



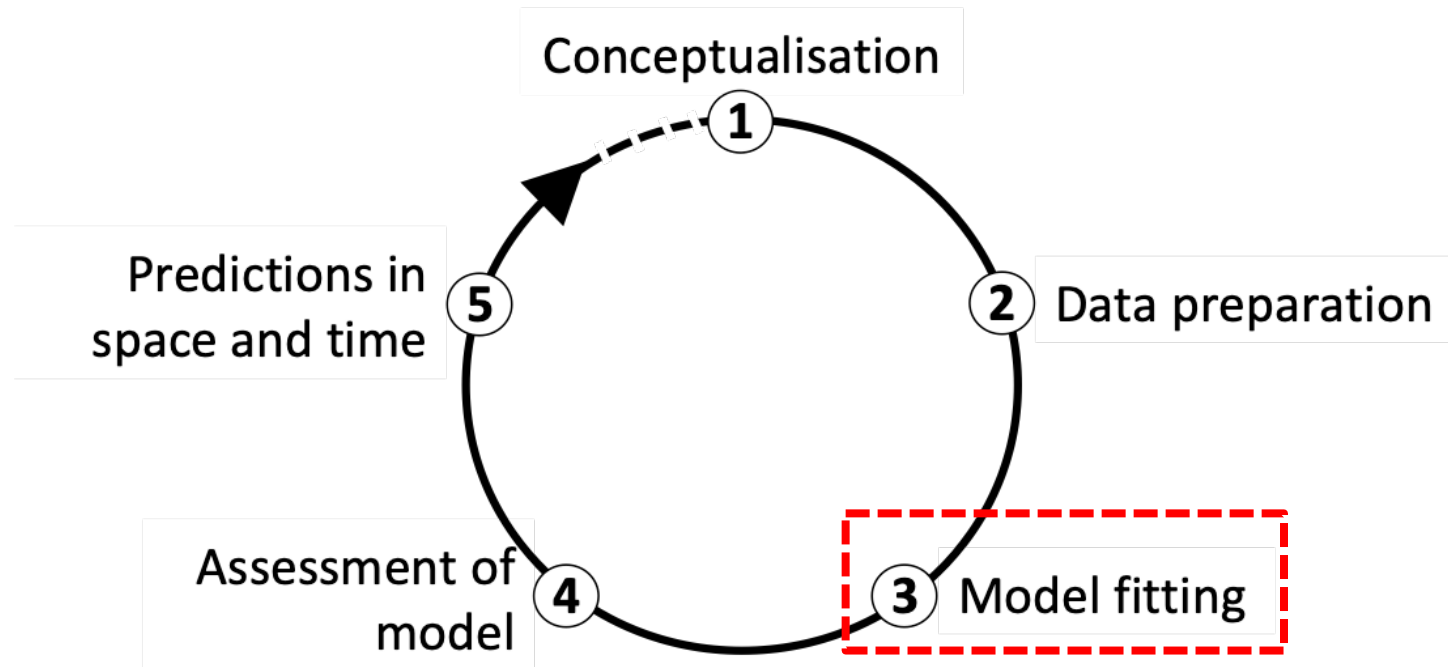
SDMs algorithms & ensembles

Damaris Zurell

<https://damarisurell.github.io>

 @ZurellLab

SDM – model building steps



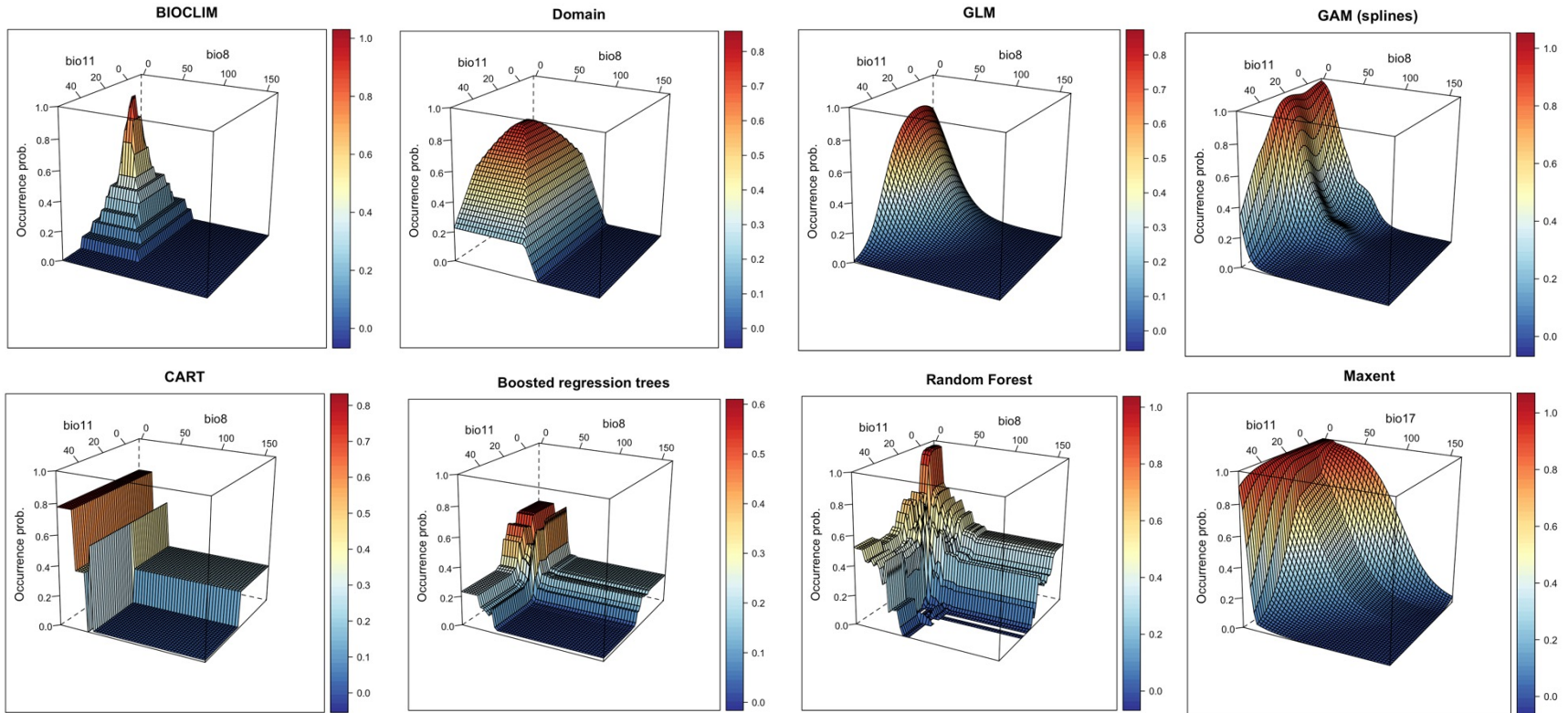
SDM algorithms

Many different algorithms available for SDMs:

- Profile methods
- Regression
- Machine-learning

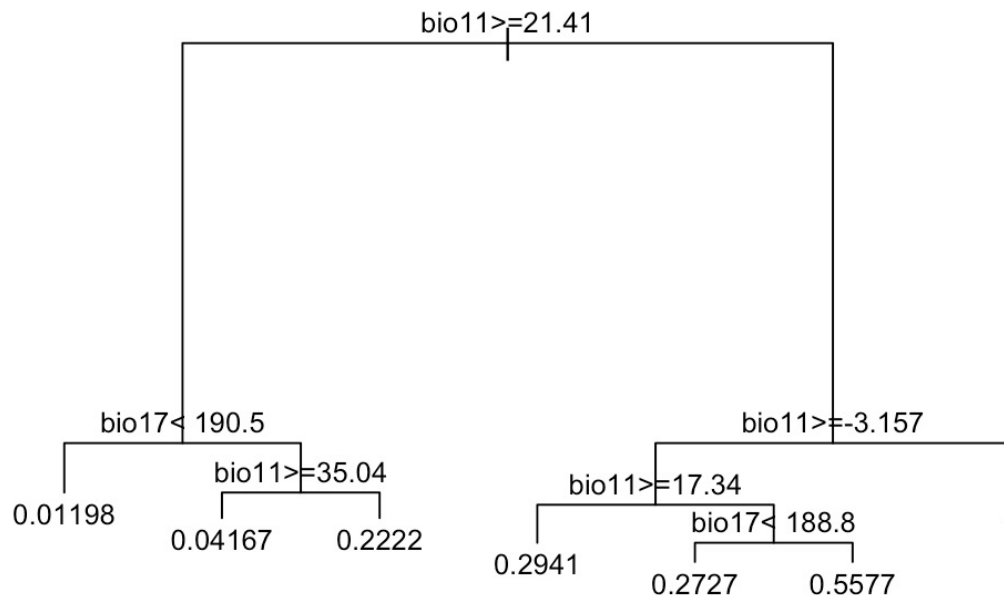
- **Profile methods** only consider species presences; use simple statistical techniques, e.g. environmental distance to known sites
 - e.g. BIOCLIM, DOMAIN, Mahalanobis distance
- **Regression-based** techniques and **machine-learning** algorithms use presence and absence (or background) data to contrast used and unused sites
 - **Regression:** e.g. generalised linear model (GLM), generalised additive model (GAM), multivariate adaptive regression splines (MARS), ...
 - **Machine-learning:** e.g. classification and regression tree (CART), artificial neural network (ANN), generalised boosted model/boosted regression trees (GBM/BRT), random forest (RF), maximum entropy (Maxent), genetic algorithms, ...

SDM algorithms



Machine-learning: CART

- Classification and regression trees (CARTs)
- Recursive partitioning method to divide the data into homogeneous subgroups
- Find splits (nodes) that best separate the observations
- Interactions between variables fitted automatically

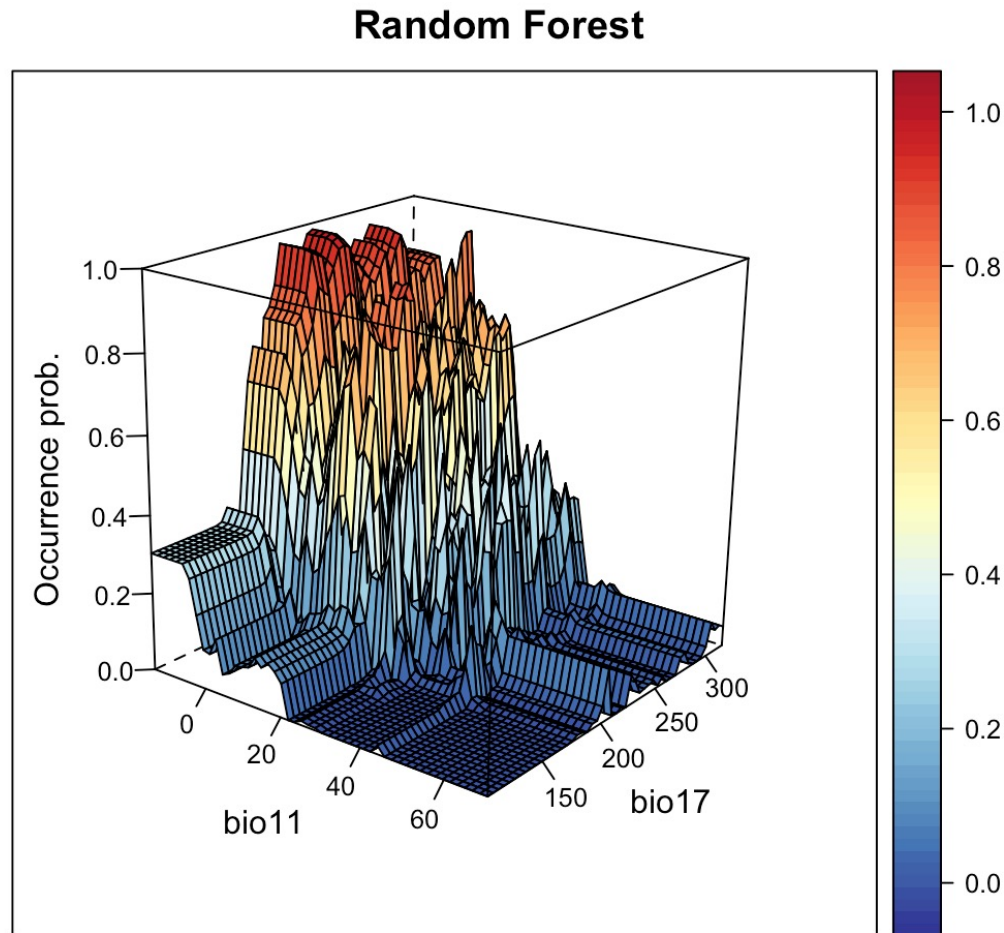


Machine-learning: CART extensions

- CARTs sensitive to noise: typically show low bias and high variance
- One solution: model averaging
 - ❖ Bagging = bootstrap aggregation: fit many CARTs to bootstrapped samples of data and average results
 - ➔ Random Forest
 - ❖ Boosting: fit relatively simple CARTs sequentially in adaptive way = each model depends on the previous ones
 - ➔ Boosted regression trees

Machine-learning: random forest

➤ R package „randomForest“



Machine-learning: random forest

➤ R package „randomForest“

```
m_rf <- randomForest( x=sp_train[,my_preds], y=sp_train$Turdus_torquatus,  
  ntree=1000, importance =T)
```

Diagram illustrating the R package `randomForest` function call:

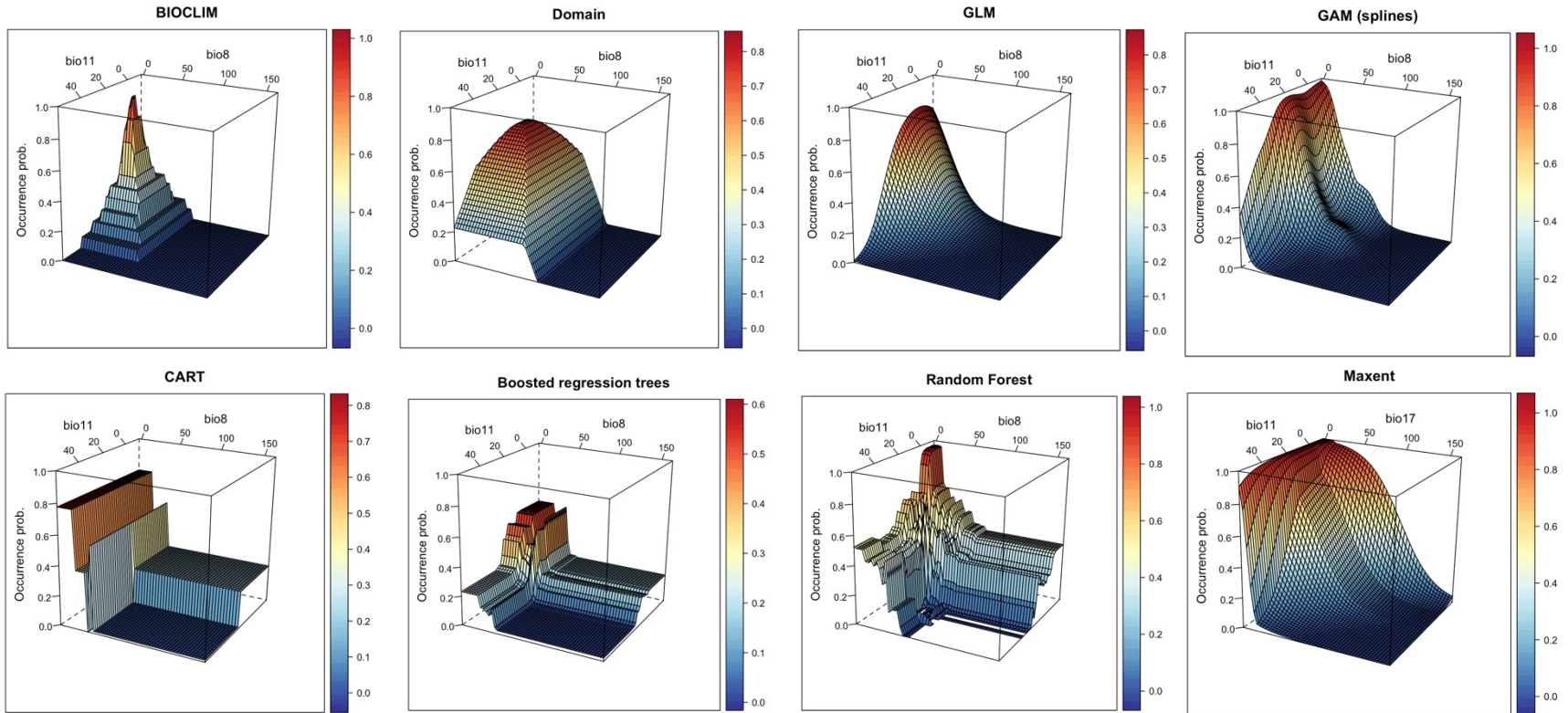
- `x=sp_train[,my_preds]`: Data frame of predictors
- `y=sp_train$Turdus_torquatus`: Response
- `ntree=1000`: How many trees to grow?
- `importance =T`: Should variable importance be computed?

```
predict(m_rf, xyz, type='prob')[,2]
```

Diagram illustrating the `predict` function call:

- `xyz`: Data frame with predictor variables
- `type='prob'`: Response type: probabilities
- `[,2]`: Probability of presence

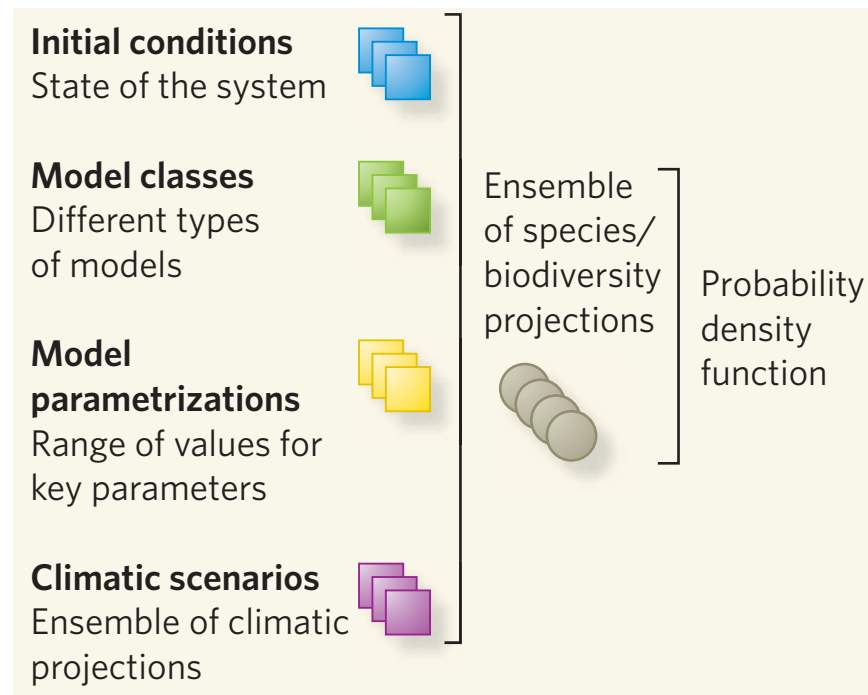
SDM algorithms



- There is no single best approach for SDMs. (I have no favourite)
- Model choice should be guided by model purpose, available data, scale, ...
- More complex models tend to better fit current species-environment relationship. Yet, it is highly debated whether more complex models make better **predictions under global change**.
- For global change analyses, the IUCN recommends to **use at least three algorithms that are as independent as possible**.

SDM ensembles

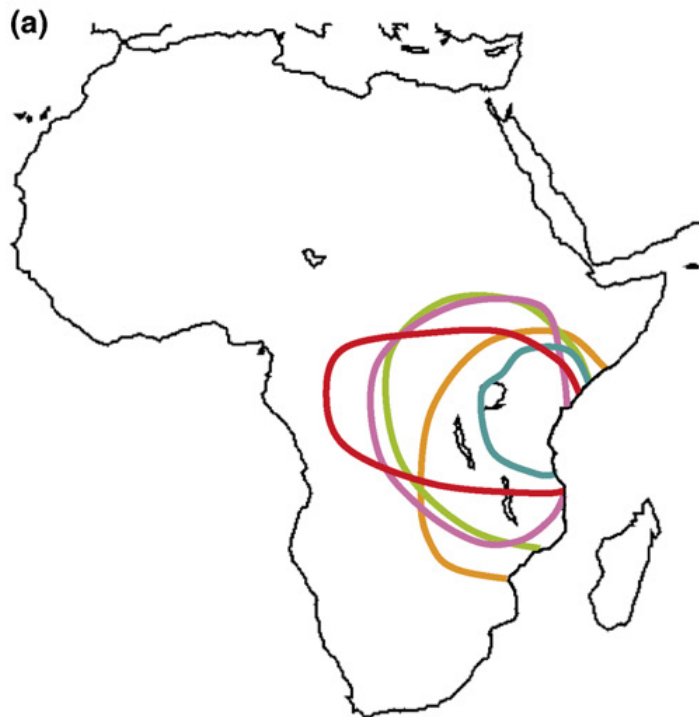
- Ensembles of forecasts are produced by making multiple simulations across more than one set of initial conditions (data), model classes, model parameterisations, and boundary conditions (scenarios)



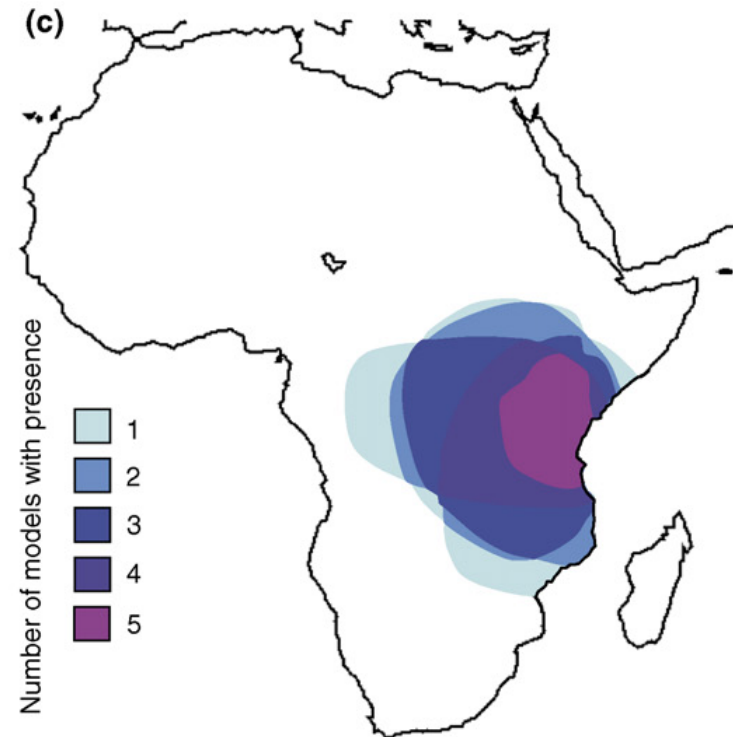
SDM ensembles

- The final predictions can be combined in different ways

Individual model predictions



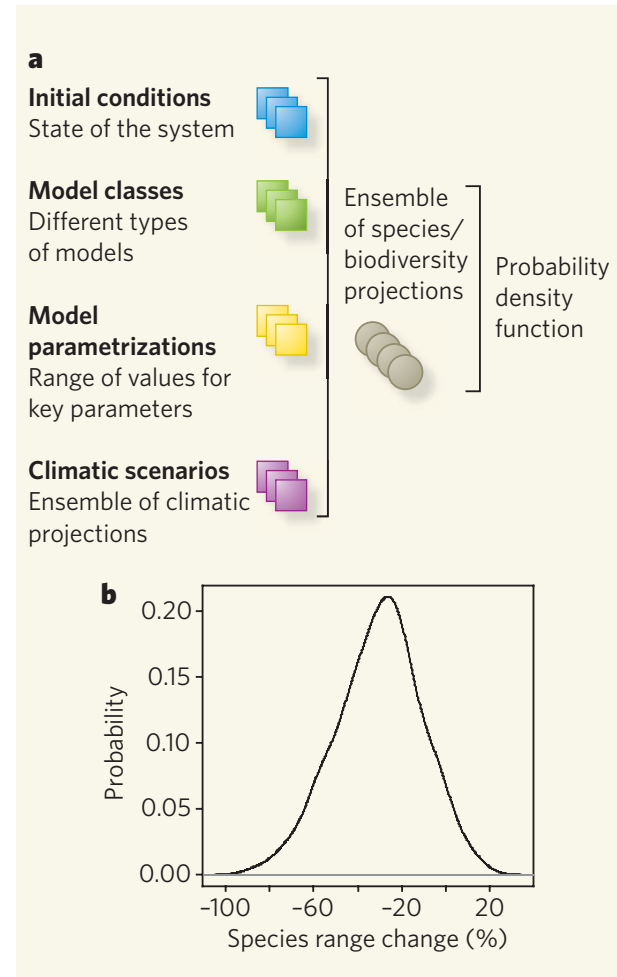
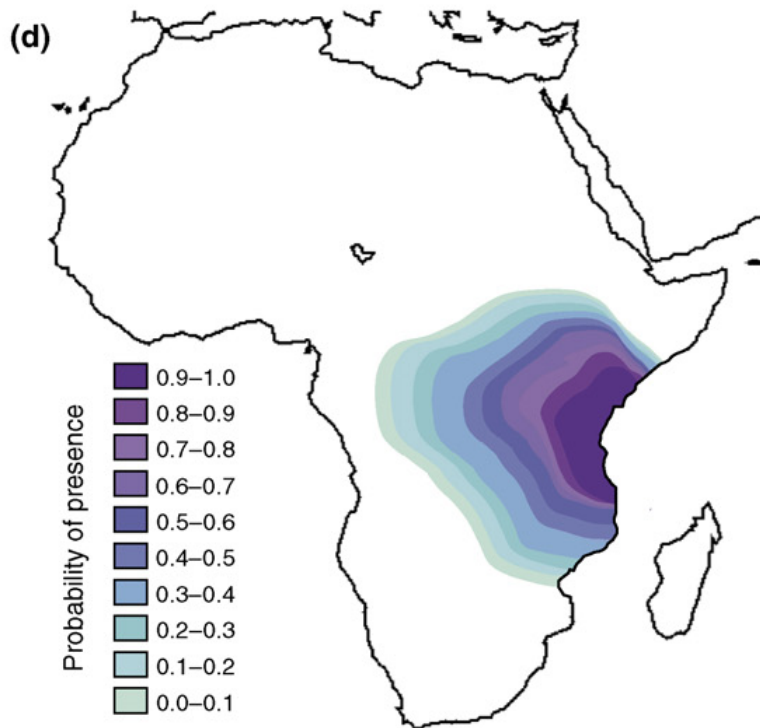
Committee average of binary predictions



SDM ensembles

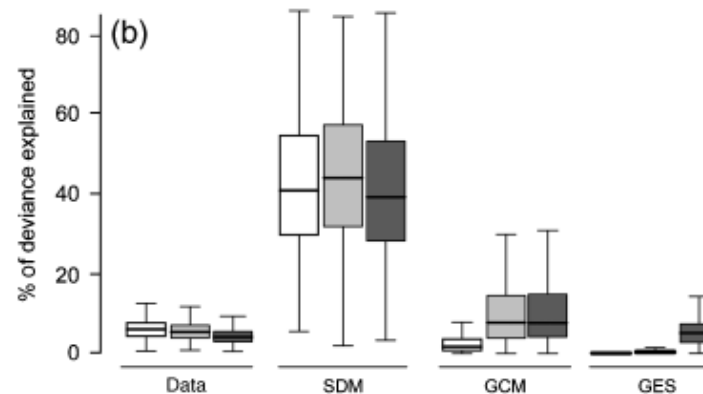
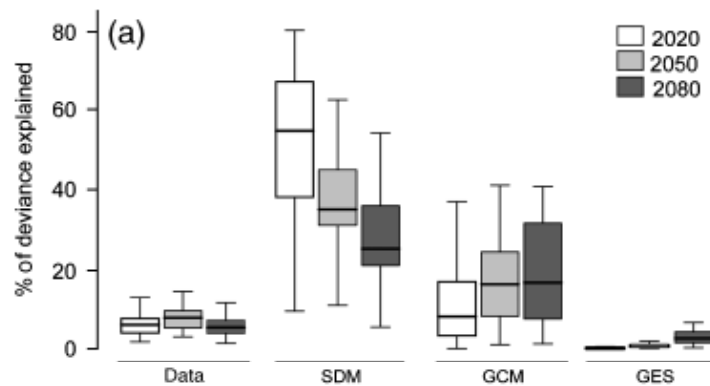
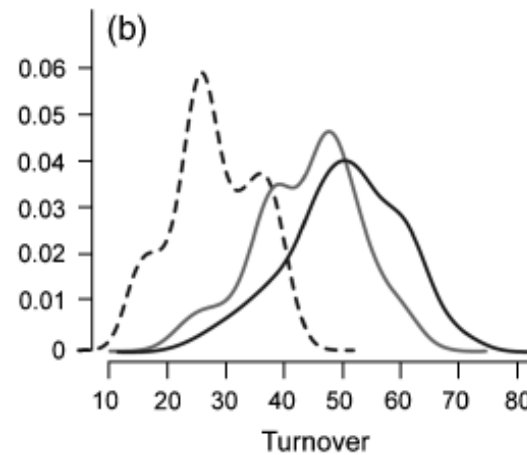
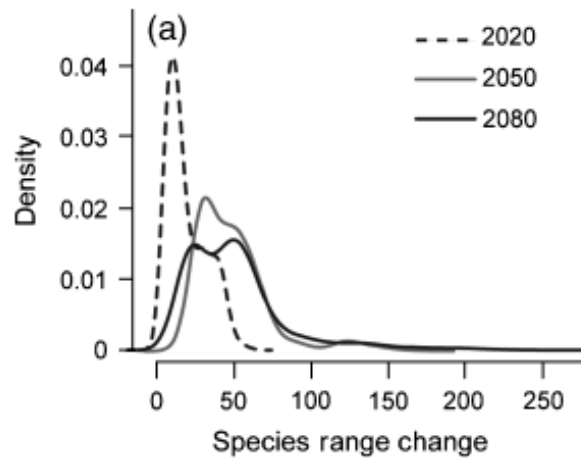
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Consensus – central tendency



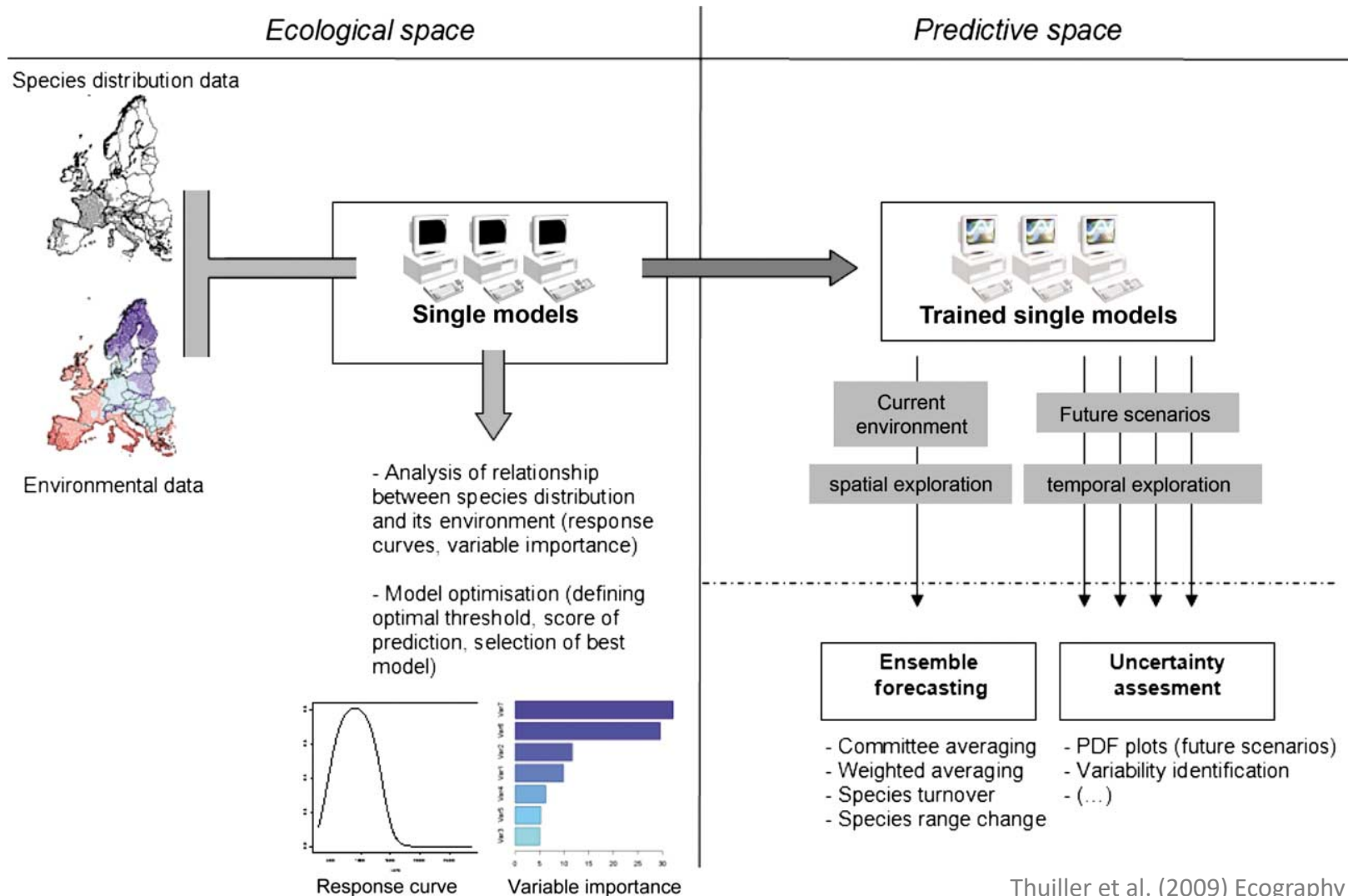
SDM ensembles

- Purpose: accounting for sources of uncertainty



SDM ensembles


- Dedicated R packages, e.g. *biomod2*



Thank you for your interest

Contact:
Damaris Zurell
Ecology & Macroecology
University of Potsdam



<https://damarisurell.github.io>
Email: damaris.zurell@uni-potsdam.de
 @ZurellLab