

# **Instructions for accessing Savanna van Mesdag's Renyi Biodiversity Analysis Data and relevant R code (edited 28<sup>th</sup> September 2024)**

Prior to and during running the code for these analyses, please read through this document.

Much of this is based on Installation of BiodiversityR: instructions for Windows users, by Richard Kindt, 2018, available on:

[https://www.researchgate.net/publication/327980349\\_Installation\\_of\\_BiodiversityR\\_instructions\\_for\\_Windows\\_users](https://www.researchgate.net/publication/327980349_Installation_of_BiodiversityR_instructions_for_Windows_users)

Please refer to this document for much of the following instructions.

## **Installing BiodiversityR.**

Please refer to pages 2 to 6 in Kindt, 2018 (not including introduction page, Steps 1 through 3).

## **Loading BiodiversityR**

It is recommended that you open R (*not* RStudio) to load the relevant packages.

Follow the Step 4 instructions in Kindt 2018 to load the BiodiversityRGUI in R to load the packages that have been installed.

Please note a warning message I received on the 29<sup>th</sup> of August 2023:

“

```
> library(BiodiversityR)
```

```
Loading required package: tcltk
```

```
Loading required package: vegan
```

```
Loading required package: permute
```

```
Loading required package: lattice
```

```
This is vegan 2.6-4
```

```
BiodiversityR 2.15-2: Use command BiodiversityRGUI() to launch the Graphical User Interface;
```

```
to see changes use BiodiversityRGUI(changeLog=TRUE, backward.compatibility.messages=TRUE)
```

```
Warning messages:
```

```
1: package 'BiodiversityR' was built under R version 4.2.3
```

```
2: package 'vegan' was built under R version 4.2.3
```

```
3: package 'permute' was built under R version 4.3.0
```

```
> BiodiversityRGUI()
```

Loading required namespace: dismo

The legacy packages maptools, rgdal, and rgeos, underpinning the sp package, which was just loaded, will retire in October 2023.

Please refer to R-spatial evolution reports for details, especially

<https://r-spatial.org/r/2023/05/15/evolution4.html>.

It may be desirable to make the sf package available;

package maintainers should consider adding sf to Suggests:.

The sp package is now running under evolution status 2

(status 2 uses the sf package in place of rgdal)

Warning in sp::CRS(...) : sf required for evolution\_status==2L

Sourced: BiodiversityGUI.R

“

If there are issues with loading the BiodiversityRGUI, please email me at [savannankvm@gmail.com](mailto:savannankvm@gmail.com), *and* [s.van-mesdag.1@research.gla.ac.uk](mailto:s.van-mesdag.1@research.gla.ac.uk), or contact me on my ResearchGate profile: <https://www.researchgate.net/profile/Savanna-Van-Mesdag>.

### **Loading the data**

Once you have opened the BiodiversityRGUI, please make sure you have downloaded the relevant Rmarkdown file and the files titled:

ADDIEWELL\_PLANT\_CHEMISTRY.csv; AddiewellPlantSpecies.csv;  
BARROW\_PLANT\_CHEMISTRY.csv; BarrowPlantSpecies.csv;  
CARNFORTH\_PLANT\_CHEMISTRY.csv; CarnforthPlantSpecies.csv;  
FALLIN\_PLANT\_CHEMISTRY.csv; FallinPlantSpecies.csv;  
HODBARROW\_PLANT\_CHEMISTRY.csv; HodbarrowPlantSpecies.csv;  
PENICUIK\_PLANT\_CHEMISTRY.csv; and PenicuikPlantSpecies.csv (available in the repository) and that you have set the directory appropriately (you will need to modify the code to do this for your own directory).

Bear in mind that to run the code in the relevant Rmarkdown file, you need to make sure you run commands from the “R Script” window, by highlighting relevant parts of the text and selecting “Submit”, at the bottom right of the R Script window. The output will then display in the Output window below.

Again, if you have any issues, please contact me by email at [savannankvm@gmail.com](mailto:savannankvm@gmail.com), *and* [s.van-mesdag.1@research.gla.ac.uk](mailto:s.van-mesdag.1@research.gla.ac.uk), or else message me on my ResearchGate profile: <https://www.researchgate.net/profile/Savanna-Van-Mesdag>.

Savanna van Mesdag