

Cross-Scale-Model-Integration-Examples

These scripts are provided to reproduce the examples given in the paper “Cross-scale integration of data and knowledge for predicting species ranges.” All source code is licensed under the GPL3, details are provided in the `LICENSE` file.

For convenience, a makefile is provided to demonstrate how to build the examples and provide an automated way to generate all necessary files. The command `make all` will build both examples, while `make example1` and `make example2` will build each example individually. Note that these will likely take a long time and consume a lot of memory, so plan your usage accordingly.

Dependencies:

- R version 3.x
- JAGS
- Rscript (optional, but recommended. Included with most R installations)

R packages:

- `sp`
- `glm2`
- `fields`
- `rjags`

Running the models:

Both examples are provided as a collection of scripts. Order matters (more so for example 2, but to some extent for example 1 as well). A list of all scripts and the proper order follows. Note that when two scripts have the same number, the order does not matter. The examples are easiest to run by invoking them with `Rscript` at the command line, as follows:

```
cd path/to/desired/example
Rscript file.r
```

Alternatively, you can run the scripts from the console by using `source()`, or by pasting one line at a time. Just make sure you set your working directory to the appropriate place, either `example_1` or `example_2`.

Example 1:

1. `Rscript ex1_m1.r` – Run the naive model
2. `Rscript ex1_m2.r` – Run the mechanistic submodel
3. `Rscript ex1_mm.r` – Run the metamodel
4. `Rscript ex1_makeSamplingFig.r ex1_Sampling.pdf` – Make figure 2 from the manuscript
5. `Rscript ex1_makePrecipFig.r ex1_precip.pdf` – Make figure 3 from the manuscript
6. `Rscript ex1_makeMapFig.r ex1_map.pdf` – Make figure 4 from the manuscript

Example 2:

1. `Rscript ex2_prepMapleData.r` – Loads data from original sources and formats it for the analysis
2. `Rscript ex2_drawPseudoAbsences.r` – Select a random subset of absences
3. `Rscript ex2_setUpSDM.r` – Use conventional methods to select the form for the metamodel
4. `Rscript ex2_mcmcSDM.r` – Run the mcmc on the naive model
5. `Rscript ex2_mcmcIntegrated.r` – Run the mcmc for the integrated model
6. `Rscript ex2_processResults.r` – Produce predictions from the posterior parameter distributions
7. `Rscript ex2_makeFigures.r` – Produce figure 5 from the manuscript