# A spatial network model of deer populations in Great Britain to inform surveillance and control strategies for Chronic Wasting Disease

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EPIC — Scottish Government's Centre of Expertise on Animal Disease Outbreaks
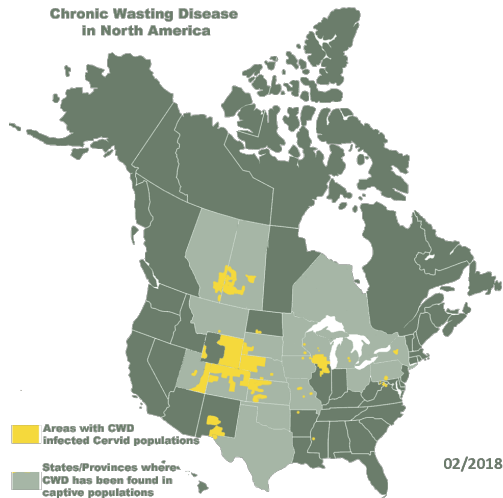
July 12, 2018

# Chronic Wasting Disease (CWD)

- Transmissible spongiform encephalopathy (TSE) affecting cervid species

- Most plausible route for CWD spread: ingestion of contaminated forage/water

- Prions excreted in faeces, saliva, urine and blood; survives in the environment for several years
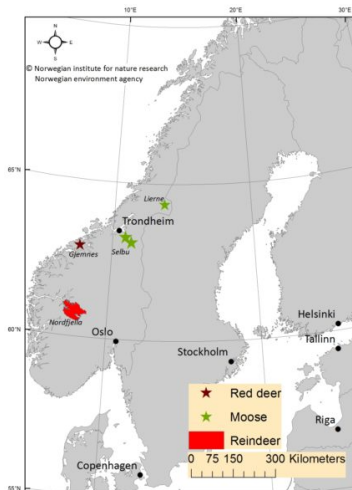
Prion accumulation in organs
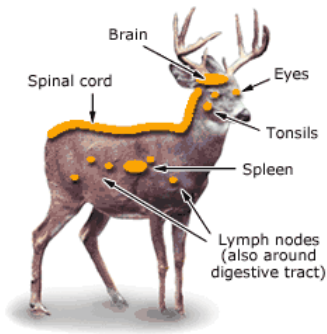


Source: Utah Division of Wildlife Resources, https://wildlife.utah.gov/diseases/cwd/

# Endemic to regions of North America



Chronic Wasting Disease in North America

Areas with CWD infected Cervid populations

States/Provinces where CWD has been found in captive populations

02/2018

Source: Chronic Wasting Disease Alliance, http://cwd-info.org

# First cases in Europe: Norway 2016



Source: Norwegian Institute for Nature Research

# Aims of our project

1. Investigate spatial structure in British deer populations

2. Inform planning of targeted surveillance

3. Inform control strategies for Chronic Wasting Disease in the event of disease incursion
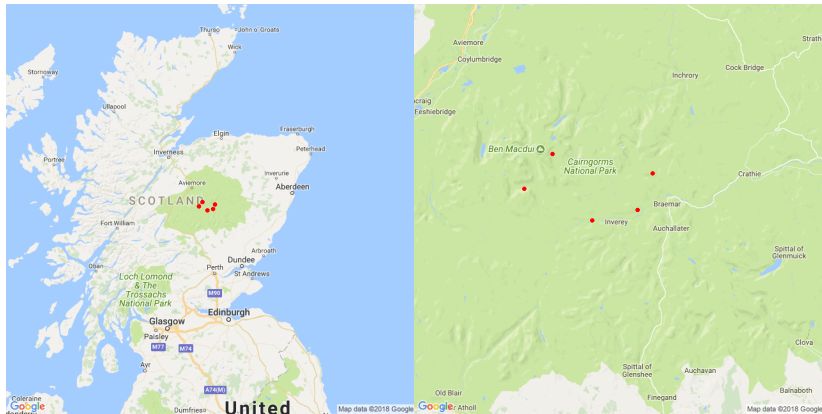
# Deer density data

Estimated deer densities based on relative likelihood of presence scores derived from presence/absence data (2005–2015)
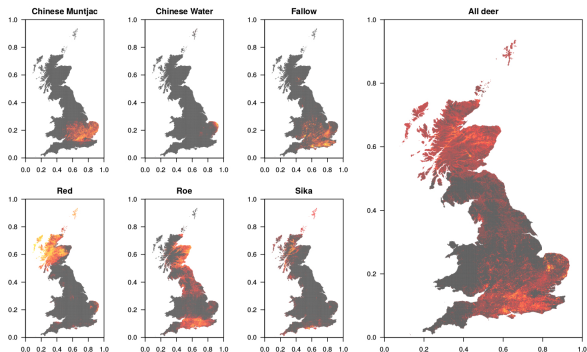


Method: similar to that described in Croft et al. (2017)

# (Limited) Tracking data

Available only for five red deer herds in Cairngorms National Park

# Modelling approach

1. Simulate deer herd locations to approximate density estimates

2. Estimate pairwise herd contact probability (direct and indirect) based on location and spread

3. Analyse constructed network representation of deer population
   - network metrics
   - disease simulation model (future)

# Model

Let $x$ be a two-dimensional random vector containing latitude and longitude coordinates.

Let $u(x)$ be a function indicating (estimated) animal densities across the landscape.

Define $h(x) = u(x)^c$ as the likelihood surface according to which we will simulate deer herd locations. Value of $c$ could be optimised according to some loss function. We used $c = 1$ for illustration.
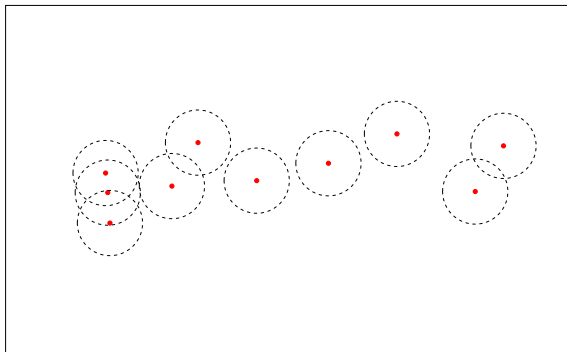
# Placement of deer herds

Random placement according to likelihood surface:
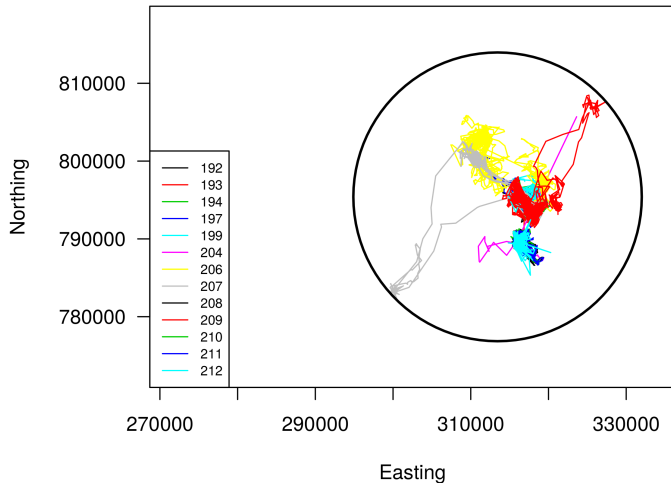$h(\mathbf{x}) = u(\mathbf{x})^c$
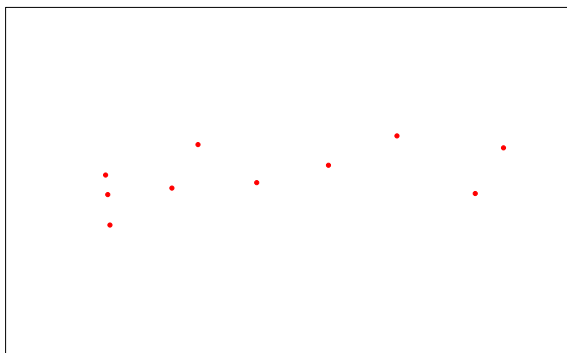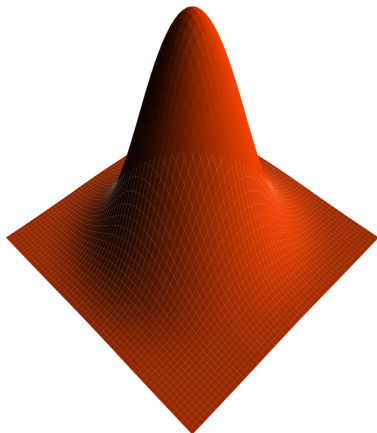
# Home range areas

Assume circular home ranges

# Use tracking data to inform home range size
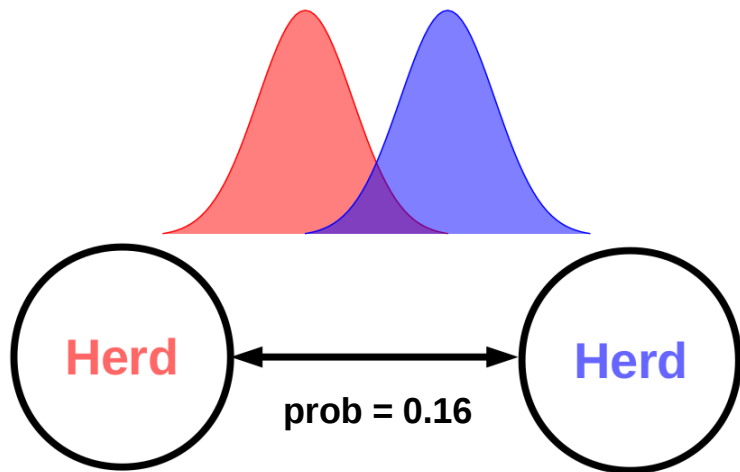


Invercauld: Red deer (2003/2004)

# Home range occupancy probability

- Assume bivariate Gaussian distribution
- Assume spread inversely related to deer density (as proxy for habitat suitability): $\sigma(\boldsymbol{x}_i) = \frac{1}{h(\boldsymbol{x}_i)^m}$
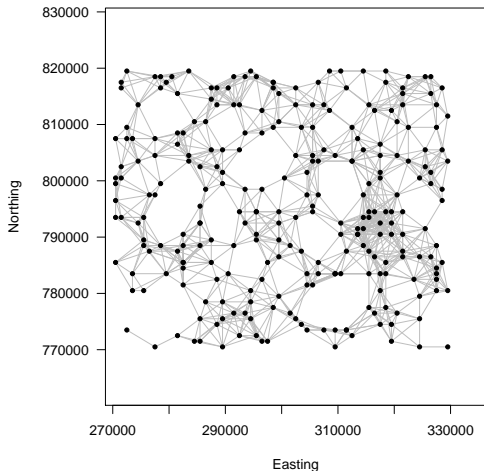
# Pairwise contact probabilities

Contact probability determined by degree of kernel overlap.
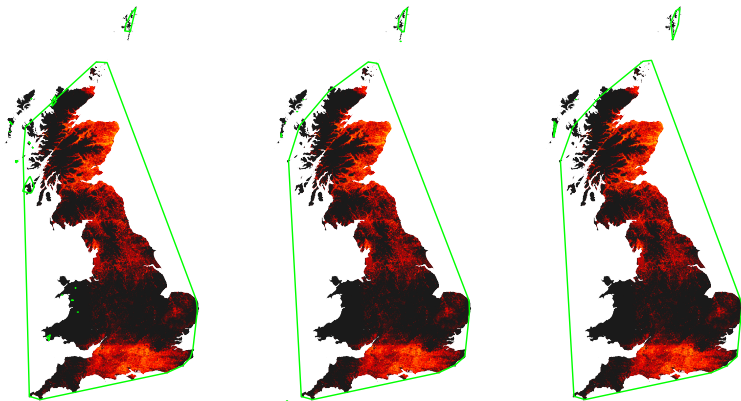Result: network representation of deer herds

# Constructed network (example)

Simulated red deer herd locations in Cairngorms National Park area (showing only edges with probability $\geq 0.5$)
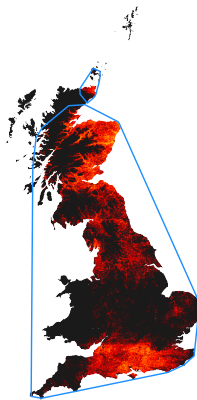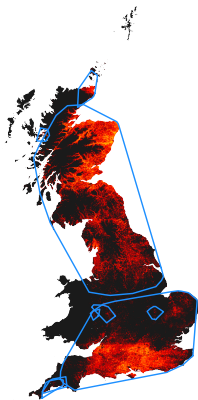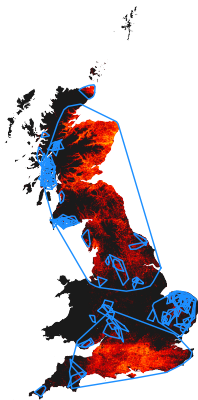
# Components in simulated red deer network
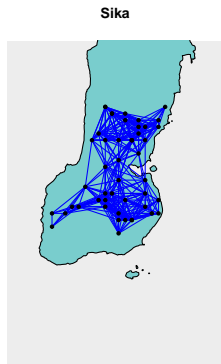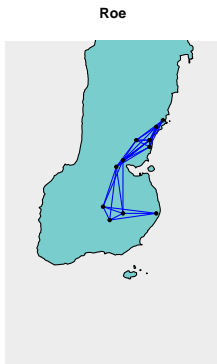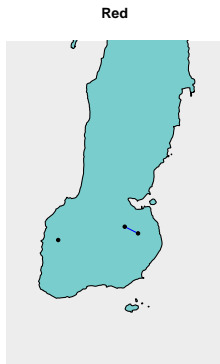
# Components in simulated roe deer network

# Sampling edges

Identify more probable infection clusters within larger roe deer network

# A recent request

Question: What do deer populations in Campbeltown area look like?



Red          Roe          Sika

# Limitations of this study

Need more/better data:

- tracking data only available for red deer
- deer herd size distribution
- inter-species transmission rate of CWD
- inter-species contact probability
- seasonal behaviour and migration

No upper or lower limits enforced on herd home range sizes.

# Potential future directions?

- Developed flexible framework which can be useful for study of other wildlife populations.

- Can incorporate data on natural barriers for deer movement—and thus disease spread—such as rivers, mountain ranges, fences, etc.

- Can combine constructed deer networks with farmed cattle/sheep/pig movement network data to study disease spread across multiple networks.

# Acknowledgements