# Campylobacteriosis in humans: a Bayesian source attribution approach.

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## Introduction

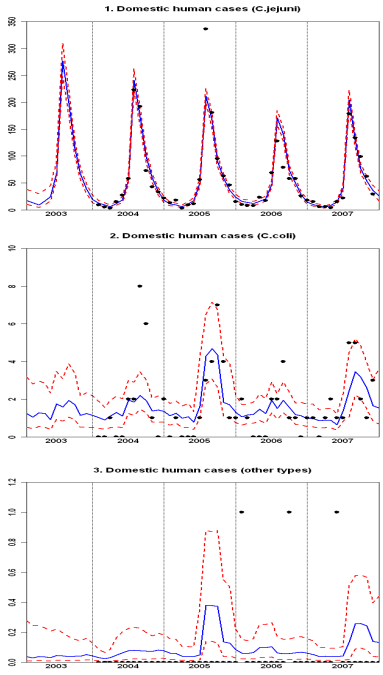
This work is part of work package 4 in CampEc-NET, a one-year network project, which in Finland is funded by Tekes, Evira, KTL and ETL. The aim of the WP is to integrate existing veterinary and medical laboratory based surveillance data, specifically towards source attribution modelling of *Campylobacter* infections. Broiler is thought to be an important source of *Campylobacter* infections. It is known that both prevalence in broiler production and incidence of human cases show a concomitant annual pattern with a peak in July-August. However, comparable data representing other sources are rare. It is known, though, that *C. coli* is typical in pigs, whereas *C. jejuni* dominates in human cases. Accounting for species specific surveillance data from humans as well as from broilers, cattle and pigs, a source attribution can be attempted. Yet, in full source attribution this depends on what is assumed about the net effect of all other exposure sources that remain.

## Data

Monthly human campylobacteriosis cases were available from the National Infectious Diseases Register, National Public Health Institute KTL. Based on travel information, only domestic sporadic cases were included from the period 2004-2007. Also monthly results (*Campylobacter* positive caecal samples) from broiler surveillance were available from 2004 to 2007 in Finland. In addition, faecal samples were available for both cattle and pigs, but only for two distinct years. Monthly consumption data were obtained from TNS Gallup Oy.

## Results and discussion

Monthly incidence of *C. jejuni* in humans follows the *C. jejuni* prevalence in broilers and broiler consumption. Other *Campylobacter* species do not show a clear concomitant pattern in human and food production data, hence the association is weaker. The overall mean share of broiler related cases was 61%-78% (cattle 4%-6%, pig 1%-2%, unknown 17%-31%), when minimum separation between two change points in the intensity of the unknowns was assumed 2-4 months, with 10 change points. I.e. the result is sensitive to the assumptions concerning the other non-monitored exposures. Nevertheless, in comparison to broiler, pigs and cattle show less probable association in all model versions. The change point model can locate times when there is an excess number of cases that are not explained by the other intensities.




Figures 1-3: expected monhtly number of domestic human cases due to *C. jejuni*, *C. coli* and other *Campylobacter*. Reported cases are shown as dots.

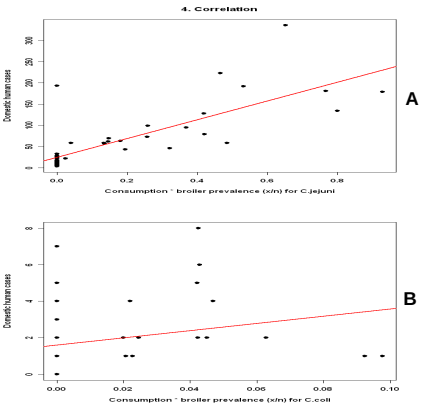



Figure 4: Correlation between human cases and the product of prevalence (x/n) and broiler consumption (**A**) *C.jejuni*, (**B**) *C.coli* (observed data).

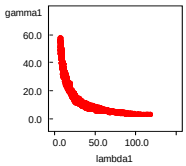



Figure 5: Posterior distribution of parameters λ (food source 1: broiler) and γ (species 1: *C.jejuni*).

## Methods

The human case intensities associated with broiler, cattle and pig were defined using prevalence surveillance (as a time series model) and consumption data for each. The intensity for the remaining sources was defined as a piecewise constant function with ten unknown change points. The source attribution probabilities can be computed from the competing intensities, $P_k=\Lambda_k/(\sum_k \Lambda_k)$. Yet, there can be no proof of direct causality due to a single source excluding all other unknown effects, only probabilities of association. The model was implemented in WinBUGS.

Probability model of registered and surely domestic cases ($Y_{i,c}$, see Fig. 1-3), species c, month i:

$$Y_{i,c} \sim Poisson\left(\sum_{k=1}^{K} \Lambda_{i,k,c} \times \hat{f}\right)$$

$\hat{f}$ is the estimated fraction of those registered as domestic cases among all domestic cases. This was assumed the same as the ratio of all cases with reported travel status and all reported cases.

Expected number of cases, species c, month i, associated with source k:

$$\Lambda_{i,k,c} = \lambda_k \gamma_c p_{i,k,c} C_{i,k}$$

$C_{i,k}$ is monthly consumption of source k, $\lambda_k$ is constant effect of source k, $\gamma_c$ is constant effect of species group c, and p is surveillance prevalence in the time series model, respectively.

Prior densities of parameters:

$$\log \lambda_k \sim N(0,1)$$
$$\log \gamma_c \sim N(0,1)$$

The complete posterior distribution is of the form:

$$P([\Lambda_{i,k,c}] | [Y_{i,c}], [x_{i,k,c}], [n_{i,k,c}])$$

where x and n represent surveillance samples from broiler, cattle and pigs, and Y are the reported human cases.

## References

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