Bayesian predictive risk modeling of microbial criteria for Campylobacter in broilers

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Bayesian Predictive Risk modeling of Microbial Criteria for Campylobacter in broilers

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Abstract

Microbial Criteria define the acceptability of food products, based on the presence or detected number of microorganisms in samples. The criteria are applied at the level of defined food lots. Generally, these are interpreted as statistical batches representing the production [1]. The batches not complying with a criterion can then be e.g. rejected. A risk reduction for consumers is therefore expected. However, a quantitative estimate of the implied risk reduction is non-trivial, because it depends on many unknown parameters. The quantity and quality of data lead to uncertainties which can be assessed by computing posterior distribution of the parameters - a Bayesian evidence synthesis. The outcome of a defined Microbial Criterion (MC) for a batch provides additional evidence concerning the batch. Posterior predictive consumer risk (probability of illness) was computed for such batch(es) with the given outcome (MC met / MC not met / MC not applied) with OpenBUGS.

Complementing evidence from two sources

Lindblad et al. [2] describe samples from a representative collection of N batches, but only one measurement (carcass) is obtained per batch. The resulting K positive outcomes provide concentrations y_k, k=1,…,K. Since batch status was not known beforehand, there is some evidence on batch prevalence q and total variance, but not on within batch prevalences p.

Hansson et al. [3] describe a collection of batches known to be positive, and batch specific samples of size N_j. Due to this selection, there is no evidence on batch prevalence, but some evidence on within batch prevalences. Sample means and sample standard deviations of positive concentrations y_{ij} were given, which provides evidence on variance components σ_w^2 (within batch) and σ_b^2 (between batch).

The concentration model is defined for $\log_{10}$-concentrations that were transformed from original data to obtain comparable log-cfu/g values, with μ as the common population mean of positive log-concentrations.

Posterior density, assuming individual measurements y_k , y_{ij}:

$$p(\mu,\sigma_w^2,\sigma_b^2,\{\mu_k\},\{\mu_j\},q,\alpha,\{p_j\}\,|\,\text{Lindbland et al. \& Hansson et al. data}) \propto$$

$$\prod_{k=1}^{K} \mathrm{N}(y_k \mid \mu_k,\sigma_w^2)\mathrm{N}(\mu_k \mid \mu,\sigma_b^2)\prod_{j=1}^{J}\prod_{i=1}^{x_j} \mathrm{N}(y_{ij} \mid \mu_j,\sigma_w^2)\mathrm{N}(\mu_j \mid \mu,\sigma_b^2)$$

$$\times \mathrm{Bin}(K \mid N, q\alpha/(\alpha+2))\prod_{j=1}^{J} \mathrm{Bin}(x_j \mid N_j, p_j)\mathrm{Beta}(p_j \mid \alpha,2)\times p(\mu,\sigma_w^2,\sigma_b^2,q,\alpha)$$

In Hansson et al., only means and SDs were reported for x_j positive concentrations. For that, we solved full conditional density for $\tau_w=1/\sigma_w^2$ to be coded in BUGS, requiring only summary statistics. For the remaining parts the likelihood was directly coded as such in BUGS.

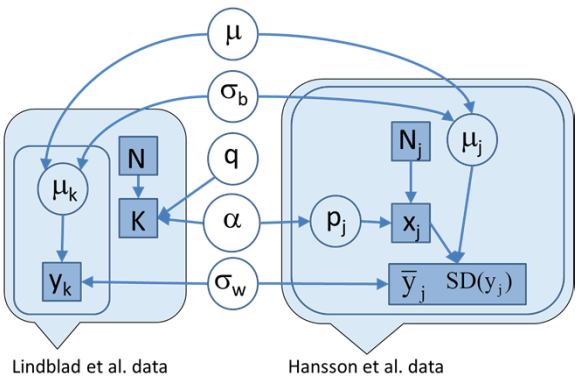

Figure 1: Directed Acyclic Graph (DAG) for the evidence synthesis.

Evidence synthesis combined with batch predictions under MC

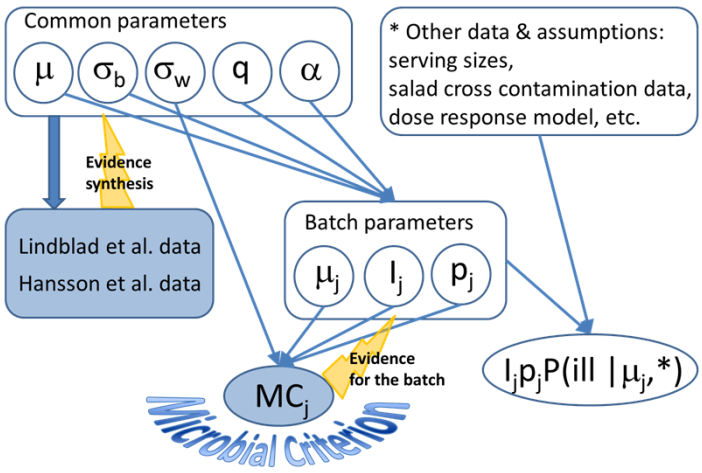

Figure 2: DAG of the Bayesian model combining both data sets for common parameters, and for predicting batch parameters to be further updated by the (binary) MC status of the batch. Risk is the probability of illness resulting from accepted batches.

From the posterior distribution of common parameters, batch parameters (batch mean μ_j, hidden contamination (binary) status l_j, within batch prevalence p_j) were predicted as a posterior predictive distribution. After adding batch specific additional evidence on the MC outcome ('MC is met'), posterior distribution of batch parameters was updated and predicted risk concerning such batch was computed. The absolute risk value also depends on other additional assumptions [4] (Fig. 2). Relative risks were compared (Table 1).

Table 1: RR = P_{batch}(ill | MC met) / P_{batch}(ill | MC not applied) for batches under different MC options 'n/c/m' = 'sample size / max positives / max cfu/g'. 10^5 MCMC iterations.

RR	m=1000	m=1000	m=100	m=100
	n=5	n=10	n=5	n=10
c=0	0.2	0.1	0.01	0.00
c=1	0.4	0.2	0.1	0.01
c=2	0.6	0.3	0.1	0.03
c=3	0.8	0.5	0.3	0.05
c=4	0.9	0.6	0.5	0.08

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References

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