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Dear Prof. S.E. Jørgensen,

Revision Submission of Paper (Ref.: Ms. No. ECOMOD2181):

Title: **USING ACCELEROMETER, HIGH SAMPLE RATE GPS AND MAGNETOMETER DATA TO DEVELOP A CATTLE MOVEMENT AND BEHAVIOUR MODEL**

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Category: Original research paper (regular paper)

We thank the reviewers for their valuable comments. The paper has been significantly revised according to the reviewers' suggestions. We are now submitting the revised paper for your consideration. Please let me know if you need other materials. Thank you.

Yours Sincerely,

Ying Guo
(on behalf of all 6 authors)

USING ACCELEROMETER, HIGH SAMPLE RATE GPS AND MAGNETOMETER DATA TO DEVELOP A CATTLE MOVEMENT AND BEHAVIOUR MODEL

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Abstract

The study described in this paper developed a model of animal movement, which explicitly recognised each individual as the central unit of measure. The model was developed by learning from a real dataset that measured and calculated, for individual cows in a herd, their linear and angular positions and directional and angular speeds. Two learning algorithms were implemented: a Hidden Markov Model (HMM) and a long-term prediction-learning algorithm. It is shown that a HMM can be used to describe the animal's movement and state transition behaviour within several "stay" areas where cows remained for long periods. Model parameters were estimated for hidden behaviour states such as relocating, foraging and bedding. For cows' movement between the "stay" areas a long-term prediction algorithm was implemented. By combining these two algorithms it was possible to develop a successful model, which achieved similar results to the animal behaviour data collected. This modelling methodology could easily be applied to interactions of other animal species.

Key words: behaviour modelling; animal movement; sensor networks; Hidden Markov models; wireless; precision ranching

1. Introduction

Grazing animals utilise a significant proportion of the global landscape, for example they occupy in excess of 50% of the Australian landscape ranging from improved pastures through to extensive rangeland environments (Gramshaw and Lloyd, 1993). Interactions between herbivores and their environments are spatially constrained and highly variable (Ash and Stafford Smith, 1996; Beecham and Farnsworth, 1999; Schwinning and Parsons, 1999; van de Koppel et al., 2002). Wild herbivores are not constrained spatially unless they exist in parks that are fenced, where they are managed in ways similar to livestock. This paper focuses on livestock modelling since the GPS and magnetometer data were collected from farmed cattle that were contained by fences. Understanding sustainable grazing systems requires modelling methods that can accurately describe the individual components of herbivore behaviour (e.g. foraging, bedding, ruminating, relocating etc.) as they interact across space and time. Accurate behavioural models provide important information about diet selection, herbage intake and how the grazing animal modifies the environment. Grassland ecosystems, which include herbivore behavioural interactions provide an ideal contextual scenario for applying innovative complex modelling procedures (Hastings and Palmer, 2003).

Previously, deterministic modelling of herbivore foraging has provided insights into the underlying processes that regulate plant animal interactions. However, methods that have used differential equations based on predator prey interaction models have the implicit and unrealistic assumption that foraging is evenly distributed in space and time (Noy-Meir, 1975). Spatial and temporal processes have been used to extend the deterministic approach and have included bite scale patches with variable foraging intervals (Parsons et al., 2001; Schwinning and Parsons, 1999). Although incorporating more realistic spatial and temporal models as the extension of deterministic models to include stochastic space and time within a stochastic mode of operation, it assumes animals defoliate bite sized patches randomly irrespective of patch state and relative location. The grazing animal's feeding choice is determined by its location in relation to the spatial arrangement of sward structural components (Grünbaum, 1998). Recent modelling has used spatially explicit methods to describe search rate and search distance, the results demonstrated the importance of spatial constraints in determining overall systems outcomes (Marion et al., 2005; Swain et al., 2007). Earlier authors have used Markov chain Monte Carlo methods within a Bayesian framework to estimate parameters for dynamic spatial models of animal behaviour using data from a field experiment exploring faecal avoidance in dairy cows (Marion et al. 2007) and a study of sheep feeding behaviour in an indoor arena (Walker et al. 2006).

This paper explores a model of cattle movement. The modelling approach was compared to behavioural data collected from cattle and could be applied to interactions of other animal species. The modelling methods estimate behavioural parameter using high sample rate spatial monitoring of cattle movement.

Monitoring data (as well as empirical data derived from numerous hours of video and human observation) shows that cows like to stay in some areas for longer periods of time than other areas (Bailey 1995, Bailey 2004). We refer to those regions where cows like to remain for prolonged periods (> one hour) as *stay* regions. Examples of stay regions could be boundary edges, shade and watering points. The remaining parts of the paddock were used to travel between stay regions and are referred to as travel regions. The cattle behaviour patterns vary between stay regions and travel regions. Animals stayed in different regions at different times of the day and each individual animal normally has its own behaviour pattern in each region. In the travel region, six cows followed almost the same trajectory. The travel regions were generally larger than the stay regions, so it is more efficient to use large scale modelling methods for travel regions. To develop a realistic model, two different modelling methodologies were implemented.

Hidden Markov Models (HMMs) were used to predict individual cattle behaviour in each stay region. MacDonald and Raubenhermer (1995) modelled behaviour sequences using a HMM where the underlying unobserved behaviour was interpreted as motivational states; the current animal state (e.g. hungry) provided an indication of both the current behaviour (foraging) and associated behaviours (e.g. relocating, drinking, etc.). Franke et. al. (2004) also used HMMs to analyse the behaviour of caribou, the probability transformation between the inferred behavioural states (bedding, foraging, relocating) was derived from observed state data (travel directional speed, travel direction, etc). The estimation procedure for HMM is based on expectation-maximization (EM) algorithm leading to an optimal state sequence.

It was also observed that animals travel directly from one stay region to another. Motion prediction can be used for objects that are able to perform trajectories as a result of an internal motion planning process or decision mechanism (e.g. persons, animals and robots). It is assumed that such plans are made with the intention to reach a specific goal, such as a water or shade area. In addition to the inferred behavioural states long-term trajectory prediction has been used to estimate future states using motion prediction (Vasquez et al. 2005). The animal trajectory and the association with inferred behavioural decisions was challenging, however, solving this problem has enabled more accurate animal behaviour models. Modelling methods that involved a two-stage process, model fitting and prediction, enabled an observed state model to be constructed and simulation estimates of future states derived based on the current knowledge (e.g. Osentoski et al. 2004). Vasquez et al. (2005) presented an on-line learning approach which was able to learn using HMMs; parameters were estimated incrementally as each observation became available using a Growing Neural Gas algorithm (Fritzke 1995). A similar methodology was used in the current study, however, rather than using HMMs, animal movement was predicted using a clustering algorithm and Maximum Likelihood.

By combining HMMs and long-term trajectory prediction, a novel methodology is presented to model cattle's individual and herd behaviour on the basis of GPS and magnetometer data from a wearable collar. Based on such models, farmers and animal scientists can potentially select for desirable qualities that were previously hard to measure or not fully understood.

2. Methods

2.1 Data collection

The dataset used for the modelling came from six cows whose GPS position was recorded every 10 seconds for 4 days in July 2005. Each animal had a monitoring collar fitted which consisted of a Fleck™ (Sikka et al., 2004) with wireless networking. The Fleck™ was specifically designed for applications in animal tracking and control (Swain et al., 2007; Butler et al., 2006; Marsh, 1999; Tiedemann et al., 1999). The collar had a number of sensors including GPS, 3-axis accelerometer, 3-axis magnetometer and data storage capacity. The animals were able to move freely around a seven hectare paddock during data collection. The collar number, time (seconds), latitude and longitude were collected and saved in the dataset (Guo et al., 2006; Wark et al., 2007). The dataset was used to learn about the properties of animal movement.

Longitude and latitude were converted to meters in the east and north directions which with time were used to show the animals' changing locations. Inter-animal distances were calculated from the positional data.

The four day dataset collected from the collar animals was split in half. The first half was used to develop the model and the second half for validation. The model training data-set was further divided and used to describe the activities within stay regions using HMMs and the movement between stay regions using long-term track prediction learning methodologies. The modelled animal movement data were implemented within a Matlab simulator to compare simulated results with the real data. Details of the model are as follows.

2.2 Model development

The model was developed using a combination of HMMs and long-term track prediction learning methodologies.

The model used a hierarchical structure (Figure 1), including several sub-models:

1. The study area was separated into sub-areas of interest (stay regions and travel regions) according to GPS data as well as empirical data derived from numerous hours of video and human observation.
2. For each stay region, HMMs were generated for each cow using the corresponding observed data collected from its monitoring collar. All the HMMs were time-dependent: each day was divided into three time periods (6 am to 2 pm, 2pm to 10 pm, and 10 pm to 6 am) according to a cow's distribution in the appropriate zone. A HMM model is developed for each time period.
3. For transition periods, the modelled cow moved from a stay region into a travel region or vice versa (from a travel region into a stay region) according to a 2D Gaussian distribution estimated from the observed positional data.
4. The path by which the cow moved from one stay region to another was generated using a long-term prediction learning process.

More details on the HMM design, the long-term prediction learning process and the transition process between models are provided in the following sections.

2.3 A Hidden Markov Model

Hidden Markov Models (HMMs) were chosen to model the stay regions because they were able to infer optimal hidden states from observational data. A HMM is a statistical model in which the system being modeled is assumed to be a Markov process with unknown parameters. A Markov process is a mathematical model for the random evolution of a memory-less system (Bharucha-Reid 1960). That is, the likelihood of a given future state at any given moment depends only on its present state and not on any past states. The most common HMM structure is a finite set of states, each of which is associated with a (generally multidimensional) probability distribution (Rabiner 1989). Transitions among the states are governed by a set of probabilities called transition probabilities. In a particular state an outcome or observation can be generated according to the associated probability distribution. It is only the outcome, not the state, that is visible to an external observer and therefore the states are said to be "hidden". To define a discrete HMM, three basic components are needed:

1. A vector containing the prior probability of each hidden state: the initial state distribution, $\pi = \pi_i$, where $\pi_i = p\{q_0 = i\}$, for $1 \le i \le N$. Here N is the number of states of the model, and q_0 denotes the initial state.
2. A set of state transition probabilities $A = a_{ij}$. Defined as

$$a_{ij} = p\{q_{t+1} = j \mid q_t = i\}, \quad 1 \le i, j \le N, \tag{1}$$

where q_t denotes the state at time *t*. Transition probabilities should satisfy the normal stochastic constraints, $a_{ij} \ge 0$ for $1 \le i, j \le N$, and $\sum_{j=1}^{N} a_{ij} = 1$ for $1 \le i \le N$.

3. The probability of the observation given the underlying (hidden) state, $B = \{b_j(k)\}$. Defined as

$$b_j(k) = p\{O_t = \upsilon_k \mid q_t = j\}, \quad 1 \le j \le N, 1 \le k \le M, \tag{2}$$

where υ_k denotes the k_{th} observation, M the number of the observation, and O_t the current parameter vector. The following stochastic constraints must be satisfied: $b_j \ge 0$ for $1 \le j \le N, 1 \le k \le M$, and $\sum_{k=1}^{M} b_j(k) = 1$ for $1 \le j \le N$.

In the current study time was treated discretely. The most likely set of state transition and output probabilities were needed to discover the parameters of the HMM based on the observed measurements. The Baum-Welch algorithm was used to solve this problem (Baum 1970). The Hidden Markov Model (HMM) Toolbox written by Kevin Murphy (Murphy 1998) was used in this study. For animal behaviour modelling, transitions between the same or different behavioural states can be predicted from the state transition matrix A, and the state-dependent observation matrices B. To develop a HMM for cow movement, we determined a set of interpretable states as the hidden state space, and what observations to make as the observation space. We defined three hidden state spaces ($N = 3$): foraging, bedding, and relocating because they accounted for the largest proportion of time for all cattle activities. The vector $\pi_i = p\{q_0 = i\}$ then refers to the likelihood that an individual's hidden state is. The hidden state could be, for example, relocating, foraging or bedding. Such likelihood was determined by the HMMs through the training process using observed data.

Using data collected from GPS collars the animals' changing location was calculated, including the directional speed v and angular speed v'. The directional speed v was defined as $v = L/\tau$ (m/s) if an animal traveled a distance L in time τ. The angular speed v' was a scalar measure of rotation rate; this is a measure of how fast an object is rotating. It was defined as $v' = |\theta/\tau|$ (radian/s) where θ are radians and τ is time. A low angular speed v' is indicative of more direct movement and was used to infer more goal directed movement by a cow. Larger temporal variation in the angular speed was used to infer foraging and drinking activity. Hence we assume that the directional speed and angular speed were suitable observations to train the HMMs. The observation state space was then set as: (1) low directional speed with low angular speed $O = 1\ (low\,\upsilon', low\ v)$; (2) low directional speed with high angular speed $O = 2\ (high\ \upsilon', low\ v)$; and (3) high directional speed with low angular speed $O = 3\ (low\,\upsilon', high\ v)$. Since high directional speed with high angular speed was not a reasonable behavioural assumption, it was not included as an observation state.

2.4 Long term prediction model

Besides using HMMs for stay regions, another model for trajectory prediction and clustering was fitted to data in the travel region. The approach was based on the idea that for a given area, moving objects tend to follow typical motion patterns that depend on the objects' nature and the structure of the environment. This learning algorithm was named the long-term trajectory prediction algorithm. It was implemented to predict cow movement.

To learn the patterns of different trajectories, a group of typical trajectories were obtained by choosing a range of trajectories in which cows were travelling between stay regions. Each trajectory can be defined as a function $d(t):[0, T] \to C$ that returns the two-dimensional position of a moving animal at time *t*. Here *T* is the duration of the trajectory, and *C* is the two-dimensional space of the animal movement. For all the training trajectories, a dissimilarity value was calculated.

The dissimilarity or time averaged distance, between two trajectories d_i and d_j was defined as:

$$\delta(d_i, d_j) = \left(\frac{1}{T} \int_{t=0}^{T} \left\| d_i(t) - d_j(t) \right\|^2 dt \right)^{1/2} \tag{3}$$

The dissimilarity matrix was used in the distance matrix for a clustering algorithm to obtain a set of clusters of trajectories. The Agglomerative Hierarchical clustering algorithm (Jain and Dobbs 1988) was used because of the simplicity of this family of approaches. In order to implement this algorithm Matlab code was written to process the data collected from the collars worn by the cattle used in this study. The agglomerative approach builds the hierarchy from the bottom up. It starts with the data objects as individual clusters and successively merges the most similar pair of clusters until all the clusters are merged into one cluster, which is the topmost level of the hierarchy (refer Jain and Dubes (1988) for a detailed description of the algorithm). Here, the similarity was calculated using equation (3). After defining a final cluster number all the trajectories were assigned to a cluster. The mean value and the standard deviation for each cluster were then calculated as

$$\mu(t) = \frac{1}{N} \sum_{i=1}^{N} d_i(t), \tag{4}$$

$$\sigma(t) = \left(\frac{1}{N} \sum_{i=1}^{N} \delta\left(d_i(t), \mu(t)\right)^2 \right)^{1/2}. \tag{5}$$

Each cluster was modelled as Gaussian sources with the mean value and standard deviation calculated during learning using equations (4) and (5). Maximum Likelihood was then used for the prediction. To predict an animal's motion, we assumed the first part of the trajectory was already known. That is, we used animal motions in the past N time steps as the known fragment and calculated the likelihood of the known fragment under each of the clusters. We then identified the cluster with the maximum likelihood. The rest of the trajectory was predicted using the mean value of the cluster with the maximum likelihood.

2.5 Transition between HMMs and long-term prediction models

After the HMMs and long-term prediction models were trained for each animal, a combination step was needed to create the completed model. The transfers between the HMMs and the long-term prediction models were based on the transition probabilities estimated by pre-processing the observed data. Each animal's locations were assumed to be 2D Gaussian distributions in each stay region. By calculating the mean and variance of easting and northing directions from the observed data for each animal in each region, it was possible to determine the animal's Gaussian distribution. These distributions were then used to calculate the transfer probability between the HMMs and the long-term prediction models.

In the final (combined) model, we assumed that the animal starts the movement in a randomly chosen stay region at discrete time steps, with a frequency of 0.1Hz (same as the GPS data). The appropriate HMM firstly simulated the next location and direction of the animal based on the current position. The new location was compared with the 2D Gaussian distribution to decide whether the animal was still within this stay region or had moved. If the new location was within the 3σ contour of the 2D Gaussian distribution of the current region, the animal continued within the region based on the model simulation. Here, σ is the standard deviation of the corresponding Gaussian distribution calculated from real data. If the modelled animal moved out of the stay region it was allocated to a travelling activity with random movement speed and direction. After the animal spent thirty minutes in the travel region, the moving trace in the travel region was used to calculate the similarity to the long-term prediction model and the best-fit model was used to calculate the moving trace until the animal enters another stay region. After applying the long-term prediction model, the modelled cow moved into another stay region and the HMM of the new region was used to continue movement within the stay region.

3. Results and discussion

3.1 Statistical properties of the data

The average distance over time between cattle and between each cow and the average location centre with standard deviations are shown in Figure 2. No obvious relationship between individual animals can be discerned from these distances. The average distances between any two cows were in the range of 5 to 35 meters. The distances from each cow to the centre position ranged between 5 to 20 meters.

GPS data suggests that cattle stayed in some areas for longer periods of time than other areas; we identified these areas using a density calculation. The density was obtained by counting the number of locations of six cows during the 4-day period in each 10 by 10 meter region. The peaks can be seen in Figure 2 which is a contour plot of the density. Peaks represent regions that had higher use by the cattle, such as corners and edges of the paddock and the location of water. Six regions were identified on the plot as those in which cows spent more of their time and these are marked with red circles. The model was generated using data from each individual cow to see the length of time that they spent in each region, what paths were followed between regions and the average time taken to move from one region to another.

3.2 Hidden Markov Model

The relationship between directional speed and angular speed was the basis for inferring individual activities, for example, high angular speed and low directional speed was used to represent foraging behaviour, low angular speed and low directional speed was used to represent bedding behaviour and high directional speed with low angular speed represented relocating behaviour in the paddock. The directional speed and angular speed were calculated from the data collected from the GPS collars on the cattle and the results are plotted in Figure 4, where the possible hidden states (foraging, bedding and relocating) are marked. The directional speed and angular speed relationships were used to train HMMs. The animal datasets were subsequently grouped into three discrete observations:

- those data where v < 0.4 m/s and v' < 90°/s were considered as "slow movement with slow body/heading direction changing" assigned observation value $O = 1$;
- those data where v < 0.4 m/s and v' >=90°/s were considered as "slow movement with quick body/heading direction changing" assigned observation value $O = 2$;
- those data where v >= 0.4 m/s and v' < 90°/s were considered as quick movement assigned $O = 3$.

Threshold values of 90°/s and 0.4 m/s were set based on reviewing video and based on field observation of animal activities. Notice there is not an observation group with high angular speed and high directional speed (v >= 0.4 m/s and v' >= 90°/s), because animals cannot physically change their heading direction (moving angle) when they are moving fast.

HMM parameters were estimated separately for the six cows by learning based on the observation time series within stay regions. For example, the HMM parameters are shown in Table 1 for cow 1 in stay region 1 from 10 pm to 6 am. From matrix B we can postulate that the hidden state $q = 1$ corresponds to the "relocating" state because it has the highest probability with the observation $O_t=3$ (high directional speed). The main difference between hidden states $q = 2$ and $q = 3$ is in the second column, where the probability $p\{O_t=2 \mid q=1\}$ is 20% and the probability $p\{O_t=2 \mid q=2\}$ is 4%. That is, the probability of the observation (high angular speed, low directional speed) given hidden state O_t=2 was five times higher than the corresponding probability given hidden state 3. Hence we can postulate that $q = 2$ was the "foraging/drinking" state, and $q = 3$ was the "bedding" state. Since cows remained in stay region 1 for the majority of the night, the prior probability of relocating and foraging were both very low, with a high probability of bedding. For instance, the probability is 0.0335 that a cow will relocate in the next time step given that it is bedding in the current time step. Similarly, if the current state is foraging, the probability is 0.0085 that the next state will be bedding. Such logic is shown in Figure 5 more clearly.

The HMMs for the six cows were different and Table 2 shows the average HMMs with the standard deviation for the six cows in stay region 1 during 10 pm to 6 am. The standard deviation is high for some values, such as $p\{O_t = 1 | q_t = 2\}$ has the standard deviation as 0.2725, indicating that the cows have different foraging patterns. Most of the standard deviations are similar, which indicates they behaved as a herd during most of the observation period.

3.3 Long-term prediction model

To model the animal's movement from one region to another, the positional training data series in the travel region was used to learn the parameters for inter-region trajectories. For example, the track of cow 1 was divided into 15 minute trajectories and used to train different trajectory clusters as described above. The trajectories for different time periods, including 15 minutes, 20 minutes, 25 minutes and 30 minutes were generated for the whole model. The whole library of trajectories was very large, and ensured the final parameters covered the full range of different moving trajectories. Four clusters are shown in Figure 6; including two quick moving clusters (longer tracks on the left) and two stable clusters (shorter tracks on the right). All tracks record the movement of an animal over 15 minutes. The stars show the average trajectory in each cluster while the solid lines show some of the training trajectories used. The learnt trajectories represent typical cattle movement patterns and represent herbivore environment interactions.

3.4 Cattle movement simulation model using a combination of the Hidden Markov Model and long-term prediction methods

The HMMs and the long-term prediction model were combined according to the transition method described in Section 2. By applying the above strategy, a final model was generated. Running the model to simulate the movement of four cows over a full day generated a location distribution from the resultant artificial data. The performance is shown in Figure 7 (a. 3D distribution, b. corresponding contour data), which shows that the artificial data had very similar statistics to the real data (Figure 3). A comparison of the modelling results and the split-half testing data are shown in Table 3. The table is in two parts: Part 1 is the data from the GPS collars but doesn't include the data that was used to construct the model. The data represents the percentage of time each animal spends in each region where the regions are defined as in previous sections and Figure 3. The measurement of the modelling results is in Part 2 of the table which records the average staying period within each region with the standard deviation. The modelling results perform similarly to the real testing data in terms of the proportion of time spent in each region and the standard deviation in the travel region is higher than in stay regions. This means the long-term prediction model has more uncertainty than the HMMs within stay regions.

3.5 How these modelling methods might be used to understand and manage herbivore-grazing behaviour

This paper has developed a hierarchical modelling methodology that successfully combines HMMs and long-term prediction methods together. One of the advantages of this model is that it models animal behaviour at both large and fine scales. For instance, the HMMs model the behaviour in the stay regions in fine resolution temporally and spatially while the long-term prediction model describes herding behaviour at a much larger scale. Such modelling methodologies might be used to differentiate and predict aspects of individual behaviour whilst simultaneously integrating overall herd behaviour. With such models farmers and animal scientists can identify and focus on understanding the impact of differences in specific behavioural traits on overall ecosystem outcomes. For example, animals that have preferences for a specific set of environmental features will exhibit a unique set of landscape movement patterns.

One important advantage of the model presented in this paper is the use of observed data to derive statistical descriptions of herbivore behaviour. The model is based on statistical learning and modelling methodologies using high sample rate accelerometer, GPS and magnetometer data, the integration of observed animal behaviour enhances the potential application of the model. Models that attempt to bridge the gap between theoretical constructs and observed realities are extremely valuable for solving many applied agriculture and environmental challenges, such as protecting environmentally sensitive areas and maintaining animal welfare etc. For instance, the model not only shows that cattle graze pastures in a non-homogeneous way but also begins to identify some of the underlying processes that lead to uneven grazing pressure. Understanding herbivore landscape grazing interactions can lead to improved management intervention strategies such as identifying the optimal location of watering points to prevent localised overgrazing effects.

4. Conclusions

Spatially explicit simulation modelling of herbivore behaviour is being increasingly used to understand grazing systems (Marion et al., 2005; Swain et al., 2007). With the advent of enhanced behavioural monitoring it is now possible to use high sample rate GPS data to derive information on both herbivore movement (Schwager et al, 2007; Swain et al., 2008) and behavioural state. By using HMMs and long-term prediction learning algorithms on high sample rate observed data this study generated a realistic model of animal movement in a herd, which explicitly recognised each individual as the central unit of measure. Model parameters were learnt from a real dataset giving the animals' positional data over time. It has been shown that HMMs can be used to describe the animal movement and state transition behaviour within several areas where cows like to stay for long periods. Model parameters were used to identify hidden behavioural states with real activities such as relocating, foraging and bedding, and accounted for stay region time budgets. For cows' movement between those HMM areas, a long-term prediction algorithm was implemented. By combining these two models, we have developed a successful simulator that achieves animal behaviour similar to the real dataset and is interpretable in terms of behavioural processes. This modelling methodology could be applied to include interactions of other animal species.

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Figure captions

Figure 1: The hierarchical structure of the animal model. Monitoring data (as well as empirical data derived from numerous hours of video and human observation) shows that cows like to stay in some areas for longer periods of time than other areas. We refer to those regions as stay regions (circles). The remaining parts of the paddock were used to travel between stay regions and are referred to as travel regions.

Figure 2: (a) The average distances between any two cows were in the range of 5 to 35 meters. (b) The average distance over time between one animal and animals' centre location ranged between 5 to 20 meters. The error bars show the standard deviation. No obvious relationship between individual animals can be discerned from these distances

Figure 3: Contour plot of the density of six cows during the 4-day period. It shows total number that cows visit the corresponding region. Cows' real location should be (x, y) × 10 meter (the grid size is 10 meter). The peaks represent higher used locations for the cattle, such as corners and edges of the paddock and the location of water. Six regions were identified on the plot as those in which cows spent more of their time, and marked as red circles

Figure 4: Relationship between the directional speed (v) and angular speed (v') were calculated from the data collected from the GPS collars on the cattle, where the possible hidden states (foraging, bedding and relocating) are marked

Figure 5: The 3-state Hidden Markov Model trained with observed data for cow 1 in stay region 1. The numbers on each arrow shows the transition probabilities between states. For instance, the probability is 0.0335 that a cow will relocate in the next time step given that it is bedding in the current time step. Similarly, if the current state is foraging, the probability is 0.0085 that the next state will be bedding

Figure 6: Four clusters of trajectories in the paddock, including two quick moving clusters (longer tracks on the left) and two stable clusters (shorter tracks on the right). All tracks record the movement of an animal over 15 minutes. Line: measured moving path. Cross: cluster results

Figure 7: (a) A 3D location distribution generated from the resultant artificial data; (b) the corresponding contour plot. The artificial data has very similar statistics to real data

Figure 1

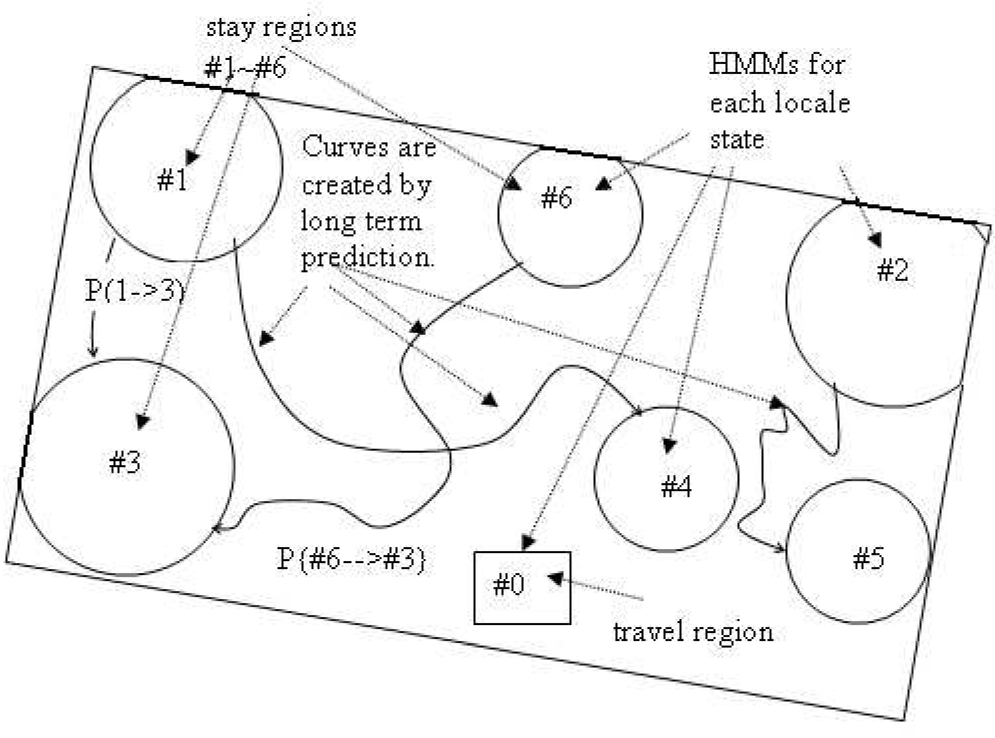
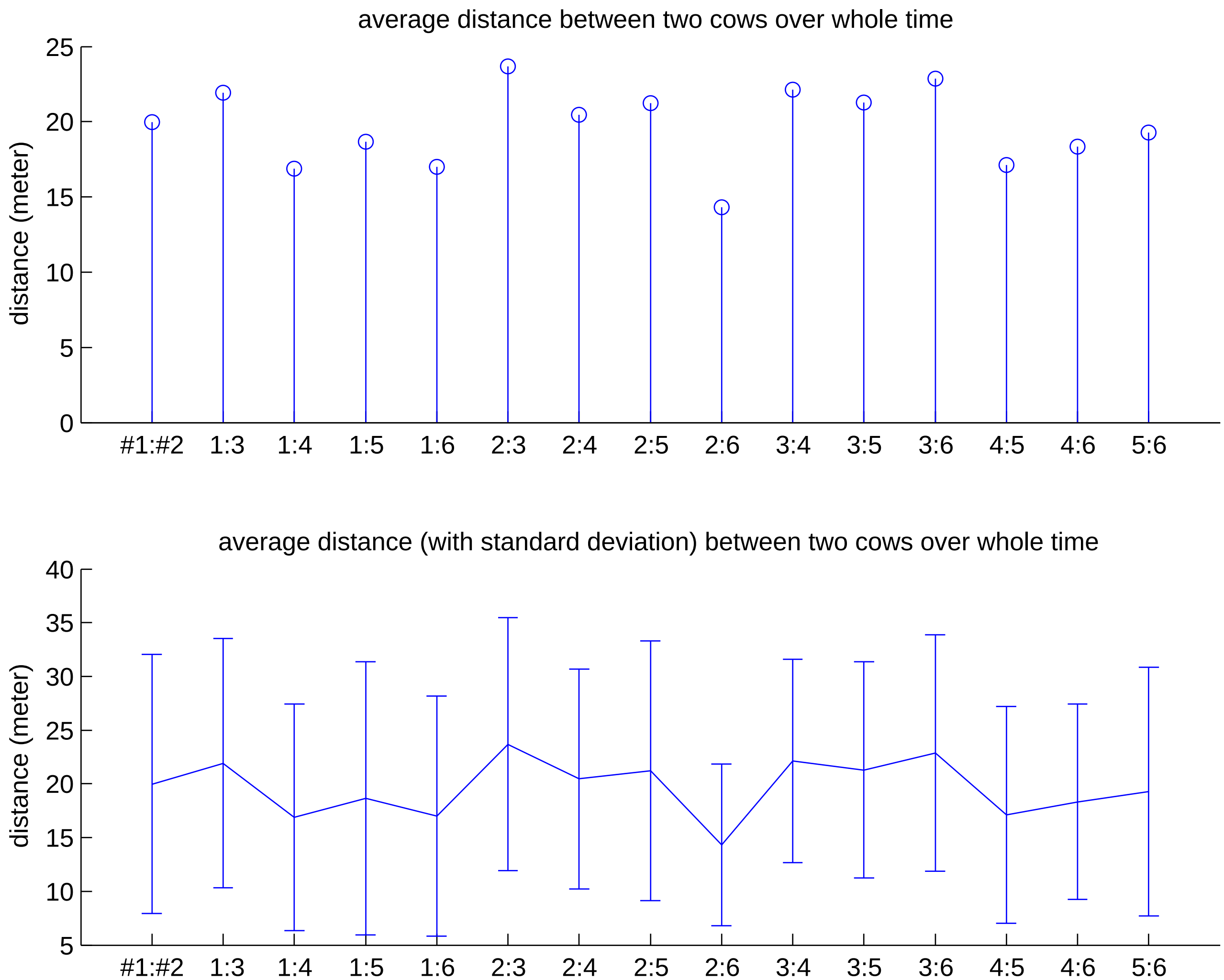

stay regions
#1~#6
HMMs for
each locale
state
Curves are
created by
long term
prediction.
#1
#6
#2
P(1->3)
#3
#4
#5
P{#6-->#3}
#0
travel region

Figure 2a



average distance between two cows over whole time
distance (meter)
25
20
15
10
5
0
#1:#2
1:3
1:4
1:5
1:6
2:3
2:4
2:5
2:6
3:4
3:5
3:6
4:5
4:6
5:6
average distance (with standard deviation) between two cows over whole time
distance (meter)
40
35
30
25
20
15
10
5
#1:#2
1:3
1:4
1:5
1:6
2:3
2:4
2:5
2:6
3:4
3:5
3:6
4:5
4:6
5:6

Figure 2b

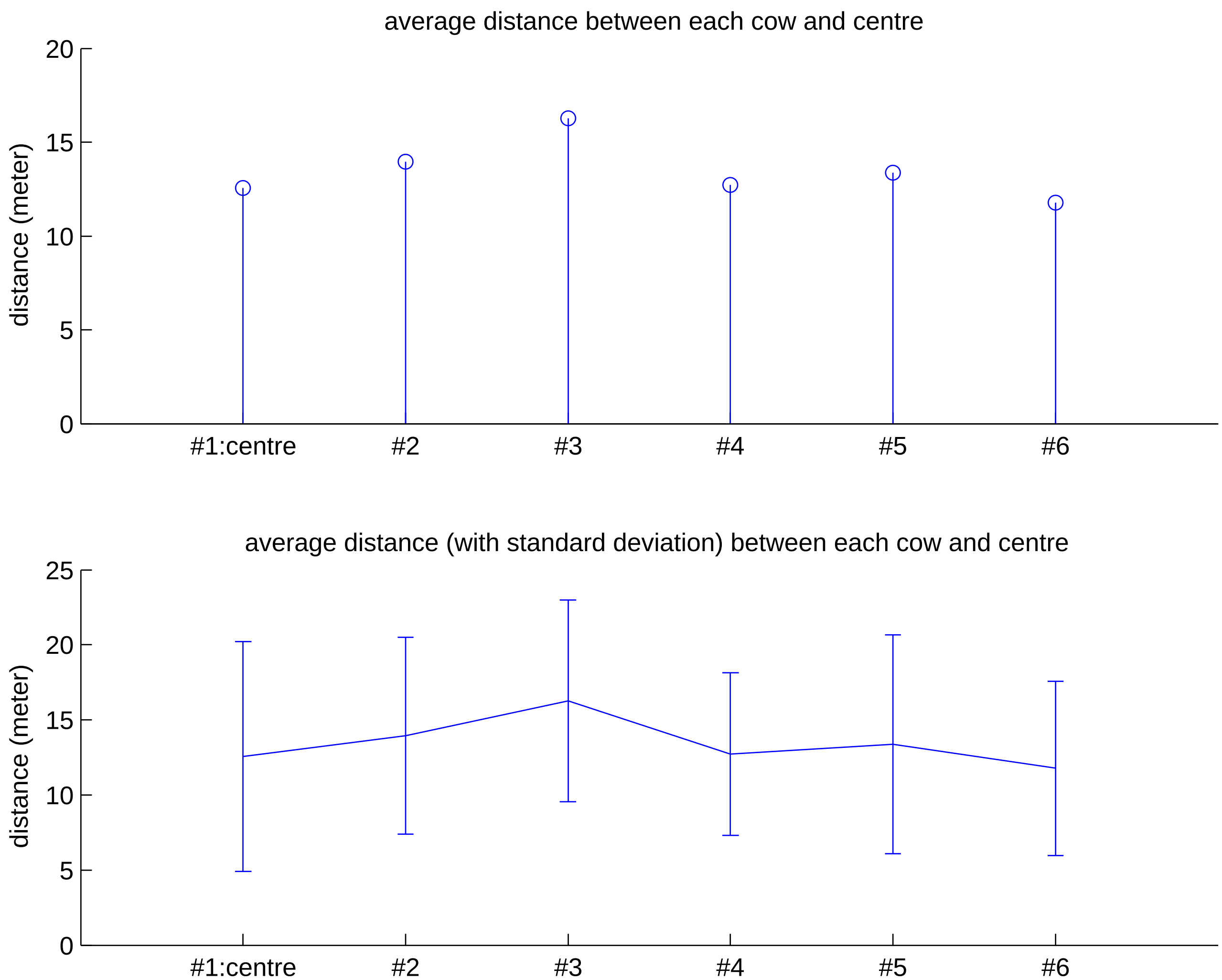

average distance between each cow and centre
distance (meter)
0
5
10
15
20
#1:centre
#2
#3
#4
#5
#6
average distance (with standard deviation) between each cow and centre
distance (meter)
0
5
10
15
20
25
#1:centre
#2
#3
#4
#5
#6

Figure 3

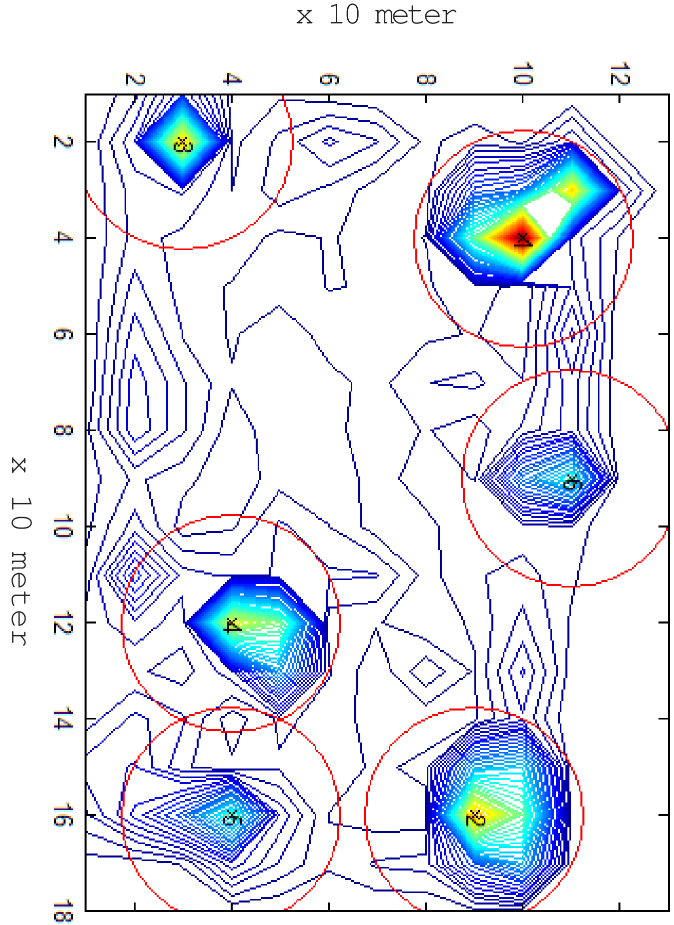
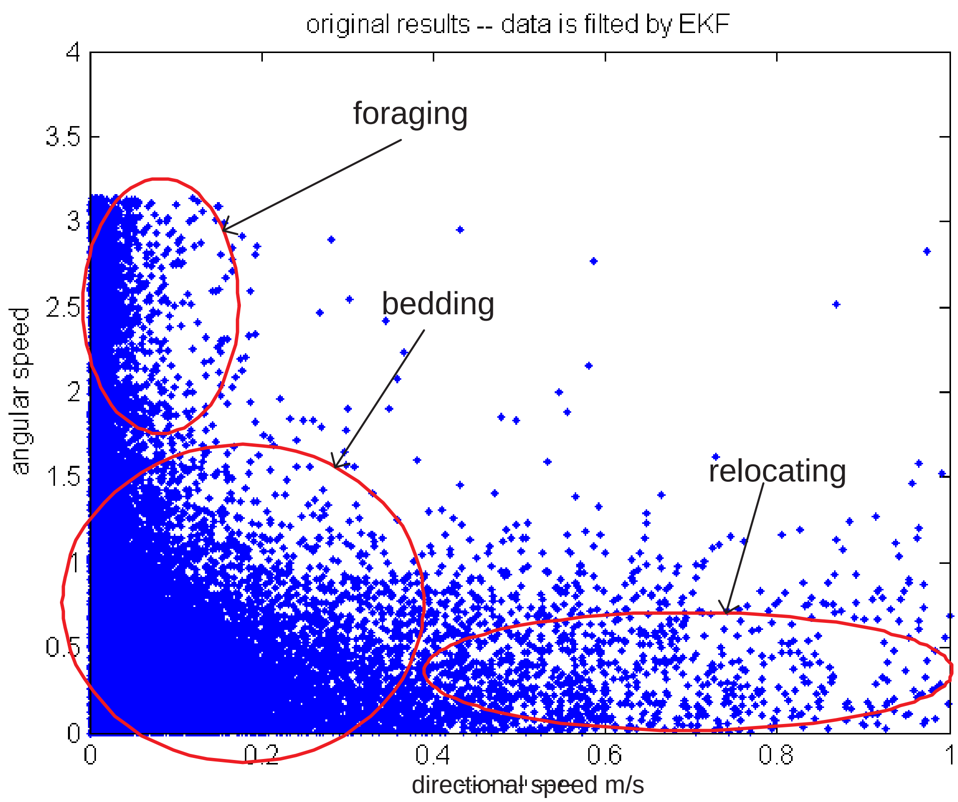


Figure 4



original results -- data is filted by EKF
foraging
bedding
relocating
angular speed
directional speed m/s
0
0.5
1
1.5
2
2.5
3
3.5
4
0
0.2
0.4
0.6
0.8
1

Figure 5

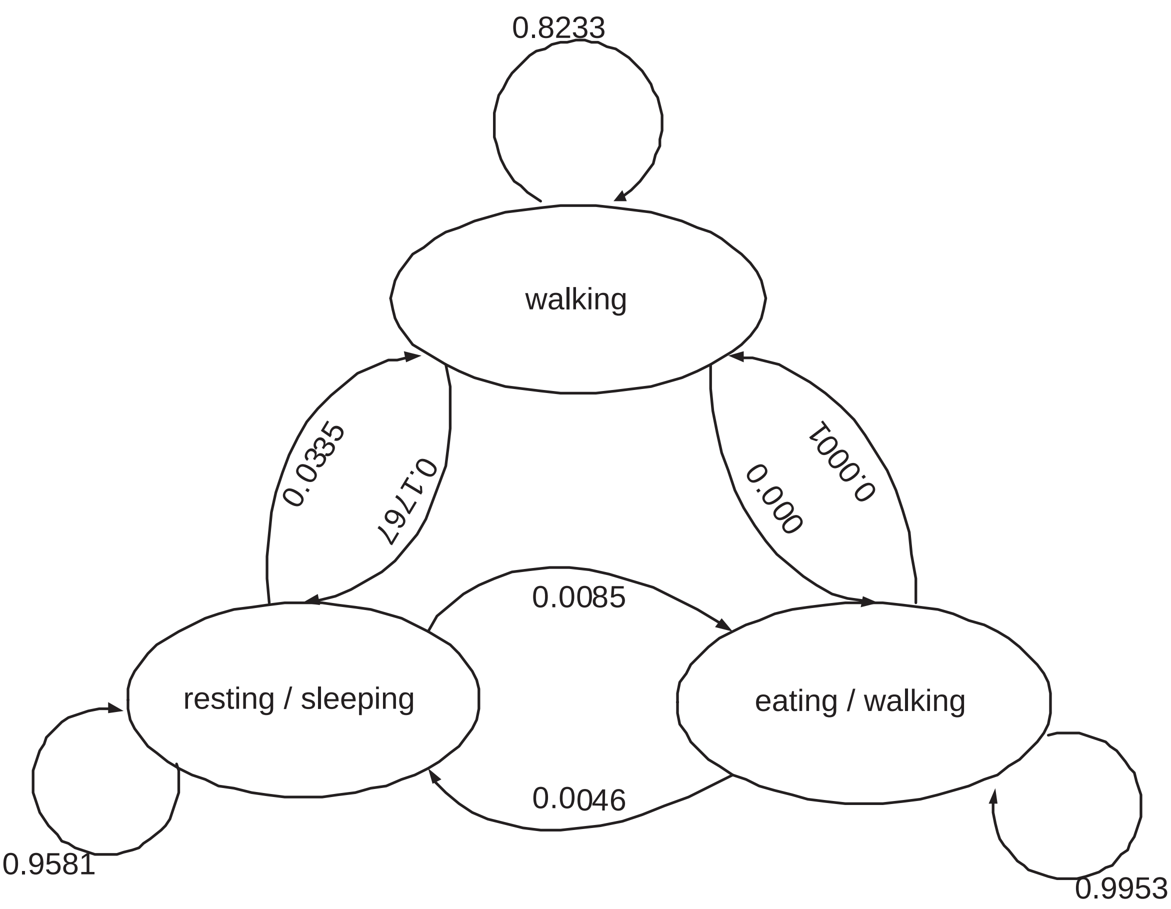

0.8233
walking
0.0335
0.1767
0.000
0.0001
0.0085
resting / sleeping
eating / walking
0.0046
0.9581
0.9953

Figure 6

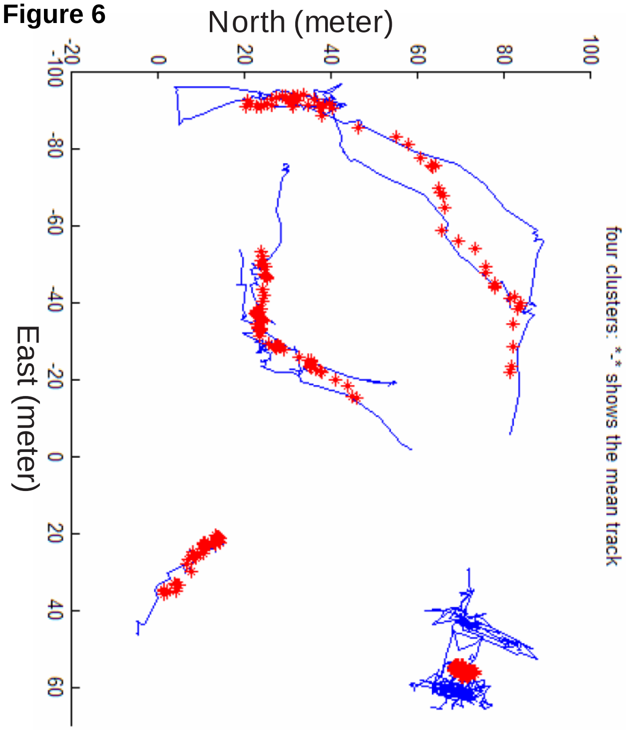


Figure 7a

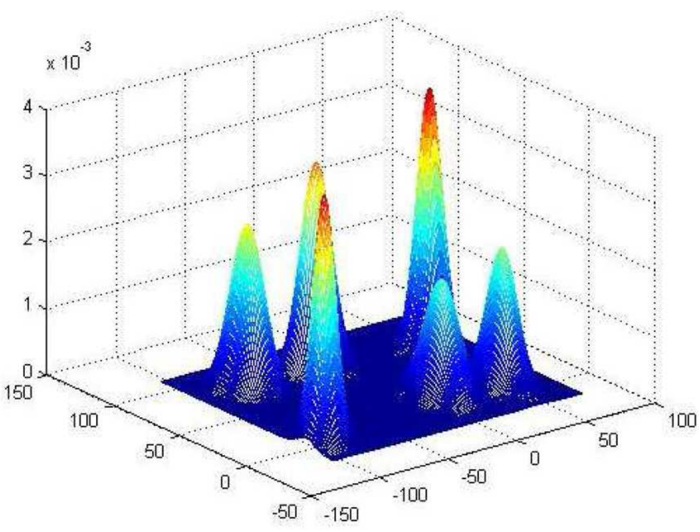


Figure 7b

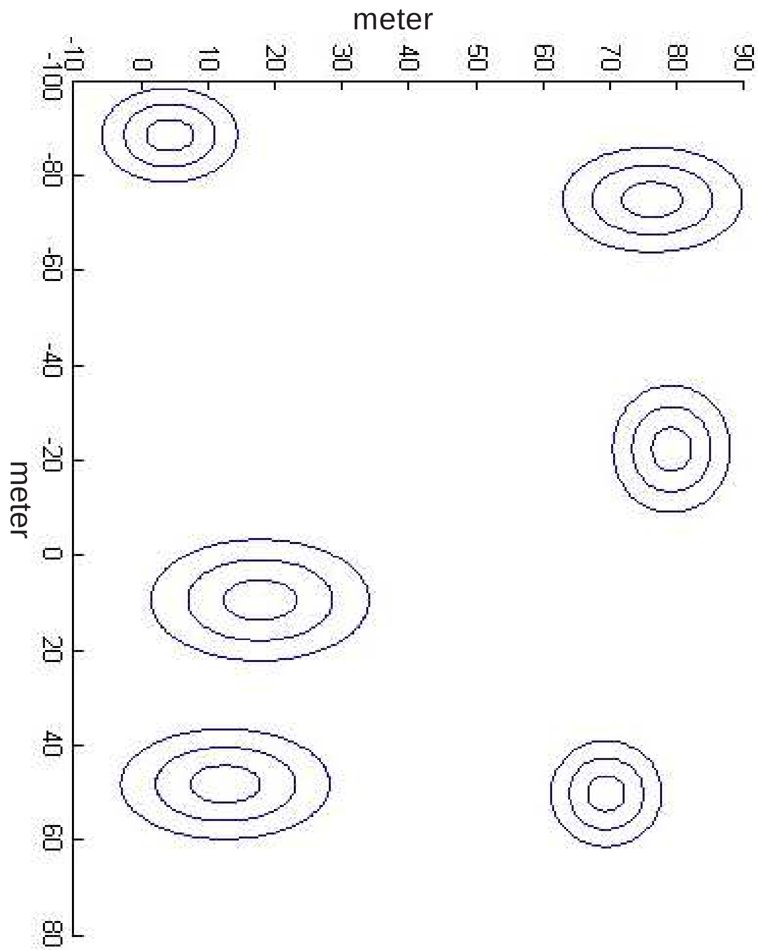

meter
-10
0
10
20
30
40
50
60
70
80
90
meter
-100
-80
-60
-40
-20
0
20
40
60
80

Table 1

Table 1: Hidden Markov Model for cow 1 in stay region 1 during 10 pm to 6 am

Λ: State transitions			
	$q_{t+1} = 1$	$q_{t+1} = 2$	$q_{t+1} = 3$
$q_t = 1$	0.8233	0.0000	0.1767
$q_t = 2$	0.0001	0.9953	0.0046
$q_t = 3$	0.0335	0.0085	0.9581
B: Probability of observation			
$p\{O_t = v_k \mid q_t = j\}$	$O_t = 1\left(low\ \upsilon', low\ v\right)$	$O_t = 2\left(high\ \upsilon', low\ v\right)$	$O_t = 3\left(low\ \upsilon',\ high\ v\right)$
$q_t = 1$	0.1058	0.0006	0.8936
$q_t = 2$	0.7951	0.2049	0.0000
$q_t = 3$	0.9570	0.0396	0.0034
π : Prior probability of each hidden state			
	$p\{q_0 = 1\}$	$p\{q_0 = 2\}$	$p\{q_0 = 3\}$
	0.0000	0.0070	0.9930

Table 2

Table 2: Mean Hidden Markov Model for six cows in stay region 1 during 10 pm to 6 am

Λ: State transitions			
	$q_{t+1}=1$	$q_{t+1}=2$	$q_{t+1}=3$
$q_t=1$	0.7164±0.1648	0.0001±0.0004	0.2833±0.0614
$q_t=2$	0.0001±0.0003	0.8919±0.2510	0.1080±0.0492
$q_t=3$	0.0091±0.0008	0.0124±0.0008	0.9734±0.1194
B: Probability of observation			
$p\{O_t=v_k \mid q_t=j\}$	$O_t=1\left(low\ \upsilon', low\ v\right)$	$O_t=2\left(high\ \upsilon', low\ v\right)$	$O_t=3\left(low\ \upsilon', high\ v\right)$
$q_t=1$	0.0351±0.1579	0.0004±0.0027	0.9648±0.1018
$q_t=2$	0.5771±0.2725	0.4229±0.2914	0.0001±0.0002
$q_t=3$	0.8582±0.2740	0.1412±0.1085	0.0006±0.0033
π : Prior probability of each hidden state			
	$p\{q_0=1\}$	$p\{q_0=2\}$	$p\{q_0=3\}$
	0.0001±0.0001	0.0103±0.0048	0.9896±0.0167

Table 3

Table 3: Comparison of the simulation results against the split-half testing data

	Travel region	Stay region 1	Stay region 2	Stay region 3	Stay region 4	Stay region 5	Stay region 6
Testing data measurement: counting number that cows in each region and the corresponding percentage over whole time							
Cow 1	7530	6411	5214	3215	4072	2304	1755
Cow 2	8116	4539	4985	3537	3968	2151	3047
Cow 3	8985	4374	4306	4337	3498	3173	1985
Cow 4	9324	4920	4602	2309	2685	2945	1785
Cow 5	8414	5584	3570	4156	2369	3589	2730
Cow 6	8140	6886	4007	3168	3572	2925	2347
Total	50509	32714	26684	20722	20164	17087	13649
percent	27.82%	18.02%	14.70%	11.42%	11.11%	9.41%	7.52%
Simulation results: average over 10 runs (10,000 steps for each run)							
average	2881	1882	1640	1262	1132	723	480
Std	1168	338	379	468	580	447	281
percent	28.8±11.7%	18.8±3.4%	16.4±3.8%	12.6±4.7%	11.3±5.8%	7.2±4.5%	4.8±2.8%