

2/1/23

Intuitively I think the next step is neutral sums in comparison to the FS over a range of parameter values. but that's something you want to do with a little bit of strategy because there are a lot of parameters and the FS computation can be intensive.

Parameters:

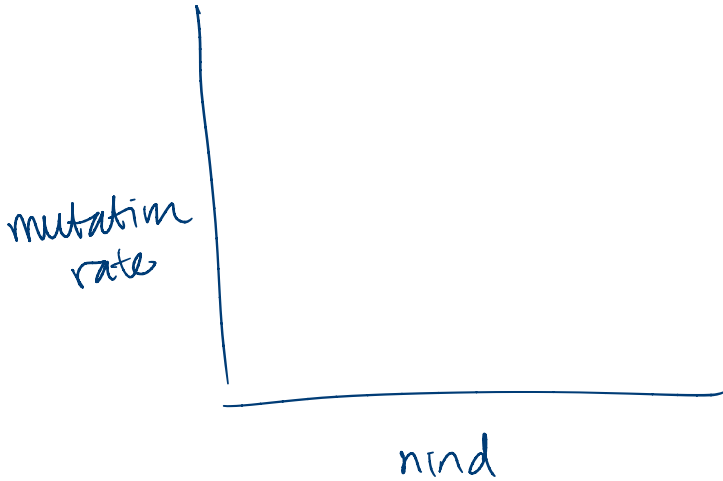
'ukb' uses mutation, mnd
can use a meta comm
but defaults not to

'mek' uses mutation &
immigration etc.

I think these are mostly
relevant for phylogenies;
there's no Δ species
richness / the SAD if you
use it. a new spp is a
new spp, right?

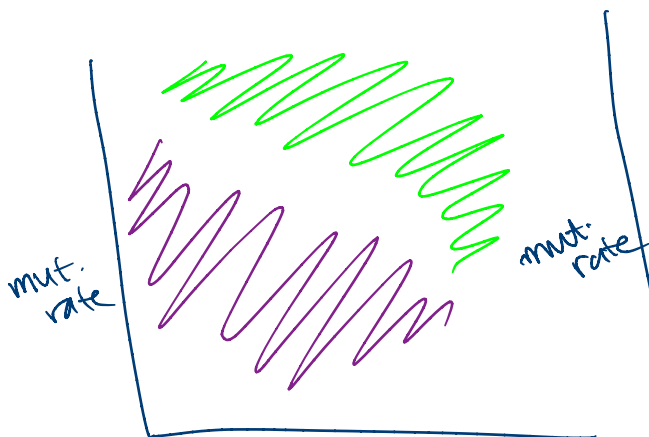
fs needs $S \neq N$
mek needs $S \neq N$

So what if you explored a matrix of

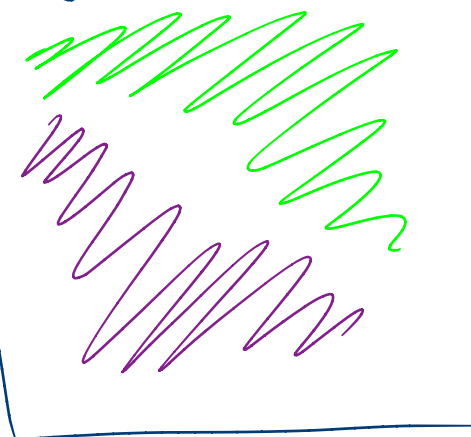


then a question is, does the mutation rate cease to matter for a given $nind$ at equilibrium or does the mutation rate modulate, for example, S @ equilibrium? (⊕ in addition to \underline{S} at equilibrium, e.g. erinness) I think it does.

So there's a first time curiosity



NO



XO

SO
(should be learnable)
(from ut)

FS of oil
(new)

~ unknown histograms ~

* at equilibrium.