Interactive comment on "Bayesian calibration of terrestrial ecosystem models: A study of advanced Markov chain Monte Carlo methods" *by* Dan Lu et al.

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Let me first clarify, that I am not the author of the paper - I was asked to review the manuscript. My comment below relates to the review of Marko. An excellent review on methodology with respect to the implementation of the AM algorithm. I concur with most of the statements made. Very useful comments to further enhance the methodological aspects of this paper.

One thing I like to comment on and that is the Gaussian mixture target example in the paper and review. The AM method will work well if the modes of the target are close to each other. Indeed, the covariance matrix of the jump distribution will then provide sufficient "width" for the proposals to transition directly between the different peaks.

Yet, if the distance between the modes becomes large, then a direct jump becomes infeasible with a reasonable covariance matrix. I would like to refer to Figure 5 of 2016 DREAM manual paper that demonstrates this with a practical example (also discussed in earlier papers). Marko explicitly states all this in his review. In those cases, one can try to use an overly dispersed proposal distribution, but this is at the expense of a very low acceptance rate as many of the jumps will fall outside the target. Multimodality becomes more and more difficult to sample with increasing dimensionality, d, of the target.

In other words, if the authors want to show that AM cannot sample multimodal distributions then the two or three modes have to be taken further apart. I do agree with Marko that, in practice, if there are many modes that one needs to have some prior information about their existence; certainly if the distance between the modes is not constant but changes with location in the parameter space! for example,

p(x) = 1/6N_d(-10,1) + 3/6N_d(-2,0.5) + 2/6N_d(10,1),

where N_d(a,b) is the d-variate normal distribution with mean a and covariance matrix b. This distribution will be harder to sample; AM will not be able to do a good job - will converge either to one mode or otherwise be highly inefficient (very large covariance matrix of jump distribution –> low acceptance rate -> even more problematic for large d). DREAM will also find it difficult as the two modes have a different separation of 8 units and 12 units respectively (and 20 for that matter). Try it out.

Regards, Jasper