

# Supplementary Material 1. HMM analysis from: Harvesting trajectories in large-scale coffee plantations: ecological and managment drivers and implications

Mora Van Cauwelaert et al., 2023

## 0. Introduction to HMM

Hidden Markov models (HMMs) are models in which the distribution that generates an observation  $Z_t$  depends on the state  $S_t$  of an underlying and unobserved Markov process (Fig.1) (Zucchini 2016). In this sense, the observations  $Z_t$  can be retrieved from one to multiple distributions related to the number of states. In the context of animal movement, the state  $S_t$  is interpreted as a proxy for the behavioral state of the animal (e.g. foraging, exploring; (Michelot, Langrock, and Patterson 2019)). The observations  $Z_t$  are bivariate time series ( $Z_t = (l_t, \phi_t)$ ) where  $l_t$  is the step length (the Euclidean distance) and  $\phi_t$  the turning angle, between two successive locations Zucchini (2016). Biologically speaking, these models try to include the process where the movement of agents (e.g. short or large steps) depends on its behavior. With these models, we can define the different originary distributions and then decode the most likely sequence of states along the trajectory of an agent, its average time within a state, and the number of switches between states.

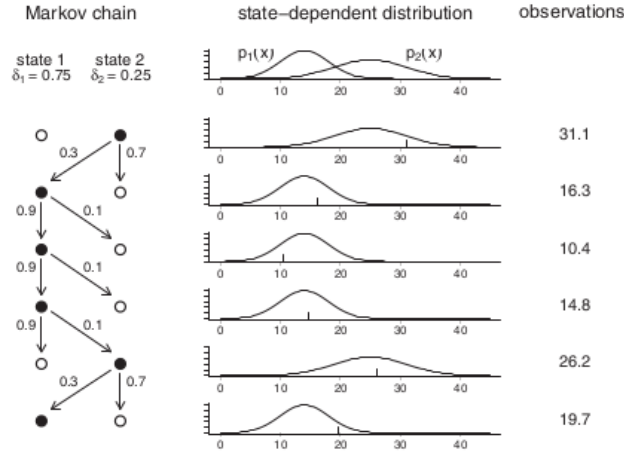


Figure 1: Process generating the observations in a two-state HMM. The chain followed the path 2, 1, 1, 1, 2, 1, as indicated on the left. The corresponding state-dependent distributions are shown in the middle. The observations are generated from the corresponding active distributions. Taken from (Zucchini, 2016)

Here we used the *movehmm* library (Michelot, Langrock, and Patterson (2019)) to i) fit the most likely distributions and HMM to the harvester movement data, ii) describe the different states and iii) decode and compare the sequence of states in the two farms (Ecological and Conventional) with the Viterbi algorithm.

# 1. Fitting of HMM

## 1.1. Preparation of data

We loaded *ggplot2*, *dplyr*, *tidyverse* and *movehmm* libraries. We then loaded the data of the trajectories and did some punctual modifications to it. We had in total 12 trajectories, with  $(x, y)$  coordinates (Fig. 2).

```
## Movement data for 12 tracks:
## E_1 -- 100 observations
## E_2 -- 80 observations
## E_3 -- 107 observations
## E_4 -- 76 observations
## C_1 -- 77 observations
## C_2 -- 70 observations
## C_3 -- 115 observations
## C_4 -- 63 observations
## C_5 -- 97 observations
## E_5 -- 104 observations
## C_6 -- 88 observations
## E_6 -- 158 observations
## No covariates.
```

A first assumption for the analysis was made: we took these time irregular trajectories (where each point represents one different tree, but where the time between two trees is variable) and treated them as a regular trajectories. This aimed to analyze the change in the movement of the workers during a day, generated by the underlying pattern of trees or by the differences in the fruit charge and ripening synchronicity. We convert this database into a *movehmm* object where the step distance  $l_t$  and the relative angle  $\phi_t$  between the  $(x, y)$  coordinates is calculated (table 1). Now, for the following analysis, we only took the step distance and treated both farms as one. We decided to exclude the angles because they didn't have a biological meaning for irregular trajectories. The input for the analysis is then the histogram presented in Fig. 3. The values of the steps lengths ranges from 1 to 117, with a mean of 5.14 and a median equal to 4.

Table 1: First lines of the *movehmm* object with harvester data

| ID  | step     | angle     | x   | y   |
|-----|----------|-----------|-----|-----|
| E_1 | 3.605551 | NA        | 146 | 117 |
| E_1 | 3.000000 | -2.158799 | 143 | 115 |
| E_1 | 3.605551 | 2.553590  | 143 | 118 |
| E_1 | 2.236068 | -1.446441 | 141 | 115 |
| E_1 | 5.000000 | 2.034444  | 139 | 116 |
| E_1 | 3.605551 | -2.158799 | 139 | 111 |

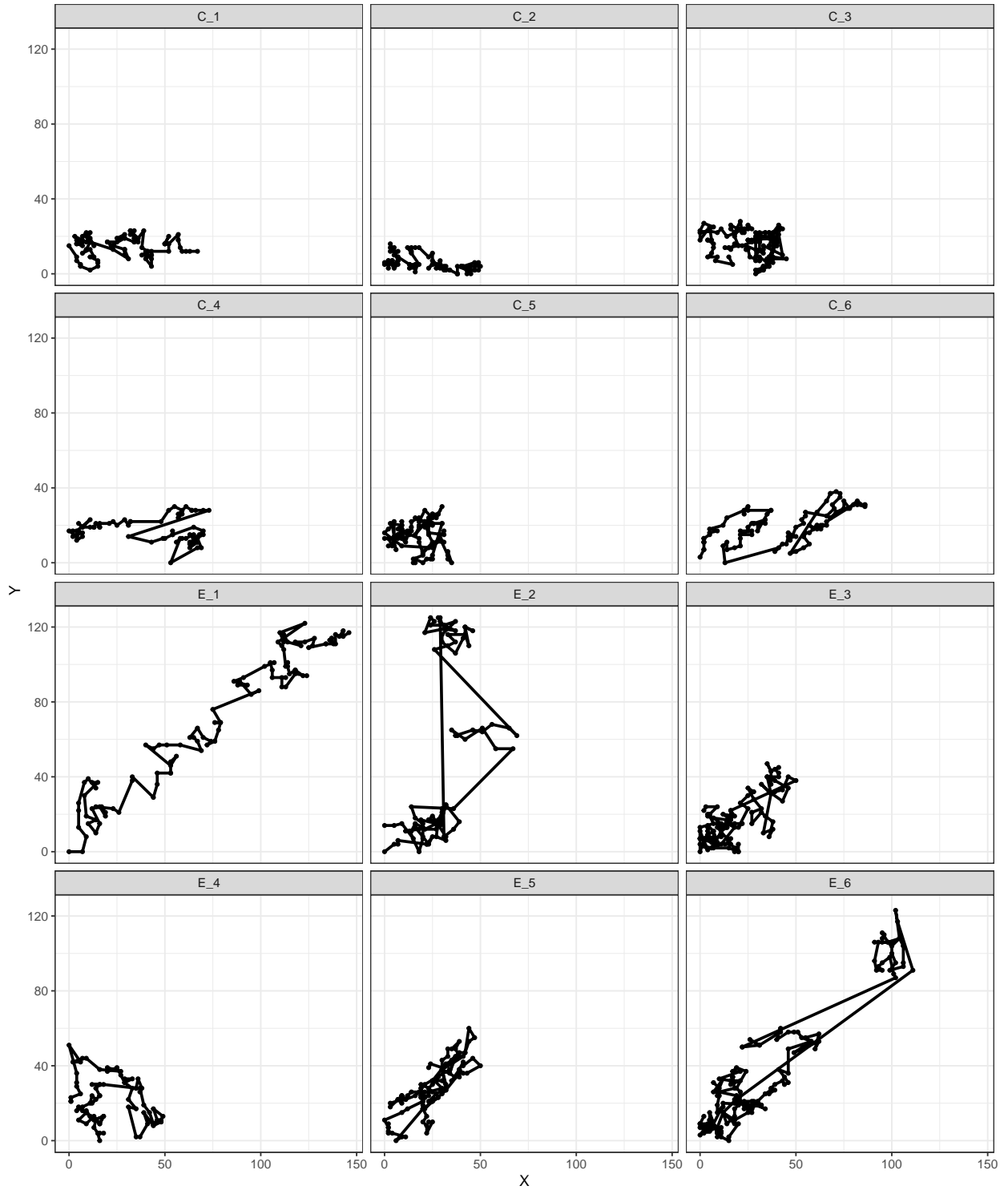


Figure 2: 12 trajectories of harvesters. The green line represent the Conventional Farm (C) and the blue line the Ecological Farm (E). Each black dot represent a tree

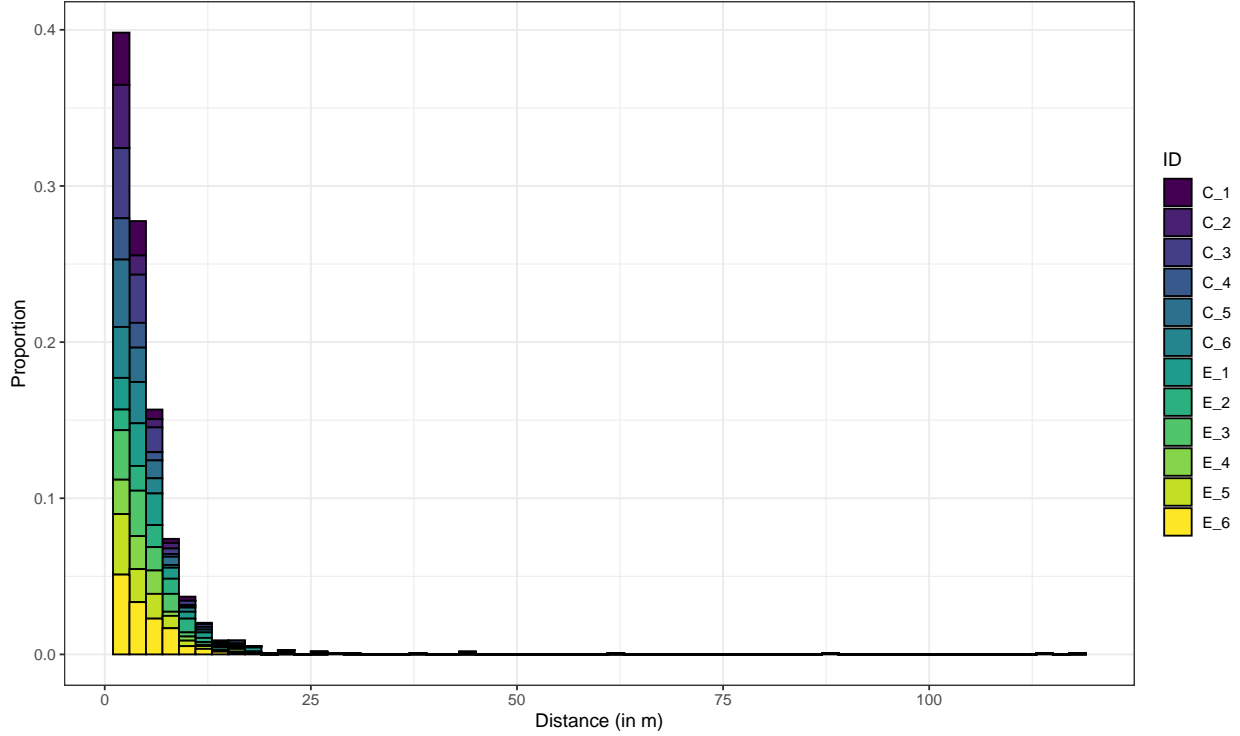


Figure 3: Histogram of the steps lengths divided by the different trajectories.

## 1.2. Fitting of the data

The algorithm of the *movehmm* library uses:

- a predefined number of states. Here we will use two. But the algorithm also explores the case when both states are equal.
- a defined family of distributions. Here we will try to fit two different exponential families (*gamma* and *weibull*).
- prior parameters for each of the distributions, for each state.
- The observations (step-lengths) (the data of harvesters)

With these inputs, the algorithm extracts the most likely two-state-distributions with their respective parameters (within the predefined family of distributions) from the data. During the fitting process, the algorithm uses the maximum-log likelihood and the *forward algorithm* (a recursive algorithm starting with the prior distributions; (Zucchini 2016)).

We ran a loop to fit the data to two different families (*weibull*, and *gamma*) and in order to avoid local maximal likelihoods, we swapped 1000 combinations across a range of prior parameters for each model (Michelot, Langrock, and Patterson 2019). For the *gamma* distribution, the minimum and maximum values of each range were chosen to encompass the full distribution (including values below and over the mean). For the *weibull* distribution, the maximum shape considered the left-skew shape and the scale was chosen to include the 120m long steps (see the ranges in table 2). It is important to note that these are only priors guesses, and the real parameters can outbound these limits. Many of these combinations of prior parameters converged to the same final distributions.

Table 2: Minimum and maximum values of the prior parameters for each distribution

| value | gamma.mean | gamma.sd | weibull.shape | weibull.scale |
|-------|------------|----------|---------------|---------------|
| min   | 0.1        | 0.1      | 0.0           | 0.1           |
| max   | 20.0       | 20.0     | 2.7           | 15.0          |

Some combinations resulted in distributions with zero variance. We decided to remove those cases as they did not make any biological sense. We then plotted the minimum negative log of the likelihood without these outliers. The minimum negative log-likelihood is equivalent to the maximum likelihood. Almost all the combinations of prior parameters converge to two models with equivalent minimum likelihoods (Fig. 6). We chose, for each family of distributions the model that had the minimum AIC value (table 3).

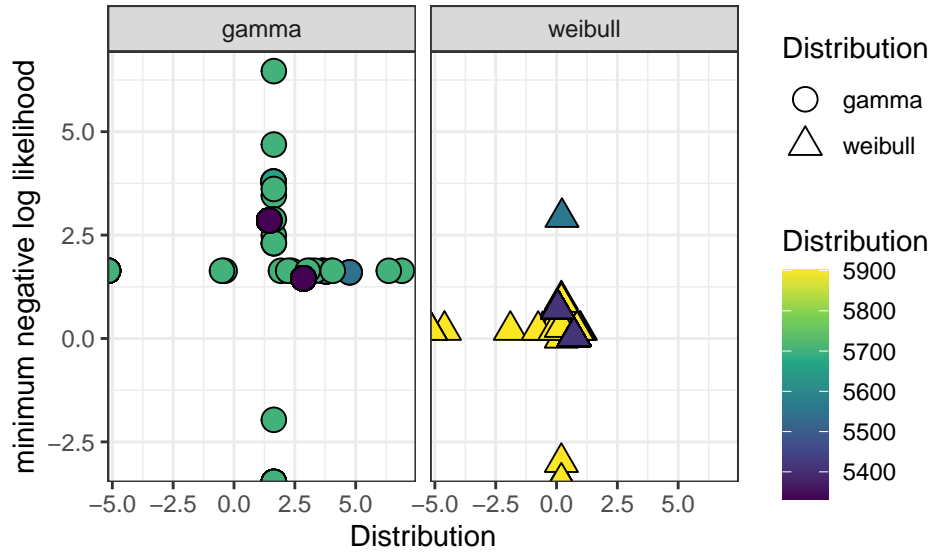


Figure 4: Parameters obtained\*

Table 3: Best models for each of the distributions. We added the prior parameters, the likelihood, AIC criteria and the final parameters. pr:prior, st1: state 1, p1: parameter 1 (shape for weibull and mean for gamma, p2: parameter 2 (scale for weibull and sd for gamma).

| model   | pr_st1_p1 | pr_st1_p2 | pr_st2_p1 | pr_st2_p2 | minNegL | AIC     | s1_p1 | s1_p2 | s2_p2 | s2_p2 |
|---------|-----------|-----------|-----------|-----------|---------|---------|-------|-------|-------|-------|
| weibull | 2.20      | 0.80      | 5.10      | 13.20     | 2700.20 | 5414.39 | 2.05  | 4.71  | 1.05  | 14.45 |
| gamma   | 1.94      | 5.61      | 6.46      | 1.15      | 2659.24 | 5332.48 | 17.34 | 15.18 | 4.28  | 2.25  |

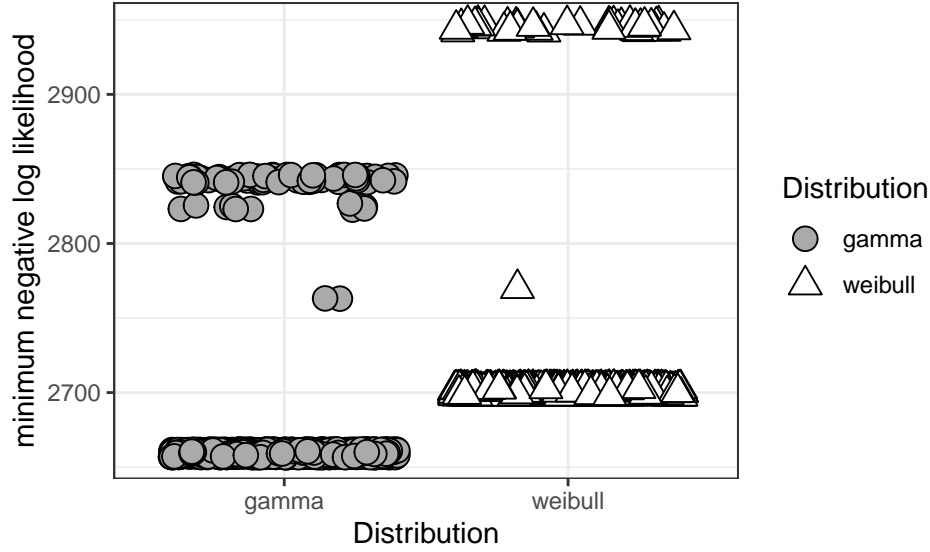


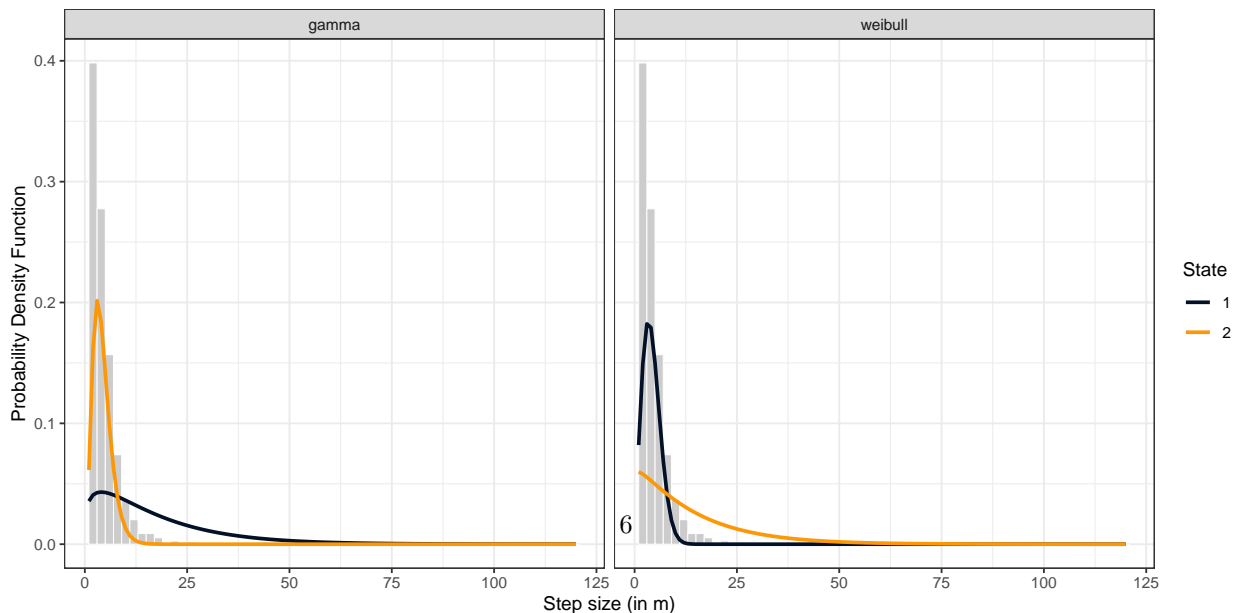
Figure 5: Minimum Negative Log-likelihood per combination of prior parameters for two different distributions

## 2. Description of the states, for each studied distribution.

We plotted the two state distributions for *gamma* and *weibull* families with the obtained parameters (see figure. 7 and table 4 for the final parameters). For both families, one of the states produced a distribution that encompass all highly frequent short steps and falls abruptly for size steps bigger than 13 m. The other state generates a long tailed distribution with a lower probability of short steps (compared to the other distribution) and a non zero probability for steps bigger than 13 m (Fig. 7 and table 4).

Table 4: Final parameters for both gamma and weibull distributions.  
For the gamma distribution  $\alpha = \mu/\sigma^2$ ;  $\beta = \mu^2/\sigma^2$ ;  $\theta = 1/\beta$ .

| Parameter        | Gamma_St1 | Gamma_St2 | Weibull_St1 | Weibull_St2 |
|------------------|-----------|-----------|-------------|-------------|
| $\mu$ (mean)     | 17.30     | 4.30      | –           | –           |
| $\sigma$ (sd)    | 15.20     | 2.25      | –           | –           |
| $\alpha$ (shape) | 1.30      | 3.62      | 2.05        | 1.05        |
| $\theta$ (scale) | 13.30     | 0.84      | 4.71        | 14.5        |
| $\beta$ (rate)   | 0.07      | 1.18      | –           | –           |



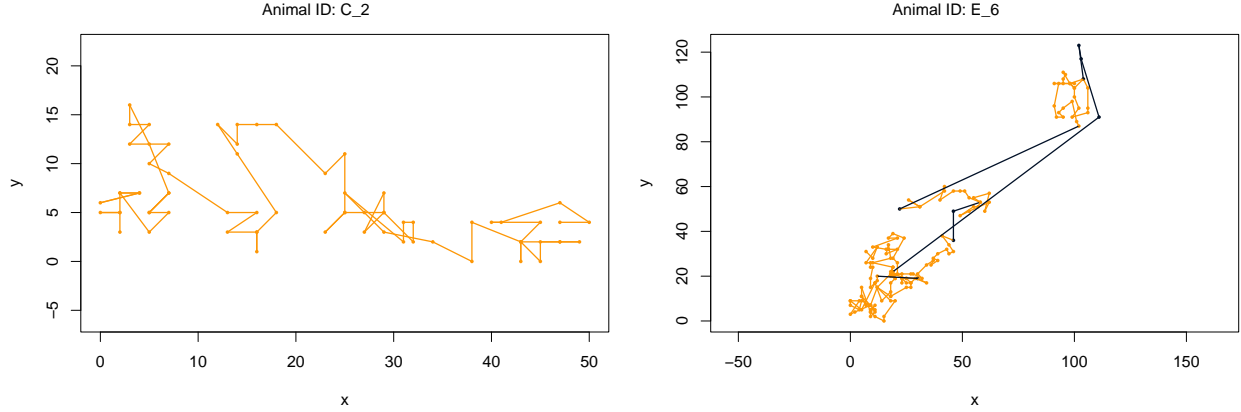


Figure 7: Distribution of states  $St$  along two trajectories. Each color follow the code of colors of Fig.7)

### 3. Probabilities of states per farm

and the most likely sequence of states (assuming a markov process).

We finally plotted the sequence of the most likely states along each of the trajectories (Fig. 9) and estimate the probability of the most unlikely state (state 1, that represent the relocalization of the workers in the plot) according to the farm the trajectory belonged to (Fig. 10). We note that the percentage of steps from state 1 correlates with the identity of the farm (Fig. 10): 4 out of 6 trajectories that belong to the Ecological Farm, presented a higher than the mean percentage of longer steps, compared to the Conventional Farm, where 5 out of 6 were below the mean.

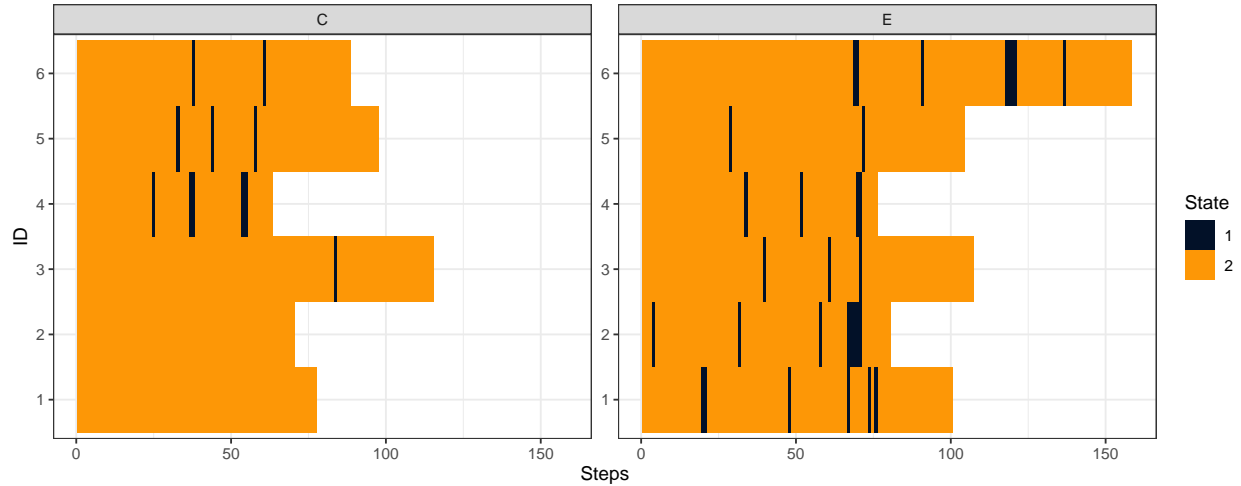


Figure 8: Sequence of states along the trajectory in two different farms (C: Conventional, E: Ecological)

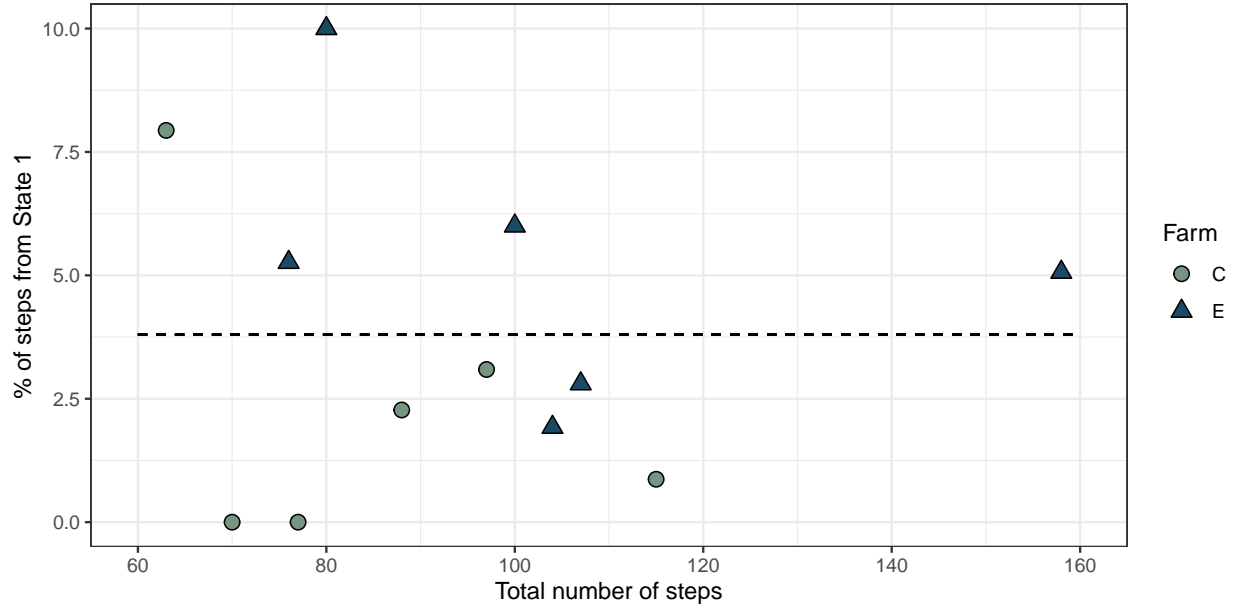


Figure 9: Relation between the probability of state 1, the total number of steps and the farm (C: Conventional, E: Ecological). The dashed line represent the average percentage of steps that belong to state 1 (3.8%).

#### 4. References

- Michelot, Théo, Roland Langrock, and Toby Patterson. 2019. “moveHMM: An r Package for the Analysis of Animal Movement Data.” *ArXiv Preprint*, 1–24.
- Zucchini, MacDonald, W. 2016. *Hidden Markov Models for Time Series: An Introduction Using r*. Chapman; Hall/CRC Press.