

# Individual contact tracing using simulated real-time data

Stephen Catterall & Sarah Brocklehurst  
Biomathematics & Statistics Scotland

## Aim

Develop tools to assist contact tracing in the event of a disease outbreak in livestock in Scotland

- Make full use of all relevant data sources e.g. ScotEID database
- Explore the potential for improved efficiency of tracing given increasingly accurate records
- Allow use of data on individual animals to constrain possible contacts, thus allowing resources to be targeted at the highest risk contacts
- Take into account uncertainty due to missing observations e.g. due to EID read errors or delays in the submission of movement records
- Focus on identifying the likely contacts of a suspected infected animal during the early stages of a disease outbreak
- Initial focus on sheep and EID read errors, but approach can be extended to other species and sources of missing observations

## Methods – basic principles

### Pre-existing methods

- Typically based on identifying contacts e.g. batch sales, between holdings, but without making use of data on individual animals e.g. EpiContactTrace package in R

### Individual-based approach

- Tracing starts by using batch movement records to identify possible movement histories for a suspected infected sheep
- Individual animal records can then be used to constrain possible contacts, identify the most likely sources of infection, and those holdings currently likely to contain most contacts of the suspect sheep.

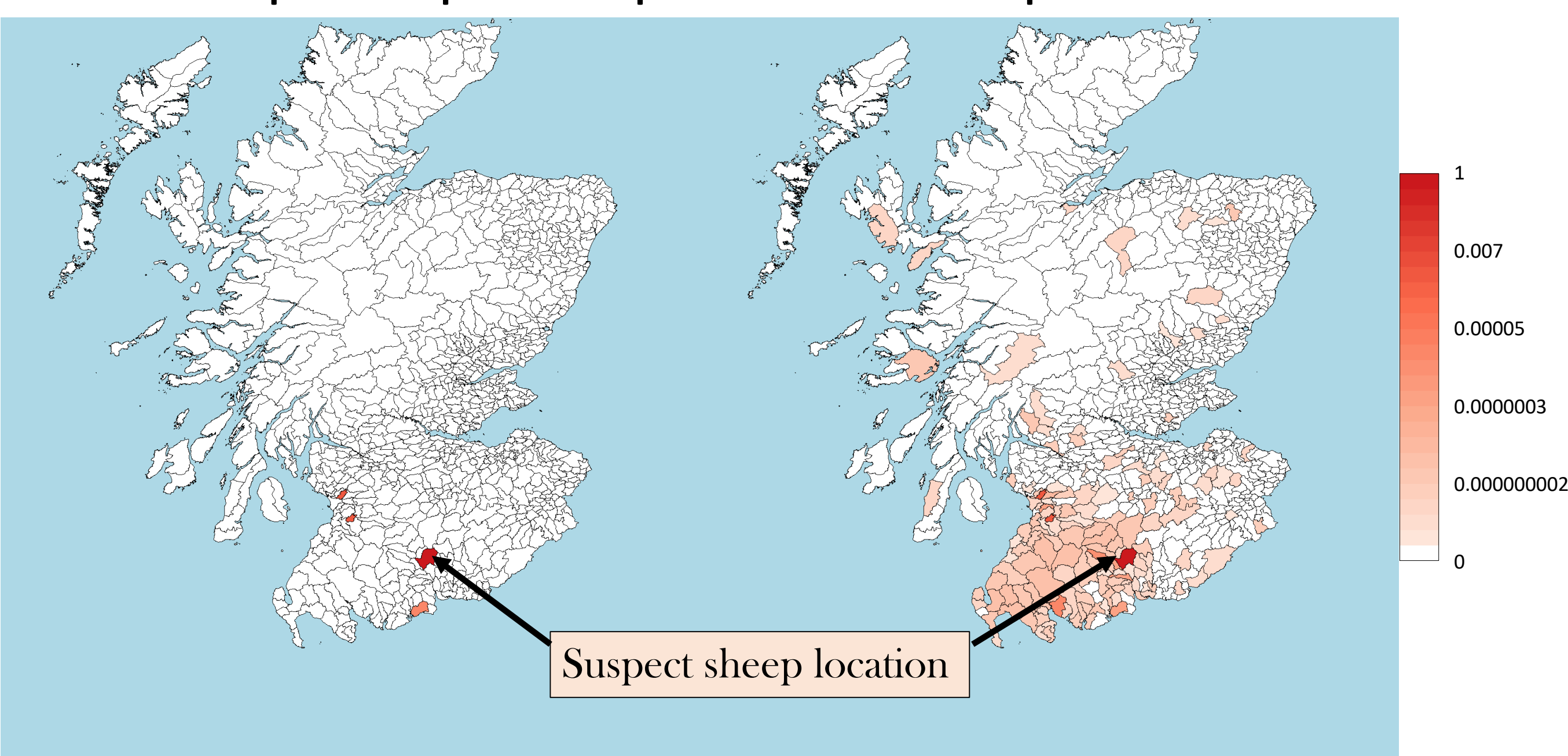
### Accounting for uncertainty

- Potential problem: information on movement of individuals is less accurate than information on movement of batches
- This is taken into account by allowing for a *distribution* of possible movement histories for the suspect sheep and each of its potential contacts

### Simulation framework

- To test and validate the methods, a simulation framework has been developed
- Individual animal movements are simulated, conditional on historic batch movement data and agricultural census data
- Electronic reads of each animal are simulated from a model with parameters derived from a GLMM fitted to EID tag read data from a pilot study
- Individual-based tracing is then performed using the simulated electronic read data in combination with the (assumed known) batch movements
- Risk maps and other outputs can be generated

### Sheep scab case study (simulated movements): estimated level of contact between a suspect sheep and sheep in all other Scottish parishes



Estimates based on perfect knowledge of all individual sheep (known from simulation)

Estimates based only on simulated EID reads at marts/abattoirs and batch movement records

## Data

Sheep EID reads were simulated

- characteristics based on the ScotEID real-time relational database for between-holding animal movements

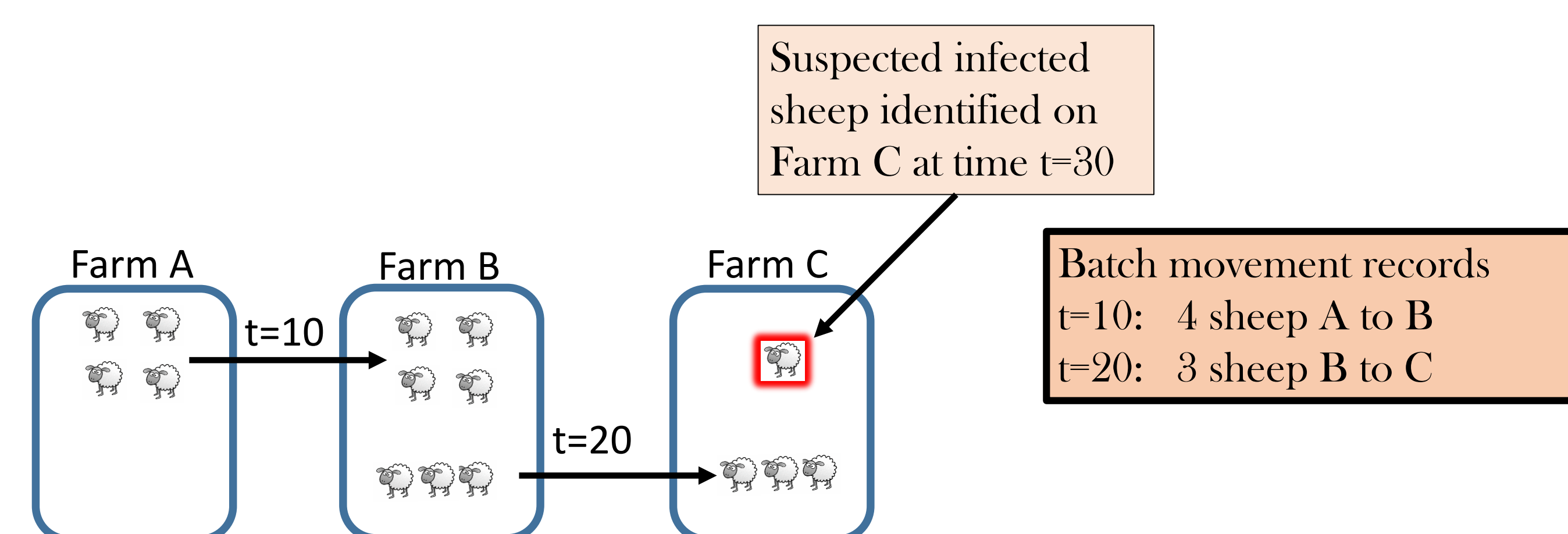
Key properties for ScotEID sheep data:

- Batch level data (source holding, destination holding, date, no. of animals) should be complete
- Individual sheep data are collected via EID tag readers at critical control points e.g. marts, abattoirs
- Although the rate at which EID tags are successfully read is high (~95%) it is still less than 100%
- EID tag data are not generally available for direct farm to farm movements

### Complexity of the network

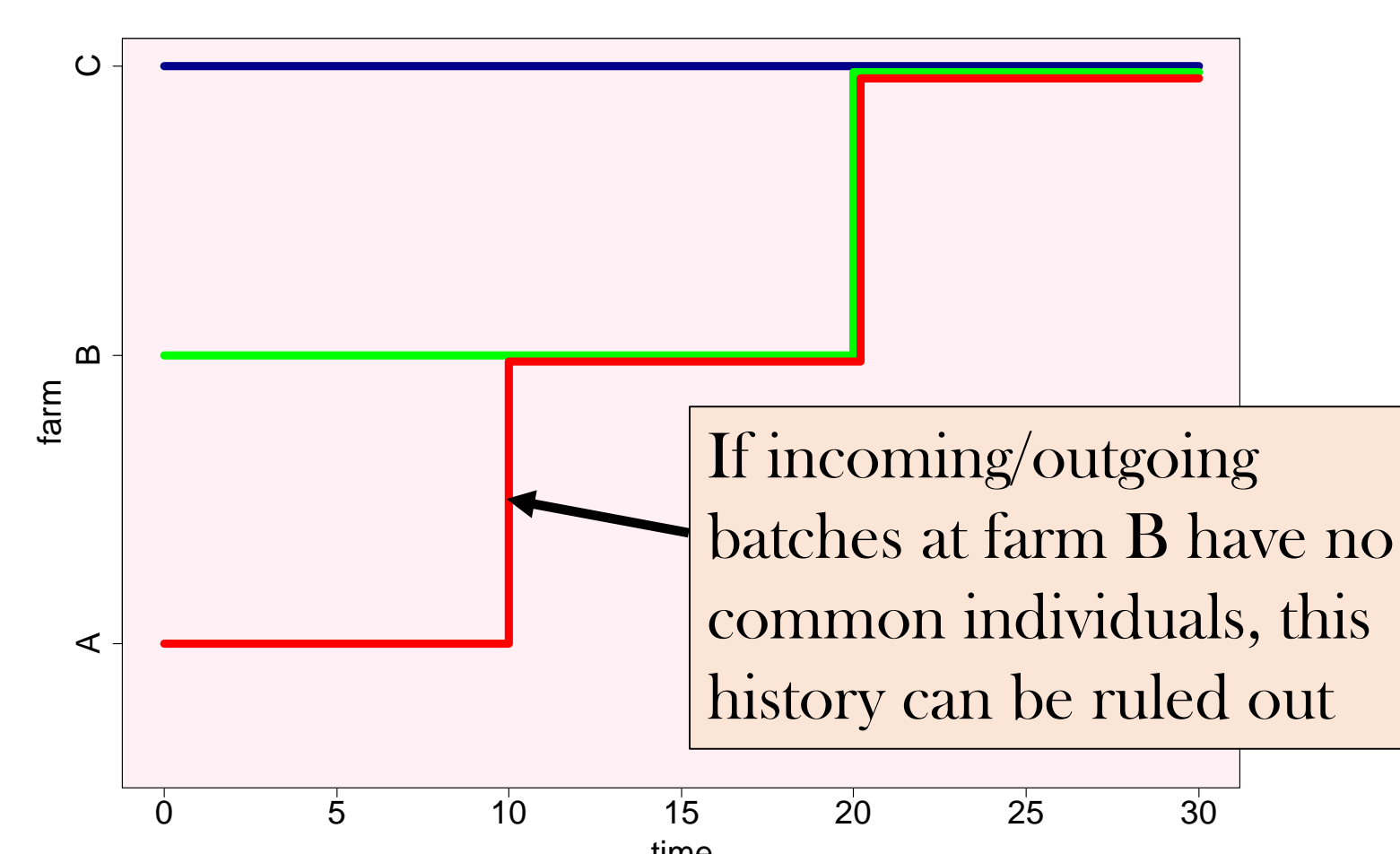
Visualization of sheep movement network in Scotland on 5th October 2010.

Two nodes (holdings) are linked if sheep move between them on that specific day.



### Individual based-approach: can Farm A be a source of the infected animal at C?

The sheep moving onto and off Farm B may or may not have any individuals in common. Individual level data can help to determine whether Farm A is likely to be a source of the infected animal.



There are three possible movement histories for the suspect sheep

### Accounting for uncertainty: where did the suspect sheep come from?

Batch movement records give us three possible movement histories for the suspect sheep. Individual level data are used to inform the probability of each movement history.

## Example: sheep scab case study

- Individual-based contact tracing is applicable to a range of infectious diseases.
- Most useful in situations where the risk of secondary transmission (i.e. from contacts of the suspect sheep to contacts of those contacts) is relatively low during the contact tracing period.

A simulated example: suppose that a sheep is discovered with sheep scab at a farm

- Individual-based tracing can be used to generate a risk map highlighting those parishes likely to contain the most contacts of the identified sheep.
- Given perfect movement data (left hand map) we can see that a handful of parishes will contain contacts of the identified sheep.
- Given only EID reads and batch movements (right hand map), the location of contacts is much less certain in this example. **However**, the highest risk parishes are precisely those that truly contain the suspect sheep's contacts (compare with left hand map), indicating that the method is valuable as a means of targeting resources.
- Important:** for many sheep there would be little difference between the two maps; this simulation was chosen as an illustration of how imperfect knowledge can change the estimated risk map.