

Predicting diversity with *Joint Species Distribution Models*

A difficult case with species rich marine benthic communities

Clément Violet, DYNÉCO - LEBCO

Aurélien Boyé, DYNÉCO - LEBCO

Olivier Gauthier, LEMAR

Jacques Grall, IUEM - Observatoire

Stanislas Dubois, DYNÉCO - LEBCO

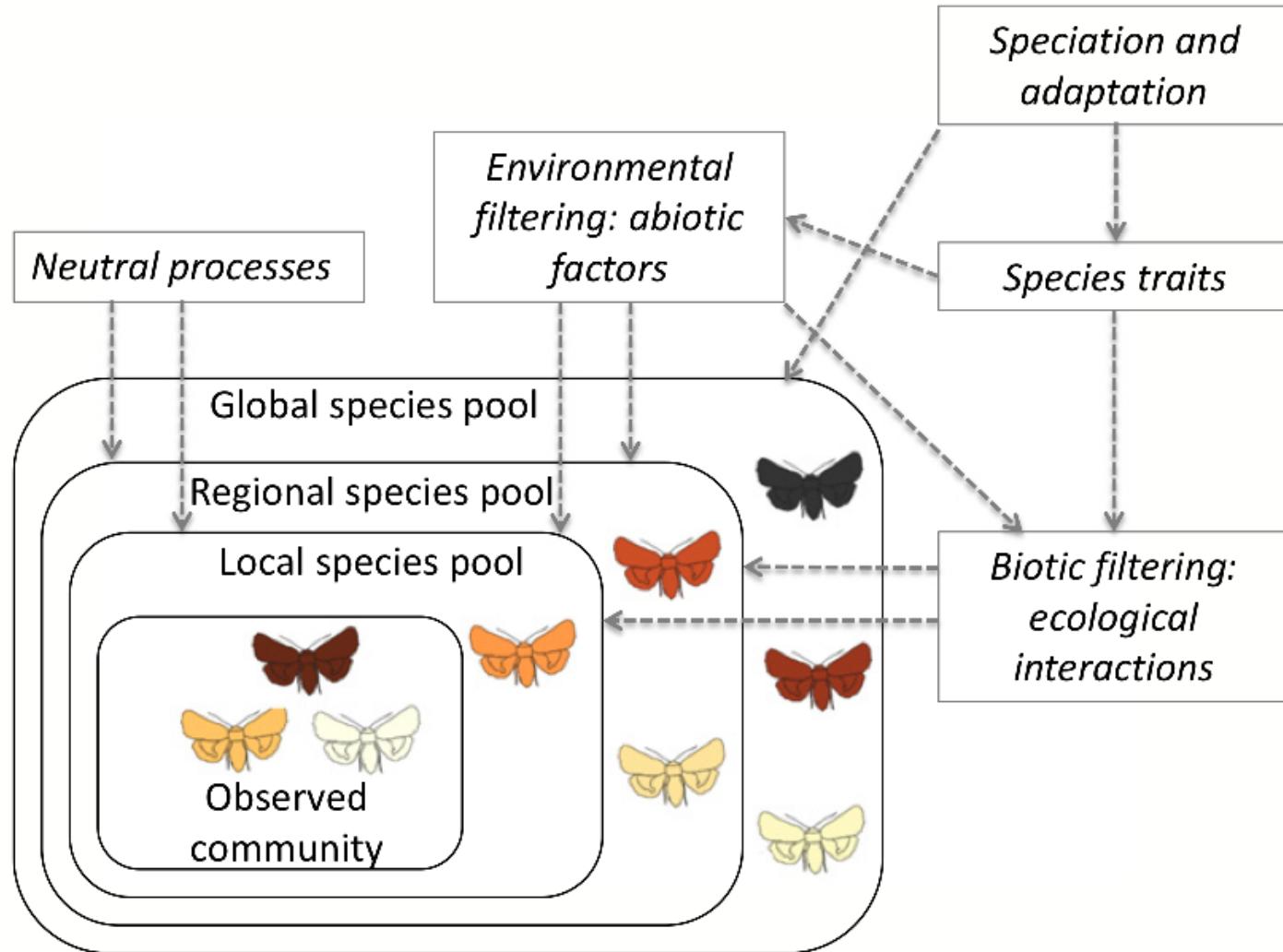
Martin Marzloff, DYNÉCO - LEBCO

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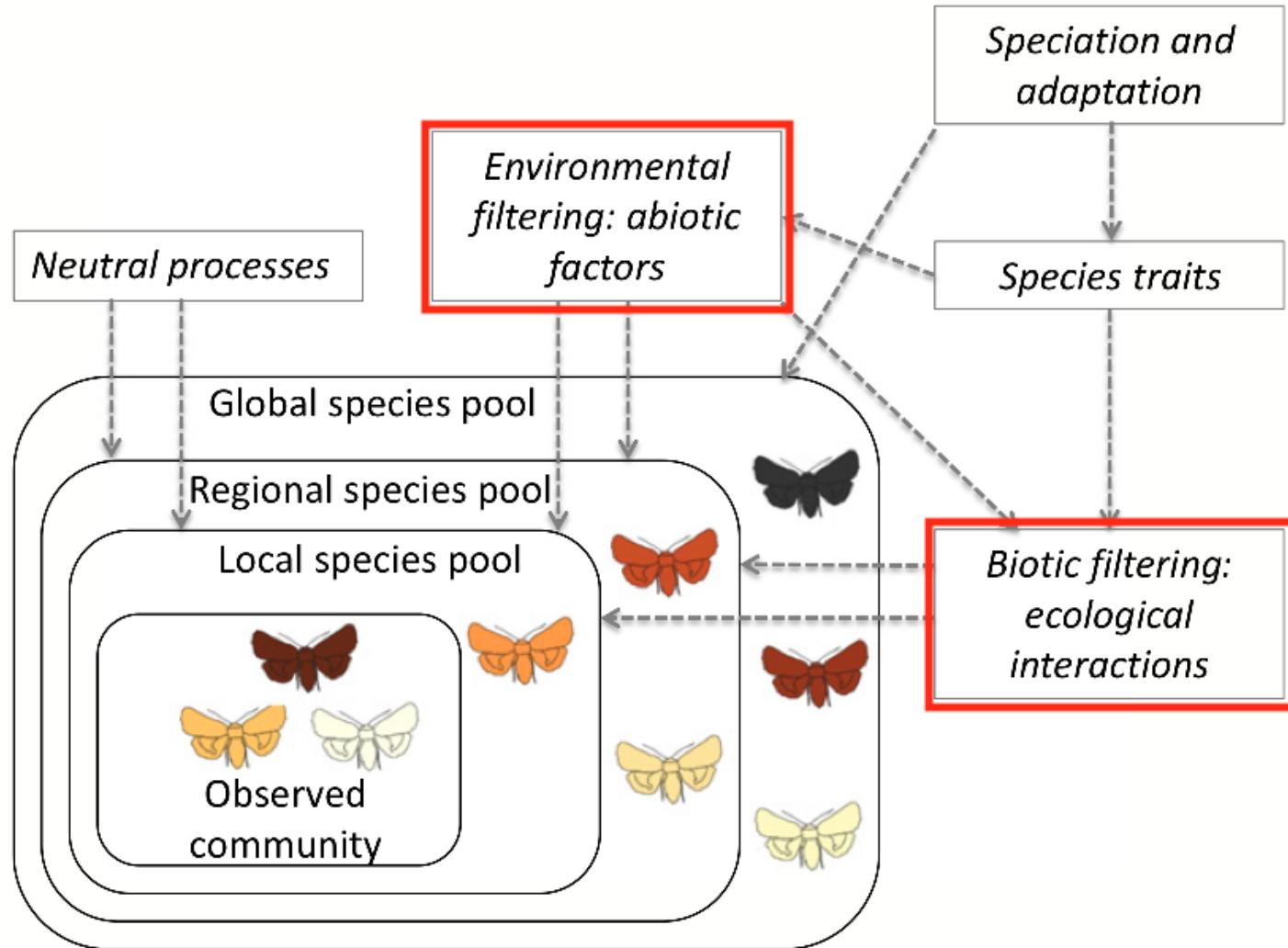


Introduction

Assembly Rules Framework



Assembly Rules Framework



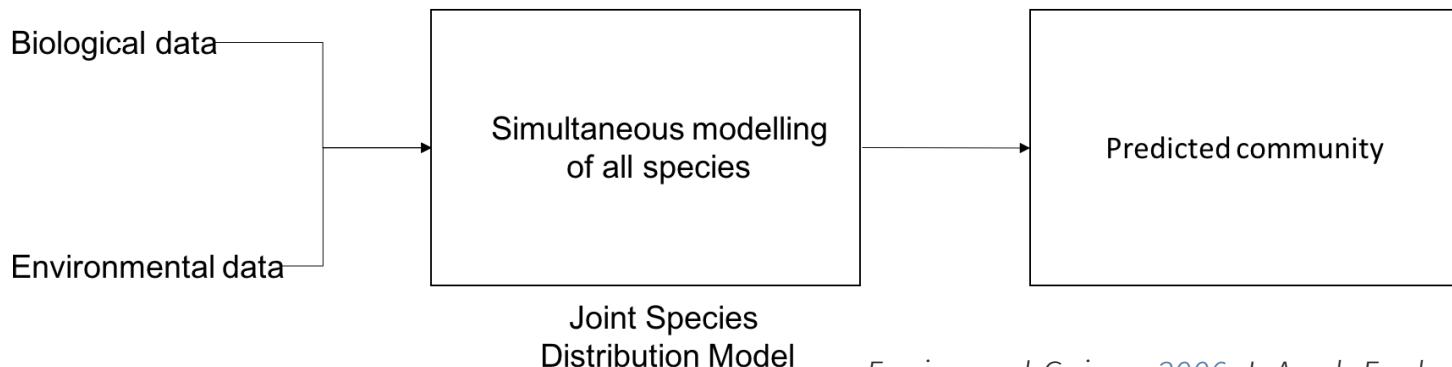
Species Distribution Models

Strategies for modelling a community:

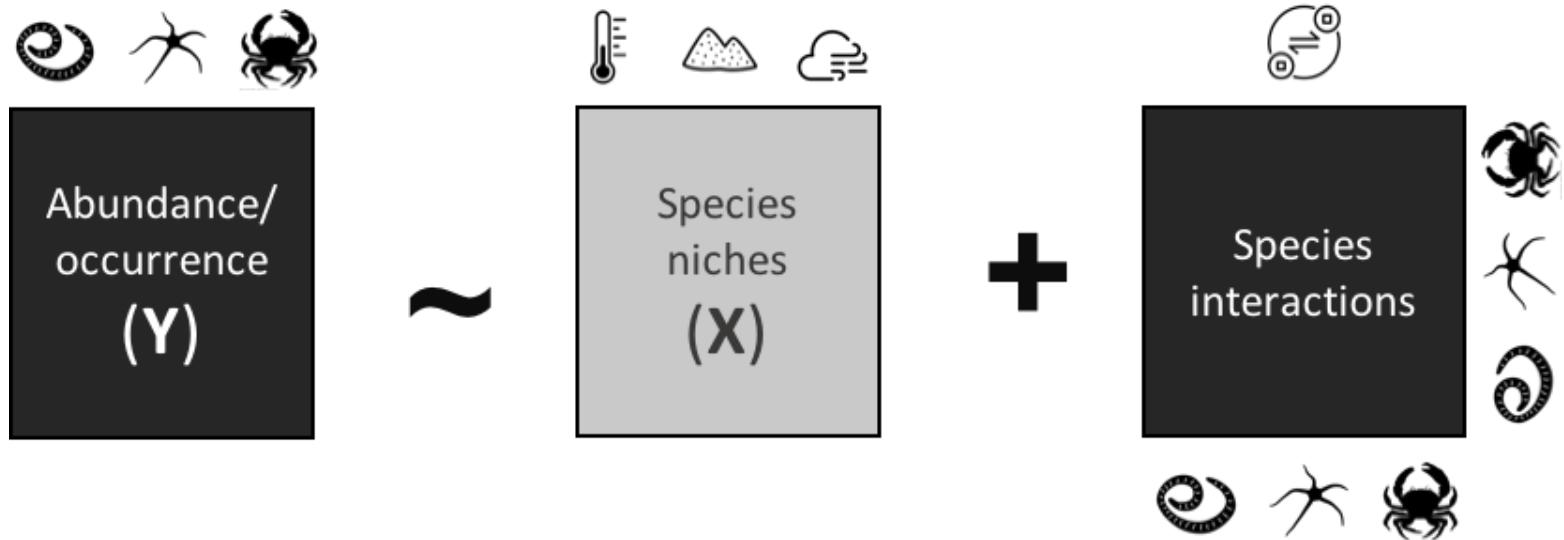
Predict first, assemble later



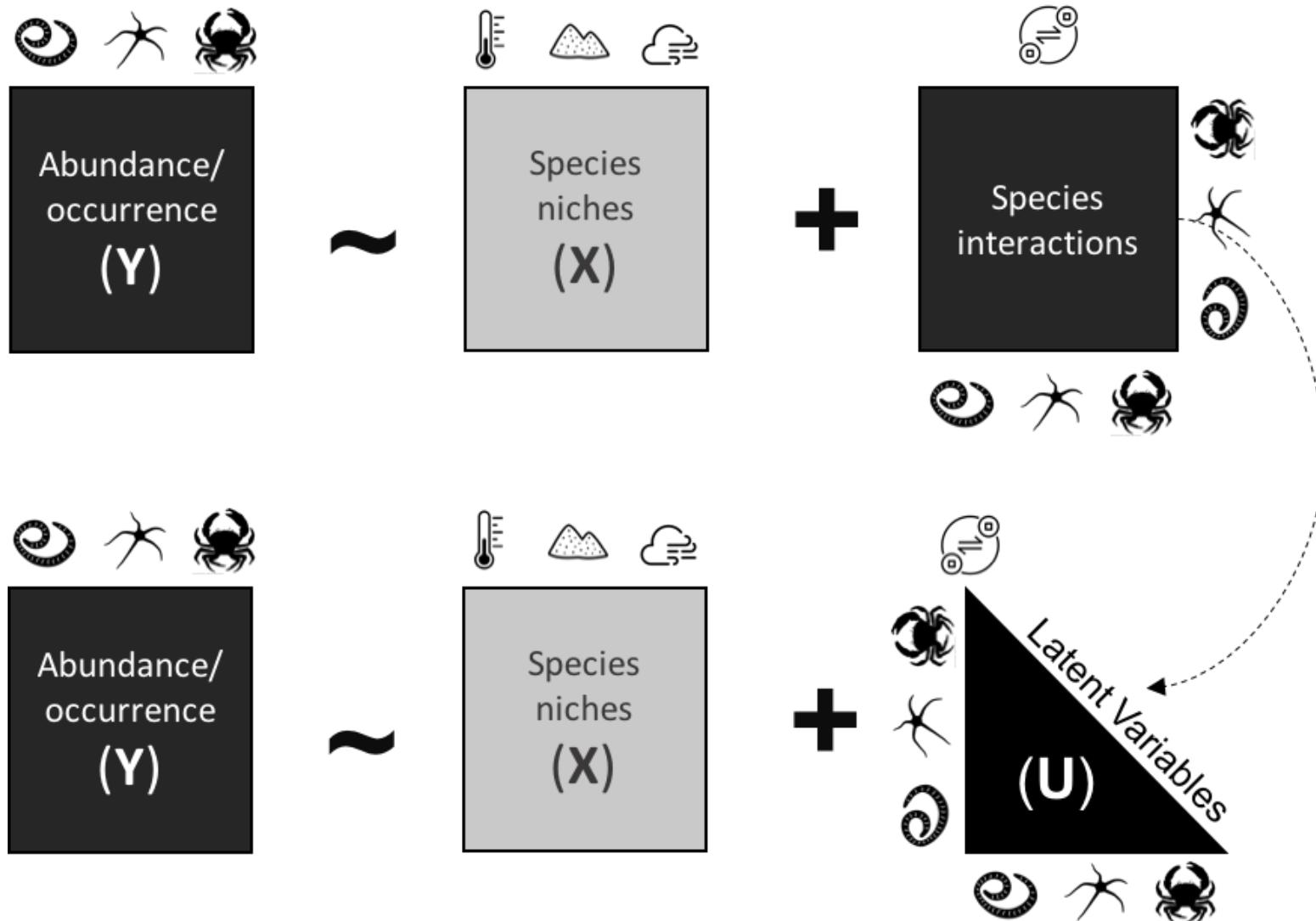
Assemble and predict together



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

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

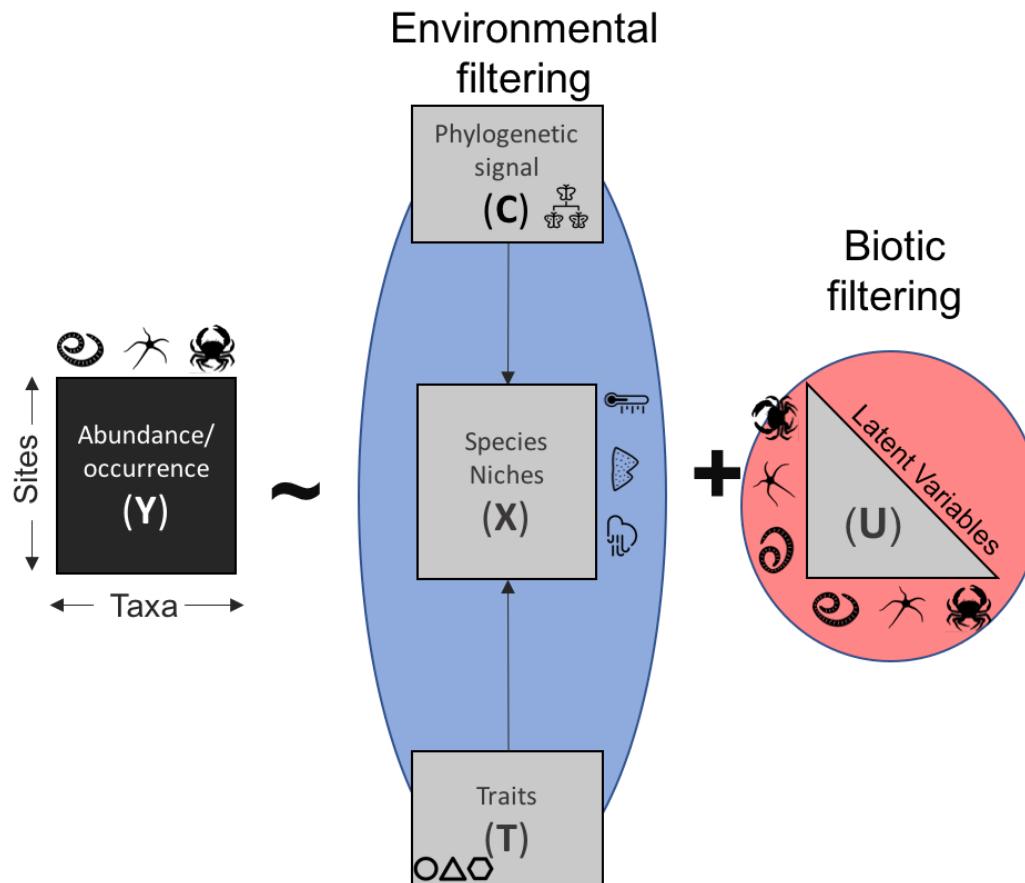
Polychaeta



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

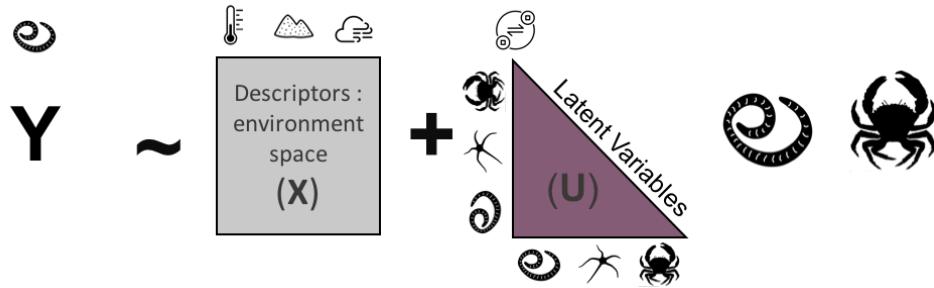
Model backbone

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

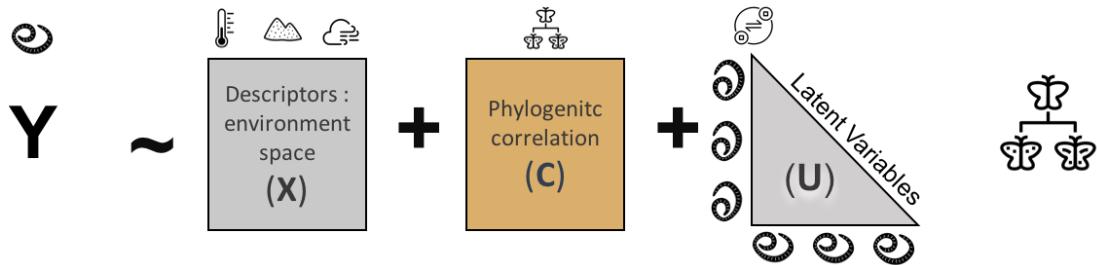


Candidate Models

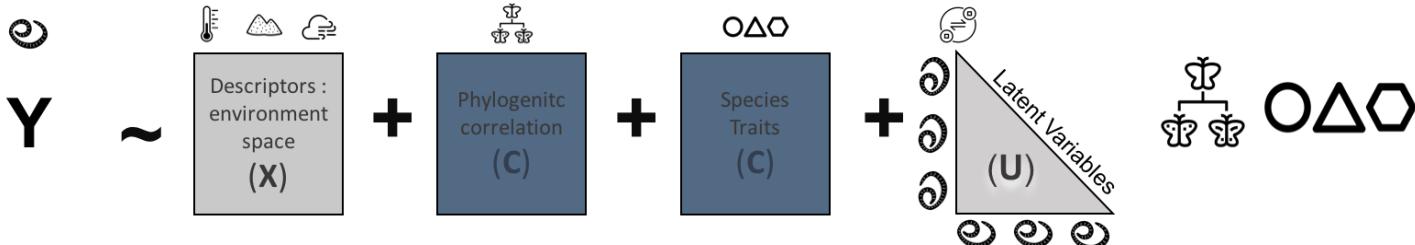
Model 1



Model 2



Model 3

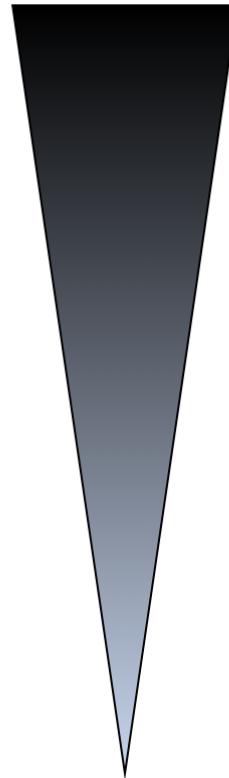


Diversity patterns

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]

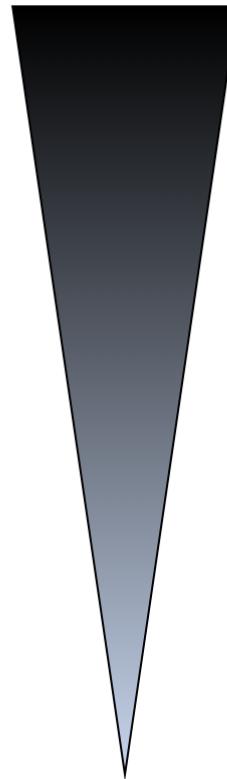
2. Species richness?

- Mean Absolute Error on species richness

3. Species-specific abundance

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

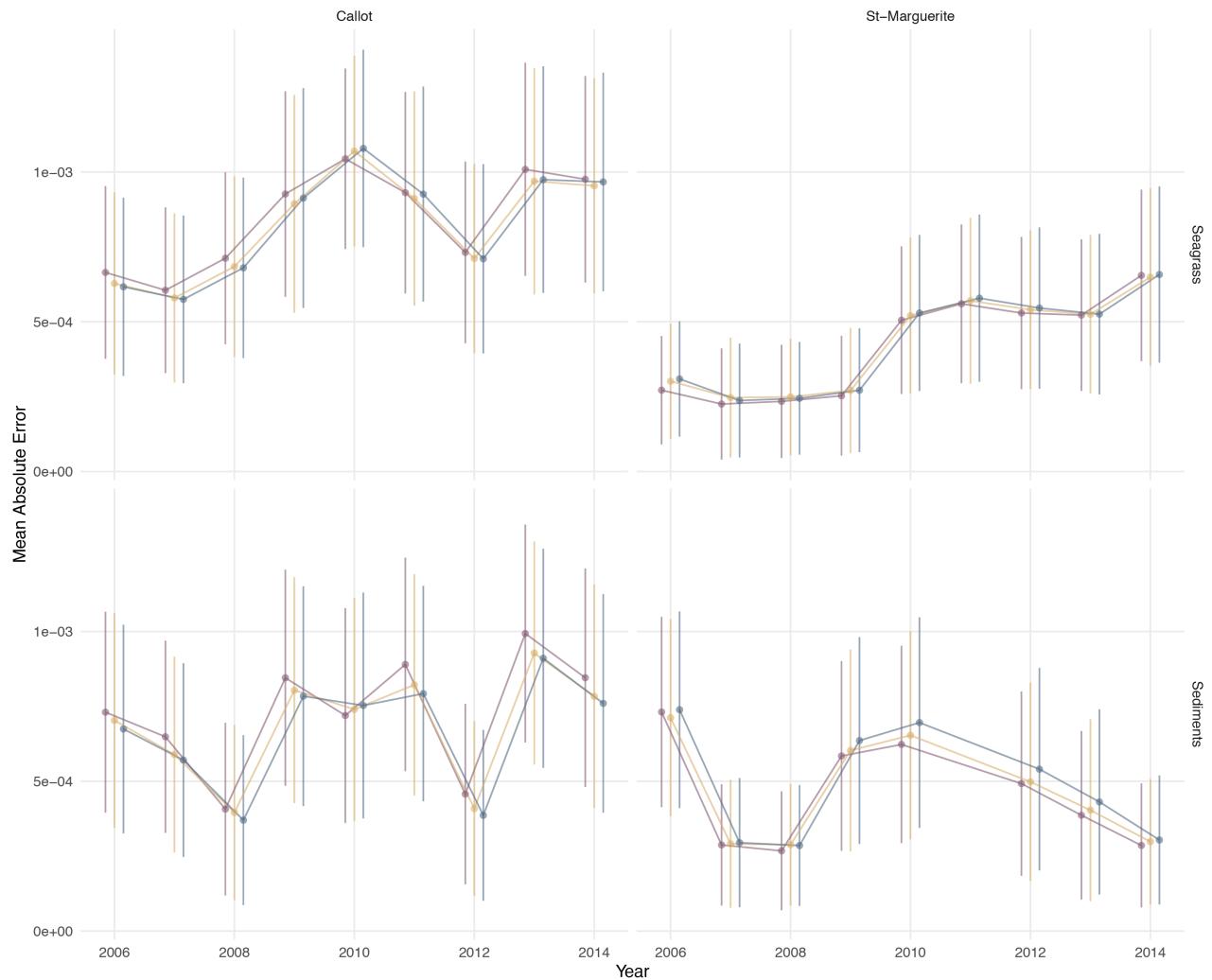
Coarse scale predictions



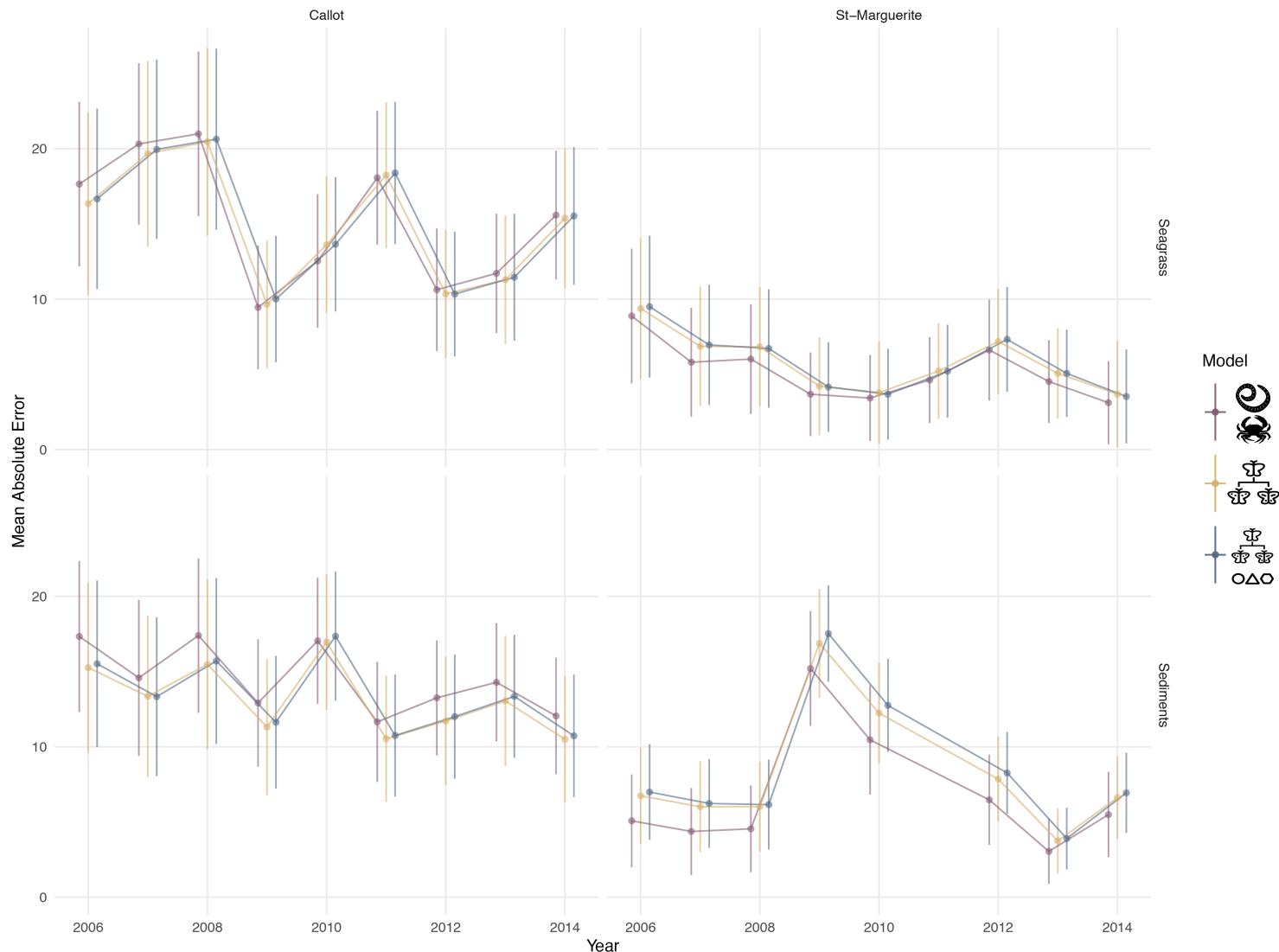
Fine scale predictions

Predict Community Structure

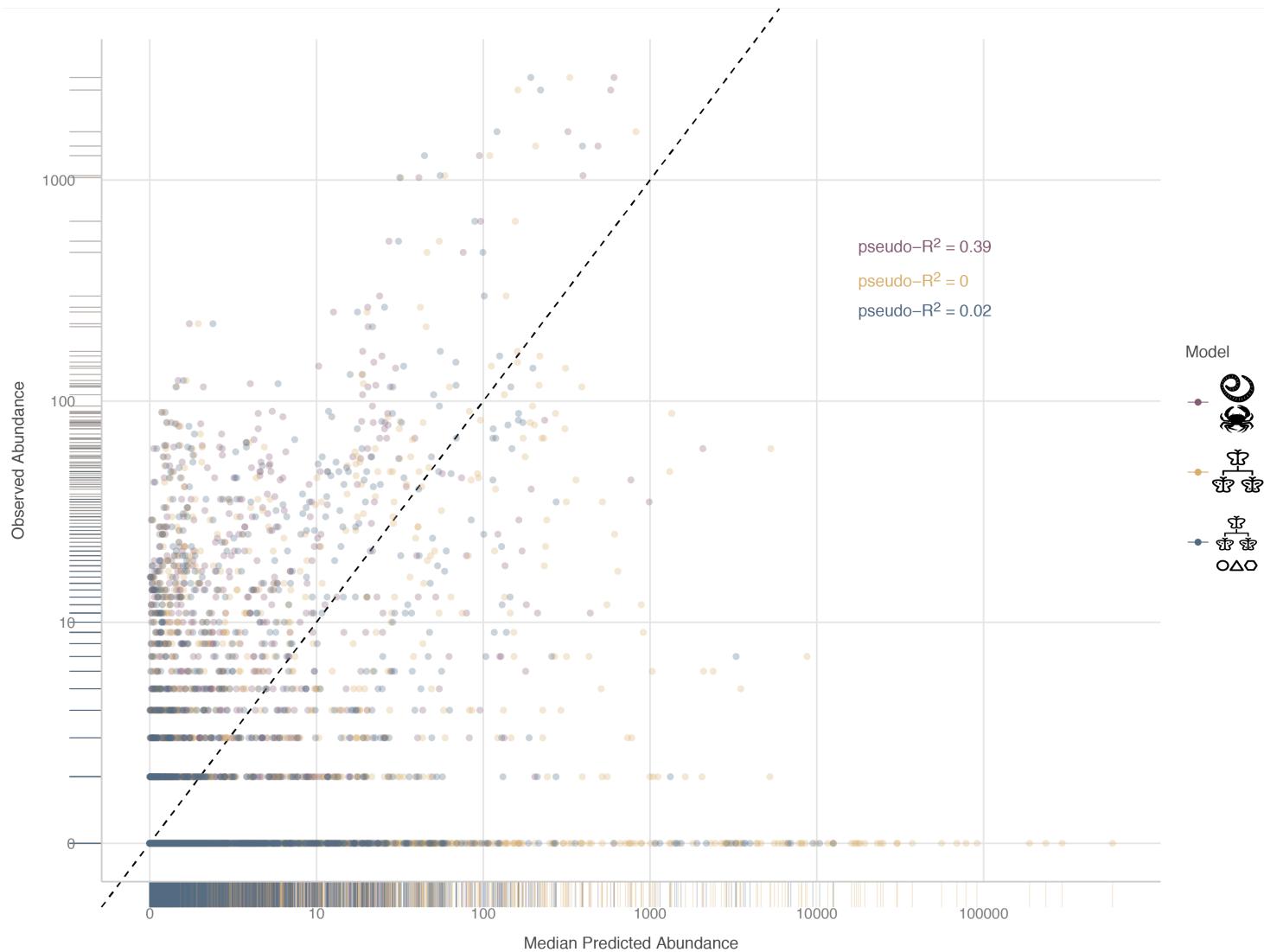
Local Contribution to Beta Diversity



Predict Species Richness



Species-specific abundance accuracy



Conclusion



Model 1 – Whole community



Model 2 - Taxonomy



Model 3 – Taxonomy + traits

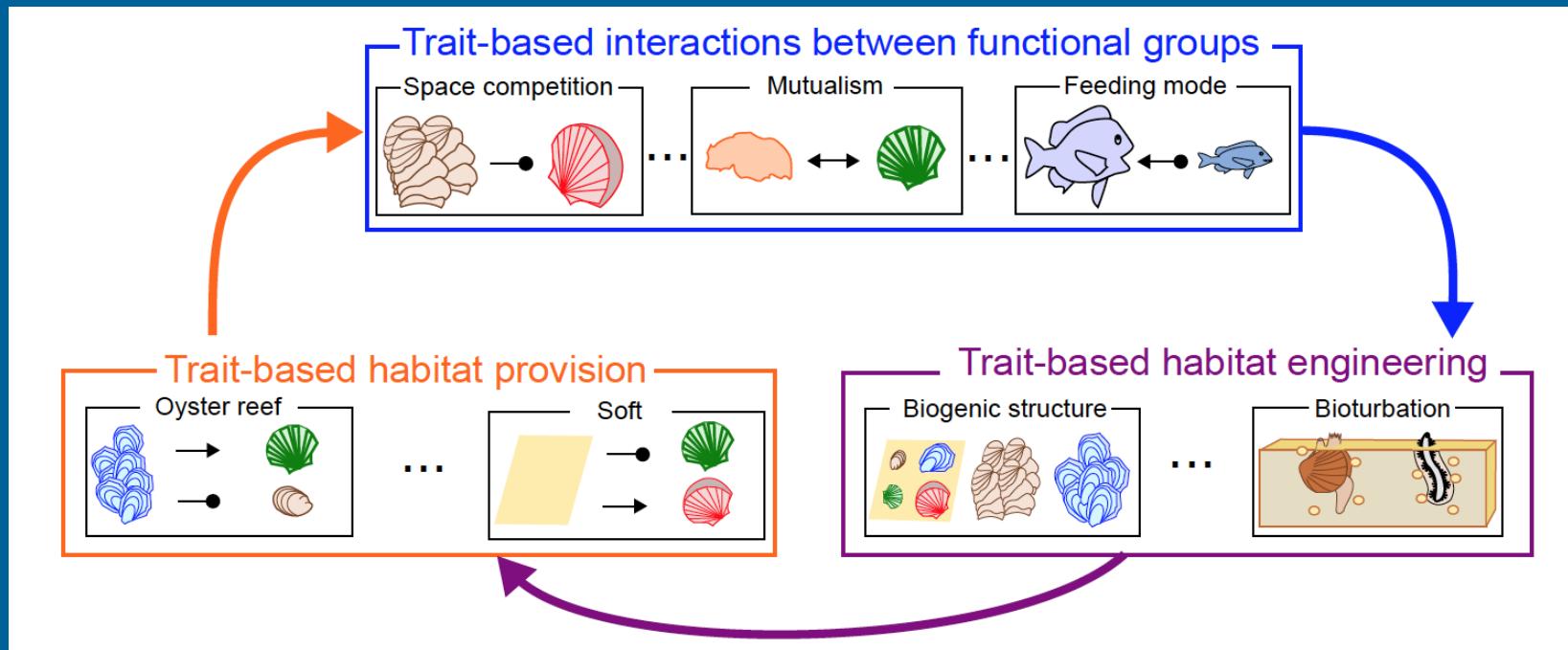
Diversity Patterns	Model 1	Model 2	Model 3
Community Structures	++	++	++
Species Richness	+/-	+/-	+/-
Species Abundance	+	-	-

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!

 clementviolet/GDREcostat21

 @ClementVIOLET

 0000-0001-6217-5891



Eunice aphroditois a.k.a Bobbit worm