



ESEB2025
BARCELONA 17-22 AUGUST 2025
CONGRESS OF THE EUROPEAN SOCIETY FOR
EVOLUTIONARY BIOLOGY

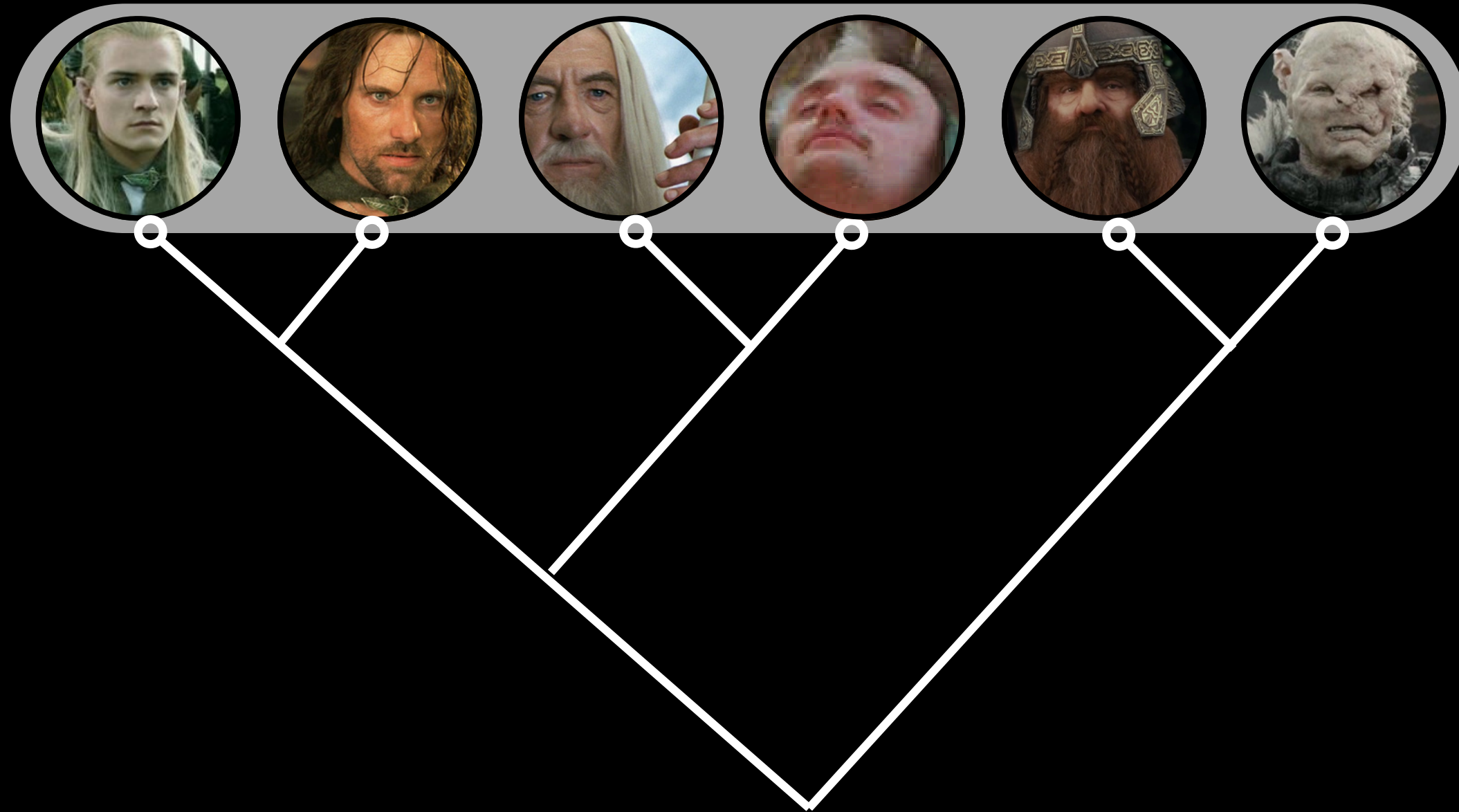
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**Mechanisms of community
assembly through the lens of
phylogenetic diversity: a
critical reappraisal.**

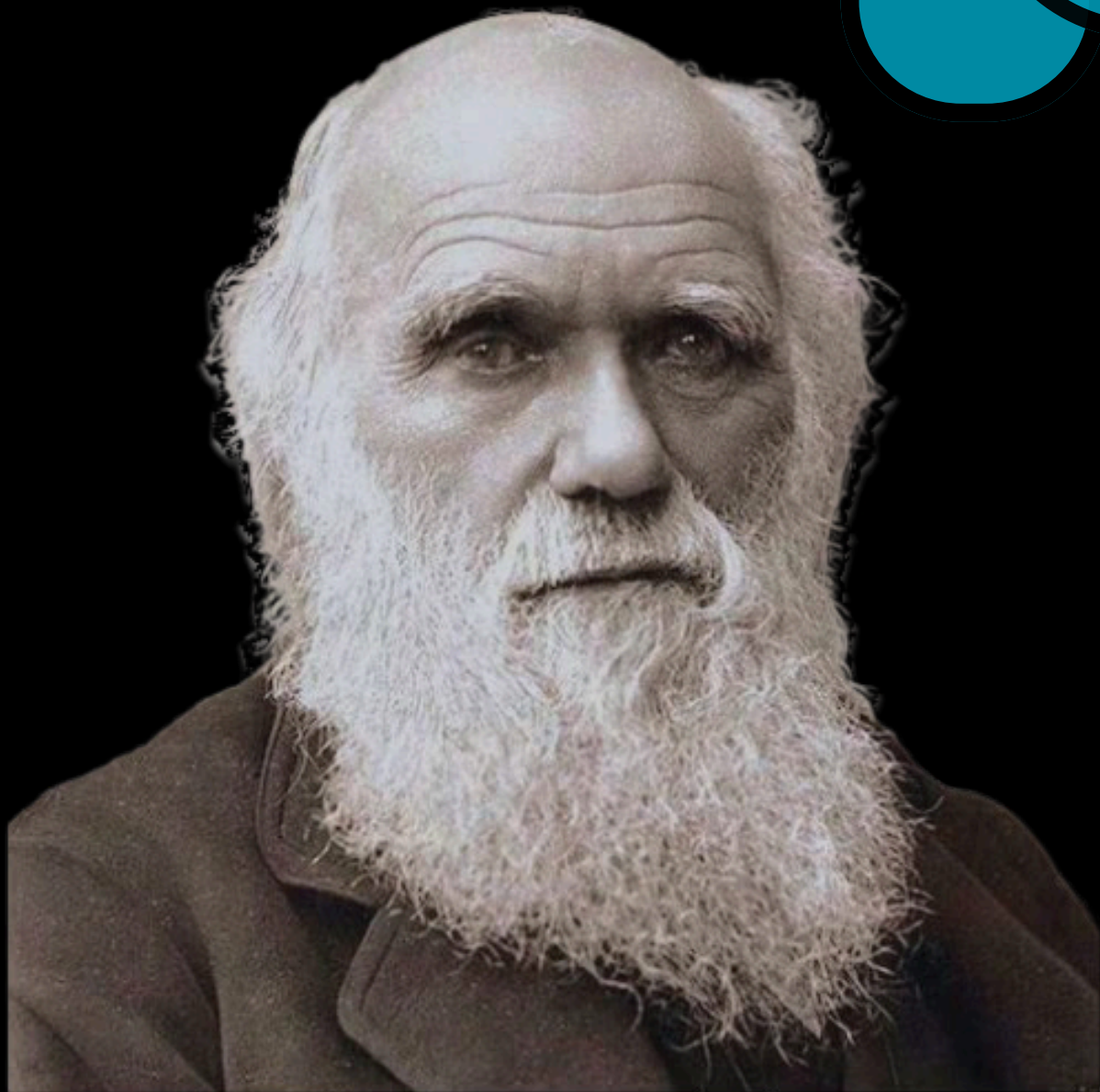
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Ecology and Biogeography
thibault.kasprzyk@uliege.be



Disclaimer: There is no need to wait for me at the end of the presentation to say that the phylogenetic tree of the Lord of The Ring characters is wrong.

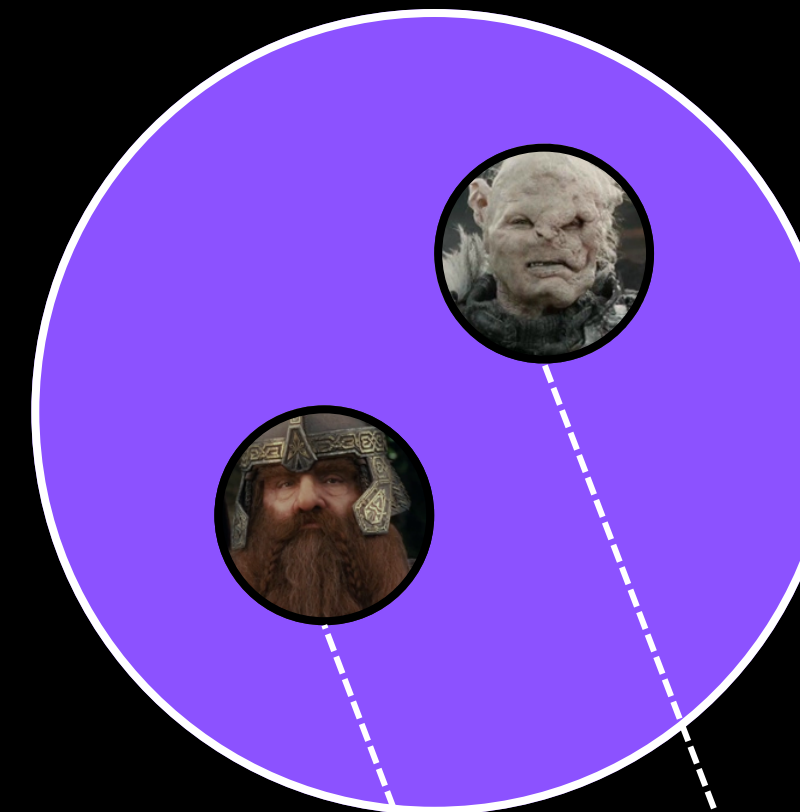
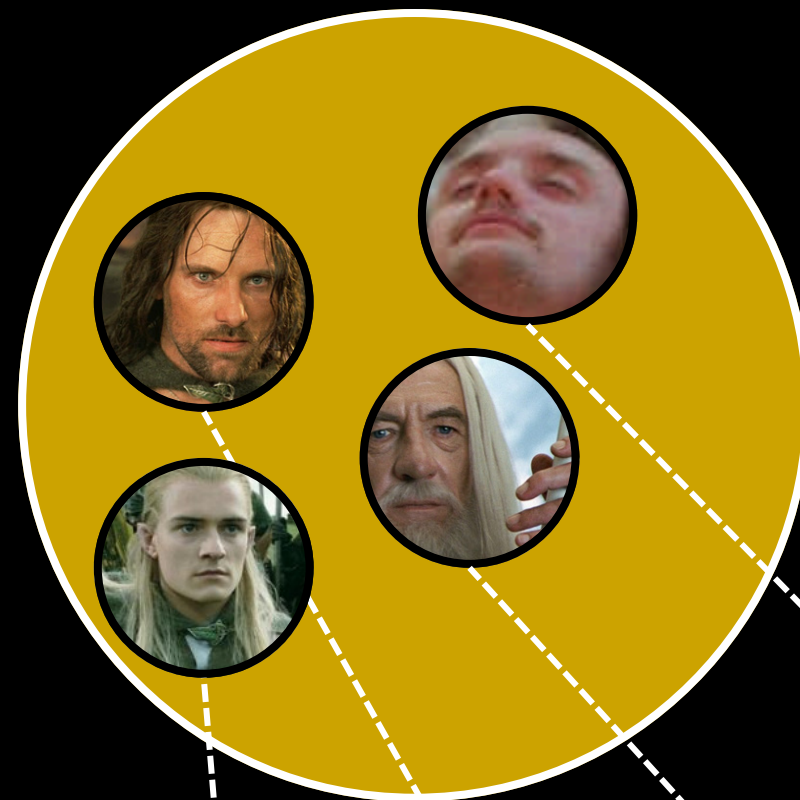
Closely related species will co-occur due to the sharing of the same adaptive traits

Habitat filtering → Phylogenetic Clustering



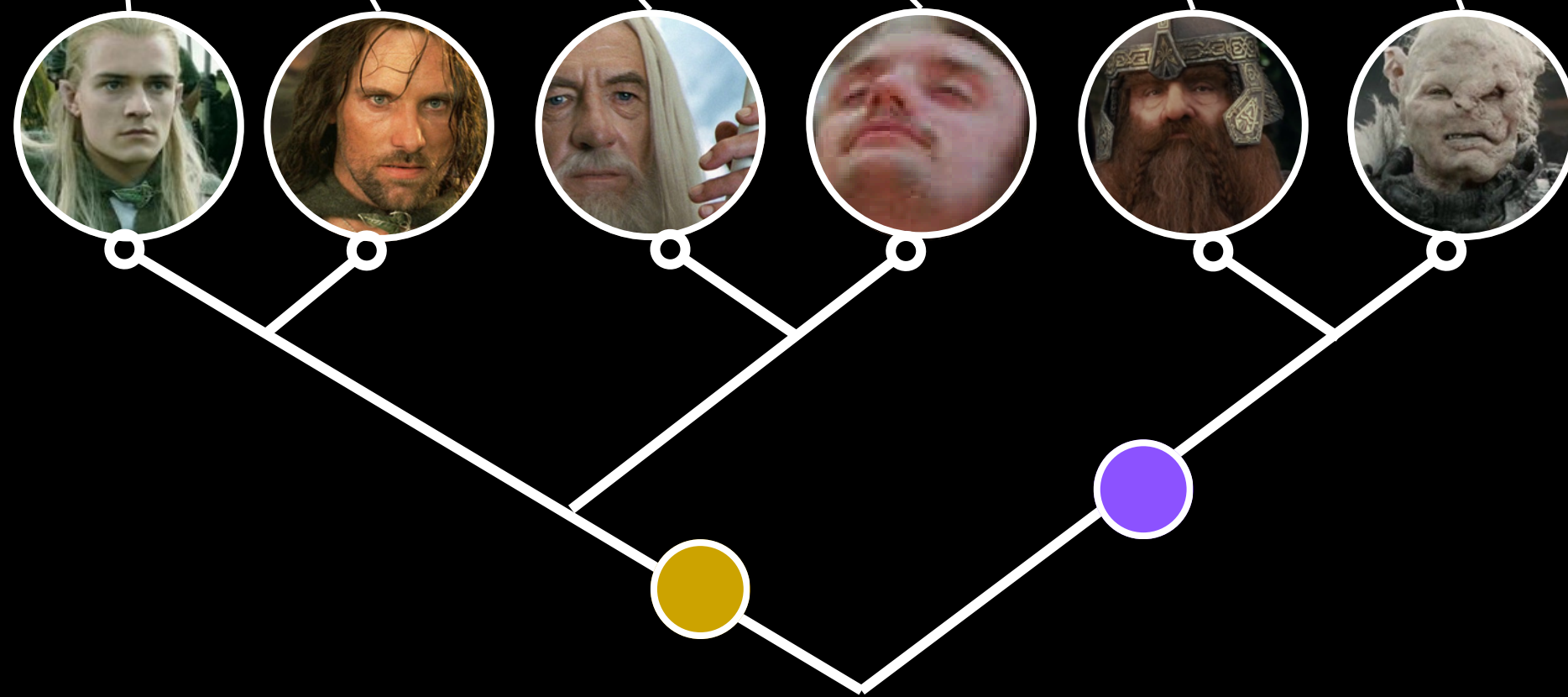


Habitat Filtering



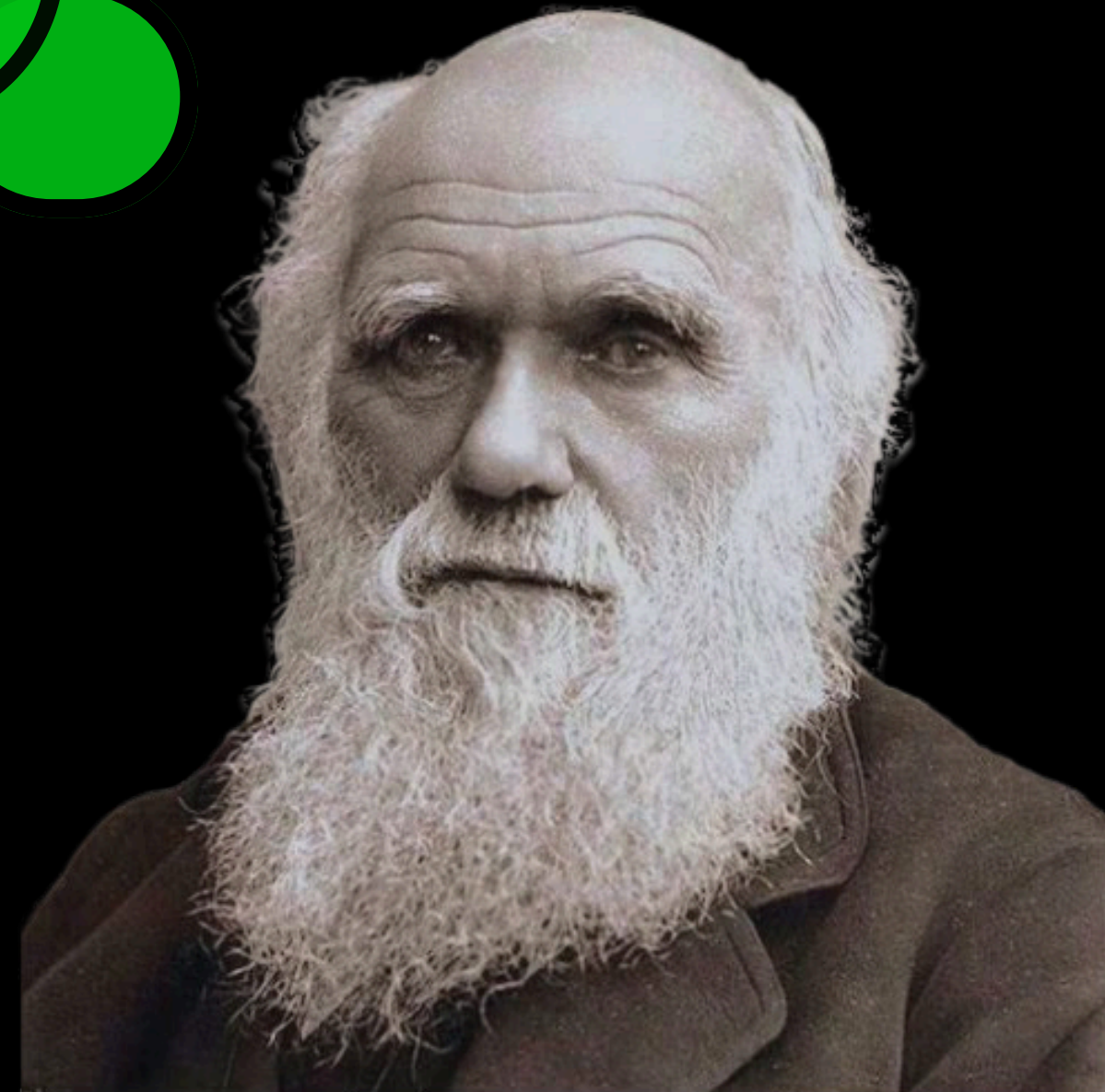
Expected community phylogenetic structure :

Phylogenetic Clustering



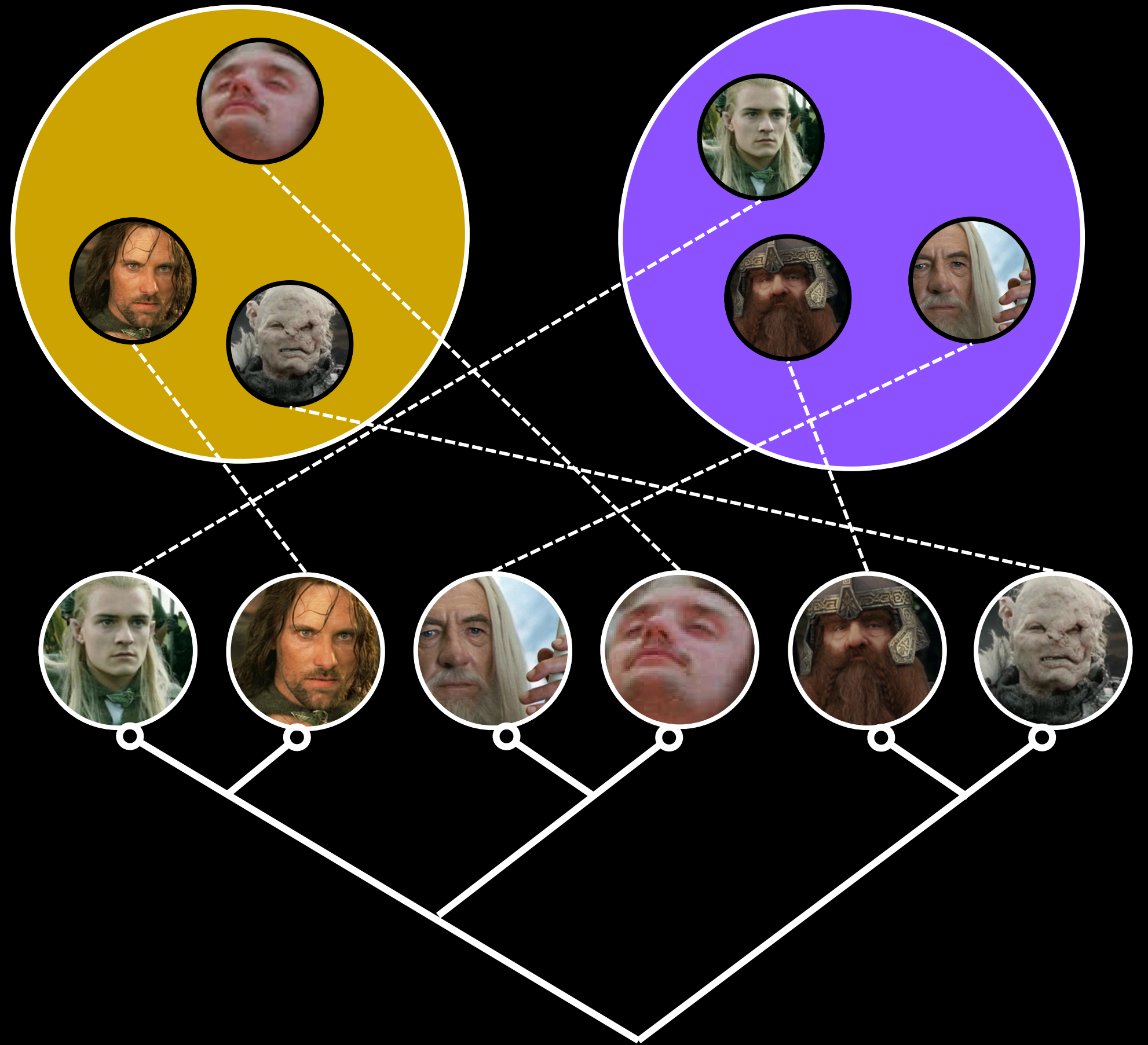
Closely related species will exclude each other due to competition for the same resources

Competition → Phylogenetic Overdispersion





Competition



Expected community phylogenetic structure :

Phylogenetic Overdispersion

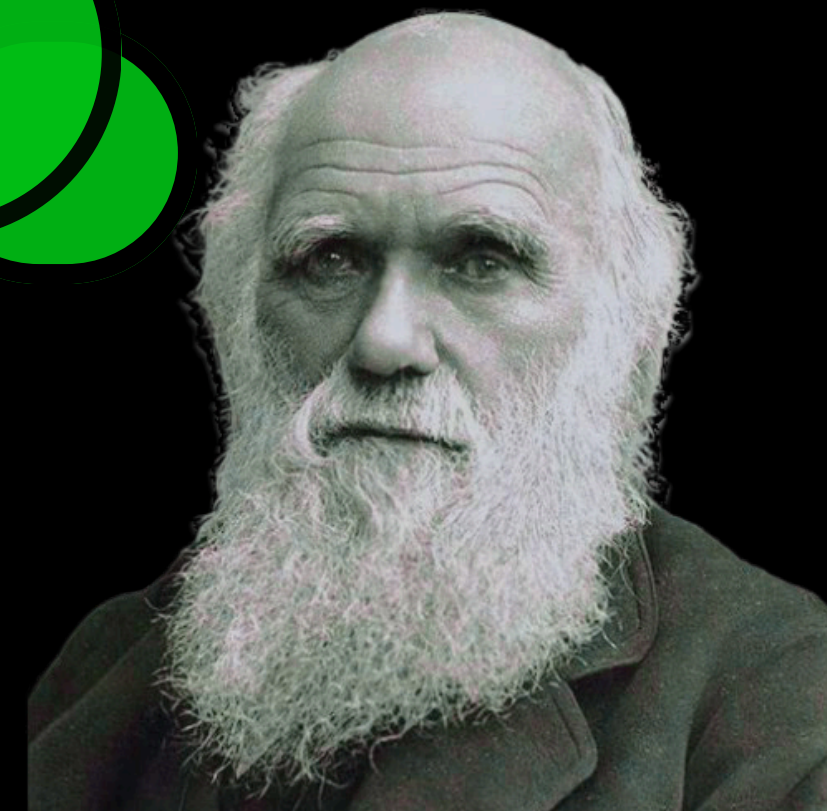
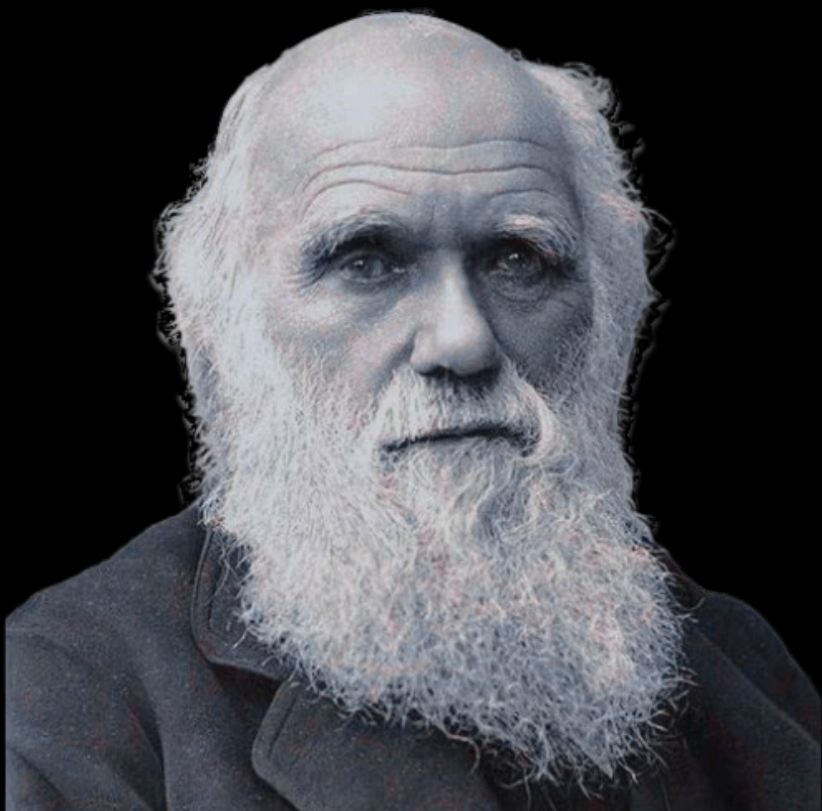
DARWIN'S CONUNDRUM

Habitat filtering → Phylogenetic Clustering

Co-occurrence of closely related species due to the sharing of the same adaptive traits

Competition → Phylogenetic Overdispersion

Mutual exclusion of closely related species due to competition for the same resources





Habitat Filtering



Phylogenetic Clustering

Competition

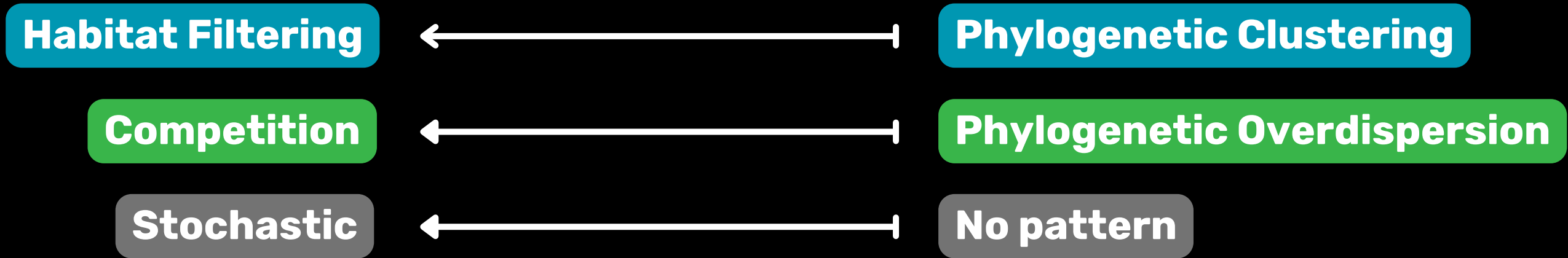
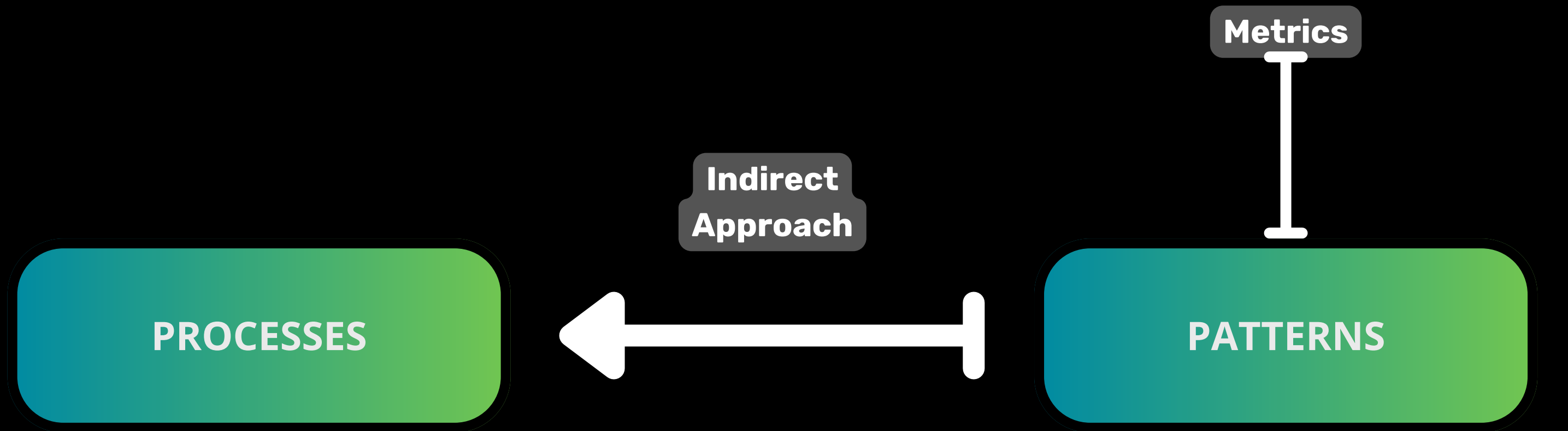


Phylogenetic Overdispersion

Stochastic



No pattern



Is the indirect approach reasonable ?

- Do different assembly processes result in different community phylogenetic patterns?
- Are these patterns reflected by variation in phylogenetic diversity metrics?

If YES

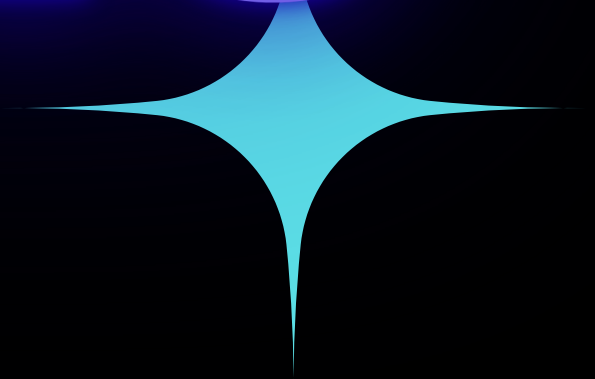
- Which metric(s) of phylogenetic diversity best perform?
- Which patterns can we correctly recover ?

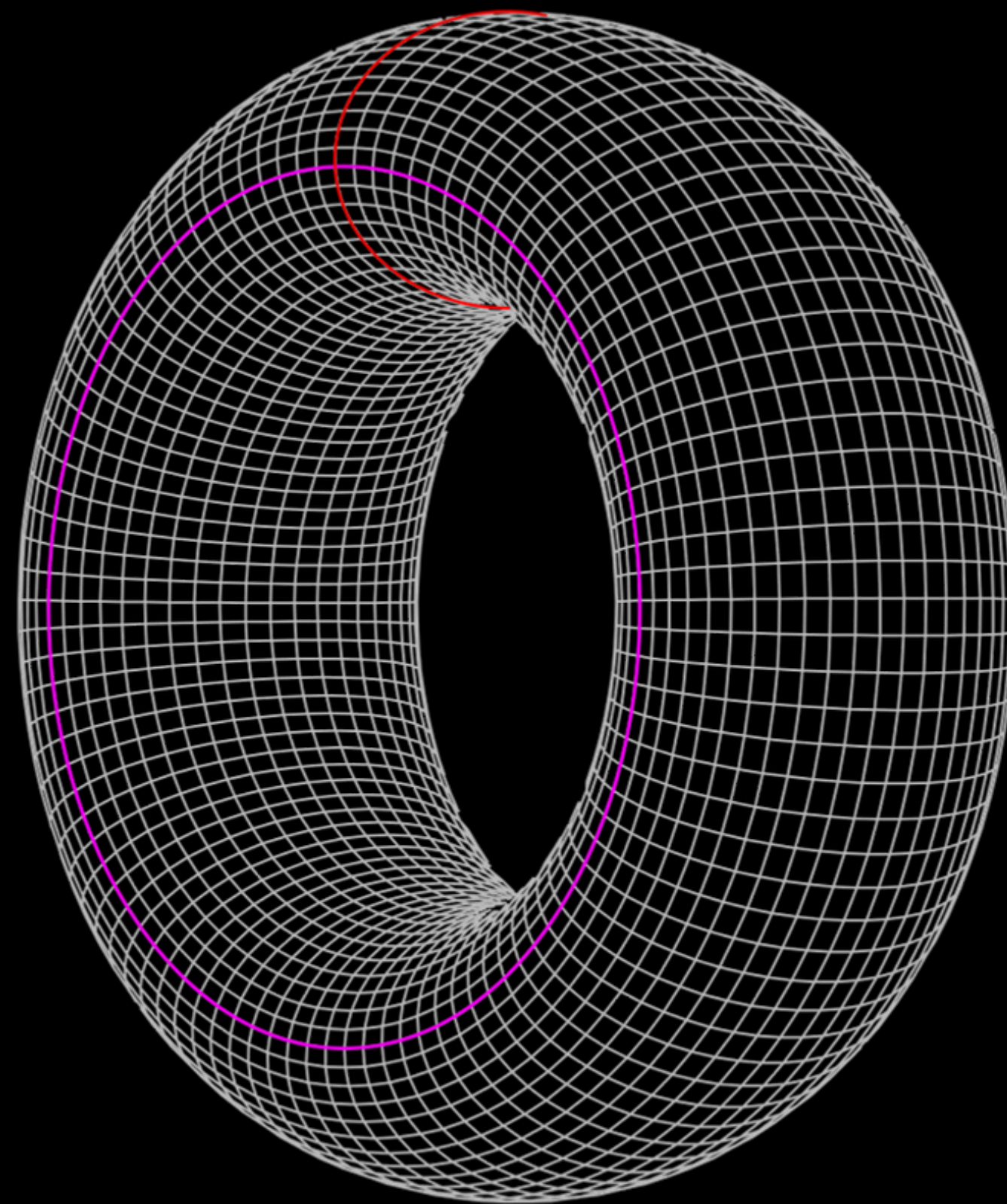
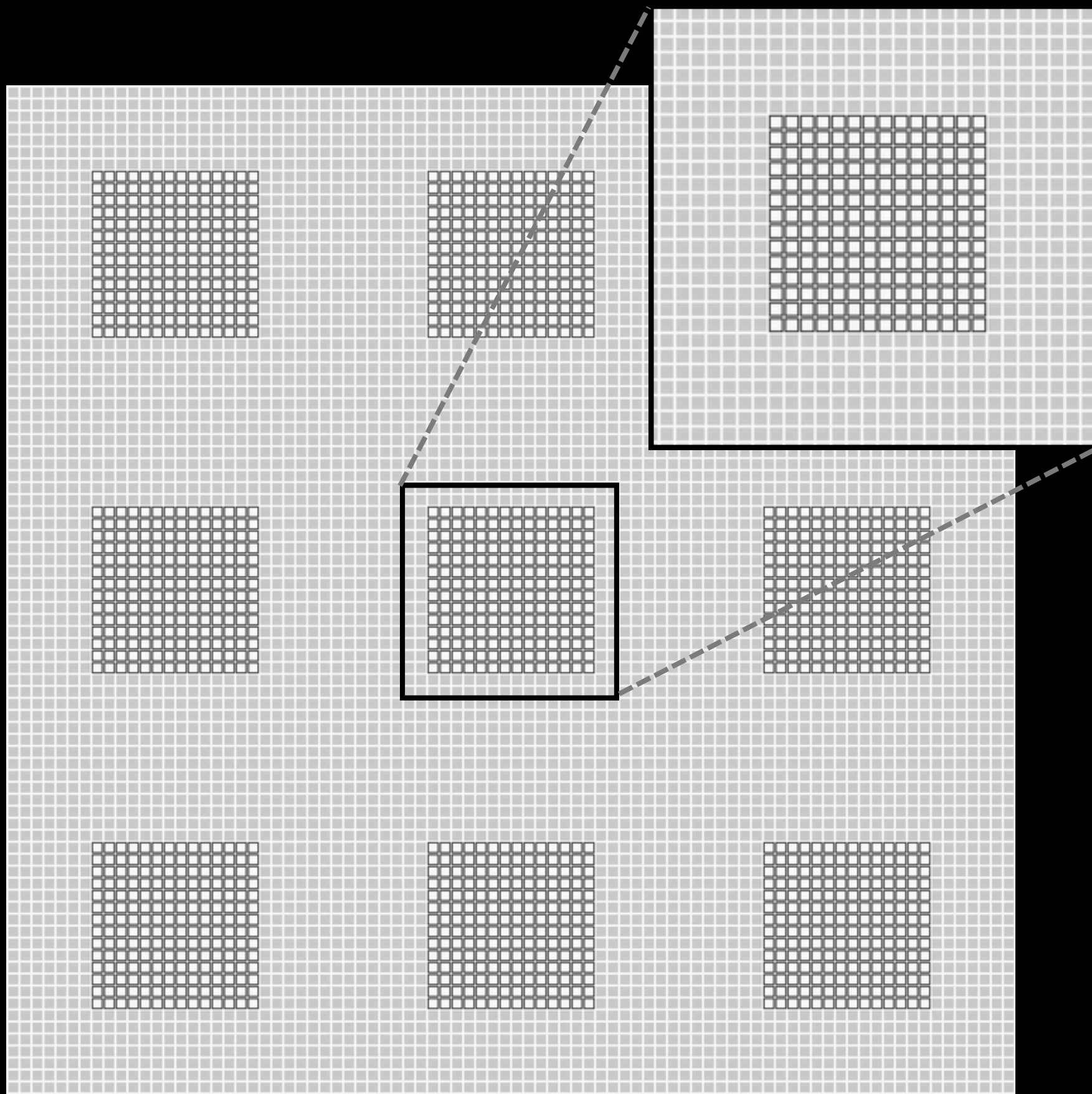


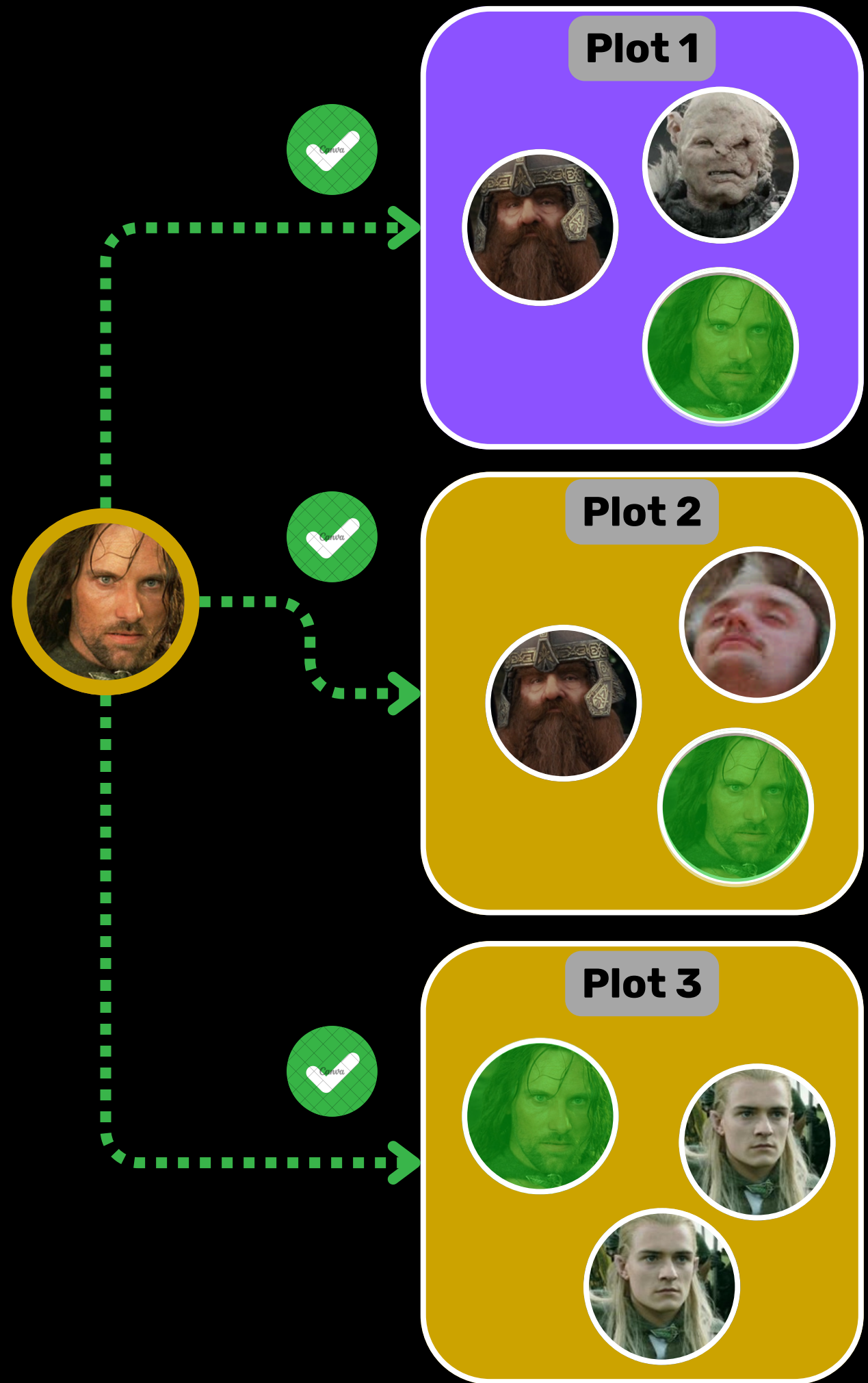
SIMULATIONS



Controlled environment where we know what
processes are at play.

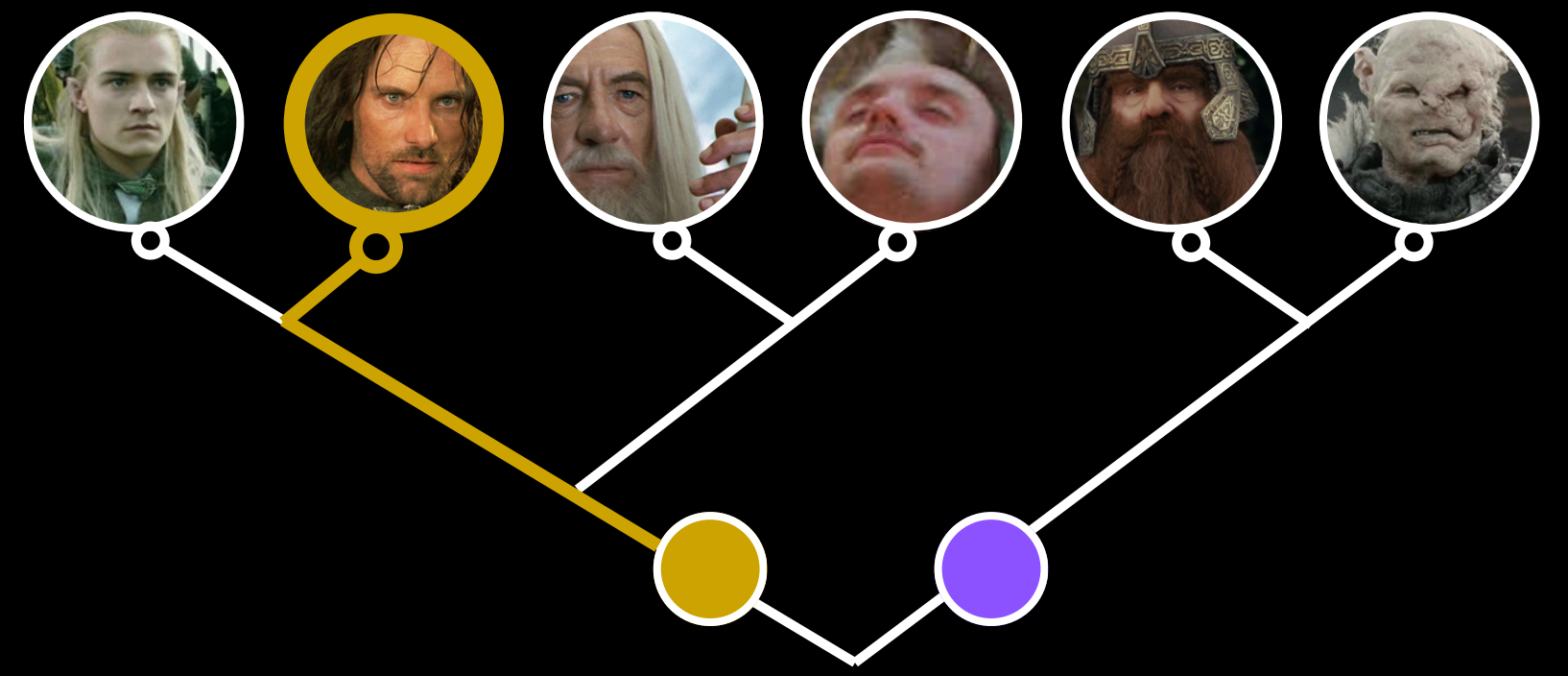


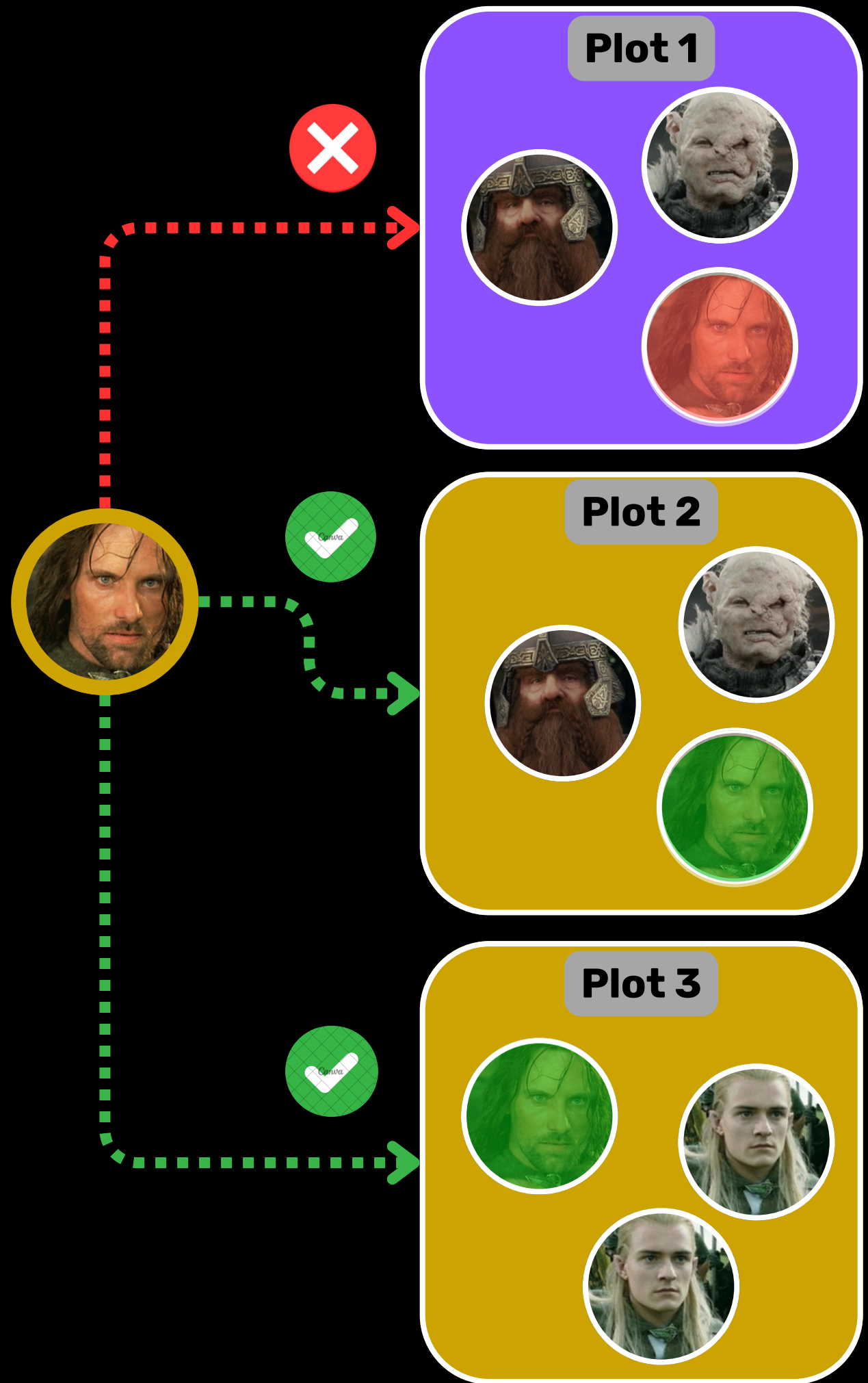




STOCHASTIC PROCESSES

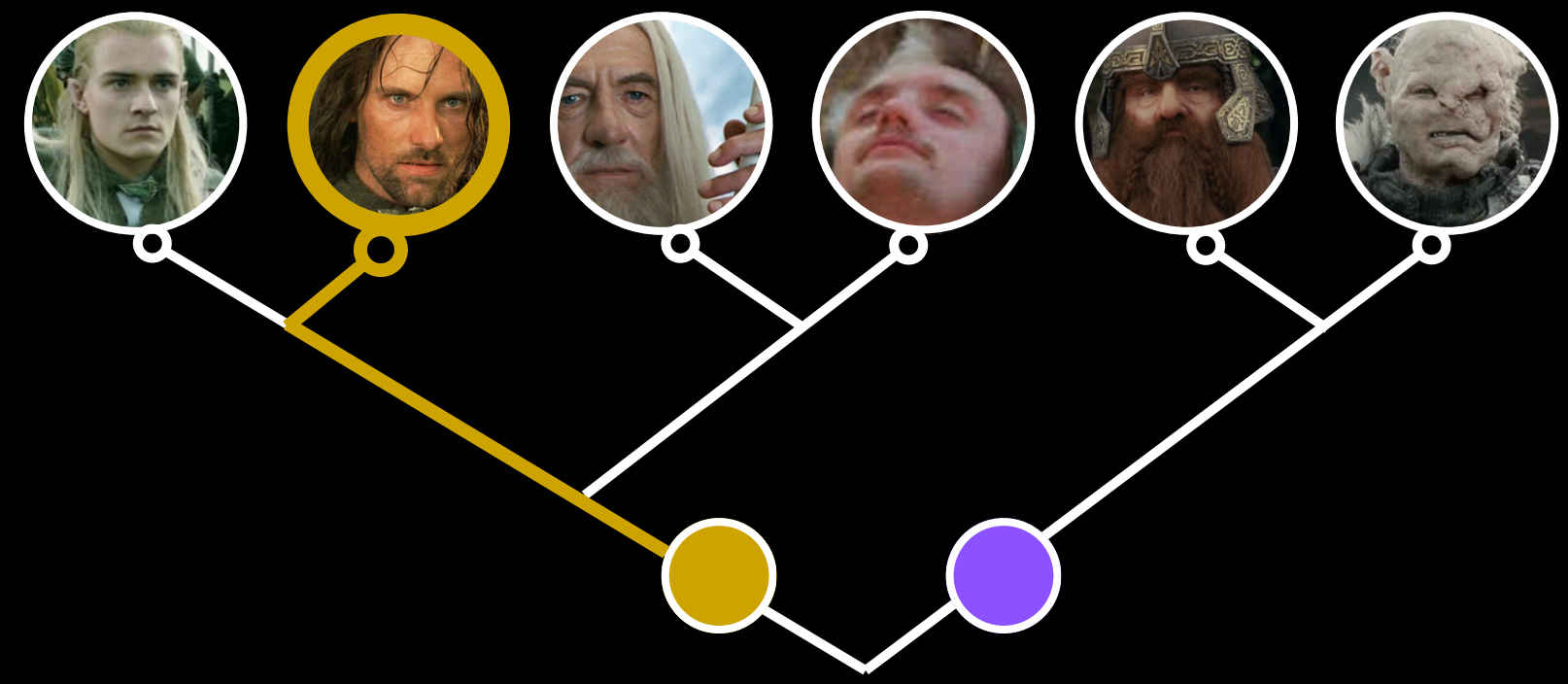
Migrants always settle.

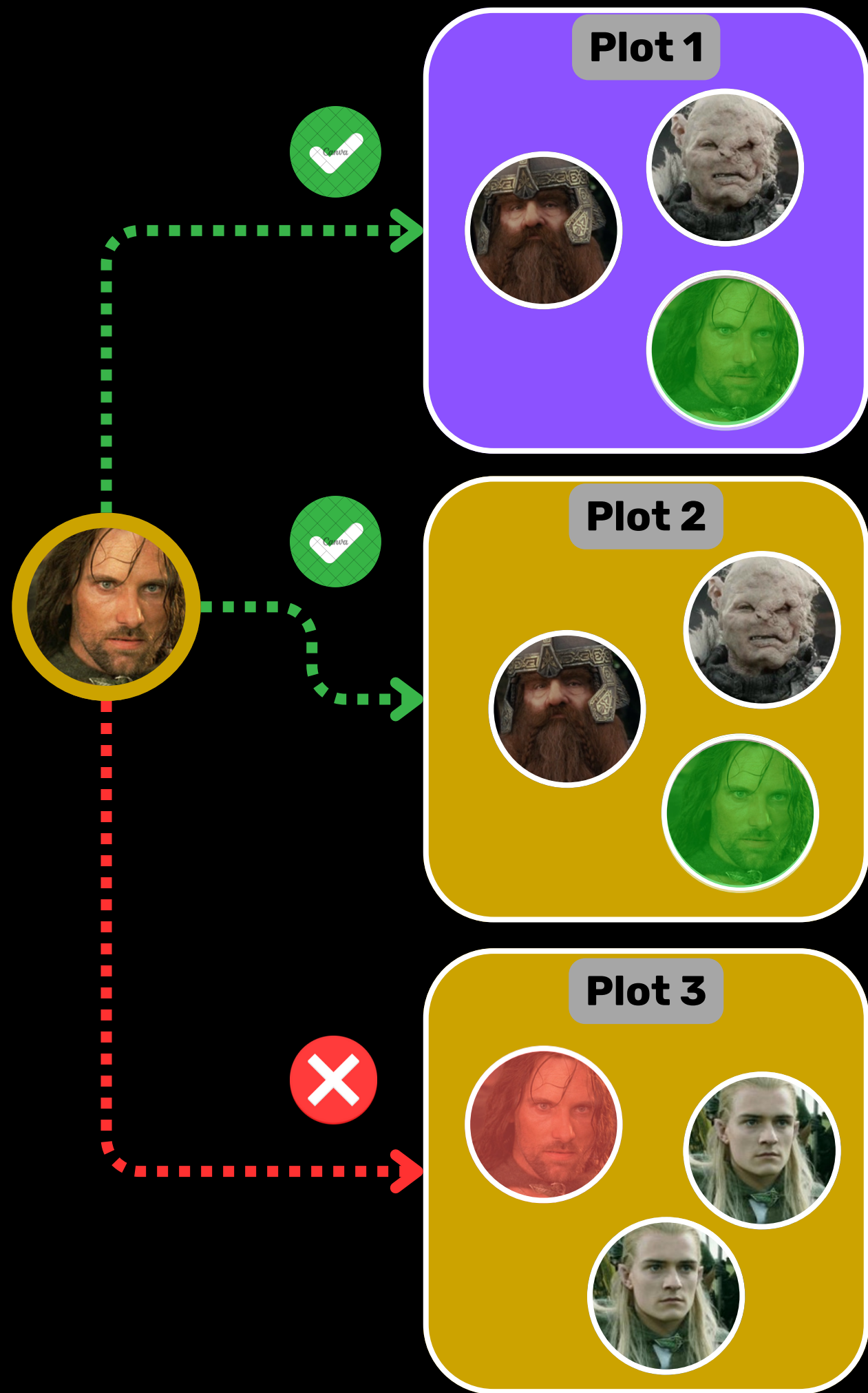




HABITAT FILTERING

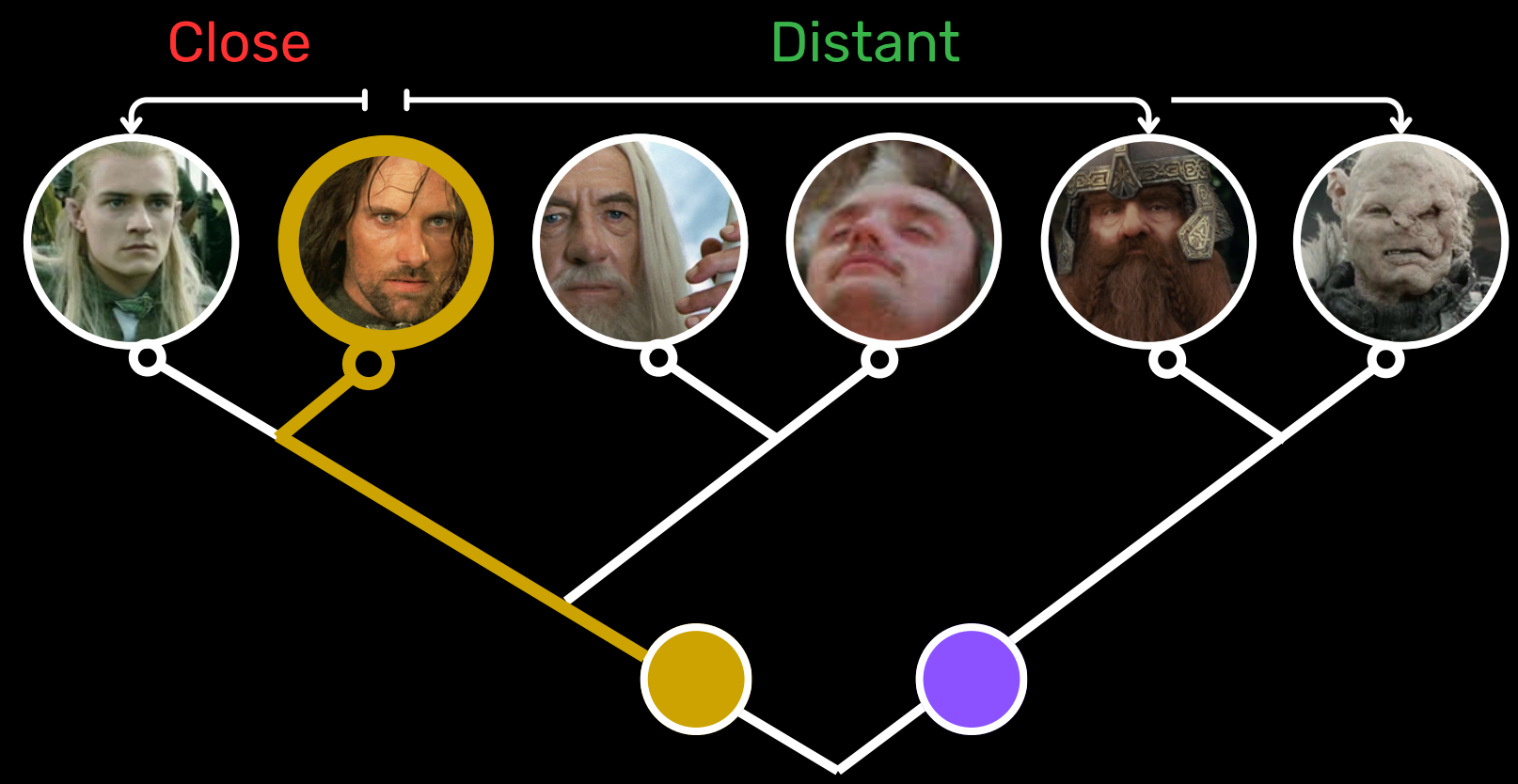
Migrants settle based on their habitat preference, minimizing trait differences and resulting in phylogenetically clustered communities.





COMPETITION

Migrants are selected based on the species already present, maximising trait differences and resulting in phylogenetically over-dispersed communities

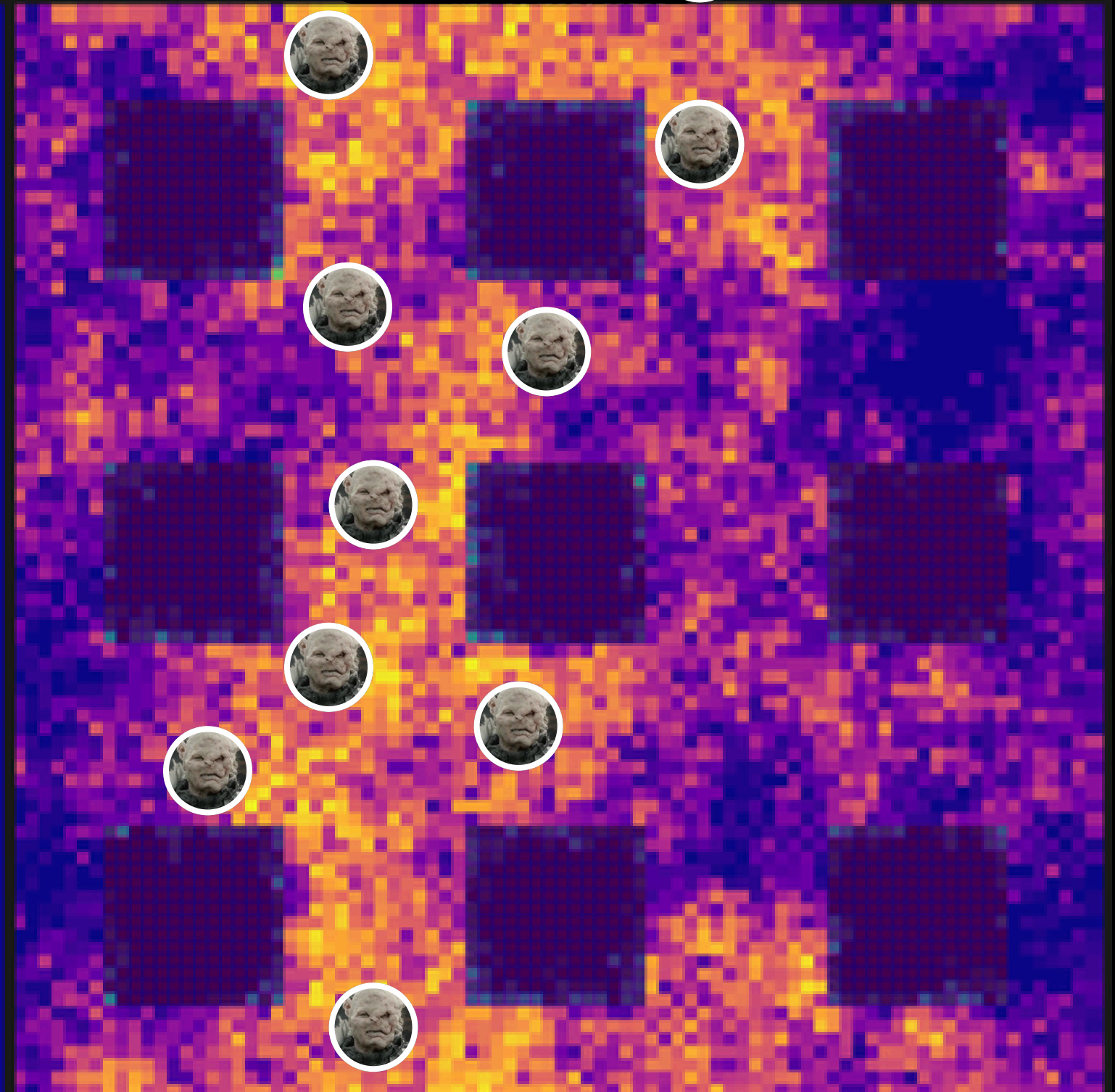
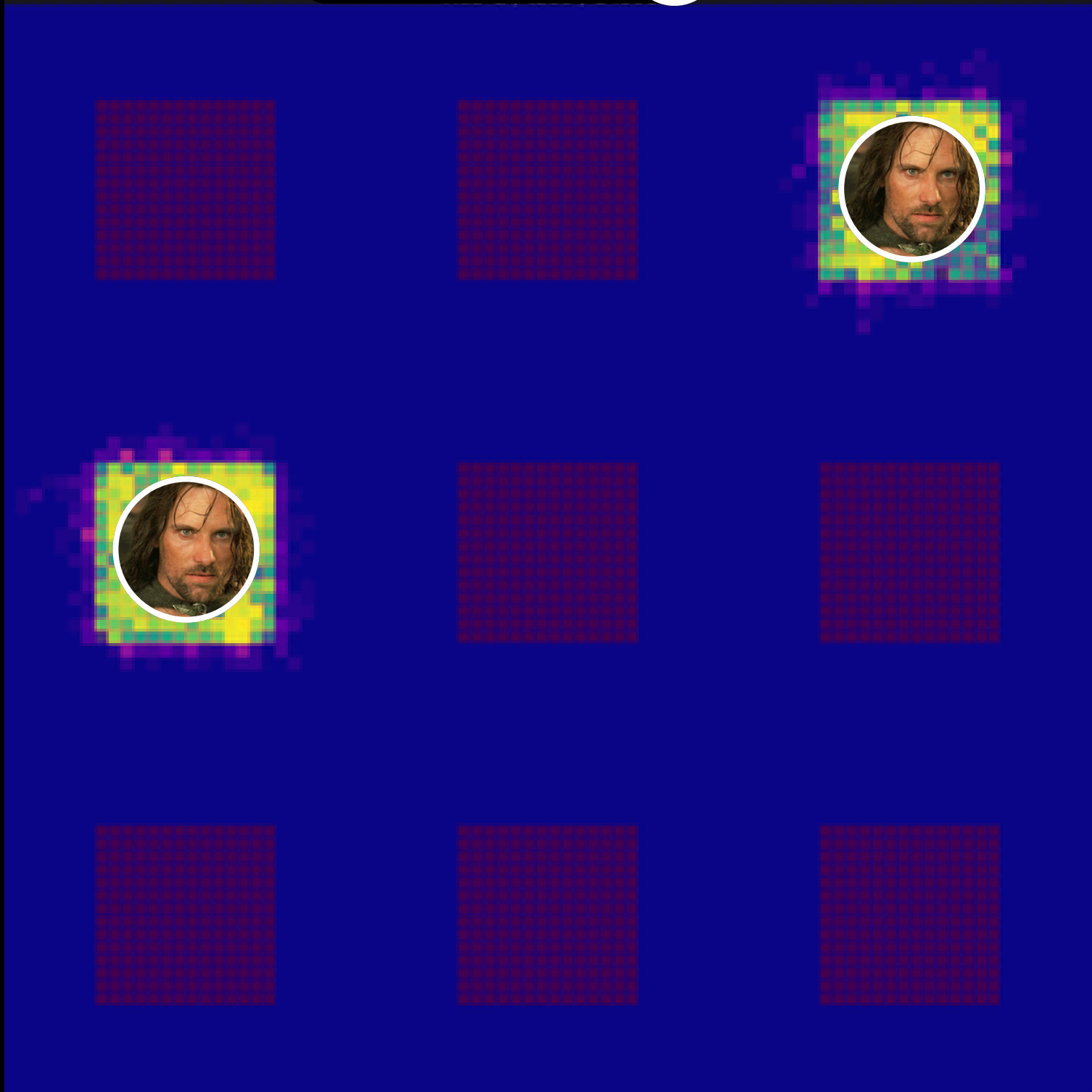


Variation of phylogenetic diversity metrics depending on community assembly processes

Species 

100% Habitat filtering

Species  *



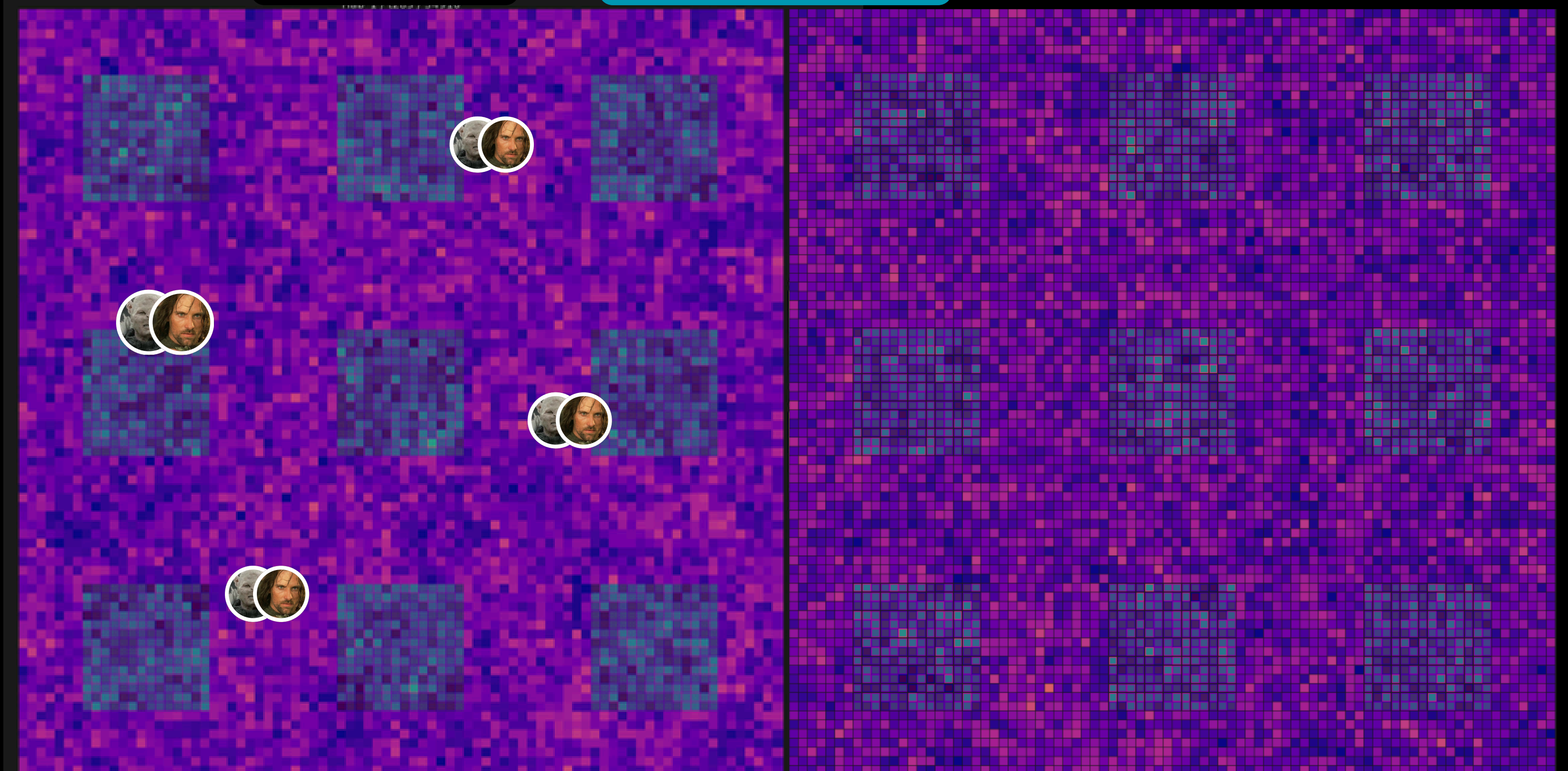
*This guy is called Gothmog

Variation of phylogenetic diversity metrics depending on community assembly processes

Species 

100% Competition

Species 

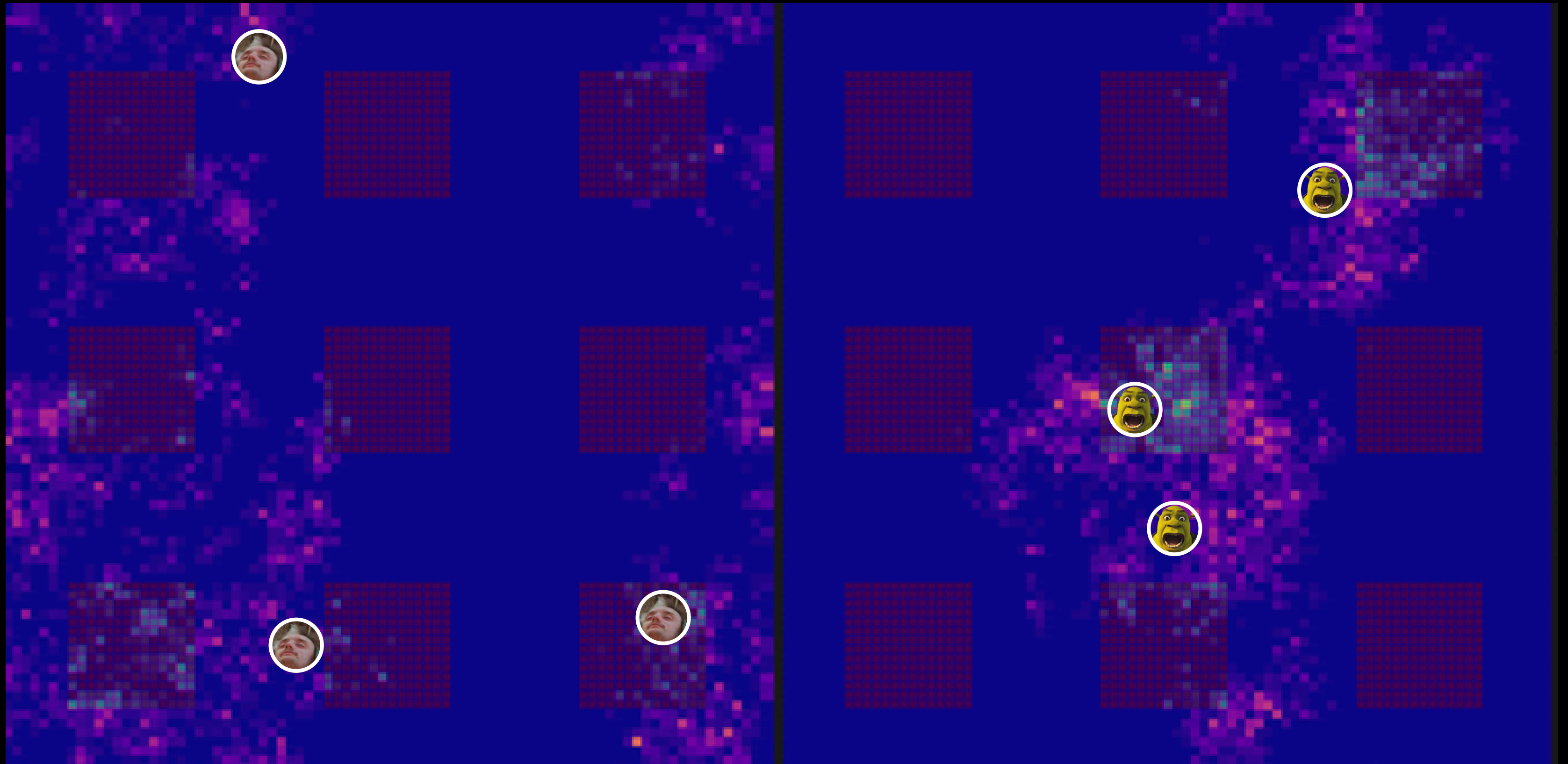


Variation of phylogenetic diversity metrics depending on community assembly processes

Species 

100% Stochastic

Species 

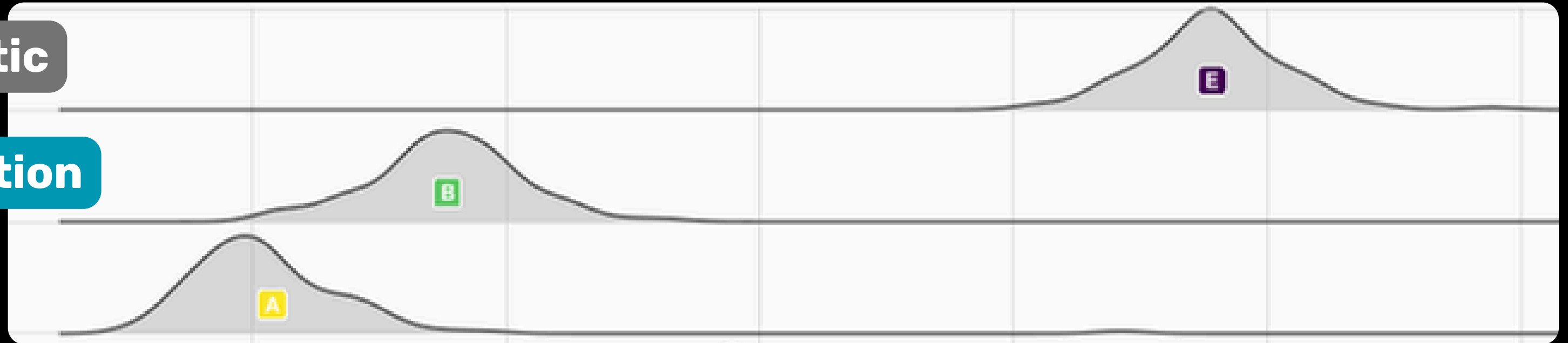


Do phylogenetic diversity metrics reflect community assembly processes?

100% Stochastic



100% Competition

100% Habitat filtering



Phylogenetic diversity (PD)

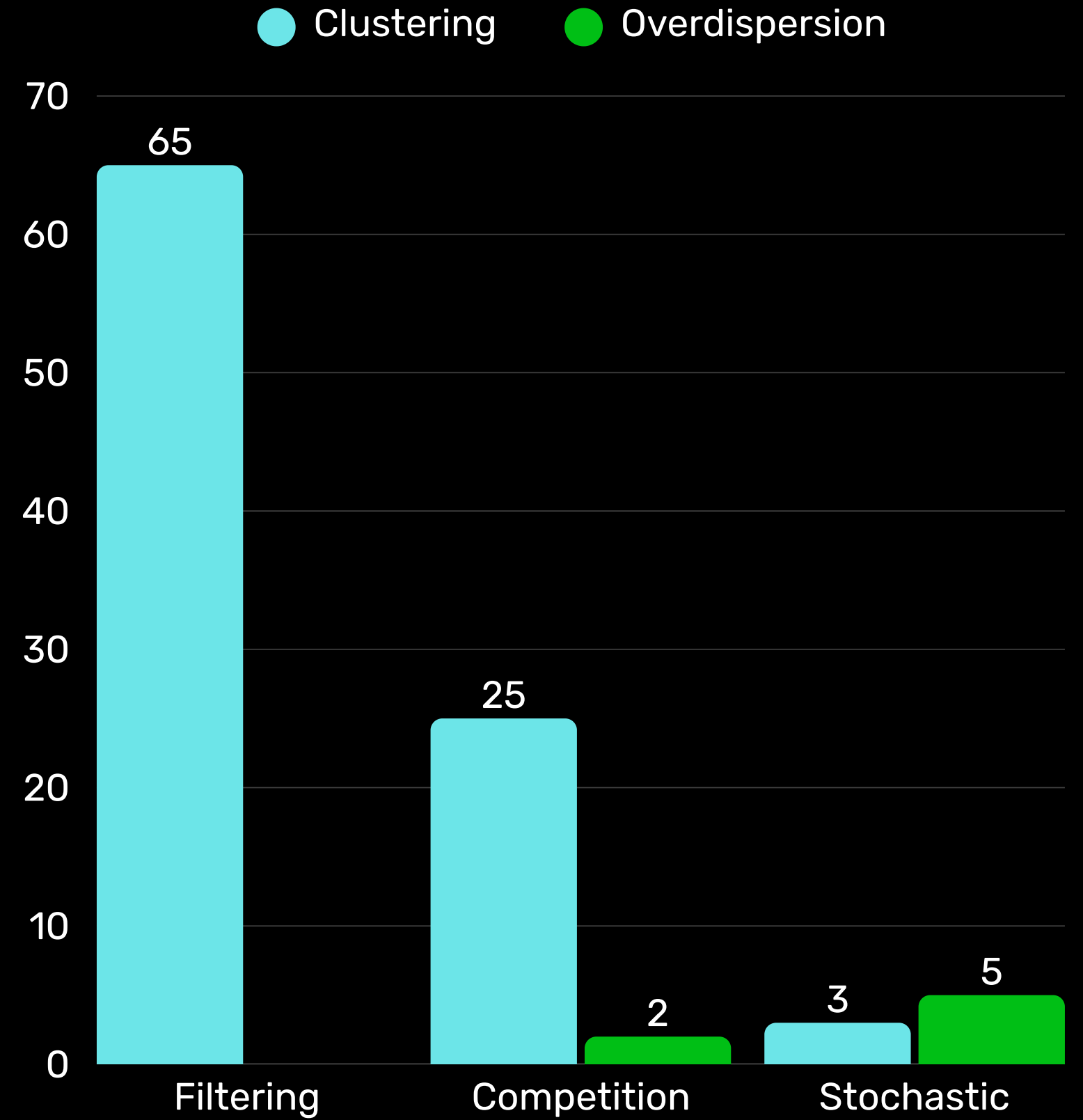
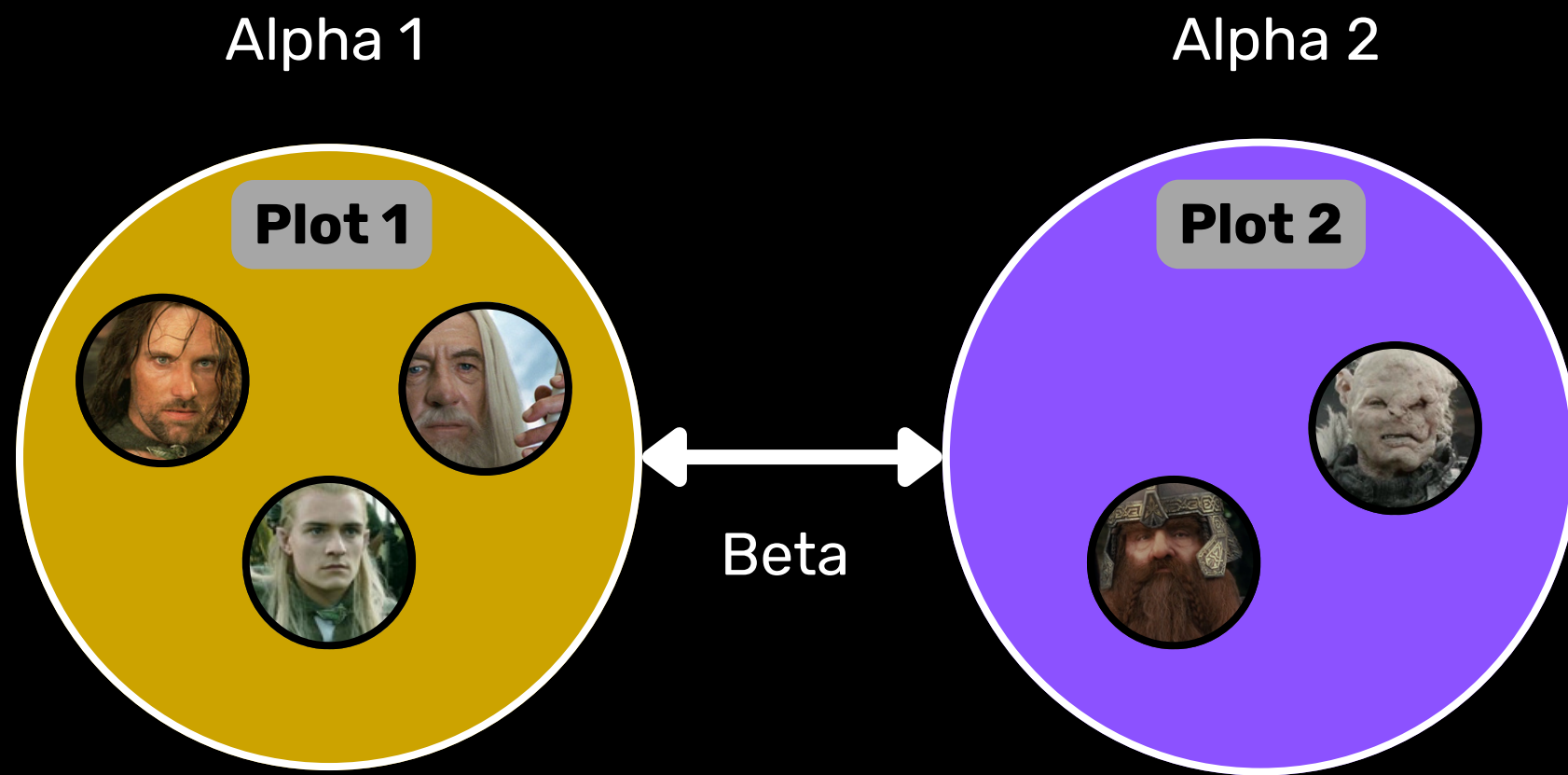
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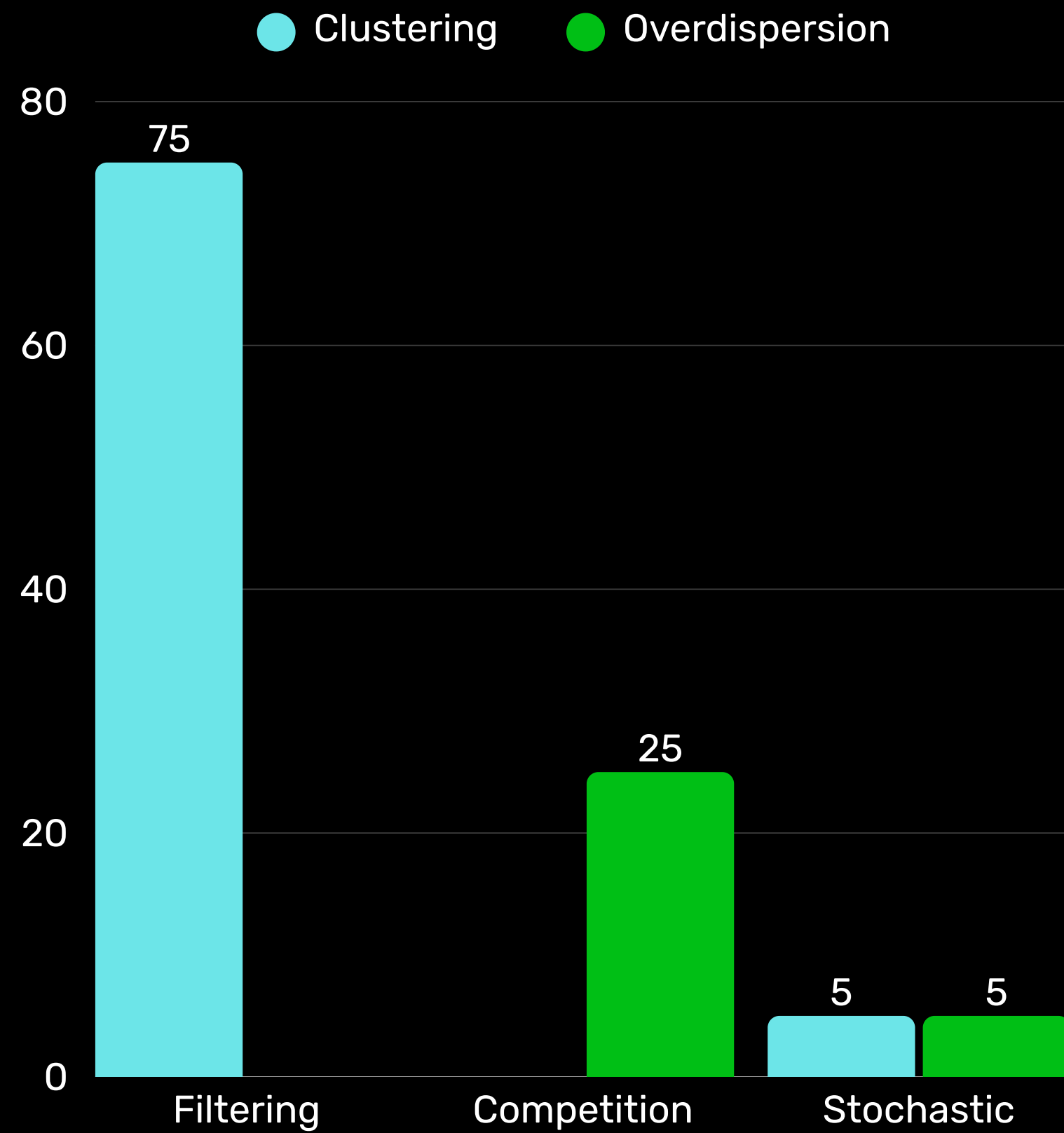
If YES

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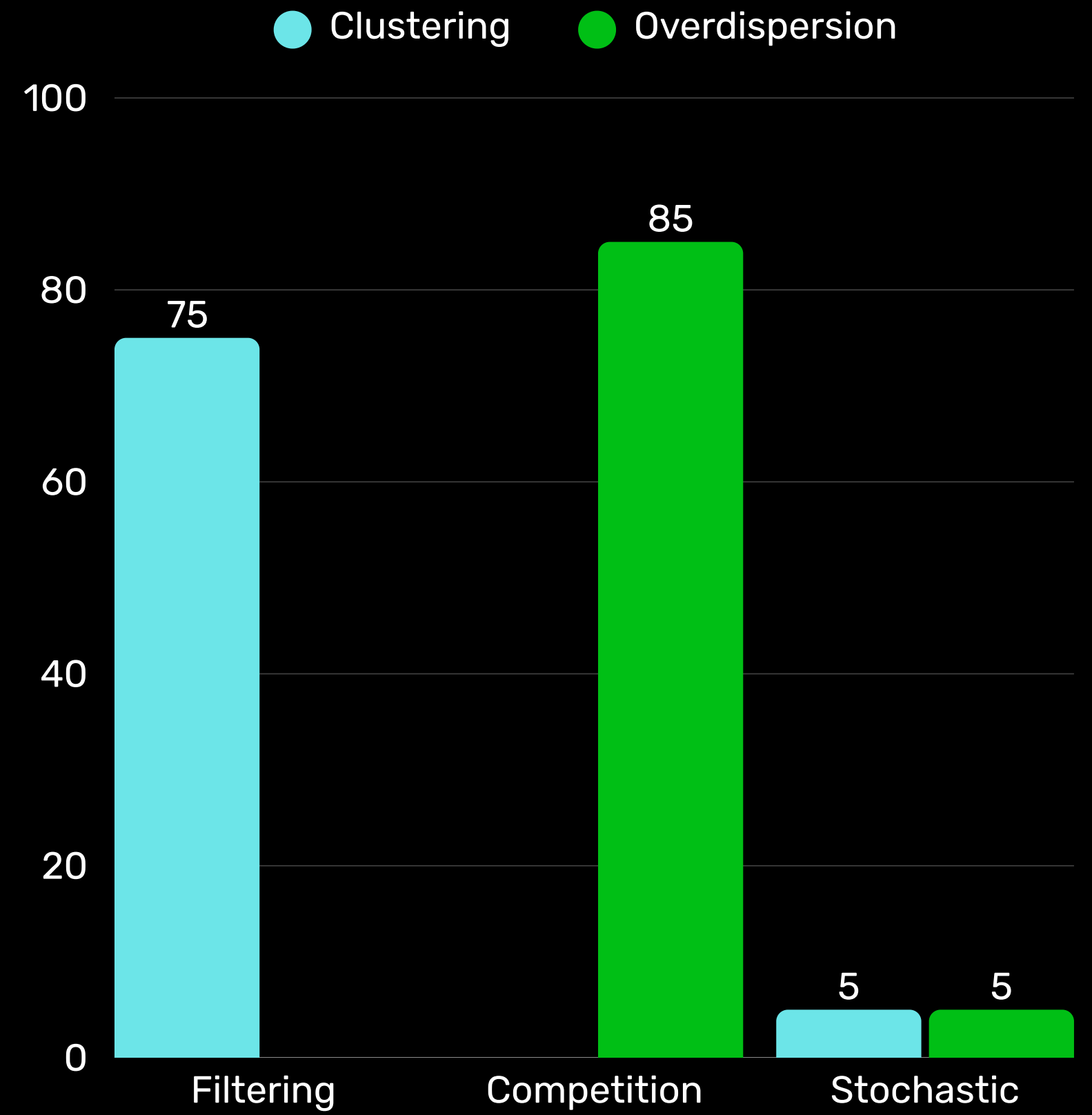
MNTD:
Mean nearest taxon distance

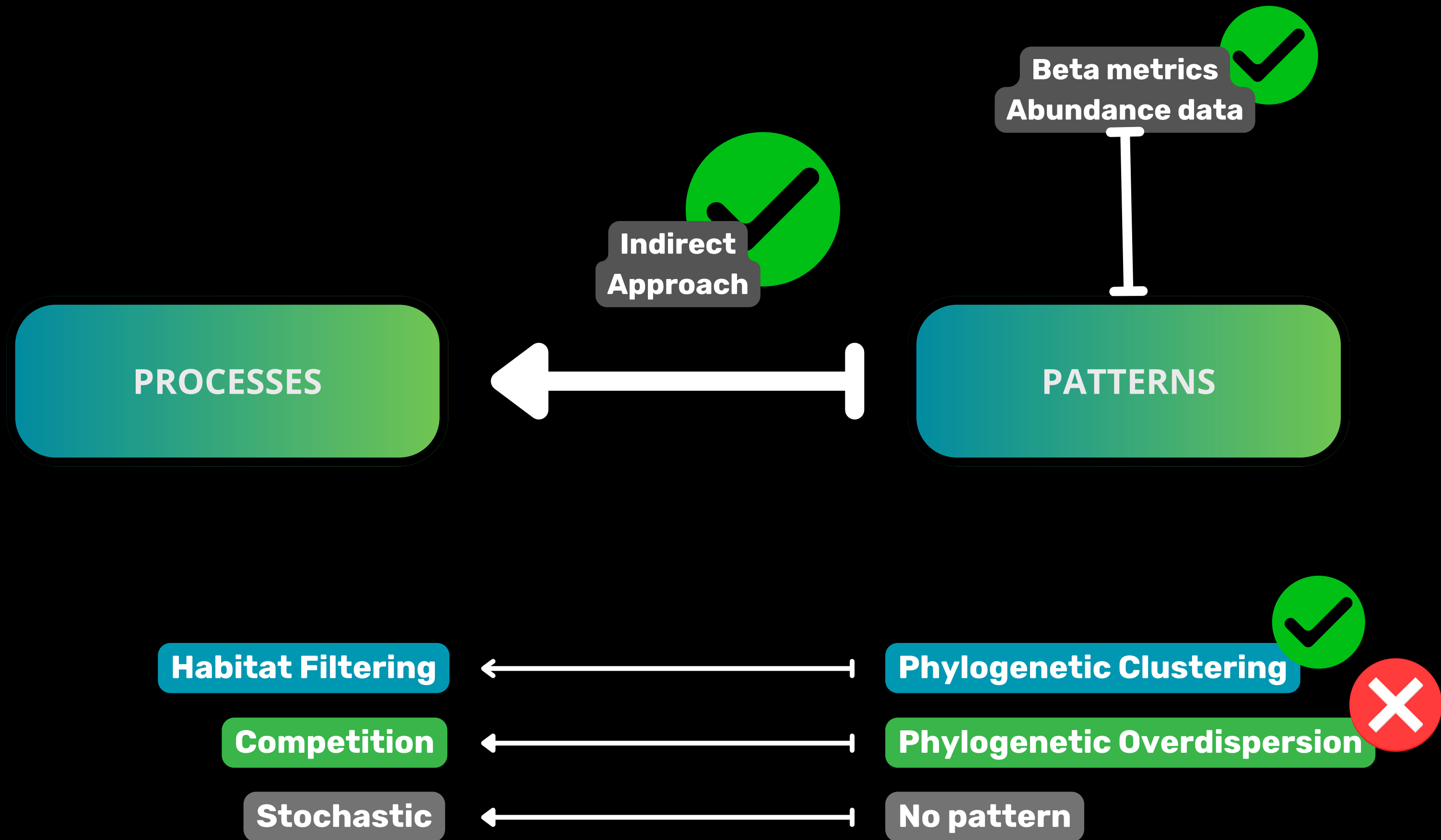


Plst (Occurrence data)



Bst (Abundance data)





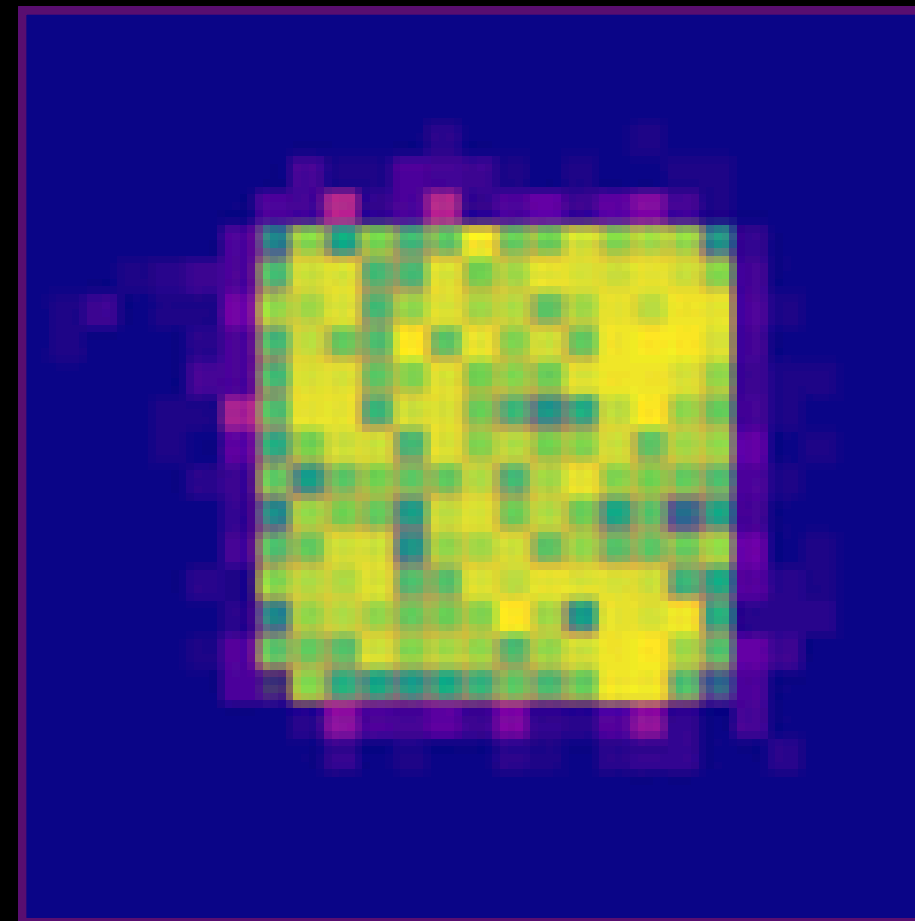
PERSPECTIVES

- In nature, we can have multiple processes acting together.

40% Competition - 40% Filtering - 20% Stochastic

- Other mechanisms can create significant phylogenetic structure.

Mass Effect



CO-AUTHORS



Vanderpoorten Alain | Research Director
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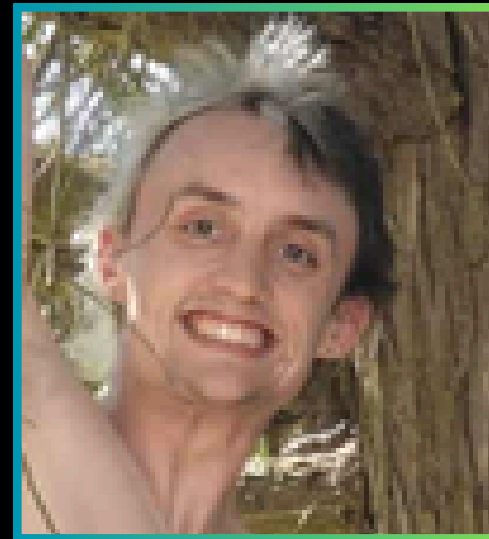


Hardy Olivier | Research Director
Free University of Brussels



Dauby Gilles | Research Associate
Institute of Research for
Development

MYSELF



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Interested in a post-doctoral position for 2026



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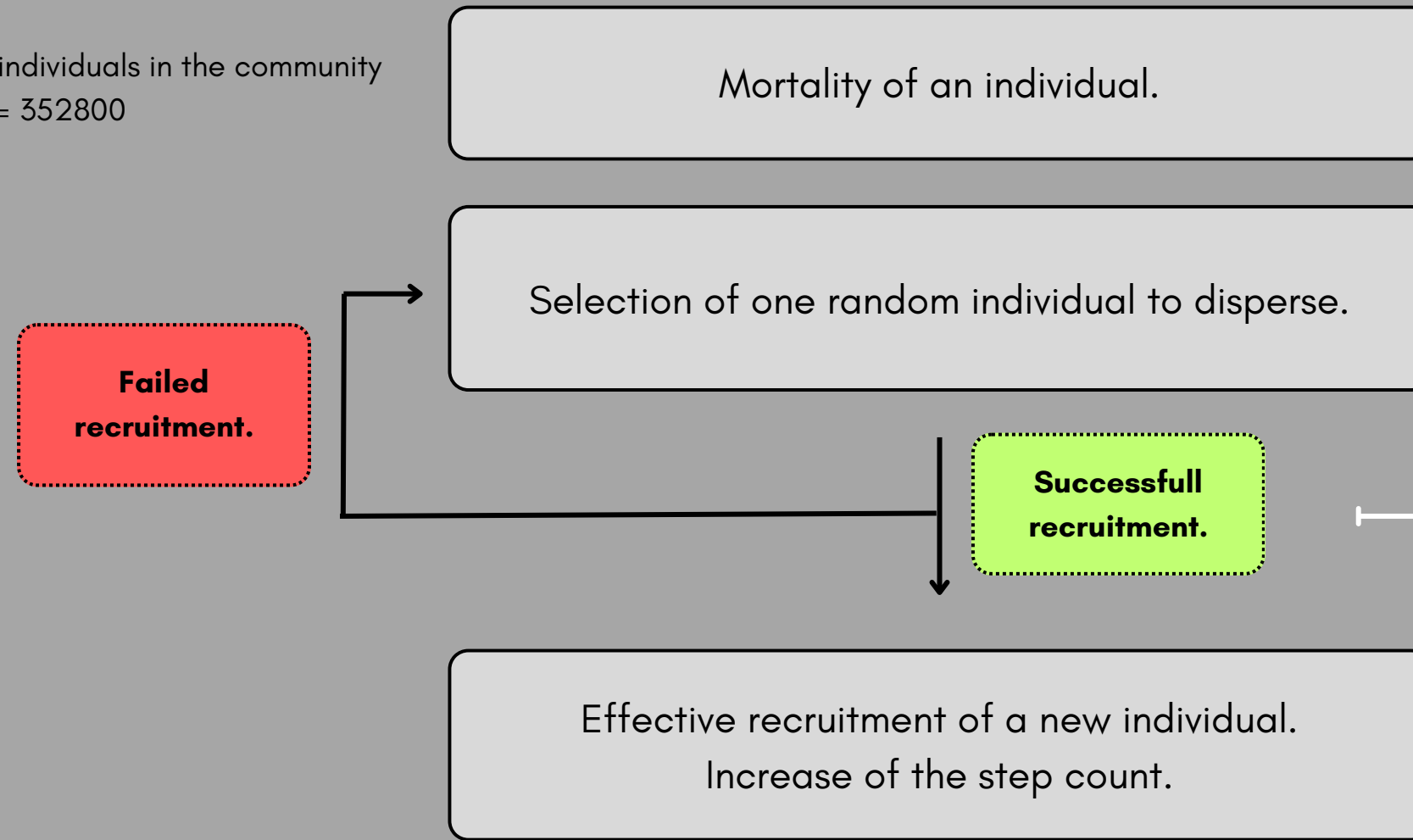
Gen 0: Distribution of the **species** randomly in the **grid**.

Gen 1 -> Gen 2000 : Community evolution across generations.

Step 1 -> Nstep : Recruitment process.

Nstep:

Total number of individuals in the community
-> $84 * 84 * 50 = 352800$



Mortality

1 individual is killed to be replaced.

Dispersion

Dispersion of a propagule based on a dispersion kernel with decreasing probability with increasing distance.

Processus

• **Stochastic:**

Every propagule is accepted, independtly from habitats and species already present.

• **Habitat filtering:**

Propagules are selected based on the correspondance between their traits and the habitat, minimizing traits differences between species inside each plots.

• **Competition:**

Propagules are selected based on the species already presents by competition, maximising trait differences.

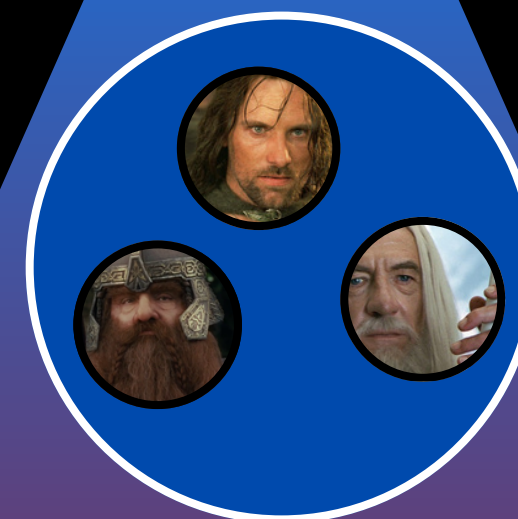
End of the simulation.

If species are impacted by niche conservatism (habitat filtering), they are threatened by climate change.

t0



t1



Recolonisation by exogenic species ?

