The manuscript "A Bayesian Penalized Hidden Markov Model for Ant Interactions" addresses an important problem in movement ecology. As technology has improved, movement data can be collected at a fine temporal scale with many behaviors of interest occurring over multiple observations. Application of a discrete-time hidden Markov model allows the possibility for the process to rapidly alternate between states, which runs counter to biological intuition. The authors instead present a penalized continuous-time HMM to analyze ant interactions and demonstrate that the decoded state sequences exhibit biologically realistic behaviors.

For this particular application it is clear that this approach returned much better results, as measured by the decoded state sequence – assuming small variability in possible state outcomes. The penalized approach for the off-diagonal entries enforces the belief that more mass should be placed on larger state-duration times that could possibly occur without the penalization. This penalization, however, simply distributes the probability to larger state-dwell times as it assumed to follow an exponential distribution. For instance, below are two plots of the state-dwell times for state 1, given the results in the paper. On the right we have the curve for the geometric distribution, which connects the probabilities of  $x=1, 2, \ldots, 300$ , and on the left the curve for the exponential distribution. Moving to continuous time, along with penalization, does seem to place more probability on a wider variety of state-dwell times.

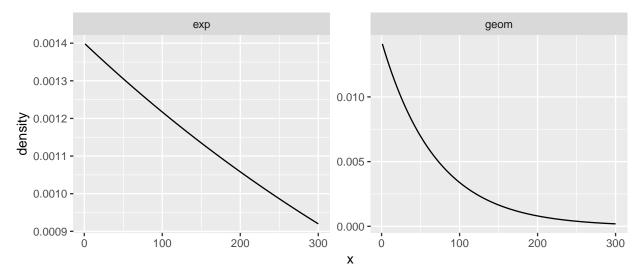
```
library(ggplot2)
library(tidyverse)

x <- 1:300
dx_geom <- dgeom(x, 0.0143)
dx_exp <- dexp(x, 0.0014)

dens <- data.frame(x = x, geom = dx_geom, exp = dx_exp)

data <- gather(dens, key, density, -x)

ggplot(data, aes(x, density)) + geom_line() + facet_wrap(~key, scales = "free_y")</pre>
```



However, it's not clear to me that simply moving to continuous-time, along with this penalization, solves the issue of not allowing such short state-dwell times (the exponential distribution is the continuous analog of the geometric distribution). In fact, simulating from the continuous-time model would still produce data that switch rapidly across states. What has typically been done in the literature to resolve this issue has been to move to a hidden semi-Markov model, which can be expressed in discrete or continuous-time. Has

this been considered?

Regarding the penalization, typically this is used because there is belief a priori that not all of the signals are different from zero. As such, there is a desire to shrink some of the signals to zero. I'm curious if the approach to penalization here could be better suited to other problems that could occur in HMMs: selecting the number of states (a subset J from a pre-defined N) or shrinking some entries of the transition matrix when there are a larger number of states defined but not all transitions occur often. Just some ideas. At the same time, shrinking some of the transition entries toward zero, or equating them to zero, has strong implications about the dynamics of the system.

Overall, I think the idea is interesting and it's clear that the decoded state sequences do produce much more realistic results than the discrete-time HMM without the penalization. At the same time, the methodology seems to be primarily motivated by the decoded state sequences under both approaches. The results here, however, are not sufficient to justify that the proposed methodology prohibits, to some extent, rapid state-switching, it does not. The type of data that the fitted continuous-time model can produce does still allows for rapid state-switching, even if that's not what occurred in the ant data set. The argument would be more convincing if the probability of switching after a single or a few seconds was in some manner shrunk toward, though not equal to, zero. The state-dwell time distributions are not discussed enough, even though this behavior seems to be the primary focus of the manuscript.

## Specific Comments

- Page 4, Lines 9-10: The observed data serves as a proxy for behaviors of interest. A slight detail but important to convey nonetheless.
- Page 4, Line 22: Some detail about what an HMM actually is could be useful for those not familiar with them.
- Page 4, Line 28/29: What does best imply here? Viterbi?
- Page 4, paragraph 2: Although I've mentioned the state-dwell time distribution, another reason that there could be rapid state-switching is because the estimated state-dependent distributions don't capture the intended behavioral states well.
- Page 7, 23/24: The MCMC should be initialized with a variety of starting values, not just one.
- Page 7, 28/29: There need to be formal checks of the behavior MCMC chain.