if

If we know all the , then it is simple to sample as the FCD is going to be normal

It is going to be tricky to sample

It is going to be tricky to sample all the breaks if I have many possible values and species.

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#-------------------------------------------------------------------

Start creating this model by assuming that z is known. We can make it latent and estimate it later on.

#-------------------------------------------------------------------

We can integrate out and do our Gibbs sampler in the following way:

Furthermore, we can have breaks that are not species specific (i.e., instead of , we would have ). This should reduce the number of breaks we are estimating at the expense of decreasing our ability to fit well these data. On the other hand, this would enable a more straight-forward interpretation of .

Can we calculate our likelihood in a very fast way for our MH algorithms?

#-------------------------------------------------------------------

How do we interpret ?

Say we have unique values for , where the q-th unique value is given by . Furthermore, assume that an area is completely dominated by community 1. Then,

In other words, there is a one-to-one mapping between and . Therefore, results can be reported either as or, more intuitively, as .

Notice that if for species s and s\* in community c, this would imply that if location l was dominated by community c *if we have global break parameters*. On the other hand, if we had species specific breaks, that might not be true.

#-------------------------------------------------------------------

Can we integrate out ?

This reduces dependency between and but makes it very hard to sample . Not sure if this is useful