CA_Ch3: Spatial cluster analysis case study - Salmonella infection in feral pigs in Australia

MASSEY UNIVERSITY
TE KUNENGA KI PŪREHUROA
UNIVERSITY OF NEW ZEALAND

3.1 Background

"A study was undertaken in north-west Australia to investigate the risk to co-grazing livestock from feral pig populations that can be infected with *Salmonella* spp. ([Ward et al., 2013](#)). The researchers wanted to identify the distribution of salmonella-infected pigs in the study area to assess the risk of their contact with grazing livestock whose range was known.

The researchers knew from previous research and reports from recreational hunters the approximate distribution of feral pigs, and the fact that they existed mainly in small family groups. They undertook a helicopter- and ground-based sampling programme to shoot and collect post-mortem samples from all the pigs they could identify in a location. They geo-referenced the location of sample collection and corresponding results of bacteriological analysis of samples collected from them."

The data derived from this study were downloaded from the 'EpiTools' website (https://epitools.ausvet.com.au) and further augmented for this case study by simulation to recreate the part of the analysis published by Ward et al. (2013). A dictionary of the study data in the "feralPigs" shape file for this exercise is provided in Table 3.1. This file and other geographic data for this example are provided in a zipped file named "AUS-FeralPigs.zip" in the "Data_CA_exercise3" folder. Click HERE to download.

ᴛable 3.1: Definitions and descriptions of variables in 'feralPigs' shape file[ss1]

Variable name	Description
id	Location ID number
nSample	Number of pigs sampled at location
nPos	Number of sampled pigs positive for salmonella infection
salmStatus	Status of pigs at location- 0 = all negative, 1 = 1 or more positive

CONTINUE

Exercise 3.1: Exploratory spatial data analysis

"**In the following exercises, you will work with both vector (point, line) and raster data to visualise the data collected in the study and information on other geographic features. You will then investigate if spatial clusters of salmonella infection in pigs exist and generate hypotheses about factors associated with your findings**.

Undertake an analysis of these data to investigate whether clusters of pigs with salmonellosis occur in the study area."

Instructions

- Create a new project in QGIS for this exercise

- Re-project the spatial data provided to the local CRS (EPSG = 3577)

- Plot each spatial layer individually and then layered in one map

- Plot separate maps with salmonella status as either a binary (negative-positive) variable as provided with the "salmStatus" variable or as a

proportion (number of salmonella pigs at location divided by number of pigs sampled at location)- you will need to create this new variable.

CONTINUE

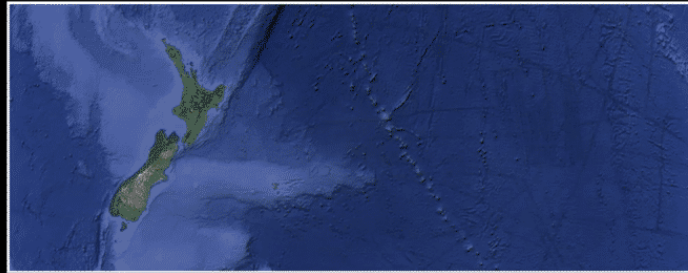Have you completed the exploratory spatial data analysis exercise?
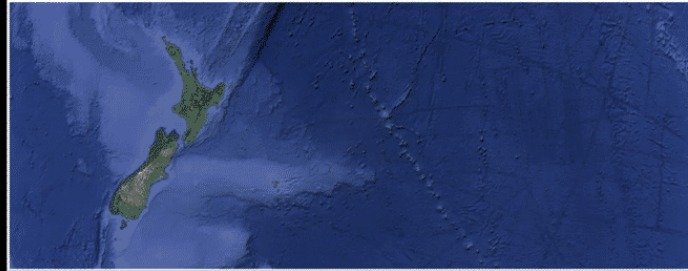
○ Yes

○ No

SUBMIT

CONTINUE

"Let's start from the beginning by creating a new QGIS project for this exercise"

Click ▶ to play the demonstration video
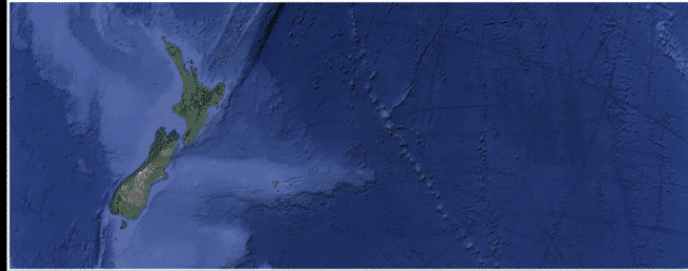

CONTINUE

CONTINUE

" The next step is to create the heatmap so we can visualise the intensity of positive herds compared with the underlying locations across the whole population"

Click ▶ to play the demonstration video

CONTINUE

Exercise 3.2: Cluster analysis by SatScan

"From the previous exercise, we found that the distribution of the population of feral pigs groups and salmonella-infected pig groups does not appear random. We will investigate this further by applying SatScan."

CONTINUE

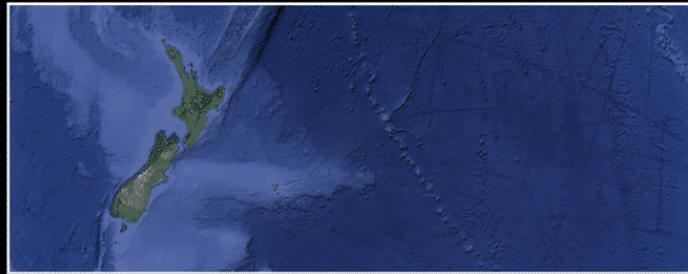Have you conducted spatial cluster analysis using SatScan?

○ Yes

○ No

SUBMIT

" **Let's begin with the data preparation and SatScan analysis process.** "
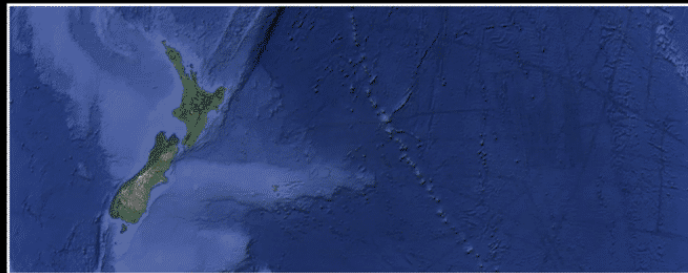
Click ▶ to view the demonstration video

> "Next, we will prepare SatScan results in CSV format.
>
> Then, import to QGIS for visualisation of spatial clusters."

Click ▶ to view the demonstration video

CONTINUE

Congratulations - end of lesson reached

Reference

Ward, M.P., B.D. Cowled, F. Galea, M.G. Garner, S.W. Laffan, I. Marsh, K. Negus, S.D. Sarre, and A.P. Woolnough. 2013. Salmonella infection in a remote, isolated wild pig population. Vet. Microbiol. 162:921–929. doi:10.1016/j.vetmic.2012.11.036