Brownian motion trait evol:



How to simulate brownian motion evolution (Dominique’s email):

In your case in particular, yes it could be simulated from a given phylogeny. But what you proposes seems ok, with a slight ajustment :

z\_t1 ~ N(z\_t0, sigma^2\_t0)

In other words, the trait of the descendant is centered on the trait value of the ancestor.

The alternative would be :

z\_t1 ~ z\_t0 + d\_t0

where

d\_t0~N(0, sigma^2\_t0)

Then,

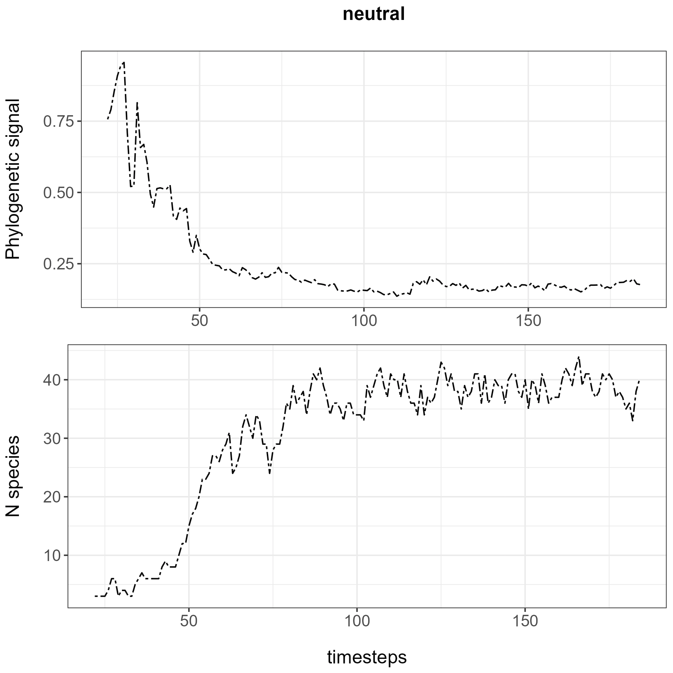
For drawing traits from new mutants, use the Brownian motion formula.

Then the probability of establishment is fixed around a mean

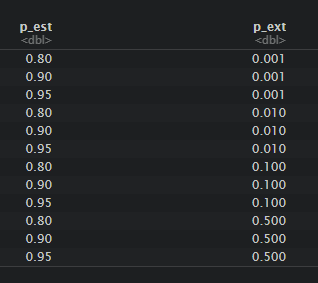
Then there is no extinctions

The way I draw mutant traits is ALREADY like that (normal distribution centered in the ancestor, with a given sd).

Dominique: what matters is whether or not there is selection afterwards. You are right, it is in the probabilities of establishment and extinction it matters.



I tried with different options



The highest value of p\_ext and lowest of p\_est that gives a successful simulation is

P\_est = 0.80

P\_ext = 0.1

Explore much more possibilities,

Find a way to save the results of each scenario

But for now, I see that it has the same effect with and without selection.

2) Come up with a method/scheme to test different scenarios and select a valid one:

🡪 1. Successful simulation (i.e. I can create a community)

🡪 2. The resulting community has properties that are observed in natural systems:

---- Network properties: connectance, modularity, degree distribution.(check papers foodweb models)

---- Network motifs: Python package of Stouffer that yields a table with their frequencies.

---- Choose natural foodwebs and measure all these metrics – obtain means and ranges and then compare how my networks compare to that. (check papers foodweb models).

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| Table X. Queries performance measures. Each query also contains the word “Quebec +…” | | | |
| Query | Fscore | Precision | Recall |
| *species* | *0.33* | *0.33* | *0.32* |
| *population + species* | *0.23* | *0.33* | *0.18* |
| *sites + species* | *0.17* | *0.31* | *0.12* |
| *occurrence + species* | *0.15* | *0.44* | *0.09* |
| *sampling + species* | *0.14* | *0.36* | *0.09* |
| *abundance + species* | *0.14* | *0.34* | *0.09* |
| *survey + species* | *0.09* | *0.35* | *0.05* |
| *collection + species* | *0.06* | *0.31* | *0.03* |
| *density + species* | *0.04* | *0.3* | *0.02* |
| *inventory + species* | *0.02* | *0.22* | *0.01* |
| *time series + species* | *0.01* | *0.25* | *0.01* |