HOW CLOSE IS TOO CLOSE?
BOVINE TB CLUSTER ANALYSIS

Animal & Plant Health Agency

Royal Veterinary College, University of London

TBEEP Project: Bovine TB (bTB) Risk Characterisation and Applied Epidemiology

TBEEP (bTB Epidemiology Enhancement Project) was established in May 2015 to design and implement improvements to Animal and Plant Health Agency (APHA) investigation of bovine tuberculosis on farms, and to the analysis and control of the bTB epidemic at regional and cluster level. The bTB Risk Characterization and Applied Epidemiology project is lead by the Epidemiology Assessment Centre (EAC) and includes analysts from the Department of Epidemiological Sciences (DES) in APHA .The project is delivered through a PhD project in collaboration with the Royal Veterinary College.

Can exploratory Spatial Analysis improve bTB disease control?

Improve understanding

bTB distribution does not follow administrative boundaries. Cluster identification sets the basis for understanding the drivers that give rise to them, to better inform disease control.

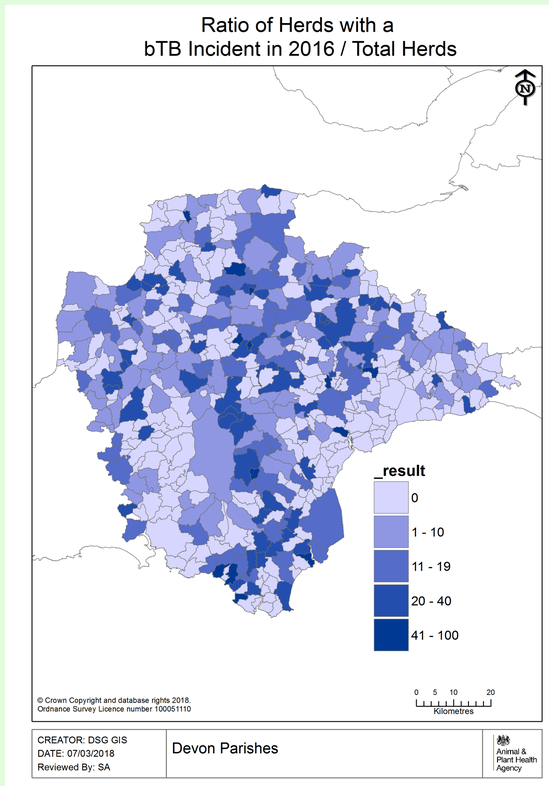
Improve reporting

Current reports use different administrative units as the basis for reporting. In the absence of a legal requirement to do so, a more informative report would be based around clusters of disease.

Improve operational delivery

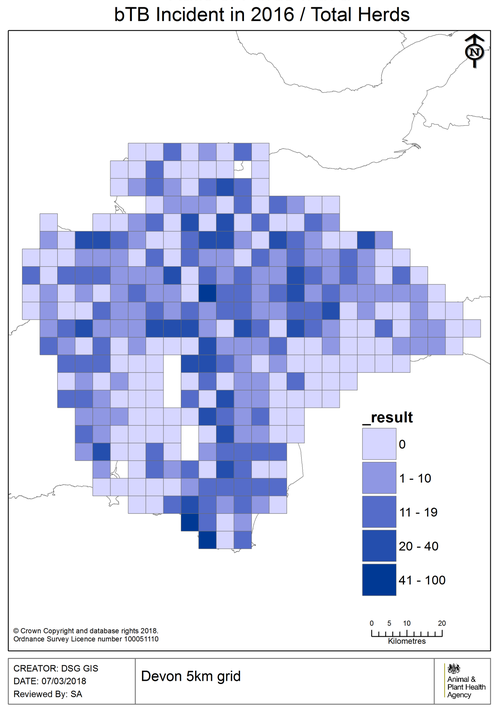
Better use of resources to target worst-affected areas more effectively.

Targeted disease control interventions applied at cluster level to improve outcomes.



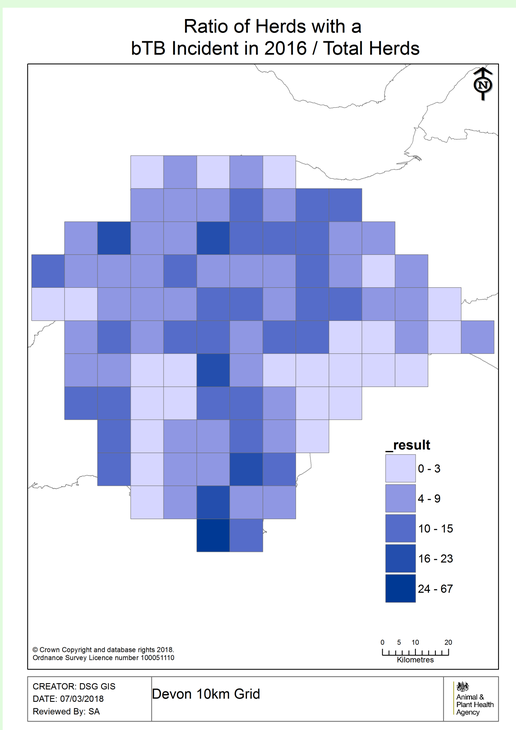
1. An Example data source:

- Ratio of bTB incidents vs total herds (2016) at parish level, within a county (Devon, England, UK).
- Is it easy to see the parishes that have a high proportion of incidents?
- Can we produce more informative outputs based on this data?

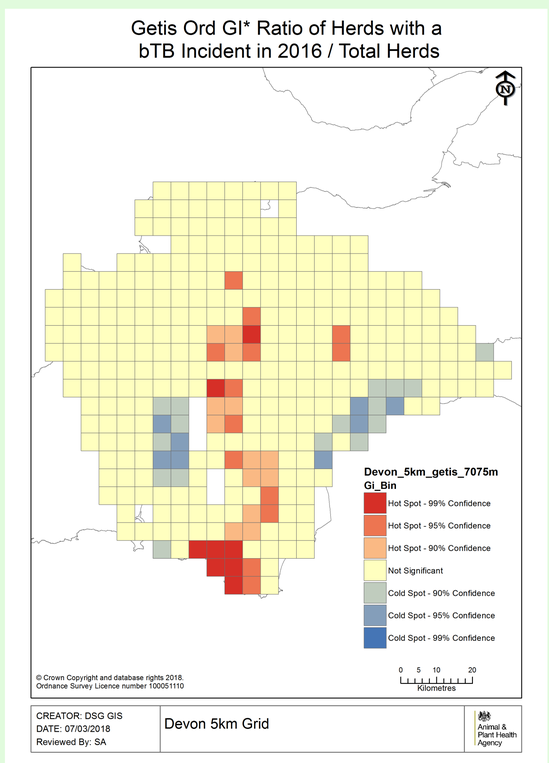


2. Standardization to 5 (left) or 10km (right) grid:

- How do we choose the best scale to aggregate data?
- Does this offer advantages?
- To what extent does it introduce bias?
- How do we treat outliers?

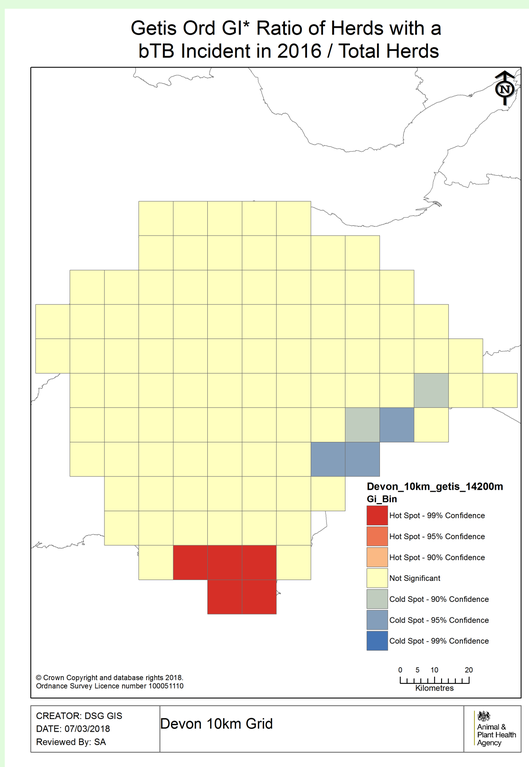


3. Exploratory **Spatial Analysis** techniques could aid in highlighting areas where further investigation may be useful, dependant on the specific question being asked. They are scale-dependant and are impacted by the selection of parameters (e.g. how local neighbourhoods are defined). Two examples are shown below:

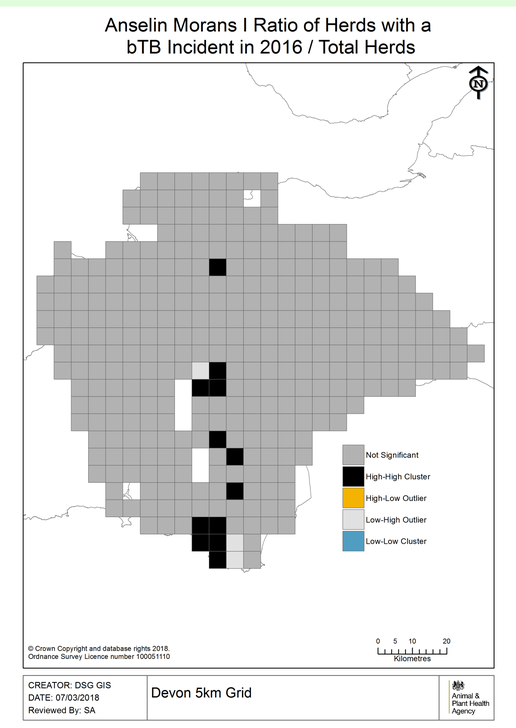


3.1. The **Getis Ord Gi*** statistic (left / below) compares the local sum for a feature and its neighbours, proportionally to the sum of all features. To be a statistically significant hot spot, a feature will have a high value and be surrounded by other features with high values as well.

- Do the outputs add insight beyond what we know already?
- What is a relevant scale given the question being asked?
- How many neighbours should be considered?
- Do these outputs combined with those above offer additional value?



3.2. Anselin Local Moran's I (right) can identify outliers within clusters; e.g. a grid cell that has a high value, surrounded by low values. These exploratory techniques can provide basic additional context to standard choropleth maps of counts and rates.



Note the impact of:

- The scale chosen.
- The methodology for selecting neighbours and their number.
- The edge effects introduced from aggregating to a grid.

4. Next steps:

- More advanced statistics may offer potential for identifying clusters of farms based on measures of similarity in spatial and non-spatial contexts.
- Analysis of farm attribute data, alongside spatial information relative to cattle and supplementary risk factors used to monitor of spatial clusters of bTB.

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