

Biodiverse Quick Start Guide

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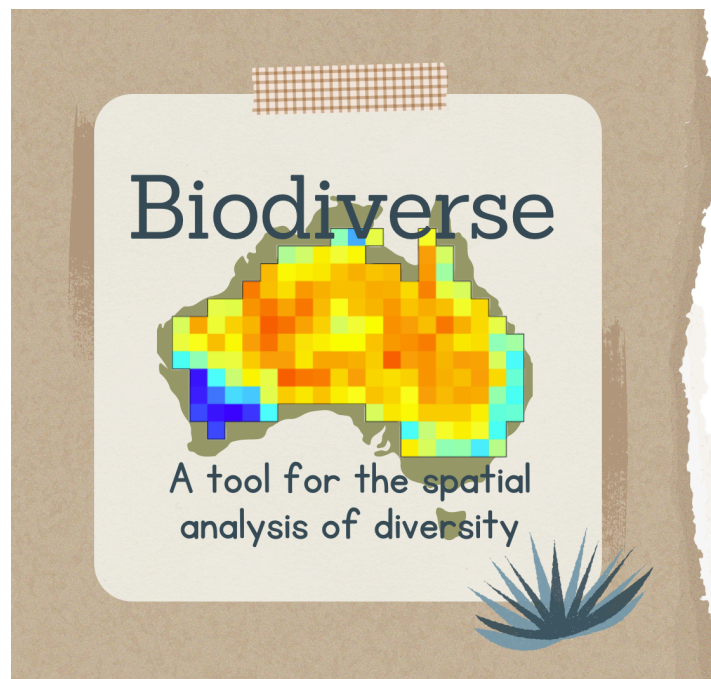
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Welcome!

Biodiverse is a free tool for the spatial analysis of diversity using indices based on taxonomic, phylogenetic, matrix and trait-based relationships. This book is made to support to new users of Biodiverse, introducing the main features of the software. It contains walk-through tutorials, explanations of key concepts and other resources to support your diversity analysis.



This book is built using [Quarto](#) and hosted via GitHub Pages, it is licensed under a [Creative Commons Attribution-NonCommercial 4.0 International License](#).

Got a question?

Please do not hesitate to reach out if you have question or feedback about the software. We encourage you to start a [GitHub Discussion](#) so we can help!

Alternatively, you can post your question at our [Google Group Forum](#). We recommend searching through past conversations to see if your question has been raised by others.

How to contribute

Biodiverse is an open source tool. While it is actively maintained, our capacity is limited. We welcome contributions that can improve the usage and understanding of Biodiverse.

There are many ways to contribute:

- Fixing grammar and typos in documentation
- Clarification or expanding on existing documentation
- Refining existing features
- Adding new features to the software
- Testing out new features

Submit your ideas in our [GitHub Discussions board](#)

Acknowledgements

This book was created on the unceded territory of the Bedegal people who are the Traditional custodians of the lands where the Kensington campus is located.

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1 Overview of Biodiverse

1.1 What is Biodiverse

Biodiverse is an open source tool for the spatial analysis of diversity using indices based on taxonomic, phylogenetic, matrix and trait-based relationships. Analyses can be run on a wide range of variables that vary across space and/or time whether they are biological, physical or lingual.

For example, the [diversity distributions of marsupials across Australia](#), or variation in rainfall across continental US, even geographic [distribution of indigenous dialects](#), can all be analysed with Biodiverse.

1.1.1 What is covered in this Quick Start Guide

This Quick Start guide introduces you to the main features of Biodiverse. It draws information from the full range of more extensive [Biodiverse help documentation](#)

Specifically we will cover how to do the following in Biodiverse:

- Importing and exporting data
- Data visualisation
- Cluster analysis
- Spatial moving window analysis
- Randomism analysis

The tutorials in this guide use the sample data sets provided in the `Biodiverse/data` folder.

This guide does not cover all the detailed aspects of Biodiverse functionality, so links to the on-line [Biodiverse documentation](#) covering more detailed information are provided throughout.

1.2 What analyses can I do with Biodiverse?

You can run a range of spatial analyses, such as:

- cluster

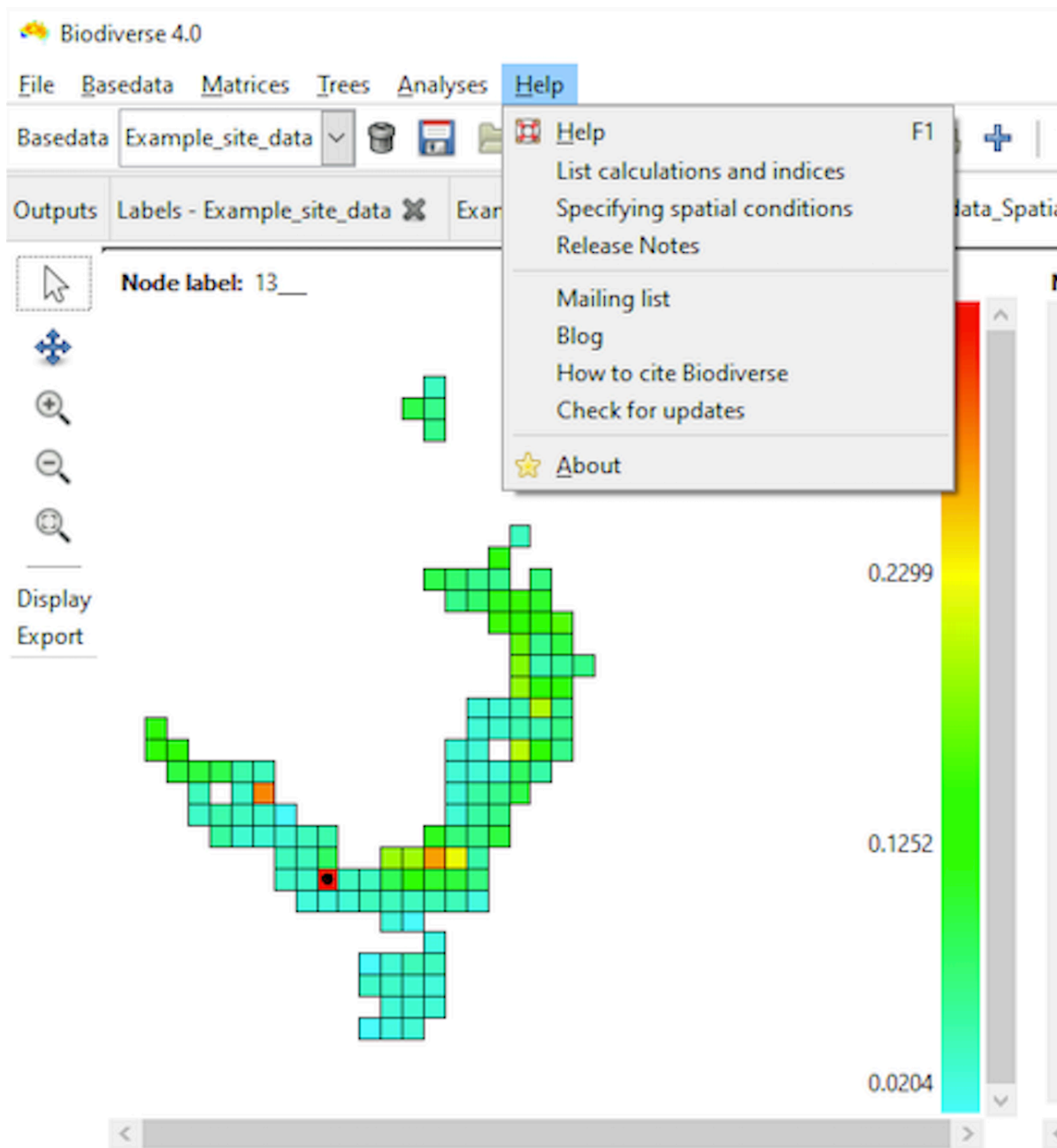
- moving window
- randomisation analyses

You can also visualise analysis results in interactive diagrams and maps, and optionally export analysis results to a variety of formats (e.g. delimited text, geoTIFF, JSON) to third party software for further analysis, such as ESRI ArcGIS, R and Matlab.

[BiodiverseR](#) - an R package to Biodiverse is currently under development to offer the same functionality as the main software

1.3 Where can I get additional help?

You can access a range of Biodiverse Help Topics by clicking on the Help option on the menu bar within the Biodiverse application



You can also hover the mouse pointer over most buttons and menu items in Biodiverse to view their associated tooltips.

Alternatively, you can post your question at our [Google Group Forum](#). We recommend searching through past conversations to see if your question has been raised by others.

1.4 Which operating systems does Biodiverse support?

Biodiverse is supported on Windows, MacOS and Linux platforms.

You can install the binary/executable or source code versions of Biodiverse at our [Installation Page](#)

The binary/executable is ‘all-in-one’ which includes the analysis engine + GUI.

If you just want the analysis engine only, follow the installation instructions for the source code version.

1.5 What programming language is Biodiverse developed in?

Biodiverse - the software itself comes in two parts:

- an analysis engine, which is written in [Pprl](#)
- a graphic user interface (GUI) which is developed using [Gtk2](#)

1.6 How do I install Biodiverse?

Follow the [Installation](#) instructions webpage for your selected version.

1.7 Key terminology

The two concepts below are important when using Biodiverse. For details of a fuller list of Biodiverse terminology, see the [Data Structures](#) page.

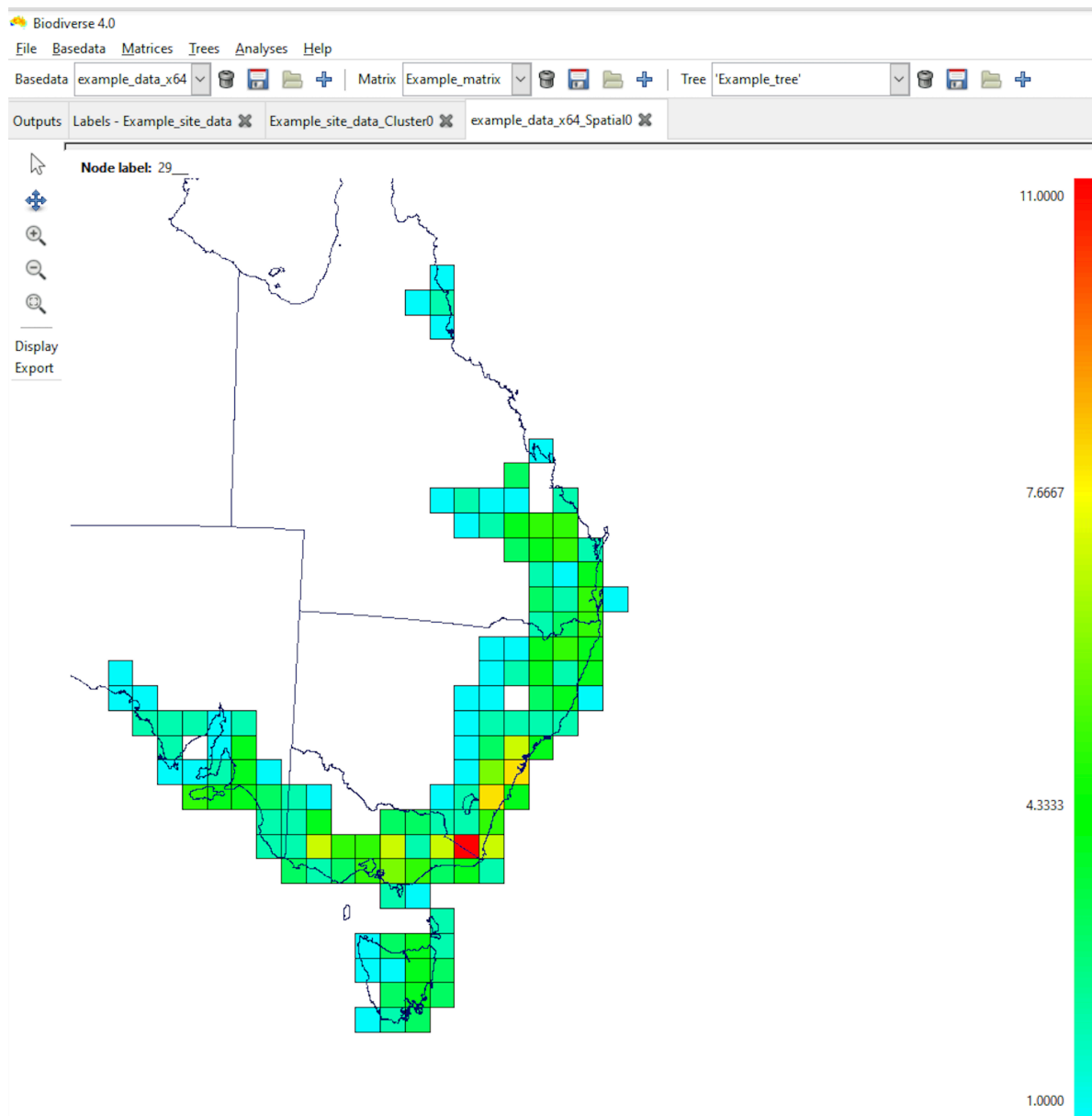
1.7.1 Labels

Typically labels represent species, but in reality they can be any named entity that is then aggregated, or ‘binned’, into a Group. Hence, an individual label could also represent other taxonomic levels, e.g. a genus, or distinct entities from other phenomena, such as lithological classes (e.g. different rock types) or linguistic structures (e.g. different phonemes).

1.7.2 Groups

Groups are cells into which the labels are aggregated (binned). These are usually square, but can represent any number of axes (x, y, z, time, population-ID, ...) with differing cell sizes (resolutions) and numeric or text types. The groups are plotted in the interactive maps that Biodiverse produces as outputs of data visualisation and spatial analyses, as in the example below. Groups are also integral to the spatial components of the moving window, cluster and randomisation analyses.

Please note however, that group coordinates are in the same coordinate system (map projection) as the input data. If you have input data in multiple files, with differing coordinate systems, then you can use GIS or other geospatial tools such as the `sf` library in R to project them into a common system.



The 'Groups' are the square cells representing the Australian mainland.