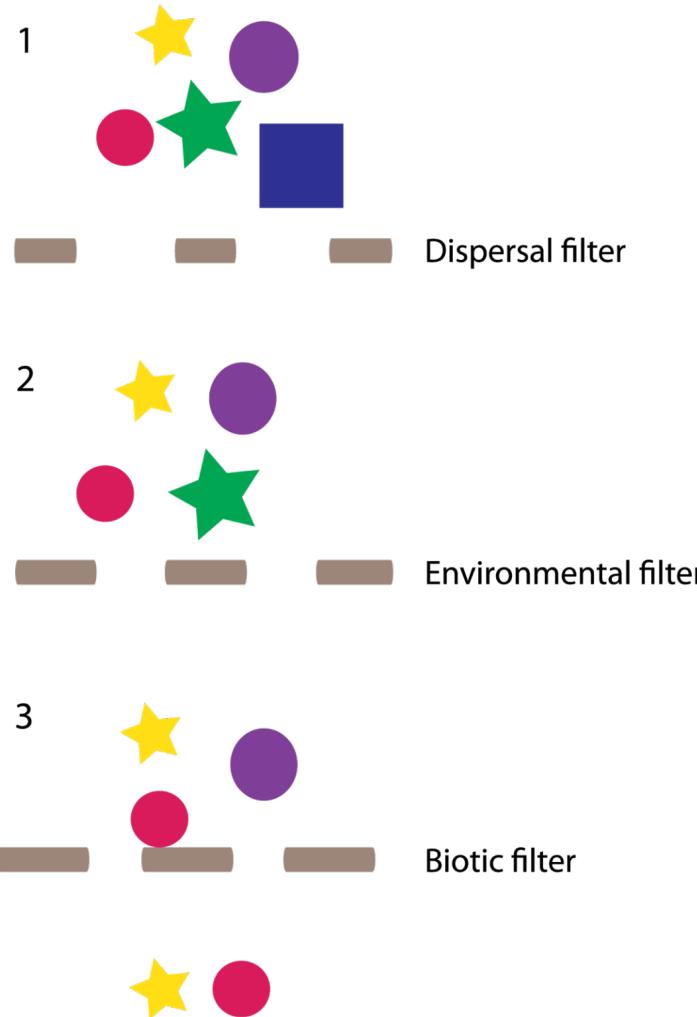


Phylogenetic community ecology

Species coexistence and phylogenetic trees

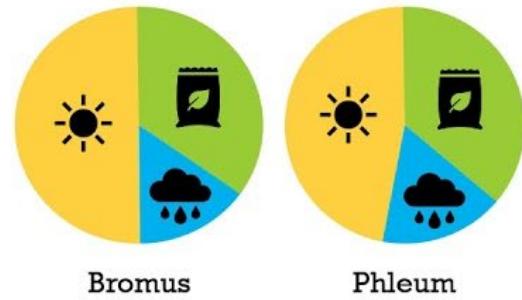


The process of community assembly



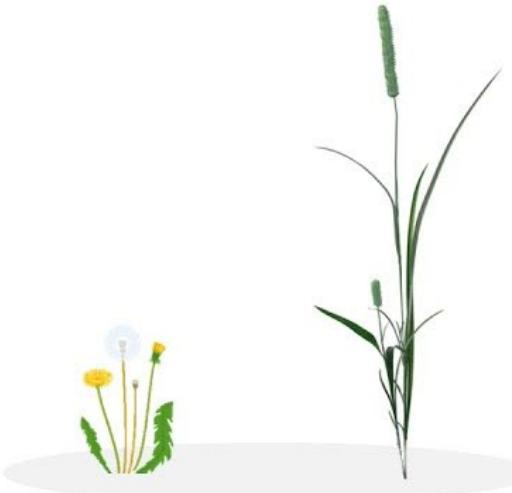
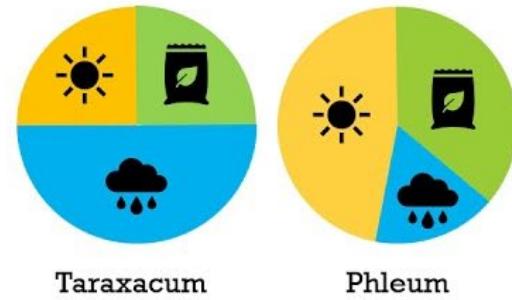
**Habitat filters
select for
species with
similar traits**

Introduction



LIMITING SIMILARITY

The environment limits
the coexistence of
functionally similar,
co-occurring species
(MacArthur and Levins 1967;
Diamond 1975; Watkins and
Wilson 2003)

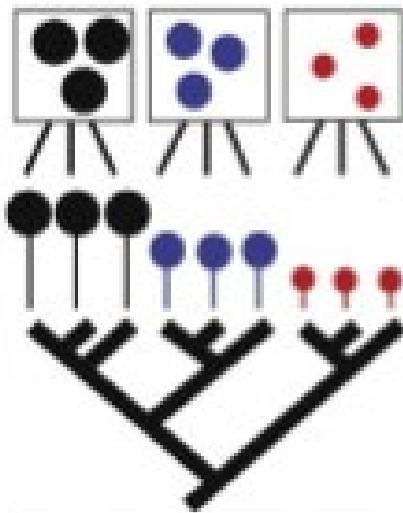


Competition selects
for species with
different traits

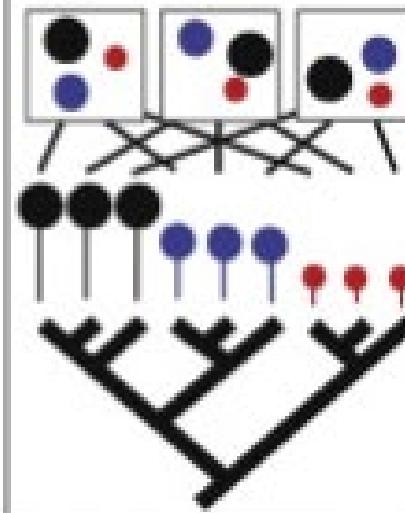
The core idea of
phylogenetic
community ecology is
that we can use the tree
as a proxy for the traits
that allow species to
coexist in communities

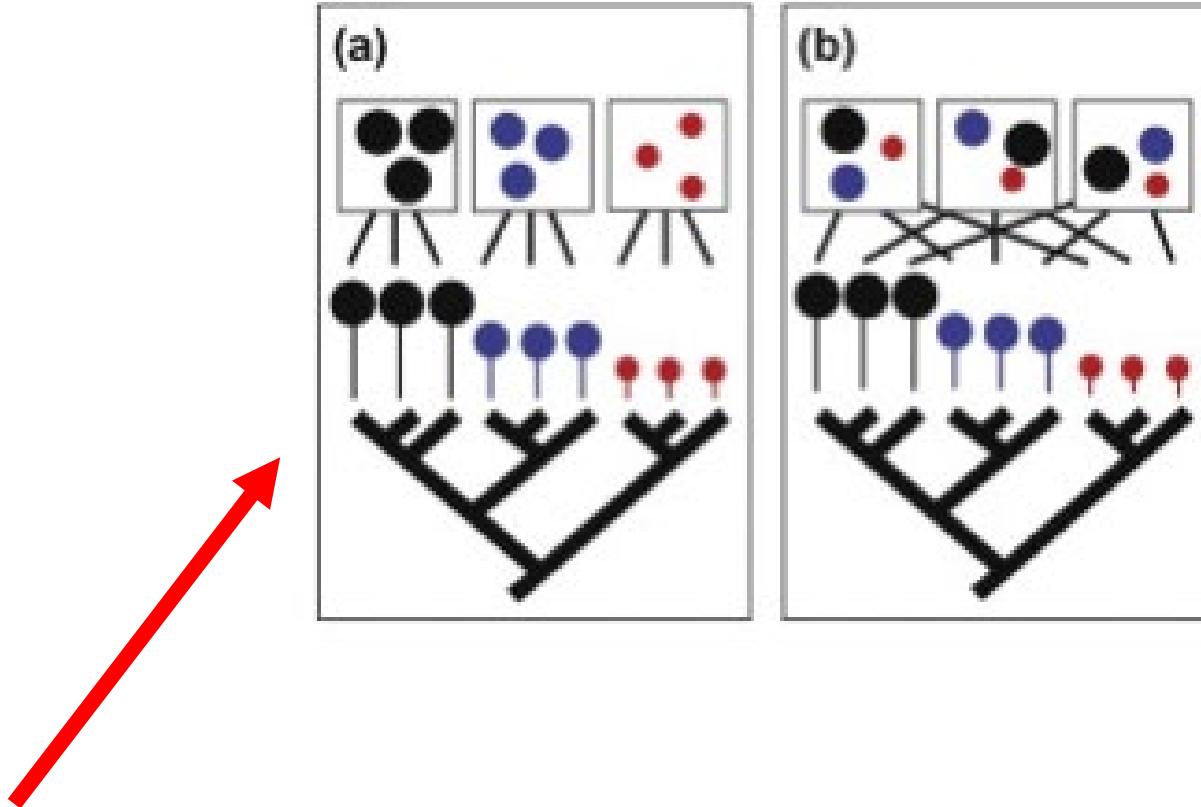
If we assume similar species have similar traits:

(a)

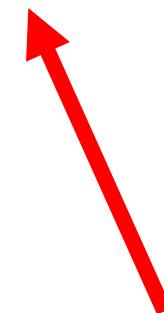
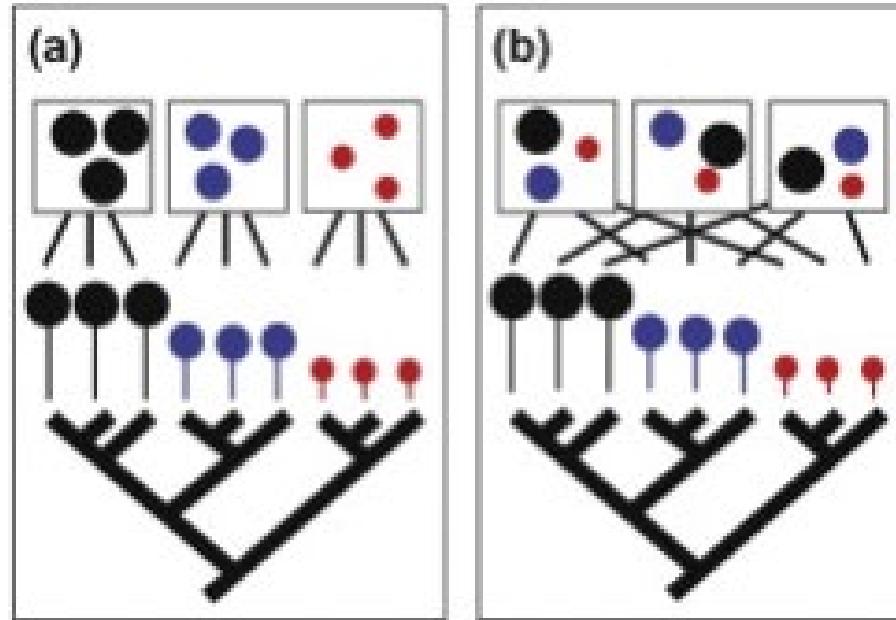


(b)



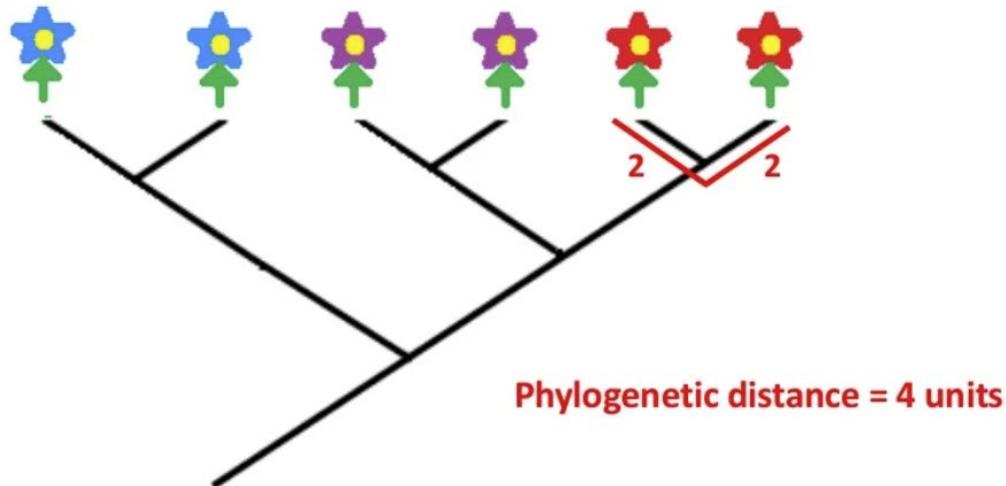


Clustered pattern = environmental filtering



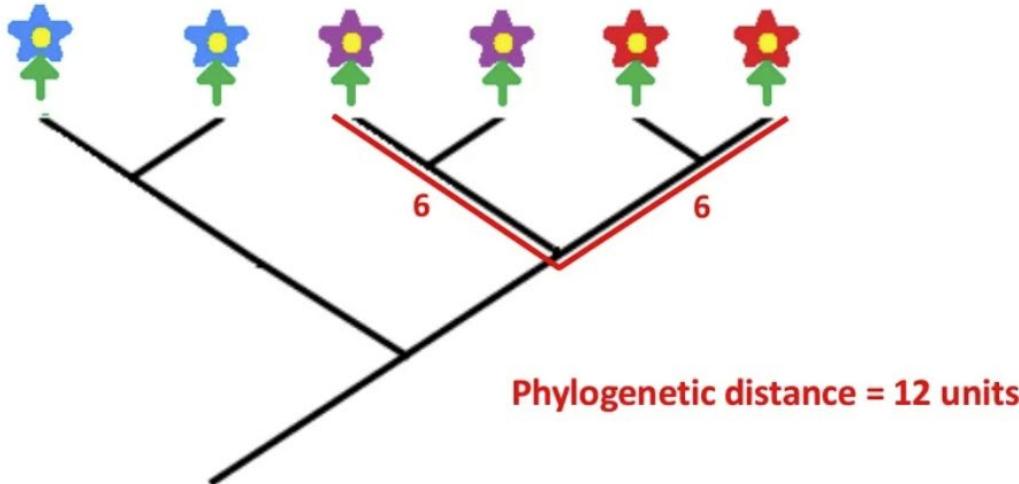
Overdispersed pattern = competition

Phylogenetic distance to estimate community relatedness



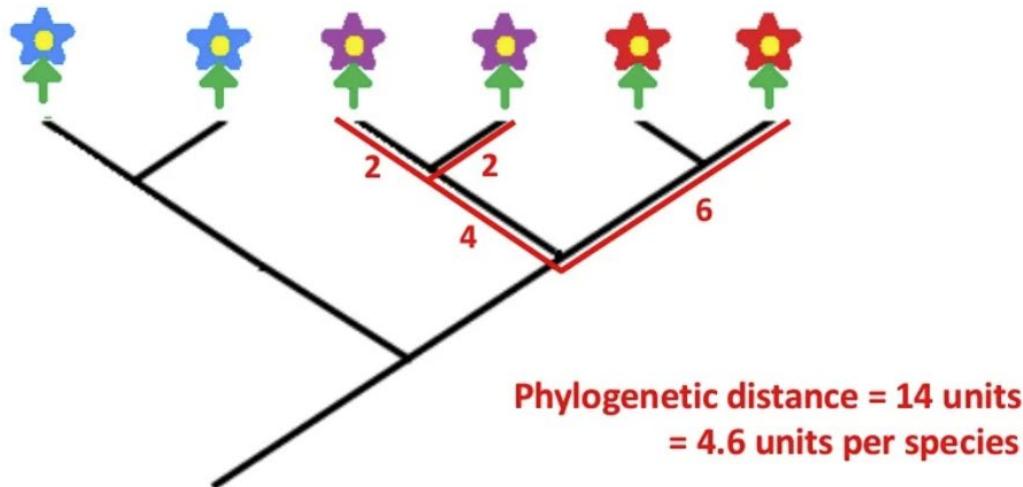
Because branch lengths are proportional to evolutionary time, we can sum them for the community

Phylogenetic distance to estimate community relatedness



Because branch lengths are proportional to evolutionary time, we can sum them for the community

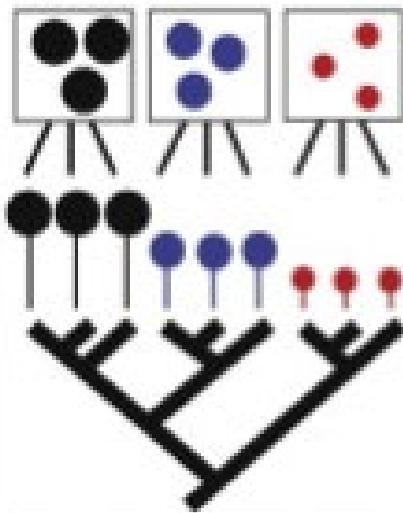
Phylogenetic distance to estimate community relatedness



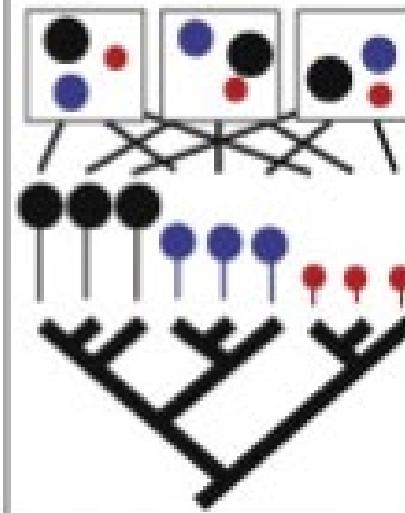
Because branch lengths are proportional to evolutionary time, we can sum them for the community

We can then compare our metrics to a null distribution of randomly assembled communities

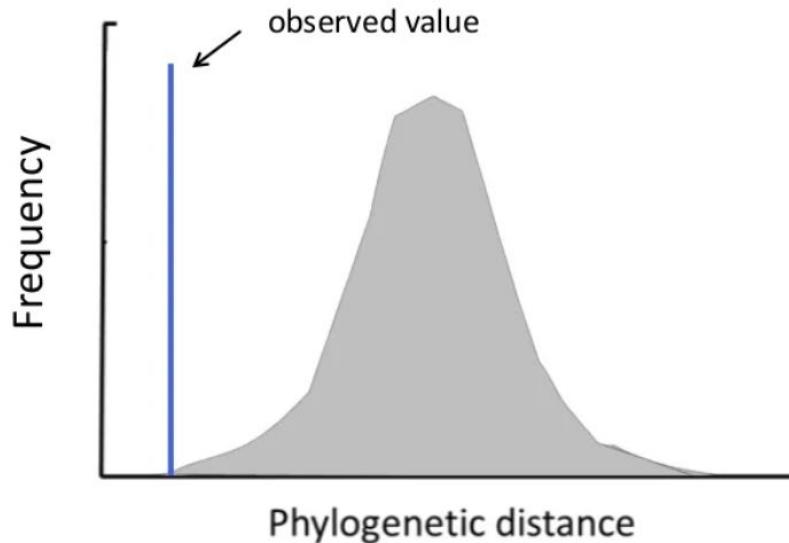
(a)



(b)

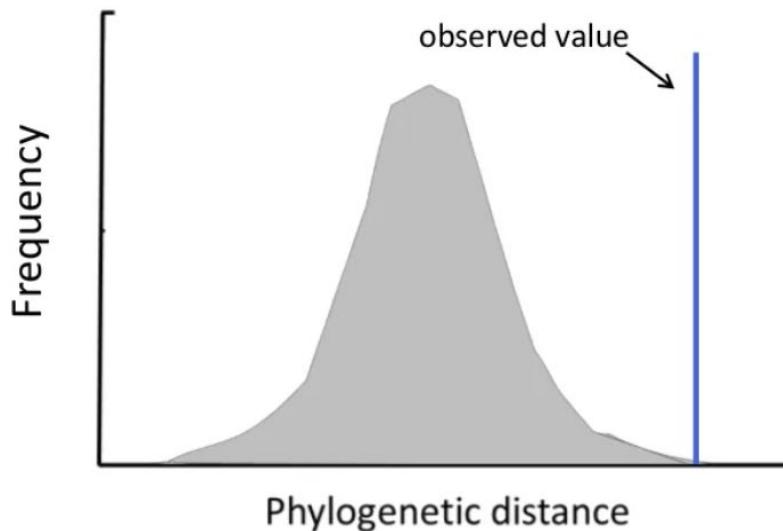


Null models in phylogenetic community analyses

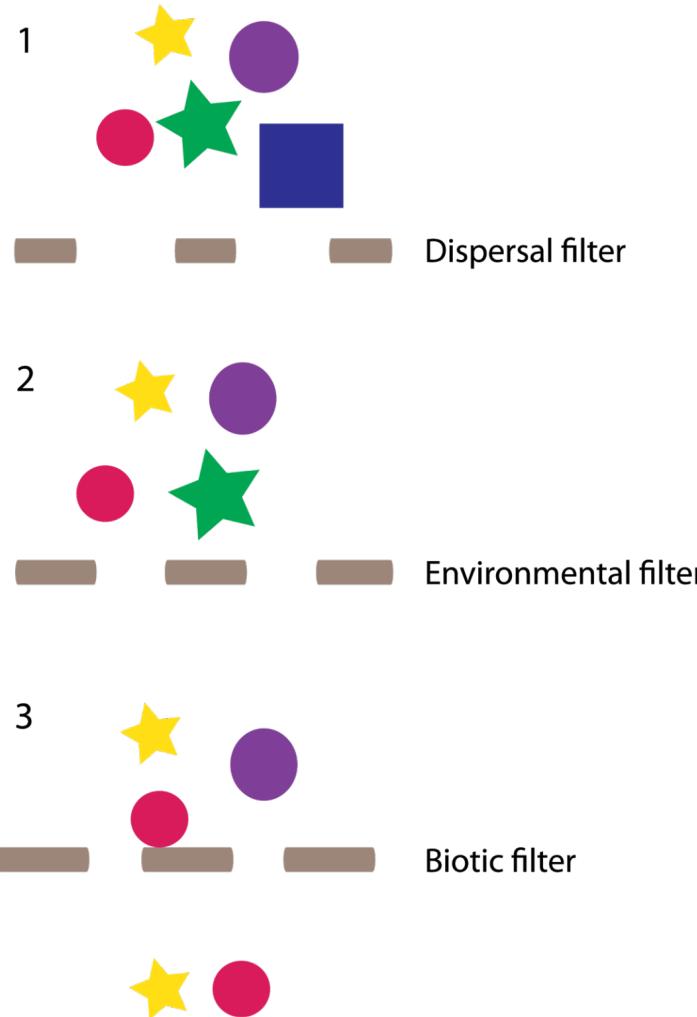


The observed value is significantly **less than** the null expectation under **environmental filtering**

Null models in phylogenetic community analyses



The observed value is significantly **greater than** the null expectation under **competition**



The process of community assembly