

Ecological Niche in R-GRASS (ENiRG) using the GUI

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1 ENFA analysis using the GUI

1.1 Preparation

For the purposes of this example, honeybees data set will be used throughout the process (Canovas *et al.*, 2002, 2008, 2014).

Reading the library.

```
> library(ENiRG)
```

Starting the GUI.

```
> enirg.GUI()
```

1.2 Data preparation

Data management can be accessed through the menu Data (Figure 1).

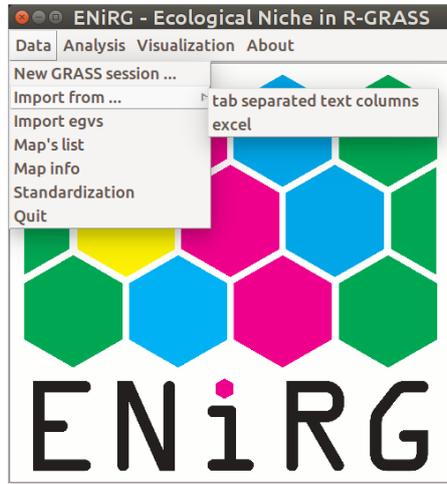


Figure 1: Data management menu.

If the user do not have a GRASS session running (i.e., Unix-systems users who started R into a GRASS session), a new one should be started before running the GUI by using the menu "New GRASS session ..." (Figure 2). NOTE: the path has to be entered manually.



Figure 2: Starting a GRASS session.

Importing species occurrence data can be performed by accessing the functions through the menu "Import from ..." (Figure 1). Two options are available: from a tab separated column text file or from an Excel file. In any case, the user should select the columns from the file, which represent position (longitude, latitude) and presence/abundance of the species (Figure 3). NOTE: Users can find two example data files in text and Microsoft Excel format into ENiRG installation folder. Users can search for the installation path of ENiRG through typing into the R terminal: `system.file(package='ENiRG')`.

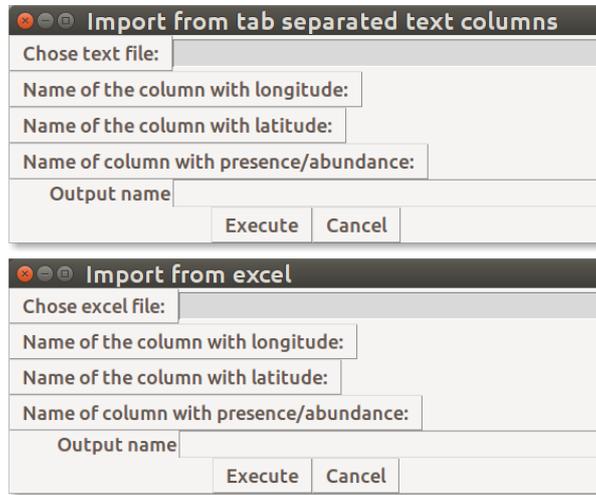


Figure 3: menu.

The ecogeographical variables should be stored in raster format. Almost all relevant formats can be used (check [GDAL library](#) for compatibility). Qualitative and quantitative predictors should represent variables of interest for the species. The importation of the raster maps can be done through the "Import egvs" menu (Figure 4). If not specified, the output name of the uploaded file is set to the original one as default. Maps are automatically uploaded to a GRASS session. NOTE: Users can find two example data files in text and Microsoft Excel format into ENiRG installation folder. Users can search for the installation path of ENiRG through typing into the R terminal: *system.file(package='ENiRG')*.

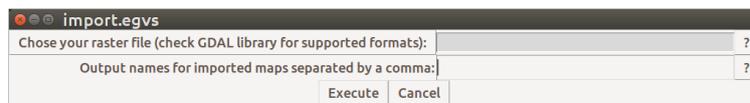


Figure 4: Importing ecogeographical variables (egvs).

Users can check metadata regarding the predictors and summarize the current settings of GRASS environment (Figure 5).

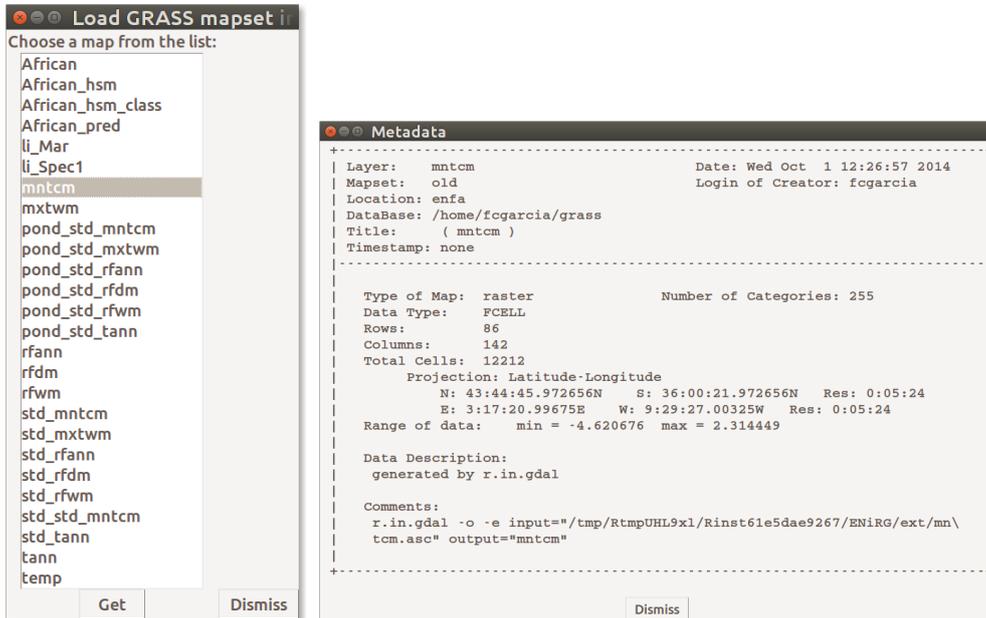


Figure 5: Getting information about a map.

A list of available maps can be imported, also searching for a particular pattern (Figure 6).

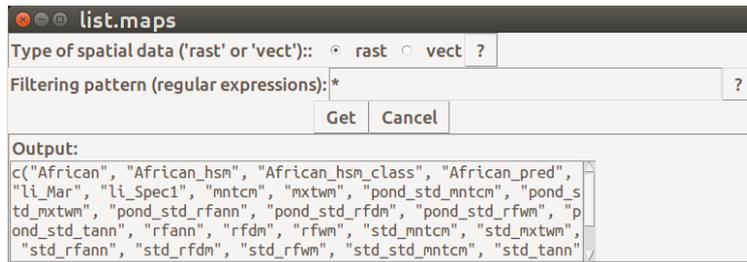


Figure 6: Listing maps in the current GRASS/ENiRG session.

When making predictions, standardization of *egv* can be advantageous, finding the maximum likelihood estimates. This process can be accessed from the "Data" menu (Figure 1). If not specified, the output name of the standardized file will contain the prefix "std_" plus the original name. More than one map can be standardized at the time.

1.3 Configuring and running ENFA analysis

The main function *enirg()* can be used through "enirg" option in "Analysis" menu (Figure 7). After setting predictor variables and occurrence points (note that the number of observations will appear closed to the data frame name in to GUI), the analysis can be run. The number of specialization factors will be interactively chosen later during the processing (chose 1 for this example). Results are returned into a list object, which will have the name set using the output boxes.

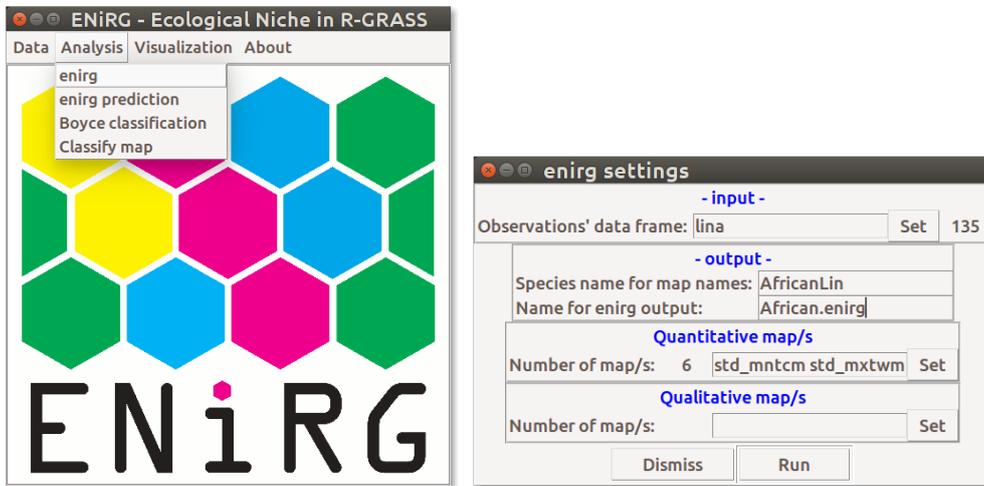


Figure 7: enirg analysis option into the analysis menu.

Habitat suitability map can be calculated using "enirg prediction" from the menu "analysis" (Figure 8). If the user does not provide a new set of maps, the calculations will be done over the same ecogeographical variables, which were used to run *enirg* function.

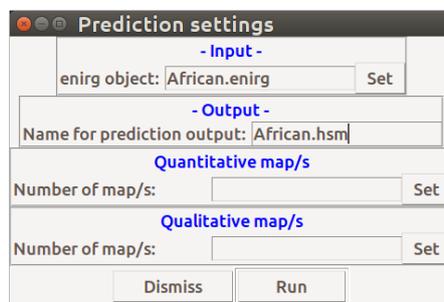


Figure 8: Calculating HSM predictions.

To perform Boyce continuous classification index on prediction results, two vector objects are needed. First, a vector containing the predictions for our observations. Second, a vector containing all the prediction values for the entire area of study. Both vectors will be automatically extracted from the results of the prediction steps.

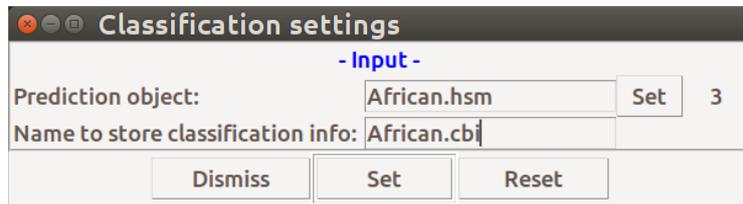


Figure 9: Classification setting menu.

Finally, the classification can be made manually, searching for the best Spearman coefficient and adjusted r^2 (Figure 10). NOTE: Try with the following intervals for the best classification fit:

- unsuitable = 0.25
- marginal = 0.69
- suitable = 0.81

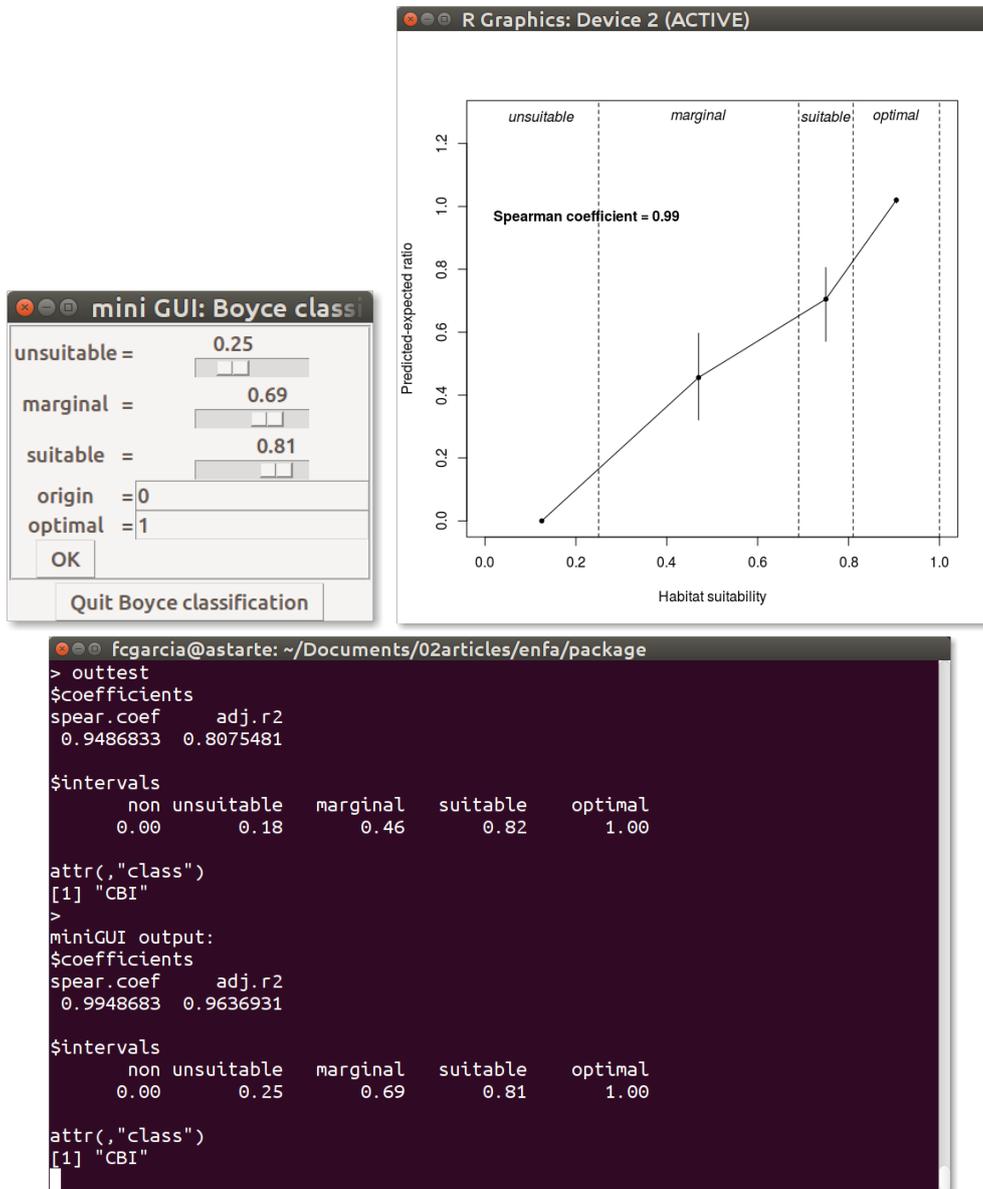


Figure 10: Classification process.

Now, the user is able to reclassify the HSM map into the four suitability classes according to (Boyce *et al.*, 2002) (unsuitable, marginal, suitable, optimal) (Figure 11).

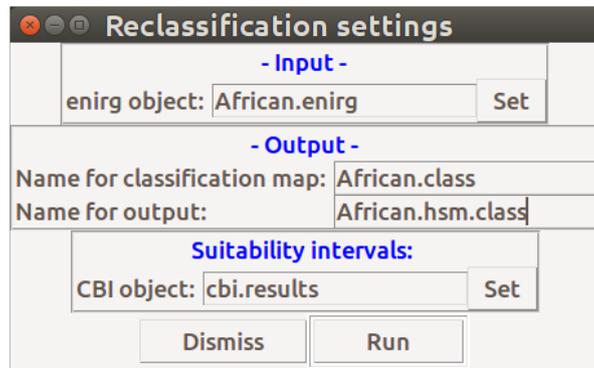


Figure 11: Reclassification window.

1.4 Visualization tools

The user is able to view the generated maps and results through the "Visualization" menu (Figure 12). The ordination results can be plotted by using "Plot enirg". (Figure 13).

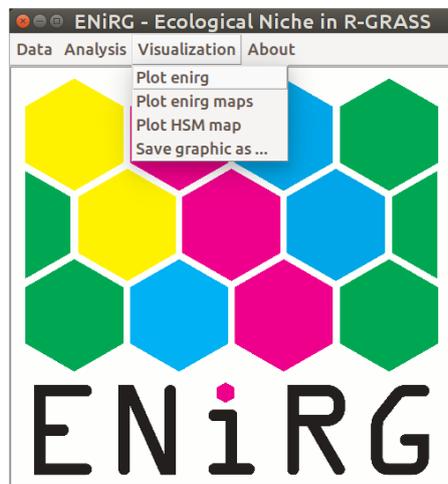


Figure 12: Visualization menu.

At any time, the user can save the current graphic into a file in any of "jpeg", "tiff" or "png" formats (Figure 16)

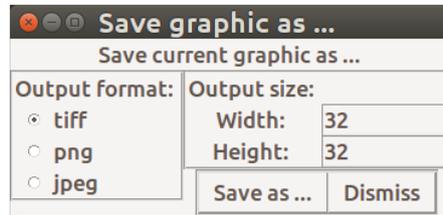


Figure 16: Saving current graphic.

2 References

References

- Boyce, M.S., Vernier, P.R., Nielsen, S.E., Schmiegelow, F.K.A. (2002). Evaluating resource selection functions. *Ecological Modelling* 157, 281-300.
- Canovas, F., De la Rúa, P. Serrano, J. and Galian, J. (2002). Mitochondrial DNA variability in *Apis mellifera iberica* populations from Galicia. *Archivos de Zootecnia*, 51: 441-448
- Canovas, F., De la Rúa, P. Serrano, J. and Galian, J. (2008). Geographical patterns of mitochondrial DNA variation in *Apis mellifera iberiensis* (Hymenoptera: Apidae). *Journal of Zoological Systematics and Evolutionary Research*, 46(1): 23-30
- Canovas, F., De la Rúa, P. Serrano, J. and Galian, J. (2014). Analysing and describing a contact area of two distinct evolutionary units. An ecological perspective. *Journal of Insect Conservation*. DOI: 10.1007/s10841-014-9701-1.