Lines 12070-12071 So the data augmentation is for the total population across all subpopulations not for each individual population ? maybe it doesn’t make a difference.

What do you gain by analyzing the data this way versus separately ? is the main advantage to share parameters since you are not explicitly linking the populations?

12106 so these are distinct groups of animals, and you have to know which group each individual belongs to. Is there a way that you could turn it around and try to estimate which group an individual belongs to? Is there a way to estimate what the groups are, for example if certain individuals are always captured near each other?

12142 How do we know what the correct structure is? Or by correct you mean the structure that we decided we want N to be? I understand if you want Ng to be Poisson M has to be Poisson as well. Maybe “desired” structure is a better word.

12165 how large is “large”?

12168-12169 so you lose information about the number of animals in each group the (B0) but regain it in the psi parameter which is counting the number of individuals in the group………..

12190: Fig 14.1 is very helpful, now I get it.

12223 “constrained” instead of constraint

12230 I suppose you could impose some sort of spatial autocorrelation term as well?

12238 FFCs “f—king forest Carnivores” as we called them in the forest service

12312 “by” instead of but

12338: isn’t this equation the same as 14.2.2

12344: So in this case can’t an individual show up in more than one group if groups=years.

12347 I think you are missing an “~” between beta0[t] and dnorm