1. The paper says to use unlinked loci; I have ddRAD snp data and retained only a single snp per locus. Should I consider pruning for LD? The Admixture manual suggests pruning data for LD using plink, removing snps where r^2 > 0.50
	1. Number of snps before pruning: 29556
	2. Number of snps after pruning: 22966
2. Layer contributions
	1. When K = 3, the third layer has an extremely small contribution (~0.1%). However, at K = 4, the fourth layer contributes moderately. Is this worth considering or should I ‘stop’ at the first value of K where layers begin to contribute marginally? (see Picture 1)
	2. I’m seeing increasing subdivision among layers at increasing values of K in my spatial model, but less so in the non-spatial model. How might I interpret this? The paper addressed spurious clusters in non-spatial models because it’s trying to partition clinal differences into discrete groups, but I’m less sure how to interpret the opposite case, which I seem to have (see Pictures 1 and 2)
		1. I reviewed the phi values for the spatial models at K = 3 and K = 4, based on an earlier question (`conStruct.results$chain\_1$MAP$layer.params$layer\_k`) (<https://github.com/gbradburd/conStruct/issues/48>)
		2. Phi values for K = 3 spatial model: K = 1: 2.41 x e-4, K = 2: 7.53 x e-5, K = 3: 5.07 x e-4
		3. Phi values for K = 4 spatial model: K = 1: 1.64 x e-5, K = 2: 4.09 x e-5, K = 3: 6.58 x e-5, K = 4: 9.36 x e-5
	3. Are the individual layers consistent across values of K for a specific model?
		1. For example, the contribution of layer 3 (when K = 3 and K = 4) is ~0.1%, while layer 4 contributes 27% when K = 4
		2. I used the function `match.layers.x.runs` prior to plotting the layer contributions, by doing so, I take it that, yes, layer 3 is the same across all values of K (for which it was assessed)
3. Layer covariance curves
	1. Is this mostly useful to visualize isolation by distance among my layers? Should I be identifying other important patterns?
	2. Looking at the graph of allelic covariance against distance, it looks like this spurious 3rd layer at K = 3 is driven by a single datapoint (Picture 3). Spurious in that it has such a marginal contribution. Combined with the small contribution of this layer, it seems that K = 3 is not biologically meaningful to describe my data; to point 2a above, should I give credence to K = 4 then?
		1. What matrix is used to build this graph? Can I look up what data point is driving the third layer? I see a point approximately the same value in each of your figures as well. Is this the allelic covariance of the sample with itself? l looked up one potentially applicable matrix (`conStruct.results$chain\_1$MAP$par.cov`), and each sample, when compared with itself, had a value approximately at this value; I’m not sure if this is what is being graphed, however
	3. If my layer covariance curves are mostly overlapping, how should I interpret this (Picture 3; layers 1 and 2)?
	4. Additionally, although the CV predictive accuracy of the spatial model outperformed the non-spatial model (indicative of IBD; Picture 4), this was marginal at K = 2. I don’t see a decay in correlation with distance in the layer covariance curves (Picture 3). Is this indicative of IBD in my system, then?
	5. Can I edit the output of the graphs? In the paper, for example, the data points on the layer covariance curves are color-coded
4. Compare two runs
	1. A naive R question, I think: how can I load two results datasets? I ran into trouble trying to ‘load’ results and assign the object a name, so I’ve only been able to load a single object at a time
5. How is variability among replicates for each value of K summarized?
	1. Ex., pie charts for a model at the same value of K look different among replicates; the code to graph pie charts (from the vignette) uses the ‘results’ object and MAP to plot the pie chart. If I understand correctly, this graphs the results with the maximum posterior probability across the replicates?