

The Internet of Animals...

## Professor Stephen Hailes UCL



# Well, kind of.

- □ Sheep (x2) (w Cambridge PDN & RVC)
- □ Leopards (RVC & BCPT)
- □ Wild dogs (RVC & BCPT)
- □ Baboons (Swansea)
- □ Birds (RVC)

This is collaborative work with
 Prof Jenny Morton (Cambridge)
 Prof Alan Wilson (RVC)
 Dr Andrew King (Swansea)
 ... and many others



# **Batten Disease (source NIH)**

## Nature

- □ A type of neurodegenerative disorder.
- Autosomal recessive
- Evidence suggests it is caused by problems with the brain's ability to remove and recycle proteins.

## Symptoms

- Abnormally increased muscle tone or spasm (myoclonus)
- Blindness or vision problems
- Dementia
- □ Lack of muscle coordination
- Mental retardation with decreasing mental function
- Movement disorder (choreoathetosis)
- Seizures
- Unsteady gait (ataxia)



## Prognosis

- □ Symptoms normally appear age 5-10
- Early signs can be subtle personality and behaviour changes, slow learning, clumsiness, or stumbling.
- Over time, affected children suffer mental impairment, worsening seizures, and progressive loss of sight and motor skills.
- Eventually, children with Batten disease become blind, bedridden, and demented. Batten disease is often fatal by the late teens or twenties.
- No specific treatment is known that can halt or reverse the symptoms of Batten disease.
- □ Palliative care (anticonvulsants, physical therapy) can help.



# NZ trip (Feb/March 2011)

## Cohort 1 (69 sheep: 40 ewes, 19 rams)

- □ 2010 (~6 month old), mixed:
  - □ Normal sheep (17)
  - □ Batten disease (CLN5/6)
    - Homozygous (11), Heterozygous (17)
  - Cataract sheep
    - Blind (11), Impaired (5), Sighted (8)

## Cohort 2 (11 ewes)

2009 (~18 month old) shed ewes, mixed:
 Homozygous (5), Heterozygous (6)

### □ Cohort 3 (11 sheep: 2 ewes, 9 rams)

2009 (~18 month old), mixed:
 Homozygous (9), Heterozygous (2)



# Cohort 1





## Cohort 2





# **GPS-based work**

Data obtained from GPS/IMU units

- GPS at 1 sample/s
- □ IMU at 50 sample/s
- Over max 22-24h periods
- □ Attached using harness...

□ Issues: C1 sheep were small, shorn and in poor condition







# Can be used to derive individual position fixes for each individual....

**UCL** 

## Cohort 3 - 3/4/11



# **Sheep 1171 - Affected**





## **Sheep 1004 - Affected**





# Which sometimes throws up some suprises....



## Sheep 1008 - Heterozygous





## **Sheep 1106 - Affected**





# Cohort 1 + 2.... 30/3/11







# Q: How can we identify phenotype from the data?

Try analysis of distance covered....by phenotype







# Try analysis of distance covered....by time of day



**UC** 



## □ What about IMU information?

## □ Produce a measure of activity:

- Take 50Hz 3D accelerometry signal, calculate magnitude of resultant
- □ (Roughly calibration offset)
- □ Integrate numerically over 1 minute for measure of activity
- Subtract mean calculated over whole day to look at variation in activity relative to the mean

□ And we get....

# Activity – Cohort 1+2 30/3/11







25

**UC** 



# Back to the GPS...







# **Path analysis**



Four cohort 2 sheep 00:06 - 00:18 22/03/11



# Path analysis - numerically

	1156 (Homo)	1123 (Homo)	1169 (Hetero)	1187 (Hetero)
Path length	16.59	253.70	36.11	46.12
Mean step size	0.023	0.352	0.050	0.064
SD step size	0.045	0.290	0.118	0.102
P(Turn same dir)	0.570	0.827	0.566	0.525
95% c.i. Psame	0.534 – 0.607	0.800 - 0.855	0.530 - 0.603	0.489 – 0.562
p-value Psame≠0.5	0.0002	<< 0.0001	0.0004	0.1784
Correlation between adj. turn angles	0.0009	0.0002	0.0017	0.0022



# **SOCIAL STRUCTURE**



# **Statistics**

# Motivation

Much of the work done on social structure lacks a mathematical foundation

## □ This matters

□We care about the identification of groups in a social network, and about the nature of change with time

Existing measures offer little in the way of robust evidence.

## □Aim:

To provide significance tests that allow the inference of social networks, or of important features of social networks such as group separation, from movement data.



# **Quick intro**

- In social network analysis, a graph is constructed to represent the social structure of a group
  = a sociogram
- □ Nodes are individuals
- Edges represent relationships
- □ Centrality (betweenness, closeness, degree)
- □ Position (structural)
- □ Strength of ties (strong/weak, weighted/discrete)
- □ Cohesion (groups, cliques)
- Division (structural holes, partition)



# **Our problem**

Typically SNA assumes that the structure of the network is observable.

□ E.g. who is friends with whom on Facebook

□Not the case for us:

□ We only have GPS data available and so...

We must infer the underlying social network before analysing it



# **Existing approaches for animals**

- □ The most common approach is..
- □ The Gambit of The Group
  - Data split into time windows
  - □ A separate social network constructed for each time window
    - Put an edge if two animals are said to be "in the same place at the same time" during that time window
  - Once we have this collection, amalgamate into a single (weighted) network
  - □ Then threshold this to remove 'weak' links
- Arguable for animals in which 'place' has a clear meaning – e.g. roosting bats
- Less clear for situations in which place has less meaning



# **Existing approaches II**

- □ There is a relationship between A and B if animal A stays within *x* metres of animal B for at least *t* seconds
  - □ But this is parameterised by x and t, and it is not clear how to choose these often arbitrary or anthropomorphic.



# **Our** approach

### □ We assume:

That the social network of the group can be directly associated with the correlation structure of the group's movement patterns

- We aim to detect any significant correlation between the movement of two members of the group
- And do this through the construction of an appropriate significance test
- Given that similarity in movement patterns is statistically significant, we place an edge in the social network. Else we don't.


# Notation

- Given a data set, we use:
  - $\square$   $N \in \mathbb{N}$  to denote the number of animals
  - $\Box H \in \mathbb{N}$  to denote the number of time points in the data set
  - $\Box$  ( $x_t$  (n),  $y_t$  (n))  $\in \mathbb{R}^2$  for position of animal  $n \in \mathbb{N}_N$  at time  $t \in \mathbb{N}_H$
  - $\Box \mathbf{x}_t$ ,  $\mathbf{y}_t \in \mathbb{R}^N$  for coordinates of the entire group at time  $t \in \mathbb{N}_H$
  - $\square \textbf{\textit{x}}_{1:H}$  ,  $\textbf{\textit{y}}_{1:H} \in \mathbb{R}^{NH}$  for coordinates of the entire group
- □ Assume that the entire group of animals is always contained within a bounded region, *D*.



## Inferring social structure

- Assume social structure corresponds to correlation structure in the movement patterns of the group.
  - □ When there is a relationship, movement patterns are correlated
  - □ When there is not, they are independent

□ A standard statistical approach to such a problem is:

- □ Construct a generative model for group movement, i.e. a probabilistic model over the space of possible movement patterns.
- Given the observed movement pattern either obtain a pointestimate of the model parameters, through e.g. likelihood maximisation, or obtain the posterior of the model parameters through Bayes' rule.
- Given the point-estimate or posterior, the correlation structure of the group's movements is then directly obtainable from the generative model.



# But...

- It is extremely difficult to construct a generative model that is both:
  - sufficiently rich to model the complex movements patterns seen in real-life data sets
  - sufficiently constrained so as to avoid over-fitting and (feasibly) allow parameter optimisation, or posterior inference.
- Various 'swarm models' have been proposed in the literature but to the best of our knowledge...
  - no statistical inference has been performed on reallife data sets through these models.



### **Our approach**

- □ By defining an appropriate null model we:
  - construct a novel significance test that infers the social structure of the group
  - obviate the need to construct a model for the collective movements of the group.
- □ Null hypothesis: the movements of each animal are independent of the other members of the group
- Given this, it is simple to train a separate generative model for each individual animal
- Given the observed movement patterns we use our set of individual generative models to determine whether any similarity in the movements of any two animals is significant, or simply due to chance.



### **Geospatial approach**

- □ Step 1: Partition space into subregions. e.g. take bounding rectangle for field and divide into equal-sized squares
- Reason: given a generative model for the movements of each animal, it is meaningful to calculate the probability that two animals are in the same sub-region of the partition at the same point in time
- ❑ Given such probabilities, we can then determine whether the number of times that two animals where observed to be in the same sub-region is significant or simply down to chance.



# The key – individual movement models

□ We learn a movement model for each animal in the group

- There are various possibilities: e.g. a multinomial distribution and a Markov model.
- To construct such models, we represent the observations of each animal's movements in terms of the partition of space
- □ for each animal,  $n \in \mathbb{N}_N$ , and each observation,  $t \in \mathbb{N}_H$ , we use the notation  $i_{t,n} \in \mathbb{N}_D$  to denote the index of the subregion that contains the point ( $x_t$  (n),  $y_t$  (n))

 $\Box$ *i.e.* ( $x_t$  (n),  $y_t$  (n))  $\in$   $D_{it,n}$ 

# Simple approach – multinomial distribution

□ Takes no account of the temporal structure of the data

□ Simply calculate the probability that animal n will be in subregion  $D_i$ 

$$\widehat{\pi}_n(i) = \frac{C_{i,n}}{\sum_{i' \in \mathbb{N}_D} C_{i',n}}$$

Where:  $C_{i,n}$  is a count of the number of times animal *n* was is region *i*.



# Not enough

Consider an animal walking in a circle
Where is has come from is important to where it is going to go next

Construct a Markov model – give a transition matrix and initial location

$$\widehat{T}_{n}(i|j) = \frac{\sum_{t=2}^{H} I[i_{t,n}, i] I[i_{t-1,n}, j]}{C_{j,n} - I[i_{H,n}, j]}$$

$$\hat{p}_n^0(i) = \boldsymbol{I}[i_{1,n}, i]$$



# **Determining significant interactions**

Determine the number of times a pair of animals were in the same sub-region at the same time

□ For each pair of animals,  $n, n' \in \mathbb{N}_N$ , we denote this count

$$e_{n,n'}^{H} = \sum_{t \in \mathbb{N}_{H}} \sum_{i \in \mathbb{N}_{D}} I[i_{t,n'}, i] I[i_{t,n}, i]$$

In the case of the Markov model, the probability of the colocation of two animals at the same time is:

$$p_{n,n'}^t = \sum_{i \in \mathbb{N}_D} \hat{p}_n(i_t = i) \hat{p}_{n'}(i_t = i)$$

□ Where the  $\hat{p}$  values are the marginals under MLE of the transition matrix and initial state distribution



- □ Using  $E_{n,n}^H$ , to denote the random variable for the number of colocations between *n* and *n*', given our generative models
- □ We can calculate  $E_{n,n'}^H$  either analytically, for the multinomial or iteratively for the Markov model
- □ We reject the null hypothesis if:

$$p(E_{n,n'}^H \ge e_{n,n'}^H) \le \alpha$$

- □ *i.e.* if the probability that there are more random colocations than actual colocations is less than a given value of significance
- □ If we reject the null hypothesis, we add an edge into the social network



# **Artificial mixing experiment**

- In the artificial mixing experiment we manipulate the data in such a manner that it is known a priori that the flock is formed of two sub-groups
  - □ To obtain two sub-groups we amalgamate pairs of data sets.
  - □ To ensure a clear demarcation between the two sub-groups we amalgamate data sets from different days, *e.g.*, 1<sup>st</sup> and 2<sup>nd</sup> March
  - We only consider pairs of data sets from the same field
- A total of twenty three different amalgamated data sets, with an average of one hundred and forty animals.
- □ Split the area into twenty five equally-sized sub-regions
- Take the median position of each individual over a five minute period as an observation
- □ Consider a Markov model, and use the data of the entire group to construct a single model. We use the significance test to construct a single binary network, and consider a 0.5% level of significance.



### **Artificial mixing experiment**





# **False positives**

- □ The proportion of connections between the two flocks, *i.e.* the false-positive rate, was 4.9 ± 1.6%,
- Slightly higher than the expected false-positive rate when using this level of significance







# **Real mixing experiment**

- □ Used a data set that consists of ninety one individuals.
- □ Flock is formed of two sub-groups that were put into the same field on the day of data collection.
- Used a six hour period during which the two sub-groups were fairly well separated to consider the social network of the group during this period.

□ Other parameters the same.







### **Real mixing experiment**





### Social network – cohort 2, NZ1





# **Classification experiment**

- □ Comparative data:
  - □ View animation
  - For each pair, consider the movements of the pair, in relation to the movements of the entire group
  - Subjectively determine whether an edge is present between the pair in the social network
- □ Construct a binary network for data from six different days.
- □ For each data set we considered a six hour period, selecting periods with a high amount of movement activity
- □ Significance test has to determine whether there is a significant amount of interaction during the six hour period.
- Each data set consists of a flock of eleven animals, so that there were fifty five possible edges in each of the six social networks.



# Result

- Over the six data sets there was a total of three hundred and thirty possible edges.
- Our significance test obtained a classification accuracy of 90.61 ± 1.61% (of the edges).
- **Comparison**:
- □ Within 3m for 3 minutes: 65.45 ± 2.62%.
- Optimise parameters to give the best results for this distance/time approach:
  - $\Box \alpha$  = proportion of 3 minute period (optimum = 0.1)
  - $\square \beta$  = threshold for formation of binary net (= 0.7)
  - $\Box$   $\gamma$  = distance (= 6.0)
- $\Box$  => classification accuracy of 89.09 ± 1.72%



### kNN-based approach

- □ Assume we have a flock consisting of two groups A and B.
- □ For each animal *n*, and each time point *t*, calculate the proportion of the 5 nearest neighbours that are from the same group as *n* at time *t*
- □ For each time point, average this across all animals
- □ Calculate the significance.... Easier in this case:
  - □ For 1000 iterations
    - □At random, split the flock into two partitions, A' and B' of the same size as A and B
    - □Calculate the proportion of nearest neighbours from the same group as before, for each time point
  - Determine what proportion of the iterations are at least as extreme as the observation



### Ewe2/Ewe3 06/09/2012





### Ewe2/Ewe3 08/09/2012 - by cohort





### Ewe2/Ewe3 28/02/2013





### Ewe2/Ewe3 01/03/2013





### 04/09/2012 - Ewe2 by genotype





### **Selfish herd behaviour**

Magazine R1

#### Correspondence

### Selfish-herd behaviour of sheep under threat

Andrew J. King<sup>1</sup>, Alan M. Wilson<sup>1</sup>, Simon D. Wilshin<sup>1</sup>, John Lowe<sup>1</sup>, Hamed Haddadi<sup>1</sup>, Stephen Hailes<sup>2</sup>, and A. Jennifer Morton<sup>3</sup>

Flocking is a striking example of collective behaviour that is found in insect swarms, fish schools and mammal herds [1]. A major factor in the evolution of flocking behaviour is thought to be predation, whereby larger and/or more cohesive groups are better at detecting predators (as for example in the 'many eyes theory'), and diluting the effects of predators (as in the 'selfish-herd theory') than are individuals during an attack has only been studied in a few cases [5,6]. In 1973, Hamilton [3] cited sheep flocking behaviour in response to a herding dog as an anecdote in support of his selfish-herd theory. We have quantified sheep flocking in response to herding by a dog in a controlled but naturalistic setting. In our experiments, a trained Australian Kelpie working dog was directed verbally to herd a flock of initially resting sheep (n = 46)individuals) to a target zone (an open gate) with minimal guidance (given the command "bring them home"). Both the sheep and the sheepdog were fitted with a 'data-logger' [7,8] on a harness (Figure 1C) that comprised a GPS module and antenna, a microcontroller, data storage card and a rechargeable battery (see Supplemental Experimental Procedures for details).

We collected data during three herding events, and re-constructed the position of all sheep in Euclidean space every second from our GPS data (see Supplemental Movies S1–S3). From this positional information, we calculated the flock's geometric centre - the centroid - and the dog's distance to this flock centroid on a second-by-second basis. Then, since sheep are predicted to move towards the centre of the flock under attack [3], we calculated the distance of all sheep to the flock centroid each second. The mean of all sheep distances to the flock centroid represented a measure of 'flock cohesion'. These data were explored, providing the first quantification of sheep flocking response to a herding dog (Figure 1).

Inter-sheep distance and overall flock configuration varied at the start of each of our trials. In each trail the flock responded to the approaching

A 10-

D

1935



# **Herding sheep**

#### JOURNAL THE ROYAL SOCIETY Interface

#### rsif.royalsocietypublishing.org



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### Solving the shepherding problem: heuristics for herding autonomous, interacting agents

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Herding of sheep by dogs is a powerful example of one individual causing many unwilling individuals to move in the same direction. Similar phenomena are central to crowd control, cleaning the environment and other engineering problems. Despite single dogs solving this 'shepherding problem' every day, it remains unknown which algorithm they employ or whether a general algorithm exists for shepherding. Here, we demonstrate such an algorithm, based on edeptive switching between collecting the accents when they are too dispersed





**Figure 1.** Interaction rules for the agents and the shepherd. (*a*) The agents are attracted to the LCM of their *n* nearest neighbours ( $\hat{C}$ ), repelled from other agents within a distance of  $r_a$  ( $\hat{R}^a$ ) and repelled from the shepherd if it is within a distance of  $r_s$  ( $\hat{R}^s$ ). The new heading of the focal agent H' is a linear combination of the three vectors  $\hat{C}$ ,  $\hat{R}^a$  and  $\hat{R}^s$ , weighted by the corresponding model parameters c,  $\rho_a$ ,  $\rho_s$ , plus a small inertia term  $d\hat{H}$  and a small noise term  $e \in$ . (*b*) In each time step, the shepherd does one out of three things depending on the position of the agents. If the shepherd is within  $3r_a$  from any agent, its speed is set to zero. Otherwise, if all agents are within a distance f(N) from the GCM of the agents, then the shepherd aims towards the driving position  $P_d$  directly behind the flock relative to the target. Finally, if at least one sheep is further away than f(N) from the GCM, then the shepherd aims for the collecting position  $P_c$  directly behind the furthest away sheep relative to the GCM. (Online version in colour.)

# Cheetah

OPEN ORCESS Freely available online

### Movement Activity Based Classification of Animal Behaviour with an Application to Data from Cheetah (Acinonyx jubatus)

# Steffen Grünewälder<sup>1,2</sup>\*, Femke Broekhuis<sup>3,4</sup>, David Whyte Macdonald<sup>4</sup>, Alan Martin Wilson<sup>5</sup>, John Weldon McNutt<sup>3</sup>, John Shawe-Taylor<sup>1,2</sup>, Stephen Hailes<sup>2,5</sup>

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#### Abstract

We propose a new method, based on machine learning techniques, for the analysis of a combination of continuous data from dataloggers and a sampling of contemporaneous behaviour observations. This data combination provides an opportunity for biologists to study behaviour at a previously unknown level of detail and accuracy; however, continuously recorded data are of little use unless the resulting large volumes of raw data can be reliably translated into actual behaviour. We address this problem by applying a Support Vector Machine and a Hidden-Markov Model that allows us to classify an animal's behaviour using a small set of field observations to calibrate continuously recorded activity data. Such classified data can be applied quantitatively to the behaviour of animals over extended periods and at times during which observation is difficult or impossible. We demonstrate the usefulness of the method by applying it to data from six cheetah (*Acinonyx jubatus*) in the Okavango Delta, Botswana. Cumulative activity data scores were recorded every five minutes by accelerometers embedded in GPS radio-collars for around one year on average. Direct behaviour sampling of each of the six







Figure 6. The figure shows effects of the season (dry/wet) on the daily activity of three individuals. The figure is similar to figure 3 with the main difference that the data is split into dry and wet season. The top row shows the activity of three individuals in the dry season and the bottom row the activity of these three individuals in the wet season. doi:10.1371/journal.pone.0049120.q006



### Leopards



Reset



### Leopards





# Wild dogs

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### Wild dogs



### **Birds**

#### LETTER

doi:10.1038/nature12939

#### Upwash exploitation and downwash avoidance by flap phasing in ibis formation flight

Steven J. Portugal<sup>1</sup>, Tatjana Y. Hubel<sup>1</sup>, Johannes Fritz<sup>2</sup>, Stefanie Heese<sup>2</sup>, Daniela Trobe<sup>2</sup>, Bernhard Voelkl<sup>2,3</sup>†, Stephen Hailes<sup>1,4</sup>, Alan M. Wilson<sup>1</sup> & James R. Usherwood<sup>1</sup>

function of these configurations is to reduce energy expenditure and entire flap cycle. In contrast, when birds fly immediately behind enhance locomotor performance of individuals in the assemblage411. The distinctive V formation of bird flocks has long intrigued researchers coherence; the wing-beats are in spatial anti-phase. This could potenand continues to attract both scientific and popular attention47,9-14. The well-held belief is that such aggregations give an energetic benefit for those birds that are flying behind and to one side of another bird through using the regions of upwash generated by the wings of feedback that would be required to perform such a feat<sup>12,4</sup>. We con-the preceding bird<sup>4,2,9,11</sup>, although a definitive account of the aero-chude that the intricate mechanisms involved in V formation flight dynamic implications of these formations has remained elusive. Here we show that in dividuals of northern bald ibises (Geronticus mates, and remarkable ability either to sense or predict it. We suggest eremita) flying in a V flock position themselves in aerodynamically optimum positions, in that they agree with theoretical aerodynamic predictions. Furthermore, we demonstrate that birds show wingtip path coherence when flying in V positions, flapping spatially in phase

Many species travel in highly organized groups<sup>1-3</sup>. The most quoted and thus enabling upwash capture to be maximized throughout the another bird-in a streamwise position-there is no wingtip path tially reduce the adverse effects of downwash for the following bird. possible for birds because of the complex flight dynamics and sensory indicate awareness of the spatial wake structures of nearby flockthat birds in V formation have phasing strategies to cope with the dynamic wakes produced by flapping wings.

Theories of fixed-wing aerodynamics have predicted the exact spanwise positioning that birds should adopt in a V formation flock to

2 0 m



Figure 1 | V formation flight in migrating ibises. a, Northern bald ibises (G. eremita) flying in V formation during a human-led migratory flight (photograph M. Unsöld). b, Three-dimensional location histogram of the 7 min flight section, showing position of individual ibises (n = 14) in the V formation, with respect to flock centroid, measured by a 5 Hz GPS data logger. The colour scale refers to the duration (in seconds) a bird was present in each  $0.25\,\mathrm{m} \times 0.25\,\mathrm{m}$  grid. A plot detailing the formation shape for the duration of the entire flight can be found in Supplementary Fig. 7. c, Histogram of number limits of optimal relative positioning, based on fixed-wing aerodynamics.

of flaps (colour coded) recorded in each 0.25 m × 0.25 m region between all birds and all other birds. Most flaps occurred at an angle of approximately 45° to the bird ahead (or behind). Transects denoted by dashed lines, directly behind or along the most populated V favoured position (just inboard of wingtip to wingtip), are the same as those detailed in Fig. 3. d. Histogram detailing the total number of flaps recorded between each bird-bird pair, with respect to position of the following bird. The shaded area (ii-i) denotes the

2.0 m

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### **Hefted Sheep**



Pause

Reset
## **New Frontiers in IoT**



## **Experimental Computer Science?**





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