The goal of this model is to estimate breakpoints such that each time segment is relatively homogeneous in relation to the visitation frequency of individual grid cells.

We start by letting denote the grid cell label for individual i at time t. Each potential model is characterized by a set of breakpoints. In other words, model consists of breakpoints , where , where is the number of observations for individual i. Given a particular model , its breakpoints define time segments and we assume that, for any given time segment c, we have that:

where is a vector of probabilities that sum to one. Our prior is given by:

To enable the algorithm to visit multiple models, we need to integrate out the parameters. Therefore, the probability of time segment c, after integrating out , is given by:

where is the number of times the animal was seen in location l in time segment c. Based on this result, we can define the probability of model as:

In this expression, the prior probability for model k (i.e., ) is given by:

**Birth:**

When we increase the number of breakpoints, we get the following ratio:

Notice that the proposal distribution in this case is given by whereas the reverse move is

Therefore, we get:

**Death:**

When we decrease the number of breakpoints, we get the following ratio:

Notice that the proposal distribution in this case is given by whereas the reverse move is

Therefore, we get: