

RangeMapper 0.0-1

- quick graphical user interface guide -

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rangeMapper is a suite of tools for easy generation of biodiversity (species richness) or life-history traits maps. **rangeMapper** performs range maps interpolation with an user defined grid, then computes at each grid cell a chosen statistic and displays the resulting map.

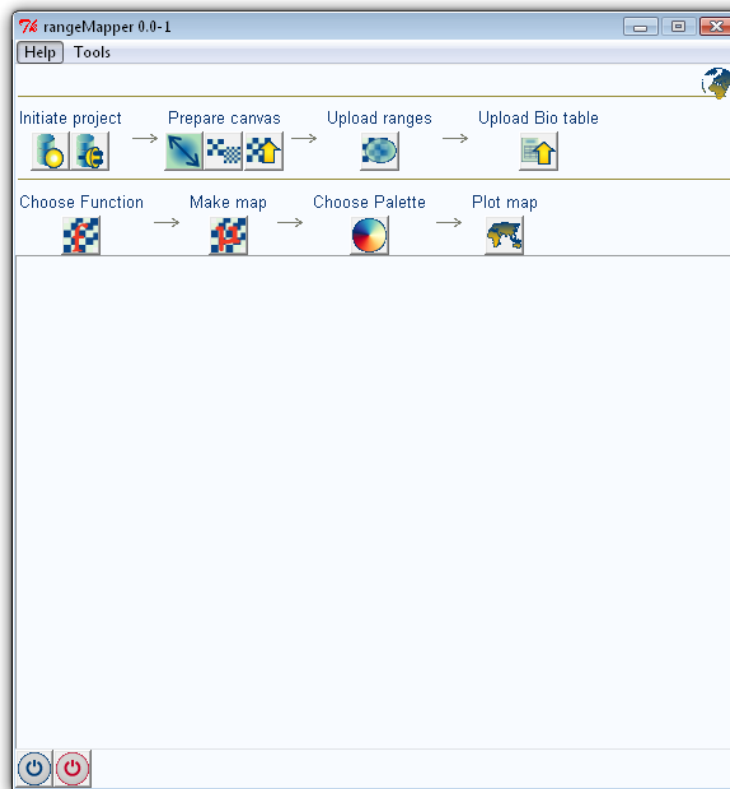
All the **rangeMapper** functions are build on the framework provided by the `sp`¹, `maptools`² and `rgdal`³ packages using `sqlite`⁴ support to store data.

rangeMapper comes with an user-friendly platform-independent tcltk graphical user interface (gui).

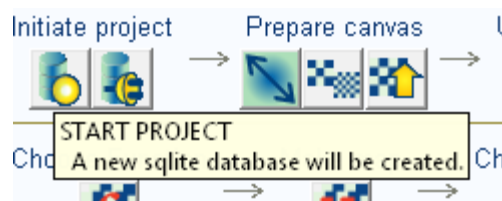
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Once the package is loaded you can open the gui by typing:
`rangeMapper()`.



To quickly get started, work through all the steps from “Initiate project” to “Plot map” using the dataset and the range files which come together with the package (to find where they are located go to Help/Example files). Place the mouse over each button to get tool-tips.



To get further help type `?rangeMapper` or `?<function name>` and the name of the function indicated by the tool-tip.

1. Initiate/open a new project

Initiate project



At this step a new project is initiated by creating a new sqlite database and populating it with a few preformatted tables.

You can interrupt at any of the next steps and resume latter by opening the same project.

2. Prepare canvas

Prepare canvas



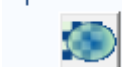
Once the project was initiated the next step is to prepare a canvas. The canvas is simply a regular grid of a given resolution (in map units) defined for the rectangular area encompassing all the ranges.

At this step you have to:

- define the global bounding box by selecting all the range polygon files (*.shp format),
- input the desired resolution (a sensible default is provided) and
- upload the canvas to the project's database.

3. Process and upload ranges

Upload ranges

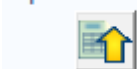


At this step every range polygon is overlaid on the canvas and the result of the overlap is saved to the database.

If there are thousands of range map polygons with complex geometries to be processed and/or the canvas resolution is relatively high this step is going to be time consuming. For example processing all amphibians of the world⁵ (5816 ranges, total 252 MB) using a grid of 0.25 deg resolution takes 544 minutes on a 64-bit machine with 4 GB of RAM running Windows Vista and R 2.10.0. However, once this step has been performed and the results saved to the database, the other operations are very fast.

4. Upload external 'BIO' data (e.g. life history data)

Upload Bio table



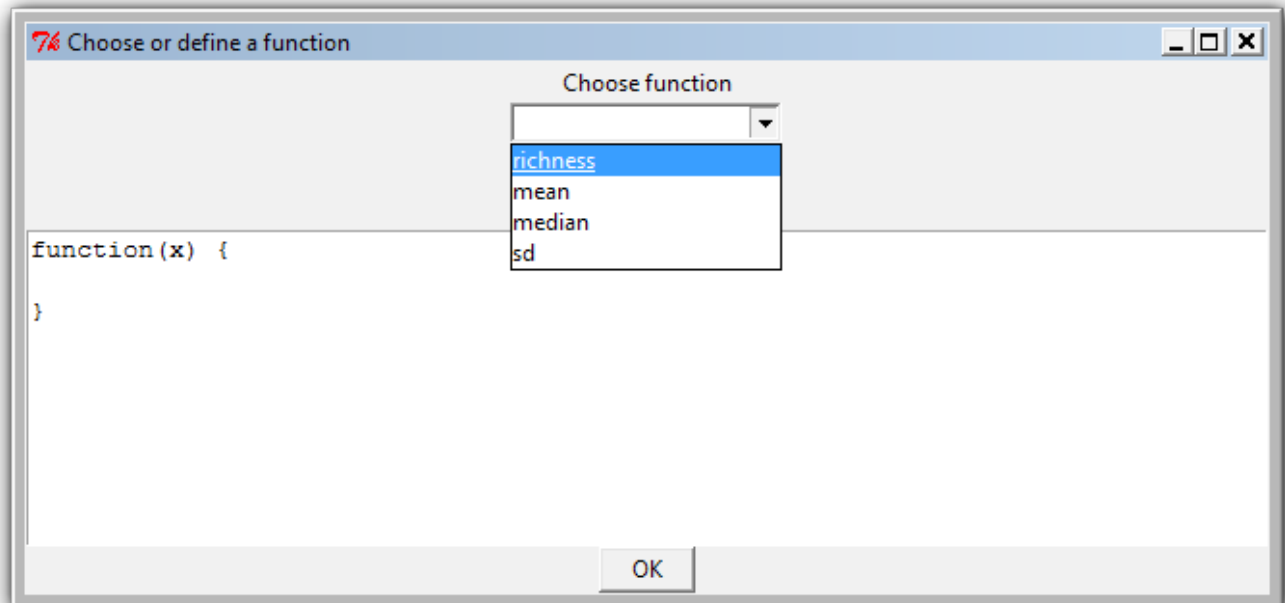
If you are only interested in species richness this step is optional. Data should be in .csv format (";" separated!). However, any `data.frame` can be imported from the command line. Type `?bio.save` for details. The 'BIO' table should contain a column with the file names of the range polygons (without the file extension). This column is used to link data in the 'BIO' table and range polygons.

5. Choose or define a function

Choose Function



At this step you can choose or define a function to be applied at each canvas cell.



6. Make a MAP

Make map



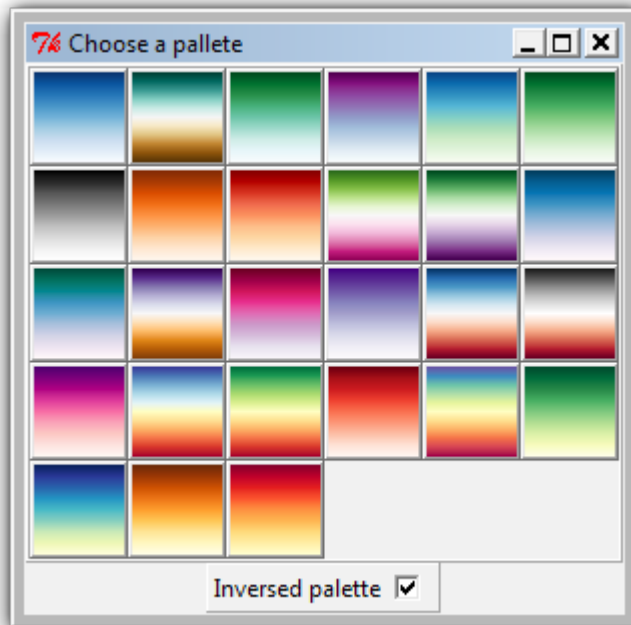
Compute the previously chosen statistic (richness, average, median or any user-defined function) at each canvas cell and save the results to the database as a "MAP" table.

7. Choose a color palette

Choose Palette



Choose one of the available color palettes.

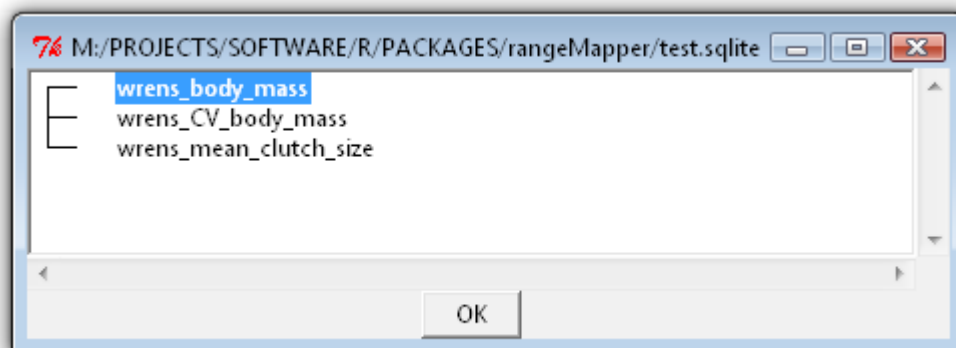


8. Plot one of the previously saved maps

Plot map

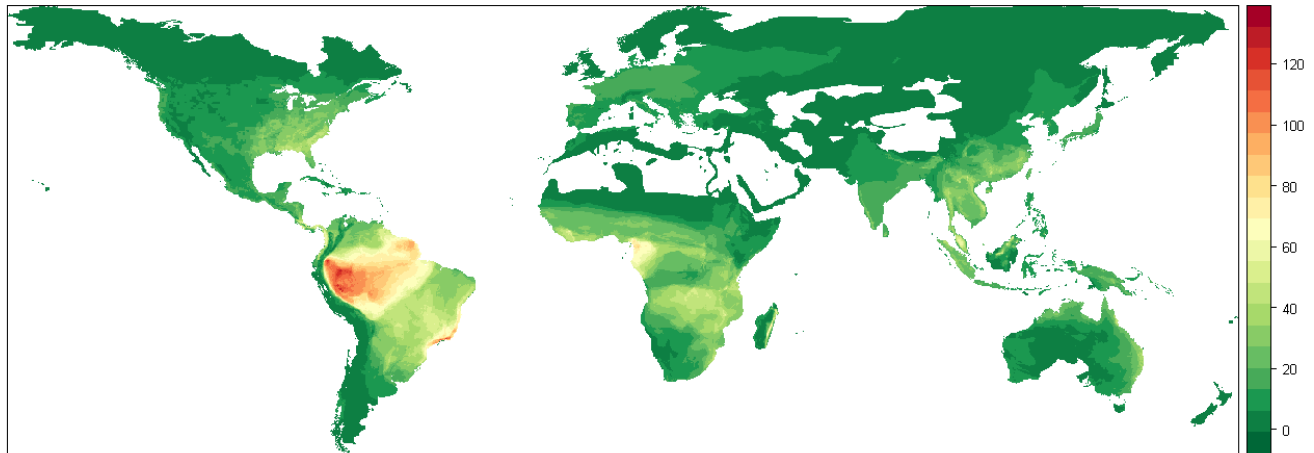


Example of a map choice dialog



Below are a few examples of maps. Note that the map resolution is arbitrary and was chosen only for testing purposes. For more information on how to choose an appropriate grid size see ⁶.

8.1 Amphibians of the world ⁵: 5816 species, grid resolution = 0.25deg



8.2. Wren species of N and S-America (40 species), grid resolution = 250000 m.

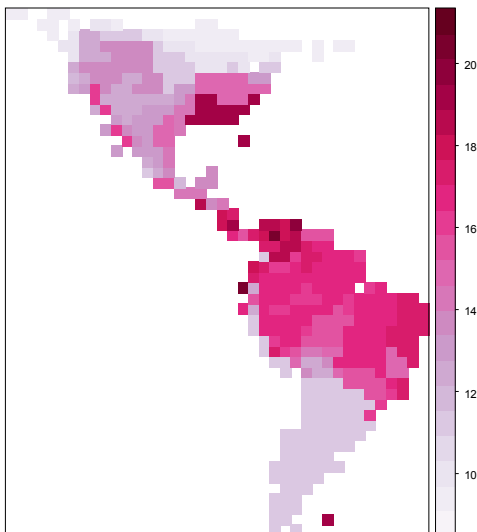
Type `?wrens` for more information.

Type

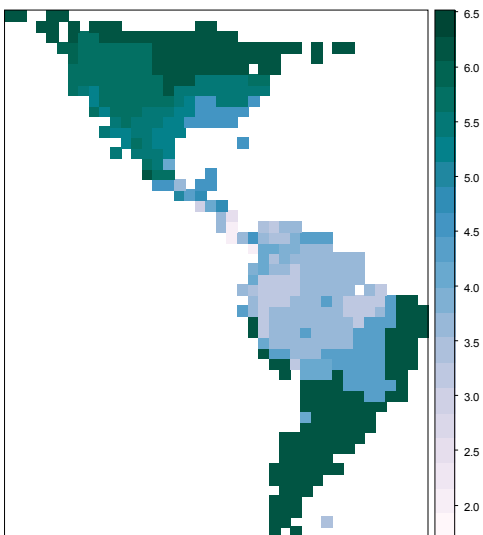
```
data(wrens)
wrens
```

to see the dataset.

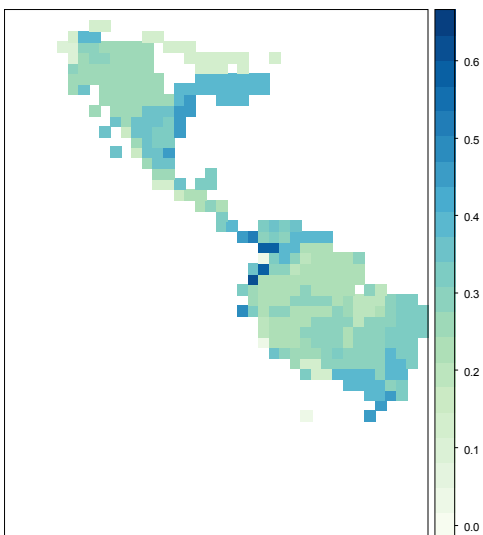
8.2.1 Mean body mass map



8.2.2 Mean clutch size



8.2.3 Mean CV of body mass



References

1. Pebesma, E.J., R.S. Bivand, (2005) Classes and methods for spatial data in R. R News 5 (2), <http://cran.r-project.org/doc/Rnews/>
2. Nicholas J. Lewin-Koh, Roger Bivand, contributions by Edzer J. Pebesma, Eric Archer, Adrian Baddeley, Hans-J  rg Bibiko, St  phane Dray, David Forrester, Michael Friendly, Patrick Giraudoux, Duncan Goulicher, Virgilio G  mez Rubio, Patrick Hausmann, Thomas Jagger, Sebastian P. Luque, Don MacQueen, Andrew Niccolai, Tom Short and Ben Stabler (2009). maptools: Tools for reading and handling spatial objects. R package version 0.7-29. <http://CRAN.R-project.org/package=maptools>
3. Timothy H. Keitt, Roger Bivand, Edzer Pebesma and Barry Rowlingson (2010). rgdal: Bindings for the Geospatial Data Abstraction Library. R package version 0.6-24. <http://CRAN.R-project.org/package=rgdal>
4. David A. James (2010). RSQLite: SQLite interface for R. R package version 0.8-2. <http://CRAN.R-project.org/package=RSQLite>
5. <http://www.iucnredlist.org/technical-documents/spatial-data#amphibians>
6. Hurlbert, AH; Jetz, W (2007) Species richness, hotspots, and the scale dependence of range maps in ecology and conservation, PNAS, 13384-13389.