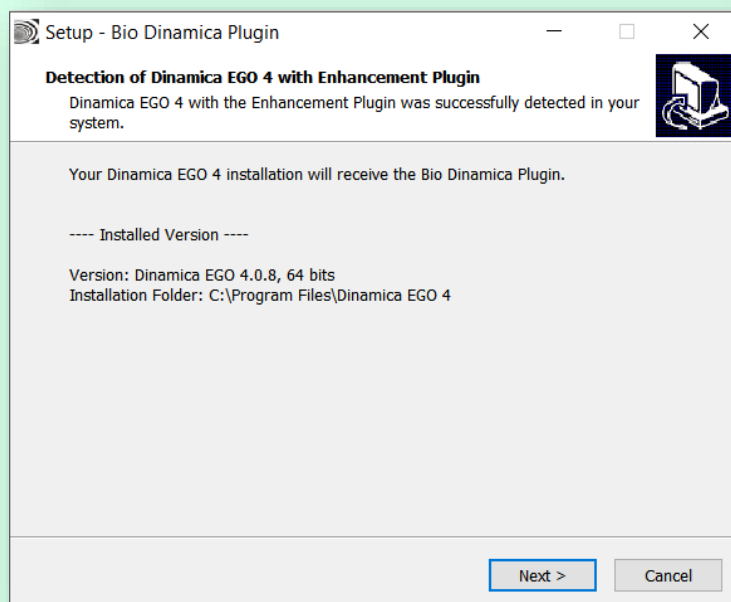
<http://csr.ufmg.br/dinamica/dokuwiki/doku.php?id=biodinamica>



4

Click on BioDinamica download button

<http://csr.ufmg.br/~ubirajara/ftp/BioDinamica-10.exe>



LIBRARY OF BIODINAMICA

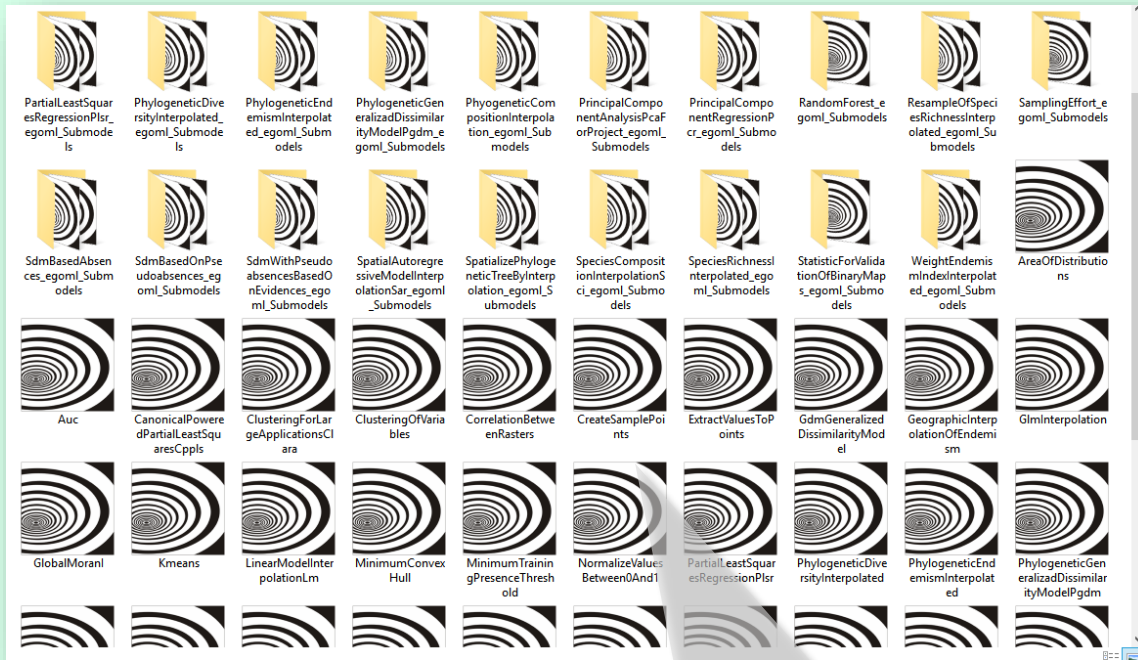


5

In Dinamica-EGO library are installed BioDinamica functions

WIZARD BIODINAMICA

You can use the capabilities of the wizard mode BioDinamica. This mode serves as a tutorial that guides the user through the analysis.

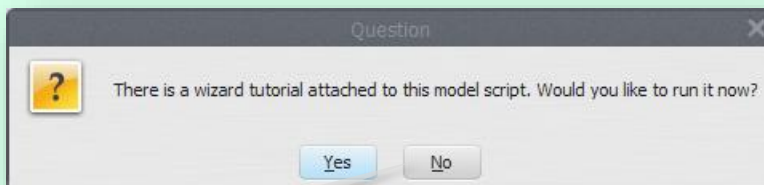


1

On the desktop computer, it installed a folder of shortcuts to BioDinamica tutorials (Wizard). Just choose the function and give a double-click to use it. Follow the Wizard and run the function.

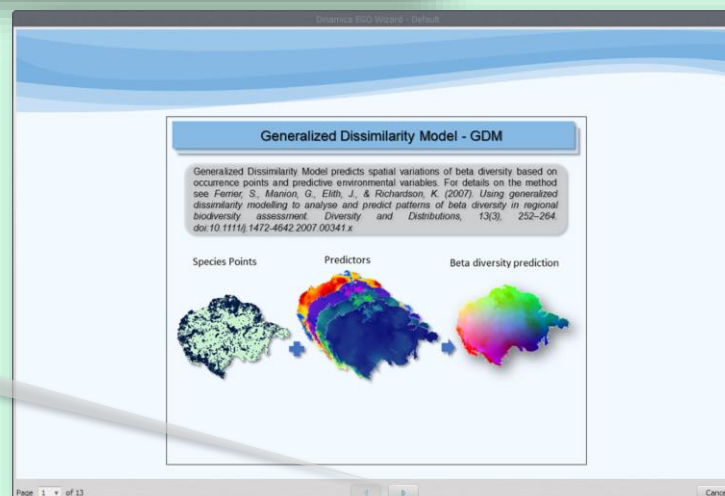
2

Choose "yes"



3

Follow the instructions and fill in the requested fields.



BIODINAMICA LIBRARY

Another option for accessing BioDinamica functions is the Dinamica-EGO library.

1 Use the tab BioDinamica library to choose the function. Move with the left mouse button, the function for the central area of the Dinamica-EGO software.

2 Double click

3 Fill in the options in the function, click ok to confirm. To run the function use the button "Run Model".

The screenshot shows the Dinamica-EGO interface. On the left, the 'Library' pane is open to the 'BioDinamica' tab, where the 'Gdm Generalized Dissimilarity Model' is highlighted. A callout box labeled '2' points to this function. In the center, a 'Documentation' pane shows the function's details. On the right, the 'Function Editor - Gdm Generalized Dissimilarity Model' dialog is open, showing configuration options like 'Input Occurrences', 'Predictors', 'Output Folder', 'Input Mask', 'Hexagons As Sample Units', and 'Hexagon Size'. A callout box labeled '3' points to this dialog. At the bottom left, a callout box labeled '1' points to the 'BioDinamica' tab in the library.

4 Click the "help" option to view the help page of function in the lower field of the screen.

The screenshot shows the Dinamica-EGO interface with the 'Gdm Generalized Dissimilarity Model' function selected in the library. A callout box labeled '4' points to the 'help' icon in the function's toolbar. Below the library, the 'Documentation' pane is open, displaying the help page for the 'Generalized Dissimilarity Model - GDM'. The help page includes a 'Description' section and an 'Inputs' section. A callout box labeled '3' points to the function icon in the library.

Generalized Dissimilarity Model - GDM

Description

This functor predicts the beta-diversity patterns by using environmental predictors. For more details, see: Ferrier, S., Manion, G., Elith, J., & Richardson, K. (2007). Using generalized dissimilarity modelling to analyse and predict patterns of beta diversity in regional biodiversity assessment. Diversity and Distributions, 13(3), 252–264. doi:10.1111/j.1472-4642.2007.00341.x

Inputs

- Input Occurrences
- Predictors
- Output Folder
- Input Mask
- ☒ Hexagons As Sample Units
- Hexagon Size
- Minimum Number Of Samples
- ☒ Project In Another Scenario
- Folder Scenarios Raster



INPUT DATA

INPUT OF OCCURRENCES

The input data are standardized, there are four basic formats, each format used in certain analyses. All input files of events (species, values or coordinates) should be as a csv table.

```
sp, x, y
Amaurospiza_carrizalensis, -62.6, 8.09
Amazilia_brevirostris, -62.43, 8.17
Amazilia_viridigaster, -62.6, 8.09
Anthracothonax_nigricollis, -62.43, 8.17
Aratinga_pertinax, -62.39, 8.01
Aratinga_pertinax, -62.6, 8.09
Aratinga_pertinax, -62.4, 8.01
Aratinga_pertinax, -62.4, 8.01
Arremonops_conirostris, -62.4, 8.02
Arremonops_conirostris, -62.6, 8.09
Arremonops_conirostris, -62.03, 8.23
Attila_cinnamomeus, -62.03, 8.23
```

```
dependent,x,y
0.374873087,-62.5,8.5
0.223601681,-61.5,8.5
0.920603089,-65.5,7.5
0.590162478,-64.5,7.5
0.654559192,-63.5,7.5
1.141030639,-62.5,7.5
0.066875409,-61.5,7.5
-0.207549216,-60.5,7.5
0.567730694,-59.5,7.5
0.531714651,-58.5,7.5
0.868004655,-66.5,6.5
1.083130427,-65.5,6.5
-0.031537805,-64.5,6.5
1.310974319,-63.5,6.5
0.328827238,-62.5,6.5
0.179027994,-61.5,6.5
```

```
x, y
-62.6,8.09
-62.43,8.17
-62.6,8.09
-62.43,8.17
-62.39,8.01
-62.6,8.09
-62.4,8.01
-62.4,8.01
-62.4,8.02
-62.6,8.09
-62.03,8.23
-62.03,8.23
-62,8
```

```
Haplotype, x, y
1, -63.413600000000, 2.359920000000
3, -59.915000000000, 4.904300000000
2, -66.983000000000, 4.692320000000
1, -63.413600000000, 0.875488000000
2, -65.357300000000, 5.787900000000
4, -64.650500000000, 4.056270000000
3, -61.823300000000, 5.646480000000
3, -60.939800000000, 4.727720000000
```

INPUT OF OCCURRENCES

1

The inputs of occurrences should be in csv format. This format consists of a text file with the columns separated by commas. You can save this format in spreadsheet software (Excel, for example). However, be aware that some software may use ";" (semicolon) as the separator for columns, this will cause a parse error. In this case, replace the ";" (semicolon) by "," (comma) in Notepad.

2

The first column must contain the name of the species. The title of the column should be "sp". The genere should be separated from the specific epithet for "_", do not use space.

3

The second and third columns should contain geographical coordinates of points of occurrence of the species. The coordinates must be in decimal degrees, with the decimals separated by a point.

```
sp, x, y
Amaurospiza_carrizalensis, -62.6, 8.09
Amazilia_brevirostris, -62.43, 8.17
Amazilia_viridigaster, -62.6, 8.09
Anthracothorax_nigricollis, -62.43, 8.17
Aratinga_pertinax, -62.39, 8.01
Aratinga_pertinax, -62.6, 8.09
Aratinga_pertinax, -62.4, 8.01
Aratinga_pertinax, -62.4, 8.01
Arremonops_conirostris, -62.4, 8.02
Arremonops_conirostris, -62.6, 8.09
Arremonops_conirostris, -62.03, 8.23
Attila_cinnamomeus, -62.03, 8.23
```

INPUT OF OCCURRENCES

1

The first column must contain the dependent variable. The title of the column should be "dependent" and values must be numeric.

2

The second and third columns should contain geographical coordinates of points. The coordinates must be in decimal degrees, with the decimals separated by a point.

dependent,x,y
0.374873087,-62.5,8.5
0.223601681,-61.5,8.5
0.920603089,-65.5,7.5
0.590162478,-64.5,7.5
0.654559192,-63.5,7.5
1.141030639,-62.5,7.5
0.066875409,-61.5,7.5
-0.207549216,-60.5,7.5
0.567730694,-59.5,7.5
0.531714651,-58.5,7.5
0.868004655,-66.5,6.5
1.083130427,-65.5,6.5
-0.031537805,-64.5,6.5
1.310974319,-63.5,6.5
0.328827238,-62.5,6.5
0.179027994,-61.5,6.5

INPUT OF OCCURRENCES

Points: columns must contain the geographical coordinates of points. The coordinates must be in decimal degrees, with the decimals separated by a point.

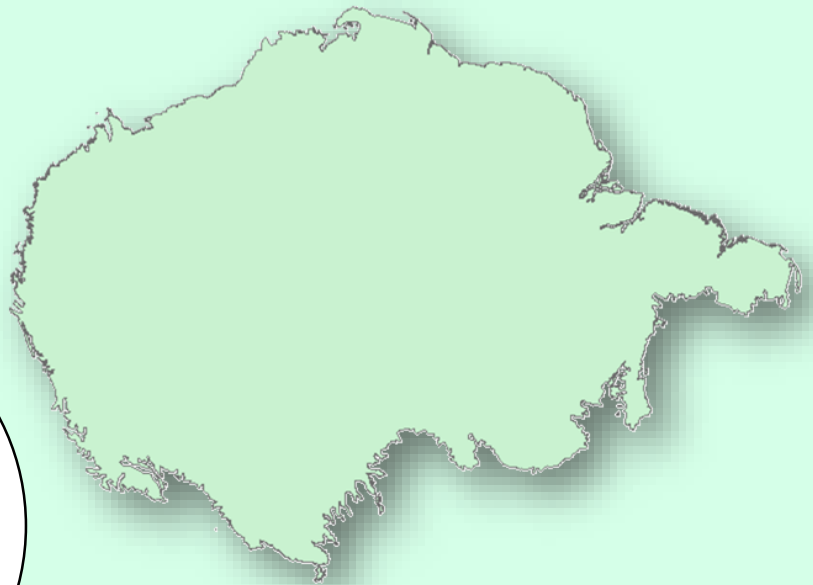
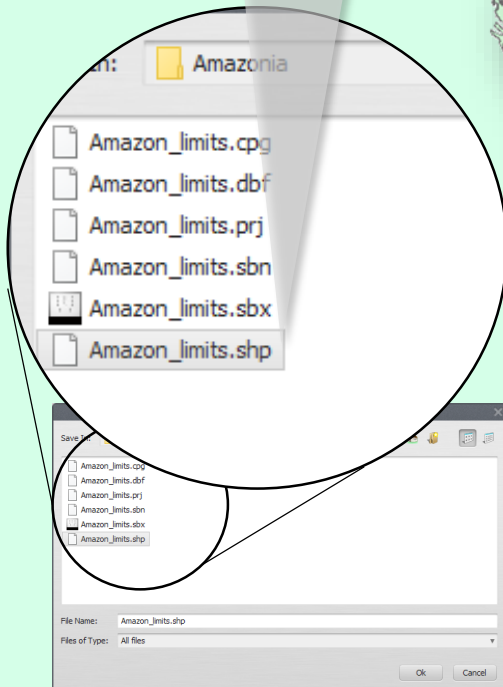
```
x, y
-62.6,8.09
-62.43,8.17
-62.6,8.09
-62.43,8.17
-62.39,8.01
-62.6,8.09
-62.4,8.01
-62.4,8.01
-62.4,8.02
-62.6,8.09
-62.03,8.23
-62.03,8.23
-62,8
```

Genetic data table (haplotypes): columns must contain the haplotypes in each population (identified by numbers) and the geographical coordinates of points of samples. The coordinates must be in decimal degrees, with the decimals separated by a point. The columns should be: Haplotype, x, y.

```
Haplotype, x, y
1, -63.41360000000, 2.35992000000
3, -59.91500000000, 4.90430000000
2, -66.98300000000, 4.69232000000
1, -63.41360000000, 0.87548800000
2, -65.35730000000, 5.78790000000
4, -64.65050000000, 4.05627000000
3, -61.82330000000, 5.64648000000
3, -60.93980000000, 4.72772000000
```

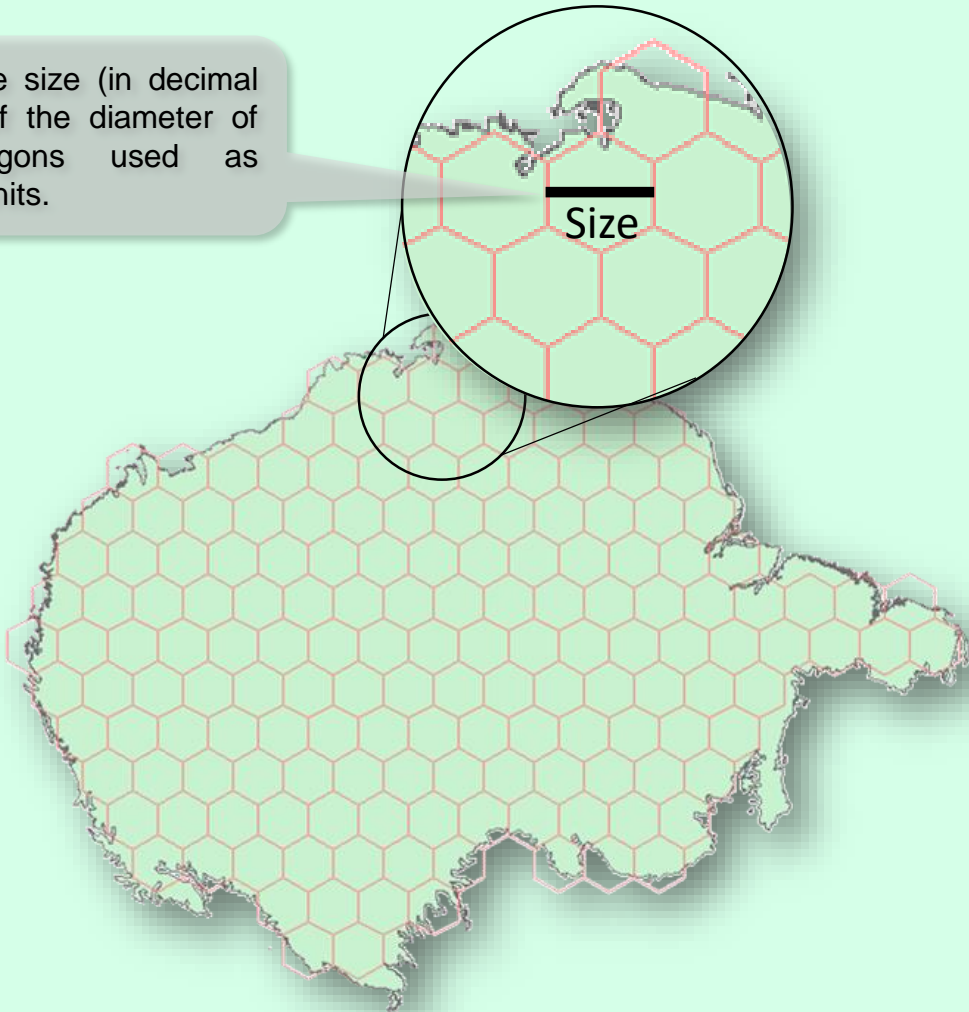
MASK

Choose a shape (shp) file to be used as a mask (limits of study area).



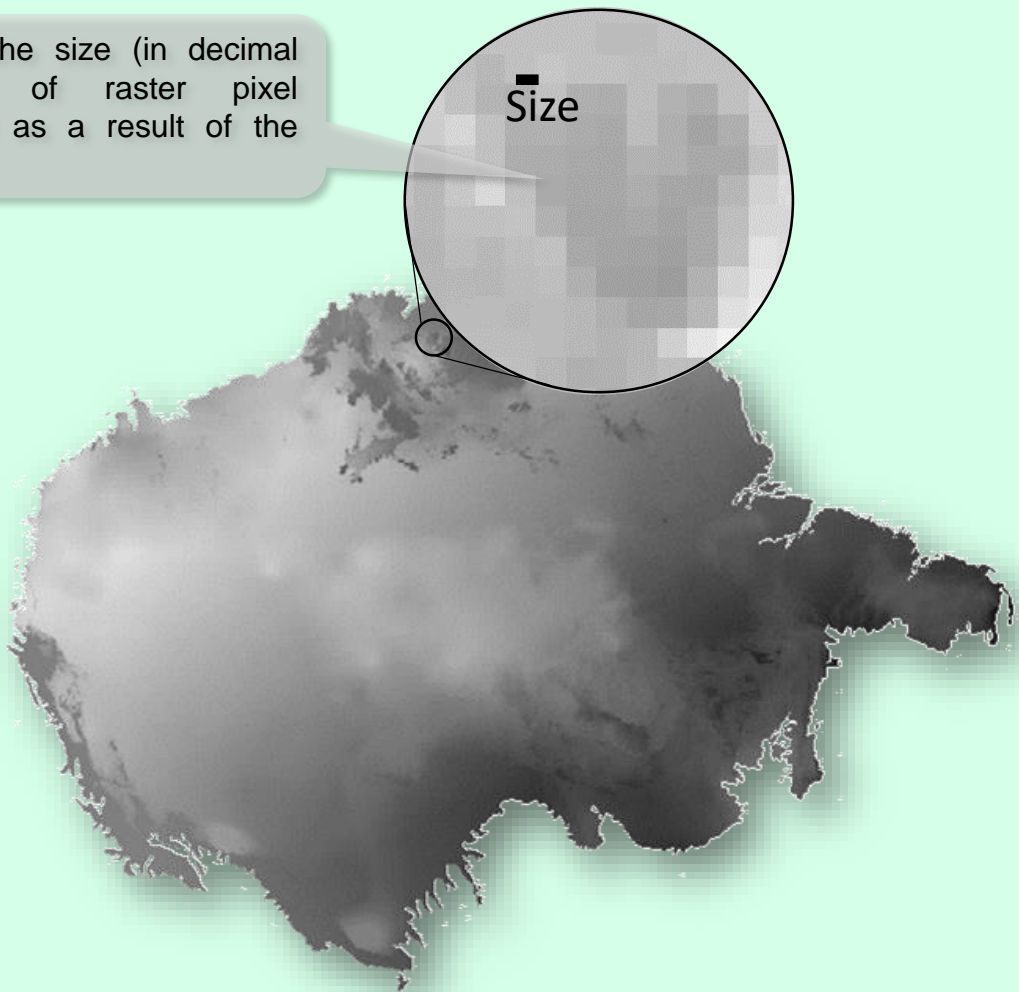
HEXAGON SIZE

Choose the size (in decimal degrees) of the diameter of the hexagons used as sampling units.



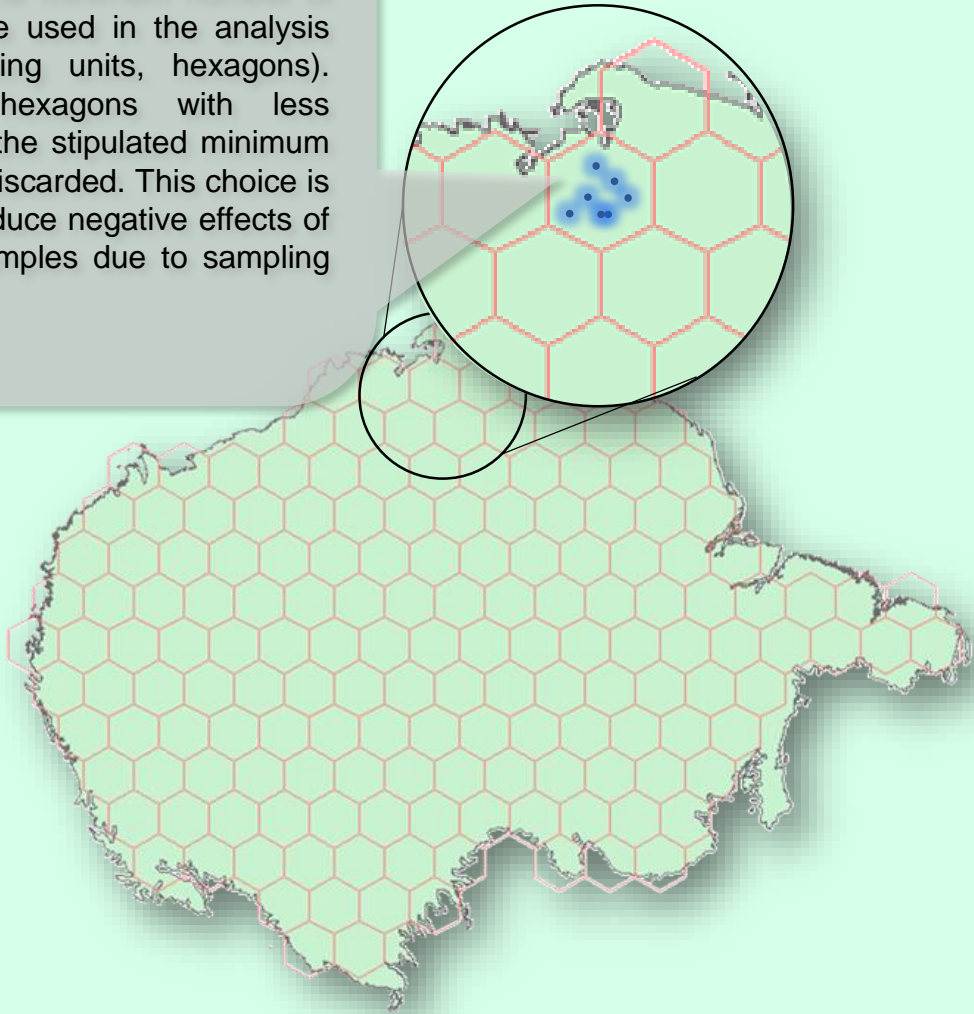
PIXEL SIZE

Choose the size (in decimal degrees) of raster pixel produced as a result of the analysis.



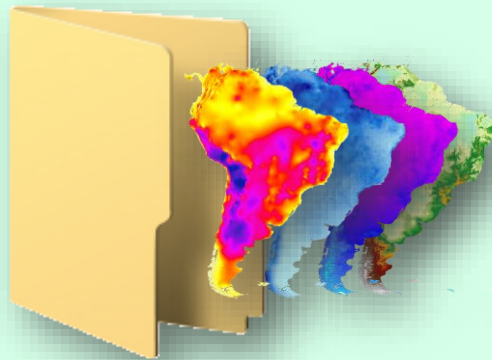
MINIMUM NUMBER OF SAMPLES

In several BioDinamica functions you can choose the minimum number of samples to be used in the analysis (within sampling units, hexagons). With that, hexagons with less samples than the stipulated minimum value will be discarded. This choice is required to reduce negative effects of very small samples due to sampling differences.



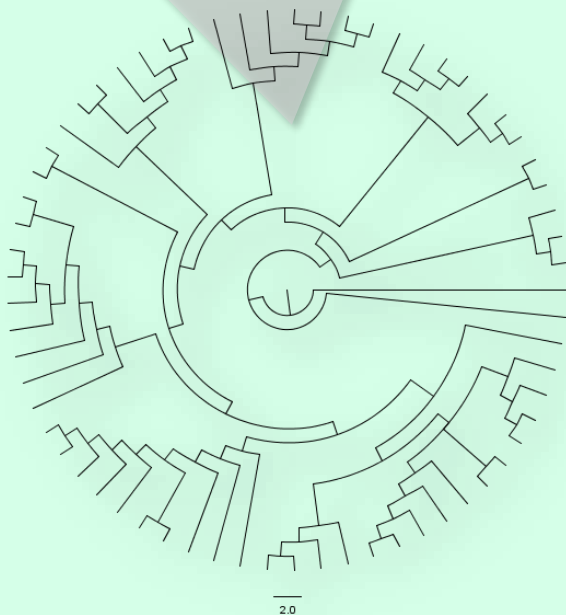
PREDICTIVE VARIABLES

As the Predictor variable BioDinamica uses map files in raster format (GeoTiff). These files must be cut to the same length (mask) and with the same pixel size.



PHYLOGENETIC TREE

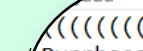
The phylogenetic tree file must be in the format tre (newick format tree files). The input tree does not need to have a complete match between the terminals and the occurrence data. That is, the tree may have more species than the present occurrence points, or vice versa. However, the names of species must have the same spelling in the tree and occurrence points.



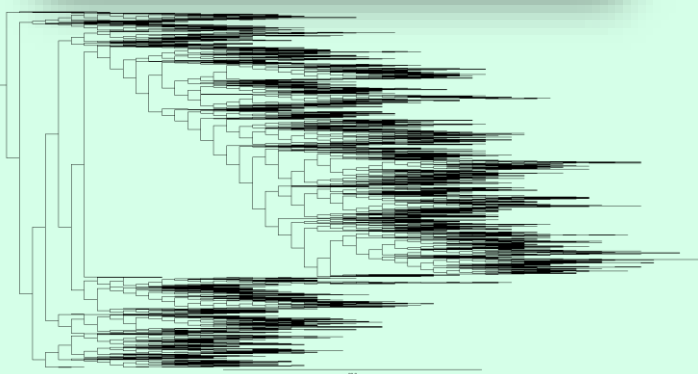
```
(((((Apteryx_australis:0.265821595,Apteryx_mantelli:0.265821595):  
:6.797034465):20.99100666,Crypturellus_strigulosus:27.78804113):16.  
79235434,(Anser_cygnoides:0.7294401477,Anser_anser:0.7294401477):1.  
australis:1.302378968):1.6156344,((Aythya_fuligula:1.100869807,(Ayt  
993497593,(Chloephaga_melanoptera:1.740536401,Neochen_jubata:1.740  
nigra:9.313972276):1.567691591):1.143444512):0.8287346259):0.17519  
as_chlorotis:0.2961105225):0.1174381328,Anas_nesiotis:0.4135486553)  
:5.629349646):5.450411418,Stictonetta-naevosa:19.88880376):3.462218  
468):26.88733024,(((Oreophasis_derbianus:13.21078574,((Nothocrax_  
72,(Penelopina_nigra:7.234880945,((Chamaepetes_unicolor:2.952991629  
:1.775400834,Callipepla_californica:1.775400834):3.439489955,(Calli  
975205):1.692201023,((Percidula_asiatika:11.74746793,Ammoperdix_hey  
0.1097507471,Syrmatius_elliotti:0.1097507471):3.796522883):3.590101  
64331,((Lagopus_muta:4.260828896,Lagopus_lagopus:4.260828896):2.21  
bscurus:1.974497968):8.9247796):4.290158492,((Tragopan_blythii:4.75  
nus_levallantoides:0.1895954946):2.373062648):0.3353232823):1.3189  
5):0.9126870492):9.415533226,(Rollulus_rouloul:15.19576277,Caloperd
```

LENGTHS OF BRANCHES IN PHYLOGENIES

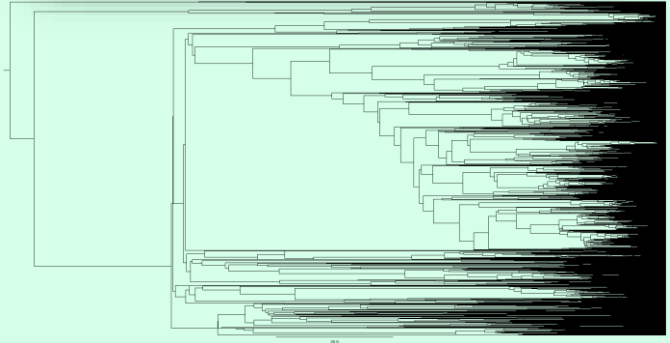
Can be used two types of phylogenetic trees-with length of branches or without branches length. If the tree does not have length of branches will be assumed between each event of cladogenesis branch length is equal to 1.



Thraupis cyanocephala



alis:0.2658219100666,Cryptu
 ygnoides:0.729440
 78968):1.6156344,(
 yphaga_melanoptera
 (((((((Apteryx_australis:0.265821595):8.1895471,
 :6.797834465):28.99100666):1.567691591):7.78804113):16.74374968):7
 79235434,(Anser_cygnoides:0.7294401477):1.049795287)
 australis:1.302378968):1.61563444):1.100869807,(Aythya_affinis
 993497593,((Chlorophaga_melanoptera:0.7294401477),Neochen_jubata:1.748536401):6.4
 nigra:9.313972270):1.567691591):1.143444512):0.8287346259):0.1751908269):1.6
 as_chlorotis:0.2961108725):0.1174381328,Anas_nesiotis:0.4135486553):1.5013457
 :5.6294349646):5.450411418,Stictonetta-naevosa:19.88880376):3.462218282):0.561

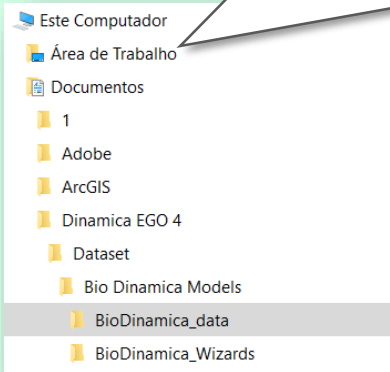


EXAMPLE DATA

To perform the functions, with the purpose of training, sample files are available from leading BioDinamica entries in the folder:

[\Documents\Dinamica EGO 4\Dataset\Bio Dinamica Models\BioDinamica_data](#)

It is recommended that you move this folder BioDinamica_data preferably in the root of a drive of the computer because the long address may not allow the execution of analyses. The icons below, representing each file for example, appear in the Guide to indicate which file can be used as an example in each analysis.



Point data (samples)



Sp_data

Points of occurrence of species (sp, x, y), used in most of analysis functions of biodiversity.



Cont_data

Numerical data of discrete values (dependent, x, y), used in most interpolation functions and ordering functions that use dependent variables.



Bin_data

Numerical data of discrete values (dependent, x, y), used only on CPPLS ordination function.



XY_data

Data from geographic coordinates (x, y), used in the sampling effort and sampling parameter in the SDM.

Phylogenetic data



Phylo_data

Phylogenetic data (format newick) may contain or not branch lengths.

Spatial data (raster and shapefile)



Rasters

Rasters of predictive variables used in analyses that use these variables as predictors.



Scenario

Predictive variables rasters in a scenario different from the one presented in the folder Rasters. Are used in analyses that use these variables to project the results in another scenario.



Predictors

Rasters of predictive variables derived from a PCA, used in analyses that employ these variables as predictors.



Scenario Predictors

Rasters of predictive variables derived from a PCA, in a scenario different from the one presented in the folder Rasters. Are used in analyses that employ these variables to project the results in another scenario.



Mask

Shapefile file used as a mask in several analyses.



Species Maps

Binary rasters that represent the distribution of species. These files are used in analyses such as calculation of area of distribution.



Gen_data

Folder with all the files needed for the analysis of genetic connectivity.



Spatialize phylo

Folder with the files needed for the analysis of spatialization of phylogenetic tree.



FUNCTIONS GUIDE

FUNCTIONS GUIDE

To perform the functions of BioDinamica and examples, the functions guide will show how to proceed and the details about each parameter of the function. Below, see the General schema for the reading of the functions guide.

Name of BioDinamica function.


Function description.

Function icon.

Description of each field of the function.

GDM – GENERALIZED DISSIMILARITY MODEL

Essa função especializa padrões de β -diversidade (composição de espécies) por meio de variáveis preditoras. Para detalhes sobre a metodologia veja: Ferrier et al. 2007 (<https://onlinelibrary.wiley.com/doi/abs/10.1111/j.1472-4642.2007.00341.x>).



Aba geral (principal)

Input Occurrences

csv with species and coordinates of localities (with columns: sp, x, y)

E: BioDinamica_data\Species_Occurrences.csv

Predictors

Folder with raster files of predictors (variables) in geotif format

E: BioDinamica_data\PCA_SA

Input Mask

Shapfile (.shp) of area of study

E: BioDinamica_data\Mask\Mask.shp

Output Folder

Folder of outputs. The folder address can not display spaces (in folder names). Use addresses like: "C:\results"

E: BioDinamica_Test\GDM

Hexagone As Sample Units


Use hexagone as sample units to generate the species data table by location (recommended when data is sparse and with gaps).

☒ Hexagone As Sample Units


Hexagone Size

Define size of hexagone


1.5



Sp_data



Predictors



Mask

Main window.

<http://csr.ufmg.br/dinamica/dokuwiki/doku.php?id=gdm&all=gdm>



INTERPOLATION

GLM – GENERALIZED LINEAR MODEL INTERPOLATION



This function interpolates spatially values by predictive variables, using a generalized linear model. As a result are generated reports informing the model and setting the parameters, and a map in raster format (GeoTiff) with the predicted values.

General tab (main)

Table in csv format (comma separated columns). First column with continuous numeric values (DON'T USE CATEGORICAL VALUES OR CLASSES), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named: dependent, x, y, written with lowercase letters.

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Indicate the folder in which the files of results will be saved.

Funcion Editor - Glm Interpolation

General Advanced

? **Input Points**

Input points (csv format) with dependent variable (with columns: dependent, x, y)

C:/data/Cont_data.csv

Predictor Variables

Folder with predictors raster files (variables) in geoTif format

C:/Predictors

Output Folder

C:/temp/output

OK Cancel



Cont_data



Predictors

Advanced tab

Choose the corresponding numbers, the distribution of errors that will be used in the GLM.

Select the reference coordinate system. The default option is WGS84 system. If you want to change this option, use the standard format Rgdal to change coordinate system.

Funcion Editor - Glm Interpolation

General Advanced

Error Distribution In Function Glm

Choose error distribution: 1 - binomial; 2 - gaussian; 3 - Gamma; 4 - inverse gaussian; 5 - poisson; 6 - quasi; 7 - quasibinomial; 8 - quasipoisson;

2

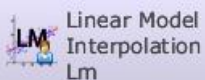
Coordinate Reference System

Define Coordinate Reference System with standard Rgdal formatting

+proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0

OK Cancel

LM –LINEAR MODEL INTERPOLATION



This function interpolates spatially values by means of predictive variables, using a linear model. As a result are generated reports informing the model and setting the parameters and map in raster format (GeoTiff) with the predicted values.

General tab (main)

Table in csv format (comma separated columns). Being the first column with continuous numeric values (DON'T USE CATEGORICAL VALUES or CLASSES), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named: dependent, x, y, written with lowercase letters.

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Indicate the folder in which the files of results will be saved.

Funcion Editor - Lm Interpolation

General Advanced

? **Input Points**

Input points (csv format) with dependent variable (with columns: dependent, x, y)

C:/data/Cont_data.csv

Predictors

Folder with predictors raster files (variables) in geoTif format

C:/Predictors

Output Folder

C:/temp/output

OK Cancel

Advanced tab

Select the reference coordinate system. The default option is WGS84 system. If you want to change this option, use the standard format Rgdal to change coordinate system.

Funcion Editor - Lm Interpolation

General Advanced

Coordinate Reference System

Define Coordinate Reference System with standard Rgdal formatting

+proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0

OK Cancel

SAR – SPATIAL AUTOREGRESSIVE MODEL INTERPOLATION



This function interpolates spatially values by predictive variables, using a space-filling model autoregressive. As a result are generated reports informing the fit and the parameters of the model and map in raster format (GeoTiff) with the predicted values .

General tab (main)

Table in csv format (comma separated columns). Being the first column with continuous numeric values (DON'T USE CATEGORICAL VALUES or CLASSES), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named: dependent, x, y, written with lowercase letters.

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Indicate the folder in which the files of results will be saved.



Cont_data



Advanced tab

Choose the cell size (pixel size) used in the sample analysis. This is not the VALUE of the FINAL SIZE of the PIXELS, is only used to generate the calculations. After that, the final map will be generated in the same resolution of the cells of the predictors.

Select the reference coordinate system. The default option is WGS84 system. If you want to change this option, use the standard format Rgdal to change coordinate system.

NNI - NEAREST NEIGHBOUR INTERPOLATION



This function interpolates spatially values, through the spatial pattern of the variables using the interpolator nearest neighbour. As a result is generated a map in raster format (GeoTiff) with the predicted values.

General tab (main)

Table in csv format (comma separated columns). Being the first column with continuous numeric values (DON'T USE CATEGORICAL VALUES or CLASSES), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named: dependent, x, y, written with lowercase letters.

Specify a file in the shapefile (.SHP) format to serve as a mask (area in which will be held the interpolation)

Enter the name and location of the raster file format (GeoTiff) that is saved with the test results.

Functor Editor - Nni

General Advanced

Input Points
Input points (csv format) with dependent variable (with columns: dependent, x, y)
E:\BioDinamica_data\Cont_data.csv

Input Mask
Shapefile (shp) of area of study
E:\BioDinamica_data\Mask\Mask.shp

Output Raster
Filename of output raster
E:\BioDinamica_data\nni.tif

OK Cancel



Cont_data



Mask



Predictors

Advanced tab

Choose the maximum number of neighbors that will be used in the calculation of interpolation.

Choose the cell size of the resulting map (interpolated). The value must be in the same unit of the coordinate system used.

Choose if the interpolation will be smoothed by the average neighbor.

If you have chosen the smoothing by the average of the neighbors, choose the number of neighbors that will be used in the calculation of the average.

Select the reference coordinate system. The default option is WGS84 system. If you want to change this option, use the standard format Rgdal to change coordinate system.

Functor Editor - Nni

General Advanced

Number Of Neighbours
Maximum number of neighbours
5

Cell Size
Cell size of output
0.05

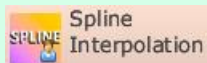
☒ **Smooth Map**
Smooth interpolation map by neighbours
No Smooth Map

Number Of Pixels In Smooth
30

Coordinate Reference System
Define Coordinate Reference System with standard Rgdal formatting
+proj=longlat +datum=WGS84 +no_defs
+ellps=WGS84 +towgs84=0,0,0

OK Cancel

SPLINE INTERPOLATION



This function interpolates spatially values, through the spatial pattern of the variables using the simple function (Spline). As a result is generated a map in raster format (GeoTiff) with the predicted values.

General tab (main)

Table in csv format (comma separated columns). Being the first column with continuous numeric values (DON'T USE CATEGORICAL VALUES or CLASSES), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named: dependent, x, y, written with lowercase letters.

Specify a file in the shapefile (.SHP) format to serve as a mask (area in which will be held the interpolation)

Enter the name and location of the raster file format (GeoTiff) that is saved with the test results.

Funcion Editor - Spline Interpolation

General Advanced

? **Input Points**

Input points (csv format) with dependent variable (with columns: dependent, x, y)

C:/data/Cont_data.csv

? **Input Mask**

Shapefile (shp) of area of study

C:/limits/mask.shp

? **Output Raster**

Filename of output raster

C:/temp/output/result.tif

OK Cancel



Cont_data



Mask

Advanced tab

Choose the cell size of the resulting map (interpolated). The value must be in the same unit of the coordinate system used.

Choose the parameter of smoothing (Lambda) of spline interpolation

Select the reference coordinate system. The default option is WGS84 system. If you want to change this option, use the standard format Rgdal to change coordinate system.

Funcion Editor - Spline Interpolation

General Advanced

IR **Cell Size**

Cell size of output

0.05

IR **Lambda**

Smoothing parameter the ratio of error variance to process variance

40

a **Coordinate Reference System**

Define Coordinate Reference System with standard Rgdal formatting

+proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0

OK Cancel

SIMPLE KRIGING INTERPOLATION



This function interpolates spatially values, through the spatial pattern of the variables using the kriging function. As a result is generated a map in raster format (GeoTiff) with the predicted values.

General tab (main)

Table in csv format (comma separated columns). Being the first column with continuous numeric values (DON'T USE CATEGORICAL VALUES or CLASSES), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named: dependent, x, y, written with lowercase letters.

Specify a file in the shapefile (.SHP) format to serve as a mask (area in which will be held the interpolation)

Enter the name and location of the raster file format (GeoTiff) that is saved with the test results.

Funcion Editor - Simple Kriging Interpolation

General Advanced

? **Input Points**
Input points (csv format) with dependent variable (with columns: dependent, x, y)
C:/data/Cont_data.csv

? **Input Mask**
Shapefile (shp) of area of study
C:/limits/mask.shp

? **Output Raster**
Filename of output raster
C:/temp/output/result.tif

OK Cancel



Cont_data



Mask

Advanced tab

Choose the corresponding numbers, the variogram model used on kriging

Choose the number of "Lags" used in the construction of the variogram.

Choose the cell size of the resulting map (interpolated). The value must be in the same unit of the coordinate system used.

Select the reference coordinate system. The default option is WGS84 system. If you want to change this option, use the standard format Rgdal to change coordinate system.

Funcion Editor - Simple Kriging Interpolation

General Advanced

IR **Model**
Specification of the variogram model: 1- spherical, 2- exponential, 3- gaussian
1

IR **Lags**
Number of lags
2

IR **Cell Size**
Cell size of output raster
0.05

a **Coordinate Reference System**
Define Coordinate Reference System with standard Rgdal formatting
+proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0

31
OK Cancel

ORDINARY KRIGING INTERPOLATION



This function interpolates spatially values, through the spatial pattern of the variables using the ordinal kriging function. As a result is generated a map in raster format (GeoTiff) with the predicted values.

General tab (main)

Table in csv format (comma separated columns). Being the first column with continuous numeric values (DON'T USE CATEGORICAL VALUES or CLASSES), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named: dependent, x, y, written with lowercase letters.

Specify a file in the shapefile (.SHP) format to serve as a mask (area in which will be held the interpolation)

Enter the name and location of the raster file format (GeoTiff) that is saved with the test results.

Funcion Editor - Ordinary Kriging

General Advanced

? **Input Points**
Input points (csv format) with dependent variable (with columns: dependent, x, y)
E:\BioDinamica_data\Cont_data.csv

? **Input Mask**
Shapefile (shp) of area of study
E:\BioDinamica_data\Mask\Mask.shp

? **Output Raster**
Filename of output raster
E:\BioDinamica_data\OK.tif

OK Cancel



Cont_data



Mask

Advanced tab

Choose the corresponding numbers, the variogram model used on kriging

Choose the cell size of the resulting map (interpolated). The value must be in the same unit of the coordinate system used.

Choose whether the Tween will be smoothed by the average of the neighbors.

If you have chosen the smoothing by the average of the neighbors, choose the number of neighbors that will be used in the calculation of the average.

Select the reference coordinate system. The default option is WGS84 system. If you want to change this option, use the standard format Rgdal to change coordinate system.

Funcion Editor - Ordinary Kriging

General Advanced

IR **Model**
Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4 - Matern
1

IR **Cell Size**
Cell size of output
0.05

☒ **Smooth Map**
Smooth interpolation map by neighbours
☐ No ☒ Smooth Map

N **Number Of Pixels In Smooth**
30

a **Coordinate Reference System**
Define Coordinate Reference System with standard Rgdal formatting
proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0

32

OK Cancel

UNIVERSAL KRIGING INTERPOLATION



This function interpolates spatially values, through the spatial pattern of the variables using the universal kriging function. As a result is generated a map in raster format (GeoTiff) with the predicted values.

General tab (main)

Table in csv format (comma separated columns). Being the first column with continuous numeric values (DON'T USE CATEGORICAL VALUES or CLASSES), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named: dependent, x, y, written with lowercase letters.

Specify a file in the shapefile (.SHP) format to serve as a mask (area in which will be held the interpolation)

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Enter the name and location of the raster file format (GeoTiff) that is saved with the test results.

Functor Editor - Universal Kriging

General Advanced

Input Points
Input points (csv format) with dependent variable (with columns: dependent, x, y)
E:\BioDinamica_data\Cont_data.csv

Input Mask
Shapefile (shp) of area of study
E:\BioDinamica_data\Mask\Mask.shp

Predictor Variables
Folder with predictors raster files (variables) in geoTiff format
E:\BioDinamica_data\Predictors

Output Folder
E:\BioDinamica_data\UK

OK Cancel

Advanced tab

Choose the corresponding numbers, the variogram model used on kriging

Choose the cell size of the resulting map (interpolated). The value must be in the same unit of the coordinate system used.

Choose the cell size of the resulting map (interpolated). The value must be in the same unit of the coordinate system used.

Choose the parameter of smoothing (Lambda) of spline interpolation

Select the reference coordinate system. The default option is WGS84 system. If you want to change this option, use the standard format Rgdal to change coordinate system.

Functor Editor - Universal Kriging

General Advanced

Model
Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4 - Matern
1

Cell Size
Cell size of output
0.05

Smooth Map
Smooth interpolation map by neighbours
☒ No ☐ Smooth Map

Number Of Pixels In Smooth
30

Coordinate Reference System
Define Coordinate Reference System with standard Rgdal formatting
+proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0

OK Cancel

IDW INTERPOLATION



This function interpolates spatially values, through the spatial pattern of the variables using the gravitational function, or the inverse of the square of the distance (IDW). As a result is generated a map in raster format (GeoTiff) with the predicted values.

General tab (main)

Table in csv format (comma separated columns). Being the first column with continuous numeric values (DON'T USE CATEGORICAL VALUES or CLASSES), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named: dependent, x, y, written with lowercase letters.

Specify a file in the shapefile (.SHP) format to serve as a mask (area in which will be held the interpolation)

Enter the name and location of the raster file format (GeoTiff) that is saved with the test results.

Functor Editor - Idw

General Advanced

Input Points
Input points (csv format) with dependent variable (with columns: dependent, x, y)
E:\BioDinamica_data\Cont_data.csv

Input Mask
Shapefile (shp) of area of study
E:\BioDinamica_data\Mask\Mask.shp

Output Raster
Filename of output raster
E:\BioDinamica_data\IDW

OK Cancel



Cont_data



Mask

Advanced tab

Choose the cell size of the resulting map (interpolated). The value must be in the same unit of the coordinate system used.

Select the reference coordinate system. The default option is WGS84 system. If you want to change this option, use the standard format Rgdal to change coordinate system.

Functor Editor - Idw

General Advanced

Cell Size
Cell size of output
0.05

Coordinate Reference System
Define Coordinate Reference System with standard Rgdal formatting
+proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0

OK Cancel

GWR – GEOGRAPHICALLY WEIGHTED REGRESSION



This function interpolates spatially values, using a non-stationary regression model based on predictors (raster format) and the spatial pattern of relations between variables.

General tab (main)

Table in csv format (comma separated columns). Being the first column with continuous numeric values (DON'T USE CATEGORICAL VALUES or CLASSES), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named: dependent, x, y, written with lowercase letters.

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Specify a file in the shapefile (.SHP) format to serve as a mask (area in which will be held the interpolation)

Enter the name and location of the raster file format (GeoTiff) that is saved with the test results.

Funcion Editor - Gwr

General Advanced

Input Points
Input points (csv format) with dependent variable (column names: dependent, x, y).
E:\BioDinamica_data_curso\Cont_data.csv

Predictor Variables
Folder with rasters of predictor variables in tif format
E:\BioDinamica_data_curso\Predictors

Mask
Shapefile (shp) with area of study
E:\BioDinamica_data_curso\Mask\Mask.shp

Output Folder
Folder to save outputs
S:\temp

OK Cancel



Cont_data



Mask

Advanced tab

Choose the cell size of the resulting map (interpolated). The value must be in the same unit of the coordinate system used.

Choose the number of samples that will be used in the calculation of the GWR.

Funcion Editor - Gwr

General Advanced

Cell Size
Cell size
0.05

Number Of Samples
Number of samples in GWR prediction
1000

OK Cancel



ORDINATION AND STATISTICAL ANALYSIS

PCA – PRINCIPAL COMPONENT ANALYSIS



Pca
Principal
Component
Analysis

This function generates maps of principal components of specialized variables (raster format). The principal component analysis (PCA) is done pixel by pixel. As a result are generated for each axis of PCA rasters and a cube of rasters with all components. In addition, reports are generated with the test results.

Enter the folder that contains the rasters (in GeoTiff format) that will be used. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Indicate the folder in which the files of results will be saved.

Funcion Editor - Principal Component Analysis Pca

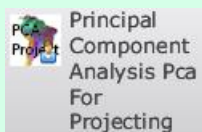
Input Folder
Folder with variables raster files in geoTif format
C:\data_test\Predictors

Output Folder
C:\temp\21032018 modelos\PCA

OK Cancel



PRINCIPAL COMPONENT ANALYSIS – PCA FOR PROJECTING



This function creates a map of principal components (PCA) based on variables and projects the axes of PCA in a new scenario (e.g. climate change). Are generated as a result a cube of rasters with each band represents an axis of PCA, moreover, are generated reports with details of the analysis.

General tab (main)

Enter the folder that contains the rasters (in GeoTiff format) that will be used. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors of projection scenarios. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. The rasters should be appointed in the same manner as were named the rasters predictors.

Indicate the folder in which the files of results will be saved.

PCR - PRINCIPAL COMPONENT REGRESSION



Principal
Component
Regression
Pcr

This function generates maps based on principal component regression (PCR) through spatialized variables (raster format). The PCR is performed pixel by pixel. As a result are generated for each axis rasters of PCR and a cube of rasters with all components. In addition, reports are generated with the test results.

General tab (main)

Table in csv format (comma separated columns). Being the first column with continuous numeric values (DON'T USE CATEGORICAL VALUES or CLASSES), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named: dependent, x, y, written with lowercase letters.

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Enter the name and location of the raster file format (GeoTiff) that is saved with the test results.

Funcion Editor - Principal Component Regression Pcr

General Advanced

? **Input Points**

Input points (csv format) with dependent variable (with columns: dependent, x, y)

C:/Cont_data.csv

Predictors

Folder with predictors raster files (variables) in geoTif format

E:/Predictors

Output Folder

C:/temp/output

OK Cancel



Cont_data



Predictors

Advanced tab

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors of projection scenarios. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. The rasters should be appointed in the same manner as were named the rasters predictors.

Choose whether it will be held the projection of the PCR in another scenario.

Funcion Editor - Principal Component Regression Pcr

General Advanced

Folder Scenarios Raster

Folder with rasters for project in another scenario. The rasters should be named in the same way of predictors.

x:/variables_scenario

☒ **Project In Another Scenario**

Project PLSR in another scenario (future or past)

yes Project In Another Scenario

OK Cancel

CPPLS - CANONICAL POWERED PARTIAL LEAST SQUARES



This function generates maps based on canonical powered partial least squares (CPPLS) through variables (raster format). The CPPLS is done pixel by pixel. As a result are generated for each axis of the rasters CPPLS and a cube of rasters with all components. In addition, reports are generated with the test results.

General tab (main)

Table in csv format (comma separated columns). Being the first column with numeric or categorical binary values (not USING CONTINUOUS VALUES), the second column x-coordinates (longitude) and third column with coordinates y (latitude). The columns must be named: dependent, x, y, written with lowercase letters

Enter the folder that contains the rasters (in GeoTiff format) that will be used. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Indicate the folder in which the files of results will be saved

Functor Editor - Canonical Powered Partial Least Squares Cp...X

General Advanced

Input Points
Input points (csv format) with dependent variable (with columns: dependent, x, y). Dependent variable must have a binary value.
C:/data/bin_data.csv

Predictors
Folder with predictors raster files (variables) in geoTiff format
C:/Predictors

Output Folder
C:/temp/output

OK Cancel



Bin_data



Predictors

Advanced tab

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors of projection scenarios. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. The rasters should be appointed in the same manner as were named the rasters predictors.

Choose whether the projection of the CPPLS will be held in another scenario.

Functor Editor - Canonical Powered Partial Least Squares Cp...X

General Advanced

Folder Scenarios Raster
Folder with rasters for project in another scenario. The rasters should be named in the same way of predictors.
C:/variables_scenario

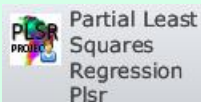
☒ **Project In Another Scenario**
Project PLSR in another scenario (future or past)
☒ Yes ☐ No Project In Another Scenario

OK Cancel



Scenario

PLSR - PARTIAL LEAST SQUARES REGRESSION



This function generates maps based on partial least square regression (PLSR) through spatialized variables (raster format). The pixel by pixel PLSR is performed. As a result are generated for each axis of PLSR rasters and a cube of rasters with all components. In addition, reports are generated with the test results.

General tab (main)

Table in csv format (comma separated columns). Being the first column with continuous numeric values (DON'T USE CATEGORICAL VALUES or CLASSES), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named: dependent, x, y, written with lowercase letters.

Enter the folder that contains the rasters (in GeoTiff format) that will be used. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Indicate the folder in which the files of results will be saved.

Funcion Editor - Plsr Partial Least Squares Regression

General Advanced

Input Points
Input points (csv format) with dependent variable (with columns: dependent, x, y)
C:/data/Cont_data.csv

Predictors
Folder with predictors raster files (variables) in geoTif format
C:/Predictors

Output Folder
C:/temp/output

OK Cancel



Cont_data



Predictors

Advanced tab

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors of projection scenarios. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. The rasters should be appointed in the same manner as were named the rasters predictors.

Choose whether the projection will be held in another scenario PLSR.

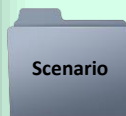
Funcion Editor - Plsr Partial Least Squares Regression

General Advanced

Folder Scenarios Raster
Folder with rasters for project in another scenario. The rasters should be named in same way of predictors.
C:/variables_scenario

☒ **Project In Another Scenario**
Project PLSR in another scenario (future or past)
☒ Yes ☐ No Project In Another Scenario

OK Cancel



Scenario

CORRELATION BETWEEN RASTERS



This function calculates the correlation between a set of rasters. Are saved reports on the analysis.

Enter the folder that contains the rasters (in GeoTiff format) that will be analyzed. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Indicate the folder in which the files of results will be saved.

Choose the corresponding numbers, the raster format that will be analyzed.

Funcion Editor - Correlation Between Rasters

Input Folder
Folder with variables raster files in geoTif format
C:/Predictors

Output Results
C:/temp/correlations.txt

Raster Input Format
Raster input format: 1- tif, 2- asc
1

OK Cancel

GWCORRELATION



This function calculates the non-stationary correlation by GWcorrelation between samples and a set of rasters. Are generated r maps of correlations.

General tab (main)

Table in csv format (comma separated columns). Being the first column with continuous numeric values (DON'T USE CATEGORICAL VALUES or CLASSES), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named: dependent, x, y, written with lowercase letters.

Enter the folder that contains the rasters (in GeoTiff format) that will be analyzed. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Specify a file in the shapefile (.SHP) format to serve as a mask (area in which will be held the interpolation).

Indicate the folder in which the files of results will be saved.

Functor Editor - Gwcorrelation

General Advanced

Input Points
Input points (csv format) with dependent variable (column names: dependent, x, y).
E:/BioDinamica_data_curso/Cont_data.csv

Predictor Variables
Folder with rasters of predictor variables in tif format
E:/BioDinamica_data_curso/Predictors

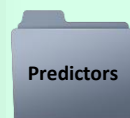
Mask
Shapefile (shp) with area of study
E:/BioDinamica_data_curso/Mask/Mask.shp

Output Folder
Folder to save outputs
C:/temp

OK Cancel



Cont_data



Mask

Advanced tab

Choose the cell size of the resulting map (interpolated). The value must be in the same unit of the coordinate system used.

Choose the number of samples that will be used in the calculation of the GWR.

Functor Editor - Gwcorrelation

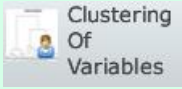
General Advanced

Cell Size
Cell size
0.05

Number Of Samples
Number of samples in GWcorrelation prediction
1000

OK Cancel

CLUSTER OF VARIABLES



This function computes the cluster of variables (ClusofVar) of a given set of variables rasterized. Are generated reports with the results of the analysis.

Enter the folder that contains the rasters (in GeoTiff format) that will be used. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Choose the corresponding numbers, the raster format that will be analyzed.

Choose the number of clusters of variables that is desired.

Indicate the folder in which the files of results will be saved.

Functor Editor - Clustering Of Variables

Variables
Folder with variables raster files
C:/Predictors

Raster Format
1- tif, 2- asc
1

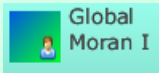
Number Of Clusters
Choice the number of cluster of variables
5

Output Folder
C:/temp/output

OK Cancel

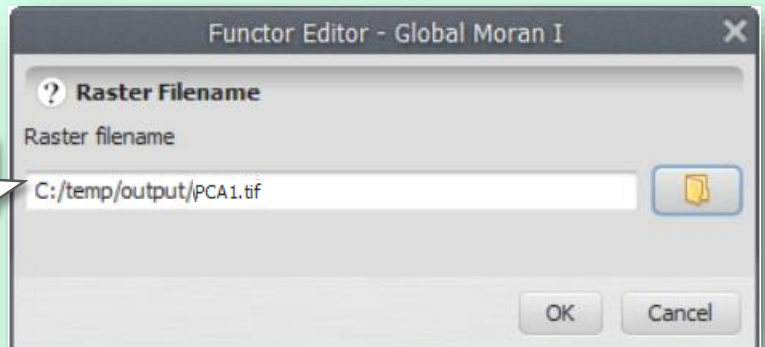


GLOBAL MORAN I



This function performs the test of Moran (I) global, to test for the existence of Spatial autocorrelation in a given raster.

Indicate the raster file format (GeoTiff) that will be used in the calculation of the index of Moran (I).



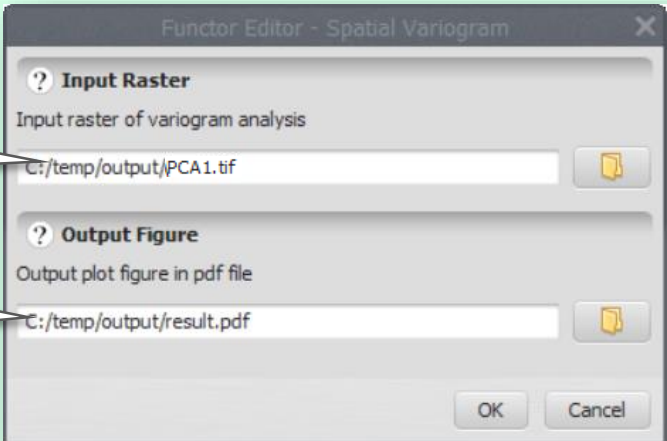
SPATIAL VARIOGRAM



This function generates a graph of a spatial variogram based on values in a given raster.

Choose the raster file format (GeoTiff).

Choose the location and name of the pdf file will be saved with the graphic analysis.





CLASSIFIERS

K-MEANS CLASSIFICATION



This function performs an unsupervised raster classification with k-means clustering.

General tab (main)

Enter the folder that contains the input rasters (in GeoTiff format). The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Choose the number of classes in which the map will be classified.

Indicate the folder to saved result map.

Functor Editor - Kmeans

General Advanced

Input Folder
Folder with predictors raster files (variables) in geoTif format
C:/Predictors

Number Of Classes
Number of classes in classification
5

Output KMeans
Output raster of k-means classification
C:/temp/output/result.tif

OK Cancel



Advanced tab

Choose the number of interactions that will be used to search for the best solution in k-means classification.

Choose the number of random starts that will be used to optimize the k-means clustering.

Functor Editor - Kmeans

General Advanced

Number Of Interactions
Maximum number of interactions in k-means classification
1000

Start Random Sets
Number of start random sets
10

OK Cancel

CLARA (CLUSTERING FOR LARGE APPLICATIONS) CLASSIFICATION



This function performs an unsupervised rasters classification with CLARA (Clustering for Large Applications).

General tab (main)

Enter the folder that contains the input rasters (in GeoTiff format). The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Choose the number of classes in which the map will be sorted.

Indicate the folder to saved result map.

Functor Editor - Clara

General Advanced

Input Folder
Folder with predictors raster files (variables) in geoTif format
C:/Predictors

Number Of Classes
Number of classes in classification
5

Output Clara
Output raster of clara classification
C:/temp/output/result.tif

OK Cancel

Aba avançada

Choose the number of samples used to generate optimization.

Choose the number corresponding to the distance metric used by classifier.

Functor Editor - Clara

General Advanced

Sample Size In Clara
500

Distance Metric In Clara
1 - euclidean; 2 - manhattan;
1

OK Cancel

RANDOM FOREST CLASSIFICATION



This function performs an unsupervised raster classification with random forest.

General tab (main)

Enter the folder that contains the input rasters (in GeoTiff format). The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Choose the number of classes in which the map will be sorted.

Indicate the folder to saved result map.

Functor Editor - Random Forest

General Advanced

Input Folder
Folder with predictors raster files (variables) in geoTif format
C:/Predictors

Number Of Classes
Number of classes in classification
5

Output Random Forest
Output raster of Random Forest classification
C:/temp/output/result.tif

OK Cancel

Advanced tab

Choose the number of samples used to generate the random forest optimization.

Choose the number of trees that will be used in the classification by random forest.

Functor Editor - Random Forest

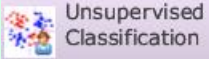
General Advanced

Sample Size In Random Forest
500

Number Of Trees
Number of trees in Random Forest
500

OK Cancel

UNSUPERVISED CLASSIFICATION



This function performs a unsupervised raster classification by three classifiers: K-means clustering; CLARA (Clustering for Large Applications) and random forest.

General tab (main)

Enter the folder that contains the input rasters (in GeoTiff format). The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Choose the number of classes in which the map will be sorted.

Choose if use the k-means classification.

Choose if use CLARA rating.

Choose if use the classification by random forest.

Enter the name of the raster (GeoTiff format) of the result that will be saved to the k-means classification.

Enter the name of the raster (GeoTiff format) of the result that will be saved to the CLARA classification.

Enter the name of the raster (GeoTiff format) of the result that will be saved to the classification by Random Forest.

UNSUPERVISED CLASSIFICATION

Advanced tab

Choose the number of interactions that will be used to search for the best solution rating for k-means clustering

Choose the number of random starts will be used to optimize the k-means clustering.

Choose the number of samples used to generate CALRA optimization.

Choose the number corresponding to the distance metric used by CLARA classifier.

Choose the number of samples used to generate the random forest optimization.

Choose the number of trees that will be used in the classification by random forest.

The screenshot shows the 'Functor Editor - Unsupervised Classification' dialog box with the 'Advanced' tab selected. The dialog contains several configuration options for unsupervised classification algorithms:

- IR Number Of Interactions**: Maximum number of interactions in k-means classification. Value: 1000.
- IR Start Random Sets**: Number of start random sets. Value: 10.
- IR Sample Size In Clara**: Value: 500.
- IR Distance Metric In Clara**: 1 - euclidean; 2 - manhattan. Value: 1.
- IR Sample Size In Random Forest**: Value: 500.
- IR Number Of Trees**: Number of trees in Random Forest. Value: 500.

At the bottom right, there are 'OK' and 'Cancel' buttons.

MINIMUM CONVEX HULL



This function generates a minimum convex polygon map through points of distribution of a species.

Table in csv format (comma separated columns). First column with the name of the species (sp), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

Specify a file in the shapefile (.SHP) format to serve as a mask (area in which will be held the interpolation).

Indicate the output folder.

Choose the cell size of the resulting map (interpolated). The value must be in the same unit of the coordinate system used.

Choose if save a csv file with the contents of the results, showing the area of minimum convex polygon for distribution for each species.

Functor Editor - Minimum Convex Hull

Input Occurrences
csv table with species and coordinates of localities (with columns: sp, x, y)
C:/data/Sp_data.csv

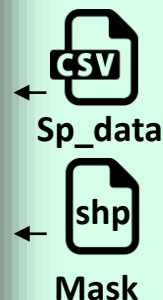
Input Mask
Shapefile (shp) of area of study
C:/limits/mask.shp

Output Folder
C:/temp/output

Cell Size
Cell size of output raster
0.05

☒ **Save Table**
Save Table with summary results in csv format
☒ Yes ☐ No Save Table

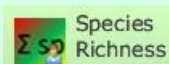
OK Cancel





ANALYSIS OF BIODIVERSITY

SPECIES RICHNESS INTERPOLATED



This function generates maps of species richness in hexagons and interpolated by three methods: spline, kriging and nearest neighbor. As a result are generated maps in raster format (GeoTiff) with the values interpolated from the species richness.

Oliveira U, et al. 2019. Modelling Highly Biodiverse Areas in Brazil. Scientific Reports 9:6355.

General tab (main)

Table in csv format (comma separated columns). First column with the name of the species (sp), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

Indicate the folder in which the files of results will be saved.

Specify a file in the shapefile (.SHP) format to serve as a mask (area for the interpolation).

Choose the size of the hexagon will be used as a sampling unit. The size must be in decimal degrees (approximately 100 km in Ecuador).

Choose whether to save the maps in hex format.

Choose whether it will be held the nearest neighbor interpolation.

Choose whether held splined interpolation.

Choose whether it will be held the interpolation by kriging.



SPECIES RICHNESS INTERPOLATED

Advanced tab

Choose the cell size of the resulting map. The value should be in decimal degrees.

Choose the minimum number of samples (in the sampling unit hexagonal) that will be considered in the analysis. The hexagons with values below the chosen will be discarded from the analysis.

Choice of smoothing interpolation factor for nearest neighbor.

Choose the smoothing factor by spline interpolation.

Choose smoothing factor interpolation by kriging.

Choose the corresponding numbers, the variogram model used on kriging.

Funcion Editor - Species Richness

General Advanced

IR Output Raster Resolution
Define resolution of raster cells in outputs
0.05

IR Minimum Number Of Samples
Minimum number of samples in hexagons
10

N Smooth Factor Of Nearest Neighbor
Number of neighboring pixels
8

N Smooth Factor Of Spline
Number of neighboring pixels in smooth
8

N Smooth Factor Of Kriging
Number of neighboring pixels in smooth
8

IR Model In Kriging Interpolation
Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4 - Matern
3

OK Cancel

SPECIES RICHNESS MODEL



This function predicts, by use predictors, the species richness through three models: GLM (generalized linear model), SAR (Spatial autoregressive model) and universal kriging. (adapted from: Oliveira U, et al. 2019. Modelling Highly Biodiverse Areas in Brazil. Scientific Reports 9:6355.)

General tab (main)

Table in csv format (comma separated columns). First column with the name of the species (sp), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

Specify a file in the shapefile (.SHP) format to serve as a mask (area for the interpolation).

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Indicate the folder in which the files of results will be saved.

Choose whether to save the maps in hex format.

Choose whether held splined interpolation.

Choose whether it will be held the nearest neighbor interpolation.

Choose whether it will be held the interpolation by kriging.

Choose whether the prediction is performed by GLM.

Choose whether the prediction is performed by SAR.

Choose whether it will be held by universal kriging prediction.

Choose the size of the hexagon will be used as a sampling unit. The size must be in decimal degrees (approximately 100 km in Ecuador).

Functor Editor - Srm

General Advanced

Input Occurrences
csv table with species and coordinates of localities (with columns: sp, x, y)
E:\BioDinamica_data_curso\Sp_data.csv

Input Mask
Shapefile (shp) with area of study
E:\BioDinamica_data_curso\Mask\Mask.shp

Predictor Variables
Folder with rasters of predictor variables in tif format
E:\BioDinamica_data_curso\Predictors

Output Folder
Folder of outputs
C:\temp

☒ **Save Hexagon NmDs**
Save hexagon NMDS raw values map?
☐ No ☐ Save Hexagon NmDs

☒ **Nearest Neighbor Interpolation**
Interpolate by nearest neighbor?
☐ No ☐ Nearest Neighbor Interpolation

☒ **Spline Interpolation**
Interpolate by Spline?
☐ No ☐ Spline Interpolation

☒ **Kriging Interpolation**
Interpolate by kriging?
☐ No ☐ Kriging Interpolation

☒ **Glm**
Run GLM prediction
☐ No ☐ Glm

☒ **Sar**
Run SAR prediction
☐ No ☐ Sar

☒ **Universal Kriging**
Run Universal Kriging prediction
☐ No ☐ Universal Kriging

Hexagon Size
Define size of hexagons (degree). Distance between centroid of hexagons
1

OK Cancel



Sp_data



Mask



Predictors

SPECIES RICHNESS MODEL

Advanced tab

Choose the cell size of the resulting map. The value should be in decimal degrees.

Choose the minimum number of samples (in the sampling unit hexagonal) that will be considered in the analysis. The hexagons with values below the chosen will be discarded from the analysis.

Choice of smoothing interpolation factor for nearest neighbor.

Choose the smoothing factor by spline interpolation.

Choose smoothing factor interpolation by kriging.

Choose the corresponding numbers, the variogram model used on kriging.

Choose the corresponding numbers, the distribution of errors that will be used in the GLM.

Choose the cell size (pixel size) used in sampling SAR analysis. This is not the VALUE of the FINAL SIZE of the PIXELS, is only used to generate the calculations. After that, the final map will be generated in the same resolution of the cells of the predictors.

Choose the corresponding numbers, the variogram model used in universal kriging.

Functor Editor - Srm

General Advanced

IR Cell Size

Cell size

0.05

IR Minimum Number Of Samples

Minimum number of samples in hexagons

10

N Shooth Factor Of Nearest Neighbor

Number of neighboring pixels

8

N Smooth Factor Of Spline

Number of neighboring pixels in smooth

8

N Smooth Factor Of Kriging

Number of neighboring pixels in smooth

8

IR Model In Kriging Interpolation

Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4 - Matern

3

IR Error Distribution In Function Gln

Choose error distribution: 1 - binomial; 2 - gaussian; 3 - Gamma; 4 - inverse gaussian; 5 - poisson; 6 - quasi; 7 - quasibinomial; 8 - quasipoisson;

2

IR Cell Size Of Analysis In Sar

Choose a value (cell size) for sampling the variables. Very small values (high resolution) can cause error.

0.5

IR Model In Universal Kriging

Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4 - Matern

1

OK Cancel

RESAMPLE OF SPECIES RICHNESS INTERPOLATED



This function generates maps of resampled species richness in hexagons and interpolated by three methods: spline, kriging and nearest neighbor. The resampling function to simulate a uniform sampling in the study area.

Oliveira U, et al. 2019. Modelling Highly Biodiverse Areas in Brazil. Scientific Reports 9:6355.

General tab (main)

Table in csv format (comma separated columns). First column with the name of the species (sp), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

Indicate the folder in which the files of results will be saved.

Specify a file in the shapefile (.SHP) format to serve as a mask (area for the interpolation).

Choose the number of times that resampling will be round to generate average values of wealth on uniform sampling simulation.

Choose the minimum number of samples to be used for resampling. NOTE: If this number is too high may have left few samples (hexagons) for examination, which could harm the interpolation.

Choose how many sub-samples will be accounted for in each round of sampling. Remember that this value must be less than the minimum number of samples (field above). It is desirable that this value does not exceed 50% of the minimum value of the samples.


Choose the size of the hexagon will be used as a sampling unit. The size must be in decimal degrees (approximately 100 km in Ecuador).

Choose whether to save the maps in hex format.

Choose whether it will be held the nearest neighbor interpolation.

Choose whether held splined interpolation.

Choose whether it will be held the interpolation by kriging

←  Sp_data

←  Mask

RESAMPLE OF SPECIES RICHNESS INTERPOLATED

Advanced tab

Choose the cell size of the resulting map. The value should be in decimal degrees.

Choice of smoothing interpolation factor for nearest neighbor.

Choose the smoothing factor by spline interpolation.

Choose smoothing factor interpolation by kriging.

Functor Editor - Resample Species Richness

General Advanced

IR Cell Size

Cell size of output raster

0.05

N Shooth Factor Of Nearest Neighbor

Number of neighboring pixels

8

N Smooth Factor Of Spline

Number of neighboring pixels in smooth

30

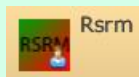
N Smooth Factor Of Kriging

Number of neighboring pixels in smooth

30

OK Cancel

RSRM - RESAMPLE OF SPECIES RICHNESS MODEL



This function predicts, by use predictors, the species richness resampled using three models: GLM (generalized linear model), SAR (Spatial autoregressive model) and universal kriging.

(adapted from: Oliveira U, et al. 2019. Modelling Highly Biodiverse Areas in Brazil. Scientific Reports 9:6355.)

General tab (main)

Table in csv format (comma separated columns). First column with the name of the species (sp), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

Specify a file in the shapefile (.SHP) format to serve as a mask (area for the interpolation).

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Indicate the folder in which the files of results will be saved.

Choose whether to save the maps in hex format.

Choose whether held splined interpolation.

Choose whether it will be held the nearest neighbor interpolation.

Choose whether it will be held the interpolation by kriging.

Choose whether the prediction is performed by GLM.

Choose whether the prediction is performed by SAR.

Choose whether it will be held by universal kriging prediction.

Choose the size of the hexagon will be used as a sampling unit. The size must be in decimal degrees (approximately 100 km in Ecuador).

Choose the number of times that resampling will be round to generate average values of wealth on uniform sampling simulation.

Choose the minimum number of samples to be used for resampling. NOTE: If this number is too high may have left few samples (hexagons) for examination, which could harm the interpolation.

Functor Editor - Rsrn

General Advanced

Input Occurrences
csv table with species and coordinates of localities (with columns: sp, x, y)
E:\Biodinamica_data_curso\Sp_data.csv

Input Mask
Shapefile (shp) with area of study
E:\Biodinamica_data_curso\Mask\Mask.shp

Predictor Variables
Folder with rasters of predictor variables in tif format
E:\Biodinamica_data_curso\Predictors

Output Folder
Folder of outputs
C:\temp

☒ **Save Hexagon NmDs**
Save hexagon NMDS raw values map?
☐ No ☐ Save Hexagon NmDs

☒ **Spline Interpolation**
Interpolate by Spline?
☐ No ☐ Spline Interpolation

☒ **Nearest Neighbor Interpolation**
Interpolate by nearest neighbor?
☐ No ☐ Nearest Neighbor Interpolation

☒ **Kriging Interpolation**
Interpolate by kriging?
☐ No ☐ Kriging Interpolation

☒ **Glm**
Run GLM prediction
☐ No ☐ Glm

☒ **Sar**
Run SAR prediction
☐ No ☐ Sar

☒ **Universal Kriging**
Run Universal Kriging prediction
☐ No ☐ Universal Kriging

Hexagon Size
Define size of hexagons (degree). Distance between centroid of hexagons
1

Number Of Resamples
Number of runs in resampling
1000

Minimum Number Of Samples
Minimum number of samples in hexagon
50

Size Of Samples In Resampling
Size of samples in each resampling round
10

OK Cancel



Sp_data



Mask



Predictors

Choose how many sub-samples will be accounted for in each round of sampling. Remember that this value must be less than the minimum number of samples (field above). It is desirable that this value does not exceed 50% of the minimum value of the samples.

RSRM - RESAMPLE OF SPECIES RICHNESS MODEL

Advanced tab

Choose the cell size of the resulting map. The value should be in decimal degrees.

Choose the corresponding numbers, the distribution of errors that will be used in the GLM.

Choose the cell size (pixel size) used in sampling SAR analysis. This is not the VALUE of the FINAL SIZE of the PIXELS, is only used to generate the calculations. After that, the final map will be generated in the same resolution of the cells of the predictors.

Choose the corresponding numbers, the variogram model used in universal kriging.

Functor Editor - Rsrn

General Advanced

IR Cell Size

Cell size

0.05

IR Error Distribution In Function Gln

Choose error distribution: 1 - binomial; 2 - gaussian; 3 - Gamma; 4 - inverse gaussian; 5 - poisson; 6 - quasi; 7 - quasibinomial; 8 - quasipoisson;

2

IR Cell Size Of Analysis Sar

Choose a value (cell size) for sampling the variables. Very small values (high resolution) can cause error.

0.5

IR Model In Universal Kriging

Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4 - Matern

1

OK Cancel

WEIGHT ENDEMISM INDEX



This function generates maps of endemism by index endemism weighing (WE) in hexagons and interpolated by three methods: spline, kriging and nearest neighbor.

Williams PH, Humphries CJ. 1994. Biodiversity, taxonomic relatedness, and endemism in conservation. Oxford: Oxford University Press.

General tab (main)

Table in csv format (comma separated columns). First column with the name of the species (sp), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

Indicate the folder in which the files of results will be saved.

Specify a file in the shapefile (.SHP) format to serve as a mask (area in which will be held the interpolation).

Choose the size of the hexagon will be used as a sampling unit. The size must be in decimal degrees (approximately 100 km in Ecuador).

Choose whether to save the maps in hex format.

Choose whether it will be held the nearest neighbor interpolation.

Choose whether it will be held by spline interpolation.

Choose whether it will be held the interpolation by kriging.

← Sp_data

← Mask

WEIGHT ENDEMISM INDEX

Advanced tab

Choose the cell size of the resulting map. The value should be in decimal degrees.

Choose the minimum number of samples (in the sampling unit hexagonal) that will be considered in the analysis. The hexagons with values below the chosen will be discarded from the analysis.

Choice of smoothing interpolation factor for nearest neighbor.

Choose the smoothing factor by spline interpolation.

Choose smoothing factor interpolation by kriging.

Choose the corresponding numbers, the variogram model used on kriging.

Functor Editor - Weight Endemism

General

Advanced

IR

Raster Resolution

Define resolution of raster cells

0.05

IR

Minimum Number Of Samples

Minimum number of samples in hexagon

10

N

Shooth Factor Of Nearest Neighbor

Number of neighboring pixels

8

N

Smooth Factor Of Spline

Number of neighboring pixels in smooth

8

N

Smooth Factor Of Kriging

Number of neighboring pixels in smooth

8

IR

Model In Kriging Interpolation

Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4 - Matern

3

OK

Cancel

WEM - WEIGHT ENDEMISM MODEL

This function predicts, by predictors, the weight index of endemism (WE) through three models: GLM (generalized linear model), SAR (Spatial autoregressive model) and universal kriging.

(adapted from: Williams PH, Humphries CJ. 1994. Biodiversity, taxonomic relatedness, and endemism in conservation. Oxford: Oxford University Press.)

General tab (main)

Table in csv format (comma separated columns). First column with the name of the species (sp), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

Specify a file in the shapefile (.SHP) format to serve as a mask (area in which will be held the interpolation).

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Indicate the folder in which the files of results will be saved.

Choose whether to save the maps in hex format.

Choose whether it will be held by spline interpolation.

Choose whether it will be held the nearest neighbor interpolation.

Choose whether it will be held the interpolation by kriging.

Choose whether the prediction is performed by GLM.

Choose whether the prediction is performed by SAR.

Choose whether it will be held by universal kriging prediction.

Choose the size of the hexagon will be used as a sampling unit. The size must be in decimal degrees (approximately 100 km in Ecuador).

Functor Editor - Wem

General Advanced

Input Occurrences
csv table with species and coordinates of localities (with columns: sp, x, y)
E:\BioDinamica_data_curso\Sp_data.csv

Input Mask
Shapefile (shp) with area of study
E:\BioDinamica_data_curso\Mask\Mask.shp

Predictor Variables
Folder with rasters of predictor variables in tif format
E:\BioDinamica_data_curso\Predictors

Output Folder
Folder of outputs
C:\temp

☒ **Save Hexagon NmDs**
Save hexagon NMDS raw values map?
Yes Save Hexagon NmDs

☒ **Spline Interpolation**
Interpolate by Spline?
No Spline Interpolation

☒ **Nearest Neighbor Interpolation**
Interpolate by nearest neighbor?
No Nearest Neighbor Interpolation

☒ **Kriging Interpolation**
Interpolate by kriging?
No Kriging Interpolation

☒ **GlM**
Run GLM prediction
No Glm

☒ **Sar**
Run SAR prediction
No Sar

☒ **Universal Kriging**
Run Universal Kriging prediction
No Universal Kriging

IR Hexagon Size
Define size of hexagons (degree). Distance between centroid of hexagons
1

OK Cancel



Sp_data



Mask



Predictors

WEM - WEIGHT ENDEMISM MODEL

Advanced tab

Choose the minimum number of samples (in the sampling unit hexagonal) that will be considered in the analysis. The hexagons with values below the chosen will be discarded from the analysis.

Choose the corresponding numbers, the variogram model used on kriging.

Choose the cell size of the resulting map. The value should be in decimal degrees.

Choose the corresponding numbers, the distribution of errors that will be used in the GLM.

Choose the corresponding numbers, the variogram model used in universal kriging.

Choose the cell size (pixel size) used in sampling SAR analysis. This is not the VALUE of the FINAL SIZE of the PIXELS, is only used to generate the calculations. After that, the final map will be generated in the same resolution of the cells of the predictors.

Functor Editor - Wem

General Advanced

IR Minimum Number Of Samples

Minimum number of samples in hexagon

10

IR Model In Kriging Interpolation

Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4 - Matern

3

IR Cell Size

Cell size

0.05

IR Error Distribution In Function Glm

Choose error distribution: 1 - binomial; 2 - gaussian; 3 - Gamma; 4 - inverse gaussian; 5 - poisson; 6 - quasi; 7 - quasibinomial; 8 - quasipoisson;

2

IR Model In Universal Kriging

Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4 - Matern

1

IR Cell Size Of Analysis Sar

Choose a value (cell size) for sampling the variables. Very small values (high resolution) can cause error.

0.5

OK Cancel

GIE - GEOGRAPHIC INTERPOLATION OF ENDEMISM



This function identifies areas of endemism through Geographical Interpolation of endemism (GIE). As a result are generated reports stating number of areas of endemism and species by area, plus, a map in raster format (GeoTiff).

Oliveira U, Brescovit AD, Santos AJ. 2015. Delimiting Areas of Endemism through Kernel Interpolation. PloS one 10:e0116673.

General tab (main)

Table in csv format (comma separated columns). First column with the name of the species (sp), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

Indicate the number of classes of GIE analysis. The classes should not contain a very small number of species (avoid a very large number of classes). On the other hand, a very small number of classes will bring together species with very distinctive scale distribution (this also should be avoided). However, if a large database, the effects of the number of classes is not significant (see supplementary material of the indicated bibliography).

Choose the size of the classes (in km). Separate the values with the "@" symbol. The number of values must be equal to the value of the number of classes (previous field) minus 1. The last class ends with the maximum value of gap in points of occurrence, so it is not necessary to include this value.

Indicate the folder in which the files of results will be saved.

Specify a file in the shapefile (.SHP) format to serve as a mask (area for the interpolation).

The screenshot shows the 'Functor Editor - Geographic Interpolation Of Endemism' dialog box with the 'General' tab selected. The 'Input Occurrences' section has a text field for 'csv table with species and coordinates of localities (with columns: sp, x, y)' containing 'C:/data/sp_data.csv'. The 'Number Of Classes' section has a text field for 'Number of classes of GIE analysis' containing '7'. The 'Value Of Classes' section has a text field for 'Maximum distance value of each class of analysis' containing '50@100@200@400@600@1000'. The 'Output Folder' section has a text field for 'C:/temp/output'. The 'Input Mask' section has a text field for 'Shapefile (shp) of area of study' containing 'C:/limits/mask.shp'. There are 'OK' and 'Cancel' buttons at the bottom right.



Sp_data



Mask

GIE - GEOGRAPHIC INTERPOLATION OF ENDEMISM

Advanced tab

Choose the minimum number of species which shall co-occurrence (synendemism) in an area to consider it an area of endemism.

Choose whether the consensus is generated with and without weighing of areas of endemism.

Indicate if you will be given more weight the areas of endemism have less area.

Choose whether to save pictures of areas of endemism.

Choose the cell size of the resulting map. The value should be in decimal degrees.

The screenshot shows the 'Funcion Editor - Geographic Interpolation Of Endemism' dialog box with the 'Advanced' tab selected. The dialog contains several settings:

- Minimum Number Of Sinendemism:** A text input field with the value '2'. Below it is the description 'Minimum number of endemic species of AoEs (sinendemism)'.
- Generate Two Consensus Map:** A checked checkbox. Below it is the text 'Generate Two consensus map (with, and without weight)?' and a button labeled 'Yes'.
- Use Weight In Consensus:** A checked checkbox. Below it is the text 'Give more weight to smaller classes (narrower endemism)' and a button labeled 'Yes'.
- Save Figures:** A checked checkbox. Below it is the text 'Save Figures' and a button labeled 'Yes'.
- Cell Size:** A text input field with the value '0.05'. Below it is the text 'Cell size of output raster'.

At the bottom right of the dialog are 'OK' and 'Cancel' buttons.

SCI – SPECIES COMPOSITION INTERPOLATION



This function is the leading standards of β -diversity (species composition) by means of hexagons and interpolation. Here are available three forms of spatial interpolation of the patterns of β -diversity: spline, kriging and nearest neighbor.

Oliveira U, Vasconcelos MF, Santos AJ. 2017. Biogeography of Amazon birds: rivers limit species composition, but not areas of endemism. Scientific Reports 7:2992.

General tab (main)

Table in csv format (comma separated columns). First column with the name of the species (sp), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

Indicate the folder in which the files of results will be saved.

Specify a file in the shapefile (.SHP) format to serve as a mask (area for the interpolation).

Choose the size of the hexagon will be used as a sampling unit. The size must be in decimal degrees (approximately 100 km in Ecuador).

Choose the corresponding numbers, the β -diversity index that will be used. 1 for Bray-Curtis and 2 for Jaccard.

Choose whether to save the maps in hex format.

Choose whether it will be held the nearest neighbor interpolation.

Choose whether held splined interpolation.

Choose whether it will be held the interpolation by kriging.

 Sp_data

 Mask



For that to be saved the pictures (view only), internet connection is needed

SCI – SPECIES COMPOSITION INTERPOLATION

Advanced tab

Choose whether to partition analysis of β -diversity at nesting and replacement. NOTE: this choice will make the analysis take triple the time to run.

Choose the cell size of the resulting map. The value should be in decimal degrees.

Choose the number of axes used in the conversion of Dissimilarity Matrix by NMDS. 3 axes is recommended, because above this value axes cannot be specialized in a map RGB.

Choose the number of search are performed rounds in NMDS.

Choose the minimum number of samples (in the sampling unit hexagonal) that will be considered in the analysis. The hexagons with values below the chosen will be discarded from the analysis.

Choice of smoothing interpolation factor for nearest neighbor.

Choose the smoothing factor by spline interpolation.

Choose the parameter of smoothing (Lambda) of splined interpolation.

Choose the corresponding numbers, the variogram model used on kriging.

Choose the number of "lags" used in the construction of the variogram.

Choose the parameter of smoothing interpolation by kriging.

Choose if the interpolated maps (for each interpolator) will be classified into discrete regions (bio-geographic regions). These regions are classified by three methods: k-means clustering, CLARA (Clustering for Large Applications), random forest.

Choose the number of classes in which the interpolated maps are classified. Note that ratings will be made with two classes to the value chosen. Choose many classes I hope more time because it will produce a larger number of classified maps.

Funcion Editor - Sci

General Advanced

☒ **Beta Diversity Partition Analysis**
Beta diversity partition analysis (Turnover and Nestedness)
☒ Beta Diversity Partition Analysis

IR Cell Size
Cell size of output raster
0.05

IR Number Of Axis
Define number of axis in NMDS analysis
3

IR Rounds Of Nmds Search
Maximum numbers of random starts in search
46000

IR Minimum Number Of Samples
Minimum number of samples in Hexagon
10

N Smooth Factor Of Nearest Neighbor
Number of neighboring pixels
8

N Smooth Factor Of Spline
Number of neighboring pixels in smooth
8

IR Spline Lambda
Smoothing parameter the ratio of error and process variance in spline interpolation
10

IR Model In Kriging Interpolation
Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4- Matern
3

IR Lags In Kriging Interpolation
Number of lags
2

N Smooth Factor Of Kriging
Number of neighboring pixels in smooth
8

☒ **Classify Nearest Neighbor**
Unsupervised Classification nearest neighbor interpolation?
☒ Classify Nearest Neighbor

N Number Of Classes Of Nearest Neighbor Interpolation
Number of classes
10

☒ **Classify Spline**
Unsupervised Classification of Spline interpolation?
☒ Classify Spline

N Number Of Classes Of Spline
Number of classes in K-means classification
10

☒ **Classify Kriging**
Unsupervised Classification of Kriging interpolation?
☒ Classify Kriging

N Number Of Classes Of Kriging
Number of classes in K-means classification
10

OK Cancel

GDM – GENERALIZED DISSIMILARITY MODEL



This function is the leading standards of β -diversity (species composition) by means of predictive variables. Also tests how the variables used to explain variation in species composition.

Ferrier S, Manion G, Elith J, Richardson K. 2007. Using generalized dissimilarity modelling to analyse and predict patterns of beta diversity in regional biodiversity assessment. Diversity and Distributions 13:252–264.

General tab (main)

Table in csv format (comma separated columns). First column with the name of the species (sp), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Specify a file in the shapefile (.SHP) format to serve as a mask (area for the interpolation).

Indicate the folder in which the files of results will be saved.

Choose whether to use hexagons as sampling units. In the case of data gaps and sampling differences, this option can reduce the effects of sampling. If you do not use this option, every point (location) will be considered as sampling unit.

Choose the size of the hexagon will be used as a sampling unit. The size must be in decimal degrees (approximately 100 km in Ecuador).

Functor Editor - Gdm

General **Advanced**

? Input Occurrences
csv with species and coordinates of localities (with columns: sp, x, y)
E:\BioDinamica_data\Sp_data.csv

Predictors
Folder with raster files of predictors (variables) in geoTif format
E:\BioDinamica_data\PCA_SA

? Input Mask
Shapefile (shp) of area of study
E:\BioDinamica_data\Mask\Mask.shp

Output Folder
Folder of outputs. The folder address can not display spaces (in folder names). Use addresses like: "C:/results"
E:\BioDinamica_Test\GDM

☒ **Hexagons As Sample Units**
Use hexagons as sample units to generate the species data table by location (recommended when data is sparse and with gaps).
Yes ☐ Hexagons As Sample Units

Hexagon Size
Define size of hexagons
1.5

OK Cancel

CSV
Sp_data

Predictors

shp
Mask



For that to be saved the pictures (view only), internet connection is needed

GDM – GENERALIZED DISSIMILARITY MODEL

Advanced tab

Choose this option to generate a scenario cast in another scenario (such as future or past).

Choose the minimum number of samples (in the sampling unit hexagonal) that will be considered in the analysis. The hexagons with values below the chosen will be discarded from the analysis.

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors of projection scenarios. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. The rasters should be appointed in the same manner as were named the rasters predictors.

Choose whether the geographical distances will be used as predictors.

Choose whether the map resulting from the GDM will be classified into discrete regions (bio-geographic regions). These regions are classified by three methods: k-means clustering, CLARA (Clustering for Large Applications), random forest.

Choose the number of classes that will be used in the classification.

Choose spline values (variable ratio curves with the dissimilarity) will be determined by the user or will be determined automatically.

Choose the value of I-which will be used in spline curves of relationship of the variables. This value should never be less than the 3.

Functor Editor - Gdm

General Advanced

☒ **Project In Another Scenario**
Project GDM in another scenario (future or past)
☐ No ☐ Project In Another Scenario

Minimum Number Of Samples
Minimum number of samples in hexagon mode
1

Folder Scenarios Raster
Folder with rasters for project in another scenario. The rasters should be named in the same way of predictors.
E:/TEMP

☒ **Use Geographical Distances**
Use geographical distances as predictors
☒ Yes ☐ Use Geographical Distances

☒ **Classify Gdm**
Classify areas in GDM
☒ Yes ☐ Classify Gdm

Number Of Classes
Number of classes in K-means classification
10

☒ **Define Spline Values**
Enter manually with the spline values used.
☒ Yes ☐ Define Spline Values

Value Of Ispline
Value of I-spline. Enter the value. The value should never be less than 3.
3

OK Cancel

Scenario Predictors

SAMPLING EFFORT



Sampling Effort

This function interpolates spatially points of occurrence (samples) to generate a map of sampling effort using the interpolation kernel.

Oliveira U, et al. 2019. Modelling Highly Biodiverse Areas in Brazil. Scientific Reports 9:6355.

General tab (main)

Table in csv format (comma separated columns). First column with x coordinates (longitude) and the second column with coordinates y (latitude). The columns must be named: dependent on x, y, written with lowercase letters.

Specify a file in the shapefile (.SHP) format to serve as a mask (area for the interpolation).

Indicate the folder in which the files of results will be saved.

Choose the search radius (area of influence) of sampling. The value must be established in meters.

Functor Editor - Sampling Effort

General Advanced

? **Points Of Sampling**
Points of sampling in csv format with two columns (x,y) in decimal degrees
C:/data/XY_data.csv

? **Input Mask**
Shapefile (shp) of area of study
C:/limits/mask.shp

Output Folder
C:/temp/output

Area Of Influence Of Sampling
Search radius of kernel density analysis (meters)
100000

OK Cancel



XY_data



Mask

Advanced tab

Choose the cell size of the resulting map. The value should be in decimal degrees.

Functor Editor - Sampling Effort

General Advanced

Cell Size
Cell size of output raster
0.05

OK Cancel

SDM – SPECIES DISTRIBUTION MODEL



This function generates species distribution models (SDM) through various algorithms. Suitability maps are generated, maps and reports with the predictive capacity of the model tests. In this function it is possible to model a large set of species at once through the table containing the species.

Elith J, Leathwick JR. 2009. Species Distribution Models: Ecological Explanation and Prediction Across Space and Time. Annual Review of Ecology, Evolution, and Systematics 40:677–697.

Table in csv format (comma separated columns).

For data that does not FEATURE the ABSENCE INFORMATION:

The first column with the name of the species (sp), the second column with the x-coordinates (longitude) and third column the coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

For data that show the information of ABSENCE:

The first column with the name of the species (sp), the second column (presence) with values 0 or 1 to indicate whether the given occurrence is corresponding to the presence or absence, the third column with the x-coordinates (longitude) and fourth column coordinates y (latitude). The columns must be named as: sp, presence, x, y, written with lowercase letters.

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Indicate the folder in which the files of results will be saved.

Choose the corresponding numbers, which the given type of absence that will be used in the analysis: true, pseudoabsences or pseudoabsences absences based on evidence.

General tab (main)

Funcion Editor - Sdm

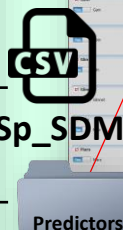
General | Advanced

Input Occurrences
csv table with species and coordinates of localities (with columns: sp, x, y for pseudoabsences, and sp,presence, x, y for true absences). In the case of true absences, the presence column should be binary indicating the presence or absence of the species.
E:\BioDinamica_data\Sp_SDM.csv

Predictors
Folder with predictors raster files (variables) in geoTiff format
E:\BioDinamica_data\Predictors

Output Folder
E:\BioDinamica_Test\SDM

Choose Absence Format
Choose an absence entry format in the model. 1 - true absences; 2 - pseudoabsences; 3 - pseudoabsences based on sampling evidences
2



SDM – SPECIES DISTRIBUTION MODEL

General tab (main)

Select which algorithms will be used in the prediction of the distribution of species.

Enter the location in which you will find the file "JAR" program Maxent. If you do not have the program, download the address:

https://biodiversityinformatics.amnh.org/open_source/maxent/

The screenshot displays the Maxent software interface, specifically the 'General' tab. The interface is divided into two main sections. The top section lists various machine learning algorithms for species distribution modeling, each with a checked checkbox and a 'Yes' button. The algorithms listed are: Bioclim, Brt, Cart, Gam, Gbm, Glm, Glnet, Mda, Mars, Rpart, Maxlike, Maxent, Maxent Jar File, Rf, and Svm. The bottom section is for the 'Maxent Jar File' and contains a text input field with the path 'C:/Maxent/maxent.jar' and a file selection icon. A red box highlights the right side of the interface, showing a list of variables and their corresponding coefficients. Arrows from the text boxes point to the 'Yes' buttons for the algorithms and the 'Maxent Jar File' input field.

Algorithm	Selected
Bioclim	Yes
Brt	Yes
Cart	Yes
Gam	Yes
Gbm	Yes
Glm	Yes
Glnet	Yes
Mda	Yes
Mars	Yes
Rpart	Yes
Maxlike	Yes
Maxent	Yes
Maxent Jar File	C:/Maxent/maxent.jar
Rf	Yes
Svm	Yes

SDM – SPECIES DISTRIBUTION MODEL

Advanced tab

Choose whether to use a custom mask for each species modeled to generate the pseudo-absences. This mask is constructed through a buffer around the points of occurrence of the species. This prevents are generated pseudo-absences in very distant and with very different conditions from which the species occurs (which can damage prediction model).

Choose the buffer distance (in meters) for the case of the choice of custom mask (previous option).

Percentage of data that will be used to generate the model, the rest of the data will be used for the calculation of the statistics of the model validation.

Choose the buffer distance (in meters) that will be used as an area in which there will be drawn pseudo-absences. This function applies only in the case of use of pseudo-absences.

Choose the number of points that will be drawn as pseudo-absences. This function only applies in the case of the use of pseudo-absences.

Choose the csv file (table) that contains the sampling points used to generate evidence-based pseudo-absences. In this choice, these points will generate a map of sampling, the evidence-based pseudo-absences will only be drawn in the places best sampled without samples of the species presence (sites with more evidence that there is a lack true). This function applies only in the case of the use of evidence-based pseudo-absences.

Choose the distance from the area of influence of the kernel used to estimate sampling, in the case of the use of evidence-based pseudo-absences.

General

Advanced

Use Custom Mask

Use a custom mask for each species. This mask is constructed by a buffer in the minimum convex polygon of the species occurrence points. This mask will be used for the select pseudo-absences.

No Use Custom Mask

Buffer In Custom Mask

Buffer distance (meters) in custom mask for pseudoabsences

100000

Percentage Of Samples To Training Model

Percentage of the data used to train the model. The rest of the data will be used to test it

60

Buffer Size

Buffer size (in meters) for sampling pseudoabsences

10000

Number Of Pseudoabsences

Number of pseudoabsences in sampling areas

100

Sampling Points

Csv filename of sampling points to pseudoabsences based on sampling evidences

C:/

Search Radius In Sampling Effort

Search radius in kernel of sampling effort in pseudoabsences based in sampling evidence

80000

Use Custom Mask

Use a custom mask for each species. This mask is constructed by a buffer in the minimum convex polygon of the species occurrence points. This mask will be used for the select pseudo-absences.

Use Custom Mask

Buffer In Custom Mask

Buffer distance (meters) in custom mask for pseudoabsences

100000

Percentage Of Samples To Training Model

Percentage of the data used to train the model. The rest of the data will be used to test it

60

Buffer Size

Buffer size (in meters) for sampling pseudoabsences

10000

Number Of Pseudoabsences

Number of pseudoabsences in sampling areas

100

Sampling Points

Csv filename of sampling points to pseudoabsences based on sampling evidences

C:/

Search Radius In Sampling Effort

Search radius in kernel of sampling effort in pseudoabsences based in sampling evidence

80000

SDM – SPECIES DISTRIBUTION MODEL

Advanced tab

Choose whether SDM projection will be held in another scenario.

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors of projection scenarios. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. The rasters should be appointed in the same manner as were named the rasters predictors.

For details about the settings of the Maxent view the bibliography about the algorithms in:
https://biodiversityinformatics.amnh.org/open_source/maxent/

Choose the number of samples used to generate the random forest optimization.

Maxent model options

Scenario Predictors

The screenshot displays the 'Advanced' tab of the SDM software interface. It is divided into two main sections: 'Maxent model options' and 'Scenario Predictors'.

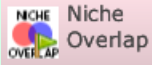
Maxent model options: This section contains various checkboxes and input fields for configuring the Maxent algorithm. Key options include:

- Project In Another Scenario:** A checkbox with a dropdown menu set to 'No'.
- Folder Scenarios Raster:** A text input field containing 'C:/Scenario_Predictors'.
- Calculate Area Of Distributions:** A checkbox with a dropdown menu set to 'No'.
- Maxent Linear Features:** A checkbox with a dropdown menu set to 'Yes'.
- Maxent Quadratic Features:** A checkbox with a dropdown menu set to 'Yes'.
- Maxent Product Features:** A checkbox with a dropdown menu set to 'Yes'.
- Maxent Threshold Features:** A checkbox with a dropdown menu set to 'Yes'.
- Maxent Hinge Features:** A checkbox with a dropdown menu set to 'Yes'.
- Maxent Maximum Iteration Done:** An input field with the value '200'.
- Maxent Minimum Number Of Samples For Quadratic ...:** An input field with the value '10'.
- Maxent Minimum Number Of Samples For Product A...:** An input field with the value '80'.
- Maxent Minimum Number Of Samples For Hinge Feat...:** An input field with the value '15'.
- Maxent Beta Linear Quadratic And Product:** An input field with the value '-1'.
- Maxent Beta Threshold:** An input field with the value '-1'.
- Maxent Beta Categorical:** An input field with the value '-1'.
- Maxent Beta Hinge:** An input field with the value '-1'.
- Maxent Beta Multiplier:** An input field with the value '1'.
- Maxent Default Prevalence:** An input field with the value '0.5'.
- Random Forest Number Of Trees:** An input field with the value '1000'.

Scenario Predictors: This section contains a list of predictors and their corresponding values. It includes a 'Use Custom Mask' checkbox and a 'Training Model' dropdown menu. The list of predictors includes:

- Number Of Pseudoreplicates
- Number Of Pseudoreplicates In Sampling Error
- Sampling Points
- Search Radius In Sampling Effort
- Project In Another Scenario
- Folder Scenarios Raster
- Calculate Area Of Distributions
- Maxent Linear Features
- Maxent Quadratic Features
- Maxent Product Features
- Maxent Threshold Features
- Maxent Hinge Features
- Maxent Maximum Iteration Done
- Maxent Minimum Number Of Samples For Quadratic A...
- Maxent Minimum Number Of Samples For Product A...
- Maxent Minimum Number Of Samples For Hinge Feat...
- Maxent Beta Linear Quadratic And Product
- Maxent Beta Threshold
- Maxent Beta Categorical
- Maxent Beta Hinge
- Maxent Beta Multiplier
- Maxent Default Prevalence
- Random Forest Number Of Trees

NICHE OVERLAP



This function computes the overlap between the predicted species niches through the indices I and Warwn D et al. (2009).

Broennimann O, et al. 2012. Measuring ecological niche overlap from occurrence and spatial environmental. :481–497.

Folder with species distribution models (do not use binary files). The files must be in GeoTiff format.

Csv table name that will be saved with the results.

Functor Editor - Niche Overlap

Folder

Folder with SDM tif files

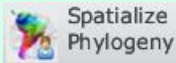
Filename

Name and path of table file to be written. File format is automatically selected based on the filename extension. If path is not specified, file location is the same of model script.

table.csv

OK Cancel

SPATIALIZE PHYLOGENY



This function plot on the map a phylogenetic tree by hexagons and interpolation. Here are available three forms of spatial interpolation: spline, kriging and nearest neighbor.

General tab (main)

Table in csv format (comma separated columns). Being the first column with the name of the species (sp), the second column with the x-coordinates (longitude) and third column the coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

A phylogenetic tree of the form tre. This tree should display as corresponding to the names Terminal taxa of csv table (field above). However, there is no need for full agreement between the two files, since the tree is pruned by the table and vice versa.

Specify a file in the shapefile (.SHP) format to serve as a mask (area for the interpolation).

Indicate the folder in which the files of results will be saved.

Indicate whether the phylogenetic tree used (field above) displays the information of the branch lengths. If not, will be considered every branch with length equal to 1.

Choose whether it will be held the nearest neighbor interpolation.

Choose whether it will be held by spline interpolation.

Choose whether it will be held the interpolation by kriging.

Functor Editor - Spatialize Phylogeny

General Advanced

Input Occurrences
csv table with species and coordinates of localities (with columns: sp, x, y)
E:\BioDinamica_data\Sp_data.csv

Input Phylogenetic Tree
Input filogenetic tree in format ".tre"
E:\BioDinamica_data\Phylo_data.tre

Input Mask
Shapefile (shp) of area of study
E:\BioDinamica_data\Mask\Mask.shp

Output Folder
E:\BioDinamica_Test\Phylogeny

☒ **The Tree Has Branch Lengths**
The file of phylogenetic tree has branch lengths?
☒ Yes ☐ The Tree Has Branch Lengths

☒ **Nearest Neighbor Interpolation**
Interpolate by NNI?
☒ Yes ☐ Nearest Neighbor Interpolation

☒ **Spline Interpolation**
Interpolate by Spline?
☒ Yes ☐ Spline Interpolation

☒ **Kriging Interpolation**
Interpolate by kriging?
☒ Yes ☐ Kriging Interpolation

OK Cancel

Spatialize phylo



Mask



For that to be saved the pictures (view only), internet connection is needed

SPATIALIZE PHYLOGENY

Advanced tab

Choose the number of search are performed rounds in NMDS.

Choose the number of axes used in the conversion of Dissimilarity Matrix by NMDS. 3 axes is recommended, more axes may not be specialized in a map RGB.

Choose the cell size of the resulting map. The value should be in decimal degrees.

Choose the parameter of smoothing (Lambda) of splined interpolation.

Choice of smoothing interpolation factor for nearest neighbor.

Choose the smoothing factor by spline interpolation.

Choose the parameter of smoothing interpolation by kriging.

Choose the corresponding numbers, the variogram model used on kriging.

Choose if the interpolated maps (for each interpolator) will be classified into discrete regions (bio-geographic regions). These regions are classified by three methods: k-means clustering, CLARA (Clustering for Large Applications), random forest.

Choose the number of classes in which the interpolated maps are classified. Note that ratings will be made with two classes to the value chosen. Choose many classes I hope more time because it will produce a larger number of classified maps.

Functor Editor - Spatialize Phylogeny

General Advanced

IR Rounds Of Nmds Search

Maximum numbers of random starts in search

10000

IR Number Of Axis

Define number of axis in NMDS analysis

3

IR Cell Size

Cell size of output raster

0.05

IR Spline Lambda

Smoothing parameter the ratio of error and process variance in spline interpolation

40

N Shooth Factor Of Nearest Neighbor

Number of neighboring pixels

8

N Smooth Factor Of Spline

Number of neighboring pixels in smooth

8

N Smooth Factor Of Kriging

Number of neighboring pixels in smooth

8

IR Model In Kriging Interpolation

Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4 - Matern

3

☒ **Classify Nearest Neighbor**

Unsupervised Classification by NNI interpolation?

☒ Yes ☐ Classify Nearest Neighbor

N Number Of Classes Of Nearest Neighbor

Number of classes

10

☒ **Classify Spline**

Unsupervised Classification by Spline interpolation?

☒ Yes ☐ Classify Spline

N Number Of Classes Of Spline

Number of classes

10

☒ **Classify Kriging**

Unsupervised Classification by Kriging interpolation?

☒ Yes ☐ Classify Kriging

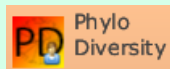
N Number Of Classes Of Kriging

Number of classes

10

OK Cancel

PD - PHYLOGENETIC DIVERSITY



This function generates maps of phylogenetic diversity in hexagons and interpolated maps through three methods: spline, kriging and nearest neighbor.

Oliveira U, et al. 2019. Modelling Highly Biodiverse Areas in Brazil. Scientific Reports 9:6355

General tab (main)

Table in csv format (comma separated columns). First column with the name of the species (sp), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

A phylogenetic tree of the form tre. This tree should display as corresponding to the names Terminal taxa of csv table (field above). However, there is no need for full agreement between the two files, since the tree is pruned by the table and vice versa.

Specify a file in the shapefile (.SHP) format to serve as a mask (area for the interpolation).

Indicate the folder in which the files of results will be saved.

Indicate whether the phylogenetic tree used (field above) displays the information of the branch lengths. If not, will be considered every branch with length equal to 1.

Choose the size of the hexagon will be used as a sampling unit. The size must be in decimal degrees (approximately 100 km in Ecuador).

Choose whether to save the maps in hex format.

Choose whether it will be held by spline interpolation.

Choose whether it will be held the nearest neighbor interpolation.

Choose whether it will be held the interpolation by kriging.

Functor Editor - Phylo Diversity

General Advanced

Input Occurrences
csv table with species and coordinates of localities (with columns: sp, x, y)
E:\Biodinamica_data\Sp_data.csv

Input Phylogenetic Tree
Input filogenetic tree in format ".tre"
E:\Biodinamica_data\Phylo_data.tre

Input Mask
Shapefile (.shp) of area of study
E:\Biodinamica_data\Mask\Mask.shp

Output Folder
E:\Biodinamica_Test\PD

☒ **The Tree Has Branch Lengths**
The file of phylogenetic tree has branch lengths?
Yes ☐ The Tree Has Branch Lengths

☒ **Save Hexagon Map**
Save hexagon with raw values map?
Yes ☐ Save Hexagon Map

Hexagon Size
1.5

☒ **Nearest Neighbor Interpolation**
Interpolate by nearest neighbor?
Yes ☐ Nearest Neighbor Interpolation

☒ **Spline Interpolation**
Interpolate by Spline?
Yes ☐ Spline Interpolation

☒ **Kriging Interpolation**
Interpolate by kriging?
Yes ☐ Kriging Interpolation

OK Cancel



Sp_data



Phylo_data



Mask

PD - PHYLOGENETIC DIVERSITY

Advanced tab

Choice of smoothing interpolation factor for nearest neighbor.

Choose the smoothing factor by spline interpolation.

Choose smoothing factor interpolation by kriging.

Choose the cell size of the resulting map. The value should be in decimal degrees.

Choose the minimum number of samples (in the sampling unit hexagonal) that will be considered in the analysis. The hexagons with values below the chosen will be discarded from the analysis.

Choose the corresponding numbers, the variogram model used on kriging.

Functor Editor - Phylo Diversity

General Advanced

N Shooth Factor Of Nearest Neighbor

Number of neighboring pixels

8

N Smooth Factor Of Spline

Number of neighboring pixels in smooth

8

N Smooth Factor Of Kriging

Number of neighboring pixels in smooth

8

IR Cell Size

Cell size of output raster

0.05

IR Minimum Number Of Sables

Minimum number of samples in hexagon

10

IR Model In Kriging Interpolation

Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4 - Matern

3

OK Cancel

PDM - PHYLOGENETIC DIVERSITY MODEL



This function predicts, phylogenetic diversity through three models: GLM (generalized linear model), SAR (Spatial autoregressive model) and universal kriging.

Adapted from: Oliveira U, et al. 2019. Modelling Highly Biodiverse Areas in Brazil. Scientific Reports 9:6355

General tab (main)

Table in csv format (comma separated columns). First column with the name of the species (sp), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

A phylogenetic tree of the form tre. This tree should display as corresponding to the names Terminal taxa of csv table (field above). However, there is no need for full agreement between the two files, since the tree is pruned by the table and vice versa.

Indicate whether the phylogenetic tree used (field above) displays the information of the branch lengths. If not, will be considered every branch with length equal to 1.

Specify a file in the shapefile (.SHP) format to serve as a mask (area for the interpolation).

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Indicate the folder in which the files of results will be saved.

Choose whether to save the maps in hex format.

Choose whether it will be held the nearest neighbor interpolation.

Choose whether it will be held by spline interpolation.

Choose whether it will be held the interpolation by kriging.

Choose whether the prediction is performed by GLM.

Choose whether the prediction is performed by SAR.

Choose whether it will be held by universal kriging prediction.

Choose the size of the hexagon will be used as a sampling unit. The size must be in decimal degrees (approximately 100 km in Ecuador).

Function Editor - Pdm

General Advanced

Input Occurrences
csv table with species and coordinates of localities (with columns: sp, x, y)
E:\BioDinamica_data_curso\Sp_data.csv

Input Phylogenetic Tree
Input filogenetic tree in format ".tre"
E:\BioDinamica_data_curso\Phylo_data.tre

☒ **The Tree Has Branch Lengths**
The file of phylogenetic tree has branch lengths?
The Tree Has Branch Lengths

Input Mask
Shapefile (shp) with area of study
E:\BioDinamica_data_curso\Mask\Mask.shp

Predictor Variables
Folder with rasters of predictor variables in tif format
E:\BioDinamica_data_curso\Predictors

Output Folder
Folder of outputs
E:\TEMP

☒ **Save Hexagon Map**
Save hexagon with raw values map?
No Save Hexagon Map

☒ **Nearest Neighbor Interpolation**
Interpolate by nearest neighbor?
No Nearest Neighbor Interpolation

☒ **Spline Interpolation**
Interpolate by Spline?
No Spline Interpolation

☒ **Kriging Interpolation**
Interpolate by kriging?
No Kriging Interpolation

☒ **Sar**
Run SAR prediction
No Sar

☒ **Glm**
Run GLM prediction
No Glm

☒ **Universal Kriging**
Run Universal Kriging prediction
No Universal Kriging

IR Hexagon Size
Define size of hexagons (degree). Distance between centroid of hexagons
1

OK Cancel



Sp_data



Phylo_data



Mask



Predictors

PDM - PHYLOGENETIC DIVERSITY MODEL

Advanced tab

Choose the cell size of the resulting map. The value should be in decimal degrees.

Choose the minimum number of samples (in the sampling unit hexagonal) that will be considered in the analysis. The hexagons with values below the chosen will be discarded from the analysis.

Choice of smoothing interpolation factor for nearest neighbor.

Choose the smoothing factor by spline interpolation.

Choose smoothing factor interpolation by kriging.

Choose the corresponding numbers, the variogram model used on kriging.

Choose the cell size (pixel size) used in sampling SAR analysis. This is not the VALUE of the FINAL SIZE of the PIXELS, is only used to generate the calculations. After that, the final map will be generated in the same resolution of the cells of the predictors.

Choose the corresponding numbers, the distribution of errors that will be used in the GLM.

Choose the corresponding numbers, the variogram model used in universal kriging.

Functor Editor - Pdm

General Advanced

IR Cell Size

Cell size of output

0.05

N Shooth Factor Of Nearest Neighbor

Number of neighboring pixels

8

N Smooth Factor Of Spline

Number of neighboring pixels in smooth

8

N Smooth Factor Of Kriging

Number of neighboring pixels in smooth

8

IR Minimum Number Of Sambles

Minimum number of samples in hexagon

10

IR Model In Kriging Interpolation

Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4 - Matern

3

IR Cell Size Of Analysis In Sar

Choose a value (cell size) for sampling the variables. Very small values (high resolution) can cause error.

0.5

IR Error Distribution In Function Glm

Choose error distribution: 1 - binomial; 2 - gaussian; 3 - Gamma; 4 - inverse gaussian; 5 - poisson; 6 - quasi; 7 - quasibinomial; 8 - quasipoisson;

2

IR Model In Universal Kriging

Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4 - Matern

1

OK Cancel

PE - PHYLOGENETIC ENDEMISM



This function generates maps of phylogenetic endemism by phylogenetic weight endemism index (PE) in hexagons and interpolated maps by three methods: spline, kriging and nearest neighbor.

Rosauer D, Laffan SW, Crisp MD, Donnellan SC, Cook LG. 2009. Phylogenetic endemism: a new approach for identifying geographical concentrations of evolutionary history. *Molecular Ecology* 18:4061–4072

General tab (main)

Table in csv format (comma separated columns). First column with the name of the species (sp), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

A phylogenetic tree of the form tre. This tree should display as corresponding to the names Terminal taxa of csv table (field above). However, there is no need for full agreement between the two files, since the tree is pruned by the table and vice versa.

Specify a file in the shapefile (.SHP) format to serve as a mask (area for the interpolation).

Indicate the folder in which the files of results will be saved.

Choose the size of the hexagon will be used as a sampling unit. The size must be in decimal degrees (approximately 100 km in Ecuador).

Indicate whether the phylogenetic tree used (field above) displays the information of the branch lengths. If not, will be considered every branch with length equal to 1.

Choose whether to save the maps in hex format.

Choose whether it will be held by spline interpolation.

Choose whether it will be held the nearest neighbor interpolation.

Choose whether it will be held the interpolation by kriging.

Functor Editor - Phylo Endemism

General Advanced

Input Occurrences
csv table with species and coordinates of localities (with columns: sp, x, y)
E:\BioDinamica_data\Sp_data.csv

Input Phylogenetic Tree
Input filogenetic tree in format ".tre"
E:\BioDinamica_data\Phylo_data.tre

Input Mask
Shapefile (shp) of area of study
E:\BioDinamica_data\Mask\Mask.shp

Output Folder
E:\BioDinamica_Test\PE

Hexagon Size
Define size of hexagons
1.5

☒ **The Tree Has Branch Lengths**
The file of phylogenetic tree has branch lengths?
Yes The Tree Has Branch Lengths

☒ **Save Hexagon Nmds**
Save hexagon NMDS raw values map?
Yes Save Hexagon Nmds

☒ **Spline Interpolation**
Interpolate by Spline?
Yes Spline Interpolation

☒ **Nearest Neighbor Interpolation**
Interpolate by nearest neighbor?
Yes Nearest Neighbor Interpolation

☒ **Kriging Interpolation**
Interpolate by kriging?
Yes Kriging Interpolation

OK Cancel



Sp_data



Phylo_data



Mask

PE - PHYLOGENETIC ENDEMISM

Advanced tab

Choose the cell size of the resulting map. The value should be in decimal degrees.

Choose the minimum number of samples (in the sampling unit hexagonal) that will be considered in the analysis. The hexagons with values below the chosen will be discarded from the analysis.

Choice of smoothing interpolation factor for nearest neighbor.

Choose the smoothing factor by spline interpolation.

Choose smoothing factor interpolation by kriging.

Choose the corresponding numbers, the variogram model used on kriging.

Functor Editor - Phylo Endemism

General Advanced

IR Cell Size

Cell size of output raster

0.05

IR Minimum Number Of Samples

Minimum number of samples in hexagon

10

N Shooth Factor Of Nearest Neighbor

Number of neighboring pixels

8

N Smooth Factor Of Spline

Number of neighboring pixels in smooth

8

N Smooth Factor Of Kriging

Number of neighboring pixels in smooth

8

IR Model In Kriging Interpolation

Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4 - Matern

3

OK Cancel

PEM - PHYLOGENETIC ENDEMISM MODEL



This function predicts the phylogenetic endemism by phylogenetic weigh endemism index (PE) through three models: GLM (generalized linear model), SAR (Spatial autoregressive model) and universal kriging.

Adapted from: Rosauer D, Laffan SW, Crisp MD, Donnellan SC, Cook LG. 2009. Phylogenetic endemism: a new approach for identifying geographical concentrations of evolutionary history. *Molecular Ecology* 18:4061–4072

General tab (main)

Table in csv format (comma separated columns). First column with the name of the species (sp), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

A phylogenetic tree of the form tre. This tree should display as corresponding to the names Terminal taxa of csv table (field above). However, there is no need for full agreement between the two files, since the tree is pruned by the table and vice versa.

Indicate whether the phylogenetic tree used (field above) displays the information of the branch lengths. If not, will be considered every branch with length equal to 1.

Specify a file in the shapefile (.SHP) format to serve as a mask (area for the interpolation).

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Indicate the folder in which the files of results will be saved.

Choose whether to save the maps in hex format.

Choose whether it will be held by spline interpolation.

Choose whether it will be held the nearest neighbor interpolation.

Choose whether it will be held the interpolation by kriging.

Choose whether the prediction is performed by GLM.

Choose whether the prediction is performed by SAR.

Choose whether it will be held by universal kriging prediction.

Choose the size of the hexagon will be used as a sampling unit. The size must be in decimal degrees (approximately 100 km in Ecuador).

Functor Editor - Pem

General Advanced

Input Occurrences
csv table with species and coordinates of localities (with columns: sp, x, y)
E:\BioDinamica_data_curso\Sp_data.csv

Input Phylogenetic Tree
Input filogenetic tree in format ".tre"
E:\BioDinamica_data_curso\Phylo_data.tre

☒ **The Tree Has Branch Lengths**
The file of phylogenetic tree has branch lengths?
☒ Yes ☐ No The Tree Has Branch Lengths

Input Mask
Shapefile (.shp) with area of study
E:\BioDinamica_data_curso\Mask\Mask.shp

Predictor Variables
Folder with rasters of predictor variables in tif format
E:\BioDinamica_data_curso\Predictors

Output Folder
Folder of outputs
E:\TEMP

☒ **Save Hexagon NmDs**
Save hexagon NMDS raw values map?
☒ Yes ☐ No Save Hexagon NmDs

☒ **Spline Interpolation**
Interpolate by Spline?
☐ No ☒ Spline Interpolation

☒ **Nearest Neighbor Interpolation**
Interpolate by nearest neighbor?
☐ No ☒ Nearest Neighbor Interpolation

☒ **Kriging Interpolation**
Interpolate by kriging?
☐ No ☒ Kriging Interpolation

☒ **Glm**
Run GLM prediction
☐ No ☒ Glm

☒ **Sar**
Run SAR prediction
☐ No ☒ Sar

☒ **Universal Kriging**
Run Universal Kriging prediction
☐ No ☒ Universal Kriging

Hexagon Size
Define size of hexagons (degree). Distance between centroid of hexagons
1

OK Cancel



Sp_data



Phylo_data



Mask



Predictors

PEM - PHYLOGENETIC ENDEMISM MODEL

Advanced tab

Choose the cell size of the resulting map. The value should be in decimal degrees.

Choose the minimum number of samples (in the sampling unit hexagonal) that will be considered in the analysis. The hexagons with values below the chosen will be discarded from the analysis.

Choice of smoothing interpolation factor for nearest neighbor.

Choose the smoothing factor by spline interpolation.

Choose smoothing factor interpolation by kriging.

Choose the corresponding numbers, the variogram model used on kriging.

Choose the cell size (pixel size) used in sampling SAR analysis. This is not the VALUE of the FINAL SIZE of the PIXELS, is only used to generate the calculations. After that, the final map will be generated in the same resolution of the cells of the predictors.

Choose the corresponding numbers, the distribution of errors that will be used in the GLM.

Choose the corresponding numbers, the variogram model used in universal kriging.

Functor Editor - Pem

General Advanced

IR Cell Size

Cell size

0.05

IR Minimum Number Of Samples

Minimum number of samples in hexagon

10

N Shooth Factor Of Nearest Neighbor

Number of neighboring pixels

8

N Smooth Factor Of Spline

Number of neighboring pixels in smooth

8

N Smooth Factor Of Kriging

Number of neighboring pixels in smooth

8

IR Model In Kriging Interpolation

Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4 - Matern

3

IR Cell Size Of Analysis

Choose a value (cell size) for sampling the variables. Very small values (high resolution) can cause error.

0.5

IR Error Distribution In Function Glm

Choose error distribution: 1 - binomial; 2 - gaussian; 3 - Gamma; 4 - inverse gaussian; 5 - poisson; 6 - quasi; 7 - quasibinomial; 8 - quasipoisson;

2

IR Model

Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4 - Matern

1

OK Cancel

PCI - PHYLOGENETIC COMPOSITION INTERPOLATION



This function is the leading standards of β -phylogenetic diversity (phylogenetic composition) by means of hexagons and interpolation. Here are available three forms of spatial interpolation : spline, kriging and nearest neighbor.

Oliveira U, et al. 2019. Modelling Highly Biodiverse Areas in Brazil. Scientific Reports 9:6355.

General tab (main)

Table in csv format (comma separated columns). First column with the name of the species (sp), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

A phylogenetic tree of the form tre. This tree should display as corresponding to the names Terminal taxa of csv table (field above). However, there is no need for full agreement between the two files, since the tree is pruned by the table and vice versa.

Specify a file in the shapefile (.SHP) format to serve as a mask (area for the interpolation).

Indicate the folder in which the files of results will be saved.

Choose the corresponding numbers, the β -diversity index that will be used: 1 for Bray-Curtis and 2 for Jaccard.

Indicate whether the phylogenetic tree used (field above) displays the information of the branch lengths. If not, will be considered every branch with length equal to 1.

Choose whether to save the maps in hex format.

Choose whether it will be held by spline interpolation.

Choose whether it will be held the nearest neighbor interpolation.

Choose whether it will be held the interpolation by kriging.

Choose the size of the hexagon will be used as a sampling unit. The size must be in decimal degrees (approximately 100 km in Ecuador).

Functor Editor - Pci

General Advanced

Input Occurrences
csv table with species and coordinates of localities (with columns: sp, x, y)
E:\BioDinamica_data\Sp_data.csv

Input Phylogenetic Tree
Input filogenetic tree in format ".tre"
E:\BioDinamica_data\Phylo_data.tre

Input Mask
Shapefile (shp) of area of study
E:\BioDinamica_data\Mask\Mask.shp

Output Folder
E:\BioDinamica_Test\PCI

Beta Diversity Index
Beta Diversity Index: 1-Bray-Curtis; 2-Jaccard

☒ **The Tree Has Branch Lengths**
The file of phylogenetic tree has branch lengths?
☒ Yes ☐ No

☒ **Save Hexagon Nmds**
Save hexagon with raw values map?
☒ Yes ☐ No

☒ **Nearest Neighbor Interpolation**
Interpolate by nearest neighbor?
☒ Yes ☐ No

☒ **Spline Interpolation**
Interpolate by Spline?
☒ Yes ☐ No

☒ **Kriging Interpolation**
Interpolate by kriging?
☒ Yes ☐ No

Hexagon Size
1.5

OK Cancel



Sp_data



Phylo_data



Mask



For that to be saved the pictures (view only), internet connection is needed

http://csr.ufmg.br/dinamica/dokuwiki/doku.php?id=phylogenetic_composition_interpolation

PCI - PHYLOGENETIC COMPOSITION INTERPOLATION

Advanced tab

Choose whether to partition analysis of β -diversity at turnover and nestedness. NOTE: this choice will make the analysis take triple the time to run.

Choose the cell size of the resulting map. The value should be in decimal degrees.

Choose the number of axes used in the conversion of Dissimilarity Matrix by NMDS. 3 axes is recommended, more axes may not be specialized in a map RGB.

Choose the number of search are performed rounds in NMDS.

Choose the minimum number of samples (in the sampling unit hexagonal) that will be considered in the analysis. The hexagons with values below the chosen will be discarded from the analysis.

Choice of smoothing interpolation factor for nearest neighbor.

Choose the smoothing factor by spline interpolation.

Choose the parameter of smoothing (Lambda) of splined interpolation.

Choose the corresponding numbers, the variogram model used on kriging.

Choose the parameter of smoothing interpolation by kriging.

Choose if the interpolated maps (for each interpolator) will be classified into discrete regions (bio-geographic regions). These regions are classified by three methods: k-means clustering, CLARA (Clustering for Large Applications), random forest.

Choose the number of classes in which the interpolated maps are classified. Note that ratings will be made with two classes to the value chosen. Choose many classes I hope more time because it will produce a larger number of classified maps.

Functor Editor - Pci

General Advanced

☒ **Beta Diversity Partition Analysis**
Beta diversity partition analysis (Turnover and Nestedness)
☒ Beta Diversity Partition Analysis

IR Cell Size
Cell size of output raster
0.05

IR Number Of Axis
Define number of axis
3

IR Rounds Of NmDs Search
Maximum numbers of random starts in search
10000

IR Minimum Number Of Samples
Minimum number of samples in hexagon
10

N Smooth Factor Of Nearest Neighbor
Number of neighboring pixels
8

N Smooth Factor Of Spline
Number of neighboring pixels in smooth
30

IR Spline Lambda
Smoothing parameter the ratio of error and process variance in spline interpolation
40

IR Model In Kriging Interpolation
Specification of the variogram model: 1- exponential, 2- spherical, 3- gaussian, 4 - Matern
3

N Smooth Factor Of Kriging
Number of neighboring pixels in smooth
30

☒ **Classify Nearest Neighbor**
Unsupervised Classification nearest neighbor interpolation?
☒ Classify Nearest Neighbor

N Number Of Classes Of Nearest Neighbor Interpolation
Number of classes
10

☒ **Classify Spline**
Unsupervised Classification of Spline interpolation?
☒ Classify Spline

N Number Of Classes Of Spline
Number of classes in k means
10

☒ **Classify Kriging**
Unsupervised Classification of Kriging interpolation?
☒ Classify Kriging

N Number Of Classes Of Kriging
Number of classes in k means
10

OK Cancel

PHYLO-GDM – PHYLOGENETIC GENERALIZED DISSIMILARITY MODEL



This function map the phylo β -diversity (phylogenetic composition) by predictor variables.

Rosauer DF, Ferrier S, Williams KJ, Manion G, Keogh JS, Laffan SW. 2014. Phylogenetic generalised dissimilarity modelling: a new approach to analysing and predicting spatial turnover in the phylogenetic composition of communities. *Ecography* 37:21–32

General tab (main)

Table in csv format (comma separated columns). First column with the name of the species (sp), the second column with x coordinates (longitude) and third column with coordinates y (latitude). The columns must be named as: sp, x, y, written with lowercase letters.

A phylogenetic tree of the form tre. This tree should display as corresponding to the names Terminal taxa of csv table (field above). However, there is no need for full agreement between the two files, since the tree is pruned by the table and vice versa.

Indicate whether the phylogenetic tree used (field above) displays the information of the branch lengths. If not, will be considered every branch with length equal to 1.

Specify a file in the shapefile (.SHP) format to serve as a mask (area for the interpolation).

Choose the size of the hexagon will be used as a sampling unit. The size must be in decimal degrees (approximately 100 km in Ecuador).

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Indicate the folder in which the files of results will be saved.

Functor Editor - Phylo Gdm

General Advanced

Input Occurrences
csv table with species and coordinates of localities (with columns: sp, x, y)
E:\Biodinamica_data\Sp_data.csv

Input Phylogenetic Tree
Input filogenetic tree in format ".tre"
E:\Biodinamica_data\Phylo_data.tre

☒ **The Tree Has Branch Lengths**
The file of phylogenetic tree has branch lengths?
Yes The Tree Has Branch Lengths

Input Mask
Shapefile (shp) of area of study
E:\Biodinamica_data\Mask\Mask.shp

IR Hexagon Size
1.5

Predictors
Folder with predictors raster files (variables) in geoTif format
E:\Biodinamica_data\Predictors

Output Folder
Folder of outputs
E:\Biodinamica_Test\Phylo_GDM

OK Cancel



Sp_data



Phylo_data



Mask



Predictors



For that to be saved the pictures (view only), internet connection is needed

PHYLO-GDM – PHYLOGENETIC GENERALIZED DISSIMILARITY MODEL

Advanced tab

Choose the minimum number of samples (in the sampling unit - hexagon) that will be considered in the analysis. The hexagons with values below the chosen will be discarded from the analysis.

Choose whether the map resulting from the GDM will be classified into discrete regions (bio-geographic regions). These regions are classified by three methods: k-means clustering, CLARA (Clustering for Large Applications), random forest.

Choose the number of classes that will be used in the classification.

Choose this option to generate a scenario cast in another scenario (such as future or past).

Enter the folder that contains the rasters (in GeoTiff format) that will be used as predictors of projection scenarios. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. The rasters should be appointed in the same manner as were named the rasters predictors.

Choose whether the geographical distances will be used as predictors.

Choose spline values (variable ratio curves with the dissimilarity) will be determined by the user or is automatically determined.

Choose the value of I-which will be used in spline curves of relationship of the variables. This value should never be less than the 3.

Choose whether a weighing by the number of samples (with the purpose of reducing the effect of sampling differences).

Functor Editor - Phylo Gdm

General Advanced

IR Minimum Number Of Samples
Minimum number of samples in hexagon
10

☒ **Classify Gdm**
Classify areas in GDM
☒ Yes ☐ Classify Gdm

IR Number Of Classes
Number of classes in classification
11

☒ **Project In Another Scenario**
Project GDM in another scenario (future or past)
☐ No ☐ Project In Another Scenario

Folder Scenarios Raster
Folder with rasters for project in another scenario. The rasters should be named in the same way of predictors.
C:/Scenario_Predictors

☒ **Use Geographical Distances**
Use geographical distances as predictors
☒ Yes ☐ Use Geographical Distances

☒ **Define Spline Values**
Enter manually with the spline values used.
☒ Yes ☐ Define Spline Values

IR Value Of Ispline
Value of I-spline. Enter the value. The value should never be less than 3.
3

☒ **Weight Samples**
Weight samples by number of samples (for data with sampling bias)
☒ Yes ☐ Weight Samples

OK Cancel

Scenario Predictors

LEAST COST PATHS HAPLOTYPES



This function calculates the lowest cost of dispersal between populations, relying for that in data on the genetics of populations (haplotypes) and a surface of cost (for example, a distribution model). For details on the methodology see: Chan & Yoder 2011. (<https://www.sciencedirect.com/science/article/pii/S1055790311000480?via%3Dihub>).

Table in csv format (comma separated columns). Being the first column with the number corresponding to the haplotype (Haplotype), the second column with the x-coordinates (longitude) and third column with the coordinates y (latitude). The columns must be named: Haplotype, x, y.

Choose a raster that is used as a friction surface. Can be used a model of distribution of the species (suitability), in this case, with the original values of the raster, check the following.

Indicate whether the map used in the previous option was a map (no change) of species distribution model (suitability).

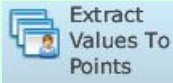
Specify a file in the shapefile (.SHP) format to serve as a mask (area for the interpolation).

Indicate the folder in which the files of results will be saved.



UTILITIES

EXTRACT VALUES TO POINTS



This function extracts the values of a set of rasters for points, creating a table with the points and the extracted values, spatially, for each point. As a result is generated a table with the points and the corresponding values of rasters.

Table in csv format (comma separated columns). First column with x coordinates (longitude) and the second column with coordinates y (latitude). The columns must be named as: x, y, written with lowercase letters.

Enter the folder that contains the rasters (in GeoTiff format or asc) that will be used to obtain the values. The rasters should be cut with the same mask (have the same dimensions) and have the cells of the same size. Never use multiple rasters bands.

Indicate the folder in which the files of results will be saved.

Choose the corresponding numbers, the raster format that is in the folder chosen.

Functor Editor - Extract Values To Points

? **Input Table**
Csv table with points (columns x and y)
C:/data/samples.csv

Raster Folder
Folder with raster files (variables)
C:/variables

? **Output Table**
C:/temp/output /table.csv

Raster Format
Choose raster format: 1 - tif; 2 - asc
1

OK Cancel



XY_data



AREA OF DISTRIBUTIONS



This function calculates the area of distribution of binary maps (e.g., species distribution maps).

Enter the folder that contains the rasters (in GeoTiff format) that will be used for the calculation of the areas of distribution. Note that will be calculated the area of pixels that present value 1.

Choose the location and name of the csv file (table) to be saved with the results.

The dialog box is titled 'Functor Editor - Area Of Distributions'. It has two main sections: 'Input Folder' and 'Output Table'. The 'Input Folder' section has a label 'Folder with binary rasters of species distributions' and a text field containing 'C:/temp/Temp_MPC'. The 'Output Table' section has a label 'Filename of output table' and a text field containing 'C:/temp/Table.csv'. There are 'OK' and 'Cancel' buttons at the bottom right. A folder icon is next to the 'Input Folder' text field, and a file icon is next to the 'Output Table' text field.



SUM OF MAPS



This function performs the sum of maps (GeoTiff format rasters).

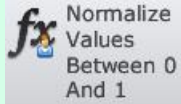
Enter the folder that contains the rasters (in GeoTiff format) that will be added. Never use multiple rasters bands.

Enter the name and location of the raster file format (GeoTiff) that is saved with the test result.

The dialog box is titled 'Functor Editor - Sum Of Maps'. It has two main sections: 'Input Folder' and 'Save Map'. The 'Input Folder' section has a label 'Folder with raster maps' and a text input field containing 'C:/variables'. The 'Save Map' section has a label 'Output map (raster tif)' and a text input field containing 'C:/temp/output/result.tif'. There are 'OK' and 'Cancel' buttons at the bottom right. A folder icon is next to the input field, and a preview icon is next to the output field.



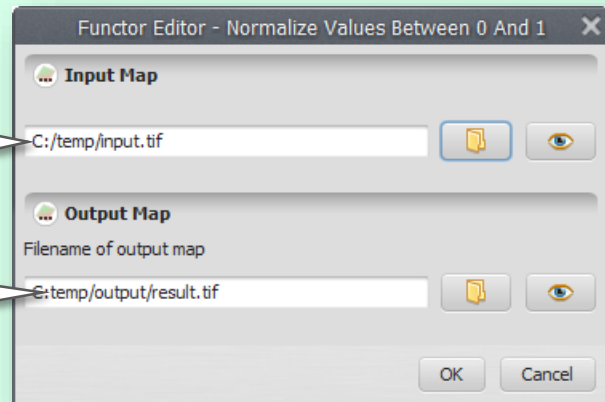
NORMALIZE VALUES BETWEEN 0 AND 1



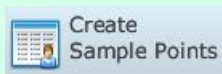
This function resample raster data values for the interval between 0 and 1

Choose the raster file format (GeoTiff).

Choose the location and name of the raster file (GeoTiff) that will be saved with the resampled values.



CREATE SAMPLE POINTS



This function creates samples of occurrence of species (in standard BioDinamica inputs), through binary distribution maps of species (which can be generated through distribution models or minimum convex polygon, for example)

Enter the folder that contains the binary rasters (in GeoTiff format) that represent the distribution of species.

Indicate the folder in which the files of results will be saved.

Choose the number of samples (by species) that will be generated.

Choose the corresponding numbers, if the samples shall be random or regular.

The dialog box is titled 'Functor Editor - Create Sample Points'. It contains four main sections: 'Input Folder' with a text field containing 'E:\BioDinamica_Test\sample_alea\bin_1' and a folder icon; 'Output Folder' with a text field containing 'E:\BioDinamica_Test\sample_alea\TEST' and a folder icon; 'Number Of Samples' with a label 'Number of points by map (species)' and a text field containing '100'; and 'Sampling' with a label '1 - random; 2 - regular;' and a text field containing '2'. At the bottom are 'OK' and 'Cancel' buttons. A folder icon labeled 'Species Maps' is shown to the right of the dialog box, with an arrow pointing to the 'Input Folder' field.

