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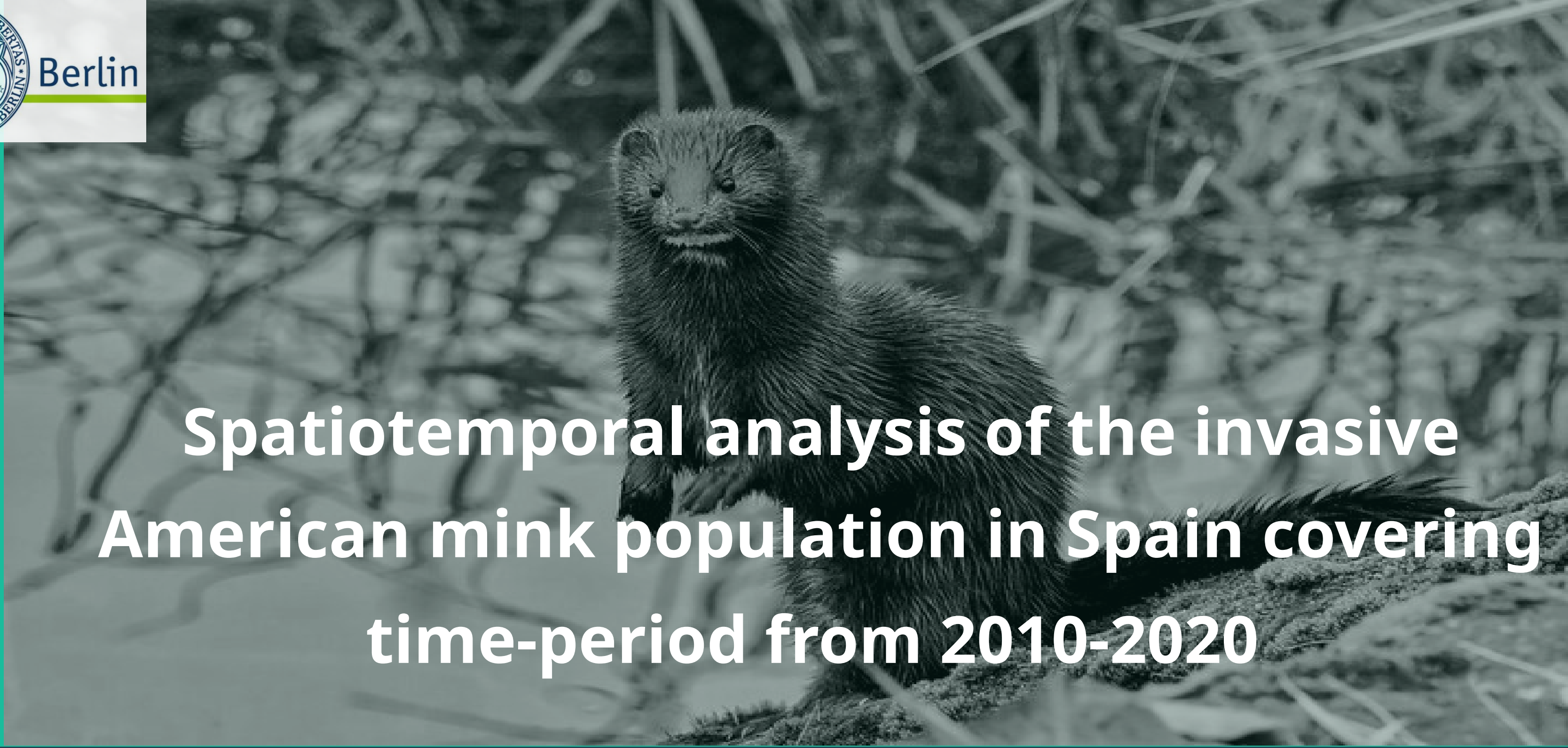


Spatiotemporal analysis of the invasive American mink population in Spain covering time-period from 2010-2020

Harsh Bardhan Gupta,

Supervision - Fiona Rickowski, Dr. Florian Ruland, Prof. Dr. Jonathan Jeschke

American Mink – An Invasive Species of Europe

- **The American mink (Neogale vison) is an high-impact invasive species invasive species in Europe that can disturb local flora and fauna.**
- **In Spain, mink farming began at the end of the 1950s, and the 1980s saw a peak in the number of farms and their escapes or deliberate releases resulted in the origin of the population.**
- **Studying and analyzing the current trend of the American mink population can be beneficial in understanding the process of invasion in the long run.**
- **For such analysis, We used I will use ML based species distribution modeling (SDM) algorithms and Agent based indivual eco-evolutionary model.**

Species Distribution Model - Spatiotemporal Trends

- **Species Distribution Modeling (SDM) and Mapping aims at explaining and mapping distribution of species as a function of ecological, environmental conditions and human influence.**
- **Typical steps in SDM include (Hijmans, 2019):**

➢ **Prepare locations of occurrence of a species or species density**

➢ **Prepare environmental predictor variables (climate, terrain, surface water)**

➢ **Fit a SDM model that can be used either to predict natural habitat / Niche and/or occurrence probability**

➢ **Predict habitat / occurrence probability across the region of interest (and perhaps for a future or past climate).**

Species Distribution Model - Spatiotemporal Trends

- Species training data often comes with occurrence-only records: ecologists often only record where some species was observed and their dynamics is often complex.
- If absence training points are not available, we have to derive pseudo-absence training points.
- Spatial interpolation is a process of estimating values of the target variable over the whole area of interest by spatial points, algorithm and values of the covariates (Enivornmental variables) at new locations. We used Ensemble Macine learning (EML) to do Spatiotemporal interpolation in both space and time.

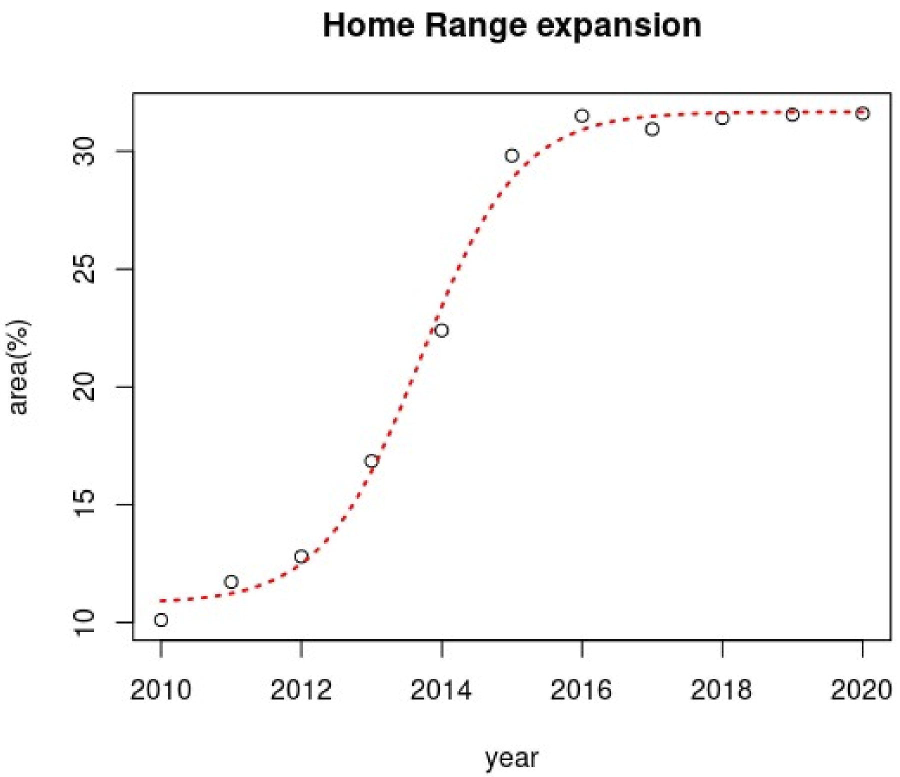
Objective

- Spatiotemporal analysis, interpolation, and visualization of invasive American mink’ s population in Spain.
- Generation of a trend map after producing predictions for American mink occurrence using different ML methods.
- Predict future population distribution over spain.
- In- Silico testing of future affect of controlling Mink population in Spain.

Study Range


1/7/2010
2010
2020
Data SIO, NOAA, U.S. Navy, NGA, GEBCO
Image Landsat / Copernicus
Imagery Date: 12/14/2015
45°50'21.32" N

Visualizing- Home range expansion



Psuedo Absence

- The quality of presence and absence data is crucial for the correlative SDM predictions to be accurate.
- So, it's crucial to determine a suitable way to describe pseudo-absences with minimum possible bias.
- Types of Pseudo-absence Selection Methods-
- Random pseudo-absence selection
- Pseudo absence points with limited geographical extent
- Pseudo-absence points based on environmental variables
- Novel Pseudo-absence Selection Method (based on environmental variables + limited geographical extent)

Psuedo Absence

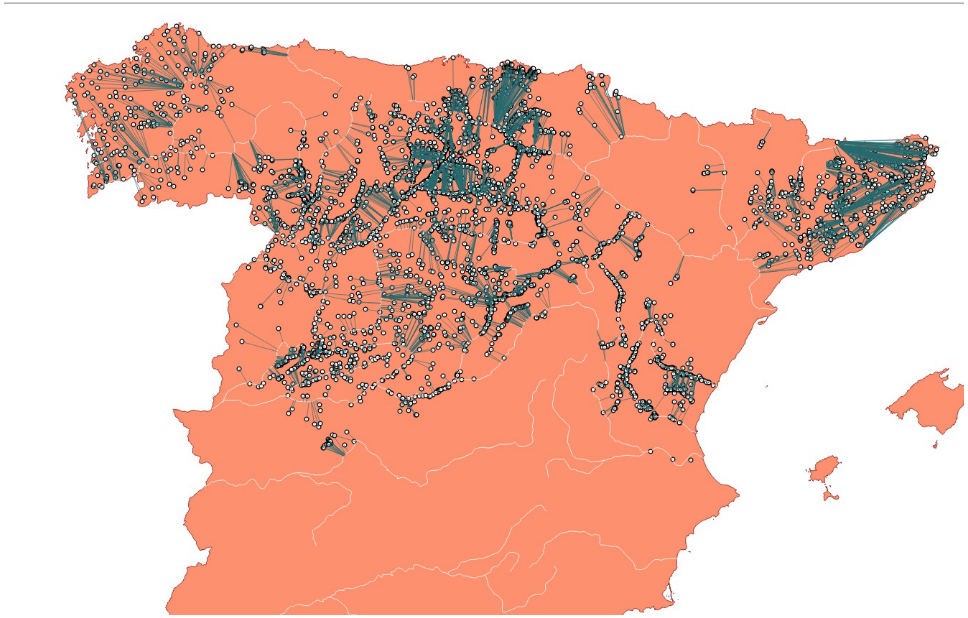
Suitable Enivorment

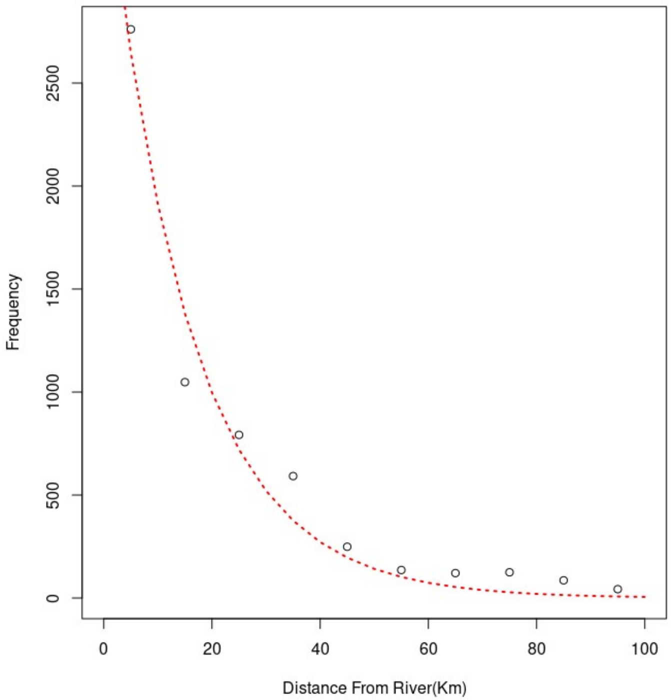
- MaxENT Algorithm
- Maximum entropy modeling for presence only data.
- compares the locations of where a species has been found to all the environments that are available in the study region

Limited geographical extent

- Elevation > 1500m
- Distance from nearest River > 60 Km

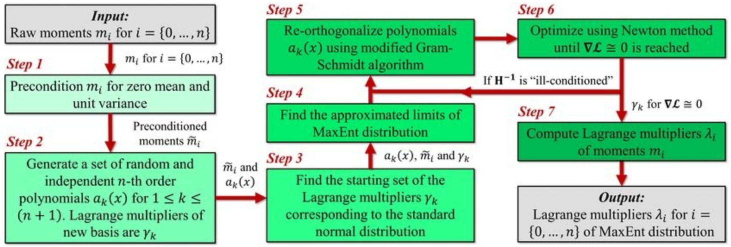
Distance from Waterways

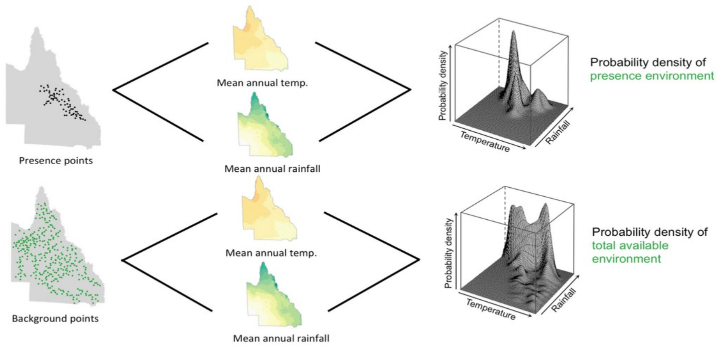




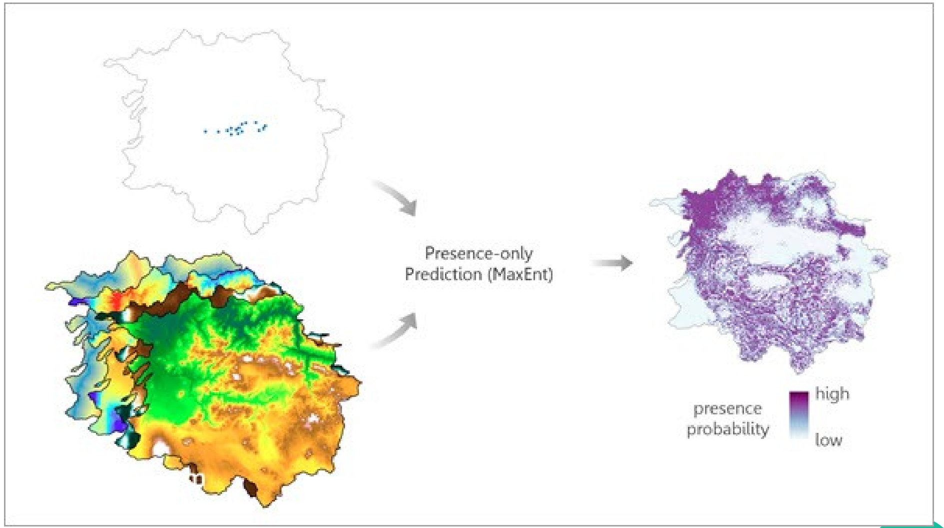
MaxENT - Algorithm

- predictions from incomplete information particularly designed for applications demanding presence-only data.
- determines how the environmental conditions at the species' occurrence localities relate to the environmental conditions across the rest of the study area.
- utilises a deterministic sequential-update algorithm that iteratively chooses and adjusts the weights of predictors until it converges to the probability distribution with the maximum entropy.

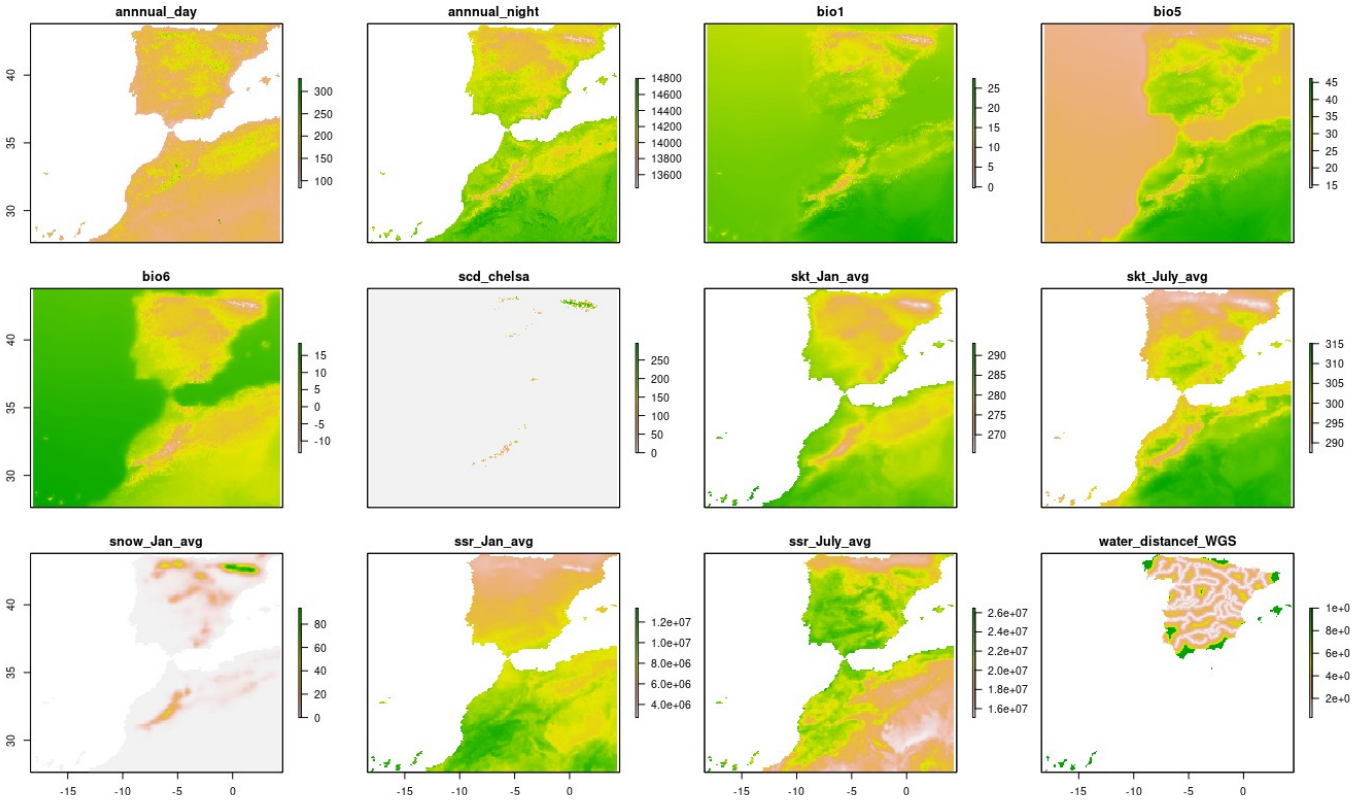




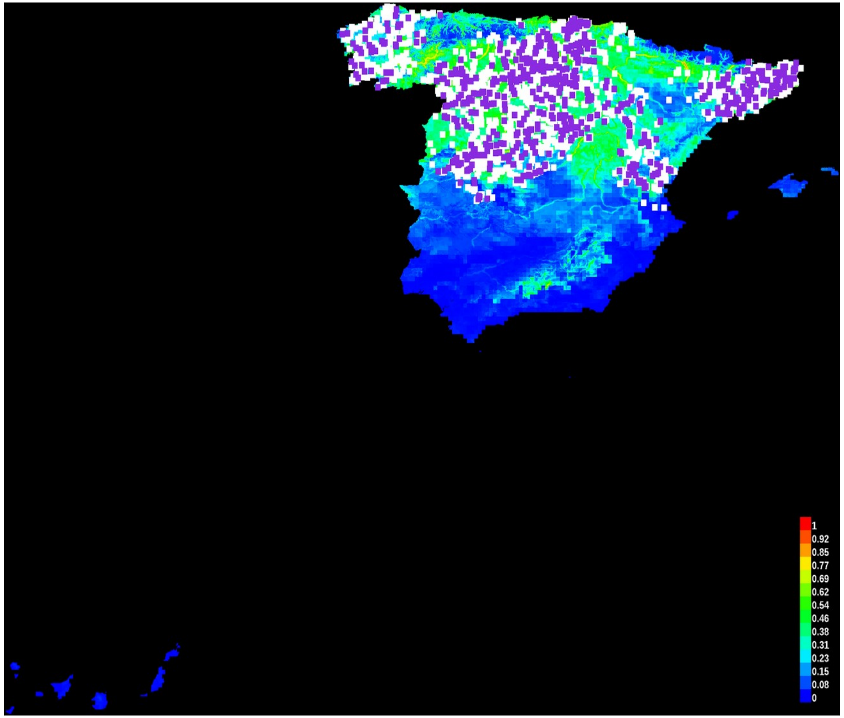
Adapted from Elith et al. (2011) *A statistical explanation of MaxEnt for ecologists*. Diversity and Distributions, 17, 43-57.

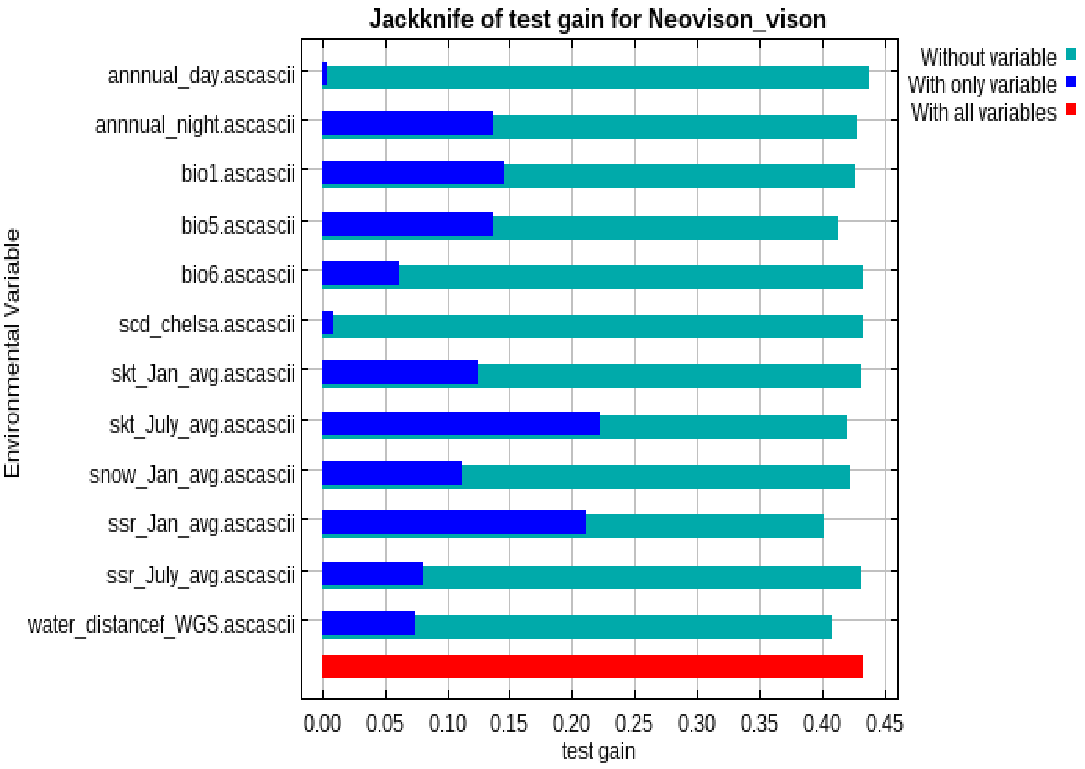


MaxEnt - Environments variables



MaxEnt Results



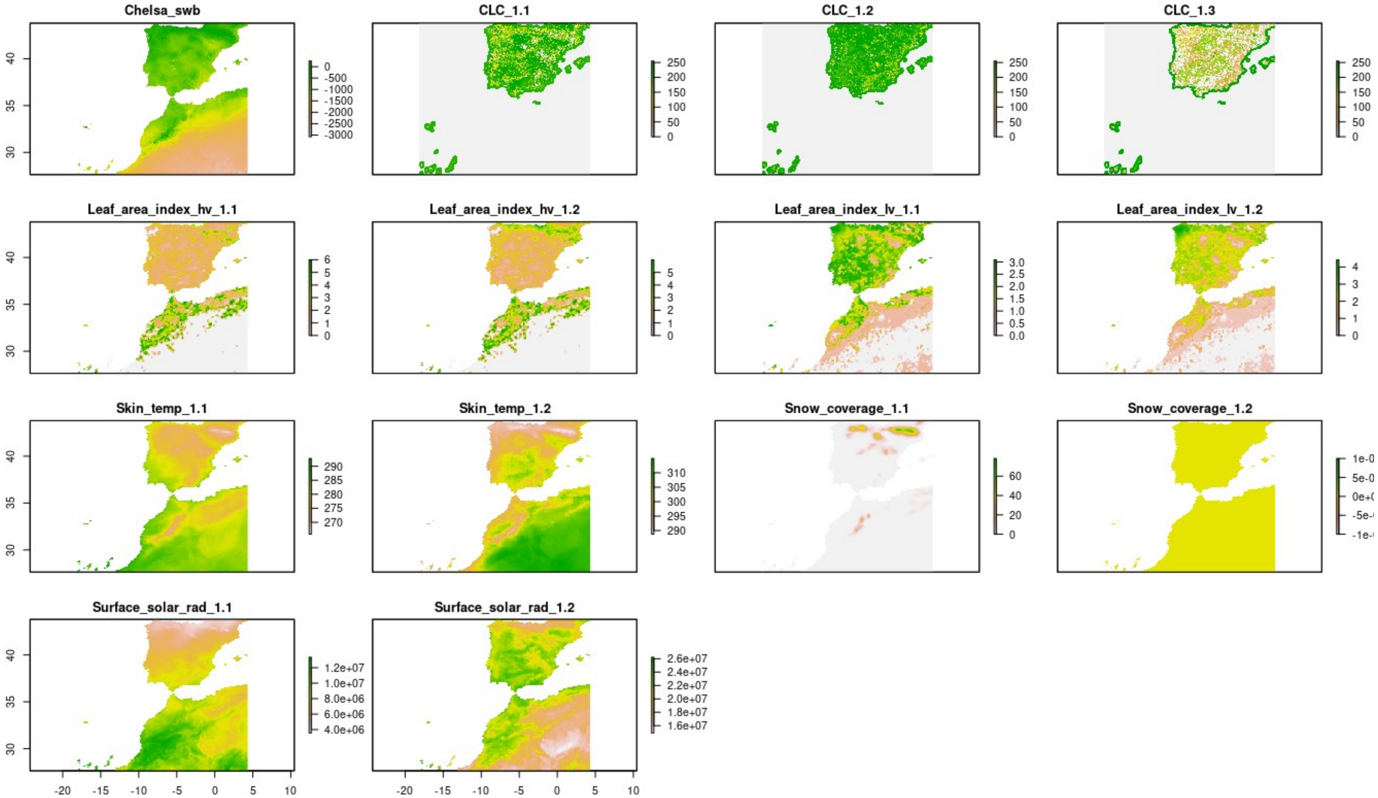


Ensemble Machine Learning

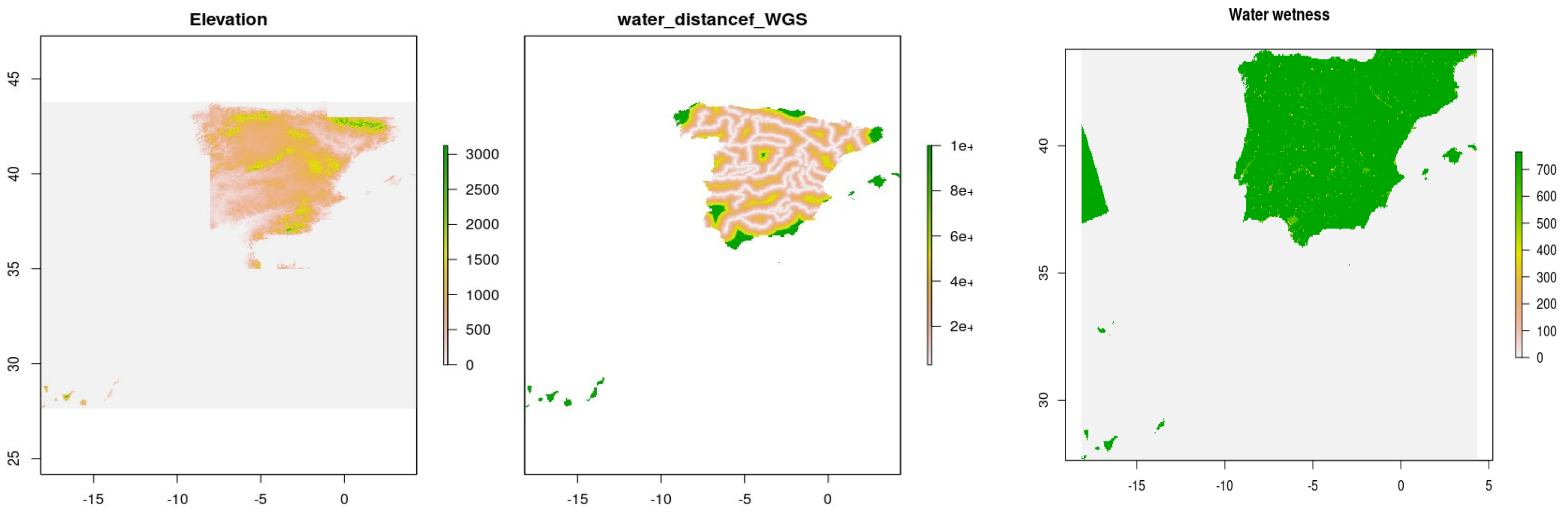
- In the Ensemble Machine Learning (EML) modelling approach, multiple strong learners are used in place of one best learner, and their predictive abilities are then combined into a single union
- lead to higher accuracy and robustness by decreasing some methodological disadvantages and Unbiasness of individual learners
- e.g.- Random Forest or neural networks (most flexible and best performing) always carry a bias in the sense that the fitting produces recognizable patterns
- Three principle three ways to apply ensembles (C. Zhang & Ma, 2012):

1) bagging: learn in parallel, then combine using some deterministic principle (e.g. weighted averaging),
2) boosting: learn sequentially in an adaptive way, then combine using some deterministic principle,
3) stacking: learn in parallel, then fit a meta-model to predict ensemble estimates.

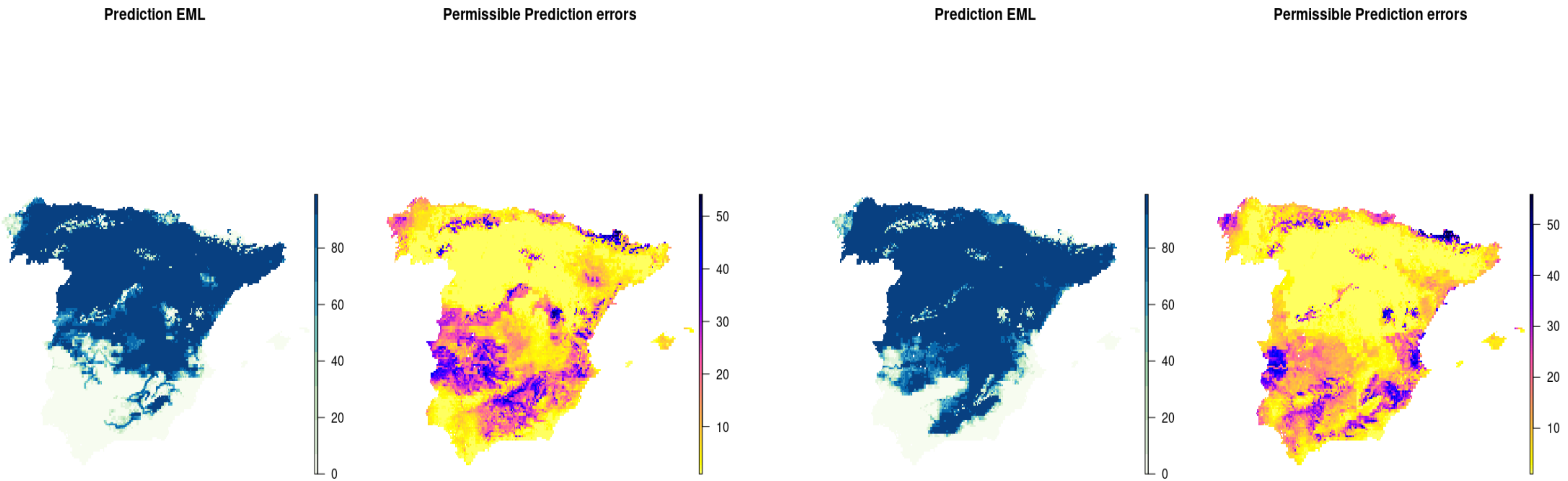
EML Methodology – Covariates (Dynamic)



EML Methodology – Covariates (Static)

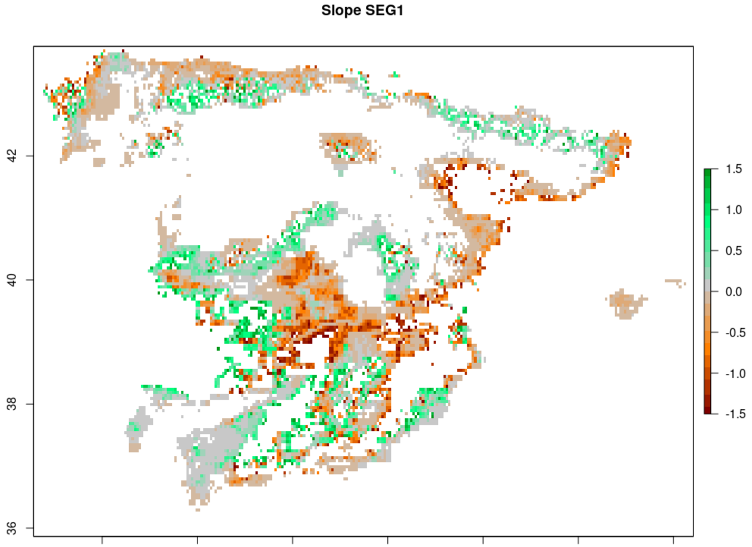


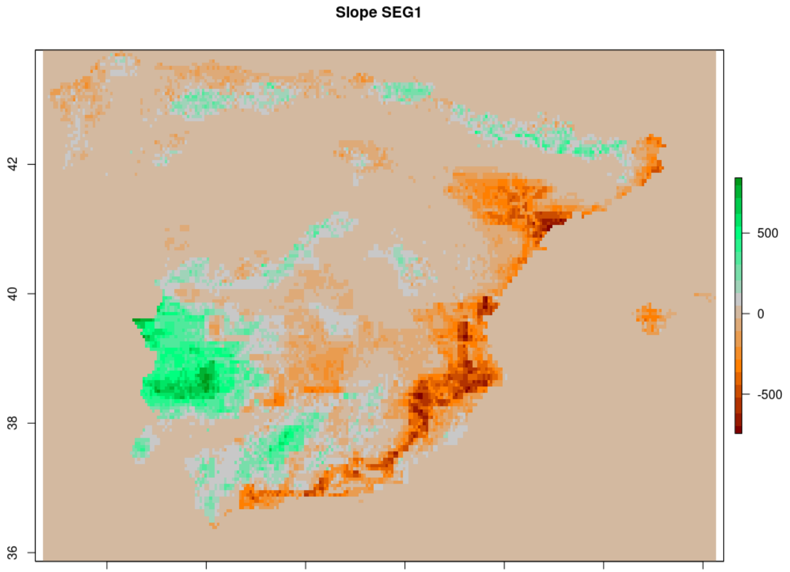
EML Results – Indv. year probability map



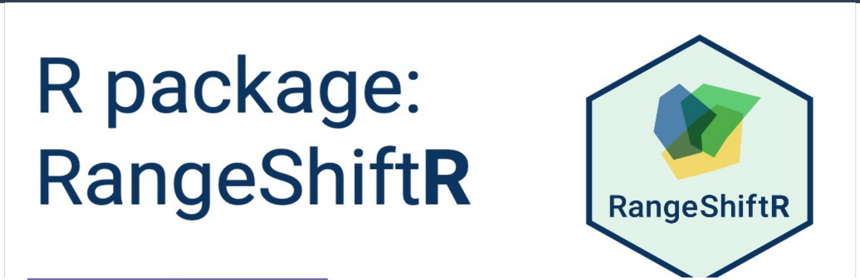
Avg Error – 0.12
Accuracy – 0.98

EML Results – Trend Map

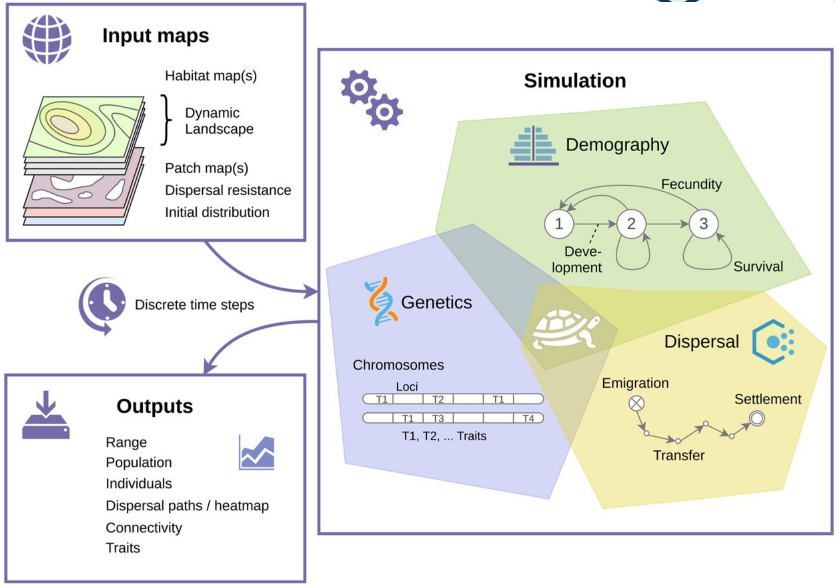


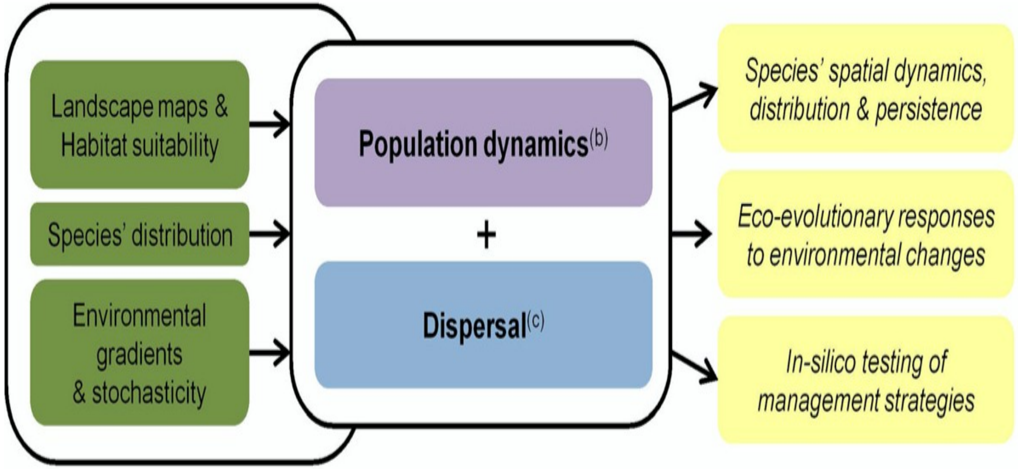


Individual Agent based model

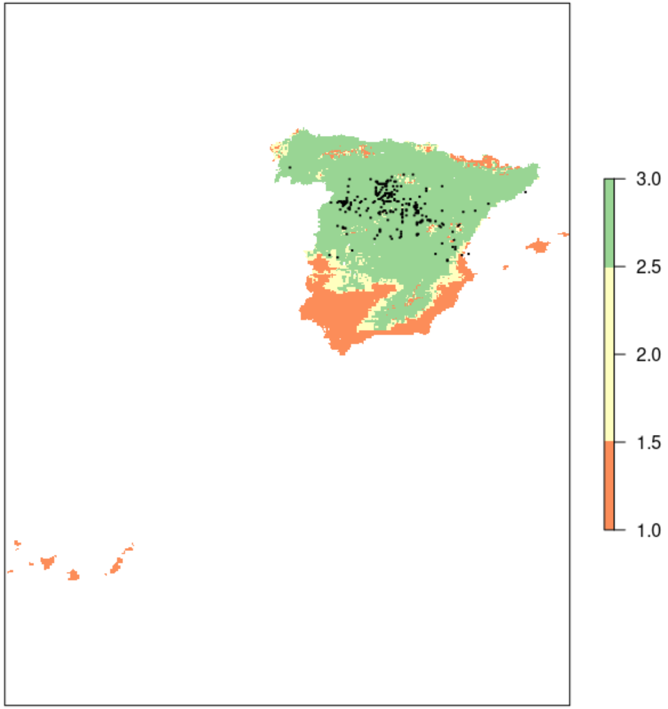


Individual-based models offer the additional capability to model inter-individual variation and evolutionary dynamics and thus capture adaptive responses Even if we don't have the known actual future environment.



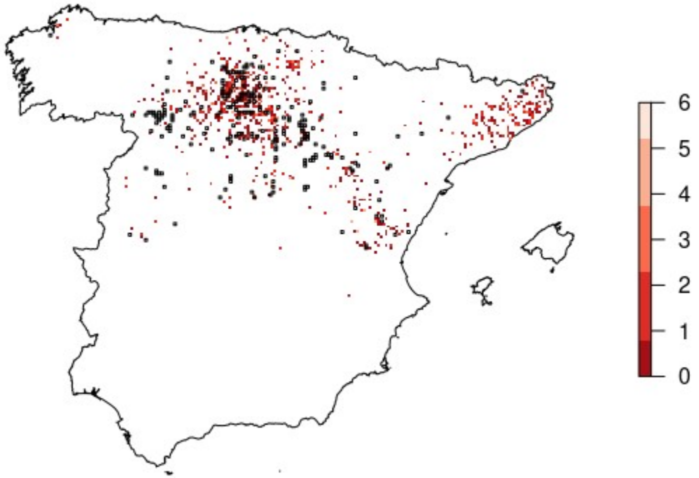


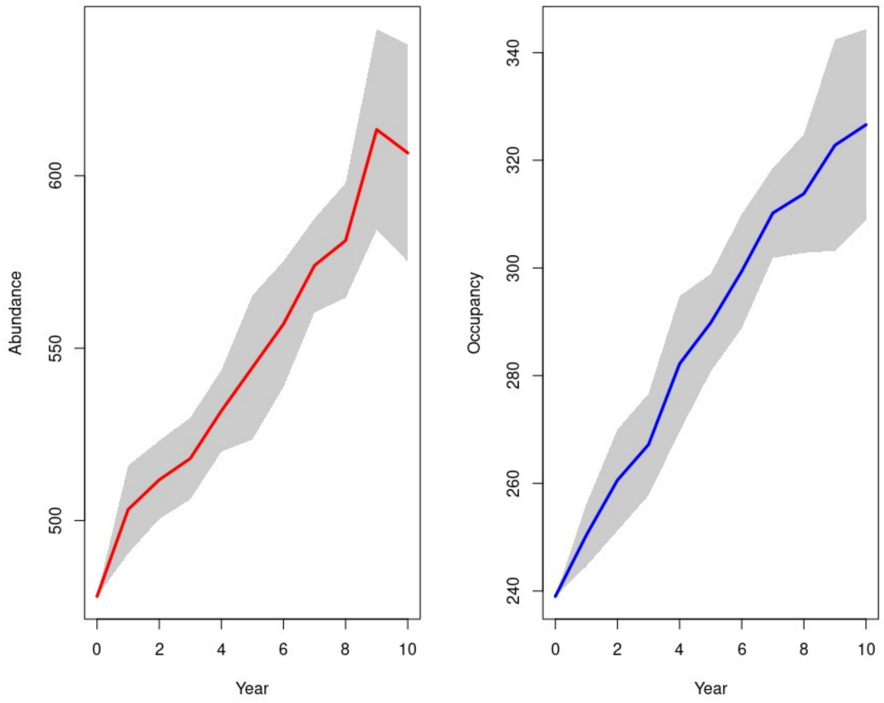
Landscape map - (Habitat Sutaibilty) and Parameters



- Grid of Cell - 5*5Km
- carrying capacity of each habitat type(0 , 3, 5) indv per cell
- Two stage juvenile stage, the adult stage
- a juvenile survival probability - 0.9 in their first year
- Asexual female model
- Only Juvenile Emigrates with mean dispersal of 40 Km
- Emigration probability – 100%
- Mean survival age – 10 years

Prediction for the 10 years starting from 2010

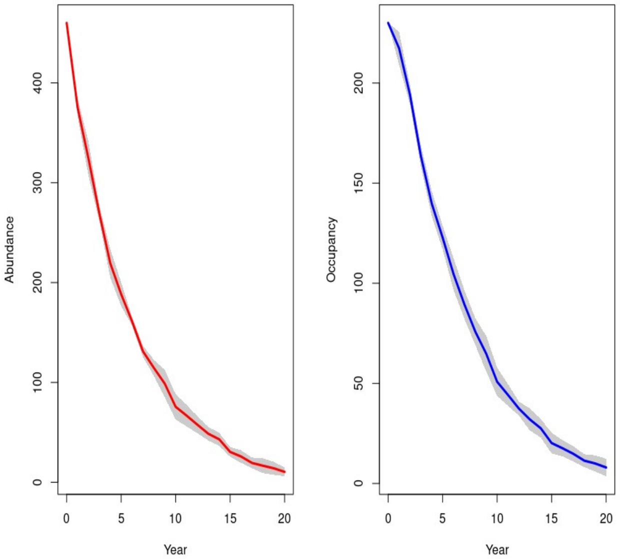




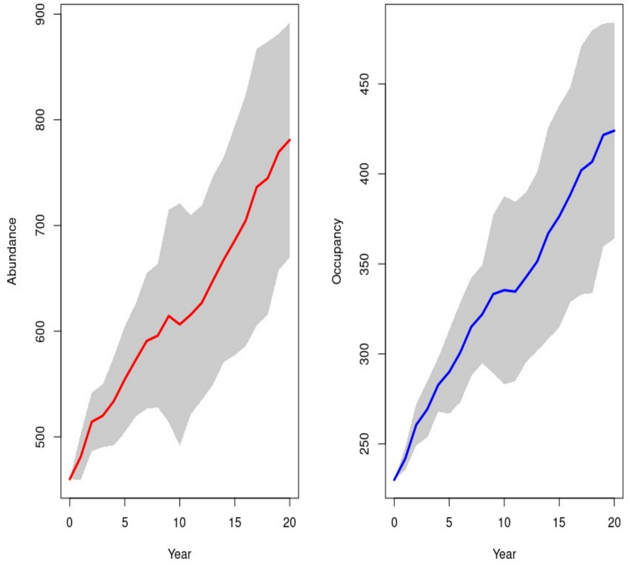
Fecundity -0.6

Survivability – 0.75

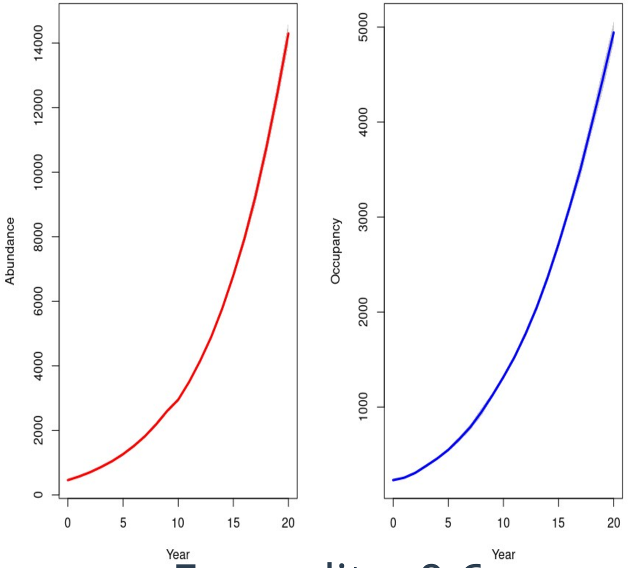
Prediction for the next 20 years with varying Survivability



Fecundity -0.6
Survivability – 0.6

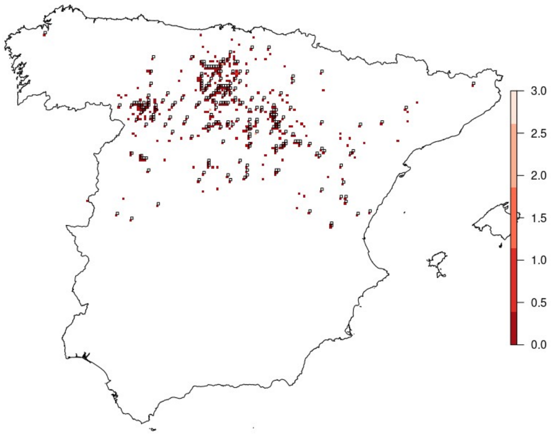


Fecundity -0.6
Survivability – 0.75

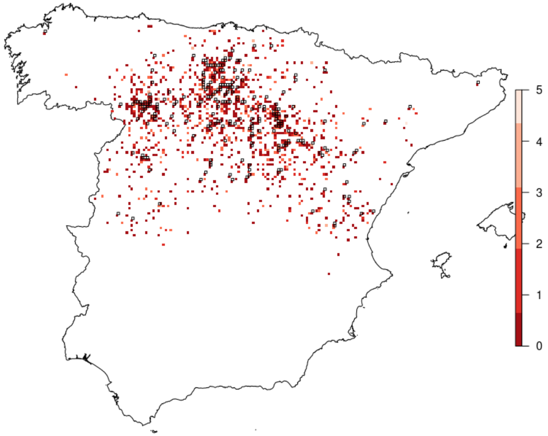


Fecundity -0.6
Survivability – 0.9

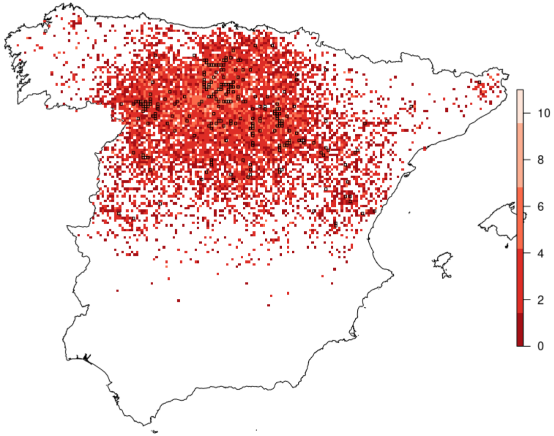
Prediction for the next 20 years with varying Survivability



Fecundity -0.6
Survivability – 0.6

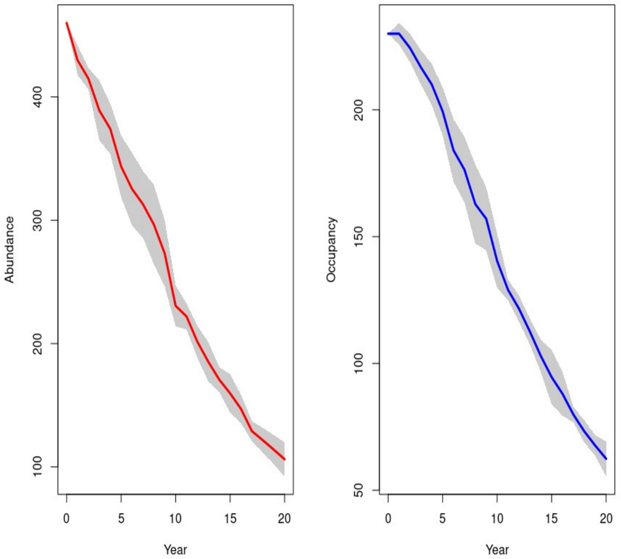


Fecundity -0.6
Survivability – 0.75

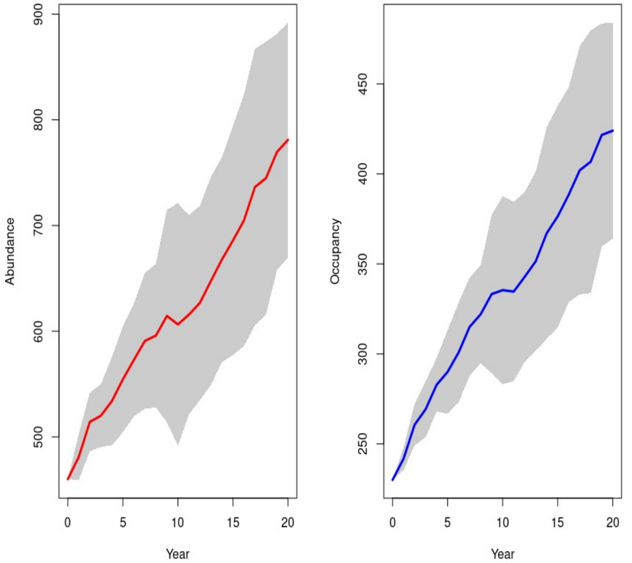


Fecundity -0.6
Survivability – 0.9

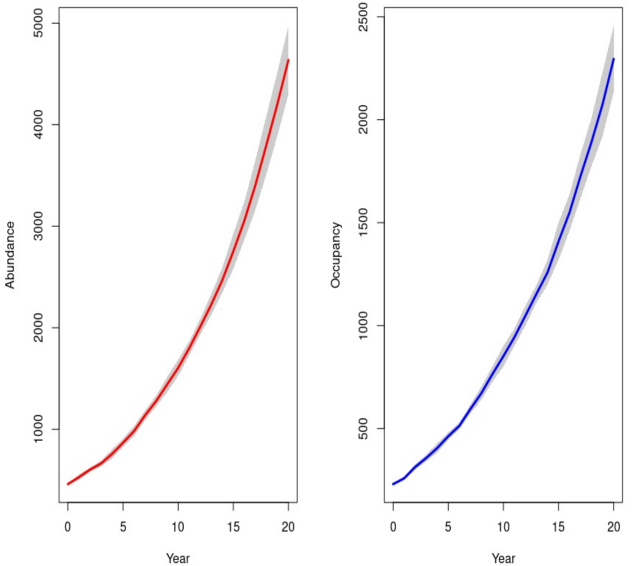
Prediction for the next 20 years with varying fecundity



Fecundity -0.4
Survivability – 0.75

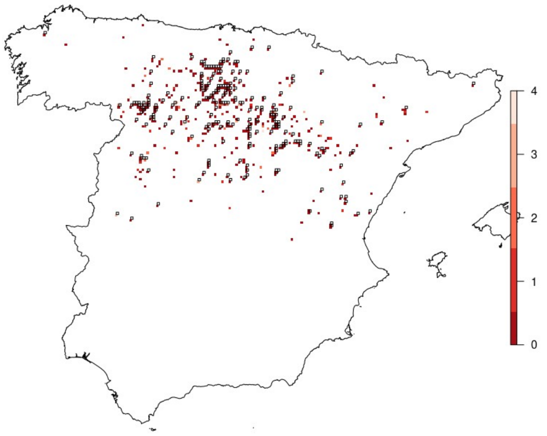


Fecundity -0.6
Survivability – 0.75

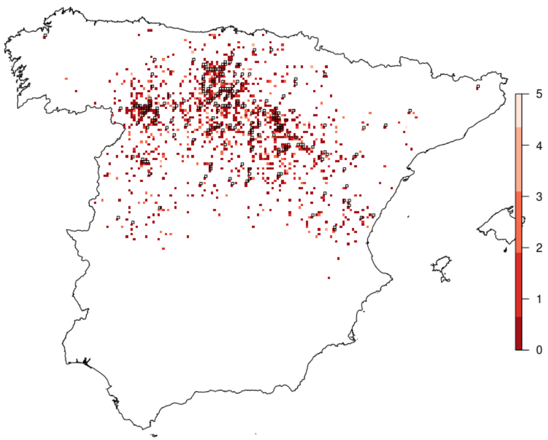


Fecundity -0.8
Survivability – 0.75

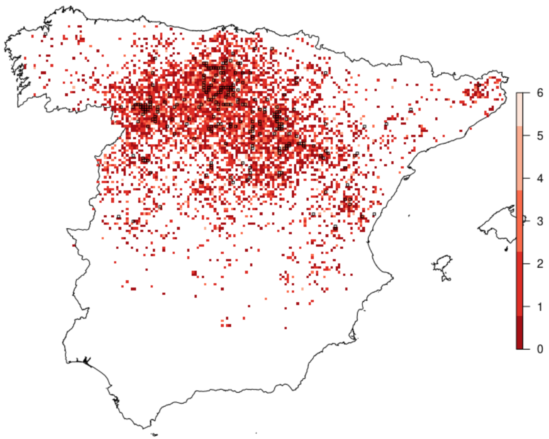
Prediction for the next 20 years with varying fecundity



Fecundity -0.4
Survivability – 0.75

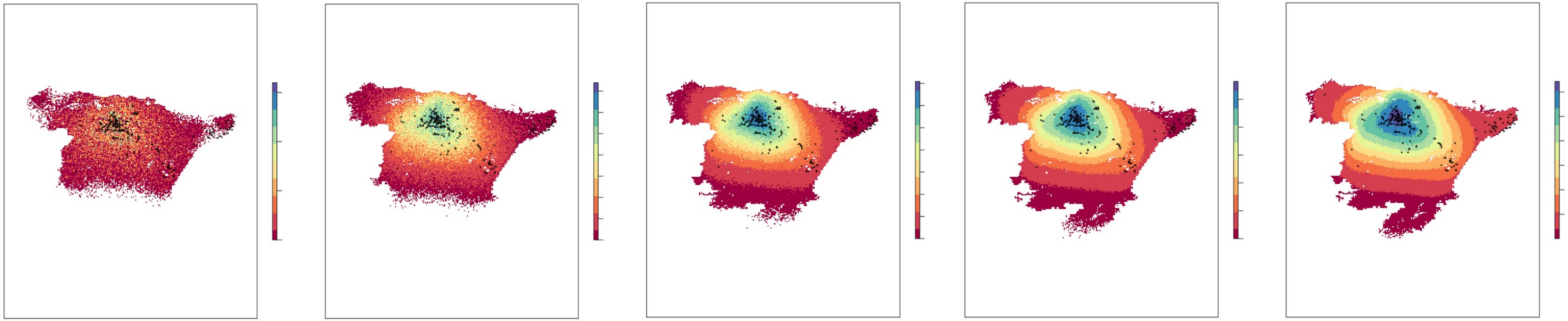


Fecundity -0.6
Survivability – 0.75



Fecundity -0.8
Survivability – 0.75

Probabilty prediction for the next 10 years with varying Rmax



Rmax – 0.6 | Rmax – 0.8 | Rmax – 1.0 | Rmax – 1.2 | Rmax – 1.4

Future Changes

- More data points in temporal scale
- Higher resolution environment maps
- Factor analysis and removing less affecting covariates
- Sexual model in individual based model
- Dyanmic environment and stochasticity in individual based model.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