

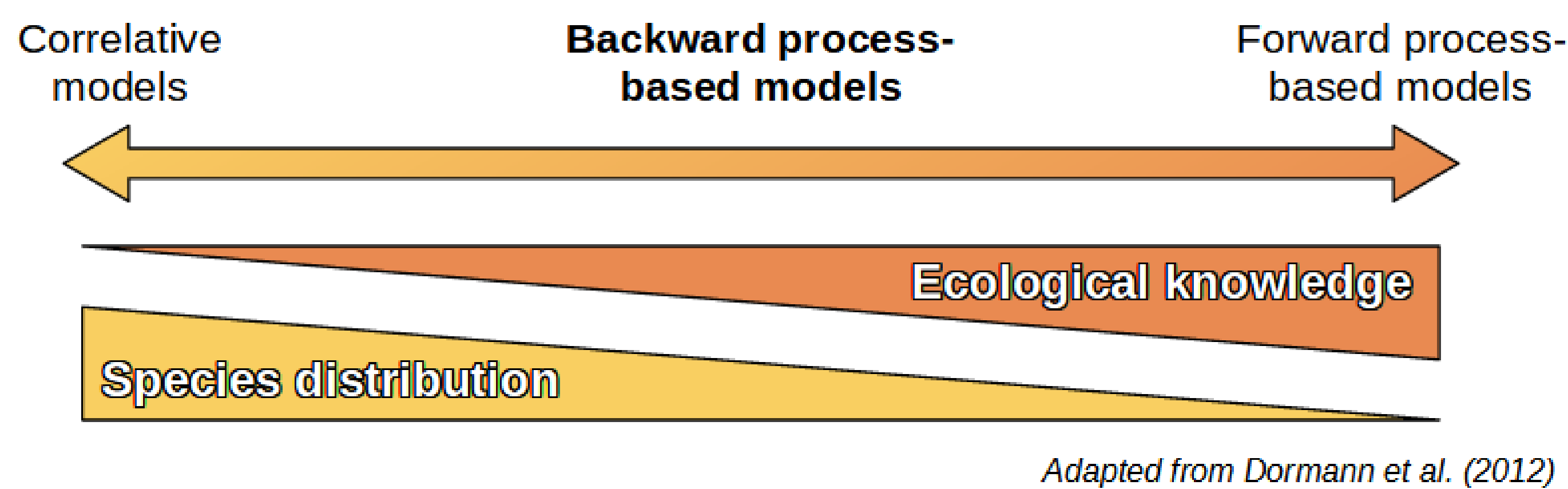
A novel method to estimate process-based model parameters from species distribution data

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1. Introduction

- Two types of species distribution models (SDMs): **correlative niche-based models** and **process-based models**
- Process-based models aim to translate into **mathematical equations** our knowledge about the **physiological and ecological processes**
- They take more time to develop: in particular, **calibration** is **challenging** and **time-consuming**



Adapted from Dormann et al. (2012)

- We explored the feasibility and interests of **calibrating process-based models using species occurrence data** as correlative SDMs do (using the geographic distributions of species), i.e. **backward calibration**

2. Data and models

Tree occurrence data

- We essentially rely on **EU-Forest** dataset
- Completed with records from **GBIF**, filtered with **Atlas Flora Europeae** and **EuroVegMap** species ranges
- For *Quercus ilex*, we also added records from **WOODIV** database

Climate and soil data

- Climatic variables were derived from **ERA5-Land** (1970-2000), 0.1° resolution
- Soil variables were extracted from **EU-SoilHydroGrids** and **SoilGrids250m**

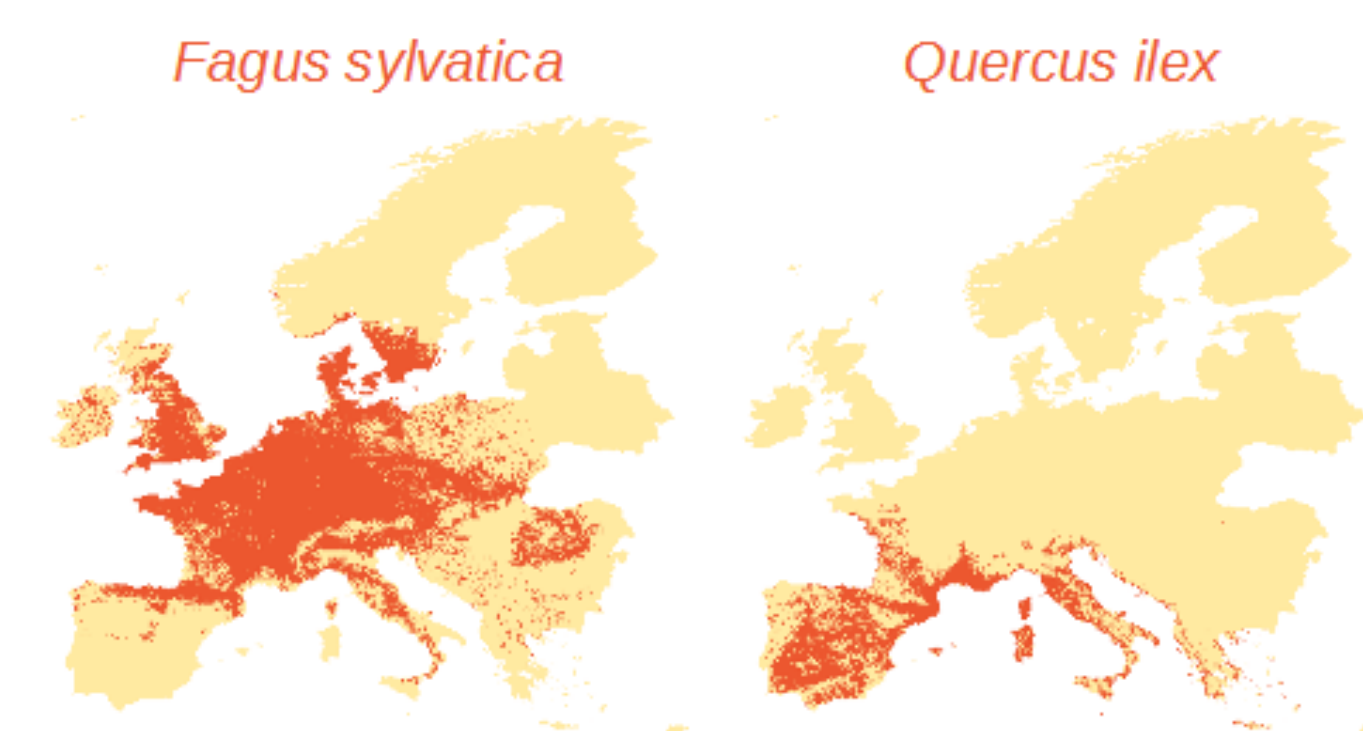


Fig. 3: Species distribution

Process-based models

- PHENOFIT**²: focuses on phenology and simulates the fitness (survival and reproductive success) of an average individual
- CASTANEA**³: simulates carbon and water fluxes in forest, with several processes (photosynthesis, stomatal conductance, respiration...)

3. Covariance matrix adaptation, evolution strategy

CMA-ES in a nutshell

- Robust optimization algorithm for **non-linear optimization problems** in continuous domain developed by **Nikolaus Hansen**¹
- Inspired by **evolutionary biology**: recombination, mutation and selection

In practice

- Parallel implementation** on two computing clusters (40 to 100 CPUs)
- Runtime :
 - PHENOFIT: ~ 24 hours
 - CASTANEA: ~ 20 days

5. Non-identifiability of parameters

- We focus here on the leaf unfolding submodel in PHENOFIT. We found a **high variability** in the **parameter estimates**

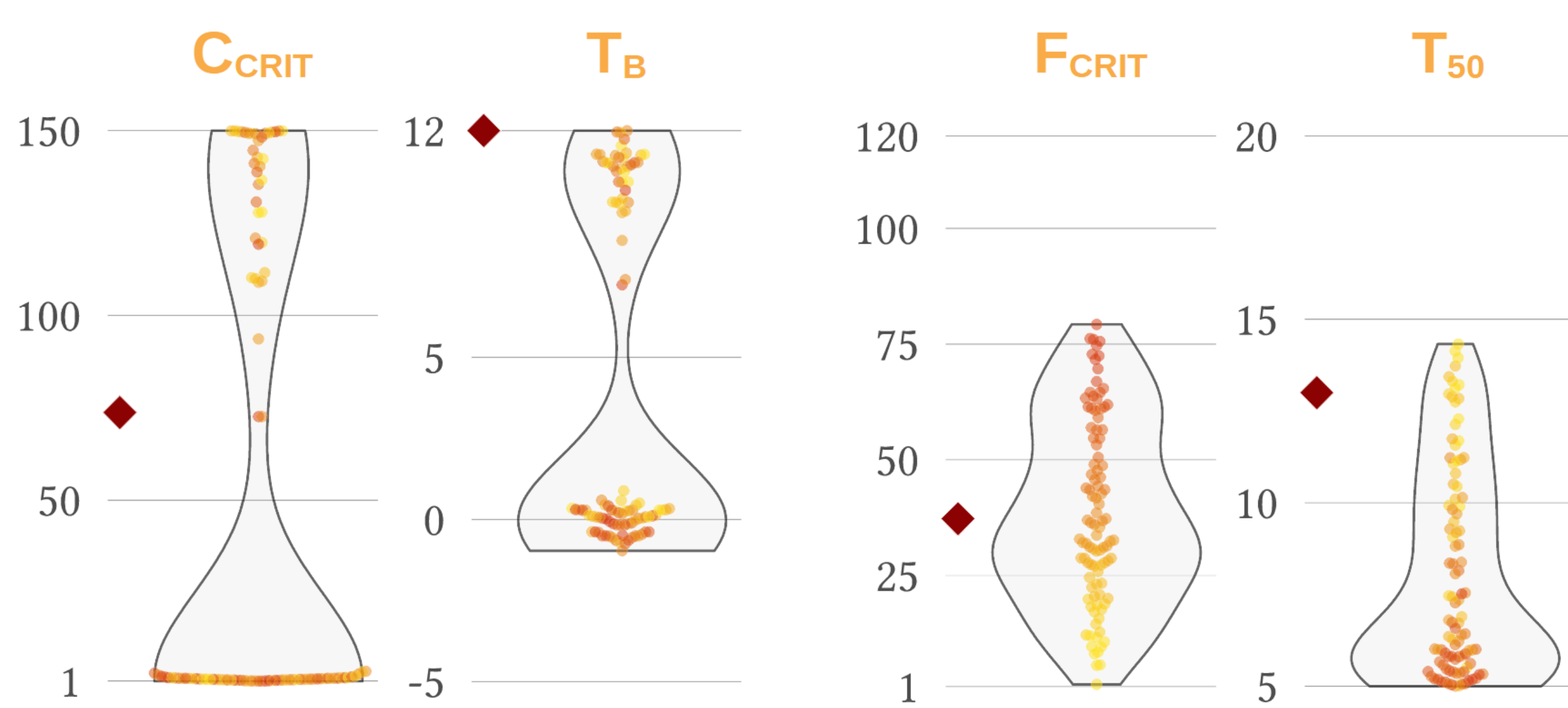


Fig. 1: Effects of stochasticity of CMA-ES calibration on PHENOFIT leaf unfolding submodel parameter

- Parameters are strongly dependent because of **structural correlations**

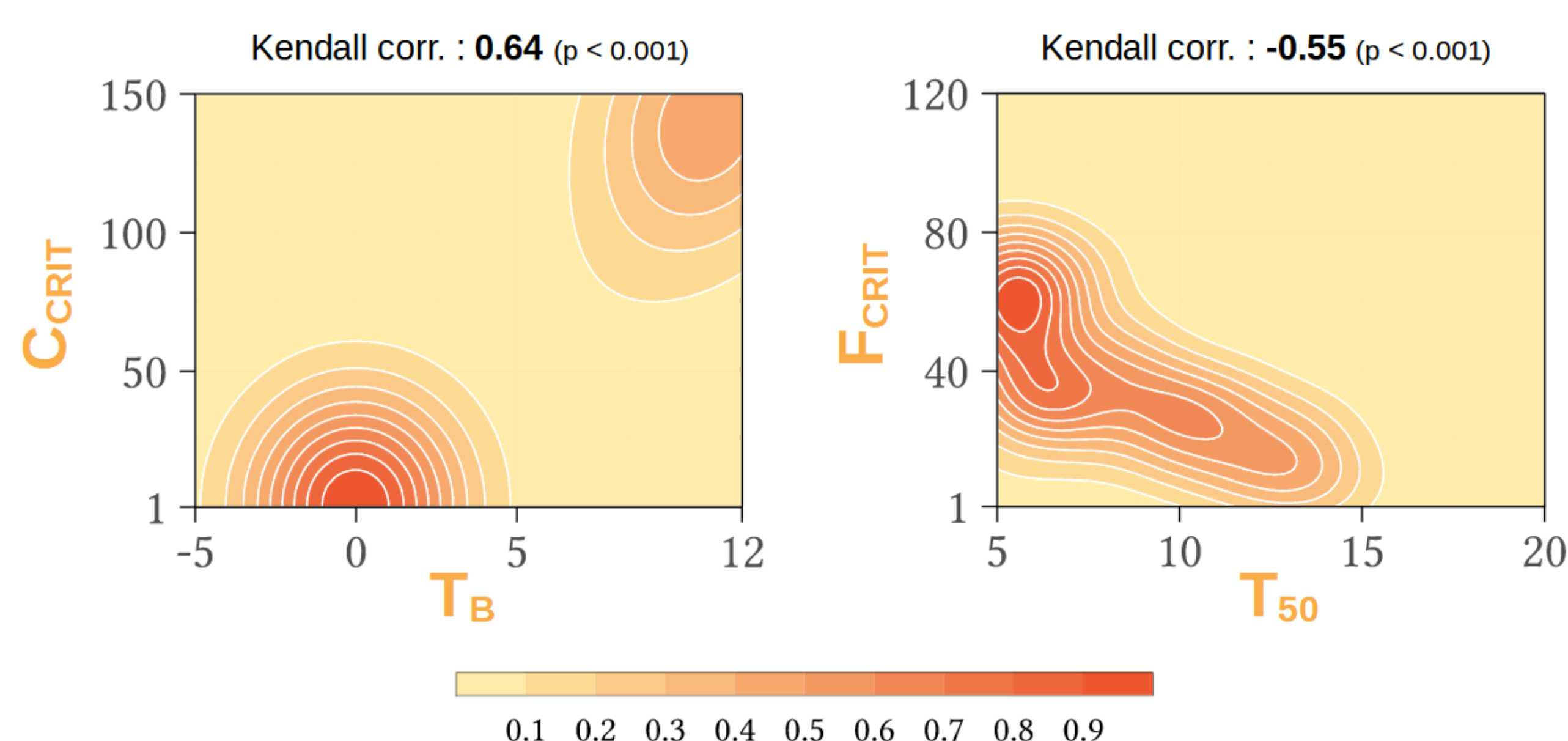


Fig. 2: Leaf unfolding submodel parameter density

- Thus, parameter values are **not necessarily ecologically relevant**

4. Calibration results

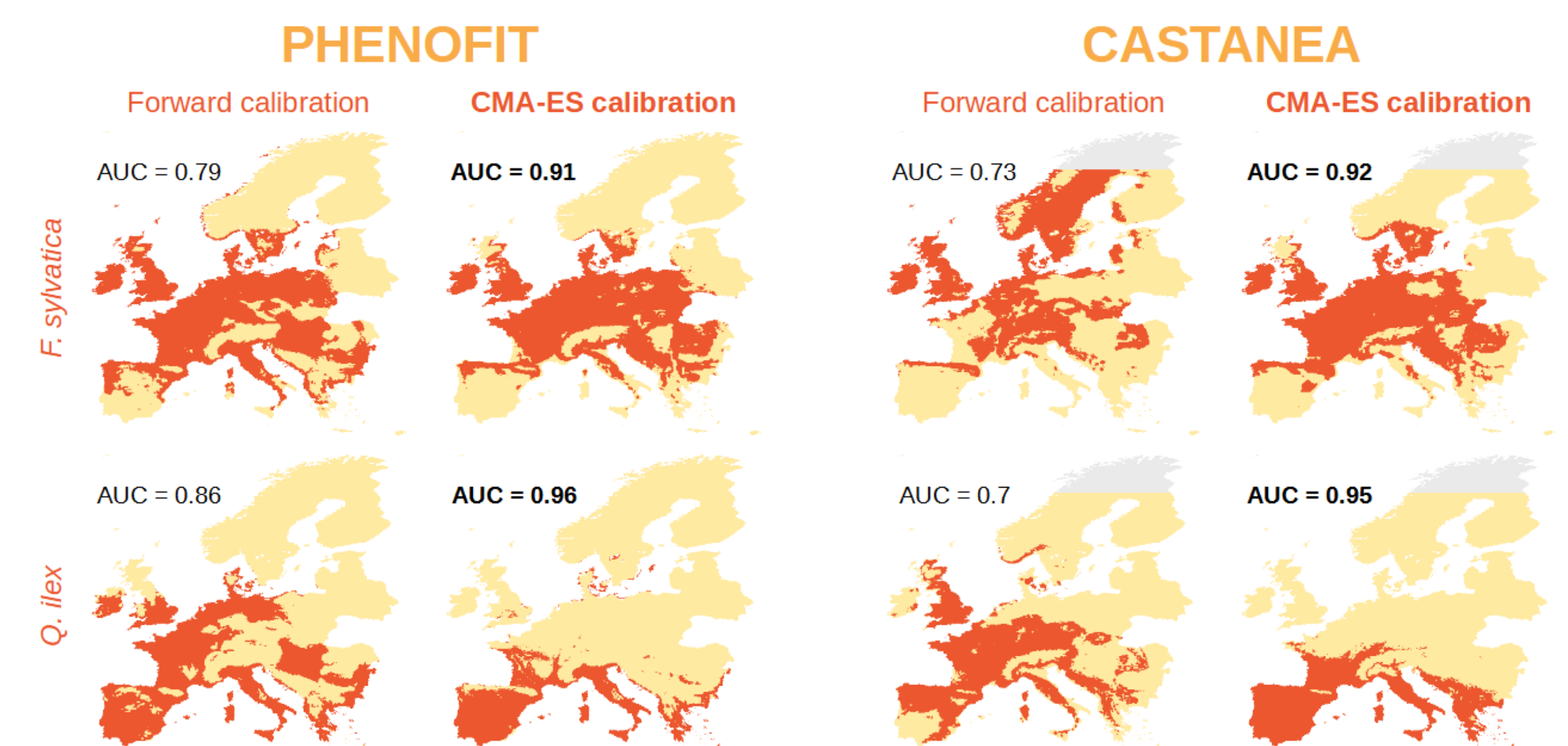


Fig. 4: Species distribution maps obtained with PHENOFIT and CASTANEA forward and backward parametrization. Optimal threshold to dichotomize model outputs is the Youden Index-based cut-off point.

6. Advantages of CMA-ES

Comparison with ABC

CMA-ES slightly **outperforms** a widely used approximate bayesian computation (ABC) optimization method

Calibration performance

- AUC is **sharply improved** compared to classical (forward) parametrization
- Easy to use**: does not require an extensive tuning
- Efficient to deal with **ill-conditioned** and **non-separable problems**
- CMA-ES backward optimization can be a **powerful technique** to calibrate submodels whose parameter values can hardly be experimentally measured

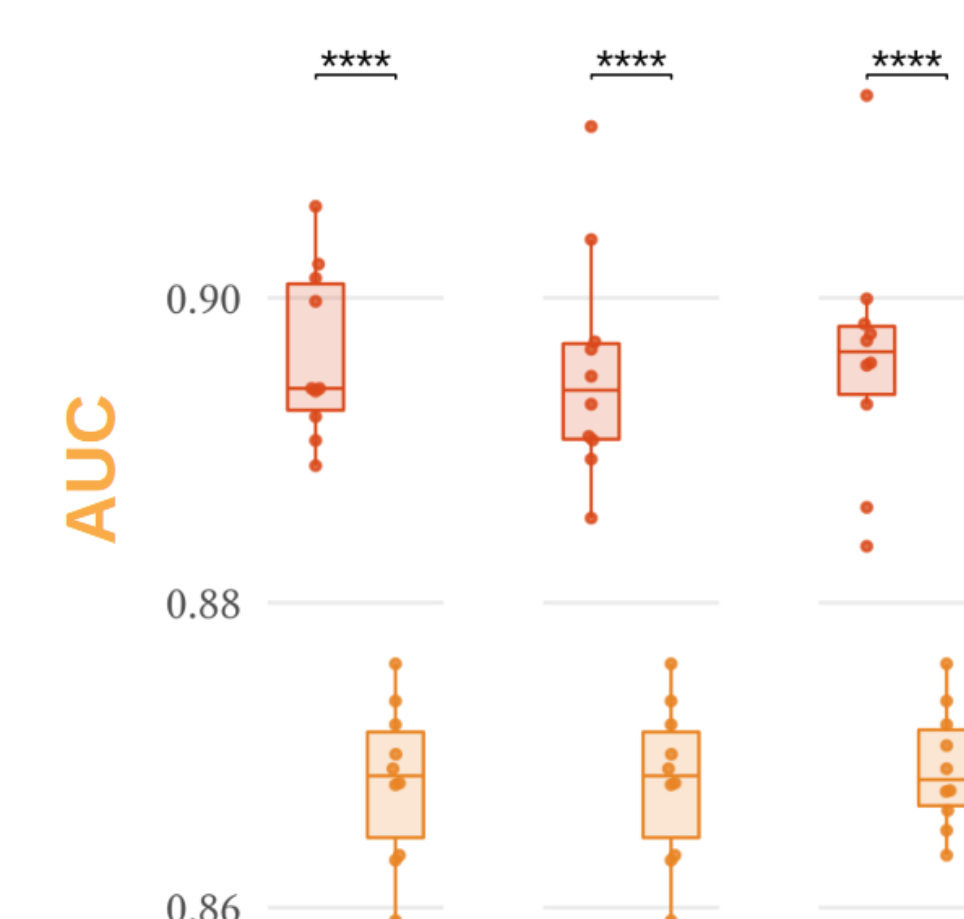


Fig. 5: Comparison of CMA-ES (red) and ABC-rejection (orange) methods, with *F. sylvatica*

References

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