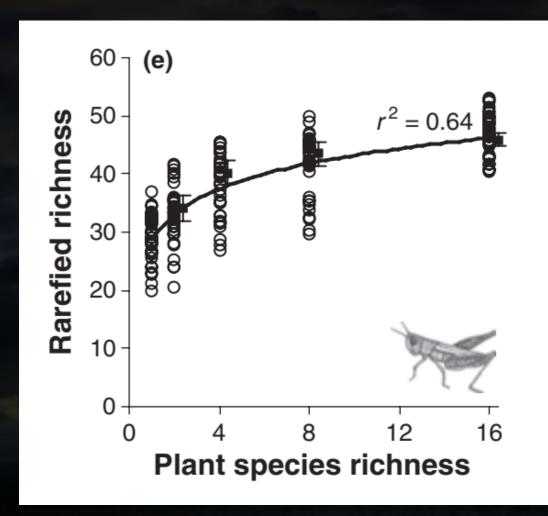
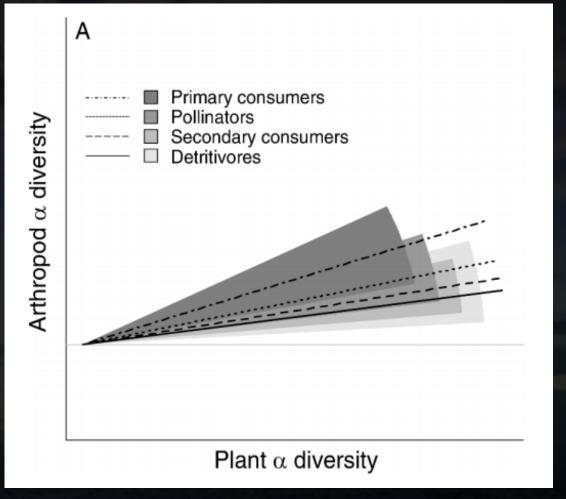
Mechanisms underlying the predatorprey diversity relationships in marine bacterioplankton

- implications from the community assembly processes

Feng-Hsun Oscar Chang

@ IONTU 422 lab meeting

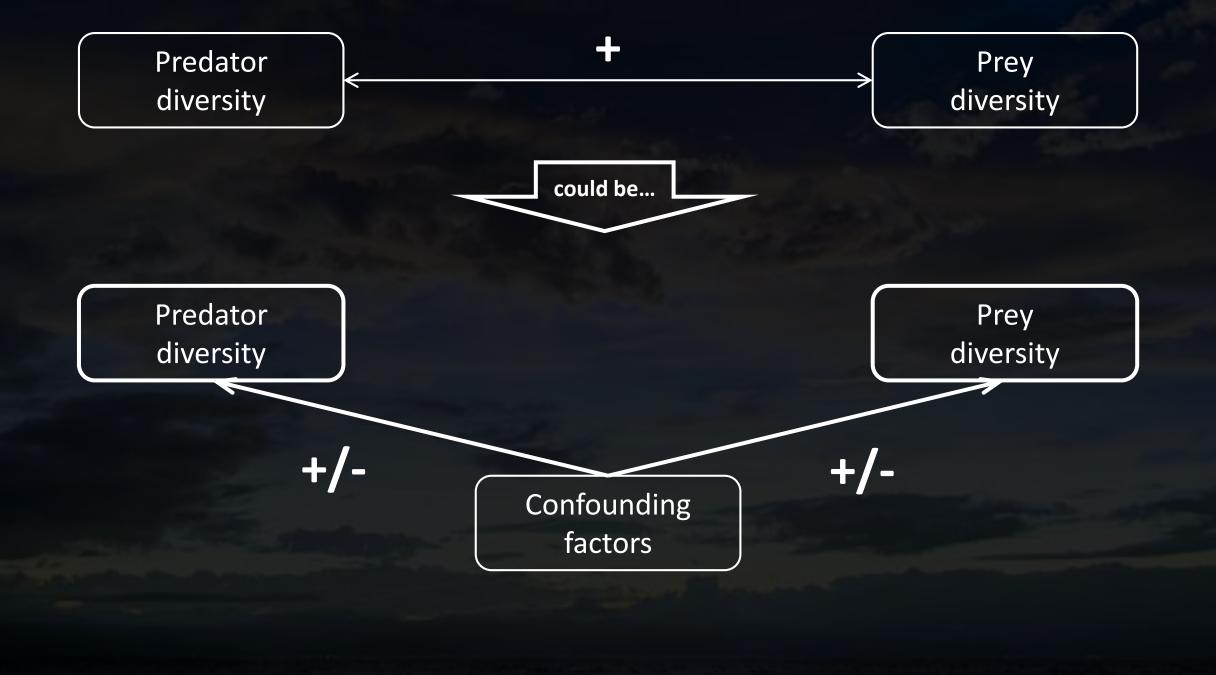


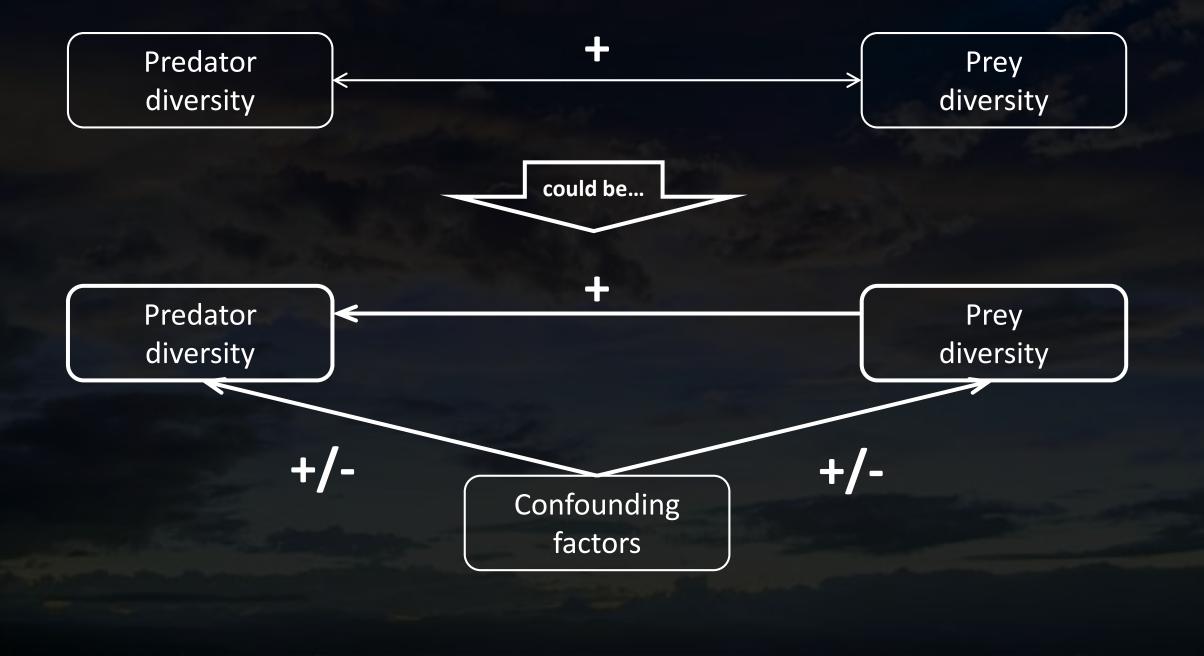


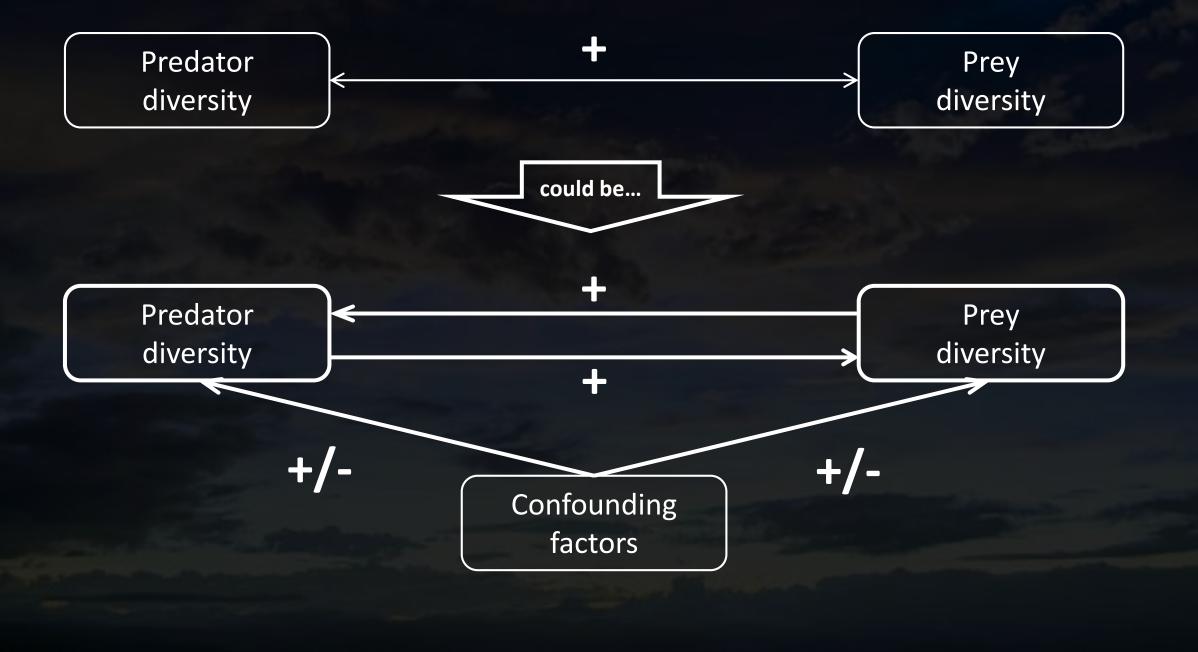
Castagneyrol et al. 2012 @ Ecology



Why the diversity of predator and prey are positively associated?







Community assembly processes





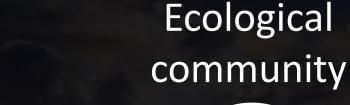
Ecological

community



- Species-area relationships
- Diversity gradients
- Relative abundance distributions
- etc...

Drift
Selection
Speciation
Dispersal





- Species-area relationships
- Diversity gradients
- Relative abundance distributions
- etc...

Random / Stochasticity

Drift

Selection Speciation Dispersal Ecological community

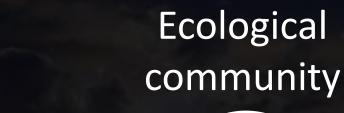


- Species-area relationships
- Diversity gradients
- Relative abundance distributions
- etc...

Random /
Stochasticity Drift

Non-random / Selection
Deterministic Speciation

Dispersal





- Species-area relationships
- Diversity gradients
- Relative abundance distributions
- etc...

Random /
Stochasticity Drift

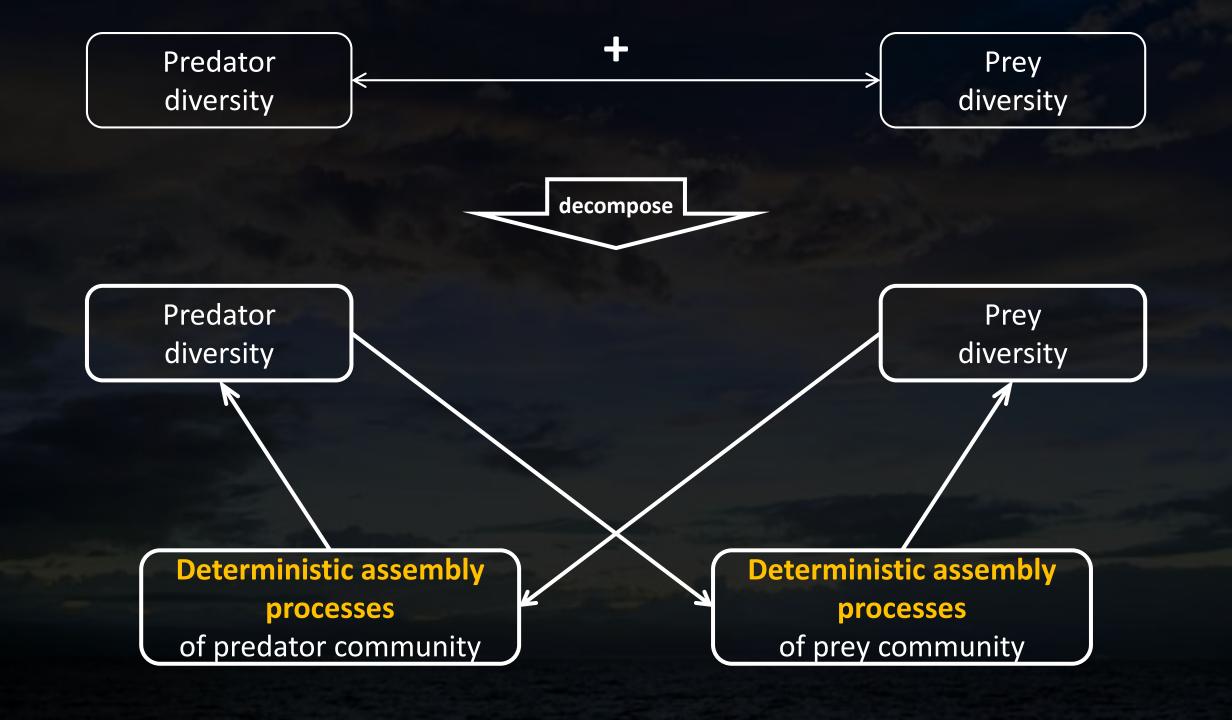
Non-random / Selection
Deterministic Speciation

Both ??? Dispersal

Ecological community



- Species-area relationships
- Diversity gradients
- Relative abundance distributions
- etc...



Divergent assembly processes

Homogeneous assembly processes



Homogeneous assembly processes



Local community



Low α diversity

Divergent assembly processes





High α diversity



Homogeneous assembly processes



Local communities







Low β diversity

Divergent assembly processes



Local communities

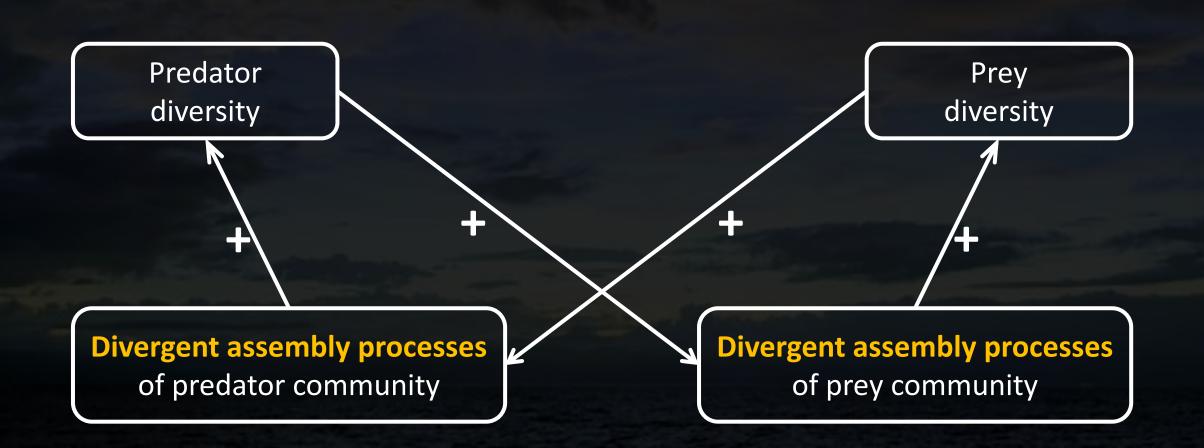




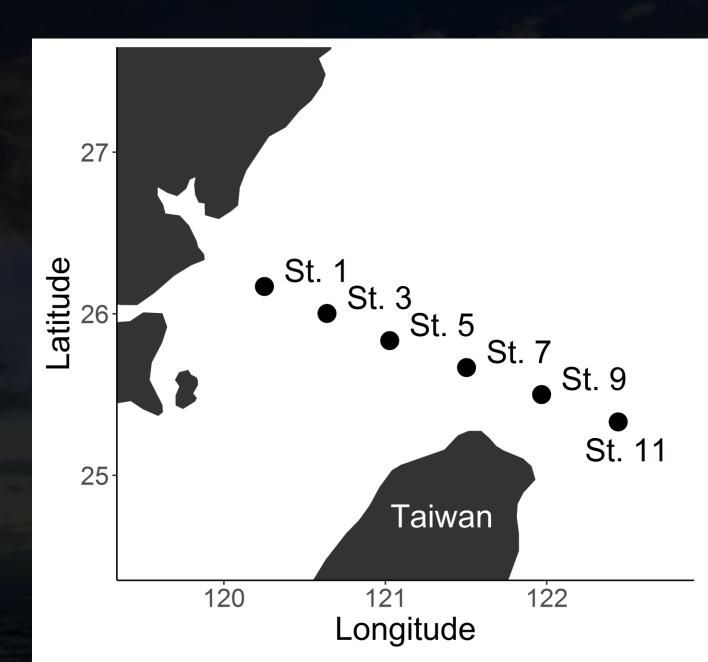


High β diversity

Predator (prey) diversity increases the divergent assembly processes of prey (predator) community, which in turn increase prey (predator) diversity, in both α and β levels



- 14 cruises
- Predator:
 Heterotrophic nano-flagellates (HNF; 18S rDNA)
- Prey: Bacteria (16S rDNA)



Deterministic assembly processes:

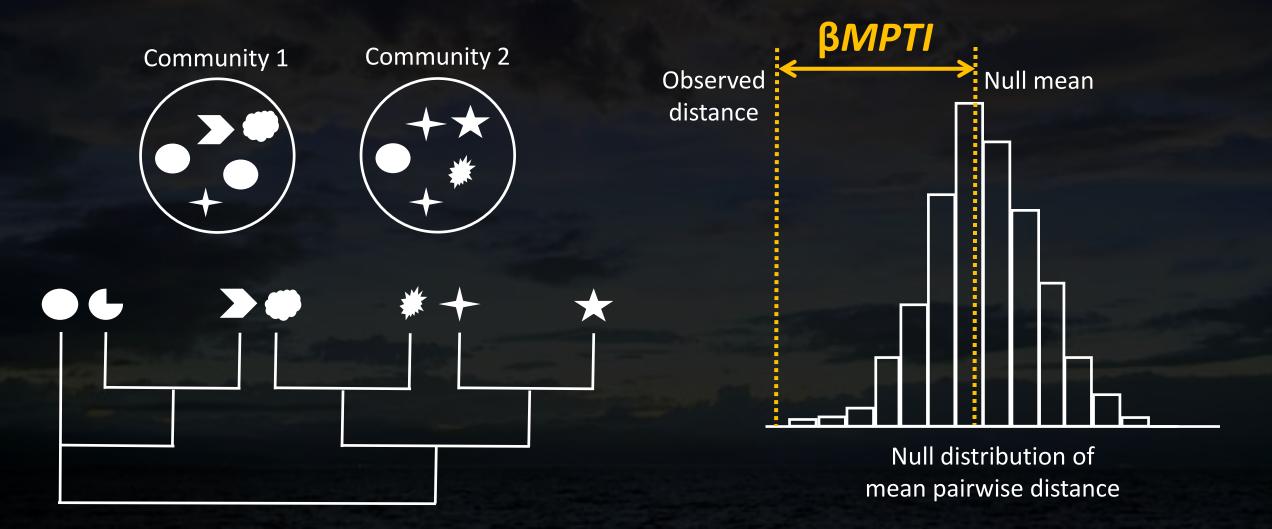
Mean Pairwise Taxa Index (MPTI),

calculated from mean pairwise phylogenetic distance

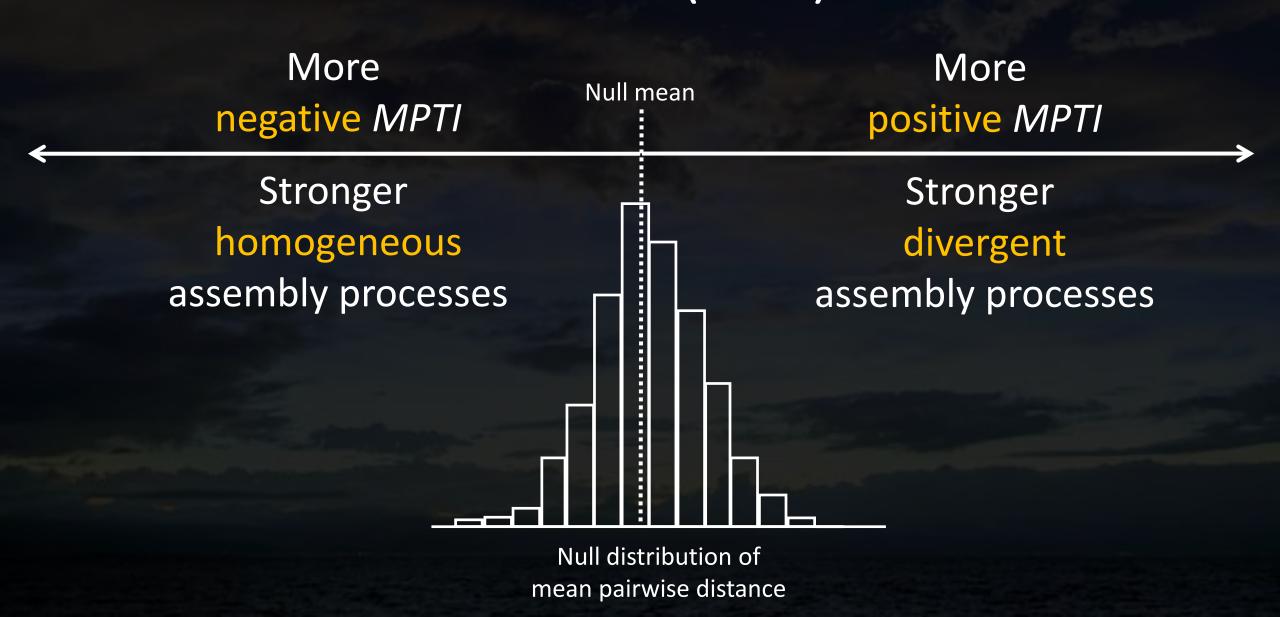


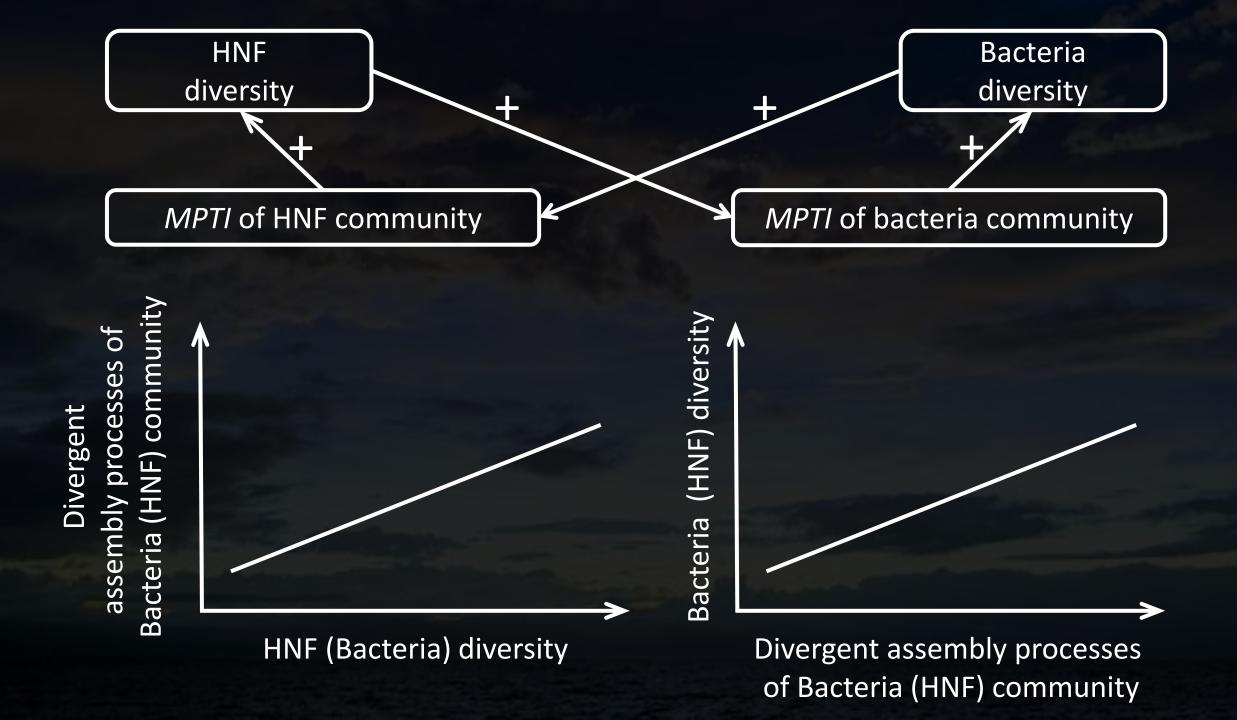
Deterministic assembly processes:

Mean Pairwise Taxa Index (MPTI), calculated from mean pairwise phylogenetic distance

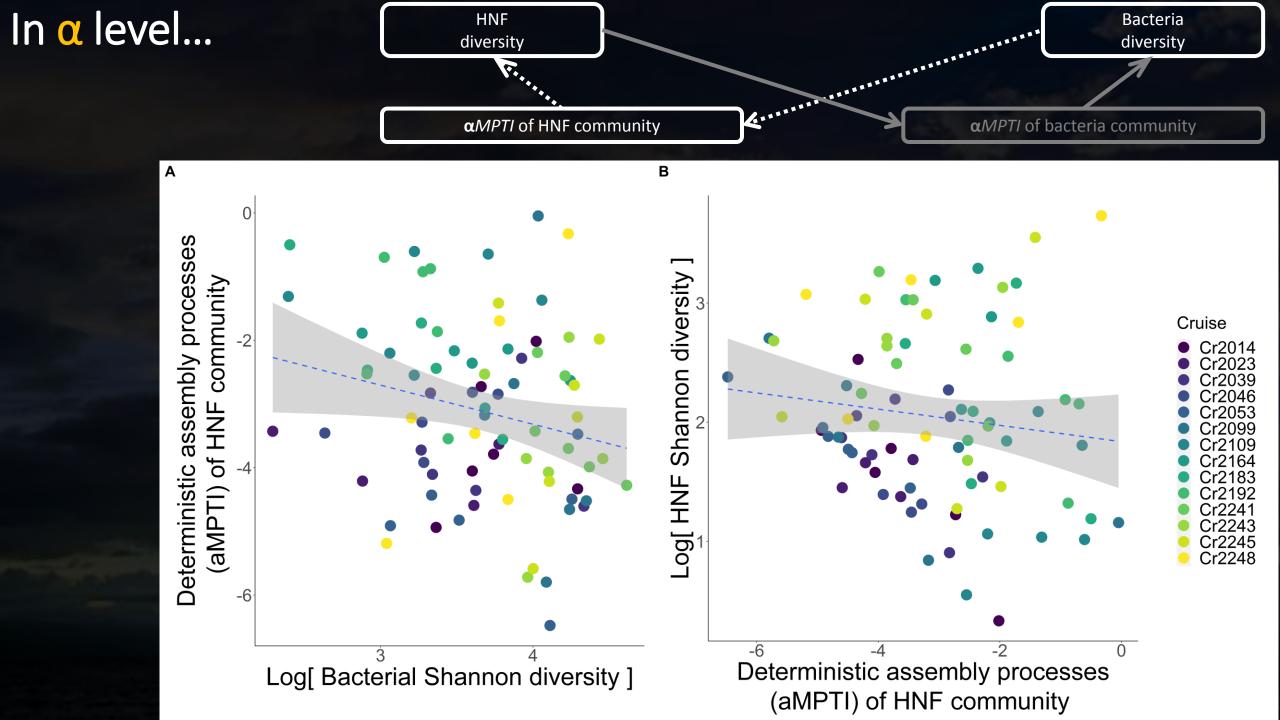


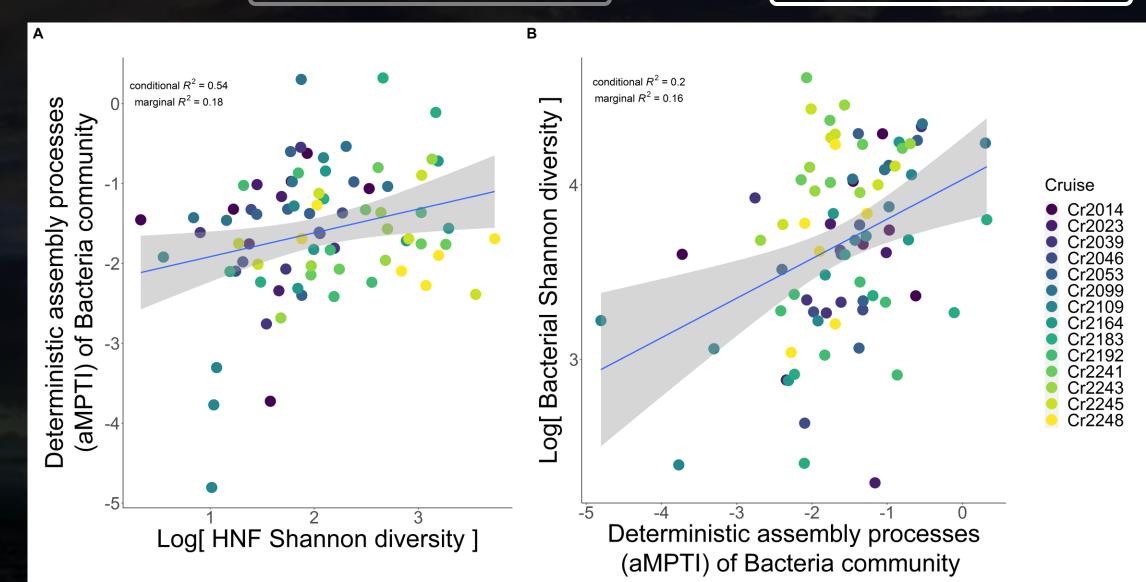
Deterministic assembly processes: Mean Pairwise Taxa Index (MPTI)

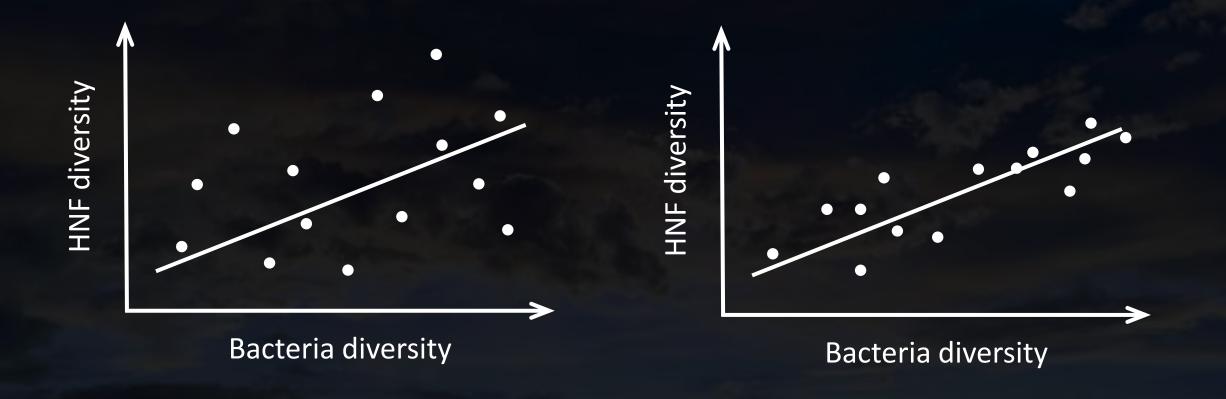




In α level... conditional $R^2 = 0.32$ marginal $R^2 = 0.1$ Shannon diversity] Cruise Cr2014 Cr2023 Cr2039 Cr2039 Cr2046 Cr2053 Cr2099 Cr2109 Cr2164 Cr2183 Cr2192 Cr2241 Cr2243 Cr2245 Cr2248 Log[HNF Log[Bacteria Shannon diversity]

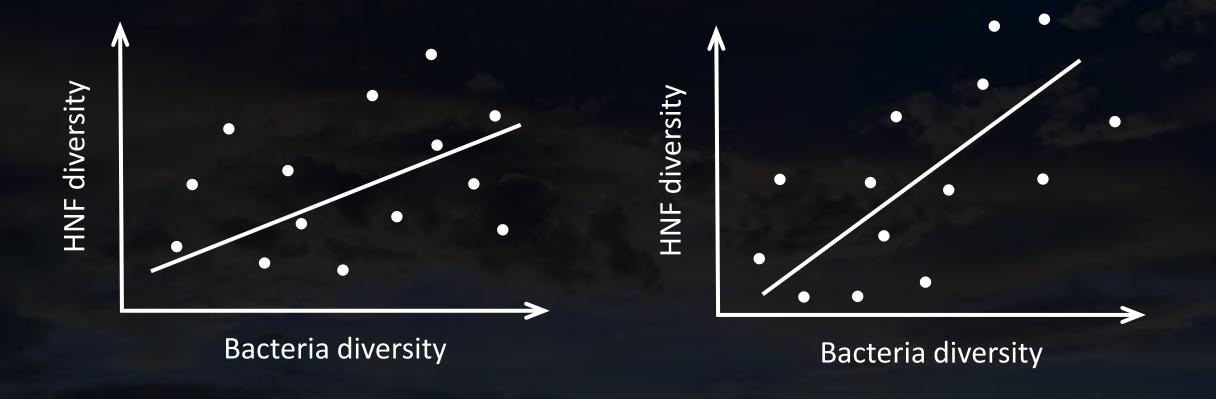






Stronger divergent processes

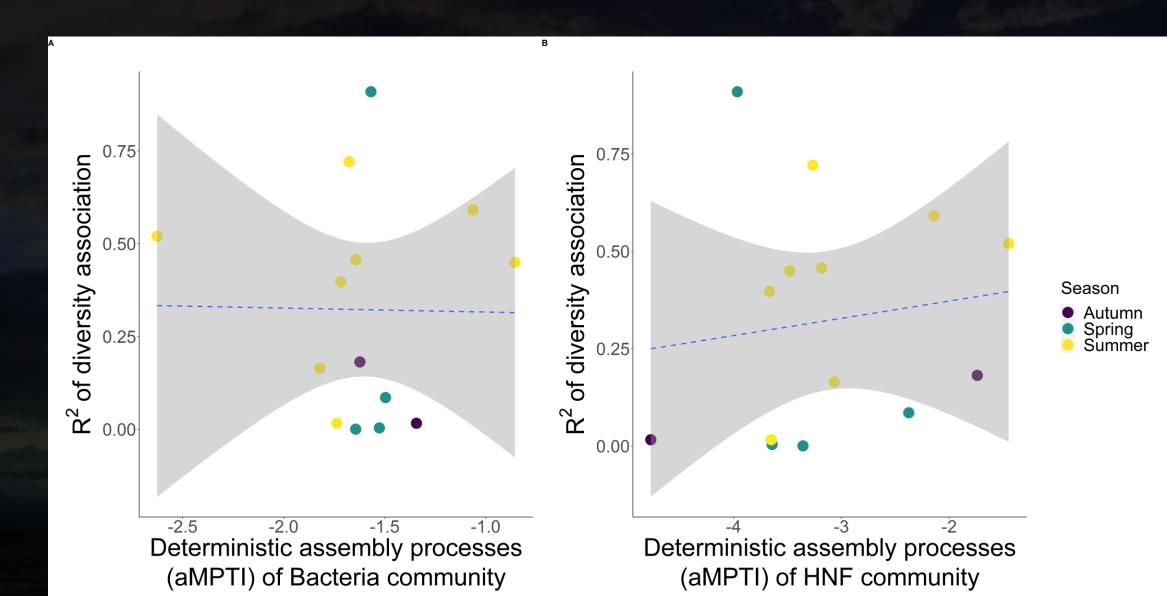
Tighter association (larger R²)?



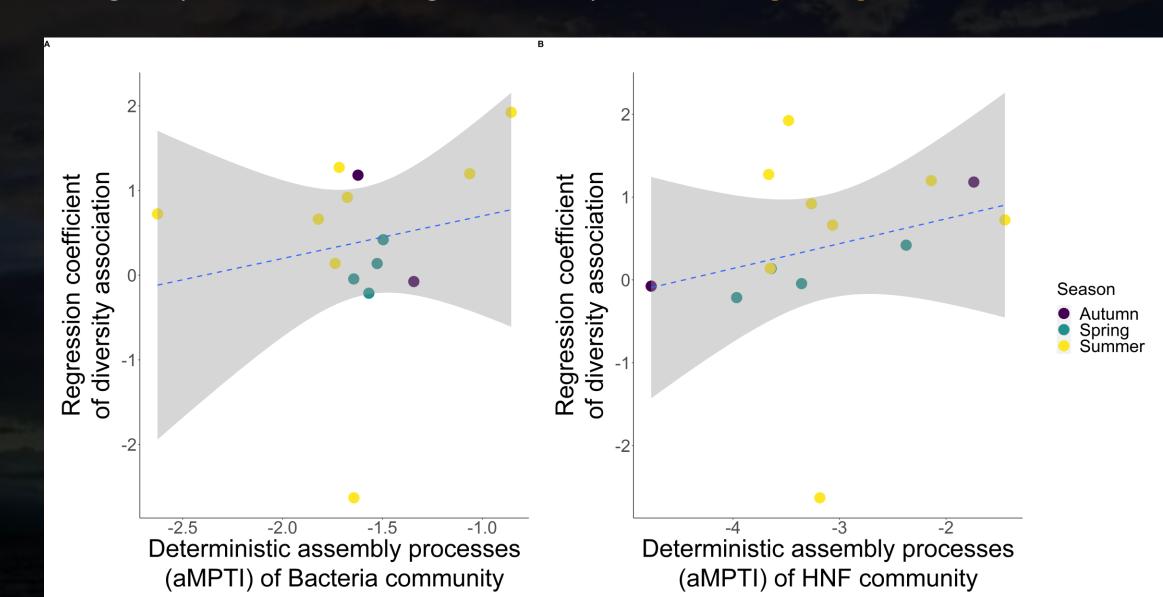
Stronger divergent processes

Larger diversity effects (larger regression coefficient)?

Stronger divergent processes ≠> Tighter association (larger R²)

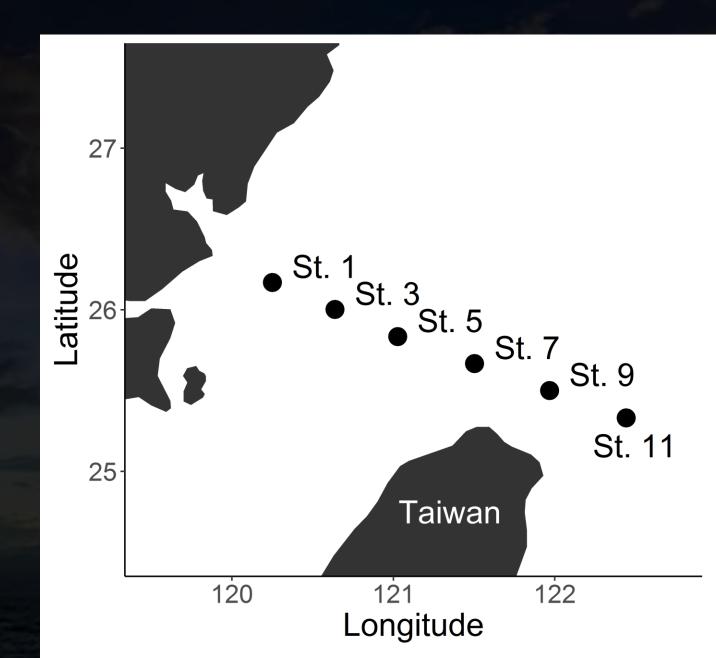


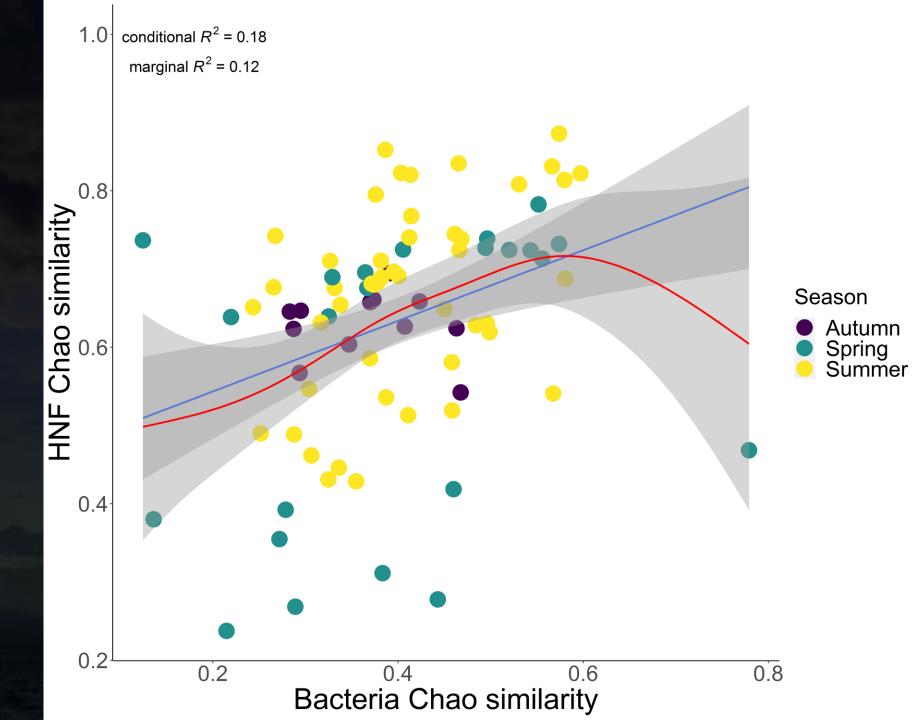
Stronger divergent processes =? Larger diversity effects (larger regression coefficient)



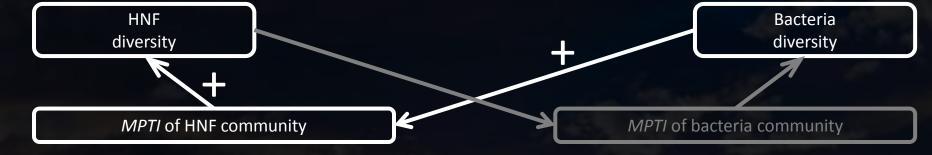


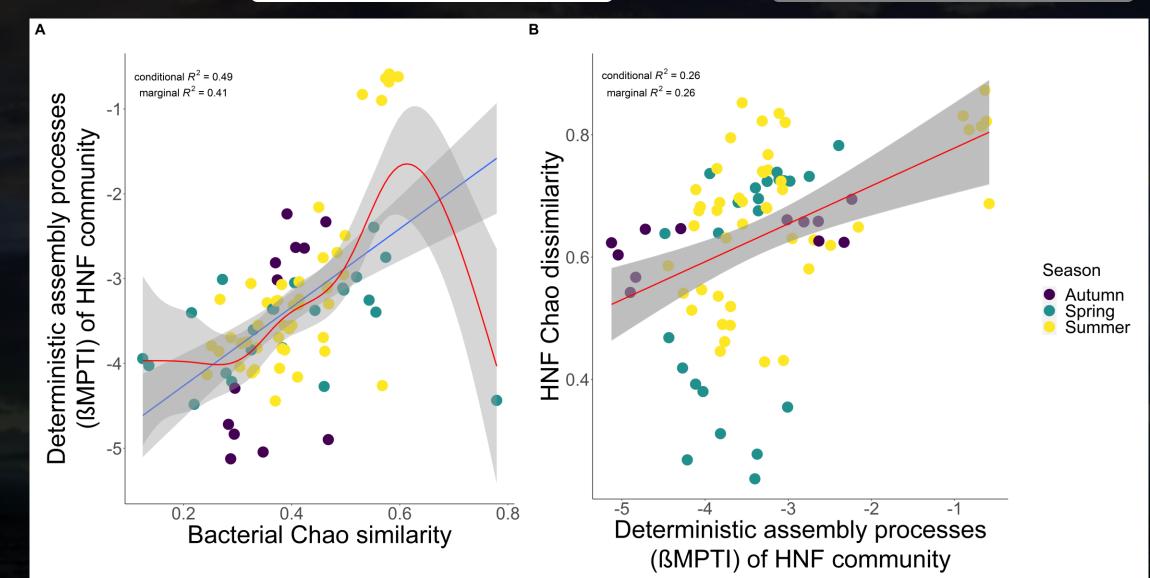
- Chao similarity
- mean pairwise similarity within a cruise

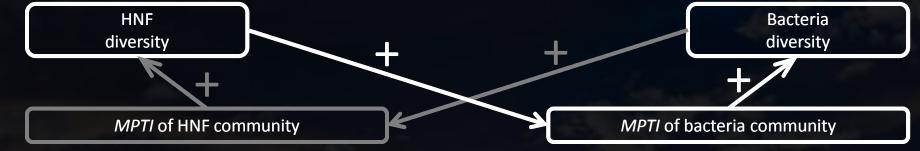


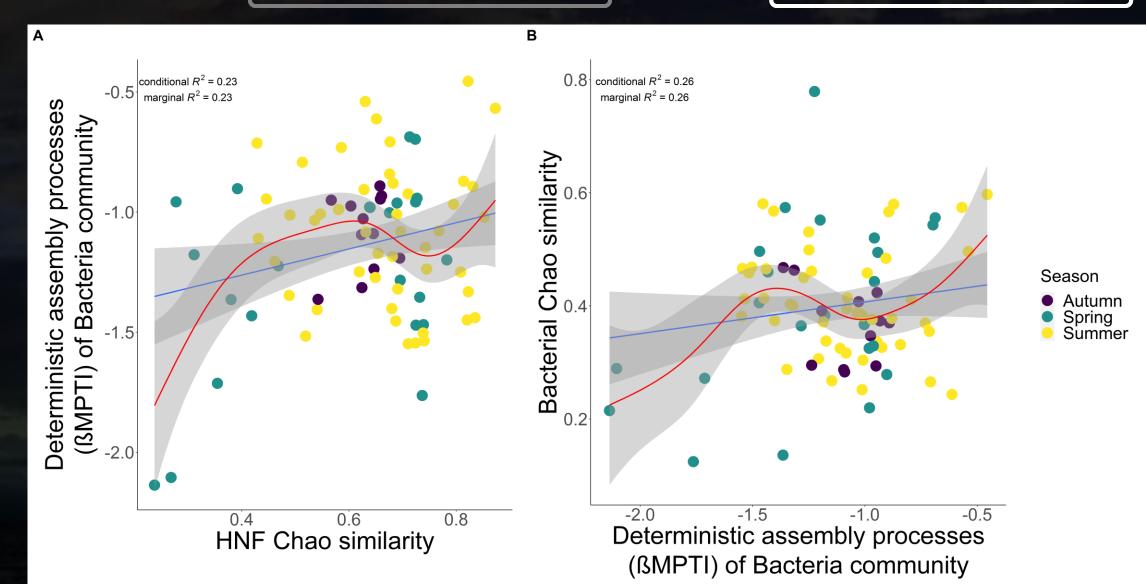




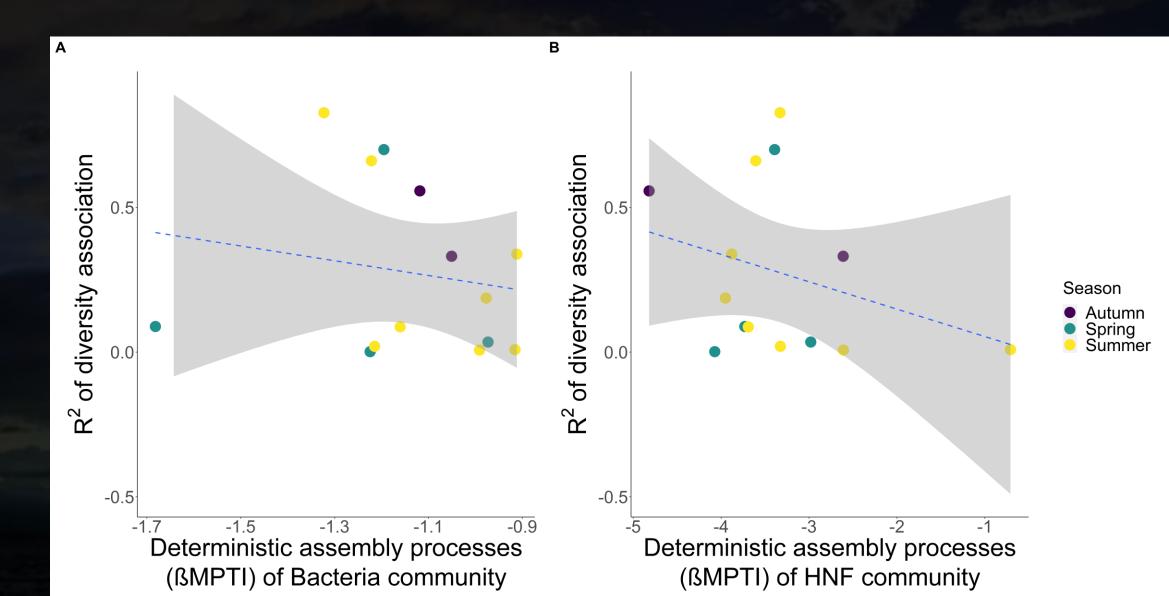




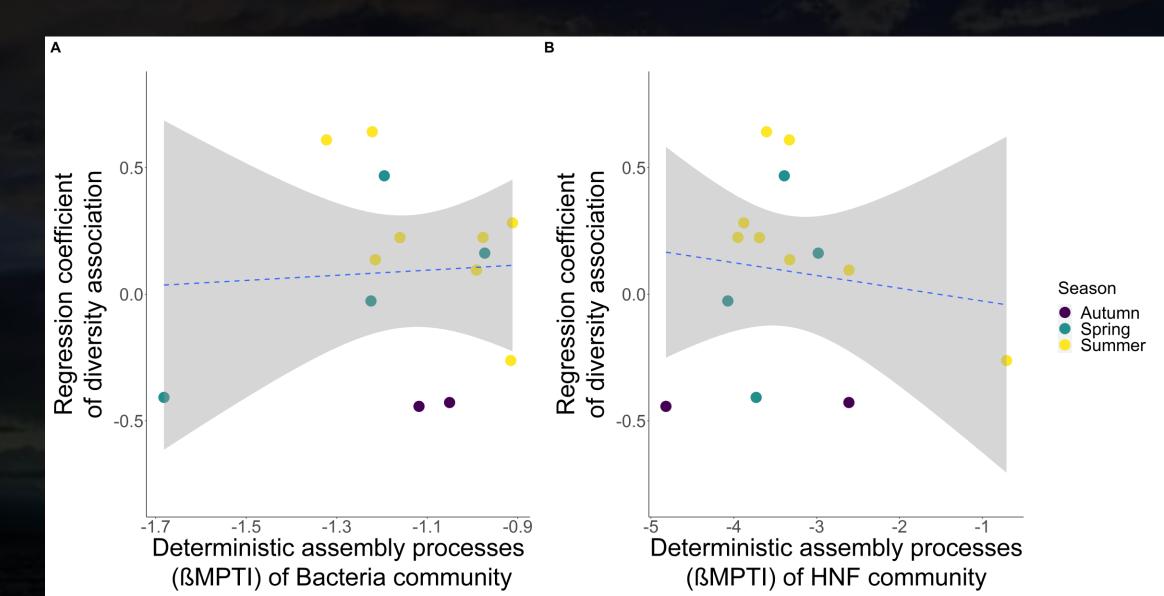




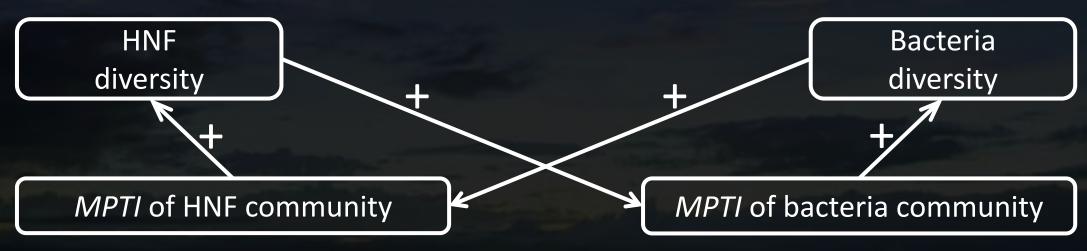
Stronger divergent processes ≠> Tighter association (larger R²)



Stronger divergent processes ≠> Larger diversity effects (larger regression coefficient)

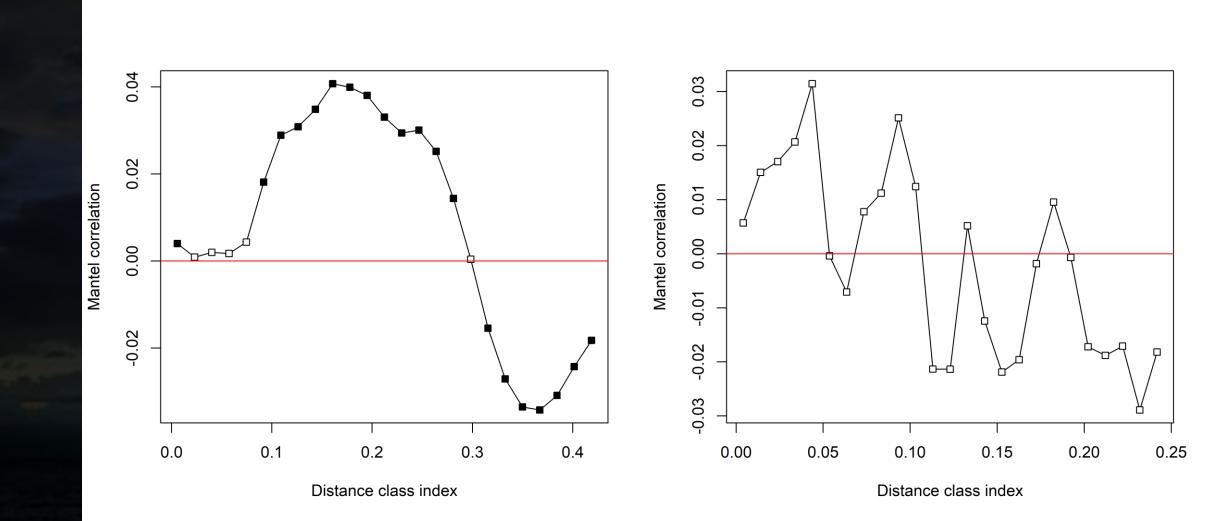


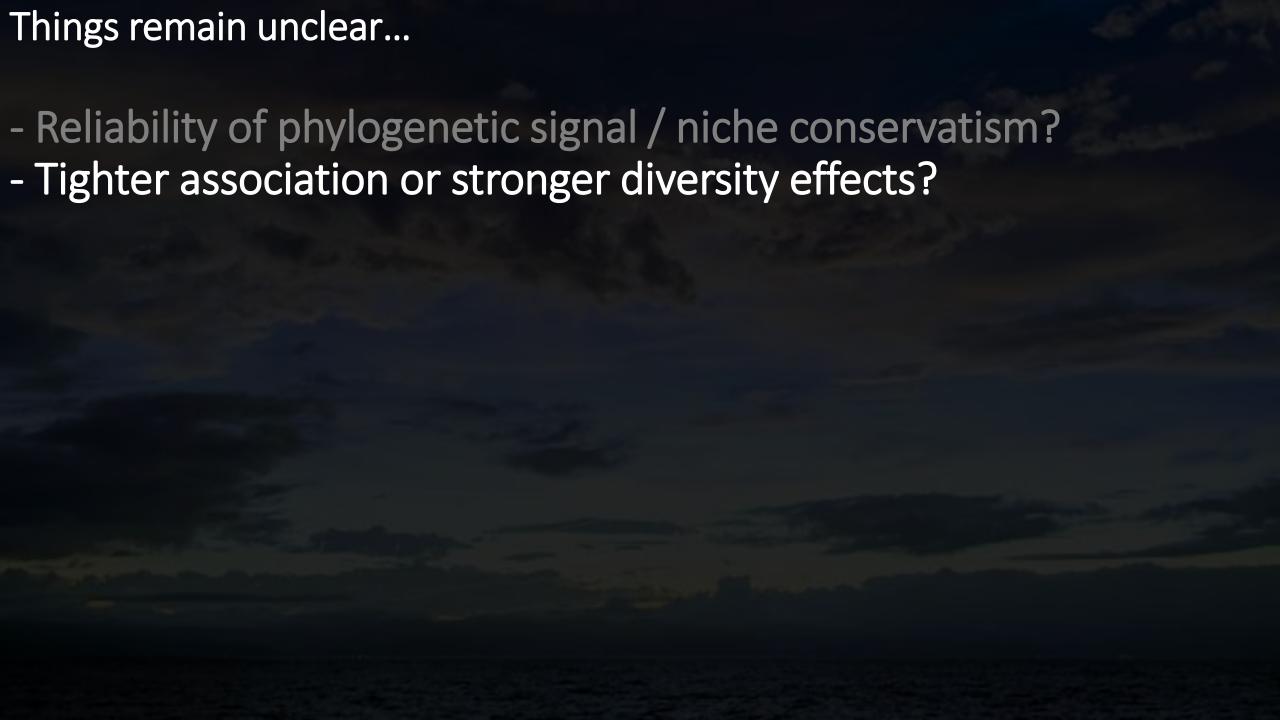




Things remain unclear...

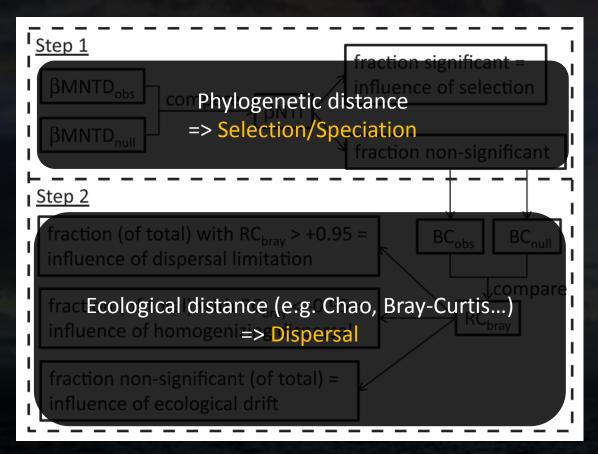
- Reliability of phylogenetic signal / niche conservatism?





Things remain unclear...

- Reliability of phylogenetic signal / niche conservatism?
- Tighter association or stronger diversity effects?
- How to quantify dispersal? Or, is it necessary to do so?



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