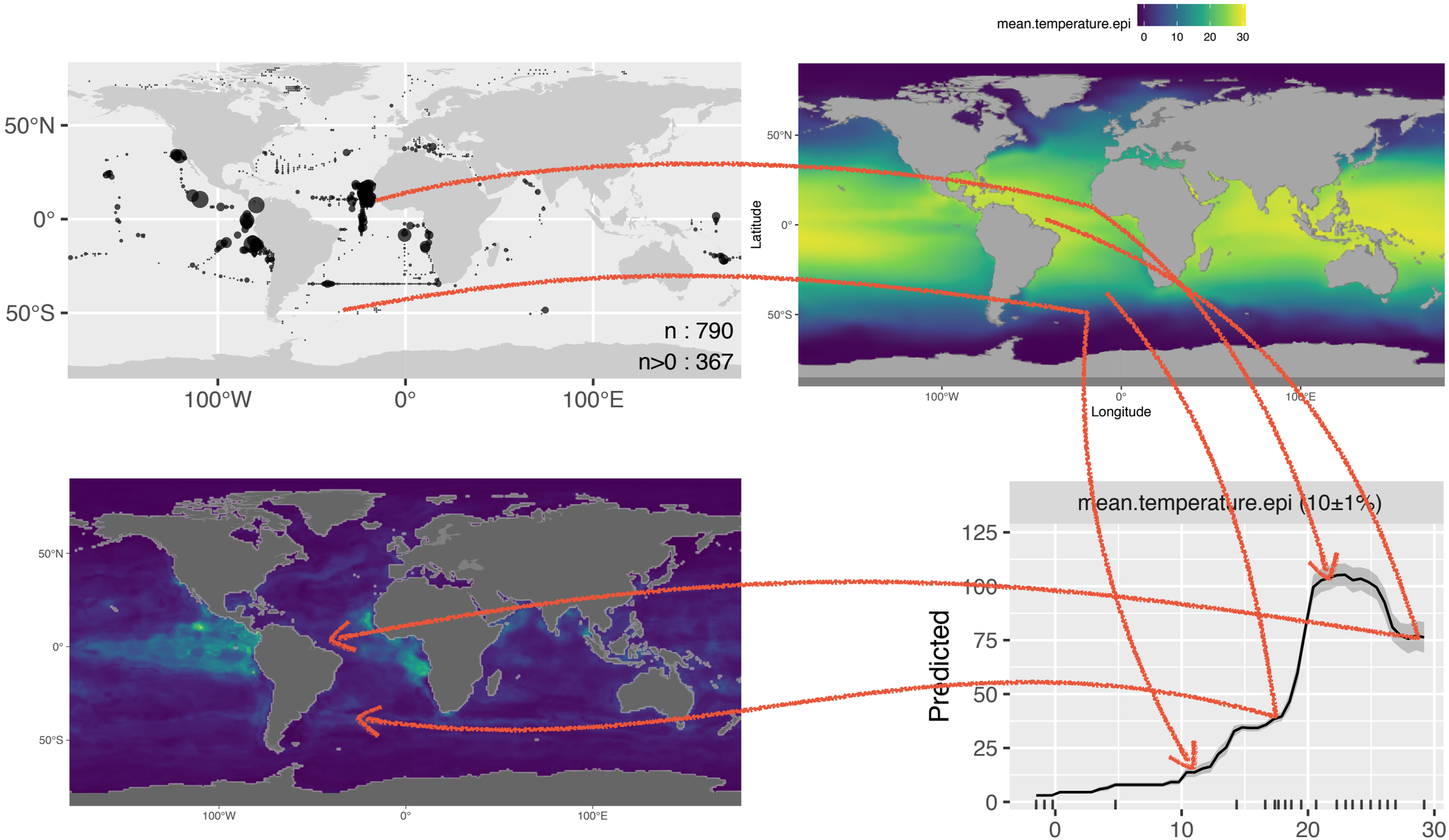
Blue Cloud Webinar, 2022-05-11

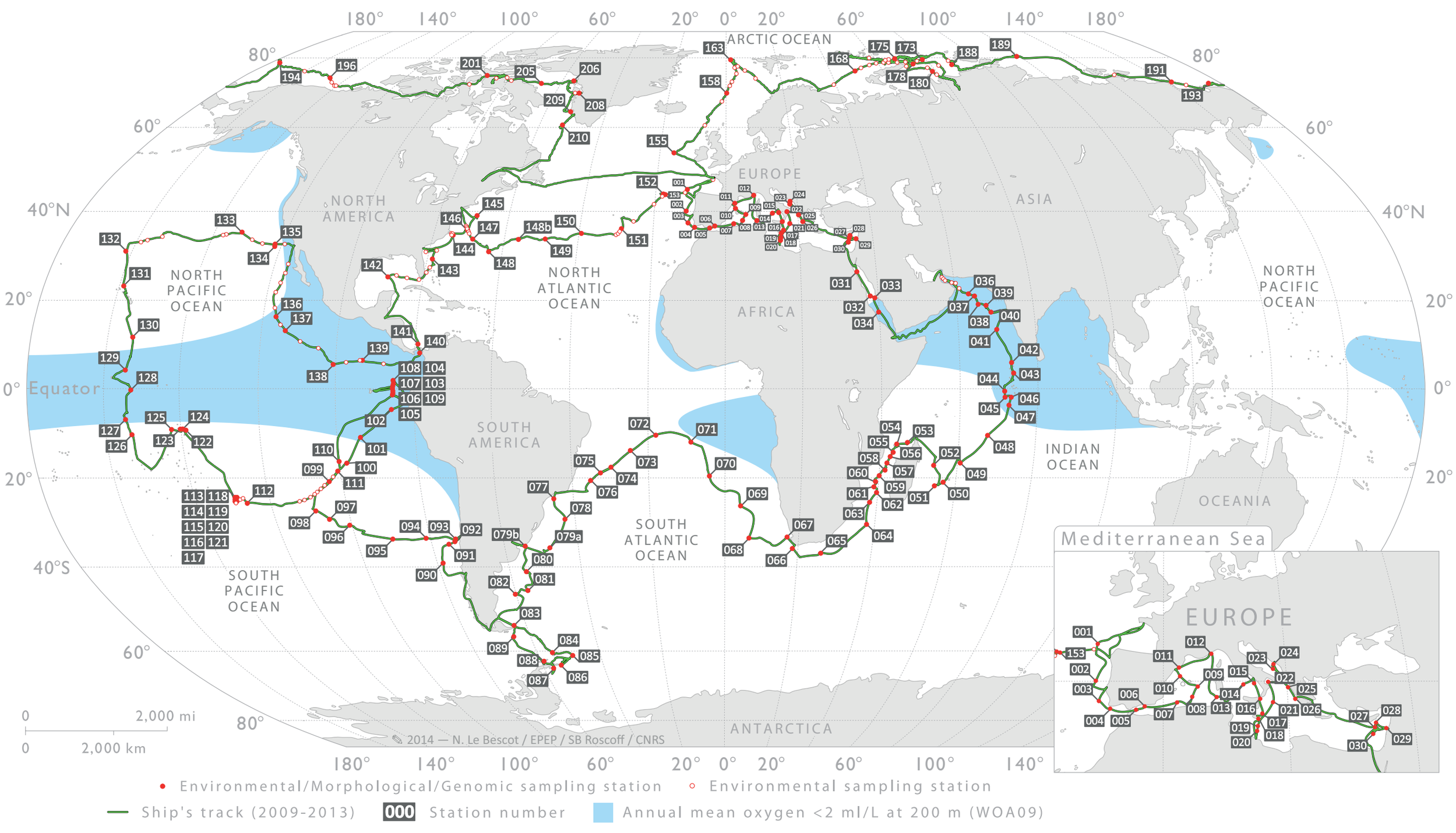
Habitat modelling

For plankton genomics

The principle of habitat modelling



Application to Tara Oceans metagenomic signal



How to construct the response curve?
= Regression trees

We need

a response variable (e.g. presence/ absence)

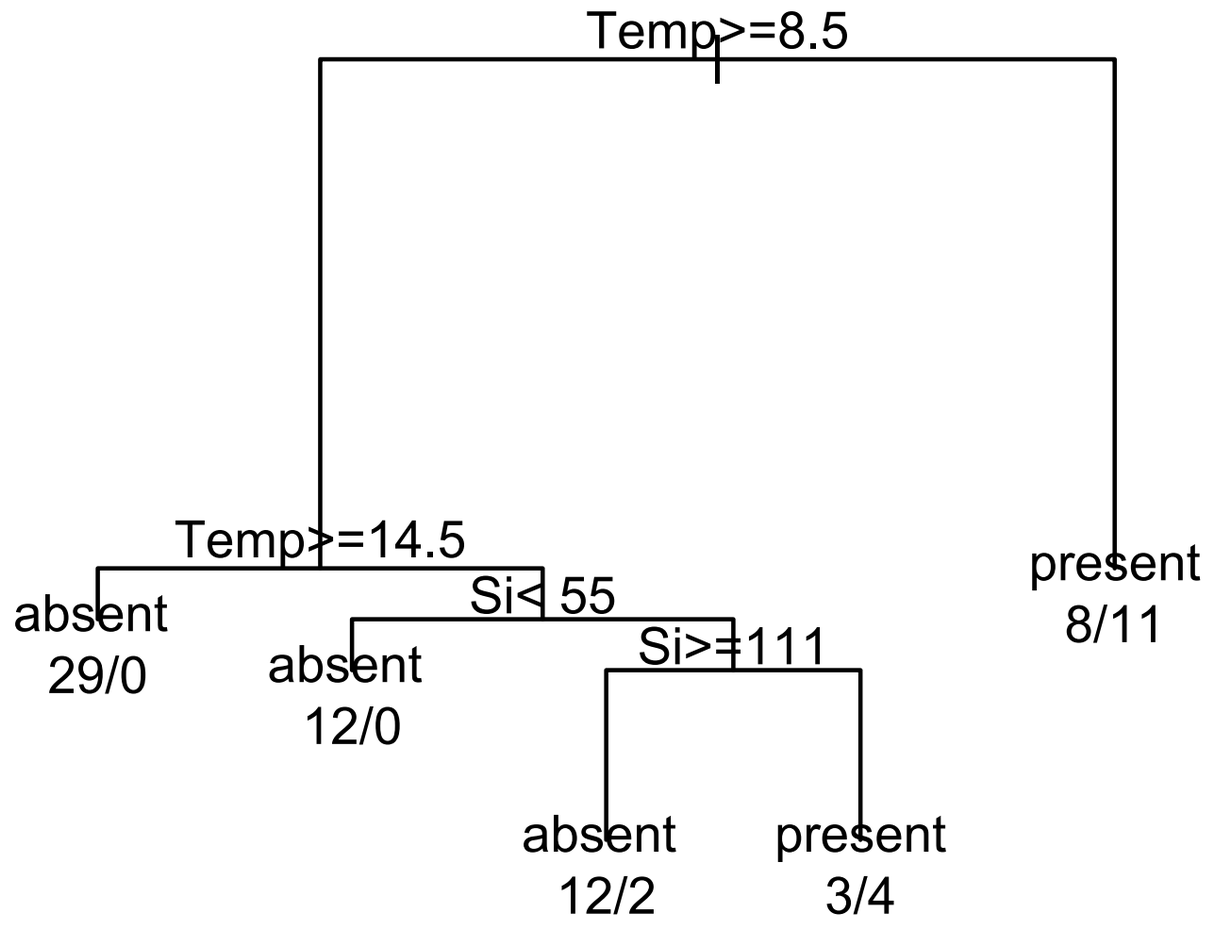
a metric to evaluate (e.g. % or correct predictions)

predictor variables (e.g. environment variables)

Then we **separate** our observations in “bags” according to values of environmental variables.

How? Try everything and see what’s best!

*That’s why it’s called **machine** learning!*



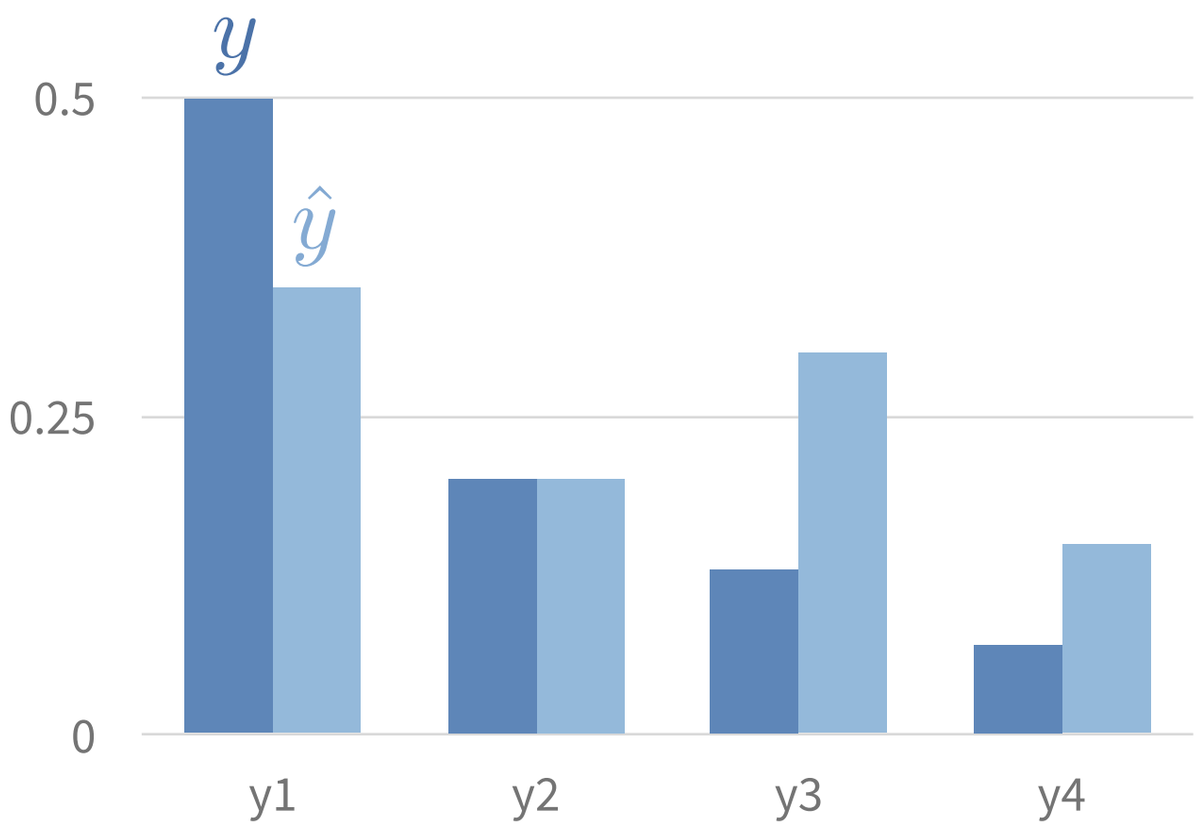
Regression trees for *multiple concentrations*

The response variable is a **vector** of concentrations

The metric is the **multiple Root Mean Square Error**

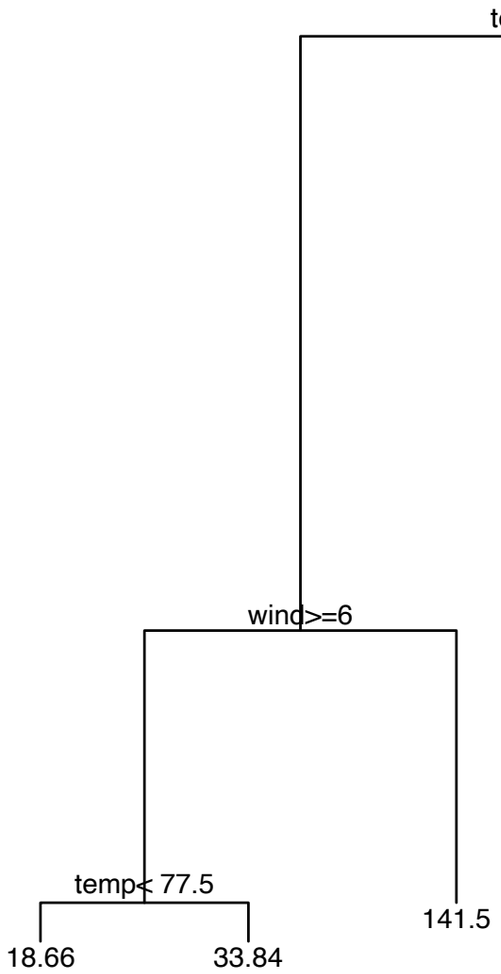
$$\sqrt{(y - \hat{y})^2}$$

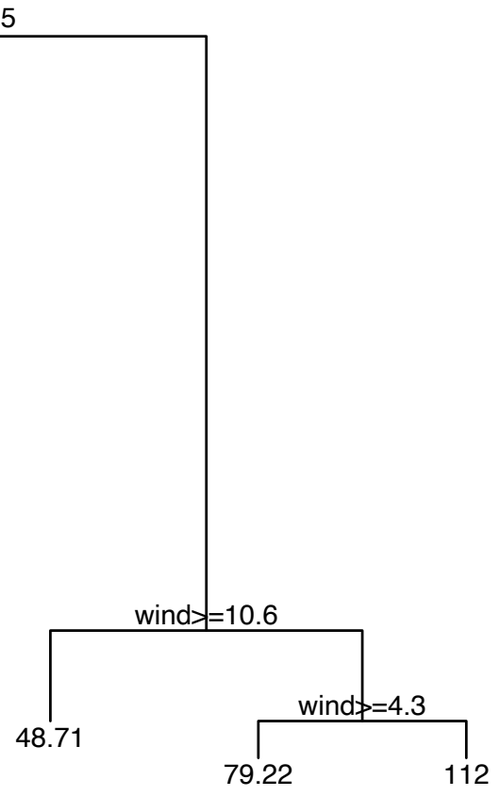
The explanatory variables are environmental **climatologies** (temperature, Chl a, mixed layer depth, etc.)



Boosted regression trees

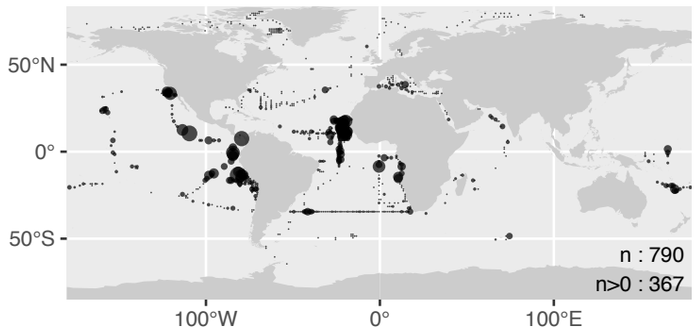
Replace one deep tree

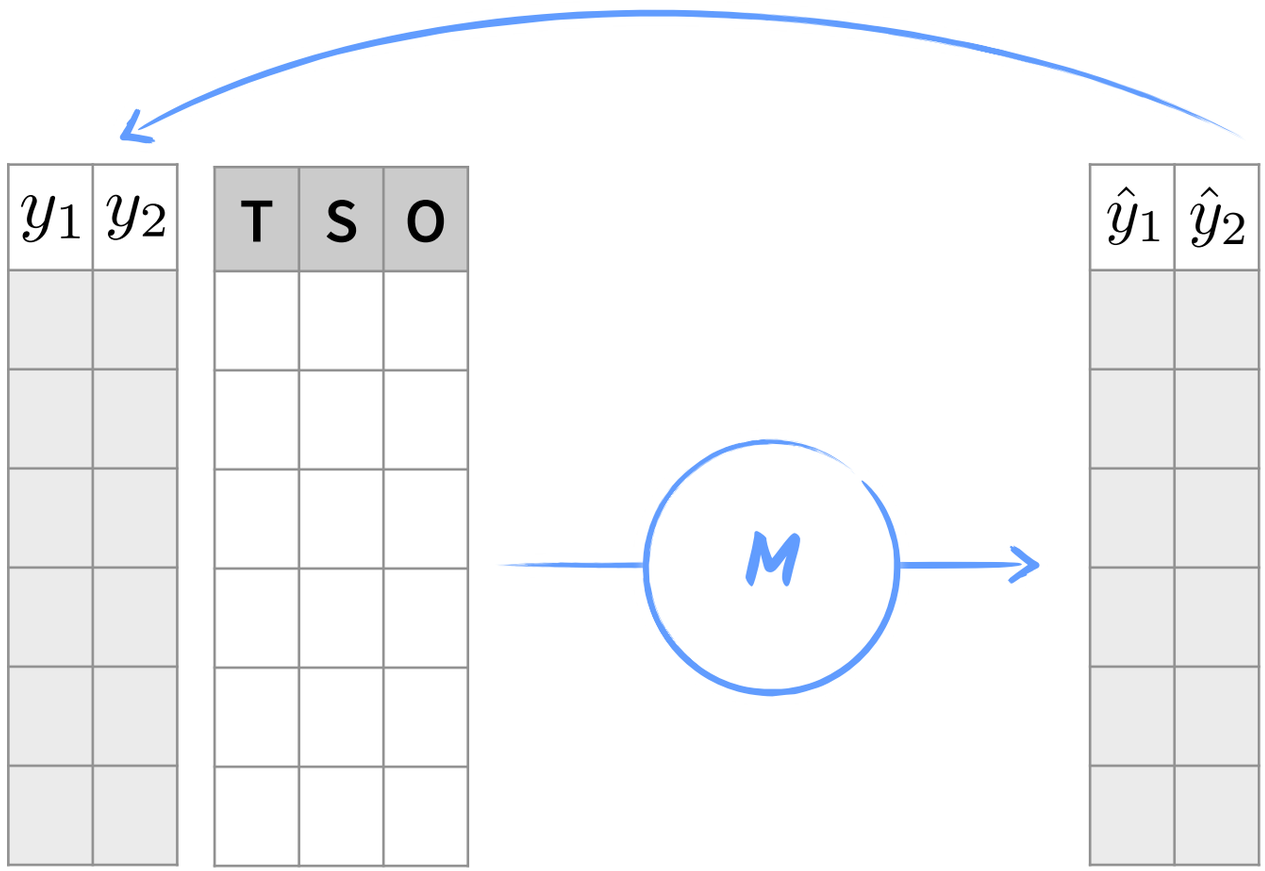




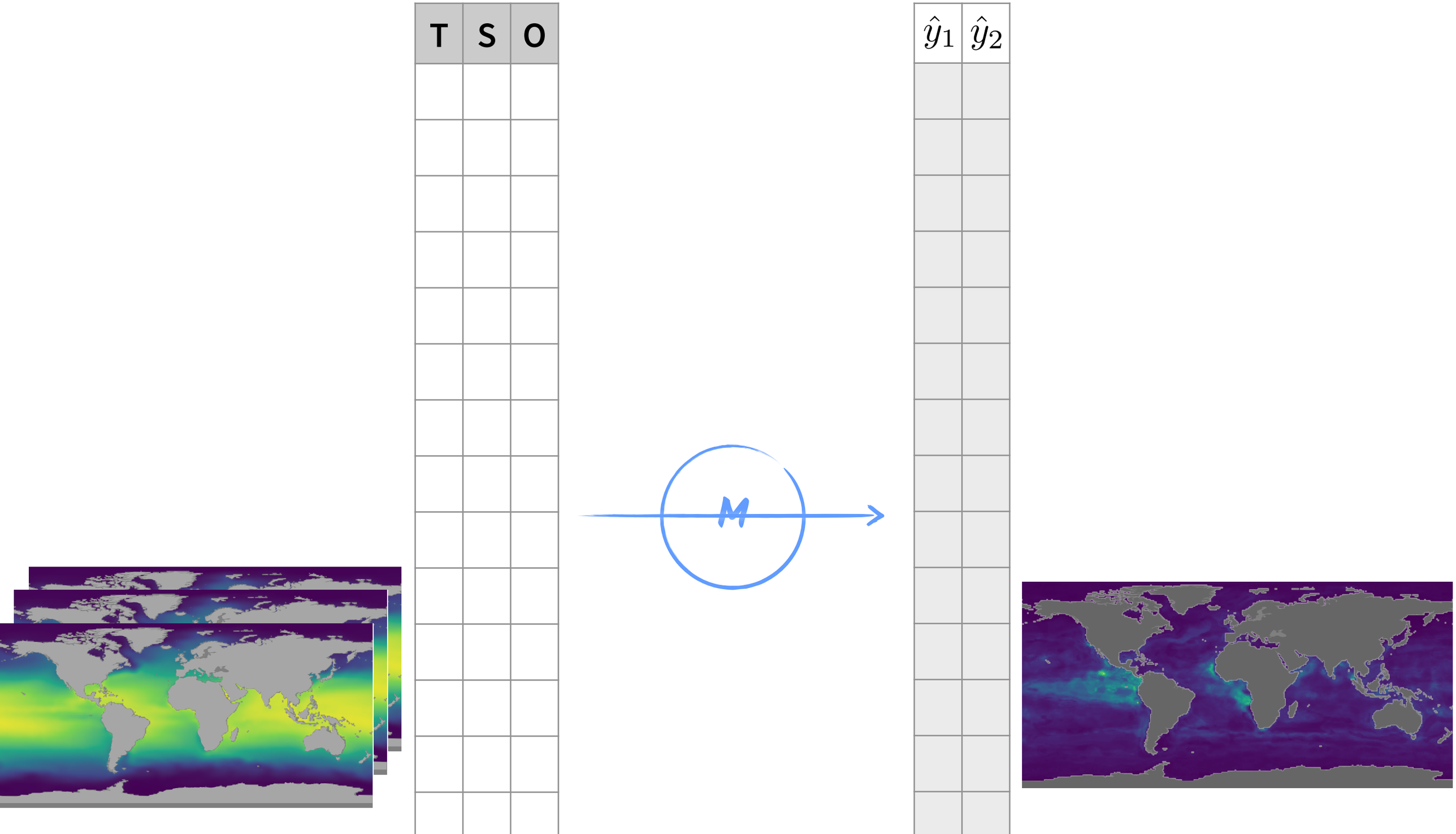
with **many** shallow ones, applied in sequence

Training

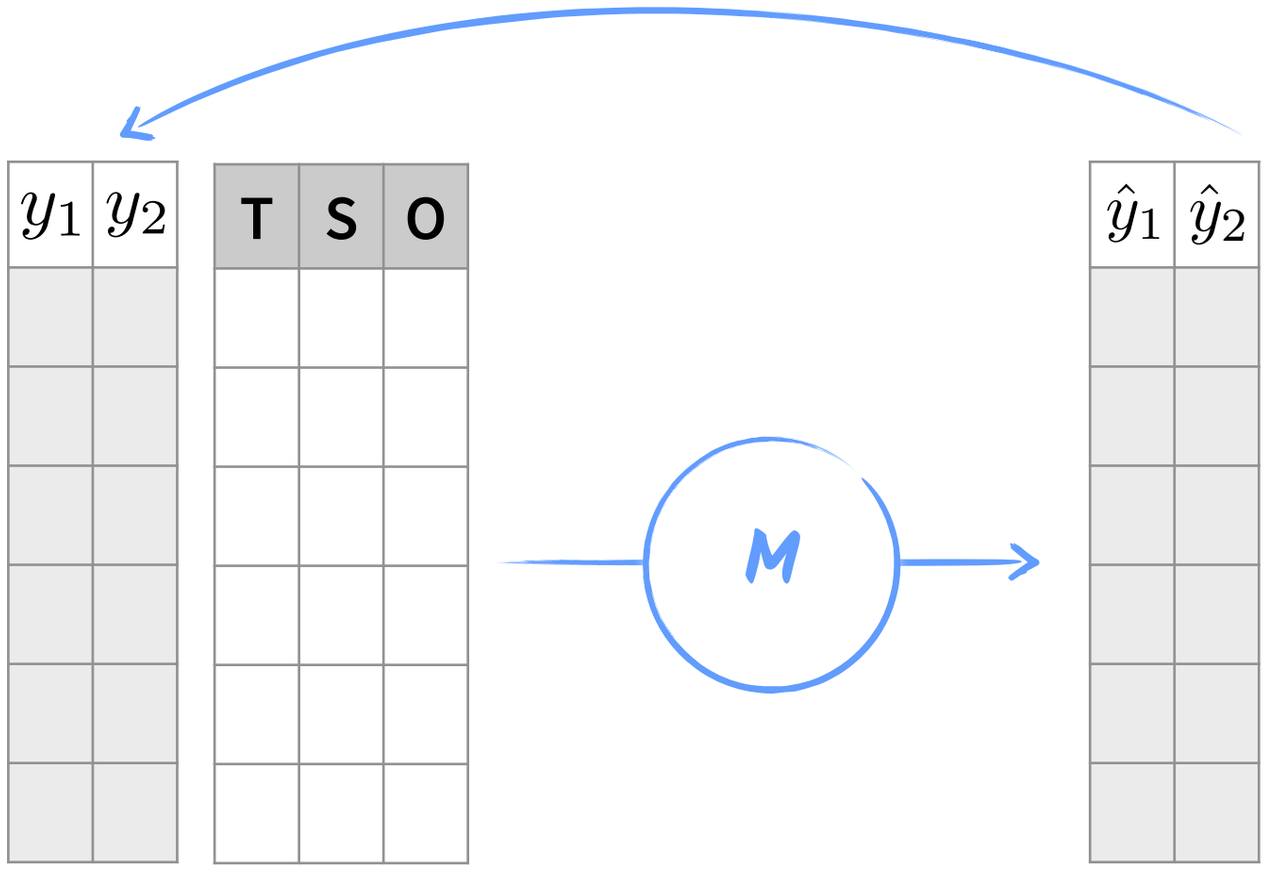




Prediction



Cross-validation during training



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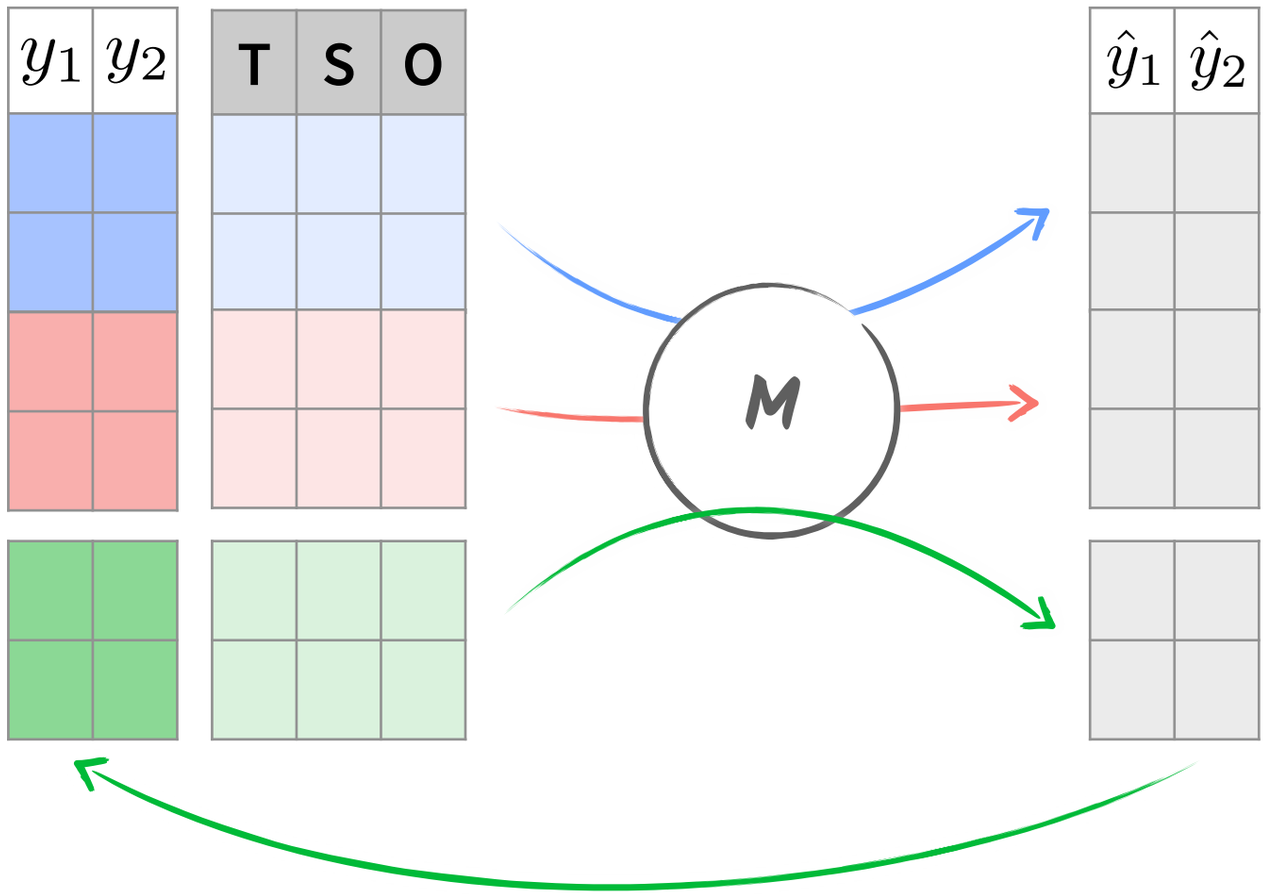

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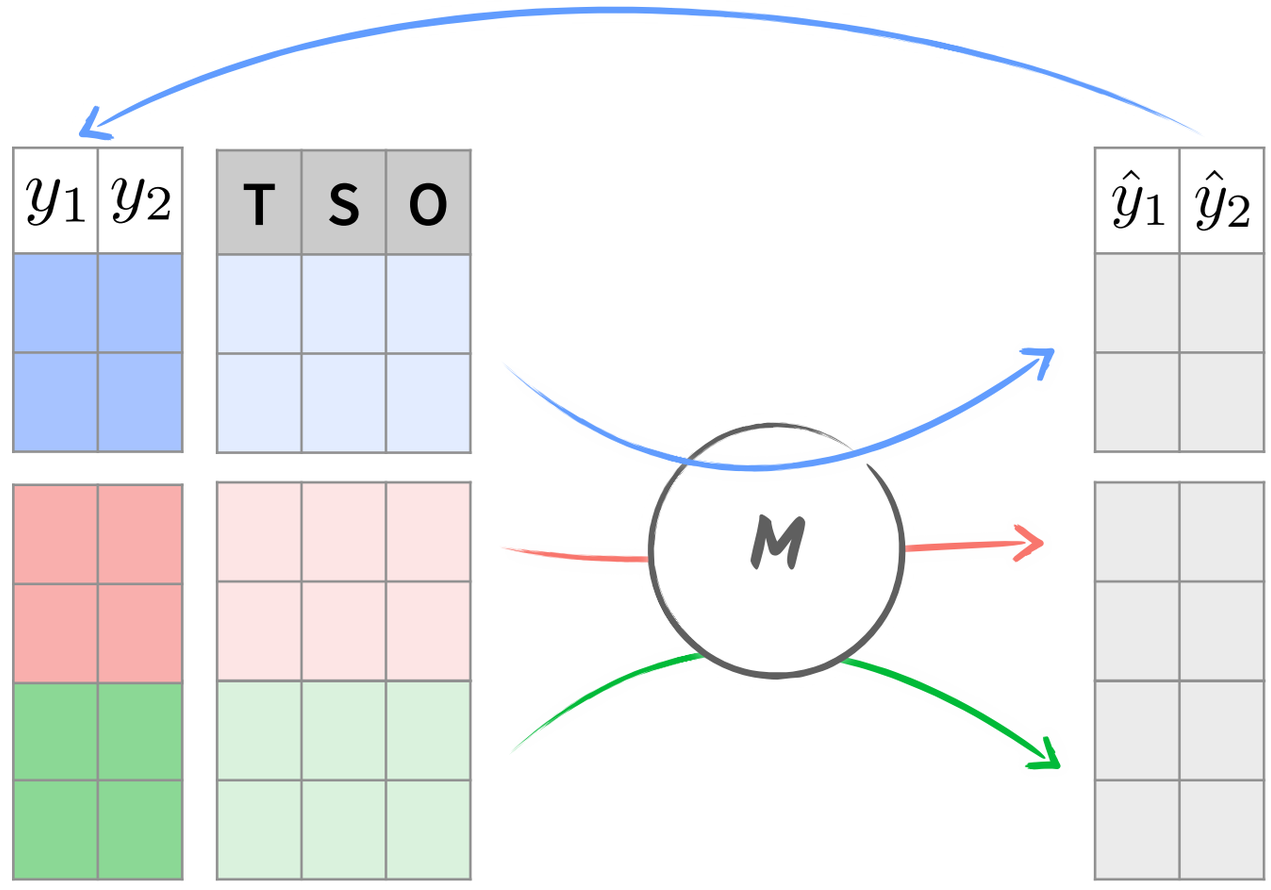

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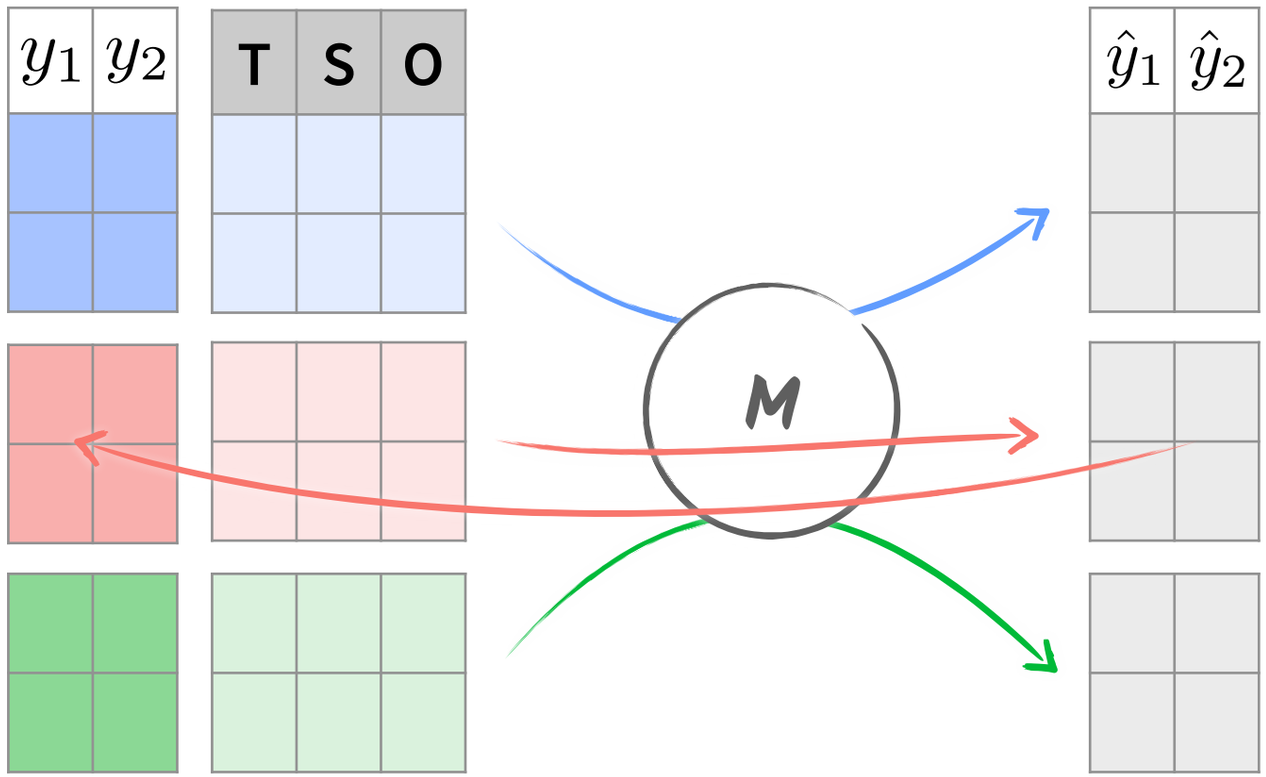
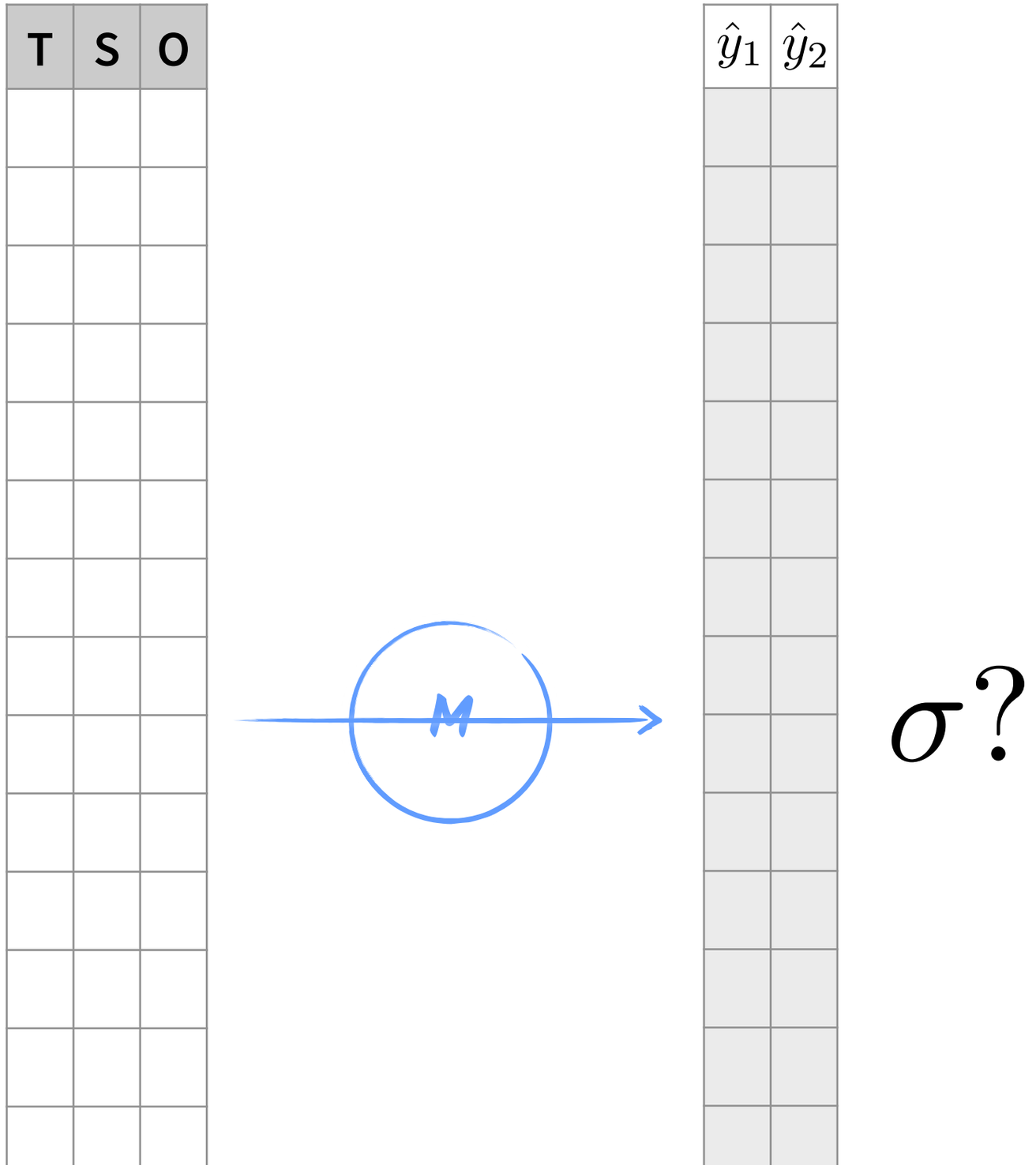


Bootstrap for prediction uncertainty



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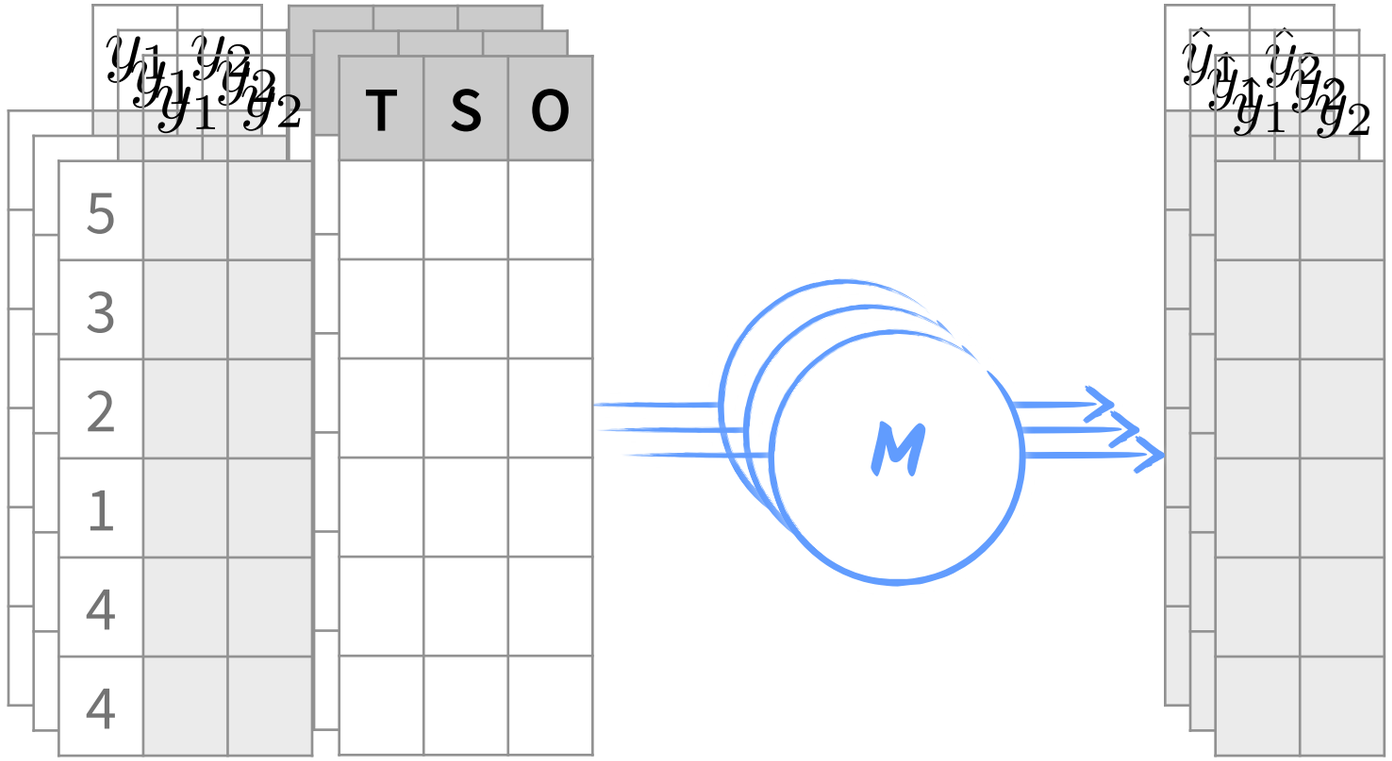
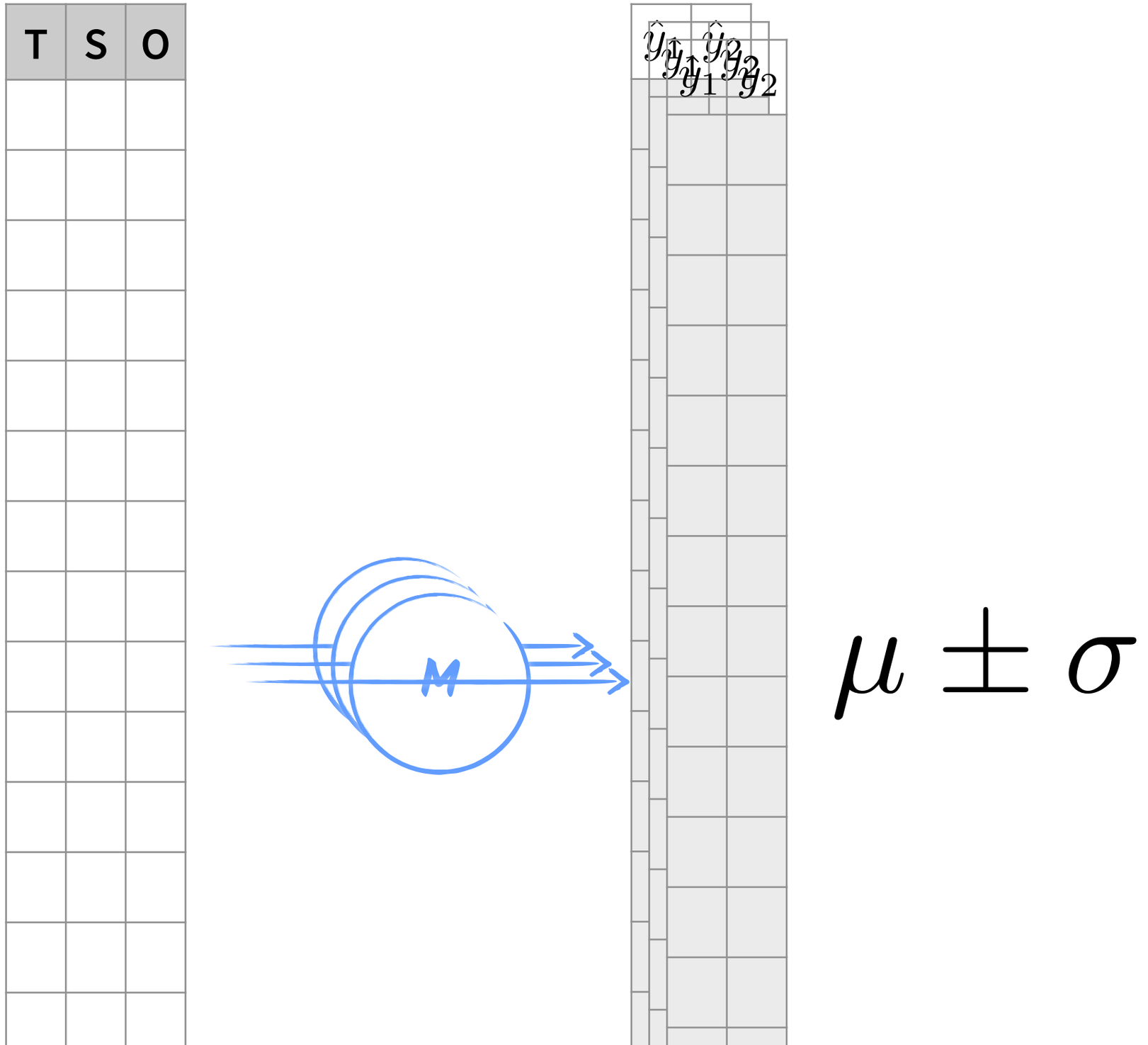


Bootstrap for prediction uncertainty



Thank you

Blue-Cloud

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