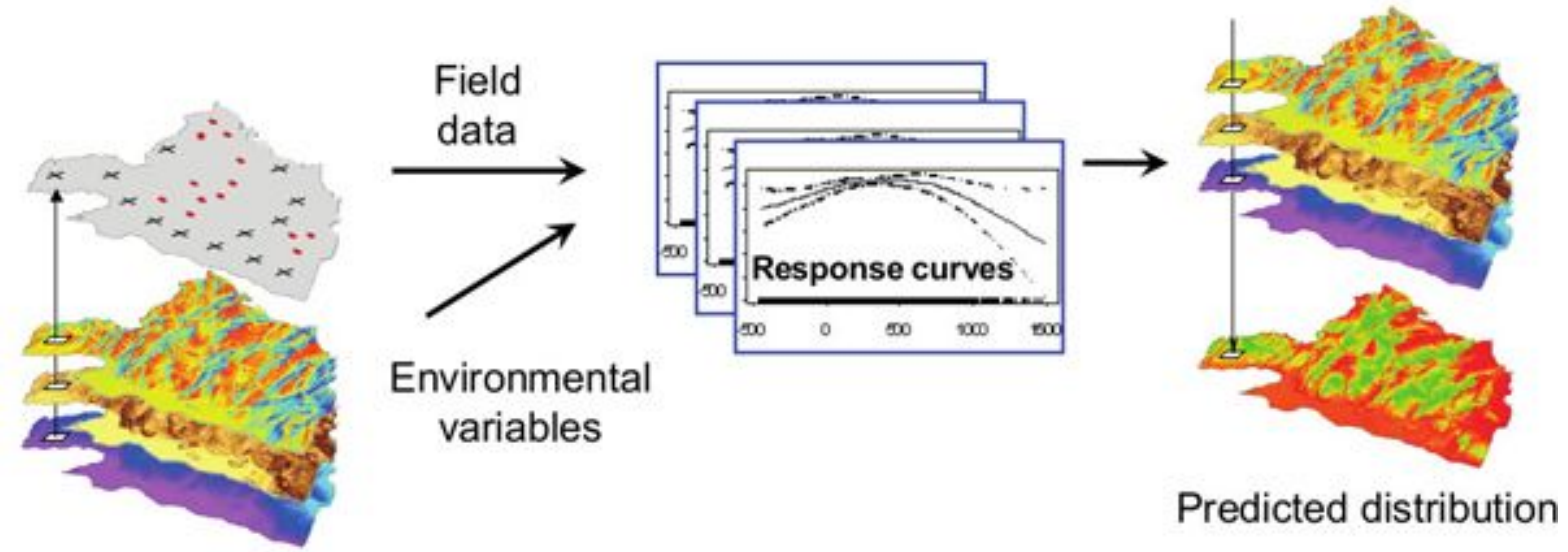
IUCN Interdisciplinary Summer School

Species Distribution Models
Practical Session



Dr. Luca Bütikofer and Caroline Martin

June 11, 2024

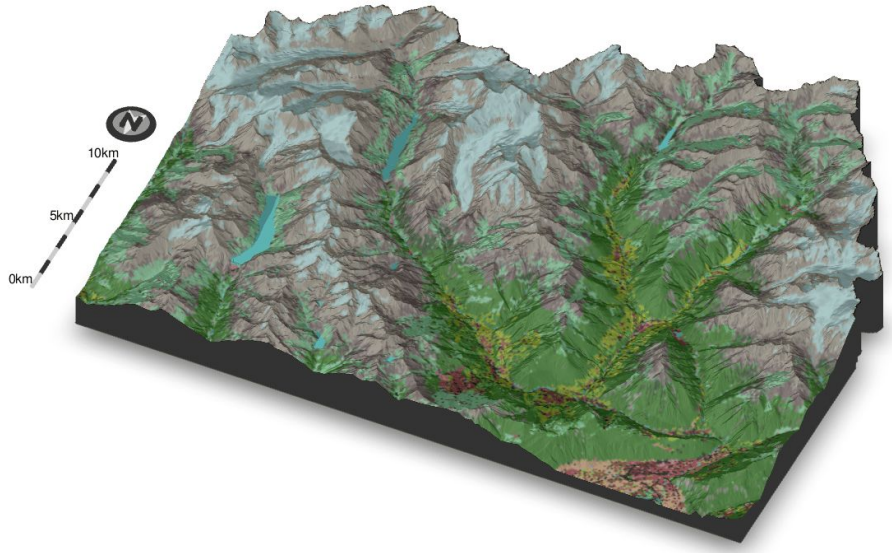
UNIL | Université de Lausanne

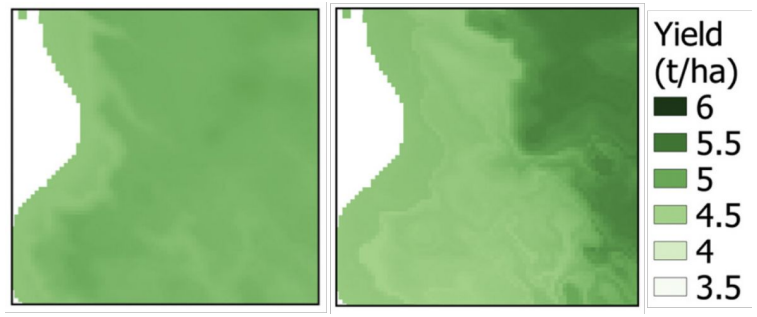
Luca Bütikofer *Spatial- Agro- Macro- Ecologist*

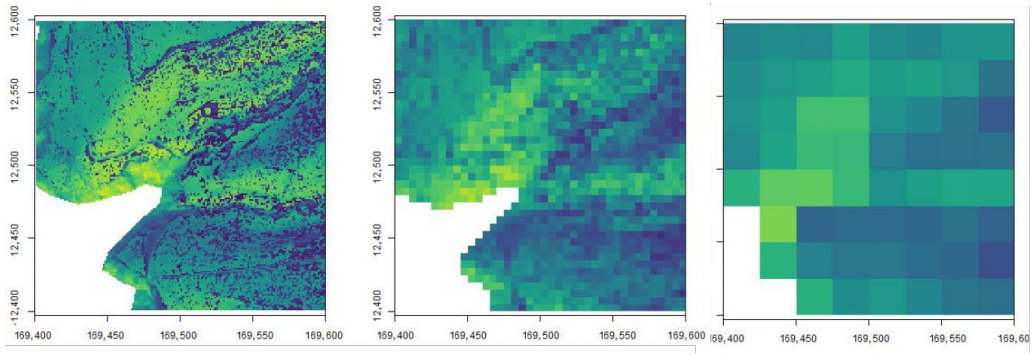
Undergrads ☞ Italy

PhD ☞ New Zealand

PostDocs ☞ UK, Switzerland







2015 - 2018
Alberta, Canada

MSc - Wildlife Ecology and Management

2018 - 2020
Saskatchewan, Canada

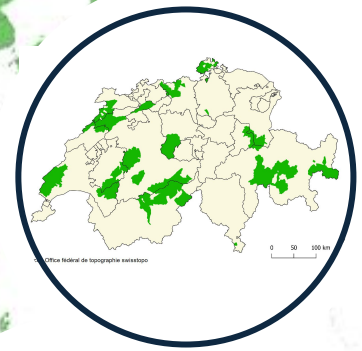
Environmental Consulting

2020 - 2022
Ontario, Canada

WWF-Canada Science, Knowledge, and Innovation Team

2022 - present
Lausanne, Switzerland

PhD Conservation Biology



Caroline Martin

Applied ecology and conservation biology

Practical Session on SDMs

Objective

Learn how to prepare data, build and fit models, visualize outputs, and interpret results of species distribution models

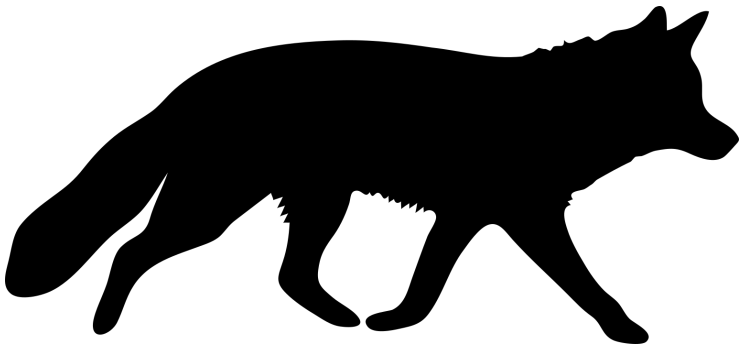
In R:

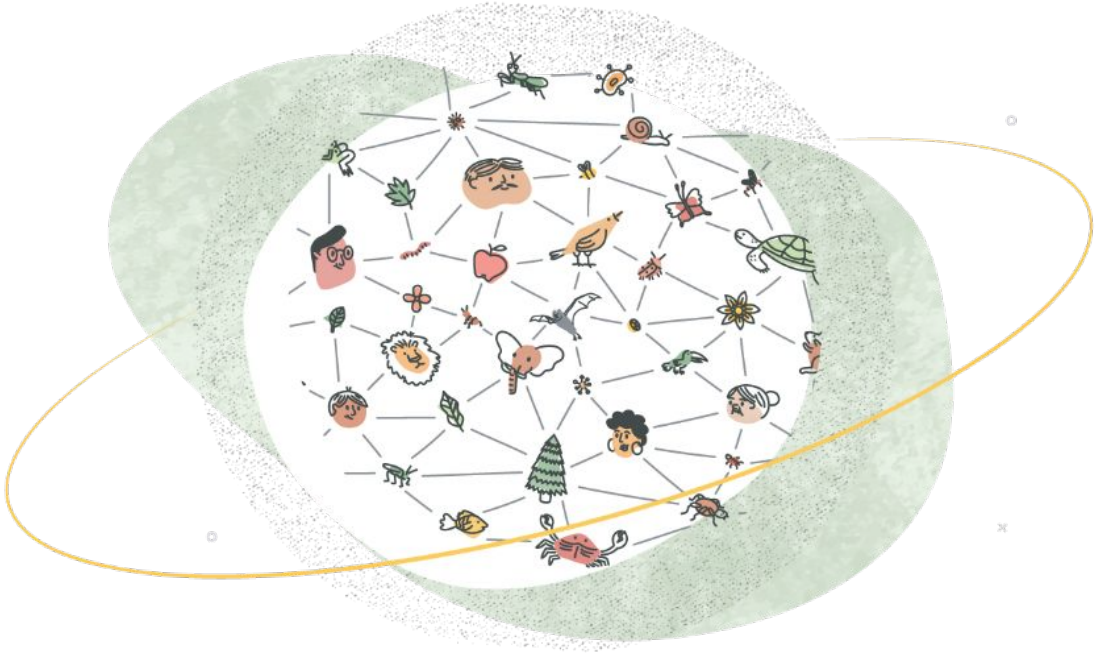
```
> install.packages("wallace")
> library("wallace")
> run_wallace()
```

Occ Data

Occurrence data: *Vulpes vulpes*

- Query Database: GBIF Global Biodiversity Information Facility
- Max. 1000 observations





Env Data

- Associate species occurrences with environmental predictor variables
- Typically in raster format (pixelated/gridded data that has been georeferenced)

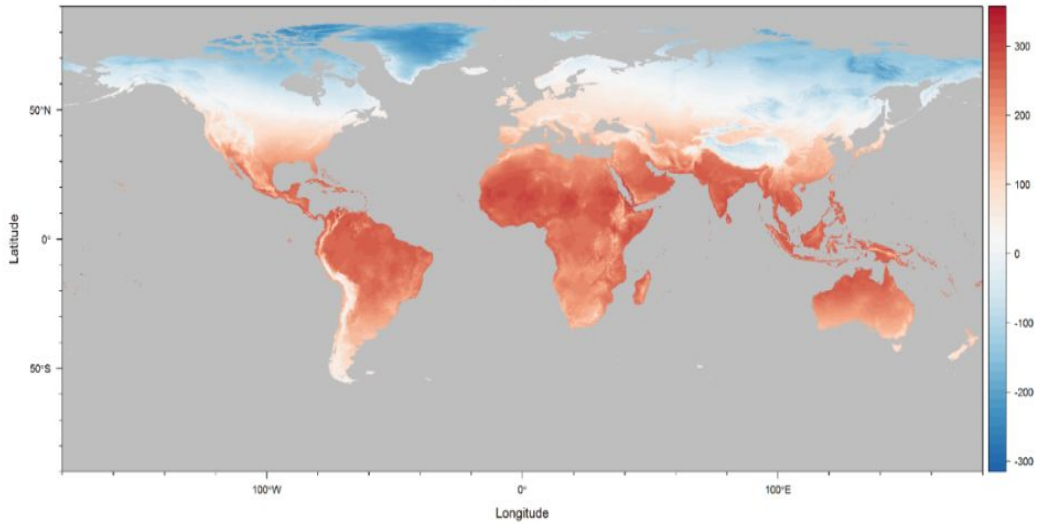
Biodiversity Informatics, 10, 2015, pp. 1-21

ECOCLIMATE: A DATABASE OF CLIMATE DATA FROM MULTIPLE MODELS FOR PAST, PRESENT, AND FUTURE FOR MACROECOLOGISTS AND BIOGEOGRAPHERS

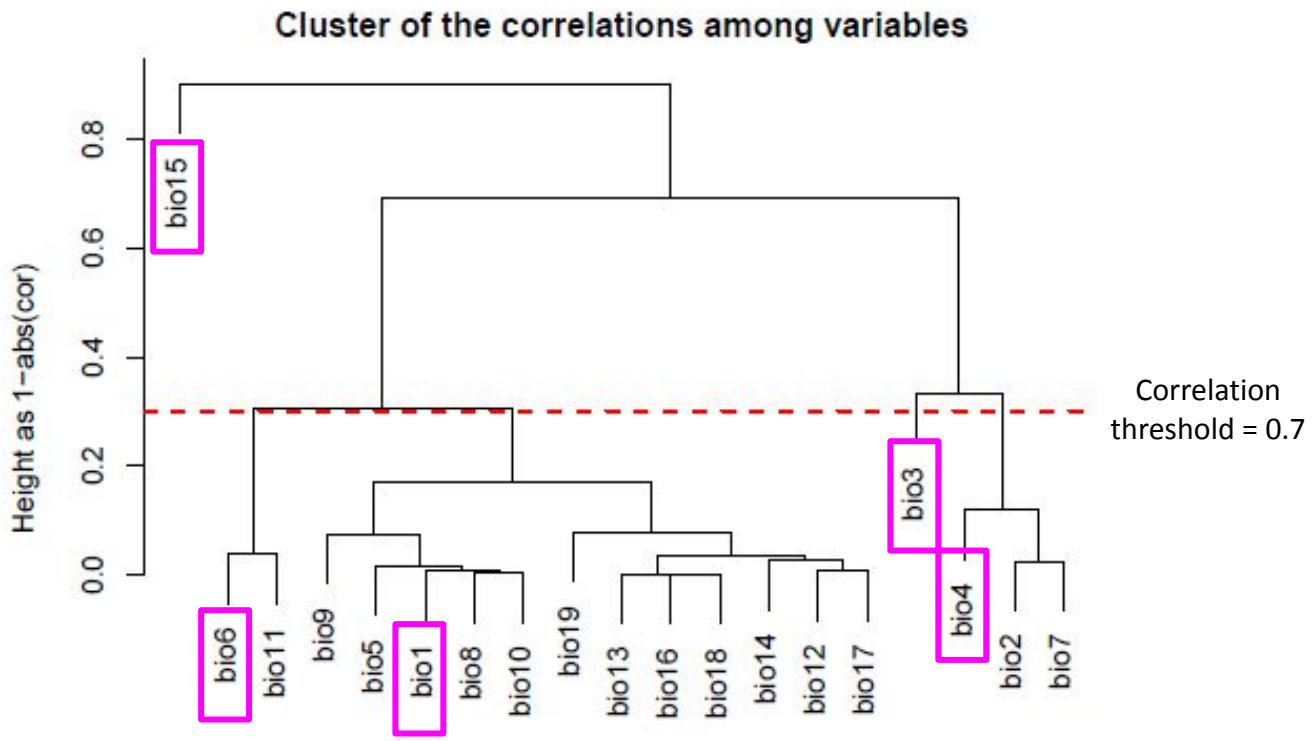
MATHEUS S. LIMA-RIBEIRO[1], SARA VARELA[2,3], JAVIER GONZÁLEZ-HERNÁNDEZ[4], GUILHERME DE OLIVEIRA[5], JOSÉ ALEXANDRE F. DINIZ-FILHO[6], LEVI CARINA TERRIBILE[1]

0.5° resolution
(~ 55km x 55km raster grid)

e.g., Mean Annual Temperature (°C)



Env Data



Biol1: Annual mean temperature (°C)

Biol3: Isothermality (%)

Biol4: Temperature seasonality (%)

Biol6: Min temperature of coldest month (°C)

Biol15: Precipitation seasonality (%)

- ecoClimate data
- Global Circulation Model: CCSM
- Temporal scenario: Present
- Bioclimatic variables:
  - biol1, biol3, biol4, biol6, biol15

Process Occs

Exclude introduced range (Australia) to test later on.

Process Envs

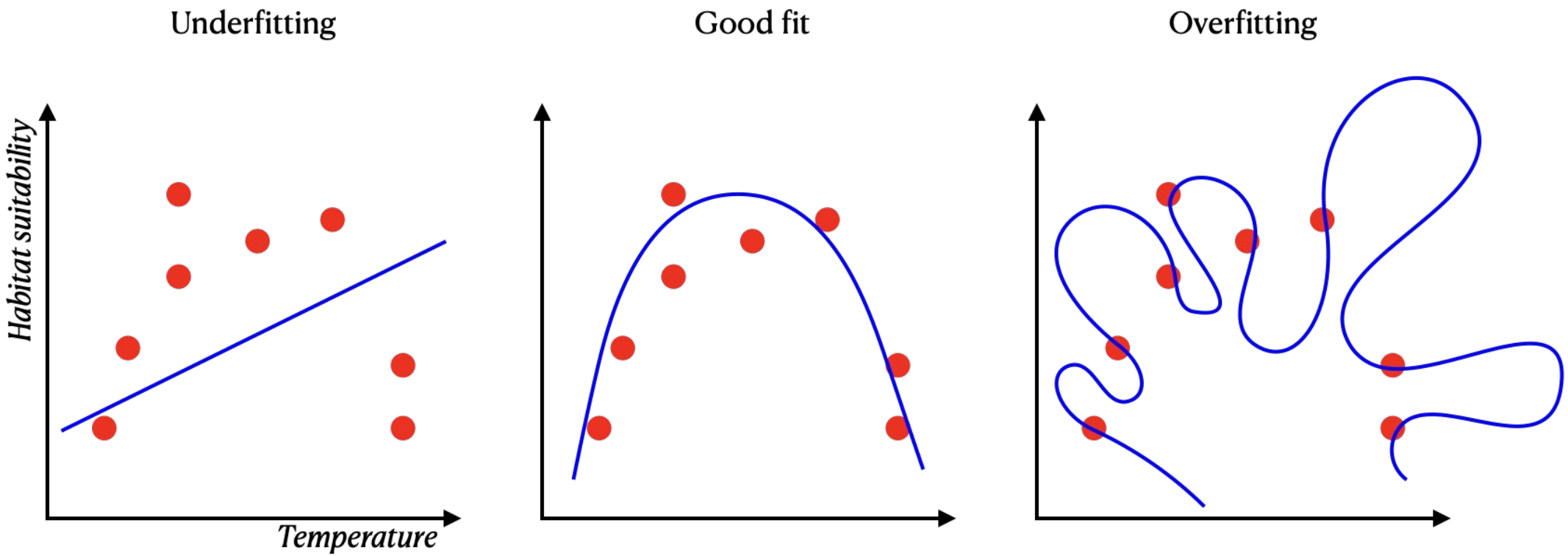
- Selection of study area by cropping predictor variables
- Sample environmental conditions where species are not recorded
  - background points or "pseudoabsence" (not a true absence)

- Select Study Region:
  - 20° point buffer around points
- Sample Background Points
  - 1000 points

Skip characterizing environmental space

Partition Occs

Model fit:

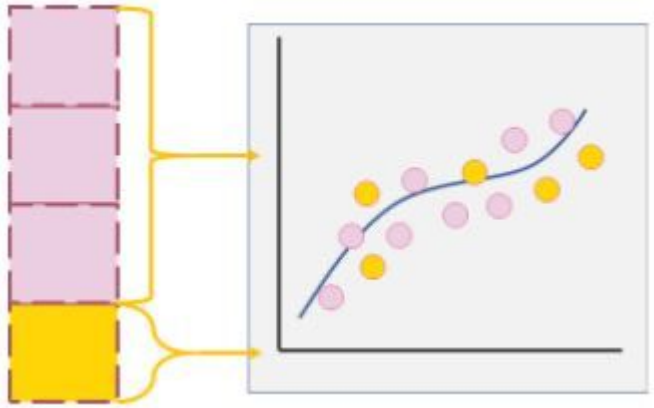


Partition Occs

Cross-validation:

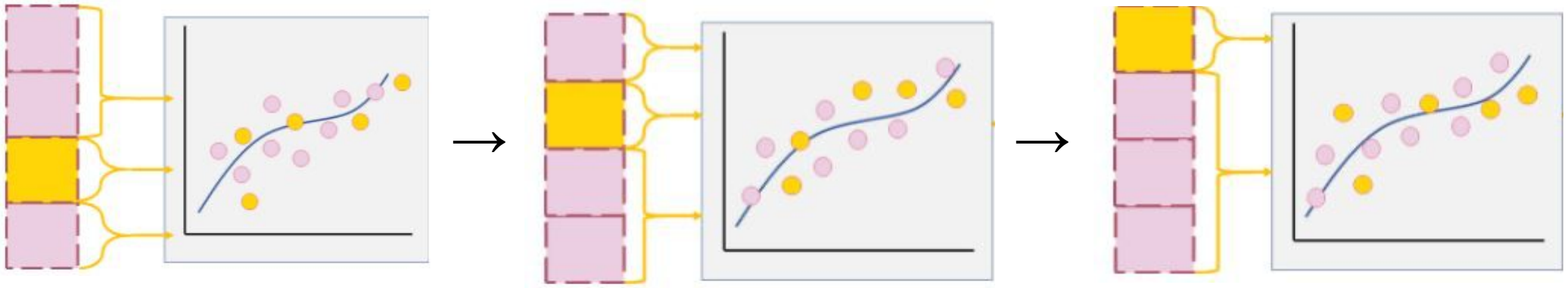
Partition Occs

Cross-validation:



Partition Occs

Cross-validation:



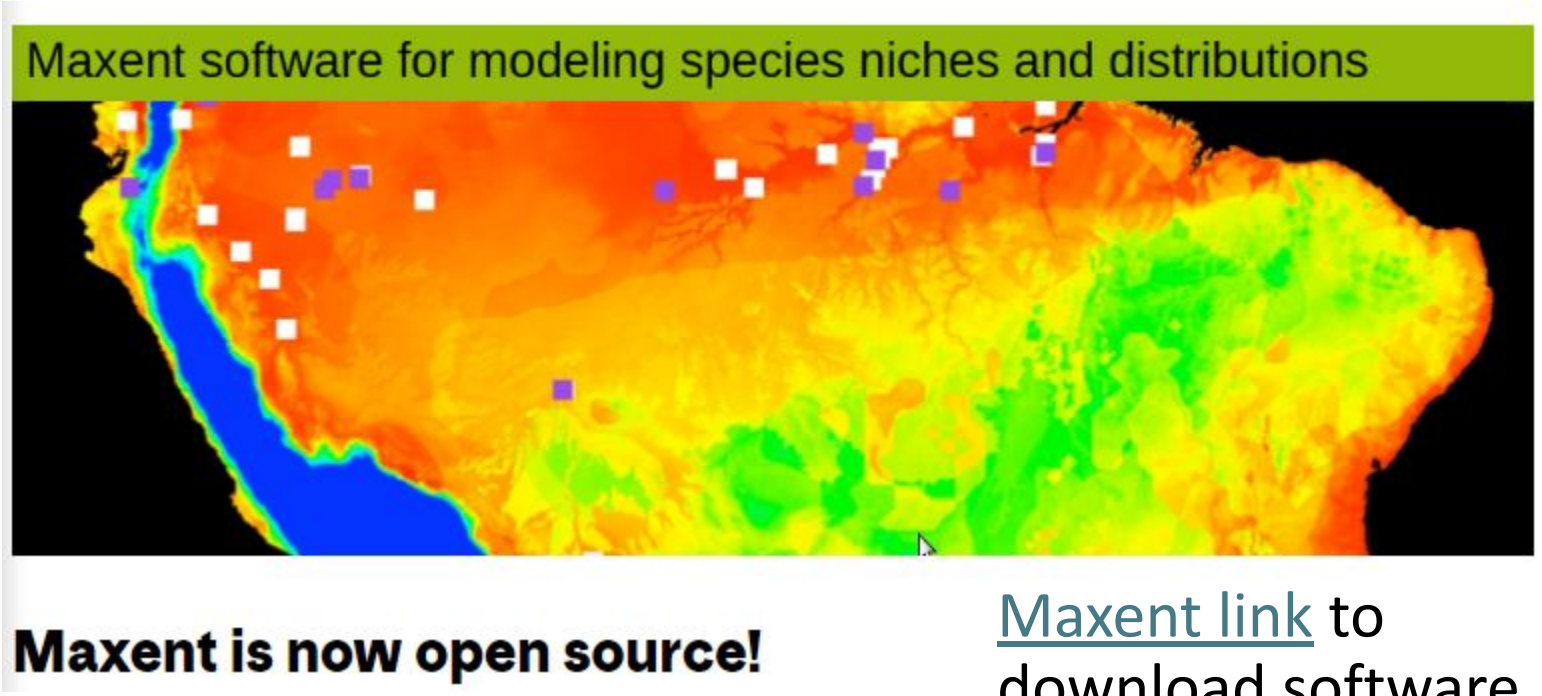
Partition Occs

Cross-validation in Wallace:

- Non-spatial Partition
- Random k-folds
- 4 partitions

Model

- Many approaches and algorithms exist to build and evaluate models for species niches/distributions
  - presence/background algorithm Maxent



Maxent link to download software

Model

- Choose Maxent module, then maxnet algorithm
- Feature classes:
  - L and LQH

- Regularization multiplier - penalization of model complexity
  - Multiplier of 1 and 4 (step value = 3)
- Categorical variables = NO
- Clamping = FALSE
- Parallel = TRUE

Model

Selecting the “best” model out of our 4 candidate models

- 2 feature classes x 2 regularization multipliers = 4 models

- Evaluation metrics
  - AUC (Area Under the Curve)
  - OR (Omission Rate)
  - CBI (Continuous Boyce Index)
  - AICc (corrected Akaike Information Criterion)

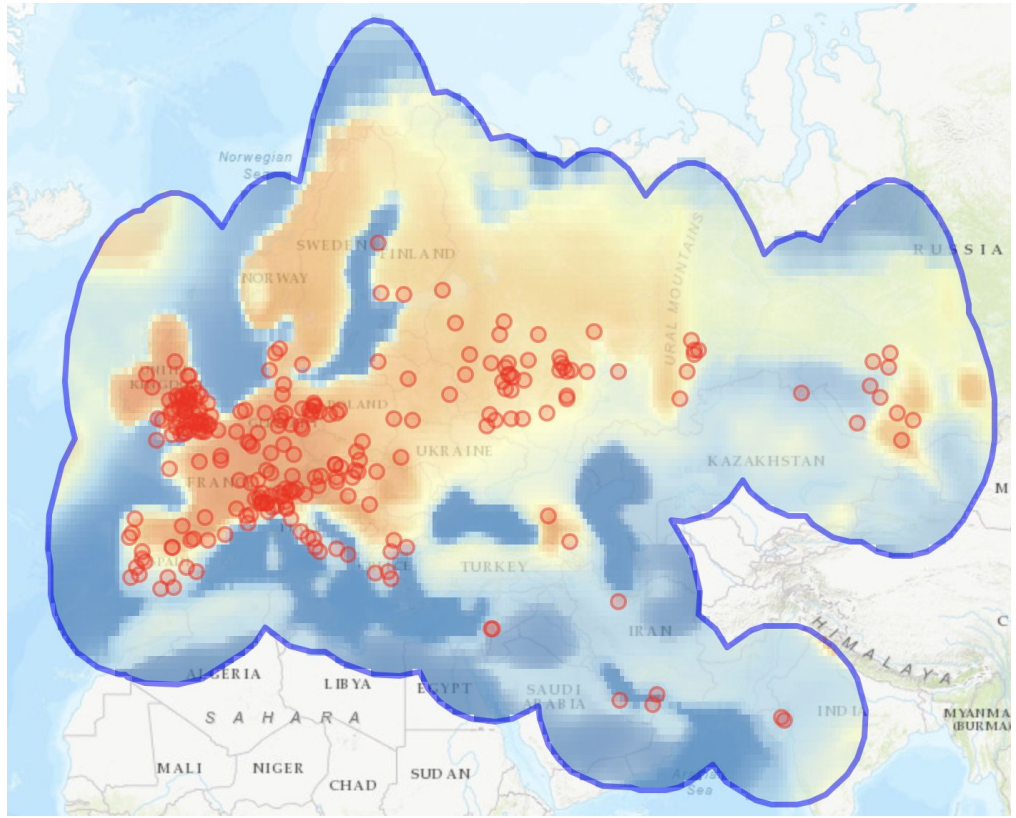
Calculated and averaged across all partitions

- Maxent Lambdas: weights for feature classes of each variable for each of the models

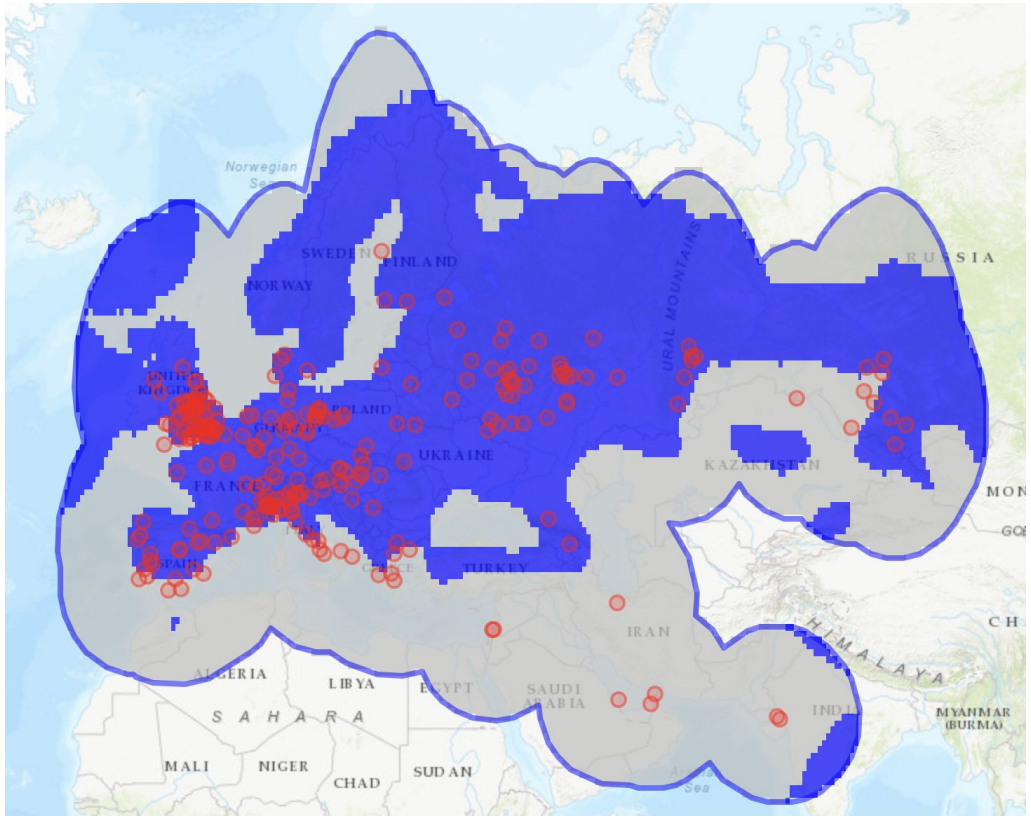
Visualize

- Map predictions

Continuous



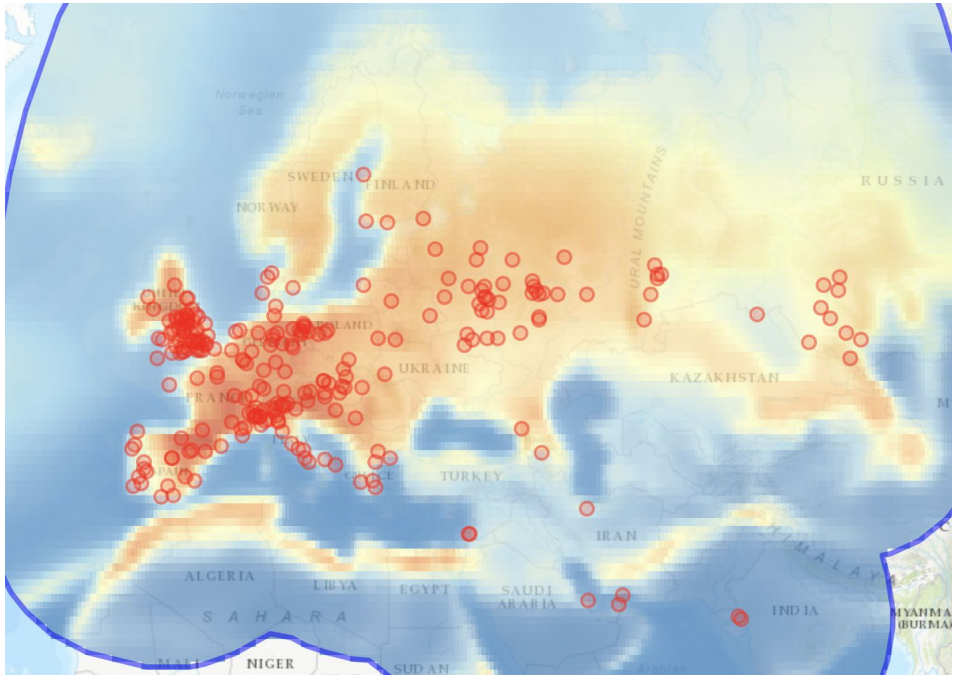
Binary



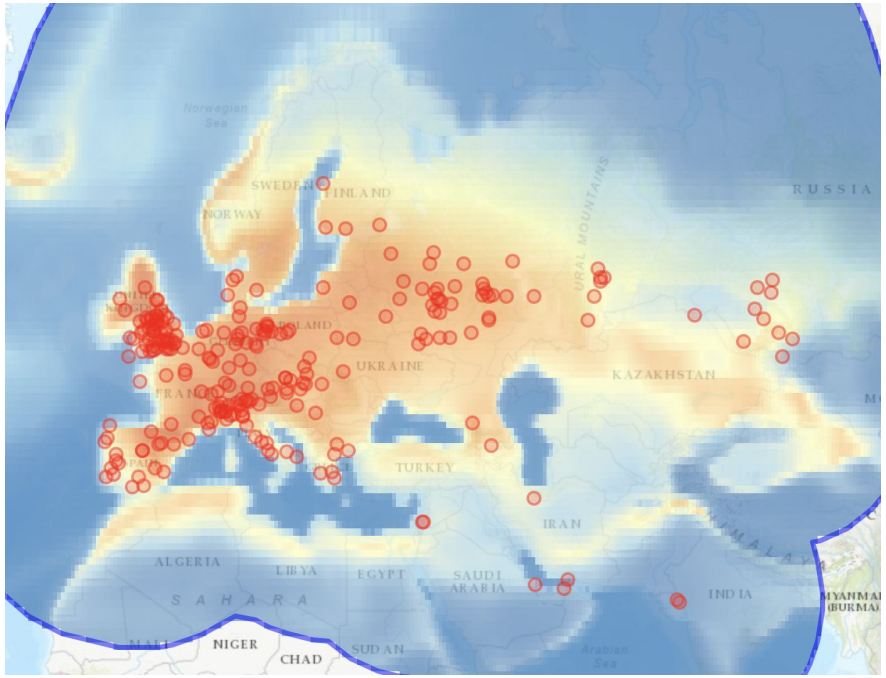
Visualize

- Map predictions

Linear



All features



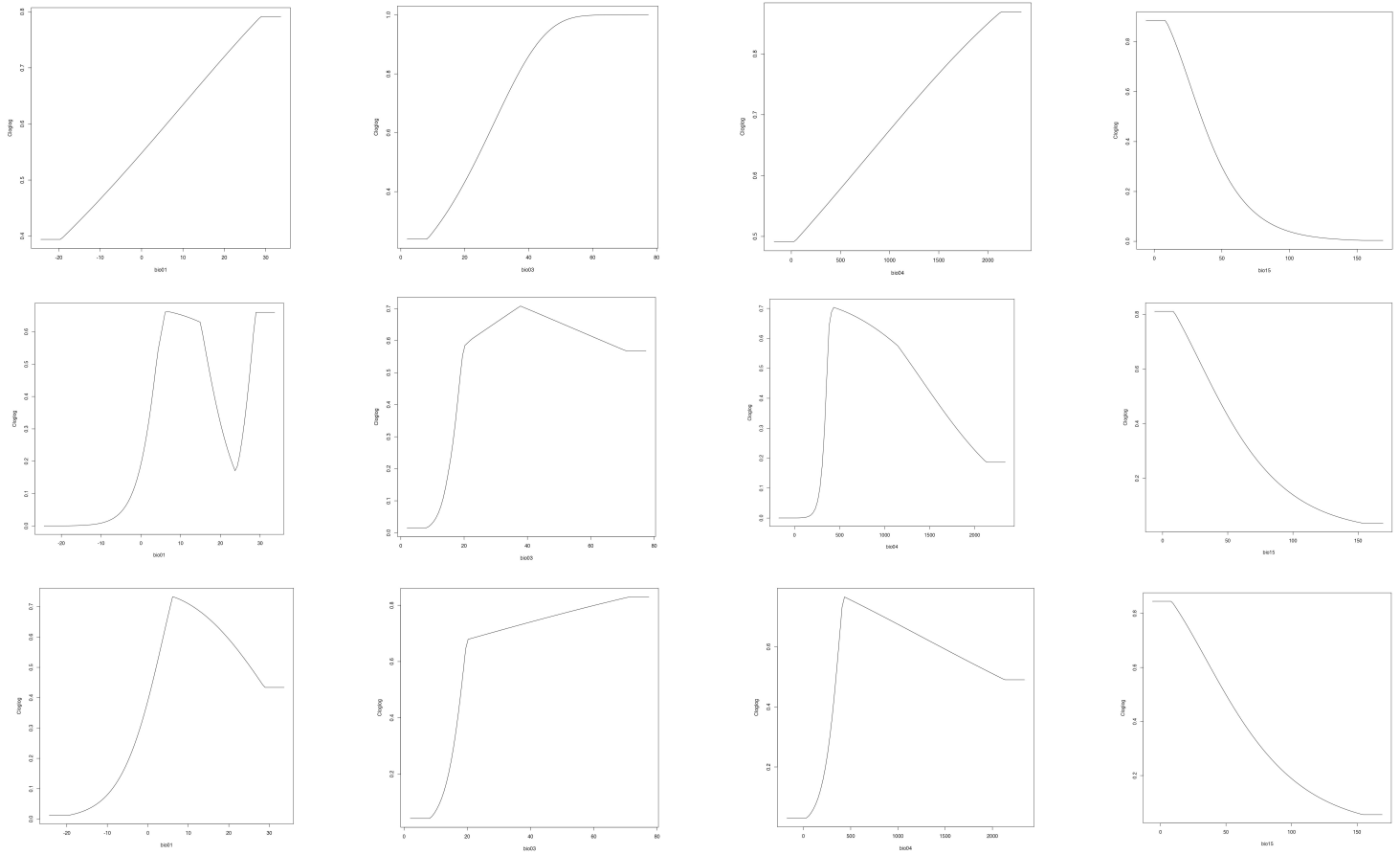
Visualize

- Response curves

Linear

All features,
No regularisation

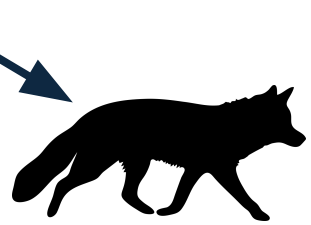
All features,
No regularisation



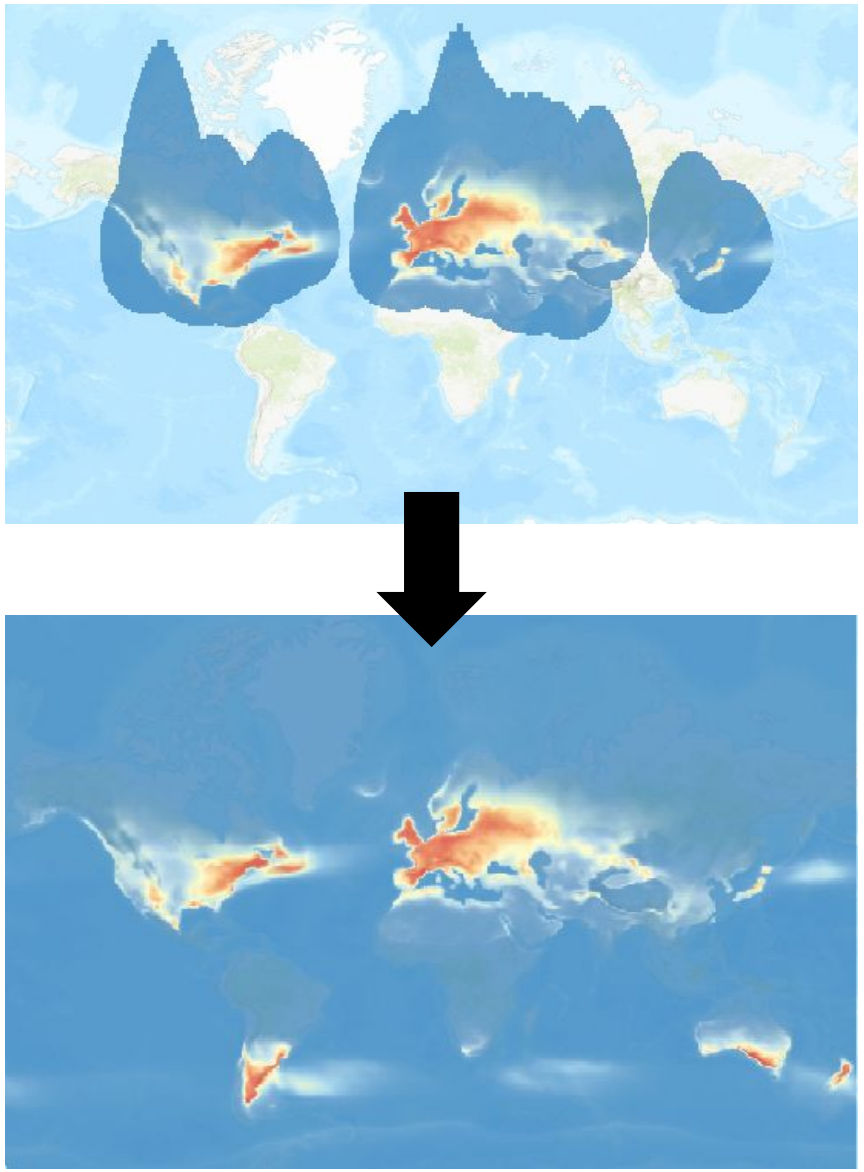
Bio 1 *Bio 3* *Bio 4* *Bio 15*

Transfer

- Predicting model in other geographic regions or time periods
  - e.g., for invasive/introduced species or effects of climate change



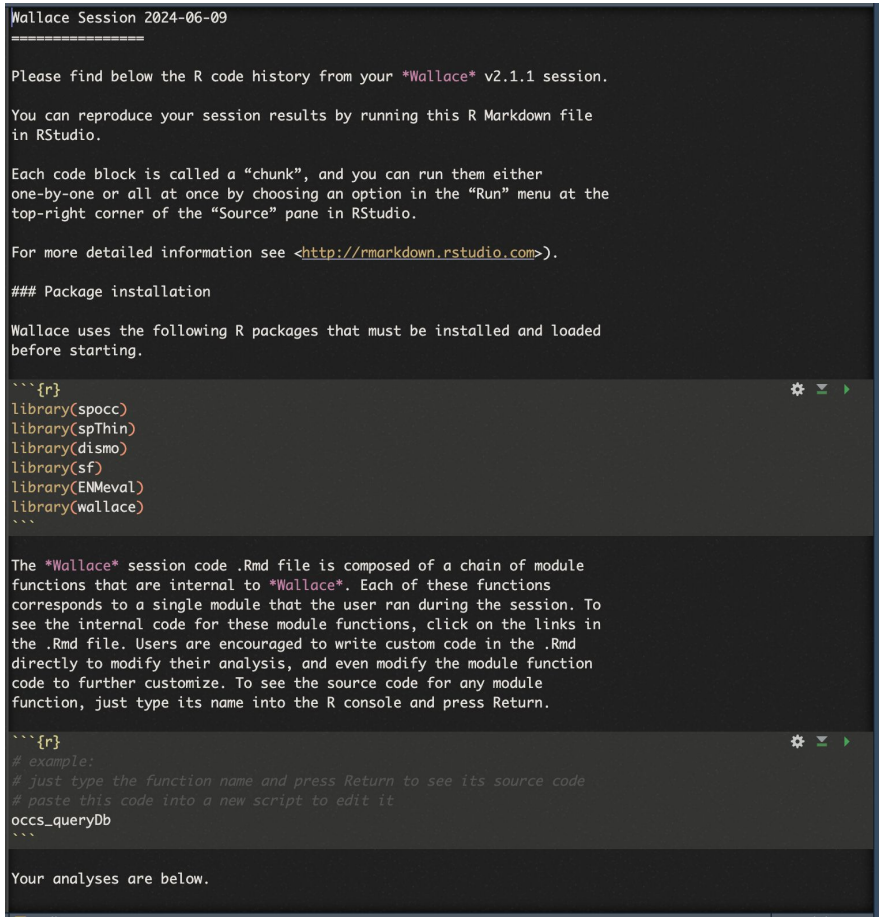
- Transfer to New Extent
  - Draw polygon to include Australia (entire world)
  - 0 degree buffer distance
- Transfer
  - No threshold: continuous



Reproduce

Download code

- Repeat analysis in one click with RStudio



Wallace Session 2024-06-09
==========

Please find below the R code history from your *Wallace* v2.1.1 session.

You can reproduce your session results by running this R Markdown file in RStudio.

Each code block is called a “chunk”, and you can run them either one-by-one or all at once by choosing an option in the “Run” menu at the top-right corner of the “Source” pane in RStudio.

For more detailed information see <http://rmarkdown.rstudio.com>).

Package installation

Wallace uses the following R packages that must be installed and loaded before starting.

```{r}
library(spocc)
library(spThin)
library(dismo)
library(sf)
library(ENMeval)
library(wallace)
```

The *Wallace* session code .Rmd file is composed of a chain of module functions that are internal to *Wallace*. Each of these functions corresponds to a single module that the user ran during the session. To see the internal code for these module functions, click on the links in the .Rmd file. Users are encouraged to write custom code in the .Rmd directly to modify their analysis, and even modify the module function code to further customize. To see the source code for any module function, just type its name into the R console and press Return.

```{r}
# example:
# just type the function name and press Return to see its source code
# paste this code into a new script to edit it
occs_queryDb
```

Your analyses are below.

For reference:

Araújo, M. B., Anderson, R. P., Márcia Barbosa, A., Beale, C. M., Dormann, C. F., Early, R., Garcia, R. A., Guisan, A., Maiorano, L., Naimi, B., O'Hara, R. B., Zimmermann, N. E., & Rahbek, C. (2019). Standards for distribution models in biodiversity assessments. Science Advances, 5(1), eaat4858. https://www.science.org/doi/10.1126/sciadv.aat4858

Feng, X., Park, D. S., Walker, C., Peterson, A. T., Merow, C., & Papeş, M. (2019). A checklist for maximizing reproducibility of ecological niche models. Nature Ecology & Evolution, 3(10), 1382–1395. https://www.nature.com/articles/s41559-019-0972-5

Merow, C., Smith, M. J., & Silander, J. A., Jr. (2013). A practical guide to MaxEnt for modeling species' distributions: what it does, and why inputs and settings matter. Ecography, 36(10), 1058–1069. https://nsojournals.onlinelibrary.wiley.com/doi/10.1111/j.1600-0587.2013.07872.x

Zurell, D., Franklin, J., König, C., Bouchet, P. J., Dormann, C. F., Elith, J., Fandos, G., Feng, X., Guillera-Arroita, G., Guisan, A., Lahoz-Monfort, J. J., Leitão, P. J., Park, D. S., Peterson, A. T., Rapacciuolo, G., Schmatz, D. R., Schröder, B., Serra-Diaz, J. M., Thuiller, W., … Merow, C. (2020). A standard protocol for reporting species distribution models. Ecography, 43(9), 1261–1277. https://nsojournals.onlinelibrary.wiley.com/doi/epdf/10.1111/ecog.04960

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GitHub page:
https://github.com/lucabutikofer/IUCN_SDM_Course