Geographic determinants for human Campylobacter cases in Scotland

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Introduction

Campylobacter spp. are a major cause of infectious gastroenteritis in Scotland. In addition to the consumption of infected food, environmental sources including surface water[1] have been linked with *Campylobacter* infection. This study investigated geographical determinants of infection within Scotland addressing the following questions:

- Can environmental risk factors for human Campylobacter cases be identified?
- Is deprivation a risk factor for Campylobacter infections?
- Are there rural-urban differences in Campylobacter infections?
- Are there differences in the reporting of Campylobacter infections between Scottish NHS boards?

Methodology

Data on human *Campylobacter* cases at the postcode sector level (920 in Scotland) from 2000 to 2006 were gathered from 12 Scottish NHS boards (Orkney, Shetland and the Western Isles were excluded) and denominator data taken from the 2001 Scottish census. The predictor data include:

- NHS board.
- The Carstairs[2] deprivation score.
- The number of private water supplies per person.
- The densities of people (proxy for rural/urban), sheep, cattle and poultry.
- The mean case rate in the five nearest neighbour postcode sectors.

Following univariate screening, predictors with p < 0.25 were entered into a multivariate GLM with a quasipoisson error term. Cases were the outcome offset against the expected number of cases. Significant (p<0.001) spatial autocorrelation in the model residuals was removed by inclusion of the neighbour case rates.
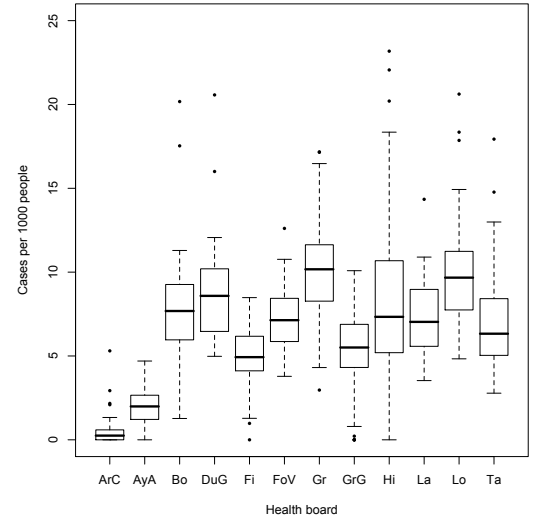

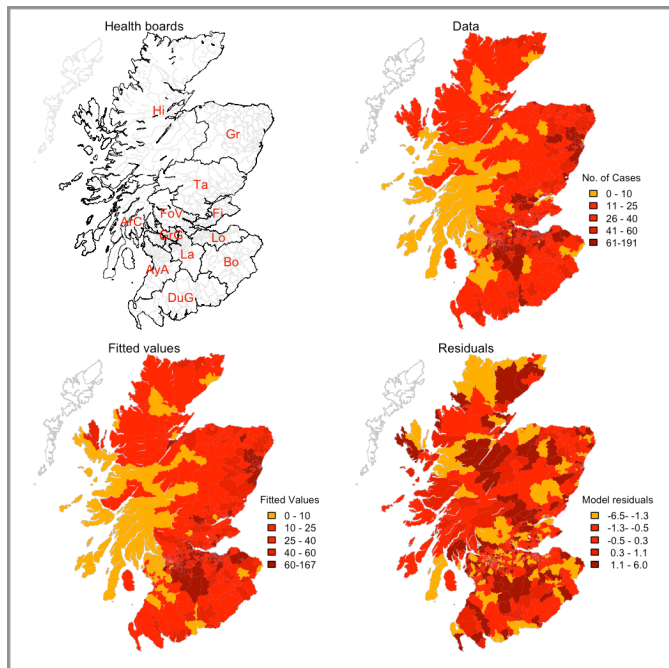Figure 1: Boxplots of case rates in each NHS board. Abbreviations are expanded in Table 1.

Figure 2: Maps of the NHS boards (abbreviations are expanded in Table 1), the case rate data, the fitted values and the model residuals. There is evidence for clustering in the data and subsequently fitted values but not the residuals (Morans I p > 0.5).

Results

32,059 cases were reported over the period of the study with substantial variation in case rates between the NHS boards (Figure 1); in particular the Ayrshire and Arran and Argyll and Clyde health boards have lower case rates.

All predictors were significant in univariate analysis with the exception of sheep and poultry densities. Despite this, the multivariate model included only four significant terms (Table 1) and the model fit was good (Figures 2 and 3).

Predictor	Unit (abbreviated)	Estimate	SE	t-value	p-value
Health Board	Argyll & Clyde (ArC)	-2.639	0.102	-25.67	<0.001
	Ayrshire & Arran (AyA)	-1.269	0.054	-23.42	<0.001
	Borders (Bo)	-0.358	0.066	-5.470	<0.001
	Dumfries & Galloway (DuG)	-0.302	0.063	-4.787	<0.001
	Fife (Fi)	-0.574	0.046	-12.49	<0.001
	Forth Valley (FoV)	-0.352	0.052	-6.776	<0.001
	Grampian (Gr)	-0.291	0.059	-4.959	<0.001
	Greater Glasgow (GrG)	-0.392	0.040	-9.669	<0.001
	Highland (Hi)	-0.445	0.055	-8.061	<0.001
	Lanarkshire (La)	-0.313	0.050	-6.312	<0.001
	(La)	-0.244	0.058	-4.225	<0.001
	Tayside (Ta)	-0.286	0.072	-3.995	<0.001
Neighbours	cases / 1000	0.064	0.006	10.87	<0.001
Carstairs score		-0.032	0.003	-12.09	<0.001
Private water supplies[1]	Supplies / person	2.251	0.658	3.419	<0.001
Human density[1]	people / km^2	0.021	0.177	-1.235	0.217
Cattle density[1]	cattle / km^2	0.020	0.028	-0.708	0.479
Sheep density[1]	sheep / km^2	0.003	0.025	-0.103	0.918
Human density[1]	people / km^2	-0.006	0.009	0.614	0.540

[1] log$_{10}$ transformed

Table 1: Multivariate GLM analysis of the case rates. The final model is in black and dropped predictors in red.
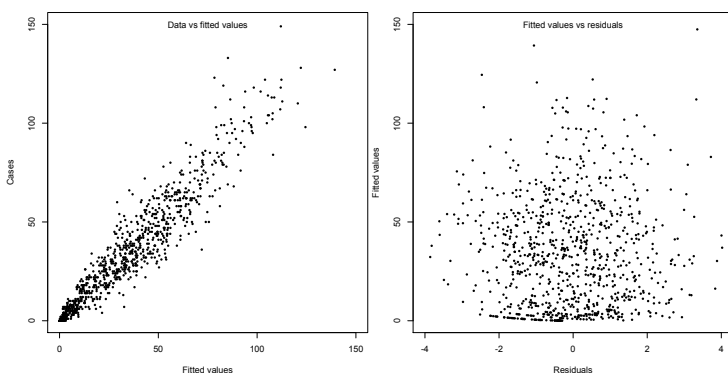

Figure 3: Plots of the data against the fitted values for the model in Table 2 and the residuals against the fitted values for this model.

Discussion

This model indicates that the pattern in *Campylobacter* reporting is not uniform across all Scottish NHS boards. As a result the NHS board is the strongest determinant in reporting for *Campylobacter*.

Many diseases have a positive association with deprivation, however this model shows that deprivation is protective for infection with *Campylobacter*. This could be a result of the development of resistance to bacterial infection, differences in the sources of infection to which individuals are exposed, or differences in diet.

The model supports previous studies which show an association with untreated water[1], but suggests that there are no rural-urban differences in risk. Livestock species were not a risk factor, however this will be investigated further by stratifying these risks by MLST.

References

[1] Sopwith W et al (2008) EID 14(11):1769 -73
[2] Carstairs V and Morris R (1990) Hea. Bull, 48:162-75