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Updating Parameters of the Chicken Processing Line Model

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A mathematical model of chicken processing that quantitatively describes the transmission of *Campylobacter* on chicken carcasses from slaughter to chicken meat product has been developed in Nauta *et al.* (2005). This model was quantified with expert judgment. Recent availability of data allows updating parameters of the model to better describe processes observed in slaughterhouses. We propose Bayesian updating as a suitable technique to update expert judgment with microbiological data. Berrang and Dickens's data are used to demonstrate performance of this method in updating parameters of the chicken processing line model.

KEY WORDS: Bayesian updating; *Campylobacter*; chicken processing; expert judgment; probabilistic inversion

1. INTRODUCTION

Campylobacter is a leading cause of zoonotic enteric infections in most developed and developing nations worldwide (WHO, 2000). Although it is generally recognized that there are many sources of *Campylobacter*, campylobacteriosis is predominantly believed to be associated with the consumption of poultry meat, especially fresh broiler meat.[1,2] As a consequence, the control of *Campylobacter* in poultry meat is a priority for food safety managers in many countries, and several quantitative microbiological risk assessments (QMRAs) dealing with this food-pathogen combination have been performed worldwide.[3]

As part of a national QMRA in the Netherlands,[4] a mathematical model of broiler chicken processing has been developed that quantitatively describes the transmission of *Campylobacter* on chicken carcasses from slaughter to chicken meat product. The model has been published in two papers, one where the model is explained and the dynamics are explored[5] and one where it is implemented in the national Dutch QMRA.[6] Whereas in other models built for that purpose the changes in concentration on carcasses are based on published microbiological data,[7,8] this model has a mechanistic basis: the parameters in this model are transfer coefficients of bacteria from the chickens' skin and intestines to the processing environment and from the environment back to the chickens' skin. This approach has the advantage that it is better suited to predict the effects of risk management interventions proposed for the control of *Campylobacter*.[3] However, a disadvantage is that the available microbiological data alone do not allow estimation of the model parameter values. Therefore, to quantify the model, structured expert judgment was used.[9] Experts were asked to assess the uncertainty regarding variables that can be predicted by the model. Their distributions were combined and then pulled back onto the parameter space of the model to obtain distributions of model parameters through probabilistic inversion.[10]

A remaining drawback of this processing model is that it does not take advantage of published microbiological data on the impact of the different processes involved in broiler chicken processing on the *Campylobacter* concentration. Such data are recently accumulating, and may be used to improve the model

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parameter estimates or to adjust them to a typical situation in a country or region in which those data are obtained.

Here we show how the parameter estimates for the industrial processing model of Nauta *et al.*[6] can be updated by the use of Bayesian inference. As an example we use the data of Berrang and Dickens,[11] who collected quantitative data on *Campylobacter* during poultry processing and published the number of colony forming units (cfu) before and after a processing stage. Because these data do not fully report the initial infection rates, we have made assumptions based on Nauta *et al.*[6] The Bayesian updating contains a new wrinkle, as the data give infection rates per flock, whereas the model being updated is per chicken.

This article is organized as follows. In Section 2, we briefly discuss the chicken processing line model. Section 3 presents Berrang's data and a general formulation of Bayesian updating, as well as an application of Bayesian updating in finding new parameters of the chicken processing line model. Performance of the updated models is tested. A final section discusses conclusions.

2. MODEL

2.1. Model Description

The chicken processing line starts with collecting poultry flocks on the farm, placing them into the truck, transporting them to the processing plant, and processing, all on the same day. At the processing plant, animals are hung upside down on a line of shackles, stunned, and killed. In the Netherlands, the process for the production of fresh meat then typically consists of the following phases: low scalding (transport through a warm water tank of 52 °C), defeathering (removal of the feathers), evisceration (extraction of intestines), washing (spraying with water), and air chilling.

During different processing stages, inactivation, removal, and cross-contamination may change the concentrations and prevalence of *Campylobacter* on the carcasses of processed flocks. The mechanics of these changes are described mathematically in the chicken processing model developed by Nauta *et al.*,[5] to which the reader is referred for a detailed description. The main output variable of the model is $N_{\text{ext,S}}(i)$, representing the number of colony forming units (cfu) of *Campylobacter* on the exterior of carcass i at the end of processing stage S (scalding, defeathering, evisceration, washing, chilling). The input variables are $N_{\text{ext,input}}$ and C_{fec}, denoting the number of cfus on the exterior and in the feces of a chicken prior to processing. The initial environmental contamination must also be specified. For each processing stage S, transfer coefficients are defined. A joint distribution expressing the uncertainty of the values of these transfer coefficients was obtained via probabilistic inversion from experts' assessments of $N_{\text{ext,S}}$ in specific conditions that are predicted by the model.[9,12]

A brief description of probabilistic inversion is as follows: a diffuse starting distribution of transfer coefficients is chosen, and sampled N times. The model is run on each sample (each vector of values for all coefficients), thereby generating a distribution of values of $N_{\text{ext,S}}$. The output is appended to the input, creating a sample of N input-output values. This sample is now reweighted in such a way that the weighted sample distribution complies with the experts' assessments (experts' assessments are in form of quantile information). Hence the joint distribution of parameters of the model is available only in the form of samples. Table I shows the means and medians of parameters of the chicken processing line model.

Table I. Means and Medians of Parameters of the Chicken Processing Line Model

	Scalding		Defeathering		Evisceration		Washing		Chilling	
Parameter	Mean	Median	Mean	Median	Mean	Median	Mean	Median	Mean	Median
a_{ext}	0.7645	0.8581	0.8652	0.9095	0.4631	0.4600	0.3421	0.3070	0.0901	0.0609
c_{ext}	0.7098	0.7141	0.0511	0.0485	0.0416	0.0420	0.2121	0.2455	0.1948	0.0348
b_{env}	8.1e−6	6.8e−6	0.0279	0.0010	1.1e−5	1e−5	0.0060	0.0010	0.0080	0.0037
c_{env}	0.0490	0.0355	0.1036	0.1145	0.0848	0.0850	0.0631	0.0619	0.0171	0.0153
$1-a_{\text{fec}}$	1.6e−6	1.4e−6	1.3e−5	1e−5	0.0062	0.0027				
w_{fec}	1.8624	1.8440	1.7097	1.7330	1.7428	1.9560				
p_{fec}	0.4840	0.4800	0.6955	0.7044	0.6573	0.6822				

Note: For a description of the parameters, see Nauta *et al.*[5]

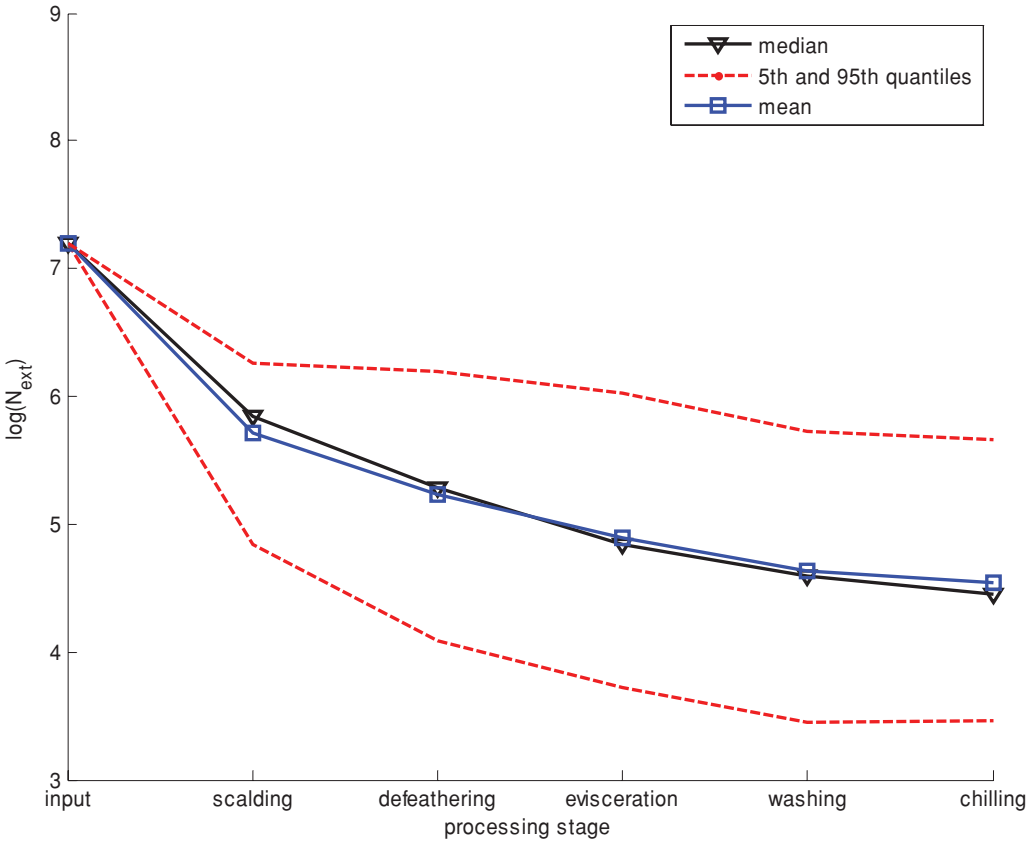

Fig. 1. Log(N_{ext}) constant initial contamination and uncertain parameters.

2.2. Model Analysis

Nauta *et al.*[6] implemented the model as a Monte Carlo simulation model, using the median values of the parameters given in Table I as constants in the baseline model.

The model requires specification of the initial distributions for external ($N_{ext,Input}$), the fecal contamination (C_{fec}), and initial contamination of the environment. It was observed in Reference 5 that quite quickly (after 10 carcasses pass through), the number of *Campylobacter* oscillates around an equilibrium value in the environment. Hence, we assume for further analysis that we start with clean line that is not contaminated.

In contrast to Nauta *et al.*,[6] we adopt here the Bayesian approach assuming that parameters of the model are not constant. Instead, we allow that the values of the parameters may depend on specific features of each chicken-line interaction. Uncertainty in parameter values is expressed in the form of prior joint distribution of parameter values obtained from experts with probabilistic inversion (we took the same 500 samples for this distribution that were used in Reference 6 to obtain medians of the parameters). We then run the model for 10,000 chickens with Monte Carlo by providing external and internal contaminations for each chicken and sampling a value of parameters from their joint distribution.

In Fig. 1, we see the median, the mean, and 5th and 95th percentile of log(N_{ext}) in the case when internal and external contaminations were assumed constant equal to 6 and 7.2 log cfu per caress, respectively. We see in Fig. 1 that even when we do not take into account the uncertainty over initial contamination large variability of output contamination can be expected due to the uncertainty in parameter values.

Whereas Fig. 1 assumes that the initial contamination is constant, Fig. 2 shows results when the internal and external contaminations of chickens in a flock are uncertain with mean 6 and standard deviation 0.73 for log(C_{fec}) and with mean 7.2 and standard deviation 0.9 for log($N_{ext,Input}$).[6] Distributions of the internal and external contamination were assumed to

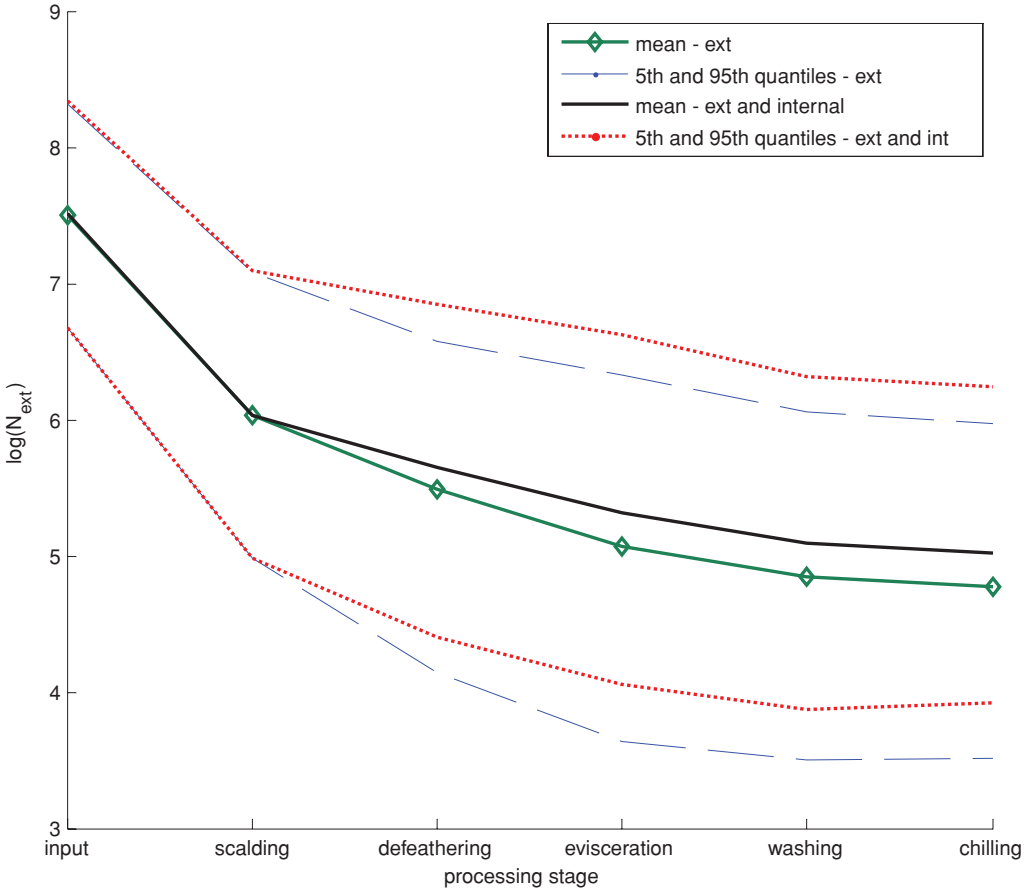

Fig. 2. Log(N_{ext}) for internally and externally versus only externally contaminated chickens.

be independent. Although this may be questioned, the present purpose is merely to illustrate the updating method, and this does not require modeling the dependence of internal and external contamination. Fig. 2 plots log(N_{ext}) for both internally and externally contaminated chickens, and for chickens contaminated only externally. We see that the internal contamination increases the predicted log(N_{ext}) as compared with only externally contaminated chickens. The biggest contribution is observed during defeathering where fecal leakage is most prominent.

3. UPDATING

The chicken processing line model was quantified with structured expert judgment.[9] Few studies collected a quantitative microbiological data on *Campylobacter* during poultry processing. In this section we show how the chicken processing line model can be updated with data. We use for this purpose data presented by Berrang and Dickens.[11] The data are not reported per chicken, but only as means and standard deviations of flocks of processed chickens. This, together with the fact that our prior distribution is given only numerically, requires an adaptation of the usual Bayesian updating schemes.

3.1. Data

Berrang's data contain the mean concentrations of cfu from the exterior of five chickens from six different flocks from a poultry processing line in the United States. Data are obtained from carcass rinses and expressed as log cfu/mL rinsing fluid, from 300 mL rinse fluid per carcass. To obtain a mean number of cfu per carcass, the published concentrations are therefore adjusted by adding a value of log(300), which gives the number of *Campylobacter* on a carcass. Within flock standard deviations were not reported, but are here assumed to be 0.5 log cfu for each flock. In the first flock no positive results

Table II. Means of Log cfu per Chicken for Flocks 2–6

	Flock 2	Flock 3	Flock 4	Flock 5	Flock 6
Input	7.5	7.5	5.6	8.3	7.1
Scalding	4.5	4.2	4.9	4.9	4
Defeathering	5.7	7	5.6	6.6	6.2
Evisceration	5.7	6.2	5	6.5	6.2
Washing	4.6	5.8	4.5	4.1	5.2
Chilling	3.7	3.6	3.4	5.7	3.6

were obtained at two of the processing stages, so this flock was excluded from our analysis, as a zero standard deviation would lead to inconsistencies, and positive standard deviation would lead to nonzero mean values.

The mean values of external contamination for five flocks are presented in Table II. We can observe that after the first stage (scalding) the number of *Campylobacter* decreases, but during the next phase (defeathering) it grows rapidly. The three phases of scalding, defeathering, and evisceration are the most critical points for cross-contamination during processing because the feces contaminated with *Campylobacter* may leak from the carcass.[6] In Reference 13, we find that after defeathering this contamination should have the highest value. For the last two stages, washing and chilling, the intestines are already removed from the carcass. Therefore, the internal infection cannot influence external contamination of the chicken and the number of cfu is decreasing. We can observe this behavior in the data. The only exception is for Flock 4, where the number of cfu at the end of the chicken processing line increases. For the first flock, after defeathering and washing, the contamination was below the detection limit and we do not have any information about the contamination after these phases.

Information about initial internal infection as well as the contamination of the environment is not available in Berrang's data. Therefore, for the further analysis we have made a few assumptions. We assume that $\log(N_{\text{ext,Input}})$ is normally distributed with mean given by data (Table II) and standard deviation 0.5 and that the log of the internal contamination is normally distributed with mean 6 and standard deviation 0.73, as used by Nauta *et al.*[6] based on Dutch microbiological data. We also assume that the process always starts with a clean environment.

Therefore, results presented here serve mainly to illustrate how initial distributions of model parameters can be updated with data.

In Fig. 3, model prediction and data for Flock 2 are plotted. The initial contamination of chickens has mean 7.5 and standard deviation 0.5. After scalding, the model predicts the mean value of contamination equal to about 6. Comparing to Berrang's data, in which the mean contamination after scalding is 4.5, we see that the model overestimates $\log(N_{\text{ext}})$. Other processing stages are not bad as the observations are contained between the 5th and 95th percentile of the distribution of $\log(N_{\text{ext}})$ predicted by the model. We must, however, realize that any change of predicted contamination after scalding will influence results in other phases. Moreover, the pattern produced by the model is clearly different from what the data show.

To see how the model predicts data for all flocks we will run the model with initial contamination that is averaged over all five flocks. We consider measurements for each flock as a realization of the contamination over the population of flocks. Hence the initial distribution of $\log(N_{\text{ext}})$ has a mean that is equal to the average mean for all flocks, which is 7.2, and its variance is equal to the sum of variances of five flocks, 2.5.

Fig. 4 confirms our findings that the model overestimates the number of cfu found after scalding. We can see that the initial variability contains all observations between the 5th and 95th percentiles. This is in contrast to the model predictions after scalding. Means for $\log(N_{\text{ext}})$ after scalding reported in Berrang's data are much smaller than the mean $\log(N_{\text{ext}})$ predicted by the model. $\text{Log}(N_{\text{ext}})$ is slightly underestimated after defeathering and evisceration and overestimated after chilling.

In the next section, the Bayesian updating method for the chicken processing line is explained and applied. We use Berrang's data to improve parameters of the chicken processing line model.

3.2. Bayesian Updating

We denote as M the chicken processing line model. M takes as an input the number of cfu on the exterior of a chicken, say x, and the number in the feces, z, and returns the output y, which indicates the number of cfu on this chicken after a processing stage. The model M has the following parameters $\theta = [a_{\text{ext}}, b_{\text{env}}, a_{\text{fec}}, c_{\text{env}}, w_{\text{fec}}, c_{\text{ext}}, p_{\text{fec}}]$ and may be therefore represented as a function $y = M(x, z; \theta)$. To simplify the exposition and because the Berrang's data do not contain information about the number of cfu in feces, we fix the distribution of internal contamination as normal with mean 6 and standard deviation 0.73 (as in previous sections) and

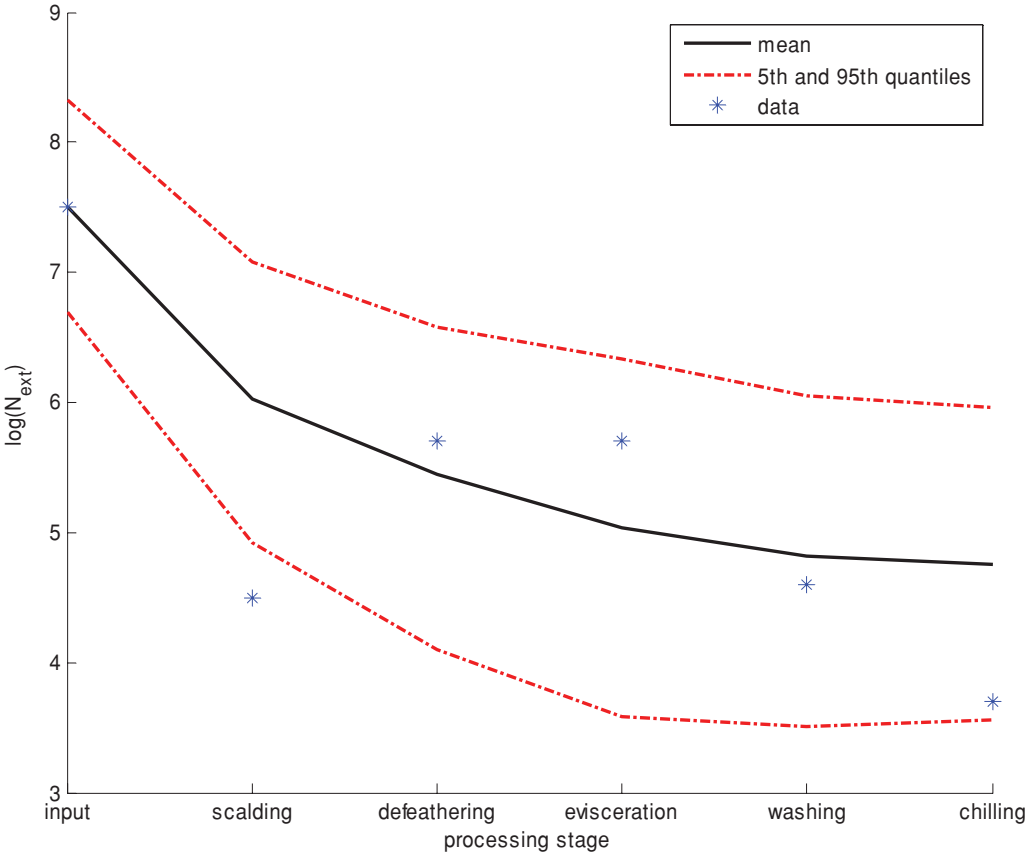

Fig. 3. Model predictions and data for Flock 2.

drop z from the model formulation. The distribution of $\boldsymbol{\theta}$, denoted as f_θ, is given in form of N samples (we took 500 samples that were used in Reference 6) obtained through probabilistic inversion from experts assessments on observable quantities predicted by M. f_θ will be considered as the prior distribution of $\boldsymbol{\theta}$.

Berrang's data do not contain information about the number of cfu on the same chicken before and after the processing stage. We know only that the number of cfu on the exterior of a random chicken from a given flock before the processing stage is a realization of a distribution, say f, and after the processing stage the number of cfu is a realization of another distribution, say g. Hence we can write the likelihood function of the data D as follows:

$$L(D \mid \theta = t) = g\left(\int_x M(x;\theta = t)\, f(x)\, dx\right),$$

where D is a number taken from Table II, for a specific flock and specific processing phase. The likelihood represents the probability of observing the number of cfu D on a random chicken drawn from distribution f calculated by the model with parameters $\boldsymbol{\theta} = t$ after the processing stage when the distribution of the number of cfu is actually equal to g.

Hence the posterior distribution of $\boldsymbol{\theta}$ updated with information about one flock can be obtained with Bayes's theorem as:

$$P'(\theta) = P(\theta \mid D) = \frac{g\left(\int_x M(x;\theta = t)\, f(x)\, dx\right) f_\theta(t)}{\int_t g\left(\int_x M(x;\theta = t)\, f(x)\, dx\right) f_\theta(t)\, dt}.$$

To combine data for all flocks together we consider information about distributions of number of cfu on a random chicken before and after the processing stage for the jth flock (f_j and g_j, where $j = 1, \ldots, k$) as independent observations from

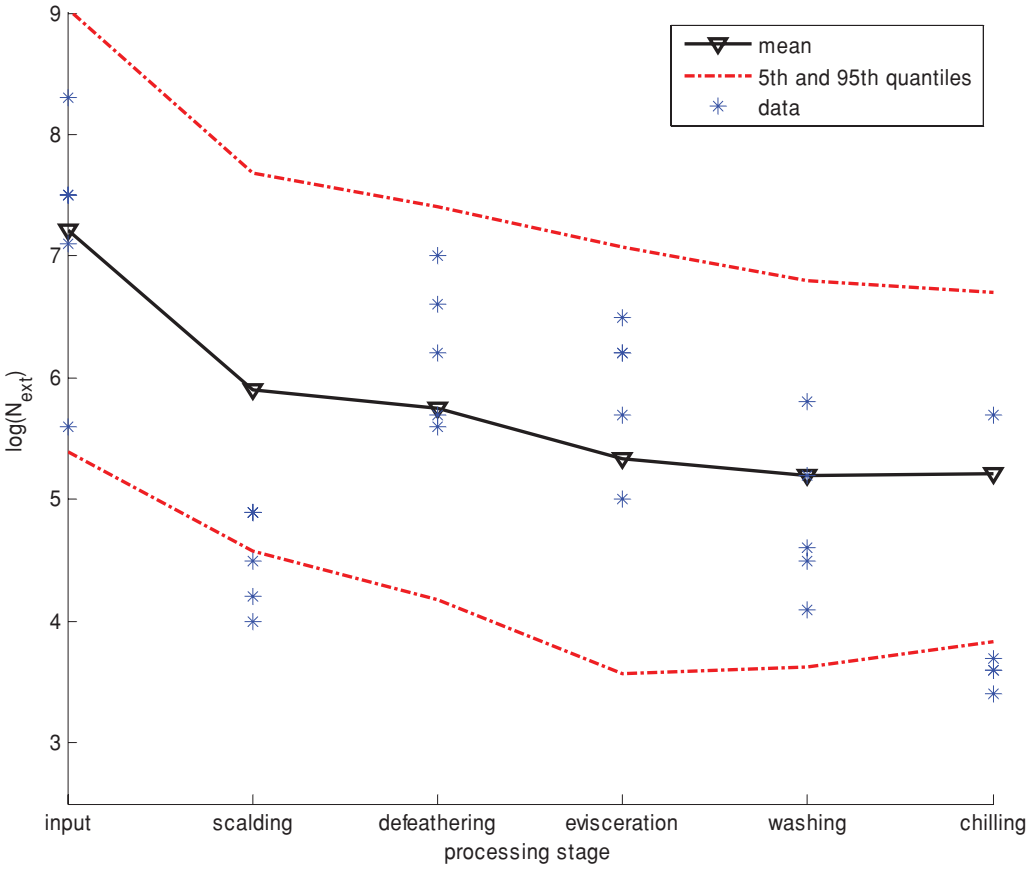

Fig. 4. Log(N_{ext}) predicted by the model with external initial contamination that is normally distributed with the mean 7.2 and variance 2.5 and Berrang's data.

population of flocks. Then the likelihood function becomes:

$$L(D \mid \theta = t) = \prod_{j=1}^{k} g_j \left(\int_x M(x;\theta = t)\, f_j(x)\, dx \right).$$

Thus, the posterior distribution of $\boldsymbol{\theta}$ including all flocks is proportional to:

$$P'(\theta) = P(\theta \mid D) \propto \prod_{j=1}^{k} g_j \left(\int_x M(x;\theta = t)\, f_j(x)\, dx \right) f_\theta(t).$$

We implemented the Bayesian updating first only for Flock 2 to see how the procedure works and then combined all data together.

We took 500 samples ($x_s, s = 1, \ldots, 500$) from the input distribution of log(N_{ext}) for Flock 2, which was normal with mean 7.5 and standard deviation 0.5 (denoted as $f \sim N(7.5, 0.5^2)$). For each sample of parameters $\boldsymbol{\theta} = t_n$, $n = 1, \ldots, N$ we obtained log(N_{ext}) after scalding predicted by the model. The histogram of log(N_{ext}) after scalding is shown in Fig. 6 (left panel). We can see that the average log concentration predicted by the model in this case is about 6. This is much higher than is observed in Berrang's data, which was 4.5. The distribution of log(N_{ext}) after scalding in Berrang's data is assumed to be normal with mean 4.5 and standard deviation 0.5 (dented as $g \sim N(4.5, 0.5^2)$).

The updating is performed as follows: for each sample of $\boldsymbol{\theta} = t_n$, $n = 1, \ldots, N$, we found the weight proportional to the likelihood of observing amount of log(N_{ext}) predicted by the model under distribution g. Hence weights w_n are proportional to $p_n = g(\frac{1}{500} \sum_{s=1}^{500} M(x_s, \theta = t_n))$. They are equal to $w_n = \frac{p_n}{\sum_{i=1}^{N} p_i}$. After resampling with these weights, the posterior sampling distribution of $\boldsymbol{\theta}$ is found. Fig. 5 shows how the distribution of the parameter a_{ext} in scalding has changed after updating with data for Flock 2.

With updated parameters we can find the posterior predictive distribution log(N_{ext}). Comparing

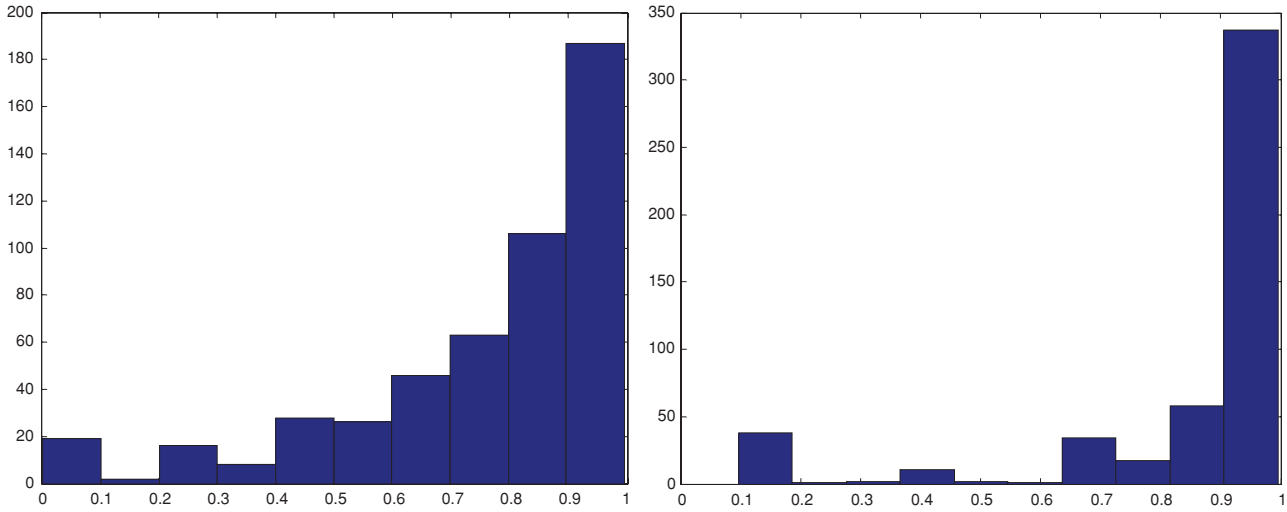

Fig. 5. Histograms of a_{ext} in scalding before (left) and after (right) update with data for Flock 2.

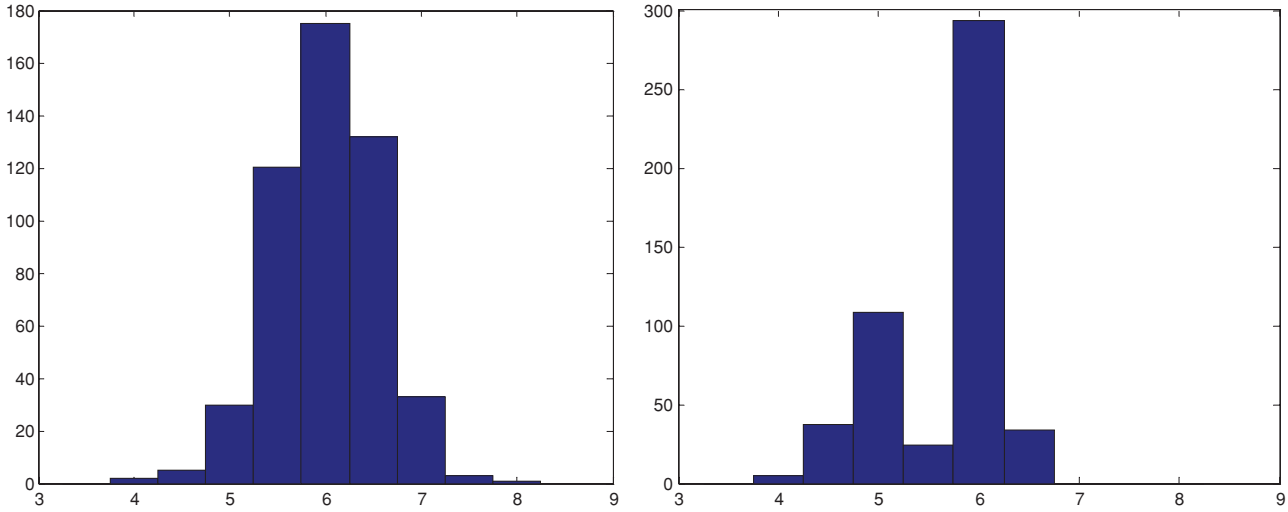

Fig. 6. Histogram of $\log(N_{\text{ext}})$ after scalding before (left) and after update (right) with data for Flock 2.

histograms in Fig. 6, we see the distribution of $\log(N_{\text{ext}})$ after update is significantly different from the one before updating; it is shifted significantly to the left.

Similarly, parameters for all processing stages have been updated with information for Flock 2. Fig. 7 shows how model predictions have changed after updating.

As expected after update $\log(N_{\text{ext}})$ after scalding is reduced. We see that the observation now lies in the 90% confidence bound of concentration after scalding predicted by the model. Moreover, we observe lower overall contamination. Notice also that after update with one flock, the uncertainty of $\log(N_{\text{ext}})$ has been slightly reduced.

Bayesian updating for all flocks leads to the significant reduction of uncertainty of the model (see Fig. 8). We observe significant changes of median contamination in scalding, washing, and chilling.

We see that the model has been calibrated so that the uptick in cfu at the defeathering stage apparent in the data is now captured.

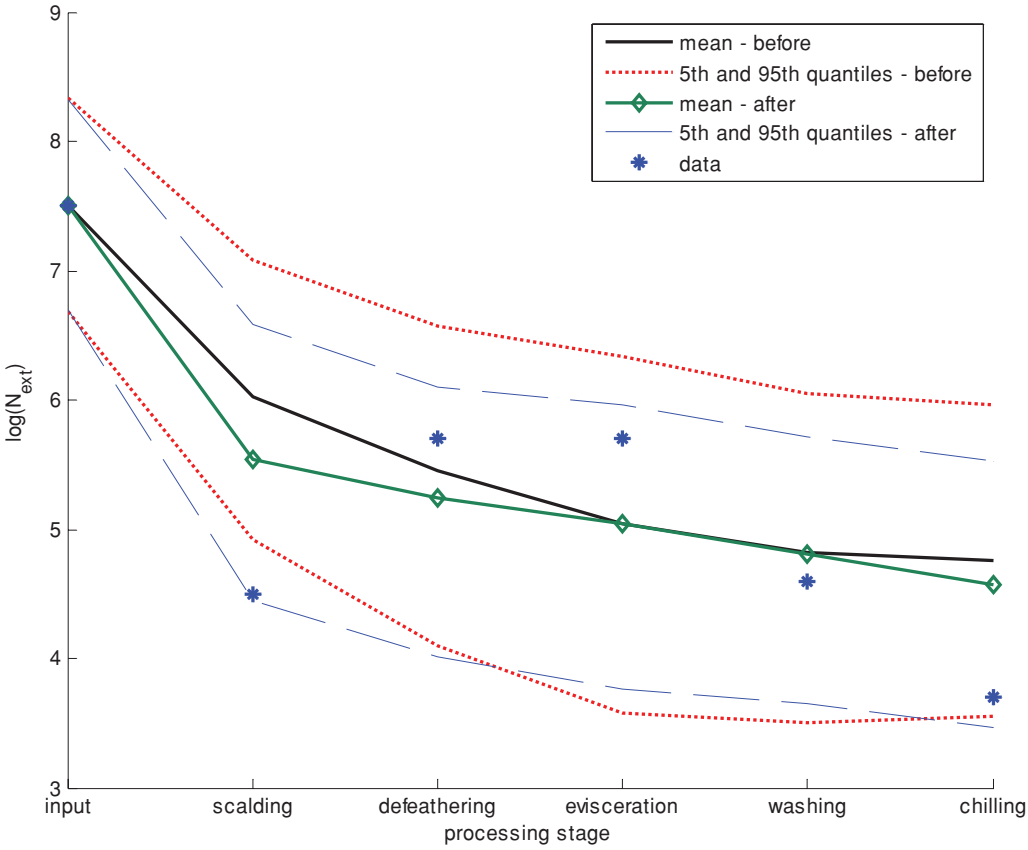

Fig. 7. Log(N_{ext}) after Bayesian updating for Flock 2.

Table III shows means of parameters of the chicken processing line model before and after Bayesian update. The biggest changes can be observed for the parameter a_{ext}, which is the percentage of cfu transferred from the exterior of a chicken to the environment.

4. DISCUSSIONS AND CONCLUSIONS

We showed that with Bayesian updating one of the disadvantages of the mechanistic model of Nauta *et al.*[5] can be overcome. The model predictions can be fitted to data, which is important when new data become available, or data for a specific country or region are to be used. The model retains the advantages of a mechanistic approach.

For the example given in this article it should be noted that these are U.S. data, which may not be representative for the Dutch situation, as *Campylobacter* levels and poultry processing methods may be different. The result should therefore not be interpreted as an update of the Dutch model, but merely as an example of the applicability of the methodology.

An important assumption in the example has been that the internal concentrations of *Campylobacter* in the feces leaking from the carcasses can be described by one and the same distribution for all flocks, as derived from a Dutch data set. Not only may values in the United States be different, these distributions will also be different per flock. As the distribution of C_{fec} has a large impact on the dynamics, this assumption must have a large impact on the resulting parameter estimates as well.

To apply the method described in this article for a specific country or region, microbiological data should be available for a set of flocks, giving the concentrations on carcass exteriors at all stages of processing from the entrance into the processing plant until chilling. Also, for the same flocks, data on concentrations in the leaking feces should be collected.

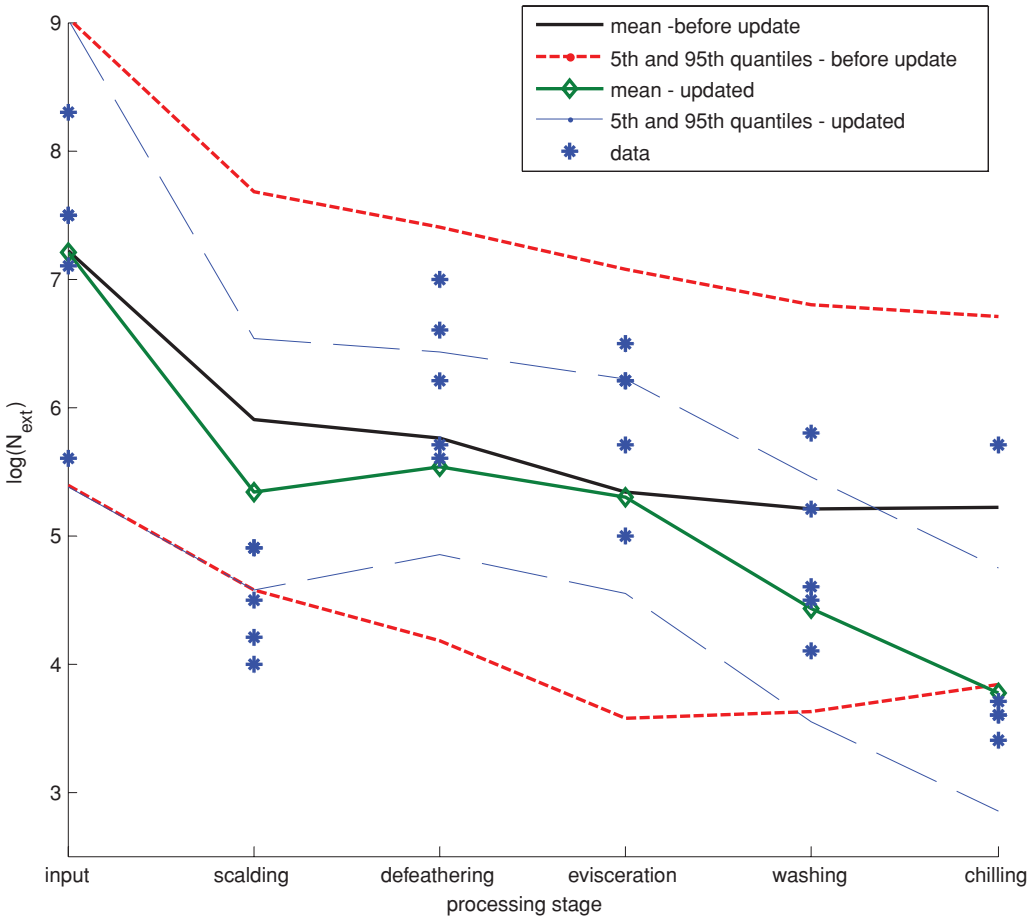

Fig. 8. Log(N_{ext}) after Bayesian updating for all flocks.

Table III. Means of Parameters of the Chicken Processing Line Model Before and After Bayesian Update

	Scalding		Defeathering		Evisceration		Washing		Chilling	
Parameter	Before	After	Before	After	Before	After	Before	After	Before	After
a_{ext}	0.7645	0.9335	0.8652	0.8403	0.4631	0.3728	0.3421	0.8099	0.0901	0.1823
c_{ext}	0.7098	0.8139	0.0511	0.0500	0.0416	0.0419	0.2121	0.2487	0.1948	0.7698
b_{env}	8.1e−6	7.6e−6	0.0279	0.0751	1.1e−5	1e−5	0.0060	0.0019	0.0080	0.0054
c_{env}	0.0490	0.0266	0.1036	0.0797	0.0848	0.0843	0.0631	0.0752	0.0171	0.0196
$1-a_{fec}$	1.6e−6	1e−6	1.3e−5	1.1e−5	0.0062	0.0061				
w_{fec}	1.8624	1.4263	1.7097	1.4541	1.7428	1.7148				
p_{fec}	0.4840	0.4533	0.6955	0.7031	0.6573	0.6600				

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