ibis.iSDM
A modelling framework for integrated species distribution models

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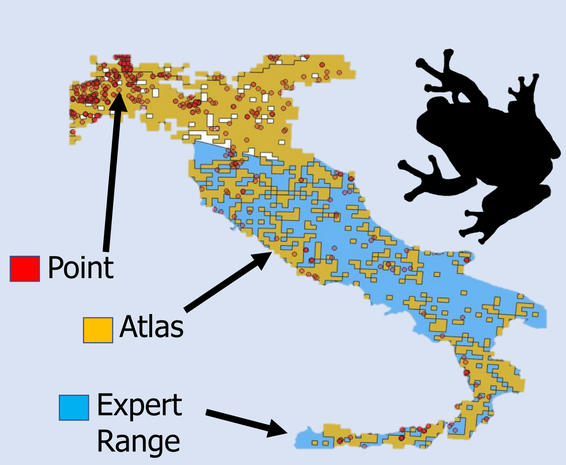
22nd – 26th 2022

Background

Species distribution models (SDMs) are widely used for creating ecological indicators.

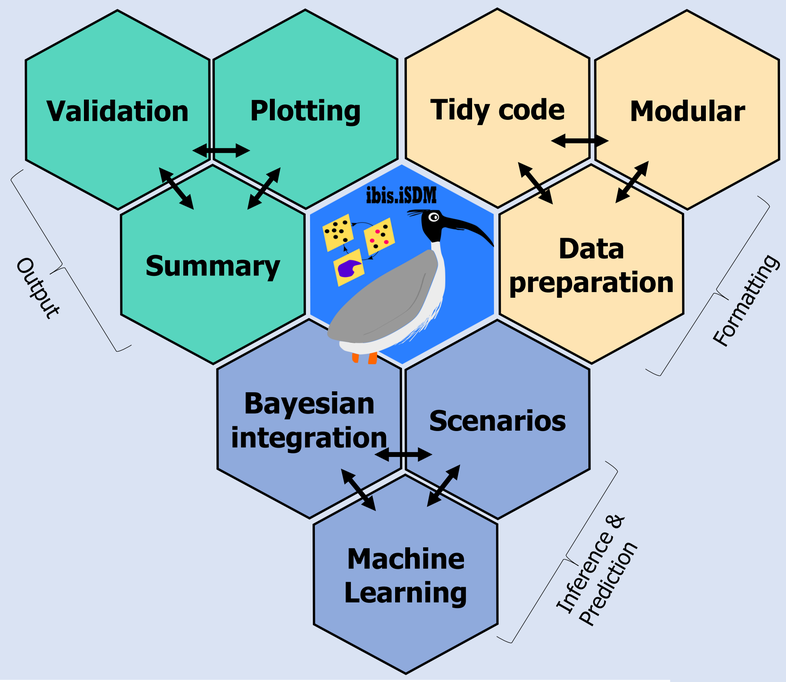
However, biodiversity data are heterogeneous, biased and of various types and origin, requiring integration.

Need for a modular and flexible framework with the ability to easily modify parameters and input data.

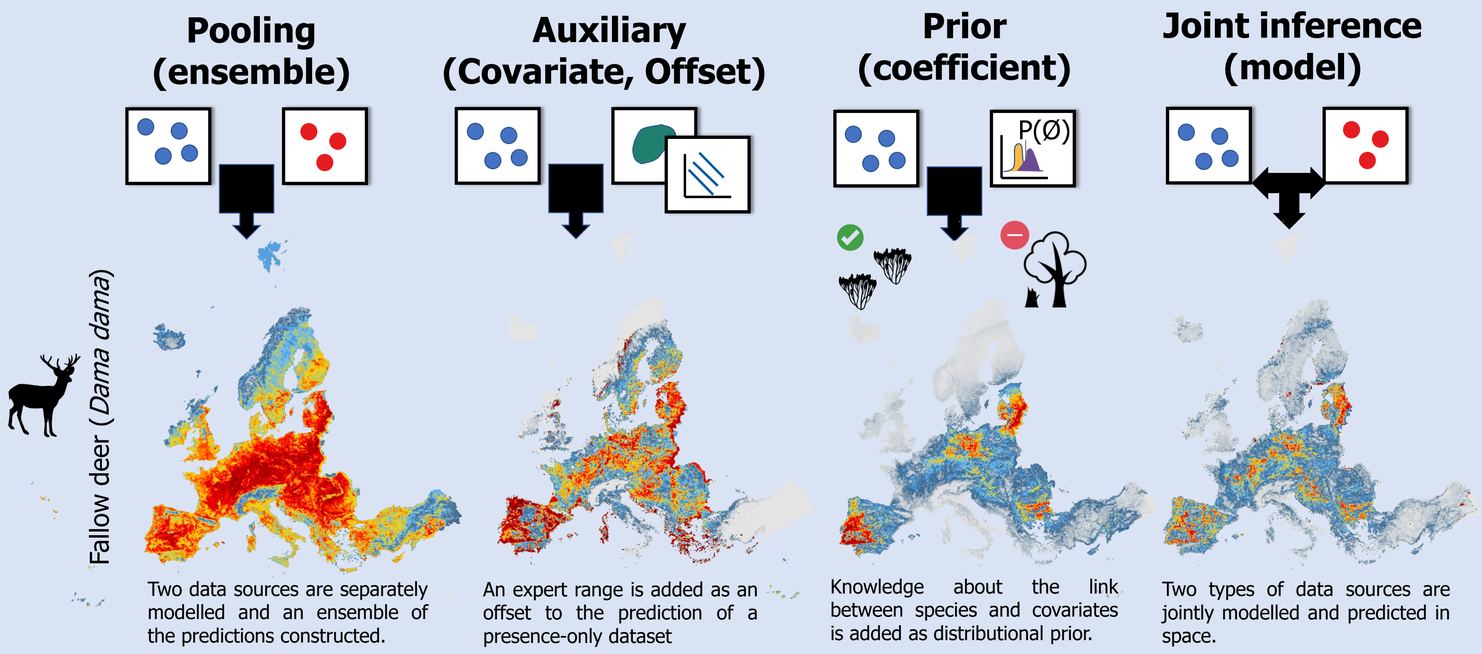


Example for the distribution of the Italian tree frog (*Hyla intermedia*). Three different data sources provide contrasting evidence of where the species persists on the Italian peninsula. Focussing on any single source would ignore substantial parts of the potential distribution.

The ibis.iSDM framework



Integrated predictions[1]



Two data sources are separately modelled and an ensemble of the predictions constructed.

An expert range is added as an offset to the prediction of a presence-only dataset

Knowledge about the link between species and covariates is added as distributional prior.

Two types of data sources are jointly modelled and predicted in space.

Code example

```
fit ← distribution(region) ▷
  add_biodiversity_poipo(species) ▷
  add_predictors(covariates, derivates = "hinge") ▷
  add_offset(expert_range) ▷
  add_latent_spatial() ▷
  engine_bart(nburn = 1000, chains = 4) ▷
  train()

results ← threshold(fit) ▷ validate(point = test_data)

fit_future ← scenario(fit) ▷
  add_predictors(future_covariates, derivates = "hinge") ▷
  threshold() ▷
  add_constrain_dispersal(method = "sdd_nexpkernel")
  project()

summary(fit_future)
```

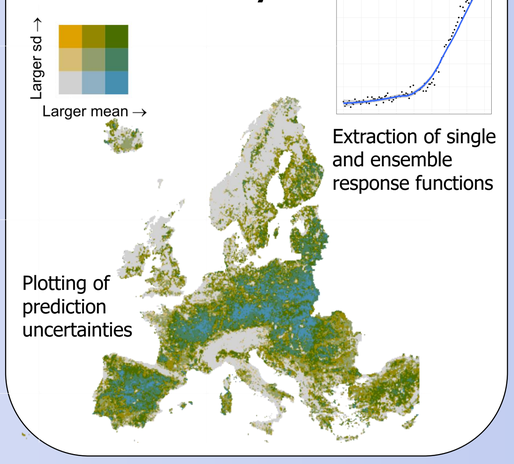
Biodiversity datasets in ibis.iSDM are added and modelled by type[2].

Features and capabilities

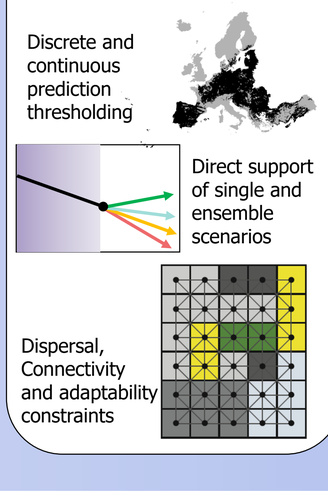
Bayesian and machine learning engines, like...

dmlc XGBoost, INLA, BART

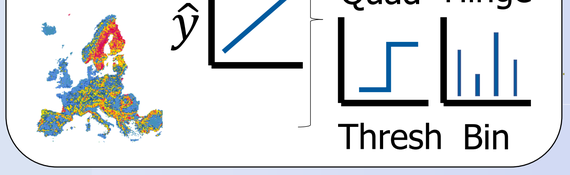
Built-in visualization of responses and uncertainty



Thresholds, scenarios & constraints



Transform-ations



What's next?

Additional engines (NNet) and further customizations.

Improved scenario dispersal and connectivity modules.

Coupling of iSDMs with other biophysical IIASA models, i.e. G4M, EPIC, cWATM and PlantFATE

iiasa.github.io/ibis.iSDM

[1] For an introduction to iSDMs see Fletcher, R. J., Hefley, T. J., Robertson, E. P., Zuckerberg, B., McCleery, R. A., & Dorazio, R. M. (2019). A practical guide for combining data to model species distributions. *Ecology*, *100*(6), e02710. https://doi.org/10.1002/ecy.2710

[2] Biodiversity datasets in ibis.iSDM are usually added either as presence-only or presence-absence datasets. In the case of the former, the point occurrences are by default assumed to follow an inhomogeneous Poisson process and are modelled as a function of an intensity λ, integrated over all occupied area A_i, where $N(A) \sim \text{Poisson}\left(\int_{A_i} \lambda(i) d_i\right)$ and $\log(\lambda(i)) = \alpha_0 + \beta_x x(i) + \varepsilon(i)$. In the case of presence-absence data, they are modelled as $\Pr(N(y_j) > 0) \sim \text{Bernoulli}(p_i)$ and as $\text{cloglog}(p_i) = \alpha_0 + \beta_x x(i) + \varepsilon(i)$. Integrated models work through products of likelihoods since $cloglog(p_i) \approx \log(\lambda(i))$. Families and link functions can be altered through parameters. Note that not every engine supported in ibis.iSDM does supports every likelihood function.

This work has been supported by the EU-Tender "European Union BIOdiversity and CLIMate strategies Assessment (Acronym: EU-BIOCLIMA)" . The R-package "ibis.iSDM" will be made openly available for download via the QR code. MJ would like to thank Matt Lewis, Florian Hofhansl, Eleanor Warren-Thomas, Juliette Martin & Jutta Beher for feedback on an earlier version of this poster.