Species Distribution Models: Models and Application for Sustainable Species Conservation Day 2

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April 27, 2024

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- These local topoclimatic habitats may need to be accounted for when evaluating climate-change impacts on biodiversity as they may constitute refugia for local populations and increase habitat connectivity for dispersal and migration (Jackson and Overpeck, 2000; Ackerly et al., 2010; Austin and Van Niel, 2011).

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- On the other hand, time lags associated with longevity of individuals established under previous conditions ["legacy" effects in plant distributions] or with breeding-area philopatry in birds may result in the occurrence of individuals in areas that no longer fall within their environmental niche space.
- Thus, ecological niche models may be prone to both omission errors (leaving out of the niche space information from places that could be occupied) and commission errors (including in the niche space places that cannot sustain the species).

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  6. format and level of technical detail of the information (e.g. maps, tables, time series).

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- Read the forecast of different models at McSweeney et al. 2015 and the definition of each acronym WCRP-CMIP CMIP6$_C$ *Vsversion* : 6.2.58.67

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  2. **boosting**, that often considers homogeneous weak learners, learns them sequentially in a very adaptative way (a base model depends on the previous ones) and combines them following a deterministic strategy

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- If we choose base models with low bias but high variance, it should be with an aggregating method that tends to reduce variance whereas if we choose base models with low variance but high bias, it should be with an aggregating method that tends to reduce bias.

- We can mention three major kinds of meta-algorithms that aim at combining weak learners:
  1. **bagging**, that often considers homogeneous weak learners, learns them independently from each other in parallel and combines them following some kind of deterministic averaging process
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  3. **stacking,** that often considers heterogeneous weak learners, learns them in parallel and combines them by training a meta-model to output a prediction based on the different weak models' predictions

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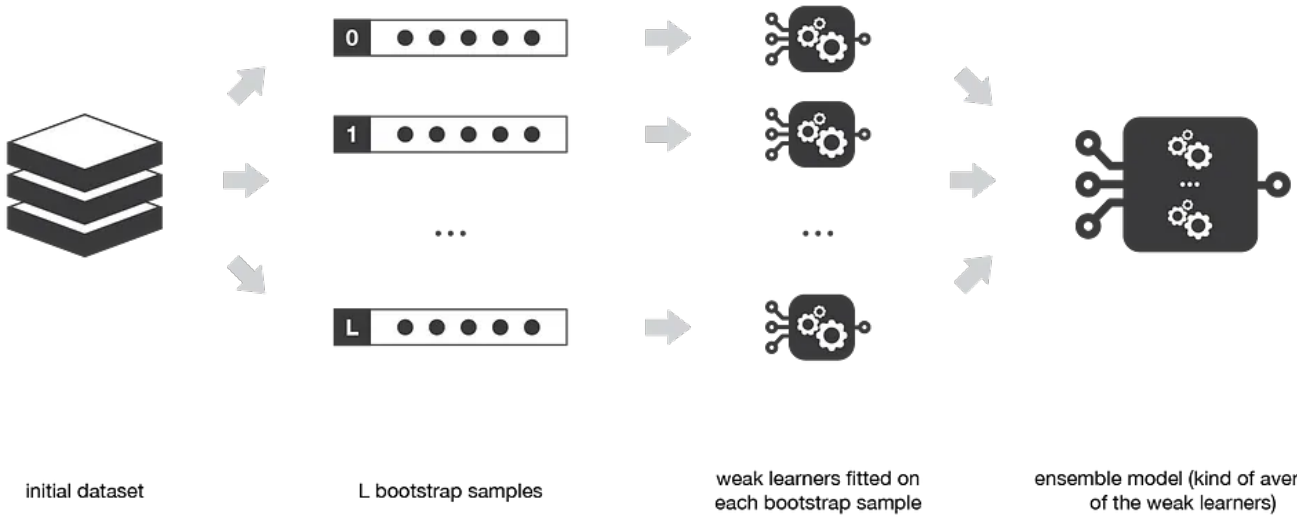
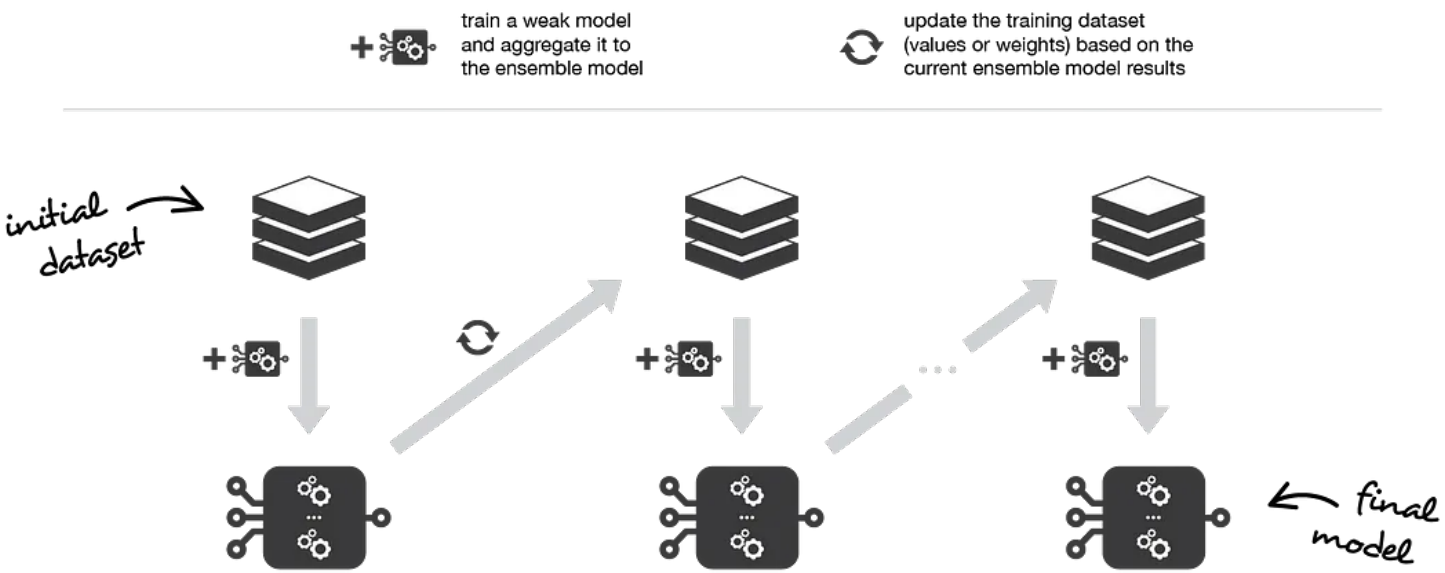
Bootstrapping

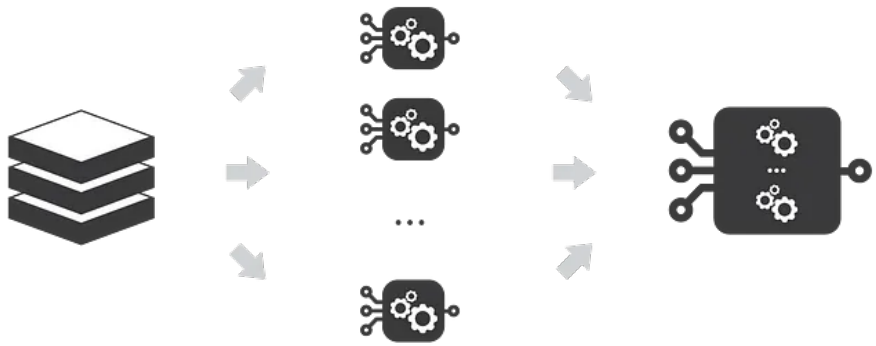
Parameter estimation while Bagging



Booting


train a weak model
and aggregate it to
the ensemble model
update the training dataset
(values or weights) based on the
current ensemble model results
initial
dataset
final
model

Stacking


initial dataset
L weak learners
(that can be non-homogeneous)
meta-model
(**trained** to output predictions based
on weak learners predictions)

Thank You

https://savikoissi.github.io/Mathematical-Biology/