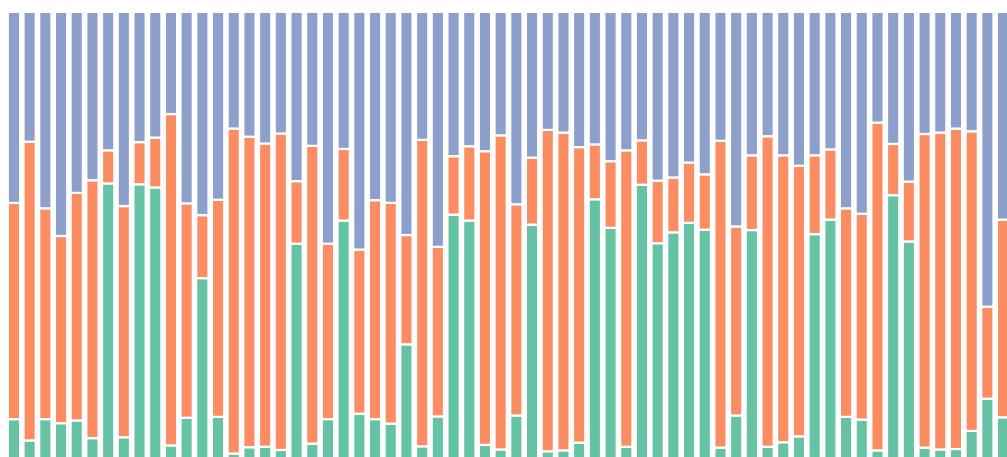


Identifying Models of Trait-Mediated Community Assembly

using random forests and
approximate Bayesian computation

Megan Ruffley, Katie Peterson,

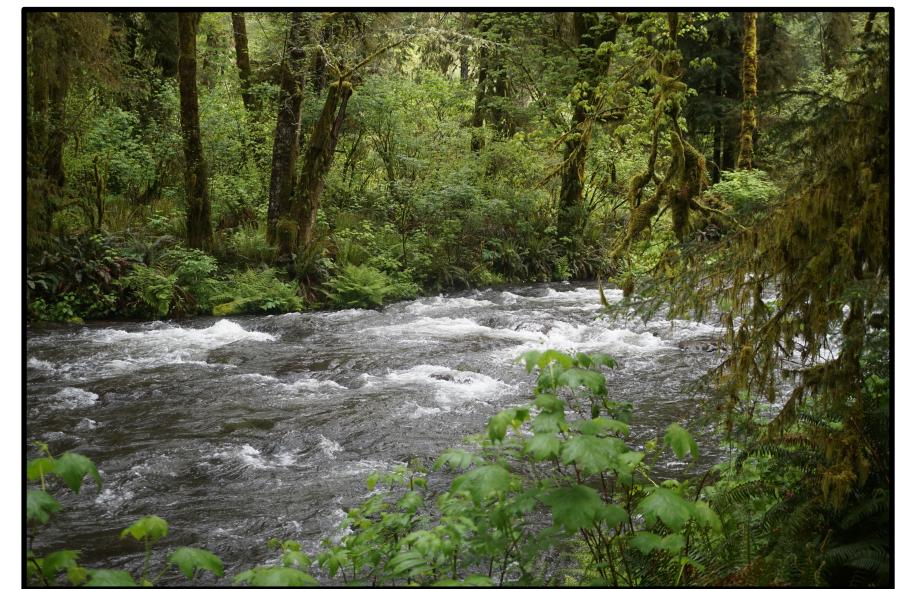
Bob Week, David C. Tank,
Luke J. Harmon



Interested in identifying neutral and non-neutral processes of assembly



Environmental Filtering



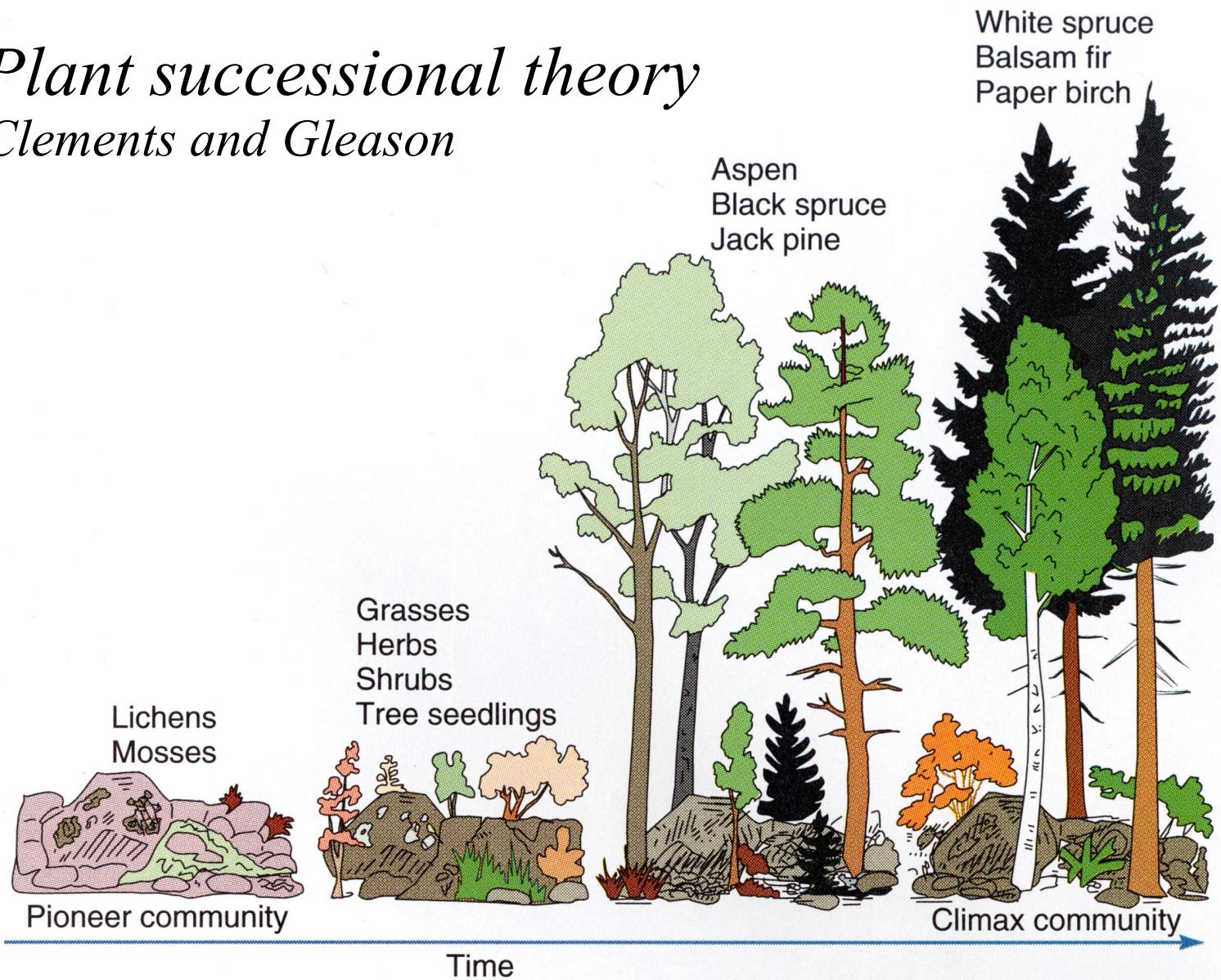
Competitive Exclusion



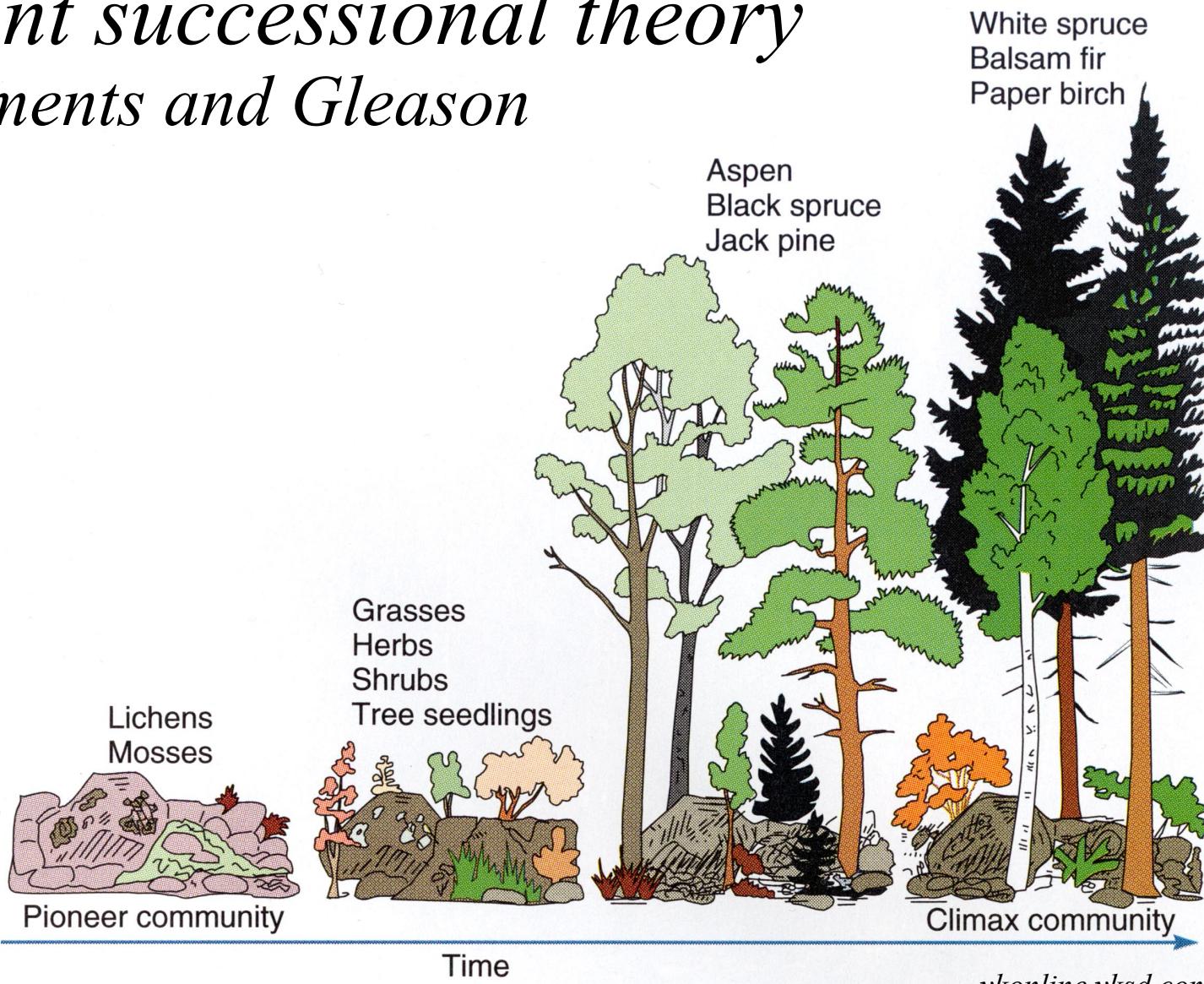
Plant successional theory

Clements and Gleason

Are communities a result of deterministic (Clements 1938) or stochastic (Gleason 1927) processes



Plant successional theory Clements and Gleason



Frederic Clements (1916)

“Succession is deterministic”

- stable ‘climax’ community that is in perfect balance with the climate

“Communities are super-organisms”

- Communities are dependent on the species interactions among members



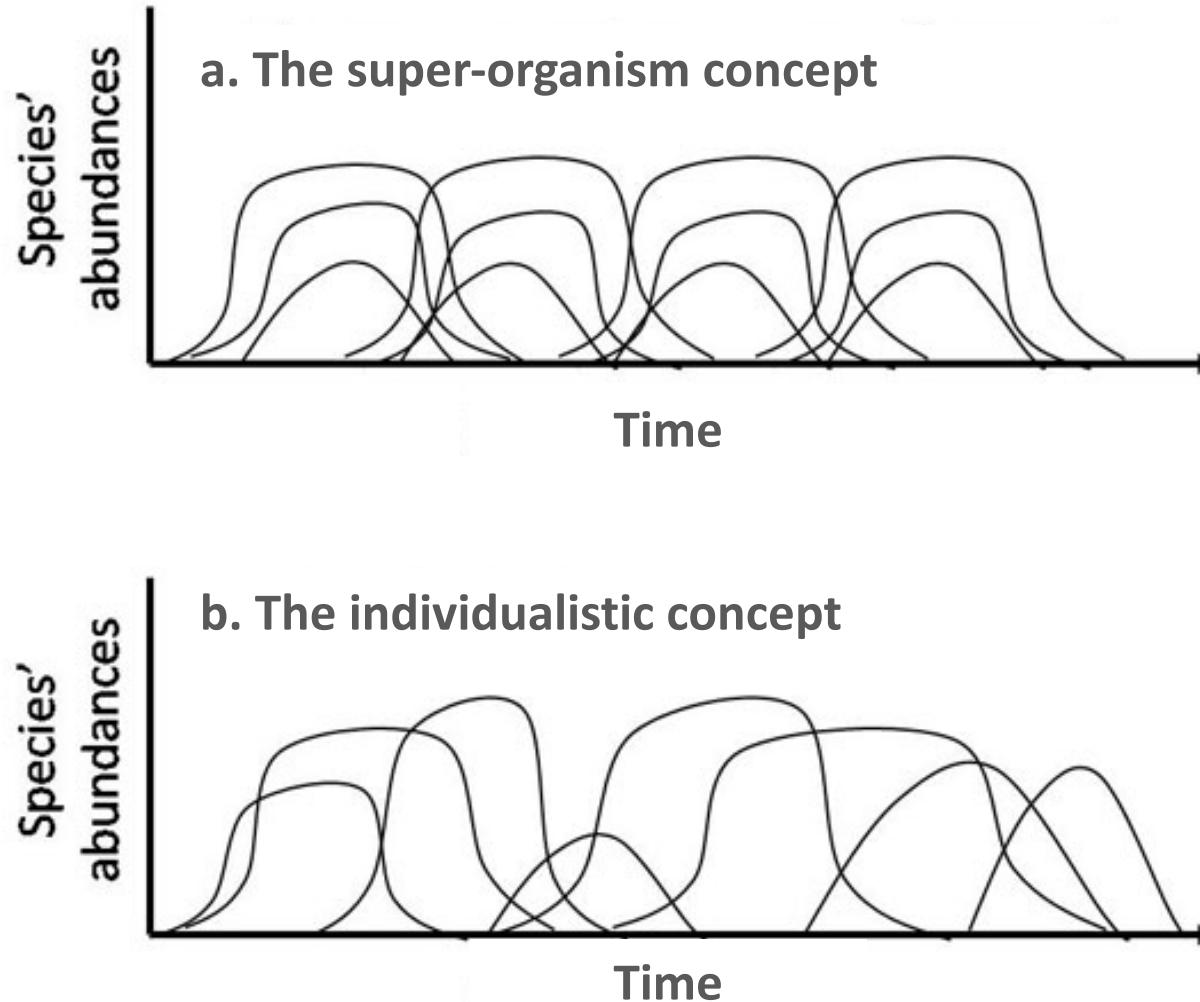
FREDERICK EDWARD CLEMENTS
1874-1945



Henry Gleason (1917)

- “Each species is an independent entity”
 - distribution of each species is due to genetics, physiology, life history, and relations to abiotic and biotic factors
 - communities are just a consequence of independent interactions among species and their environment

Introduction: Clements and Gleason debate



(A) Groups of species are tightly associated, and are supplanted by other groups of tightly associated species. (B) Individual species independently respond to environmental conditions. Each curve on the graphs represents the abundance of a single species.

What influences how communities are formed?

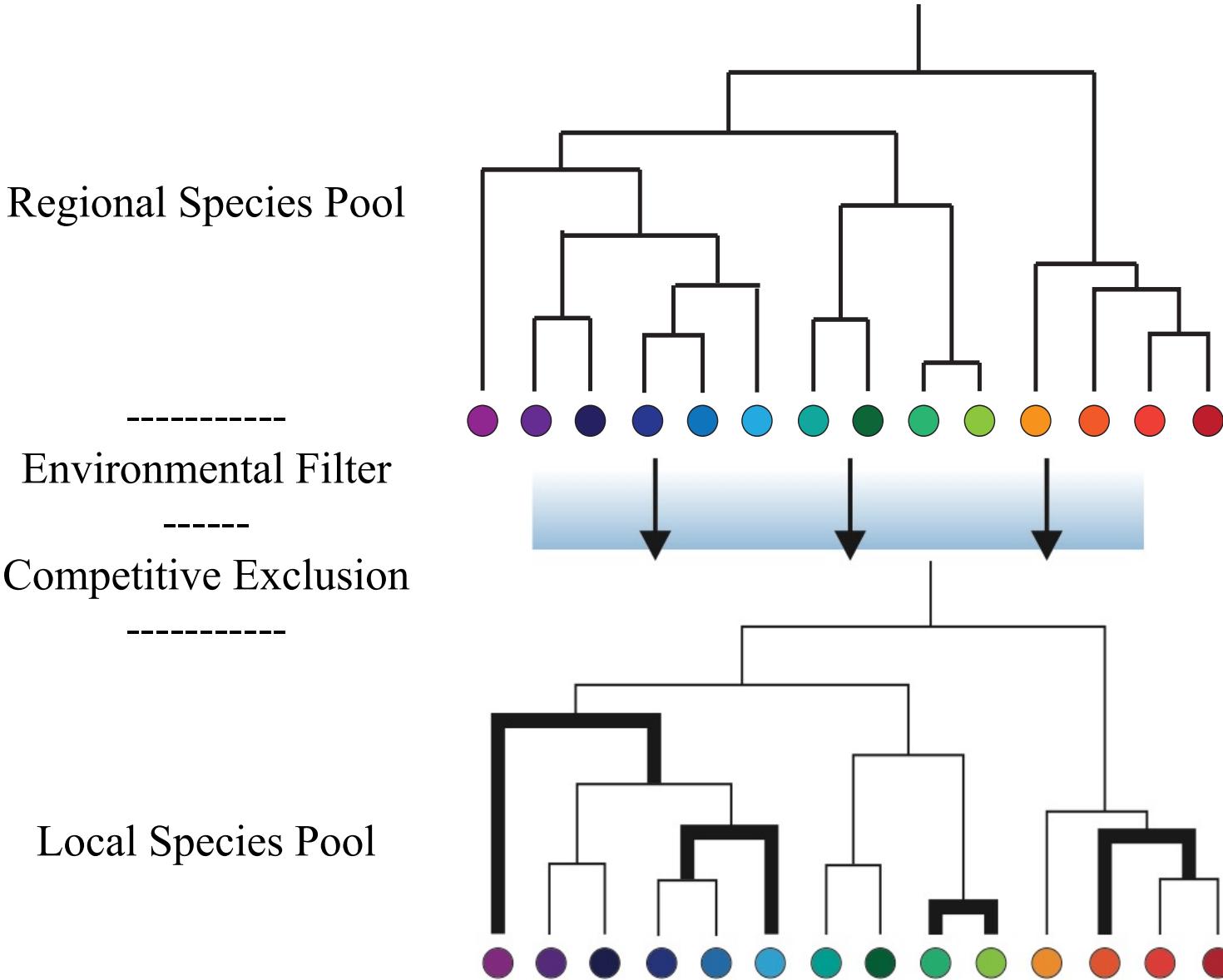
Clements – the environment

Habitat Filtering – species fail to establish in community due to incompatibility with relevant environmental factors

Gleason – the species

Competitive Exclusion – species fail to establish in a community when they cannot out-compete another species for their desired niche.

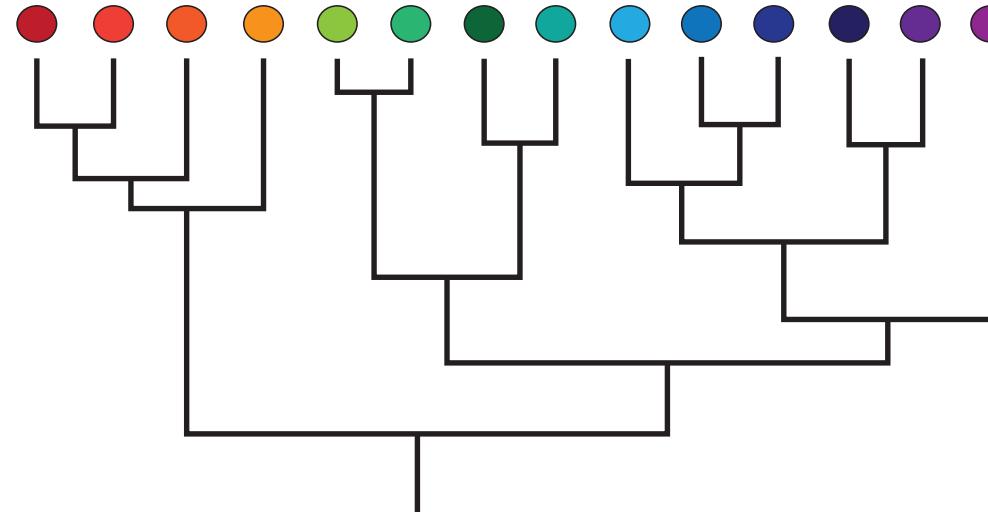
Community Assembly



How are community assembly models quantified?

Phylogenetic dispersion metrics are commonly used to detect signal for habitat filtering and competitive exclusion.

- Mean Phylogenetic Distance (MPD)
- Mean Nearest Taxon Distance (MNTD)

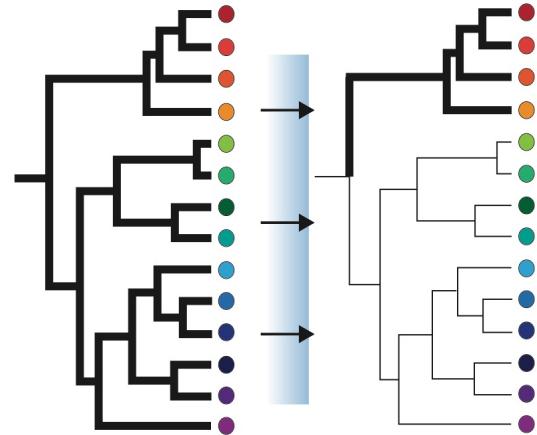


Assumption: functional traits of importance are phylogenetically conserved.

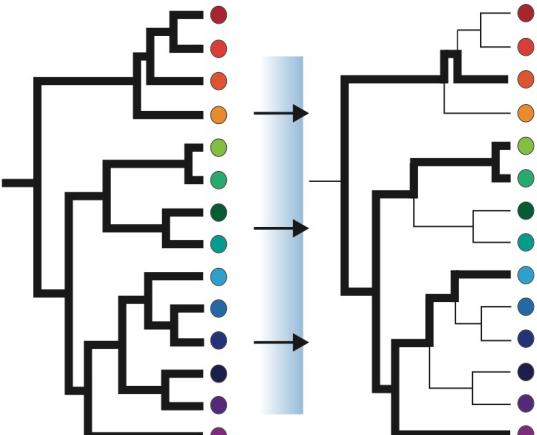
Introduction: Community Assembly

Traits are phylogenetically conserved

**Habitat Filtering =
phylogenetic underdispersion**

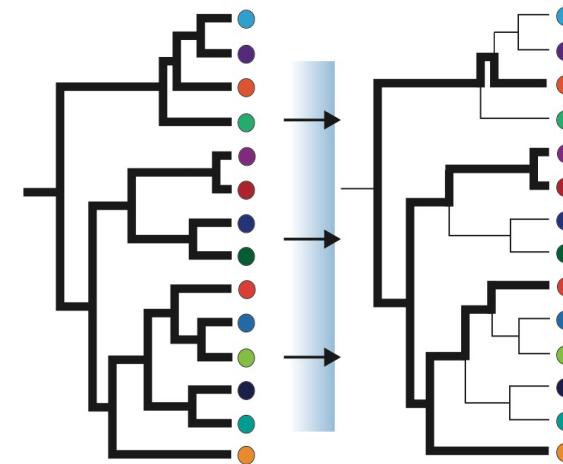


**Competitive Exclusion =
phylogenetic overdispersion**

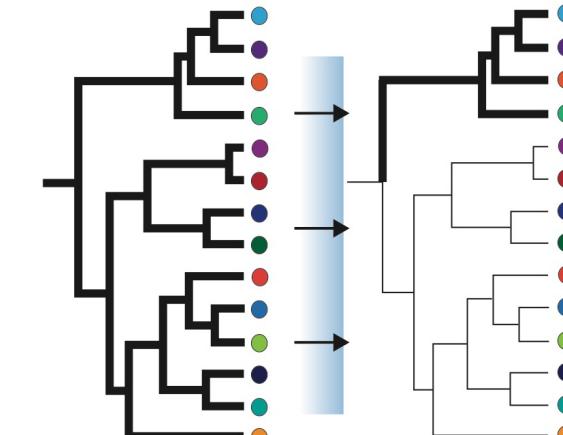


Traits are phylogenetically convergent

**Habitat Filtering =
phylogenetic overdispersion**



**Competitive Exclusion =
phylogenetic underdispersion**



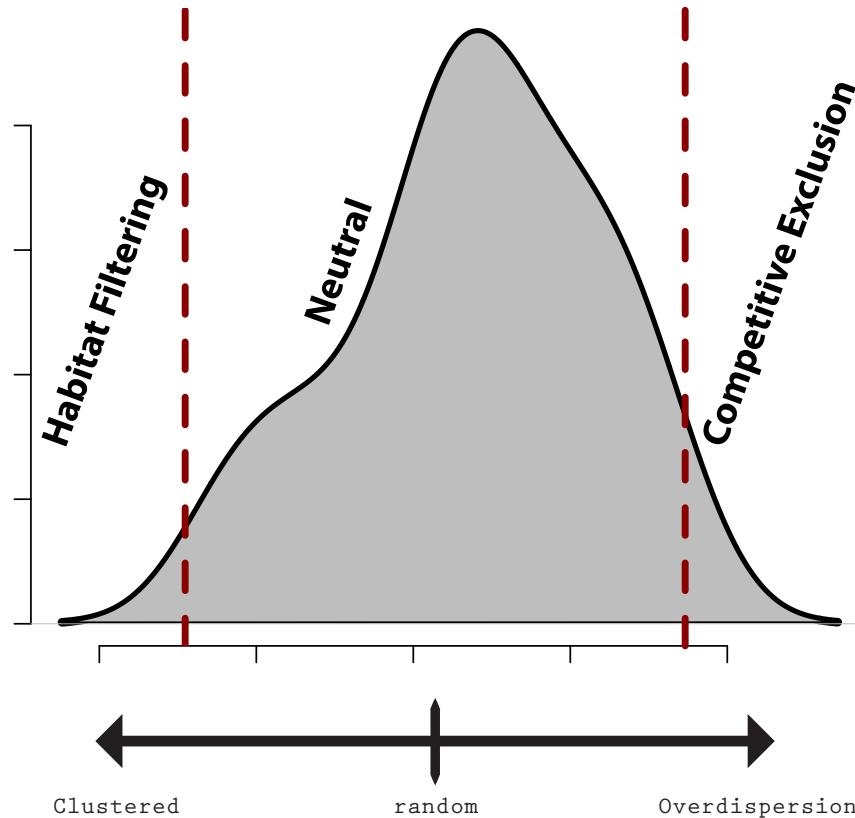
Community Assembly Inference; dispersion metrics

- Phylogenetic Community Structure

Grandcolas 1998, Webb et al. 2000, 2002,
Kraft et al. 2007

- Trait Community Structure

Weiher et al. 1999, McGill et al. 2006,
Cornwell et al. 2006, Kraft et al. 2007



Community Assembly Inference; dispersion metrics

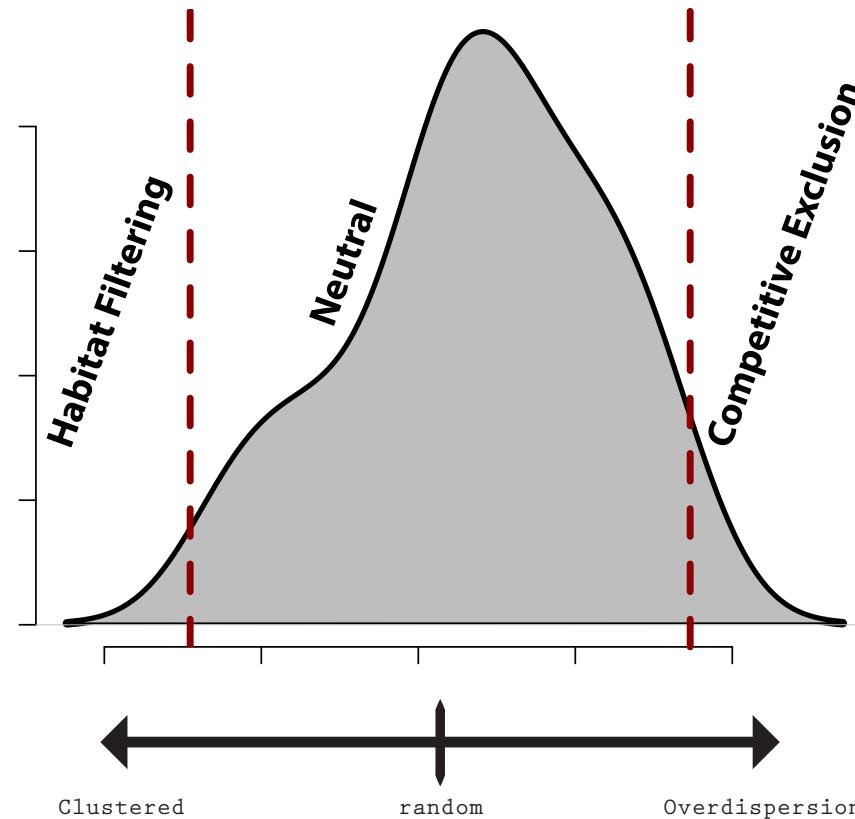
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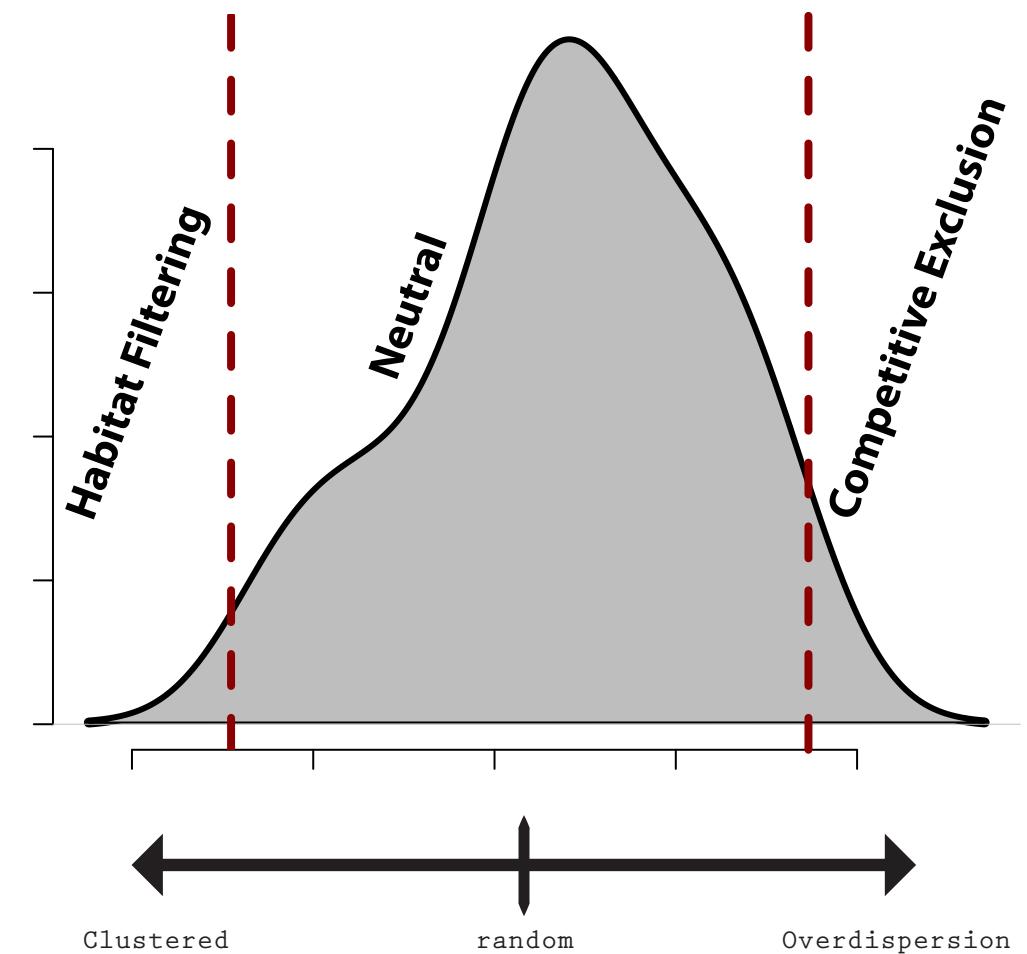
Weiher et al. 1999, McGill et al. 2006,
Cornwell et al. 2006, Kraft et al. 2007

Weiher and Keddy 1995, Kraft et al.
2007, 2010, Cavender-Bares et al.
2009; Kemble 2009; Mayfield and
Levine 2010; Gerhold et al. 2015



Current Community Assembly Inference Methods

- No uncertainty associated with the inference
- Not comparable across communities



CAMI development objectives

- 1. Implement a model-based inference procedure*

CAMI development objectives

- 1. Implement a model-based inference procedure*
 - *Compare support for neutral and non-neutral models simultaneously*

CAMI development objectives

1. Implement a model-based inference procedure

- *Compare support for neutral and non-neutral models simultaneously*
- **Cannot write down a likelihood, so we will need to use an approximate approach based on simulations*

CAMI development objectives

1. *Implement a model-based inference procedure*
 - *Compare support for neutral and non-neutral models simultaneously*
***Cannot write down a likelihood, so we will need to use an approximate approach based on simulations*
2. *Parameterize the strength of the non-neutral assembly processes*

CAMI development objectives

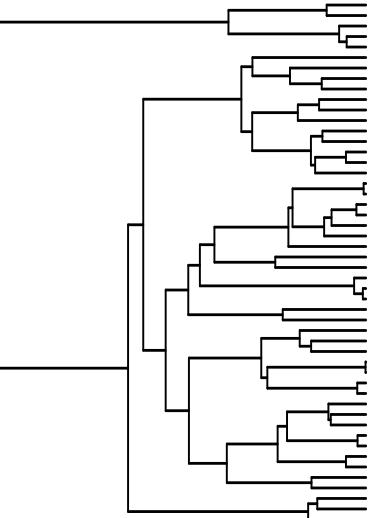
1. Implement a model-based inference procedure

- *Compare support for neutral and non-neutral models simultaneously*
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2. Parameterize the strength of the non-neutral assembly processes

Objective 1: Implement a model-based inference procedure

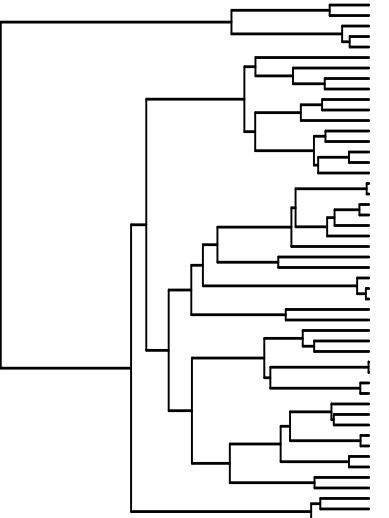
1.1 Regional community phylogeny: N, λ, μ



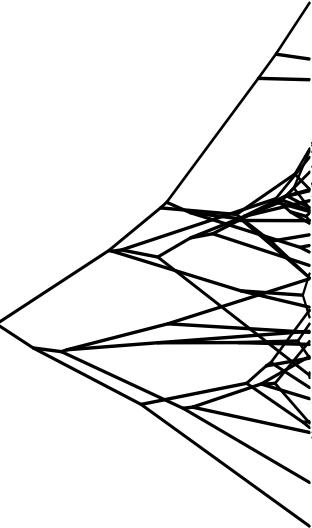
N	regional species pool
λ	speciation rate
μ	extinction rate
σ^2	rate of character change
α	strength of constraints (OU only)
n	local species pool
t_E	effect of environmental filtering
t_C	effect of competitive exclusions

Objective 1: Implement a model-based inference procedure

1.1 Regional community
phylogeny: N, λ, μ



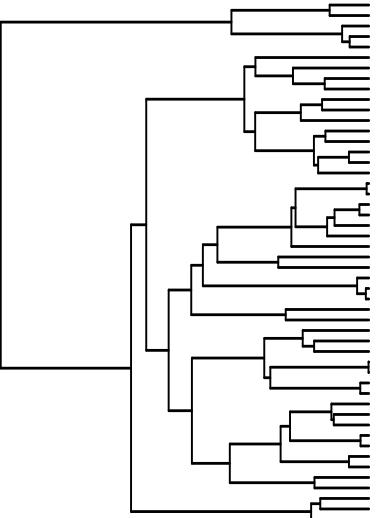
1.2 Trait evolution:
 σ^2, α



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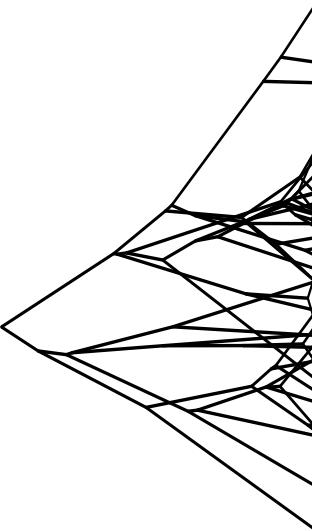
Objective 1: Implement a model-based inference procedure

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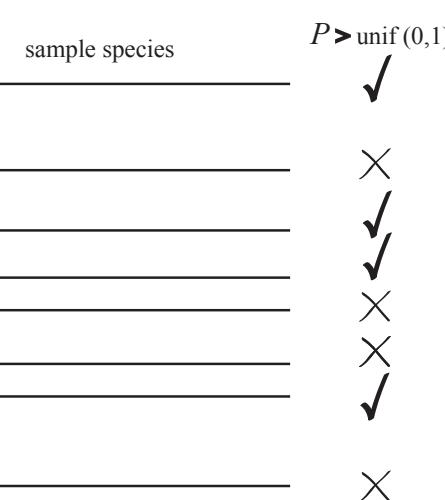


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1.2 Trait evolution: σ^2, α



1.3 Local community assembly: n, t_E, t_C



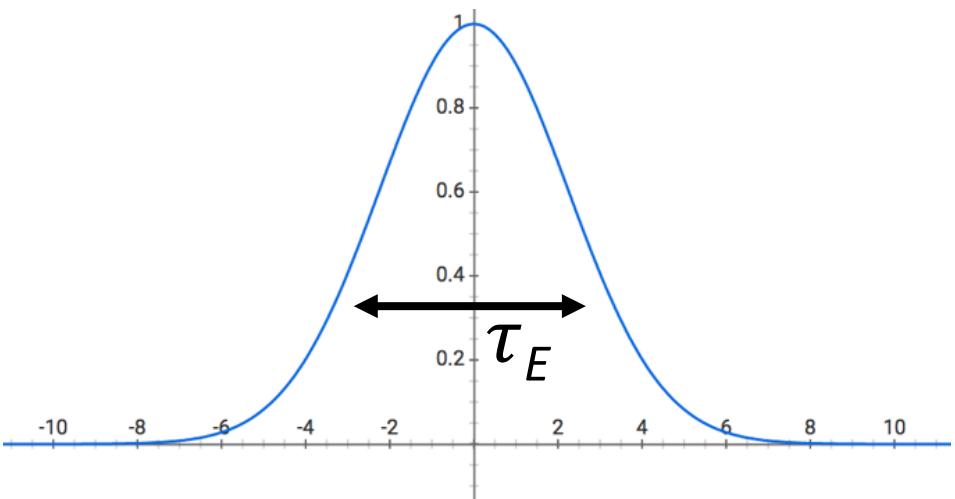
- Neutral
- Environmental Filtering
- Competitive Exclusion

Objective 2: Parameterize the strength of the non-neutral assembly processes

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Environmental Filtering

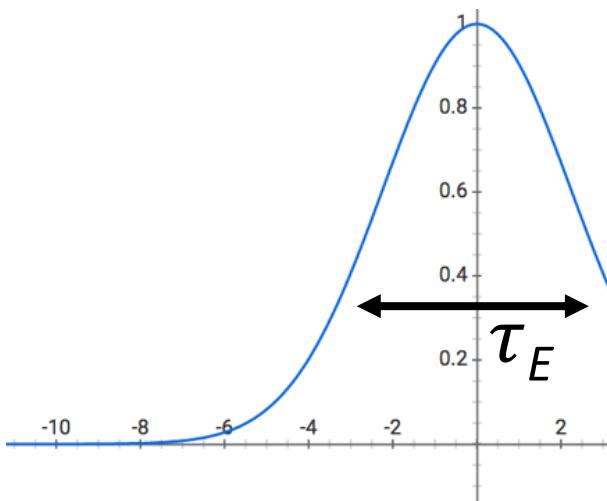
$$P = e^{-\frac{(Z_i - Z_j)^2}{\tau}}$$



Objective 2: Parameterize the strength of the non-neutral assembly processes

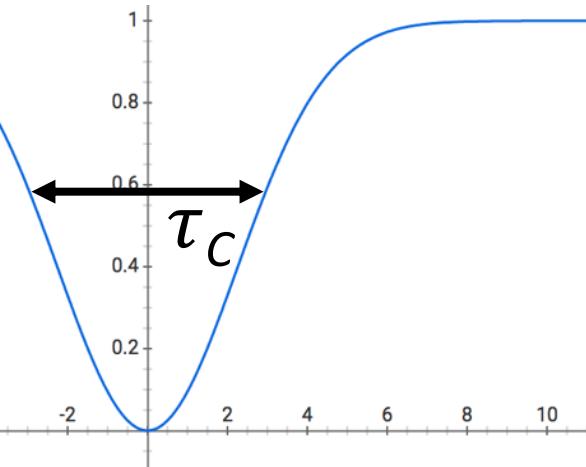
Environmental Filtering

$$P = e^{-\frac{(Z_i - Z_j)^2}{\tau}}$$



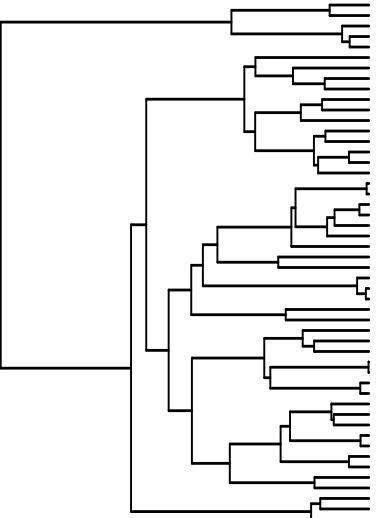
Competitive Exclusion

$$P = 1 - e^{-\frac{(Z_i - Z_j)^2}{\tau}}$$



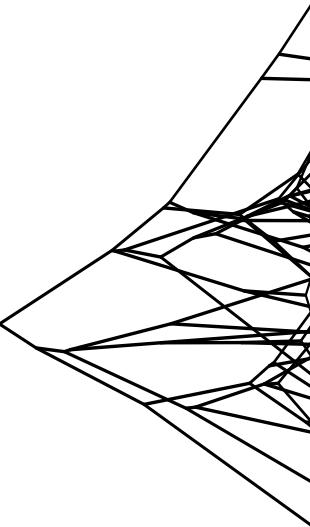
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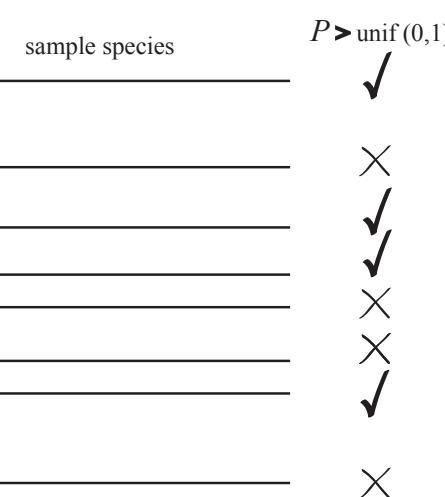


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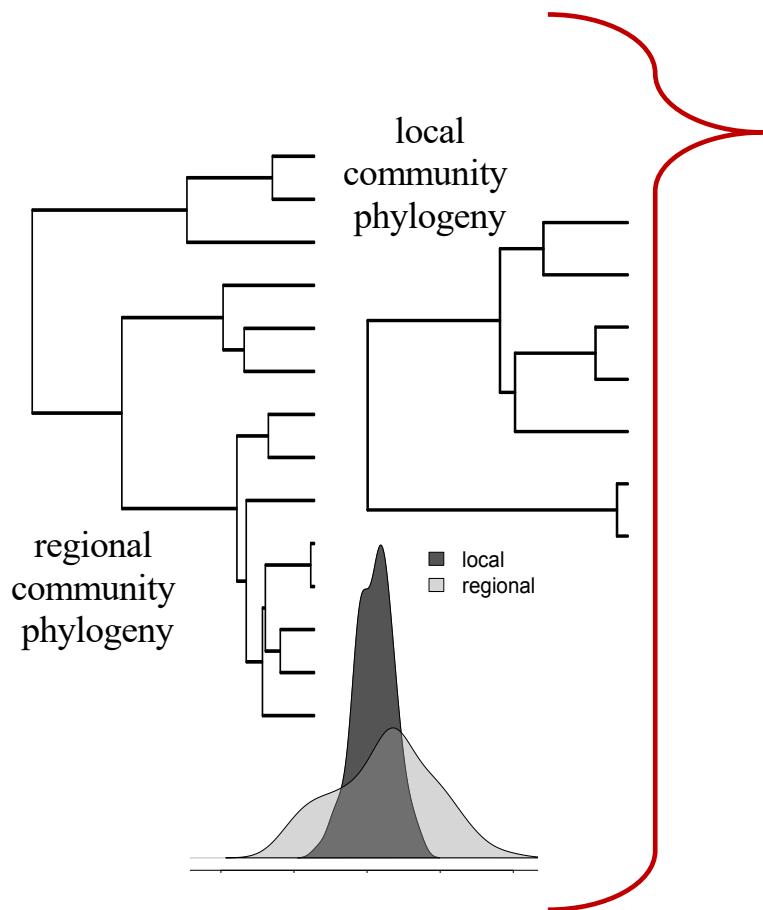


1.3 Local community assembly: n, t_E, t_C



- Neutral
- Environmental Filtering
- Competitive Exclusion

Objective 1: Implement a model-based inference procedure



Simulation #	SS.1	SS.2	SS.3	SS.30	Model
1	29.3201204	0.047795881	2.202369339	0.024039567	-0.551807157	Neutral
2	58.01018705	0.05683677	4.296006276	0.014001377	-0.141285853	Neutral
3	28.35028897	0.057748823	2.565336481	0.02472052	0.543737366	Neutral
4	54.4519145	0.058161893	4.462506196	0.006577184	-0.297716652	Neutral
5	29.52415799	0.0449925	1.332280042	-0.027307941	-0.424597011	Neutral
6	13.8002455	0.043015337	3.827085961	0.052868925	0.00038215	Filtering
7	68.51513963	0.05221236	3.773466742	0.006122832	-0.373019012	Filtering
8	6.409247373	0.067539483	1.27370363	0.056550081	-0.419361409	Filtering
9	7.869379132	0.044893904	1.621625795	0.005944114	-0.225941885	Filtering
10	56.74215972	0.042376631	3.870139564	-0.010551762	1.612683176	Filtering
11	32.21489305	0.039088122	4.436192932	-0.005017495	-0.608370405	Competition
12	35.31406132	0.055897014	1.802319164	0.00665565	0.575928644	Competition
...	15.17747744	0.052302964	2.833102254	-0.007315425	-0.343133625	Competition
10,000	176.8646799	0.046759559	3.404803136	0.003965272	-0.492954288	Competition

Objective 1: Implement a model-based inference procedure

Model-selection using approximate approaches

- randomForests (*Breiman 2001, Breiman and Cutler 2007*)
- Approximate Bayesian Computation (ABC; *Beaumont, et al. 2002, Csilléry, et al. 2012*)

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Results

- 1. Power Analysis*
- 2. Parameter Estimation*
- 3. Empirical study*

Results

1. Power Analysis

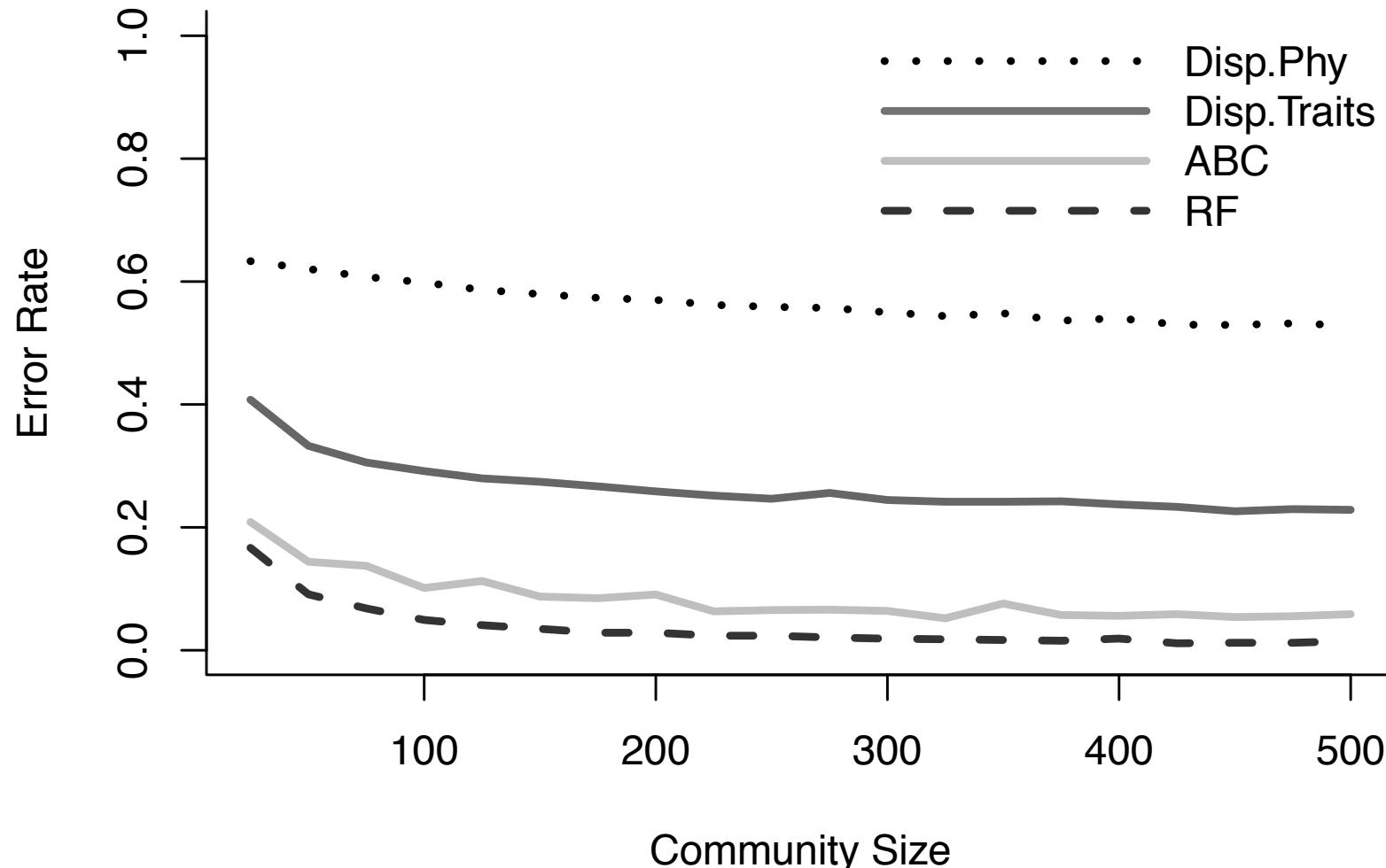
- *Dispersion Metrics*

Phylogenetic data

Functional trait data

- *randomForest (RF)*
- *ABC*

Results: Power Analysis



Results

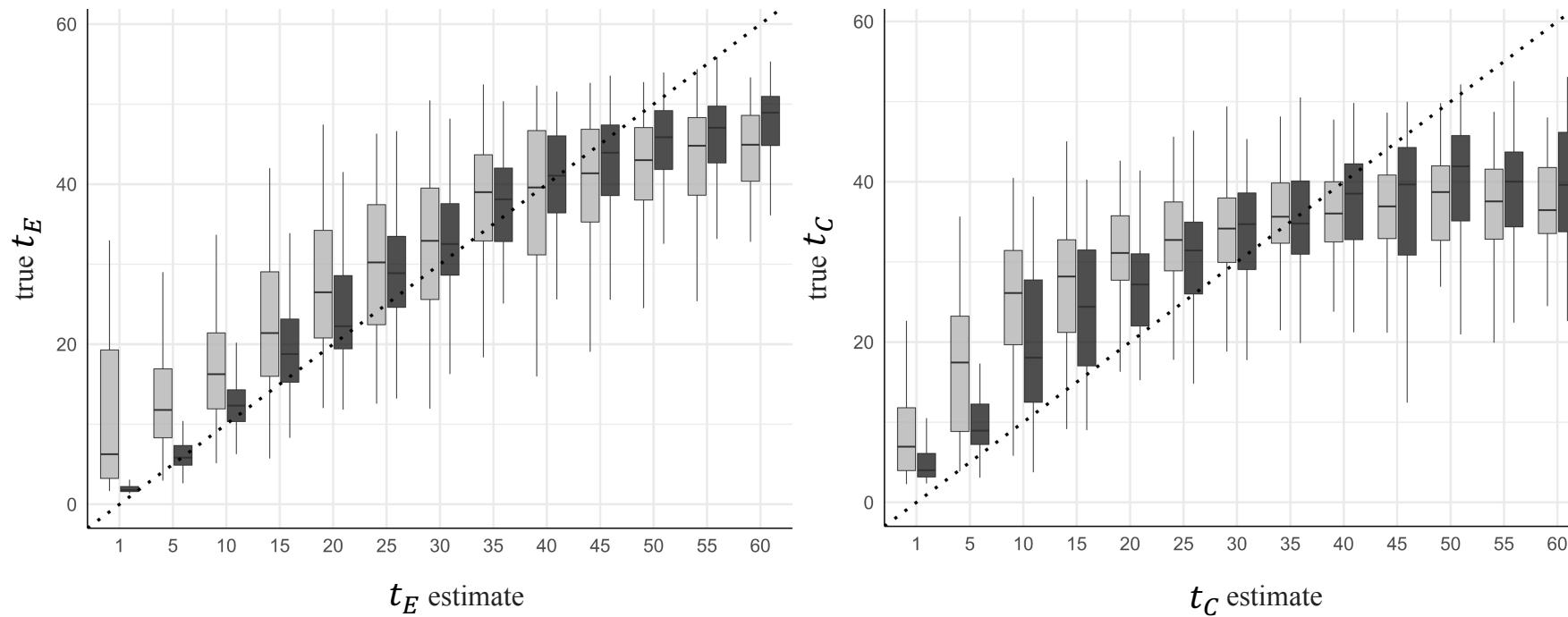
1. Power Analysis

2. Parameter Estimation

-Estimate τ_E and t_C

3. Empirical studies

Results: Parameter Estimation



- DO first tutorial and introduction to CAMI,

- Load it
- Simlate some data
- Build and RF