

# Predicting diversity with *Joint Species Distribution Models*

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## A difficult case with species rich marine benthic communities

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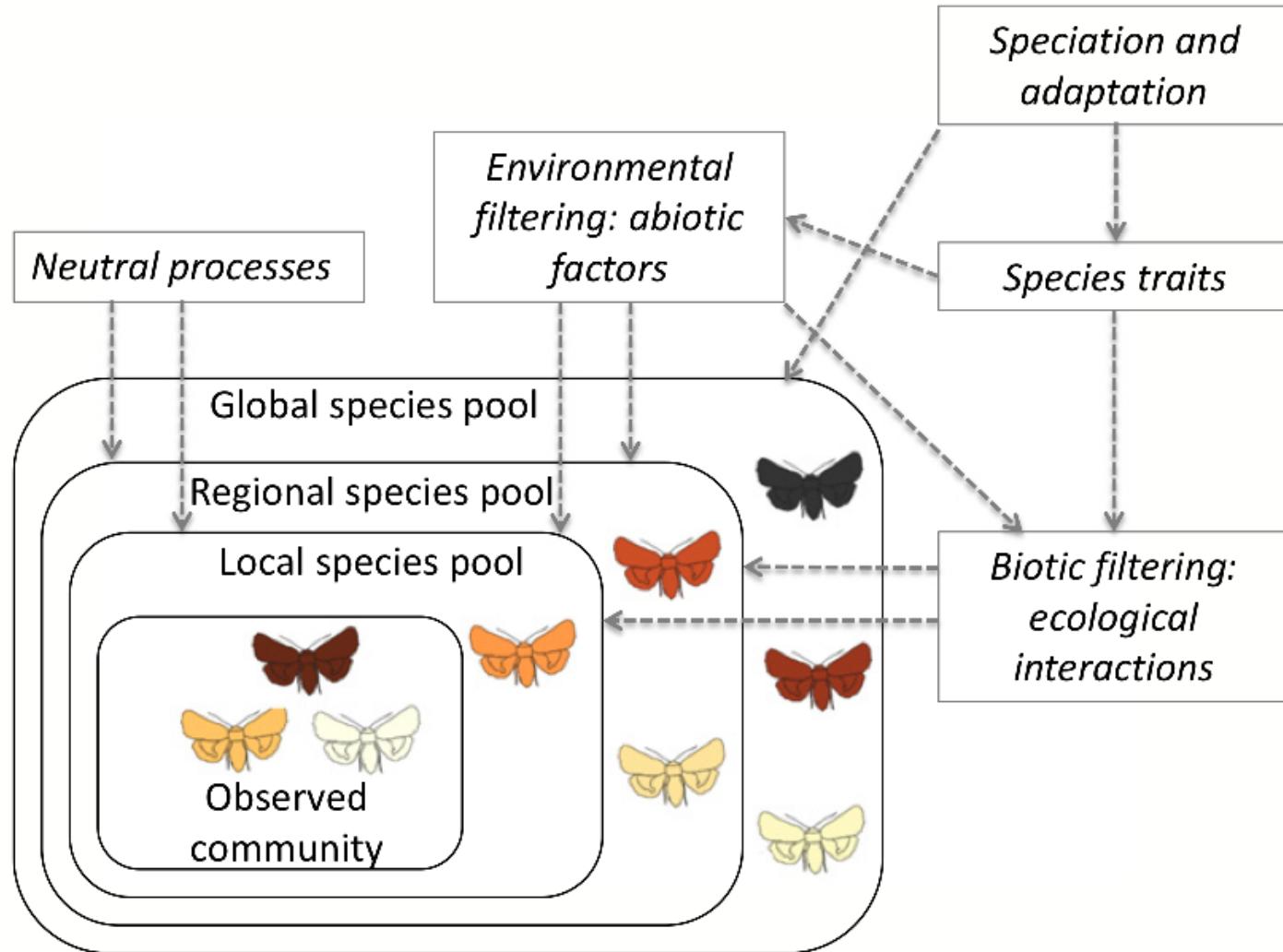
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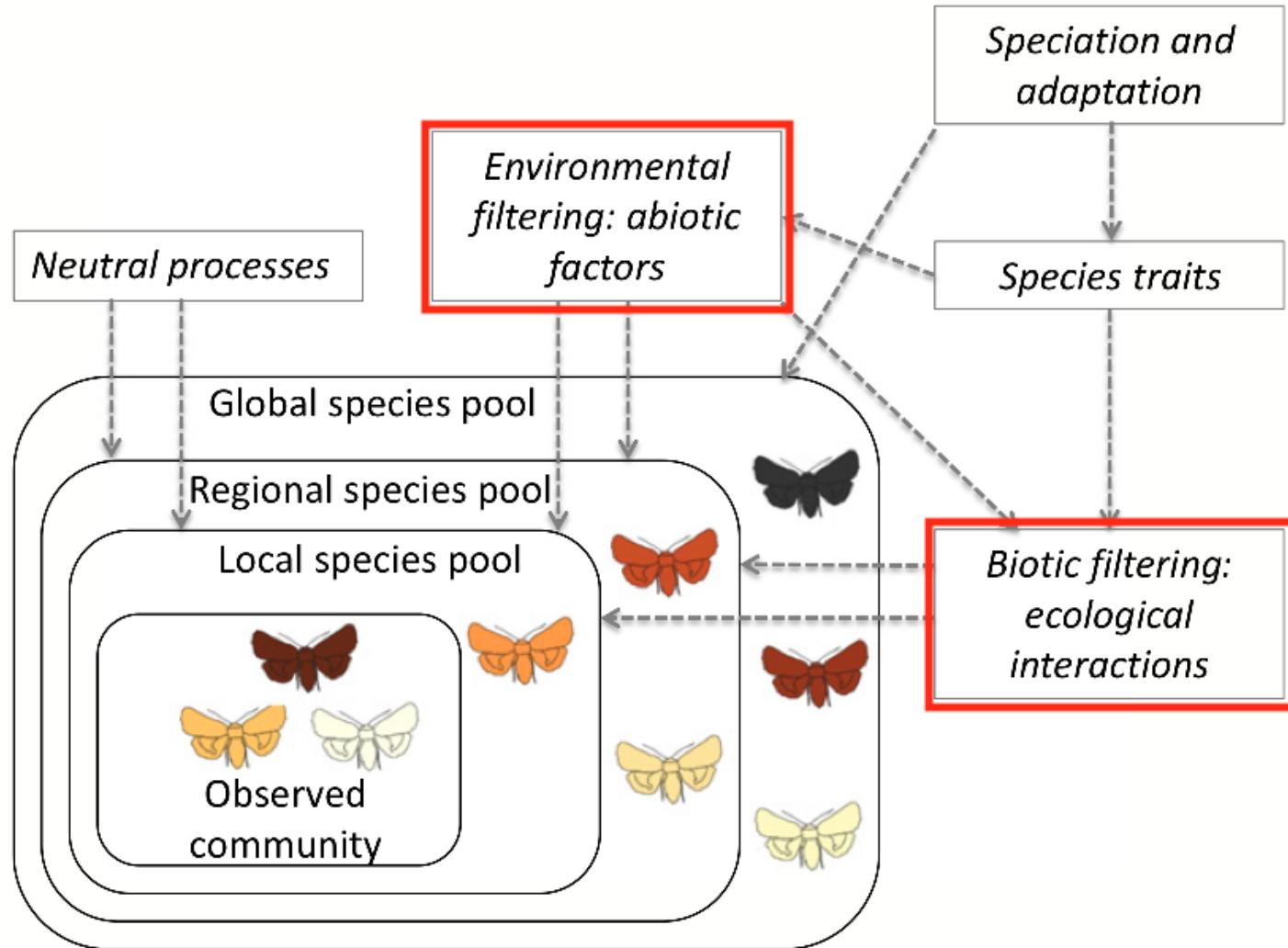
# Introduction

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# Assembly Rules Framework



# Assembly Rules Framework



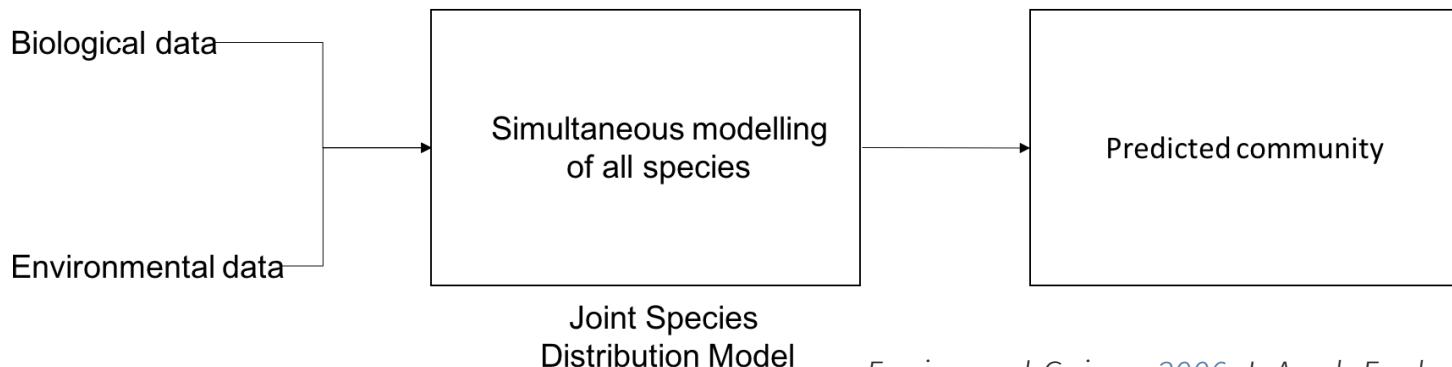
# Species Distribution Models

Strategies for modelling a community:

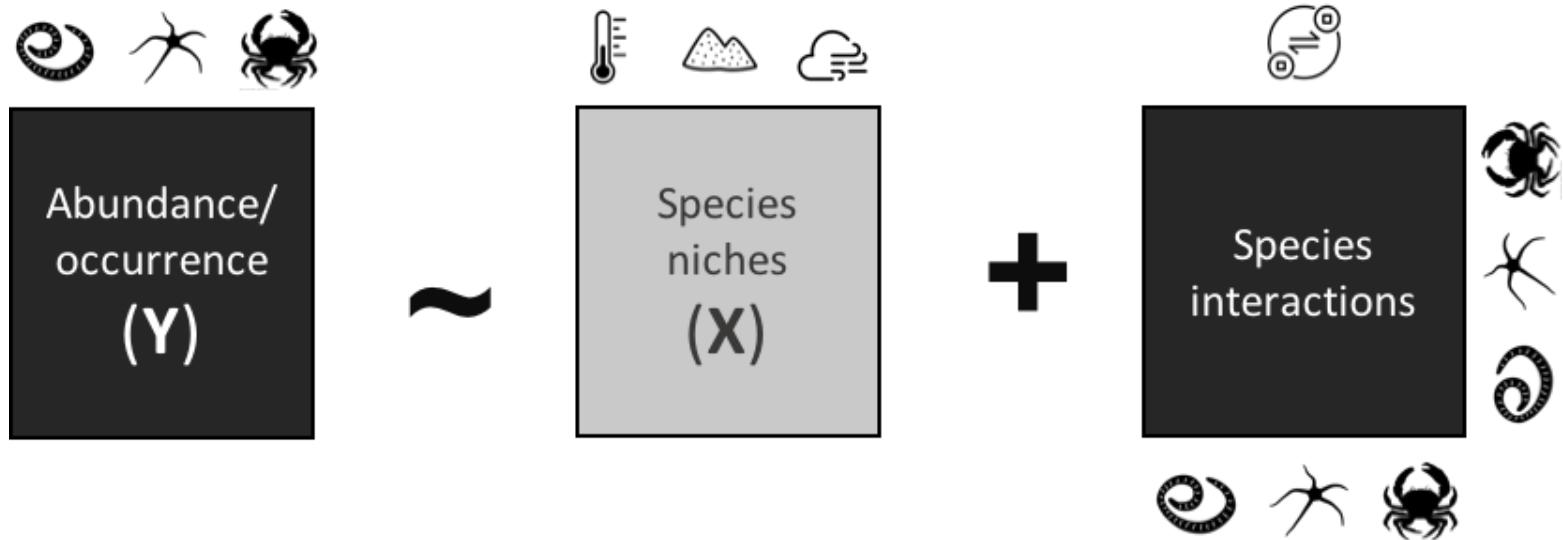
*Predict first, assemble later*



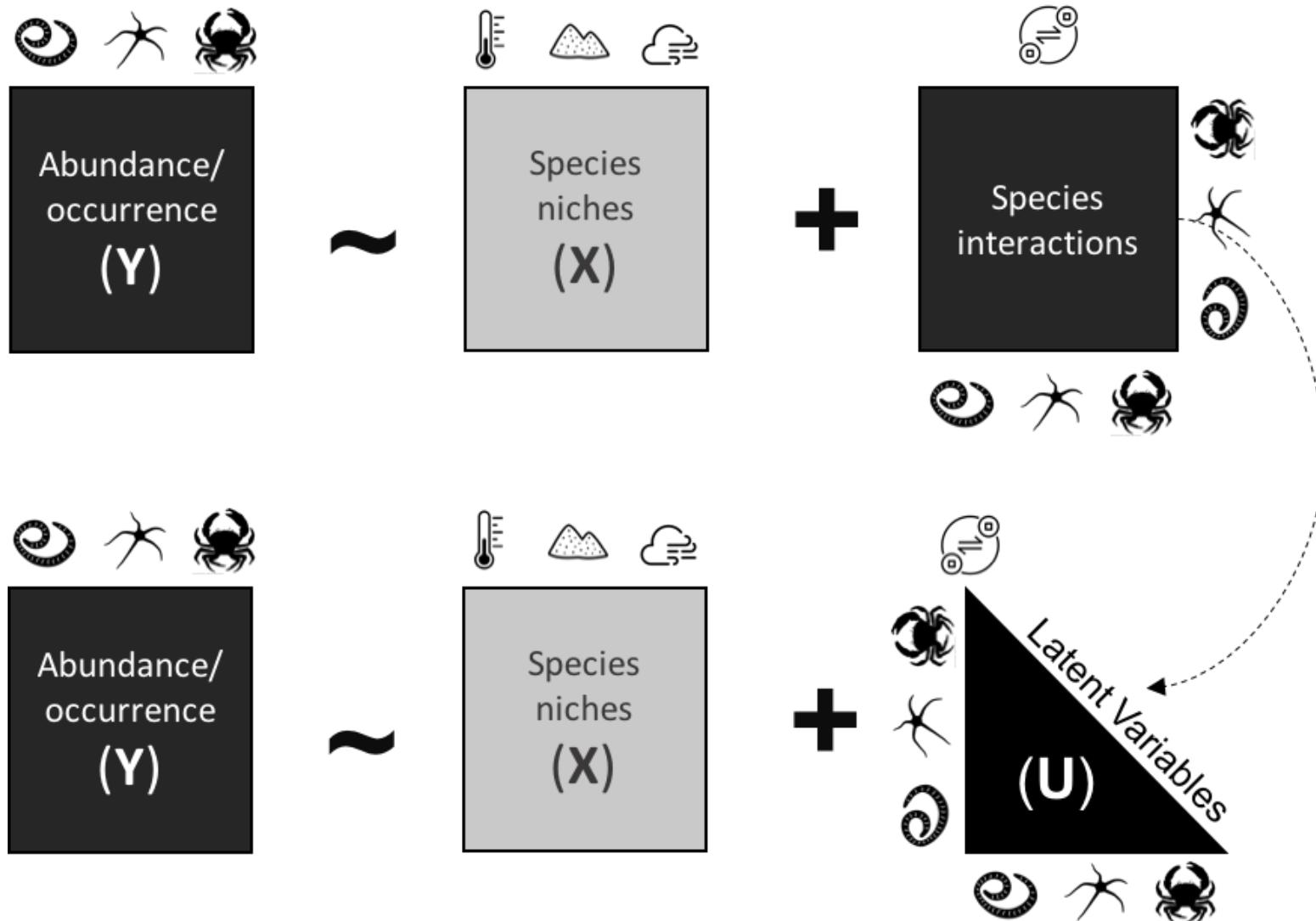
*Assemble and predict together*



# Joint Species Distribution Models



# Joint Species Distribution Models



# Prediction accuracy & species interactions

- JSMD predict the occurrence of species more accurately than SDM
  - But predict interactions is at best difficult from co-occurrence data.
- Using abundance data could be a solution to infer species interactions

Before trying to infer interactions, are we predicting accurately a community of interest?

# Material & methods

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# Study Case

December 1999...



...2003

**REBENT**  
réseau benthique

# Study Case - Habitat

- 21 training sites + 2 holdout validation sites
- 9 years of sampling (2006 - 2014)
- 2 habitats (seagrass meadows / intertidal bare sediments)



*Zostera marina*, seagrass meadow



Mont Saint-Michel, intertidal bare sediments

# Study Case - Community

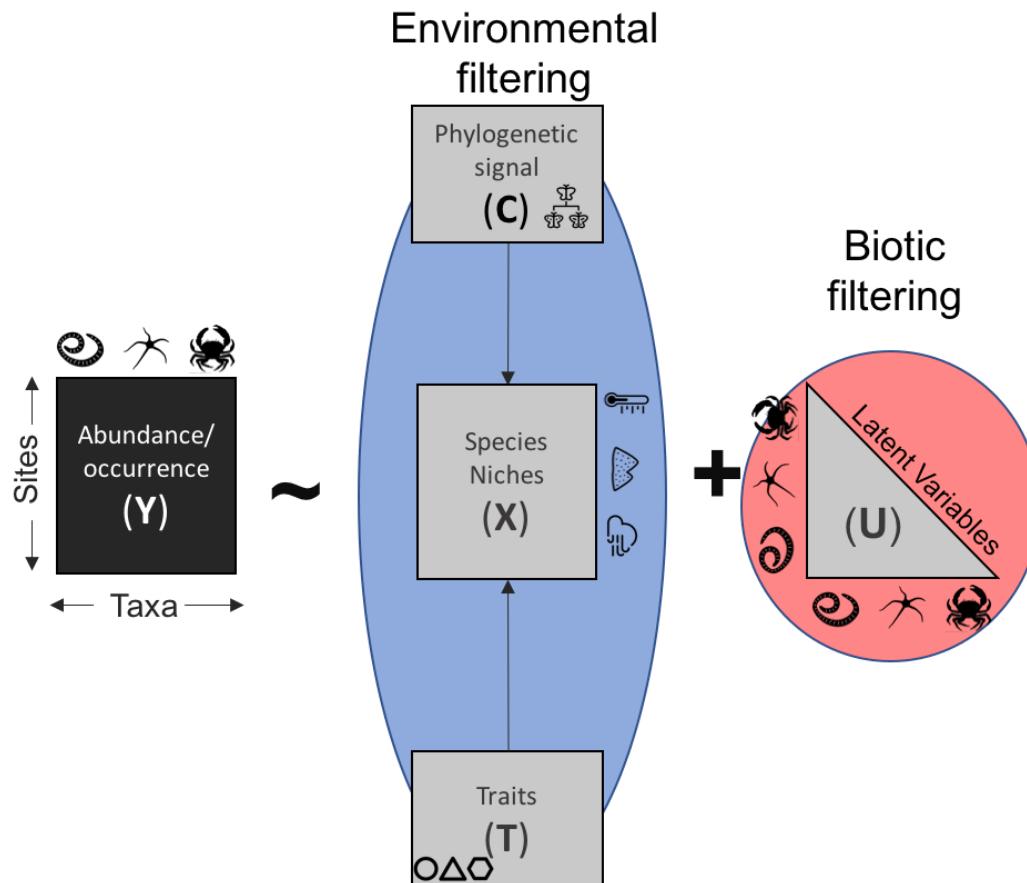
Polychaeta



*Eunice aphroditois*, which unfortunately does not inhabit our shores...

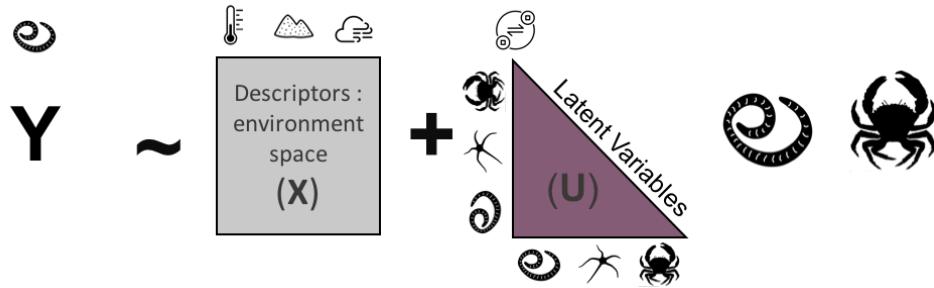
# Model backbone

- Hierarchical Modelling of Species Communities (*HMSC*)
- Multivariate hierarchical GLMM fitted with Bayesian inference
- *HMSC* relies on assembly rules framework

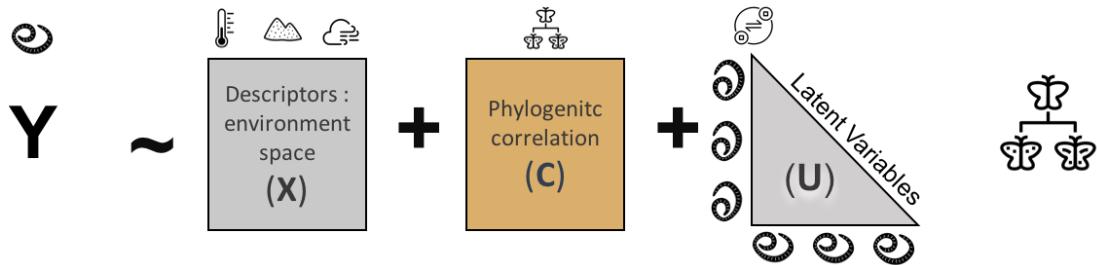


# Candidate Models

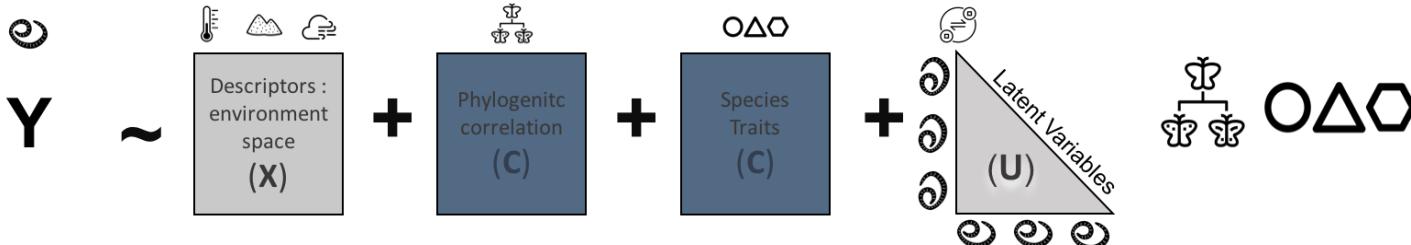
## Model 1



## Model 2



## Model 3

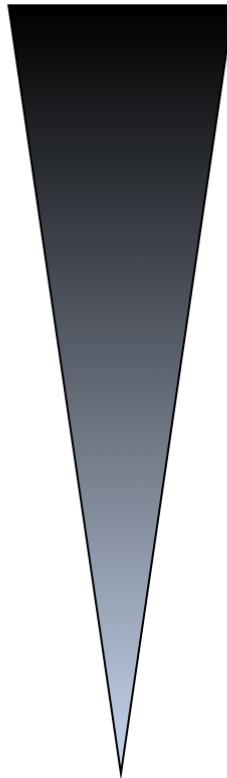


# Diversity patterns

What is the best strategy to predict:

1. Community structure?
2. Species richness?
3. Species-specific abundance

Coarse scale predictions



Fine scale predictions

# Diversity patterns

What is the best strategy to predict:

1. Community structure?

- Mean Absolute Error on Local Contribution to Beta Diversity (LCBD) [1]

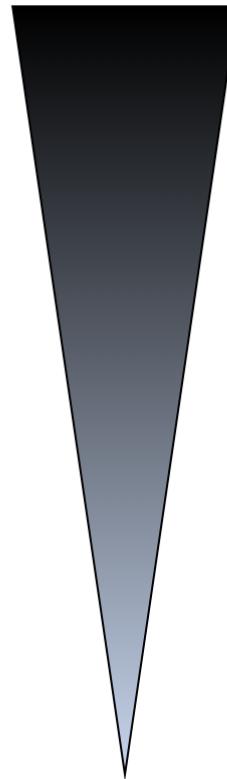
2. Species richness?

- Mean Absolute Error on species richness

3. Species-specific abundance

- $R^2 = r_p(y, \hat{y})$

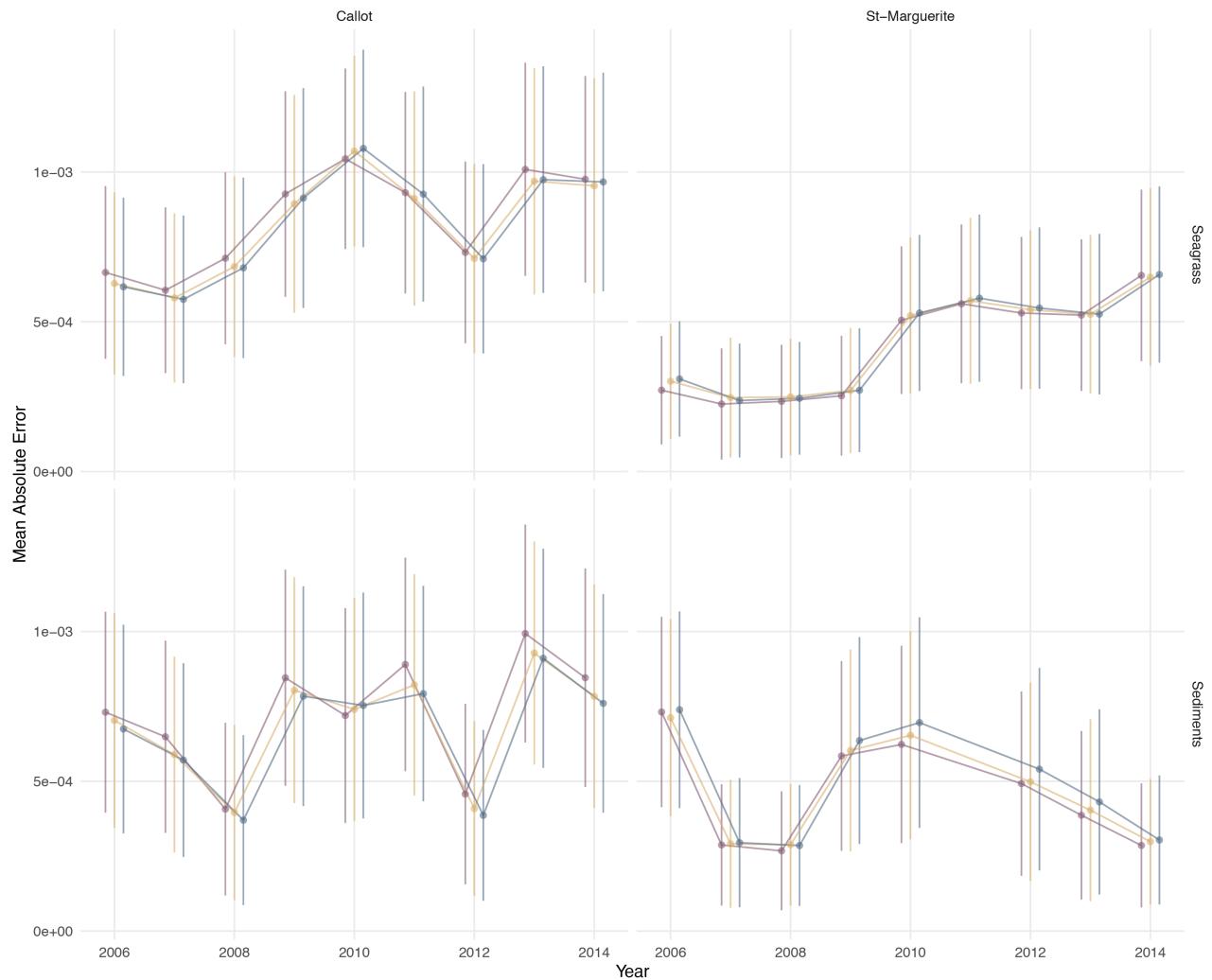
Coarse scale predictions



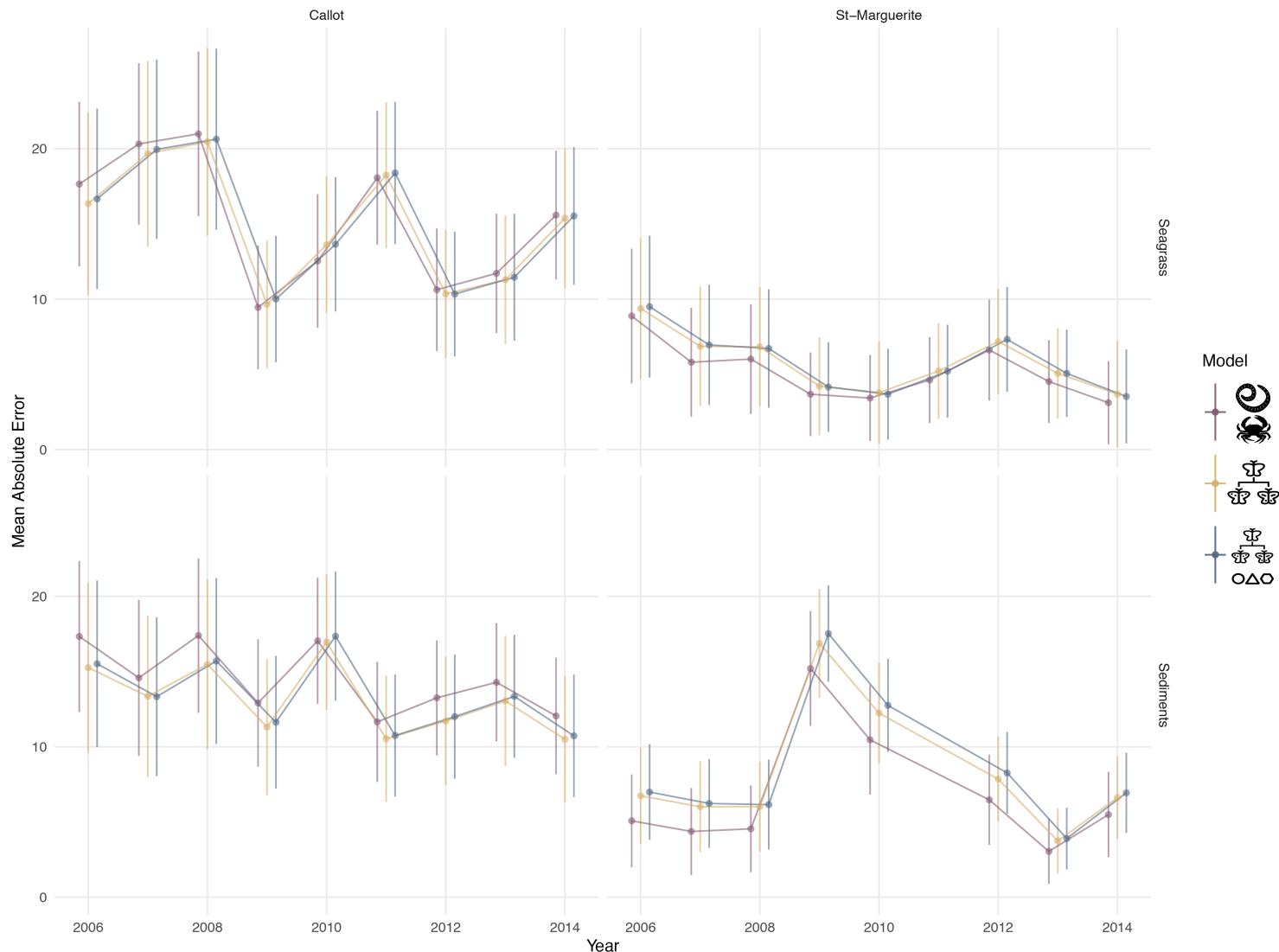
Fine scale predictions

# Predict Community Structure

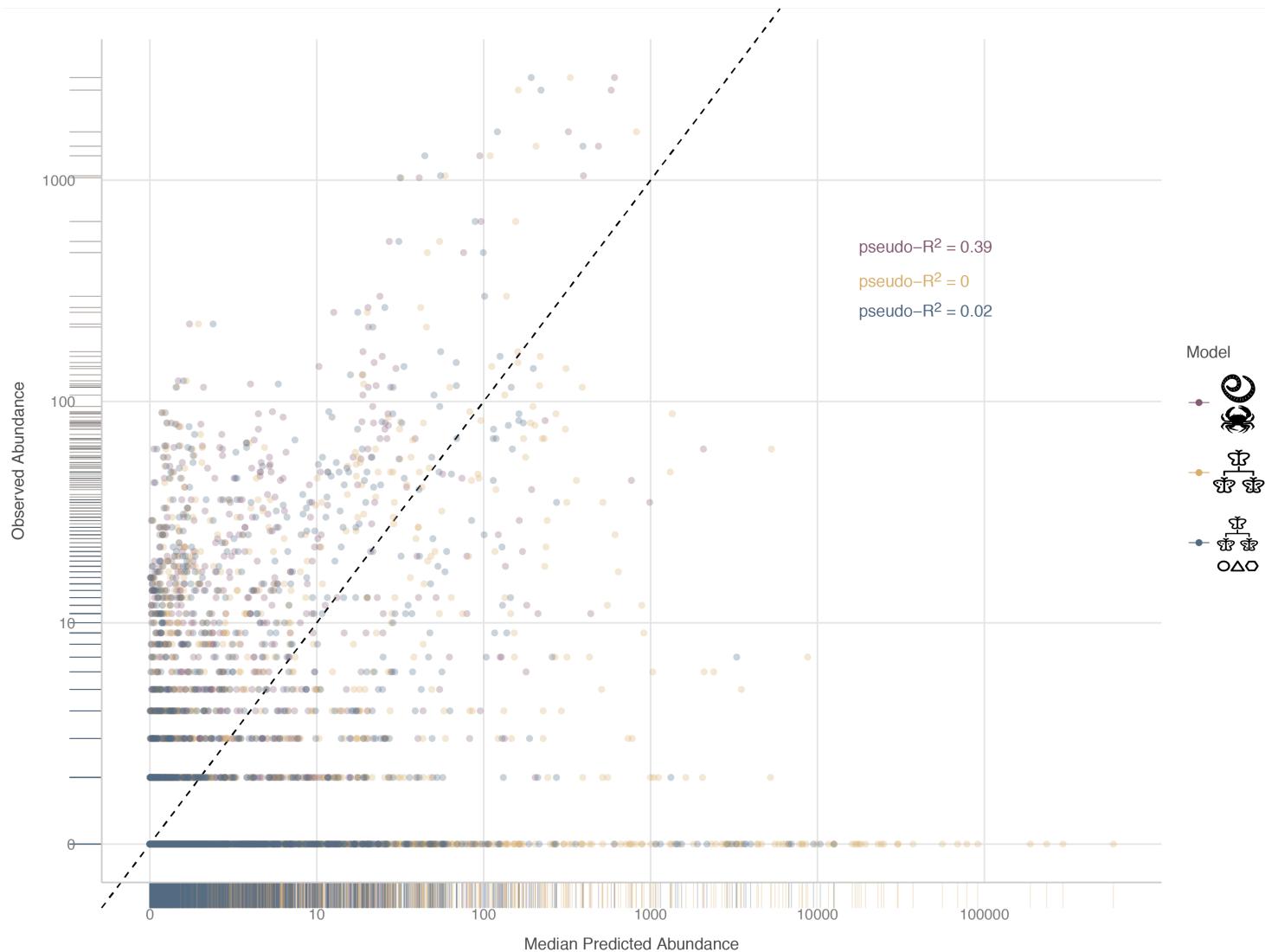
Local Contribution to Beta Diversity



# Predict Species Richness



# Species-specific abundance accuracy



# Conclusion



**Model 1 – Whole community**



**Model 2 - Taxonomy**



**Model 3 – Taxonomy + traits**

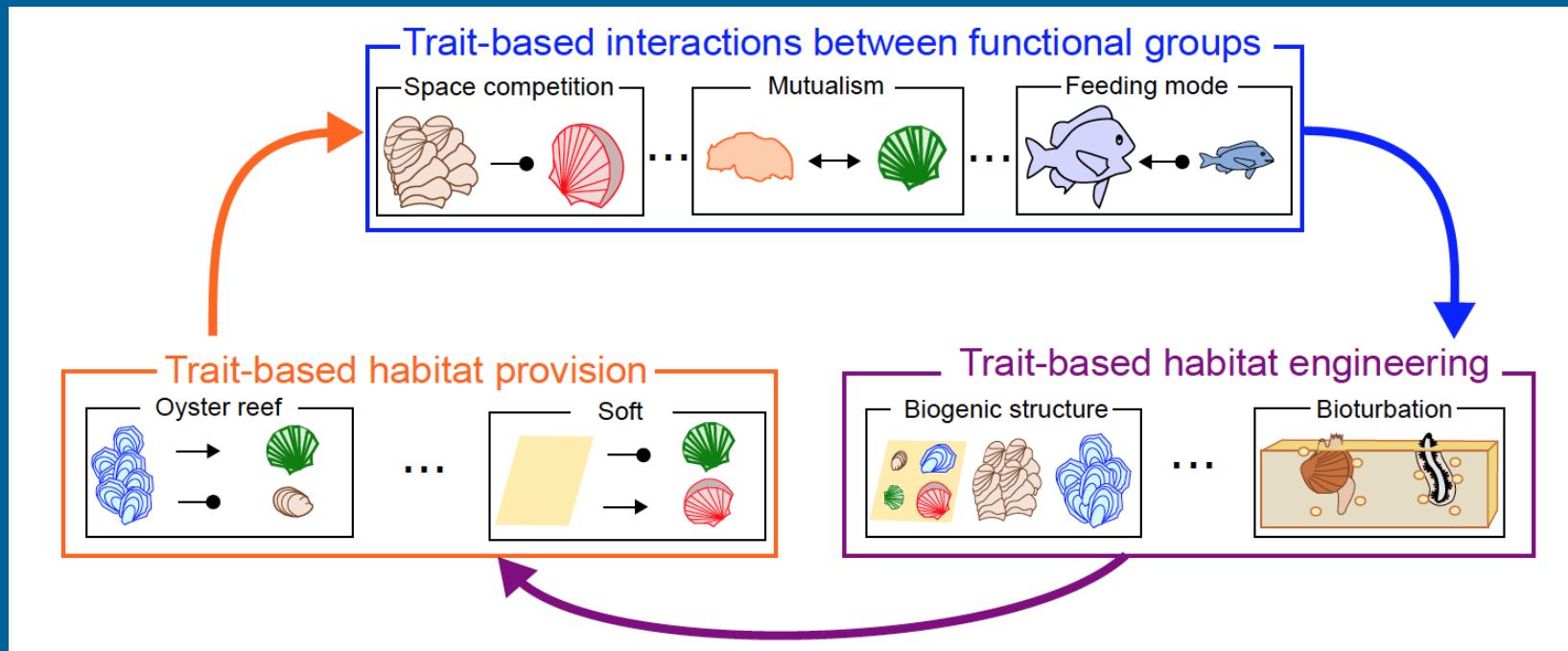
Diversity Patterns	Model 1	Model 2	Model 3
Community Structures	++	++	++
Species Richness	+/-	+/-	+/-
Species Abundance	+	-	-

Which strategy to choose?

- Best accuracy with the whole community
- Traits are a valuable addition
- Interactions ?

# Work in Progress

- Community trajectory analysis
- Add intercept models



# Thank you for listening!

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*Eunice aphroditois a.k.a Bobbit worm*