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# Updating parameters of the chicken processing line model

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# "Updating parameters of the chicken processing line model"

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# Contents

# Chapter 1

# Introduction

*Campylobacter* is a fastidious organism which can survive in a wide range of environments. This organism is routinely found in cattle, sheep, swine and avian species, and these avian species are the most common host for *Camylobacter*. They can live inside a bird, in the intestines and leak from this creature with feces. They exist on the exterior of the chicken, on the skin and in the feathers. These organisms are able to move from environment to the chicken and from the chicken to environment, so the chicken contamination can occur both on the farm and in the slaughter plants.

This bacteria is one of the main sources of *Campylobacter*-associated gastroenteritis in the Netherlands. Chicken meat may be responsible for 80.000 cases per year in a population of 16 millions of *Campylobacter*-associated gastroenteritis in the Netherlands. To find the amount of bacteria on the chicken after it is taken through the process in the slaughterhouse, the mathematical model of a typical chicken processing line was developed and it was quantified in an expert judgement study. The parameters in this model were transfer coefficients of bacteria from the chickens' skin and intestines to the processing environment, and from the environment back to the chickens' skin. Therefore experts were asked to assess the uncertainty regarding variables which 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. This process is called probabilistic inversion.

Since the model was developed [1] in 2003 quantitative data on *Campylobacter* during poultry processing have been collected. The amounts of bacteria before and after a processing stage are published. Therefore, there is a possibility to update the model with this information. Few methods can be considered at this stage and this report presents two of them.

## 1.1 Objective of the thesis

The main purpose of this thesis is to find new parameters of the chicken processing model. Using quantitative data we update these parameters to improve the model.

## 1.2 Outline of the thesis

The thesis is organized as follows. In chapter 2, the general information about the chicken processing line is presented. We introduce the mathematical model computed in 2003, which describes the number of *Campylobacter* on the exterior of a chicken and the amount of this bacteria in the environment after the chicken has passed the all process. This process contains 5 stages and during these phases bacteria can move from the chicken to the environment and from the environment to the chicken or be removed. These transport pathways of *Campylobacter* are given in form of the model parameters, which describe the probabilities that bacteria can move from the exterior of the chicken to the environment and from the environment to the exterior of the chicken, but also from the interior of the chicken to the exterior or to the environment. The lack of data yielding these parameters was the reason that expert judgement study was performed. Then using experts' knowledge, the probabilistic inversion (PI) method was applied to the model. We describe the Expert Judgement Study and PI technique in Chapter 2. We explain the elicitation procedure of experts and the classical model which was used to combine experts' opinion. Questions which were assessed by experts are presented. We have also included some examples of their answers. In the next part, we briefly explain probabilistic inversion method. We present mathematical definition of this technique and the intuitive explanation. After that, we show how this method was applied to the chicken processing line model. We finish chapter 2 of the thesis with analysis of this model.

Quantitative data on the effect of processing steps have been collected. In Chapter 3 we present data published by Berrang and Dickens. We use these data to obtain new parameters of the chicken processing line model and we implement two techniques to this model, probabilistic inversion and Bayesian inference methods. These techniques are explained in this chapter. We show how the updated model differs from the original one.
Conclusions are contained in the last chapter.

# Chapter 2

# Chicken processing line

This chapter presents the general information about the chicken processing line model [1], which describes the number of *Campylobacter* on the exterior of a chicken as a result of internal (intestinal) colonization, external contamination and exchange with the environment. To find the parameters of this model, expert judgement study was used and the method called probabilistic inversion. We explain here main results of expert judgement exercise that was performed. Moreover the probabilistic inversion technique used to get distributions of model parameters from variables predicted by the model, which were assessed by experts is briefly explained. We have redone the PI analysis for the chicken processing line model using different than previously software package. Moreover in our analysis different starting distributions were considered. In the end of this chapter model that was obtained is analyzed.

## 2.1 Model

The chicken processing line starts with collecting poultry flocks on the farm, placing into truckloads, transporting to the processing plant and processing on the same day. At the processing plant animals are hung upside down on a line of shackles and then stunned and killed. The next phases are: scalding (transport through a warm water tank), defeathering (removal of the feathers), evisceration (extraction of intestines), washing (spraying with water) and chilling. The stages of processing line are shown in figure (2.1). Two types of scalding and chilling can be considered, namely scalding using low and intermediate temperature and chilling, using air or spray.
During different stages of chicken processing line inactivation, removal and cross-contamination may change the level and prevalence of *Campylobacter*.

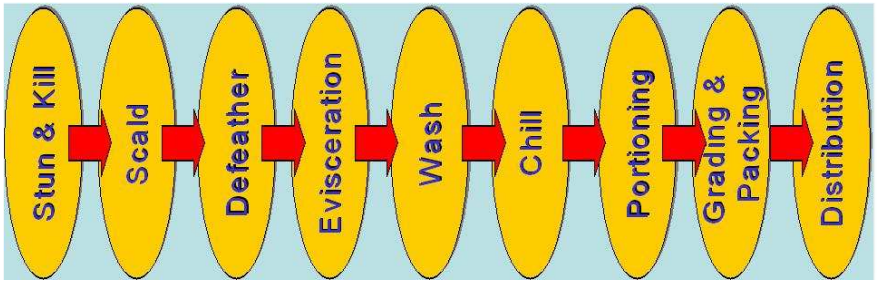


*Figure 2.1: Broiler chicken processing line .*

Each stage is modeled as a physical transport process as shown in figure (2.2). This process takes into consideration different pathways of contamination with *Campylobacters*. Bacteria can move from the exterior of the carcass to environment and from environment back to the carcass. *Campylobacters* colonized in the feces can migrate on the chickens' skin or feathers and to the environment. They can also be removed or inactivate.

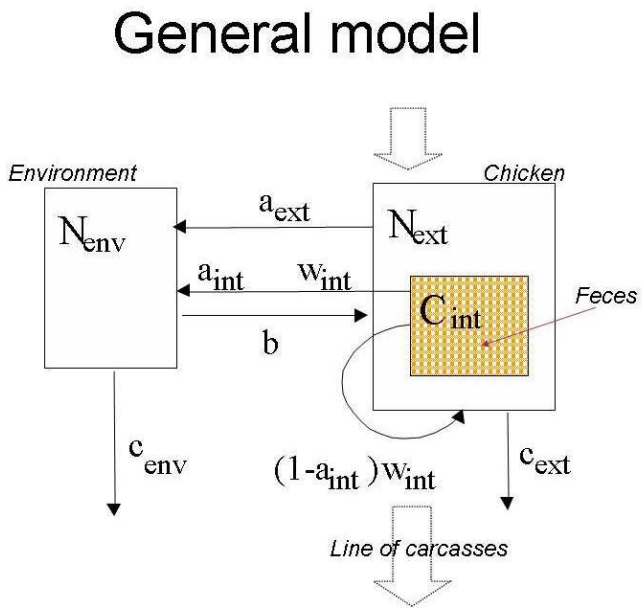


*Figure 2.2: A typical phase in the chicken processing model.*

We now present main components of the chicken processing line model. $N_{env}$ represents the number of *Campylobacter* in the physical environment of the chicken in a processing phase. This environment can be anything that gets contaminated by contact with the passing animals and from which *Campylobacter*

may be transfered back to the carcass, e.g water, equipment, hands, air. $N_{ext}$ is the number of bacteria on the exterior of the chicken, and $C_{int}$ is the concentration in the intestines, containing the feces. In this model the number of *Campylobacter* is expressed in cfu (colony forming units).

For each processing stage $S$ (scalding, defeathering, evisceration, washing, chilling) the following transfer coefficients are defined:

- $a_{ext,S}$: probability per cfu *Campylobacter* on the exterior (skin and feathers) to move from the carcass exterior to the environment, per processing stage $S$
- $b_{env,S}$: probability per cfu *Campylobacter* in the environment to move from the environment to the carcass exterior, per processing stage $S$
- $a_{int,S}$: probability per cfu *Campylobacter* in the leaking feces to move to the environment, per processing stage $S$. (With corresponding probability $1 - a_{int}$, $S$ per cfu to move from the interior to the exterior of the carcass directly)
- $c_{env,S}$: probability of inactivation or removal per cfu *Campylobacter* in the environment which is not transferred to the carcass exterior, per processing stage $S$
- $w_{int,S}(i)$: amount of feces (gram) that leaks from carcass $i$ at processing stage $S$
- $c_{ext,S}$: probability of inactivation or removal per cfu *Campylobacter* on the carcass exterior which is not transferred to the environment, per processing stage $S$

The following model equations per stage $S$ and carcass $i$ were presented in [1]:

$$\begin{aligned} N_{ext,S}(i) &= (1 - a_{ext,S})(1 - c_{ext,S})N_{ext,S-1}(i) + b_{env,S}N_{env,S}(i-1) + \\ &+ (1 - a_{int,S})w_{int,S}(i)C_{int}(i) \\ N_{env,S}(i) &= a_{ext,S}N_{ext,S-1}(i) + (1 - b_{env,S})(1 - c_{env,S})N_{env,S}(i-1) + \\ &+ a_{int,S}w_{int,S}(i)C_{int}(i) \end{aligned} \tag{2.1}$$

These equations give the the number of *Campylobacter* on the exterior of the $i$th carcass and in the environment after processing stages $S$.

At any of the consecutive processing stages, a carcass $i$ entering stage $S$ is contaminated with $N_{ext,S-1}(i)$ cfu of *Camylobacter* on the exterior and $N_{ext,S}(i)$

is the number of bacteria on carcass $i$ at the end of the stage $S$. $N_{env}(i)$ is the number of *Campylobacter* in the environment after passage of carcass $i$ in stage $S$ and $C_{int}(i)$ is the concentration of *Campylobacters* in the intestines of carcass $i$ at stage $S$.

The output of the stage $S-1$ is the input of the stage $S$. We need a value for initial number of *Campylobacters* in the environment per processing stage $N_{env}(0)$, as well as distributions of $N_{ext,input}$ and $C_{int}(0)$. Then the number of bacteria on the carcass after passing the processing line can be estimated.

It was observed in [2] that after some time, the number of *Campylobacter* does not change in the environment. This event is called the equilibrium state and for the broiler chicken processing line generally the equilibrium is approached quickly, after passage of only a few (usually $\leq 10$) carcasses. In the equilibrium we have that $N_{env,S}(i) = N_{env,S}(i-1)$, thus

$$N_{env,S} = \frac{a_{ext}N_{ext,S-1} + a_{int}w_{int}C_{int}}{b_{env} + c_{env} - b_{env}c_{env}}.$$

To perform uncertainty analysis of the chicken processing line model the distributions of the parameters, i.e. transfer coefficients are needed. However, the experimental data yielding these values cannot be obtained as transfer coefficients are not observable quantities. To obtain these parameters, experts knowledge was used. Experts couldn't have been asked directly about the parameters, they assessed variables, which can be observed and predicted by the model. Afterwards, using this information and applying method called probabilistic inversion, the parameters distributions were found. Expert judgement and PI are explained in more details in the next parts of this thesis.
First, we describe The Expert Judgement Study.

## 2.2 Expert Judgement Study

In case when data is not available, we often use experts knowledge to substitute the missing information in a particular subject. In such cases, experts are often asked to provide their assessments regarding variables in terms of some quantiles of their distributions (e.g. 5%, 50%, 95%). To check performance of experts special quantities called seed variables are also assessed by experts. The true values of these variables are known for analyst.

In the classical model of the expert judgement study [3], there are two performance measures: calibration and information. The calibration score measures

how similar the empirical distribution and the experts' uncertainty distributions are. An expert has a good calibration score on seed variables if he gives quantiles such that 5% of the realizations are less than the 5% quantile, 45% of the realizations are between the 5% and 50% quantiles and so on. The information measures the degree to which a distribution is concentrated. If the expert gives very narrow uncertainty distributions then his information score is high. Good performance corresponds to good calibration and high information.

The classical model is a method that calculates a weight for each of the participating experts as a product of the information and calibration scores. Therefore, an expert whose calibration and information scores are high is going to have a higher weights and his assessments will have a bigger influence in the study.

To obtain optimal DM we combine all experts' assessments into one combined uncertainty assessment on each query variable. The combined distributions are weighted sums of the individual experts' distributions, with non-negative weights adding to one. We distinguish three combination schemes:

- **The global weight decision maker**: The global weight decision maker uses performance based weights which are defined, per expert, by the product of expert's calibration score and his (her) overall information score on seed variables .

- **The item weight decision maker**: Item weights are determined per expert and per variable in a way, which is sensitive to the expert's informativeness for each variable. For the item weight decision maker, the weights depend on the expert and on the item.

- **The equal weight decision maker**: The equal weight decision maker assigns equal weights for each expert .

Moreover, we can optimize the DM's distribution. A crucial point of computing the calibration value for each expert is in the choice of the significance level $\alpha$ . Since the combination of the experts' results in a virtual expert (the Decision Maker), who can as well be scored with respect to calibration and information, the choice of $\alpha$ aims to maximize the virtual weight of the decision maker. [4]

For the chicken line model, experts having extensive knowledge and experience on broiler chicken processing in the Netherlands as well as behavior of pathogens, in particular Campylobacter, during the various processing stages were interviewed. Out of 21 potential experts identified, 12 experts eventually joined the panel: 5 from industry, 1 from government, 3 from science, and 3 from

combination of science and practise.

Experts respond to 16 questions about the slaughtering process of broiler chickens and their contamination with Campylobacter during the different stages of this process. They were kindly requested to give an estimate on every question by stating the 5%, 50% and 95% quantiles of their uncertainty distributions. These questions referred the number of bacteria on the first and the last carcass of the positive (internally and externally contaminated with $10^8$ and $10^5$ cfu, respectively) and negative (externally contaminated with $10^4$ cfu) flocks and the amount of manure, which leak during the slaughtering process. The experts estimation regard the slaughterhouse in the Netherlands at average day of the year, where at the beginning of the new day, the environment in this slaughterhouse is clean.
As an example we show below two questions concerned with the positive flock:

*Question A1:*
*All chickens of the particular flock are passing successively each slaughtering stage. How many Campylobacters (per carcass) will be found after each of the mentioned stages of the slaughtering process, each time on the* ***first*** *chicken of the flock?*

*Question A2:*
*All chickens of the particular flock are passing successively each slaughtering stage. How many Campylobacters (per carcass) are found after each of the mentioned slaughtering stages, each time on the* ***last*** *chicken of this flock?*

All questions can be found in Appendix.

Experts were also asked twelve seed variables, which answers were known to analysts. These variables were related to the percentage of broiler chicken flocks carrying *Campylobacter* prior to processing, levels of internal infection and external contamination of broiler chickens, and contamination levels of products. One of the questions was:

*Question A1:*
*How many Campylobacters (number per gram) are found in the caecal content just before the chicken would have been transferred to a transport crate?*

The realization of this question is equal to $5 * 10^7$ and the answers given by experts are the following.

Expert 1: $5\% = 1 * 10^4$, $50\% = 1 * 10^7$, $95\% = 1 * 10^9$
Expert 2: $5\% = 1 * 10^8$, $50\% = 5 * 10^8$, $95\% = 1 * 10^9$
Expert 3: $5\% = 1 * 10^3$, $50\% = 1 * 10^8$, $95\% = 1 * 10^{10}$
Expert 4: $5\% = 1 * 10^5$, $50\% = 1 * 10^8$, $95\% = 1 * 10^9$
Expert 5: $5\% = 1$, $50\% = 2 * 10^2$, $95\% = 1 * 10^{12}$
Expert 6: $5\% = 1 * 10^3$, $50\% = 1 * 10^6$, $95\% = 1 * 10^8$
Expert 7: $5\% = 1 * 10^6$, $50\% = 1 * 10^7$, $95\% = 1 * 10^8$
Expert 8: $5\% = 1 * 10^5$, $50\% = 1 * 10^7$, $95\% = 5 * 10^8$
Expert 9: $5\% = 1 * 10^6$, $50\% = 1 * 10^7$, $95\% = 1 * 10^8$
Expert 10: $5\% = 5 * 10^5$, $50\% = 1 * 10^7$, $95\% = 5 * 10^7$
Expert 11: $5\% = 1 * 10^6$, $50\% = 1 * 10^8$, $95\% = 1 * 10^{10}$
Expert 12: $5\% = 1 * 10^3$, $50\% = 8 * 10^3$, $95\% = 1 * 10^4$

We can present these quantiles by a range graph presented in figure (2.3). It is visible that the second expert was very close to the real value and his 90% confidence interval was narrow. Thus we can assert that an expert was almost sure about the realization of this quantity.

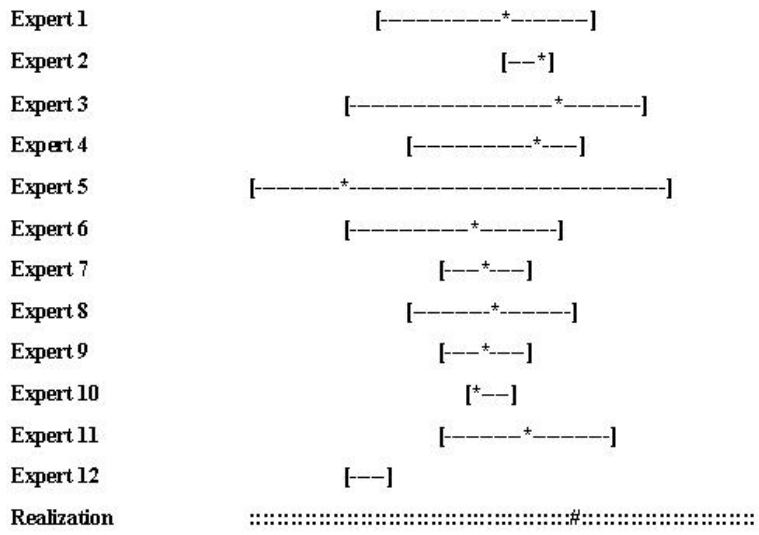


*Figure 2.3: Range graph for the seed variables A1.*

Expert 12 gave the 90% confidence interval very narrow, but the true value of variable A1 does not fall into this interval. The similar can be observed in

*Table 2.1: Results of scoring experts relative to the decision maker (DM), based on equal weighting.*

| Expert | Calibration | Information | Unnorm. weights | Norm. weights |
|---|---|---|---|---|
| 1 | 0.001 | 1.00 | 0.001 | 0.0004 |
| 2 | 0.01 | 1.34 | 0.01 | 0.01 |
| 3 | 0.68 | 0.57 | 0.39 | 0.14 |
| 4 | 0.001 | 0.74 | 0.001 | 0.0003 |
| 5 | 0.22 | 0.26 | 0.06 | 0.02 |
| 6 | 0.68 | 0.73 | 0.50 | 0.18 |
| 7 | 0.82 | 1.48 | 1.21 | 0.43 |
| 8 | 0.68 | 0.77 | 0.52 | 0.19 |
| 9 | 0.0001 | 1.13 | 0.0001 | 0.00 |
| 10 | 0.0001 | 2.12 | 0.0002 | 0.0001 |
| 11 | 0.0005 | 1.03 | 0.0005 | 0.0002 |
| 12 | 0.0001 | 1.90 | 0.0002 | 0.0001 |
| DM | 0.47 | 0.24 | 0.11 | 0.04 |

case of expert 10. Other experts' estimations contained the realization. Notice however, that few experts gave very wide confidence interval, which indicate their uncertainty in this question.

Three different weighting schemes were applied to the chicken processing line model. The results of the application of equal weighting and performance-based weighting without and with optimization of the DM are presented in tables (2.1)-(2.3). The performance of the 12 experts and the DM, expressed by calibration scores, information scores, unnormalized weights and normalized weights with DM is presented. The unnormalized weight is the global weight and the normalized weight with DM is the weight that the expert would receive if the DM had been added to the expert panel as an additional virtual expert.

Examination of the tables shows that although a few experts (Expert 3, 6, 7 and 8) succeed in combining good calibration with high information, the optimized DM coincides with the results of one expert (Expert 7).

The performance of the weighting scheme is the highest for the global optimized DM and this case was chosen for the further work. [5][6]

The uncertainty distributions given by expert 7 were used to find the parame-

*Table 2.2: Results of scoring experts relative to the decision maker (DM), based on performance-based weighting without DM optimization.*

| Expert | Calibration | Information | Unnorm. weights | Norm. weights |
|---|---|---|---|---|
| 1 | 0.001 | 1.00 | 0.001 | 0.0003 |
| 2 | 0.01 | 1.34 | 0.01 | 0.01 |
| 3 | 0.68 | 0.57 | 0.39 | 0.13 |
| 4 | 0.001 | 0.74 | 0.001 | 0.0003 |
| 5 | 0.22 | 0.26 | 0.06 | 0.02 |
| 6 | 0.68 | 0.73 | 0.50 | 0.17 |
| 7 | 0.82 | 1.48 | 1.21 | 0.41 |
| 8 | 0.68 | 0.77 | 0.52 | 0.18 |
| 9 | 0.0001 | 1.13 | 0.0001 | 0.000 |
| 10 | 0.0001 | 2.12 | 0.0002 | 0.0001 |
| 11 | 0.0005 | 1.03 | 0.0005 | 0.0002 |
| 12 | 0.0001 | 1.90 | 0.0002 | 0.0001 |
| DM | 0.47 | 0.53 | 0.251 | 0.085 |

*Table 2.3: Results of scoring experts relative to the decision maker (DM), based on performance-based weighting with DM optimization.*

| Expert | Calibration | Information | Unnorm. weights | Norm. weights |
|---|---|---|---|---|
| 1 | 0.001 | 1.00 | 0 | 0 |
| 2 | 0.01 | 1.34 | 0 | 0 |
| 3 | 0.68 | 0.57 | 0 | 0 |
| 4 | 0.001 | 0.74 | 0 | 0 |
| 5 | 0.22 | 0.26 | 0 | 0 |
| 6 | 0.68 | 0.73 | 0 | 0 |
| 7 | 0.82 | 1.48 | 1.21 | 0.50 |
| 8 | 0.68 | 0.77 | 0 | 0 |
| 9 | 0.0001 | 1.13 | 0 | 0 |
| 10 | 0.0001 | 2.12 | 0 | 0 |
| 11 | 0.0005 | 1.03 | 0 | 0 |
| 12 | 0.0001 | 1.90 | 0 | 0 |
| DM | 0.82 | 1.48 | 1.21 | 0.50 |

ters of the model through the probabilistic inversion technique, which is presented in the next part of this thesis.

## 2.3 Probabilistic inversion

Expert Judgement can be applied whenever the variables under consideration can be theoretically measured or observed. When the experts opinion is needed for model parameters, they are asked to assess functions relating the parameters and observable variables. From experts assessments on distributions of these functions, distributions of parameters can be obtained with PI method. Probabilistic inversion can be formulated mathematical as:

Let $X$ and $Y$ be $n$- and $m$-dimensional random vectors, respectively, and let $G$ be a function from $R^n$ to $R^m$. We want to find $X$ such that $G(X)$ has the same distribution as $Y$. In this case, $X$ is called a probabilistic inverse of $Y$ under $G$. If the function $G$ could be inverted analytically, then $X$ is computed very easily as $G^{-1}(Y)$. In general this is not possible, and we must find other ways to obtaine distribiution of $X$. A number of methods could be considered. One of the possibilities is technique based on sample re-weighting. [12]

We take $N$ samples from $X$ and compute $N$ samples for $Y$, yielding $N$ samples for $(X, Y)$. When we draw samples from the initial distribution, each of the $N$ samples has probability $1/N$. We wish to re-weight these $N$ samples such that, if we re-sample this distribution, drawing each sample with probability by its weight, then the quantile constraints on $Y$ are satisfied in the re-sampled distribution.

The intuitive explanation of this method is illustrated in figure (2.4). Let us consider the model $M$, which takes $A$ as an input and returns $B$ as an output, $B = M(A)$. We have given some information about $B$ and probabilistic inversion finds $A$ through the re-sampling method, such that $M(A)$ satisfies given constraints. If we have given information about $B$ in a form of 5%, 50% and 95% quantiles, then PI finds $A$ such that the values of $M(A)$ fall into intervals assigned by these quantiles. We can apply this technique, when we would like to find or change the input $A$ using the constraints imposed on $B$.

In the current context, the transfer coefficients for the model play the role of $X$, and $Y$ is computed in the following way

$$Y = (A_{1,1}, A_{2,1}, B_{1,1}, B_{2,1}, C_{1,1}, W_{int,1}, A_{1,2}, ..., B_{2,5}, ..., C_{1,5})$$

(39 components in total)

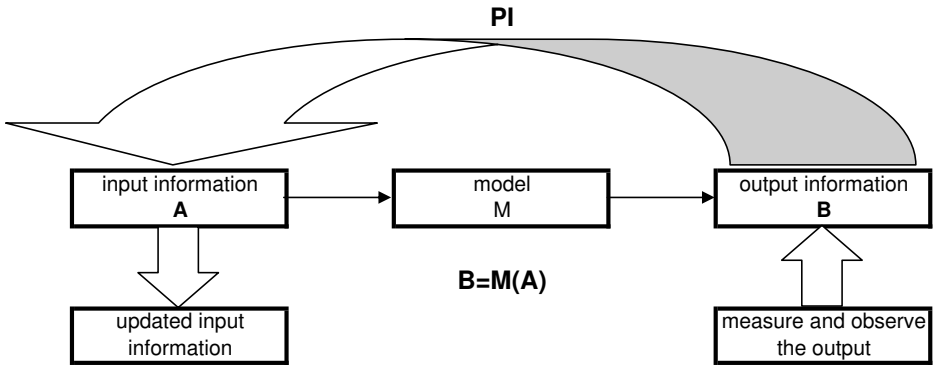


*Figure 2.4: Probabilistic inversion technique.*

where $A_{1,i}$, $A_{2,i}$, $B_{i,1}$,... were the variables assessed by the experts and $i$ denoted the $i$th stage. Questions $A_1$, $A_2$ were given in section 2.2. Questions $B_1$ and $B_2$ were similar to $A_1$ and $A_2$, but referred to a negative flock. Question $C_1$ asked for the infection on the 100th broiler of an uninfected flock, which was processed after an internally and externally contaminated flock. $W_{int}$ was a question about the amount of feces leaking from the carcass.

For three stages scalding, defeathering and evisceration, there are 6 variables $A_1$, $A_2$, $B_1$, $B_2$, $C_1$ and $W_{int}$, but last two phases, contain only 5 variables. After the intestines are removed, variable $W_{int}$ is not present.

Using the model we can find relationships between variables assessed: $A_{1,i}, ..., W_{int,i}$ and parameters of the model. These are given by the equations given below, which are computed from the model equations (2.1) and information that positive flock is internally and externally contaminated with $10^5$ and $10^8$ cfu, respectively and that the negative flock is only externally contaminated with $10^4$ cfu.

$$
\begin{aligned}
A_{1,i} &= 10^5(1-a_{ext})(1-c_{ext}) + 10^8(1-a_{int})w_{int}, \\
A_{2,i} &= A_{1,i} + b_{env}\tfrac{10^5 a_{ext}+10^8 a_{int}w_{int}}{b_{env}+c_{env}-b_{env}c_{env}}, \\
B_{1,i} &= 10^4(1-a_{ext}-c_{ext}+a_{ext}c_{ext}), \\
B_{2,i} &= B_{1,i} + b_{env}\tfrac{10^4 a_{ext}}{b_{env}+c_{env}-b_{env}c_{env}}, \\
C_{1,i} &= (1-b_{env}-c_{env}+b_{env}c_{env})^{99} b_{env}\tfrac{10^5 a_{ext}+10^8 a_{int}w_{int}}{b_{env}+c_{env}-b_{env}c_{env}}, \\
W_{int,i} &= w_{int}.
\end{aligned}
\tag{2.1}
$$

The distribution of these variables is partially specified by the 5%, 50% and 95% quantiles given by experts and the right hand sides of (2.1) constitute functions $G$ in the probabilistic inversion. We choose an initial distribution for $X$ such that, when we sample it a large number of times and compute $Y$ via (2.1), some samples fall within each interquantile interval for $Y$. We take $N$ samples from $X$ and compute $N$ samples for $Y$ and each of these $N$ samples has probability $1/N$. Now, we re-weight these $N$ samples such that, if we re-sample this distribution, drawing each sample with probability given by its weights, then quantile constraints on $Y$ are satisfied in the re-sampled distribution.

There are various strategies for finding weights. We use two of the methods, iterative proportional fitting (IPF) and parameter fitting for uncertain models (PARFUM) [7]. These techniques are quite fast and there exists a simple software to these methods. Applying these techniques, we want to find the distributions of $X$ such that $Y$ satisfy specified by experts quantiles. Each elicitation variable has four interquantile intervals, and the weighted sum of samples falling in each such interval must satisy the corresponding quantile constraints. The weight assigned to each interquantile cell is simply the total weights of the samples falling in that cell [1]. If these weights exist, we know that PI converges to a solution, we say that the problem is feasible. In this case IPF is generally preferred, because it converges faster. If the problem is infeasible, then IPF does not converge in such cases, PARFUM is more preferred as it always converges.

The results of these algorithms give a very poor fit between the re-sampled distributions and decision maker distributions. Table (2.3) shows these results for low scalding and defeathring stages. IPF and PARFUM would converge to a solution in these cases if the results of each quantiles of these methods are: 5% = 0.05, 50% = 0.5 and 95% = 0.95. Table (2.3) shows that for low scald-

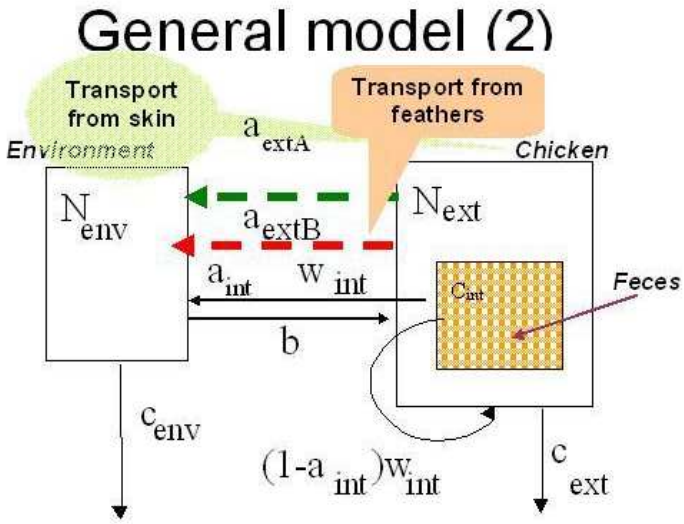


*Figure 2.5: Processing model with additional transport pathway.*

ing stage, for variables $A_2$, $C_1$ and $W_{int}$, both IPF and PARFUM provide good results and IPF gives a good solution for $A_1$ as well. However, for defeathering phase, the problem is feasible only for variable $W_{int}$ (IPF) and $C_1$ (PARFUM).

Therefore, for the chicken processing line model, PI technique shows that the expert's assessments did not support this model. The model was changed in [1] such that coefficient $a_{ext}$ was replaced by two coefficients, $a_{xa}$ and $a_{xb}$. The second pathway of transport *Campylobacter* to the environment was included, the transport from feathers. This pathway was added, because it makes a difference whether the birds have been contaminated during transport only (giving rise to only contamination of the exterior) or at the farm (resulting in intestinal colonization and contamination on the exterior). It is more difficult to remove *Camylobacter* which are in the pores of the skin than which are on the feathers or skin surface. This rational was obtained from experts narrative that acompanied expert's assessments.

*Table 2.4: Results of the probabilistic inversion method for the chicken processing model 1*

| Variable | Quantile | Low Scalding | | Defeathering | |
|---|---|---|---|---|---|
| | | IPF | PARFUM | IPF | PARFUM |
| $B_1$ | 5% | 0.0949 | 0.0682 | 0.2506 | 0.4830 |
| | 50% | 0.9500 | 0.6811 | 0.7480 | 0.4824 |
| | 95% | 0.9999 | 0.9917 | 0.8814 | 0.8987 |
| $B_2$ | 5% | 0.0903 | 0.0615 | 0.7019 | 0.2989 |
| | 50% | 0.9027 | 0.6159 | 0.9241 | 0.6495 |
| | 95% | 0.9502 | 0.9540 | 0.9815 | 0.9645 |
| $A_1$ | 5% | 0.0499 | 0.0358 | 0.2506 | 0.0468 |
| | 50% | 0.5000 | 0.3585 | 0.7459 | 0.4593 |
| | 95% | 0.9500 | 0.6811 | 0.8716 | 0.8987 |
| $A_2$ | 5% | 0.0500 | 0.0487 | 0.0047 | 0.0352 |
| | 50% | 0.5000 | 0.4876 | 0.3986 | 0.3525 |
| | 95% | 0.9501 | 0.9264 | 0.8705 | 0.6749 |
| $C_1$ | 5% | 0.0500 | 0.0487 | 0.0635 | 0.0499 |
| | 50% | 0.4999 | 0.4876 | 0.2493 | 0.4945 |
| | 95% | 0.9500 | 0.9264 | 0.9948 | 0.9408 |
| $W_{int}$ | 5% | 0.0500 | 0.0496 | 0.0500 | 0.2748 |
| | 50% | 0.4999 | 0.4958 | 0.5000 | 0.6030 |
| | 95% | 0.9499 | 0.9420 | 0.9500 | 0.9662 |

Second model equations are as follows:

$$\begin{aligned}
A_{1,i} &= 10^5(1-a_{xa})(1-c_{ext}) + 10^8(1-a_{int})w_{int},\\
A_{2,i} &= A_{1,i} + b_{env}\tfrac{10^5 a_{xa}+10^8 a_{int}w_{int}}{b_{env}+c_{env}-b_{env}c_{env}},\\
B_{1,i} &= 10^4(1-a_{xb}-c_{ext}+a_{xb}c_{ext}),\\
B_{2,i} &= B_{1,i} + b_{env}\tfrac{10^4 a_{xb}}{b_{env}+c_{env}-b_{env}c_{env}},\\
C_{1,i} &= (1-b_{env}-c_{env}+b_{env}c_{env})^{99} b_{env}\tfrac{10^5 a_{xa}+10^8 a_{int}w_{int}}{b_{env}+c_{env}-b_{env}c_{env}},\\
W_{int,i} &= w_{int}.
\end{aligned} \tag{2.2}$$

The second model performed much better with, the probabilistic inversion yielded better fits. Both IPF and PARFUM converge to a solution for low scalding and evisceration. IPF gives better results for intermediate scalding and spray chilling. PARFUM gives better results for defeathering, washing and air chilling, but it is evident that the PI is still not feasible. Finally, IPF solutions were chosen in 4 cases, for low scalding, intermediate scalding, evisceration, spray chilling and PARFUM results were preferred in 3 cases, for defeathering, washing and air chilling (tables 2.5 and 2.6).

Therefore, the chicken processing line model is built, so we can observe the number of *Campylobacter* during the processes in many possible situations. We analyze few of them in the next section.

*Table 2.5: Results of the probabilistic inversion method for the chicken processing model 2 for low scalding, intermediate scalding, defeathering and evisceration.*

| Variable | Quantile | Low Scalding | | Int Scalding | | Defeathering | | Evisceration | |
|---|---|---|---|---|---|---|---|---|---|
| | | IPF | PAR | IPF | PAR | IPF | PAR | IPF | PAR |
| $B_1$ | 5% | 0.0500 | 0.0501 | 0.0500 | 0.0597 | 0.0475 | 0.0462 | 0.0499 | 0.0500 |
| | 50% | 0.5000 | 0.5004 | 0.5000 | 0.4625 | 0.4938 | 0.4625 | 0.4999 | 0.5000 |
| | 95% | 0.9500 | 0.9502 | 0.9499 | 0.8653 | 0.9388 | 0.8787 | 0.9500 | 0.9499 |
| $B_2$ | 5% | 0.0500 | 0.0498 | 0.0500 | 0.0597 | 1.0000 | 0.9250 | 0.0499 | 0.0500 |
| | 50% | 0.5000 | 0.4995 | 0.5000 | 0.0597 | 1.0000 | 0.9250 | 0.4999 | 0.5000 |
| | 95% | 0.9500 | 0.9498 | 0.9499 | 0.0865 | 1.0000 | 0.9250 | 0.9500 | 0.9499 |
| $A_1$ | 5% | 0.0499 | 0.0500 | 0.0423 | 0.0429 | 0.2066 | 0.0462 | 0.0500 | 0.0505 |
| | 50% | 0.4999 | 0.4999 | 0.4267 | 0.4297 | 0.7452 | 0.4625 | 0.5000 | 0.5019 |
| | 95% | 0.9499 | 0.9499 | 0.8051 | 0.8165 | 0.9842 | 0.8787 | 0.9500 | 0.9503 |
| $A_2$ | 5% | 0.0499 | 0.0500 | 0.0696 | 0.0599 | 0.0052 | 0.0369 | 0.0499 | 0.0502 |
| | 50% | 0.4999 | 0.5000 | 0.6961 | 0.5996 | 0.0462 | 0.3699 | 0.5000 | 0.4984 |
| | 95% | 0.9499 | 0.9500 | 0.9749 | 0.8924 | 0.8507 | 0.7029 | 0.9500 | 0.9467 |
| $C_1$ | 5% | 0.0500 | 0.0499 | 0.0589 | 0.0429 | 0.0055 | 0.0462 | 0.0499 | 0.0499 |
| | 50% | 0.5000 | 0.5000 | 0.5899 | 0.4297 | 0.8143 | 0.4625 | 0.5000 | 0.5000 |
| | 95% | 0.9500 | 0.9500 | 0.9410 | 0.8165 | 0.9855 | 0.8787 | 0.9500 | 0.9500 |
| $W_{int}$ | 5% | 0.0500 | 0.0499 | 0.0500 | 0.0429 | 0.0500 | 0.2219 | 0.0499 | 0.0494 |
| | 50% | 0.4999 | 0.4999 | 0.4999 | 0.4297 | 0.5000 | 0.5546 | 0.5000 | 0.4997 |
| | 95% | 0.9499 | 0.9499 | 0.9499 | 0.8165 | 0.9500 | 0.8880 | 0.9500 | 0.9499 |

*Table 2.6: Results of the probabilistic inversion method for the chicken processing model 2 for washing, air chilling and spray chilling.*

| Variable | Quantile | Washing | | Air Chilling | | Spray Chilling | |
|---|---|---|---|---|---|---|---|
| | | IPF | PAR | IPF | PAR | IPF | PAR |
| $B_1$ | 5% | 0.0025 | 0.0400 | 0.0000 | 0.0000 | 0.0499 | 0.0338 |
| | 50% | 0.0250 | 0.4001 | 0.0999 | 0.3675 | 0.4999 | 0.3715 |
| | 95% | 0.0475 | 0.7600 | 0.9999 | 0.8399 | 0.9500 | 0.7661 |
| $B_2$ | 5% | 0.0025 | 0.0399 | 0.0000 | 0.0000 | 0.0499 | 0.0789 |
| | 50% | 0.0249 | 0.3998 | 0.0999 | 0.3675 | 0.4999 | 0.4894 |
| | 95% | 0.0475 | 0.7599 | 0.9999 | 0.8399 | 0.9499 | 0.7779 |
| $A_1$ | 5% | 0.0026 | 0.0410 | 0.0000 | 0.0000 | 0.0500 | 0.0338 |
| | 50% | 0.0263 | 0.4102 | 0.0999 | 0.3674 | 0.5000 | 0.3490 |
| | 95% | 0.0476 | 0.7610 | 0.9999 | 0.8399 | 0.9499 | 0.7379 |
| $A_2$ | 5% | 0.0026 | 0.0409 | 0.0999 | 0.3675 | 0.0499 | 0.8099 |
| | 50% | 0.0263 | 0.4102 | 0.9999 | 0.8399 | 0.5000 | 0.8099 |
| | 95% | 0.0500 | 0.8000 | 0.9999 | 0.8399 | 0.9500 | 0.8099 |
| $C_1$ | 5% | 0.0000 | 0.0000 | 0.0499 | 0.0419 | 0.0499 | 0.0462 |
| | 50% | 0.0000 | 0.0000 | 0.4999 | 0.4200 | 0.5000 | 0.3376 |
| | 95% | 0.0000 | 0.0000 | 0.9499 | 0.7980 | 0.9500 | 0.7537 |

## 2.4 Analysis of the model

The model of *Campylobacter* transmission in the chicken processing line is already built. This model gives the number of bacteria on the exterior of the chicken after the process. The variability of the output of this model depends on the concentration of bacteria inside the chicken, the number of *Campylobacter* on the exterior of the chicken and the contamination of the environment. This variability is important in the risk assessment study. We present medians of the numbers of *Campylobacter* ($\log(N_{ext})$) on the randomly chosen chicken at the end of all processing stages in three situations.

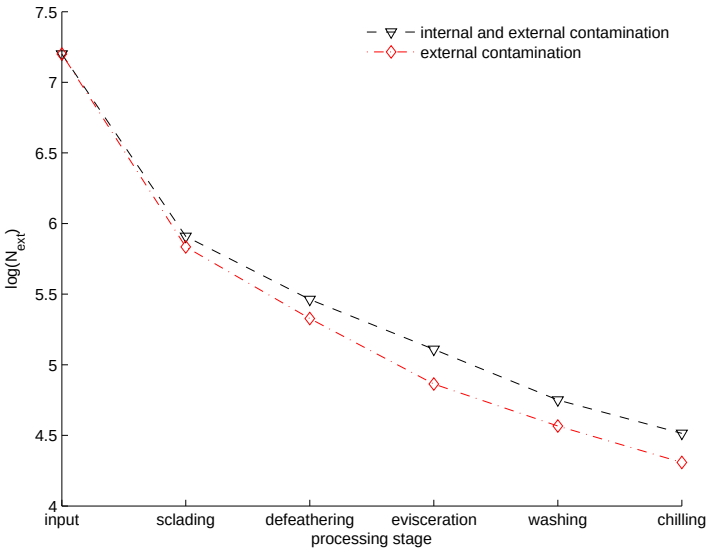


*Figure 2.6: The effect of processing on log(Next) for externally and internally and only externally contaminated flock.*

In figure (2.6) the amount of bacteria on the chicken which is internally infected with $10^6$ and externally contaminated with $10^{7.2}$ *Campylobacter* is shown. There are also presented medians of the $\log(N_{ext})$ for the chicken which is only externally contaminated with $10^{7.2}$ *Campylobacter*. We observe that the amount of bacteria decreases over all stages of the process in these two cases. Internal and external contamination has an bigger influence on the concentration of bacteria on the chicken than just the external contamination.

In the next part we take into consideration chicken, which is internally and externally contaminated.

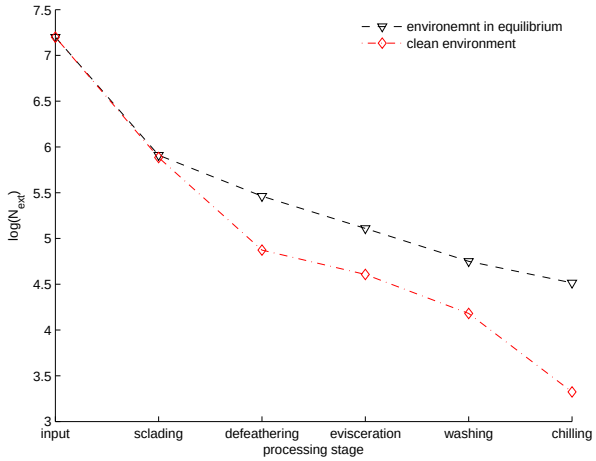


*Figure 2.7: The effect of processing on log(Next) for environment found in equilibrium and for clean environment.*

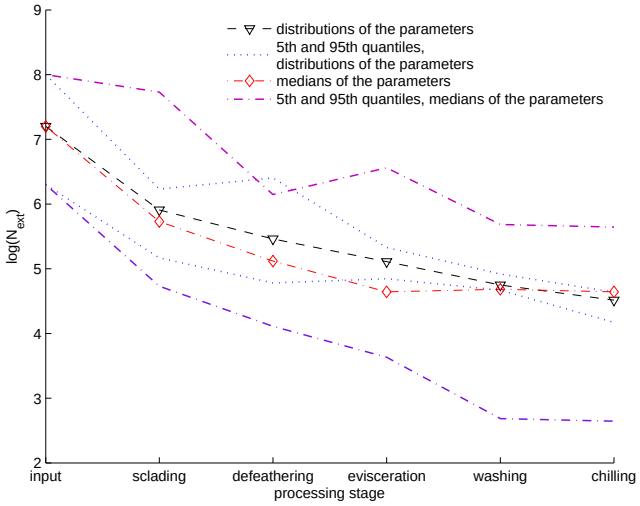


*Figure 2.8: The effect of processing on log(Next) for all the parameters samples and just for medians of the parameters.*

Now we observe the influence of the environment contamination on the output of the model (figure 2.7). *Campylobacter* can move from the chicken to the environment and from the environment back to the chicken. After few processed carcasses the contamination of the environment does not change. We see that the

concentration of bacteria in the contaminated and clean environment are slightly different. Moreover, the amount of bacteria on the exterior of the carcass is bigger when the environment is found in the equilibrium state.

In the chicken processing line model transfer coefficients are given in a form of samples. We do not know the parametric distributions of these parameters. In [9] only medians of the parameters were used. This choice neglects the uncertainty of the model and it takes into account only the uncertainty of the initial amount of bacteria on the chicken. The uncertainty of the parameters is not taken into account (figure 2.8). Moreover, when we use all parameters samples computed through probabilistic inversion technique we are able to update the model. Using quantitative data, we can find new parameters of the chicken processing line model. More information about the updating methods are contained in the next chapter of this thesis.

# Chapter 3

# Updating model parameters

The chicken processing line model is built and quantified using Expert Judgement Study, because the experimental data yielding the values of the model parameters were not available. Since that time, the quantitative data on *Campylobacter* during poultry processing in different countries have been collected. Now, when the data is published, we want to update the model. There are many possible techniques of updating, but this thesis shows two of them. The first one uses probabilistic inversion and the second one, implements Bayesian inference [3]. We implement these methods to the chicken processing line model. We are going to use "BerrangAndDickens" data as an illustration of these techniques. These data contains the amount of bacteria on the exterior of the chicken in a poultry processing line in the USA.

## 3.1 Data

In our study we use "BerrangAndDickens" data, which present the number of *Campylobacter* during poultry processing in the USA.

However, these data do not contain as much information as we would need in our calculations. It does not contain all information that would be useful for updating the model. We do not know anything about the internal contamination of the chicken and the amount of bacteria in the environment. There is no information which chicken was taken during these measurements and in what temperature carcasses were scalding and if they were chilling using air or spray.

Data presented in table (3.1) only contains means and standard deviation of the log cfu/ml rinsing water, in 300 ml per carcass, before and after each stage for five stages of the six flocks. Therefore, the mean values given in table (3.1) in-

*Table 3.1: Data.*

| | I | II | III | IV | V | VI |
|---|---|---|---|---|---|---|
| flock 1 | 2.9 | 1 | - | 1.6 | - | 0.9 |
| flock 2 | 5 | 2 | 3.2 | 3.2 | 2.1 | 1.2 |
| flock 3 | 5 | 1.7 | 4.5 | 3.7 | 3.3 | 1.1 |
| flock 4 | 3.1 | 2.4 | 3.1 | 2.5 | 2 | 0.9 |
| flock 5 | 5.8 | 2.4 | 4.1 | 4 | 1.6 | 3.2 |
| flock 6 | 4.6 | 1.5 | 3.7 | 3.7 | 2.7 | 1.1 |

*I - before scalding, II - after scalding*
*III - after defeathering, IV - after evisceration*
*V - after washing, VI - after chilling*

crease by log(300) (figure 3.1). The standard deviation is equal 0.5 for all stages. This does not seem to be very realistic.

We can observe that after the first stage (scalding) the number of *Campylobacters* decreases, but during the next phase (defeathering) it grows rapidly.

Three phases scalding, defeathering and evisceration are the most critical point for cross-contamination during processing, because the feces contaminated with *Campylobacter* may leak from the carcass [9]. In [8] we find that after defeathering this contamination has the highest value. For the last two stages, washing and chilling, the intestines are already removed from the carcass. Therefore, the internal infection does not have any influence on the external contamination of the chicken and the number of bacteria is getting smaller. The only exception is for flock 4, where the amount of bacteria 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.

For our computation we assume that the $\log(N_{ext})$ is normally distributed with mean given from data and variance $(0.5)^2$ and we assume that the measurements were taken from the random chicken. Moreover, we consider the log of the internal contamination as a normal distribution with mean 6 and standard deviation 0.73 (Enthoven data [11]). We also presume that the environment is

found in the equilibrium state. Hence, the contamination of the environment does not change.

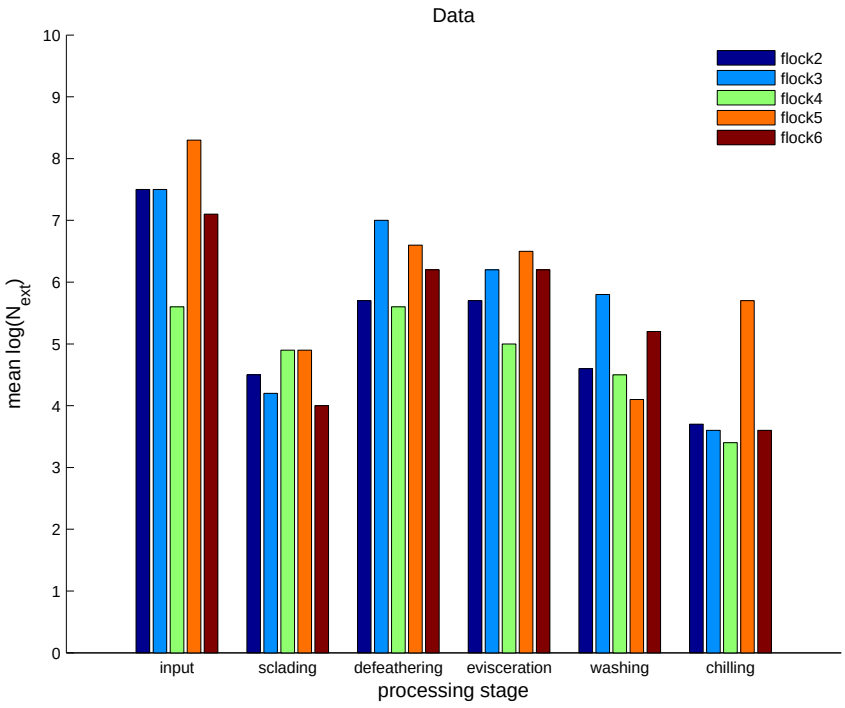


*Figure 3.1: Data.*

Usually, in the Netherlands, in the scalding process, the low temperature $50^o$-$52^o$C is used [9], so we also assume that during collecting these data carcasses were scalding using this temperature. For the chilling stages we presume that spray was used .

In our study we do not take into consideration the first flock, because of the lack of information about the amount of bacteria after defeathering and washing stage for this group of chickens.

## 3.2 Method 1 - Probabilistic Inversion

In the chicken processing line model we do not know the parametric distributions of the parameters. We only have samples computed through the probabilis-

tic inversion technique. PI was used to obtain the distributions of the parameters to comply with experts' assessments. We will now use this technique to change the distributions of the parameters to fit information from the data. We already know how to implement this technique and we would like to find new parameters of the chicken processing line model observing the output of this model.

Model is given by the equation (2.1) and parameters of this model are the transfer coefficients for each stage

$$\theta = [a_{ext}, b_{env}, a_{int}, c_{env}, w_{int}, c_{ext}].$$

Data represents only means and standard deviations of the number of bacteria before and after each stage. However, we assume that the distributions are normal with specified means and standard deviations. They are denote as $f$(before) and $g$(after).

The amount of bacteria on an average chicken after a processing stage as a function of $\theta$ is computed in a following way

$$h(\theta) = \int_x M(x;\theta)dx$$

where $x \sim f$.

We want this distribution to have 5%, 50% and 95% quantiles specified by the normal distribution $g$ of the amount of bacteria at the end of the stage given by data. Using probabilistic inversion method we can adapt $h$ to fit those quantiles.

Applying the probabilistic inversion technique to each flock separately, we update the model to the specific flock, but we can also implement this method to all flocks together and find the parameters which fit to all groups of the chickens.

We apply PI to each flock separately and to all flocks considered together. In the second case we take the average of the distributions $f$ for each flocks as a constraint.

First, we show the results of the updating for all flocks observed together in figure (3.2). We observe that for scalding and defeathering stages the 90% confidence interval is very wide and the data for almost all flocks fall into this interval. For evisceration, washing and chilling this confidence interval is narrow and only one or two values are contained between the 5% and 95% quantiles. Probabilistic inversion in this case does not converge very well (table(3.2)).

*Table 3.2: Results of the IPF method for all flocks considered together, for all stages.*

| | 5% | 50% | 95% |
|---|---|---|---|
| low scalding | 0.0000 | 0.4500 | 0.8999 |
| defeathering | 0.0500 | 0.5000 | 0.9499 |
| evisceration | 0.0000 | 0.4500 | 0.4500 |
| washing | 0.0000 | 0.4500 | 0.8999 |
| spray chilling | 0.0000 | 0.0000 | 0.4500 |

We also present our solutions for each flock separately. Updated model in such way, usually takes the distributions of the number of *Campylobacter* closer to the distributions given by data. We present the medians of these distributions for each group of chickens.

Table (3.8) contains results of IPF when we observe each flock separately and this algorithm does not always converge to the solution.

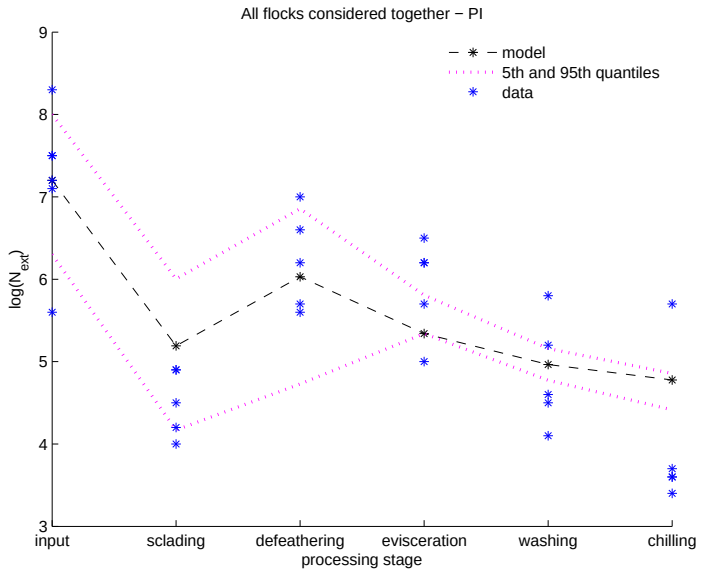


*Figure 3.2: The effect of processing on log(Next) for all flocks after updating and the uncertainty of the log(Next).*

*Table 3.3: Distribution of log(Next) in the baseline of the processing model before and after updating for* ***FLOCK 2****.*

| | | before updating | | | after updating | | |
|---|---|---|---|---|---|---|---|
| | data | 5% | 50% | 95% | 5% | 50% | 95% |
| scalding | 4.5 | 5.3797 | 6.1214 | 6.4419 | 4.1781 | 4.5920 | 6.2142 |
| defeathering | 5.7 | 4.9207 | 5.6377 | 6.5000 | 5.0108 | 5.6979 | 6.3982 |
| evisceration | 5.7 | 5.0328 | 5.2948 | 5.5286 | 5.0949 | 5.0949 | 5.5567 |
| washing | 4.6 | 4.8813 | 4.9721 | 5.1317 | 4.5232 | 4.7152 | 4.9164 |
| chilling | 3.7 | 4.3765 | 4.7203 | 4.8440 | 4.1365 | 4.5009 | 4.5009 |

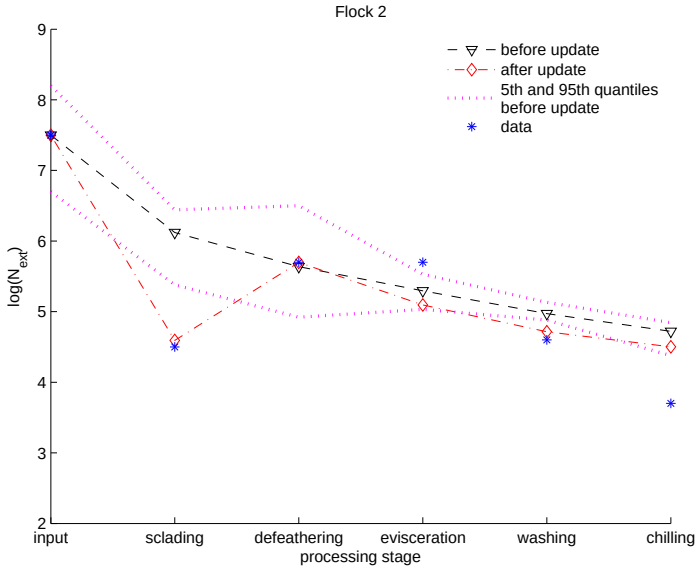


*Figure 3.3: The effect of processing on log(Next) for* ***FLOCK 2****, before and after updating and the uncertainty of the log(Next) using initial model.*

For flock 2 we observe that the medians of the number of *Campylobacter* after scalding, defeathering and washing are almost equal to the medians given by data.

*Table 3.4: Distribution of log(Next) in the baseline of the processing model before and after updating for* ***FLOCK 3****.*

| | | before updating | | | after updating | | |
|---|---|---|---|---|---|---|---|
| | data | 5% | 50% | 95% | 5% | 50% | 95% |
| scalding | 4.2 | 5.4065 | 6.1479 | 6.4692 | 4.2024 | 4.5071 | 6.2370 |
| defeathering | 7 | 4.9158 | 5.6401 | 6.4756 | 5.8229 | 6.2582 | 6.9090 |
| evisceration | 6.2 | 5.0152 | 5.2775 | 5.5074 | 5.5380 | 5.9339 | 6.0511 |
| washing | 5.8 | 4.7953 | 4.8861 | 5.0457 | 5.5590 | 5.7602 | 5.8230 |
| chilling | 3.6 | 4.3245 | 4.6683 | 4.7920 | 4.8751 | 5.5449 | 5.5449 |

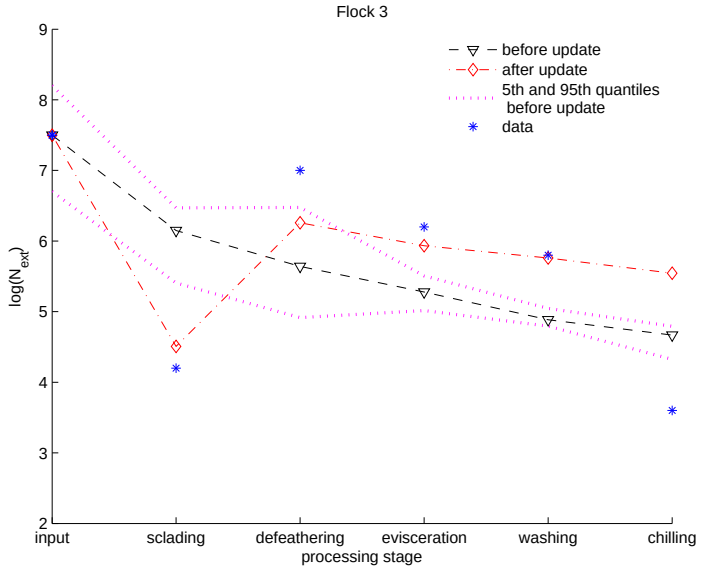


*Figure 3.4: The effect of processing on log(Next) for* ***FLOCK 3****, before and after updating and the uncertainty of the log(Next) using initial model.*

For flock 3, updated model gives good results for scalding, evisceration and washing. For washing stage, the median of the $\log(N_{ext})$ after update is almost equal to the observed median.

*Table 3.5: Distribution of log(Next) in the baseline of the processing model before and after updating for* ***FLOCK 4****.*

| | | before updating | | | after updating | | |
|---|---|---|---|---|---|---|---|
| | data | 5% | 50% | 95% | 5% | 50% | 95% |
| scalding | 4.9 | 3.6041 | 4.2814 | 4.6665 | 4.0029 | 4.5535 | 5.0951 |
| defeathering | 5.6 | 3.8767 | 4.2192 | 5.1317 | 5.3064 | 5.8732 | 6.2870 |
| evisceration | 5 | 3.9486 | 4.1831 | 4.3513 | 5.2359 | 5.2359 | 5.6982 |
| washing | 4.5 | 3.7933 | 3.8841 | 4.0437 | 4.8690 | 4.9588 | 5.0762 |
| chilling | 3.4 | 3.2745 | 3.6183 | 3.7420 | 4.0638 | 4.3365 | 4.7799 |

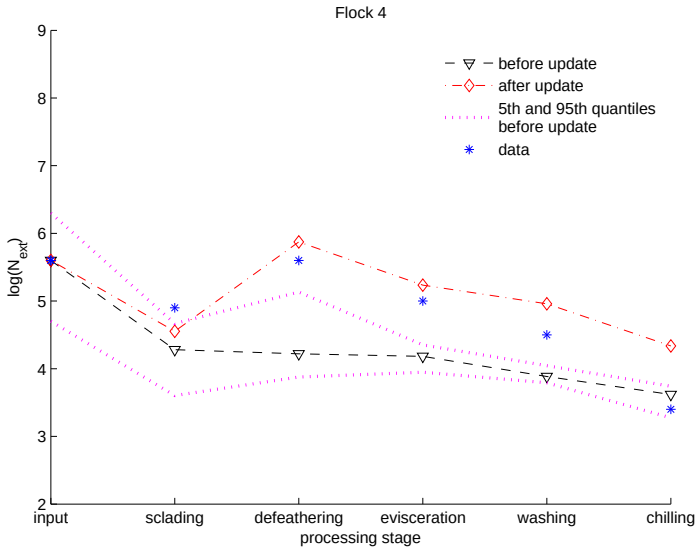


*Figure 3.5: The effect of processing on log(Next) for* ***FLOCK 4****, before and after updating and the uncertainty of the log(Next) using initial model.*

For flock 4, when we update the model we get good solutions for scalding, defeathering, evisceration and washing.

*Table 3.6: Distribution of log(Next) in the baseline of the processing model before and after updating for* ***FLOCK 5****.*

| | | before updating | | | after updating | | |
|---|---|---|---|---|---|---|---|
| | data | 5% | 50% | 95% | 5% | 50% | 95% |
| scalding | 4.9 | 6.2279 | 6.9703 | 7.2891 | 5.3006 | 5.8881 | 7.1125 |
| defeathering | 6.6 | 5.6432 | 6.4810 | 7.0262 | 5.4740 | 6.9864 | 7.0334 |
| evisceration | 6.5 | 5.8273 | 6.0910 | 6.3434 | 6.3006 | 6.5652 | 6.8017 |
| washing | 4.1 | 5.6773 | 5.7681 | 5.9277 | 5.9731 | 6.1830 | 6.3800 |
| chilling | 5.7 | 5.1905 | 5.5343 | 5.6580 | 5.5606 | 5.9955 | 6.0853 |

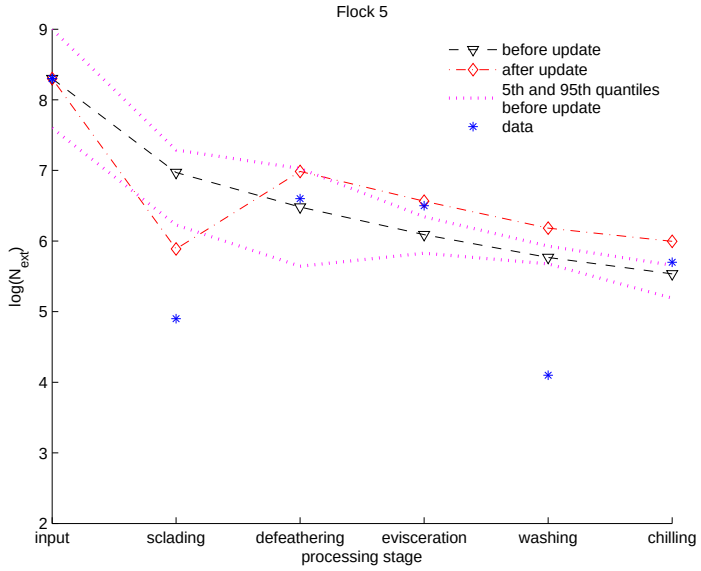


*Figure 3.6: The effect of processing on log(Next) for* ***FLOCK 5****, before and after updating and the uncertainty of the log(Next) using initial model.*

For flock 5, when we update the model the solutions are good for defeathering, evisceration and chilling stages. For the scalding and washing phases the medians of the number of *Campylobacter* are not close to the medians given by data.

*Table 3.7: Distribution of log(Next) in the baseline of the processing model before and after updating for* ***FLOCK 6****.*

| | | before updating | | | after updating | | |
|---|---|---|---|---|---|---|---|
| | data | 5% | 50% | 95% | 5% | 50% | 95% |
| scalding | 4 | 5.0597 | 5.7940 | 6.1183 | 3.8782 | 4.2757 | 5.8827 |
| defeathering | 6.2 | 4.6418 | 5.2984 | 6.2925 | 4.3099 | 5.9963 | 6.8249 |
| evisceration | 6.2 | 4.6916 | 4.9567 | 5.1685 | 5.3025 | 5.3708 | 5.8031 |
| washing | 5.2 | 4.5433 | 4.6341 | 4.7937 | 5.0030 | 5.1881 | 5.2595 |
| chilling | 3.6 | 4.0385 | 4.3823 | 4.5060 | 4.3380 | 4.9709 | 4.9709 |

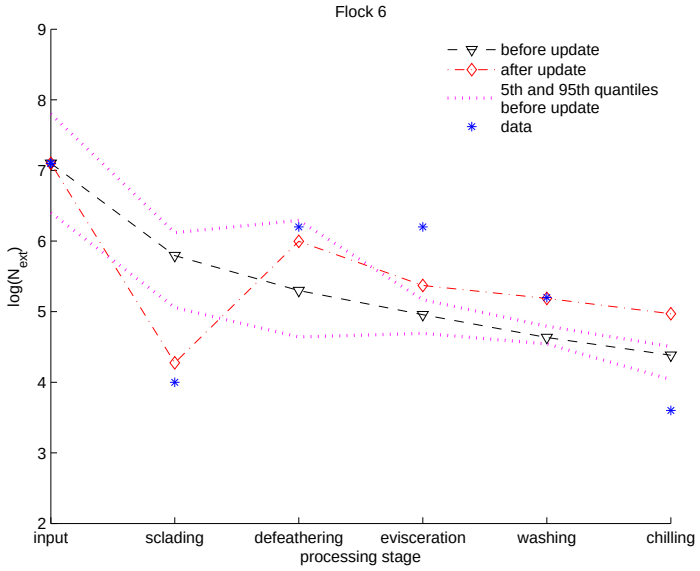


*Figure 3.7: The effect of processing on log(Next) for* ***FLOCK 6****, before and after updating and the uncertainty of the log(Next) using initial model.*

For flock 6, when we update the model using information only about this group of chicken, we get good results for scalding, defeathering and wahing stages.

*Table 3.8: Results of the probabilistic inversion method for each flock*

| | 5% | 50% | 95% |
|---|---|---|---|
| | Low Scalding | | |
| flock 2 | 0.0000 | 0.4499 | 0.8999 |
| flock 3 | 0.0000 | 0.4500 | 0.8999 |
| flock 4 | 0.0500 | 0.4999 | 0.9499 |
| flock 5 | 0.0000 | 0.4500 | 0.9000 |
| flock 6 | 0.0000 | 0.4500 | 0.9000 |
| | Defeathering | | |
| flock 2 | 0.0499 | 0.5000 | 0.9499 |
| flock 3 | 0.0499 | 0.4999 | 0.4999 |
| flock 4 | 0.0499 | 0.5000 | 0.9500 |
| flock 5 | 0.0499 | 0.5000 | 0.9500 |
| flock 6 | 0.0500 | 0.4999 | 0.9499 |
| | Evisceration | | |
| flock 2 | 0.0000 | 0.4500 | 0.4500 |
| flock 3 | 0.0000 | 0.4999 | 0.9000 |
| flock 4 | 0.0000 | 0.0000 | 0.4500 |
| flock 5 | 0.0000 | 0.0000 | 0.4500 |
| flock 6 | 0.0499 | 0.5000 | 0.5000 |
| | Washing | | |
| flock 2 | 0.0000 | 0.4499 | 0.8999 |
| flock 3 | 0.0000 | 0.4499 | 0.8999 |
| flock 4 | 0.0000 | 0.0000 | 0.4500 |
| flock 5 | 0.0000 | 0.0000 | 0.4499 |
| flock 6 | 0.0000 | 0.4499 | 0.8999 |
| | Spray Chilling | | |
| flock 2 | 0.0000 | 0.0000 | 0.4499 |
| flock 3 | 0.0000 | 0.0000 | 0.4500 |
| flock 4 | 0.0000 | 0.4499 | 0.9000 |
| flock 5 | 0.0500 | 0.4999 | 0.9499 |
| flock 6 | 0.0000 | 0.0000 | 0.4499 |

## 3.3 Method 2 - Bayesian Inference

The first method of updating the model does not always give good results. Therefore, we would like to find and check if other methods perform better on this data.

The Bayesian melding technique presented in [10] was taken into consideration and we present this method briefly.

# Bayesian Melding

The model $y = M(x;\theta)$ is given. Moreover prior distributions of inputs $(x,\theta)$ and output $y$ denoted as $q_1$ and $q_2$, respectively are available. It can be noticed however that the model and the prior distribution of inputs produce another prior distribution of the output denoted as $q^*$. The main idea of the Bayesian melding is to combine these two priors, such that

$$q^{out} \propto (q_1^*)^{\alpha} q_2^{1-\alpha}$$

where $\alpha$ is the pooling weight. The weight can be taken as e.g. $\alpha = 0.5$. [10] presents theorem that this combining priors works.

Having $q^{out}$ we invert the model (if $M$ invertible this possess no problem, however if $M$ is not invertible an inversion algorithm based on assignment proportional to input prior is proposed) and obtain new prior distribution of the inputs $q^{in}$. Having combined priors for input and output we can update distribution of input and output with observed data. The posterior function in this case is obtain in the following way:

$$\pi(x,\theta) \propto q^{in} L_{in}(x,\theta) q^{out} L_{out}(M(x,\theta))$$

where $L_{in}(x,\theta)$ and $L_{out}(M(x,\theta))$ are the likelihood functions of the input and output, respectively.

We cannot apply this method to the chicken processing line model, because we only have the prior distribution of the parameters $\theta$. We do not know prior distributions of model input $x$ and output $y$. This makes application of Bayesian melding technique not possible in our case. Therefore, to the chicken processing model we apply Bayesian Inference technique described below.

## Bayesian inference

We are given a model $M$ with parameters $\theta$,

$$\theta = [a_{ext}, b_{env}, a_{int}, c_{env}, w_{int}, c_{ext}].$$

$M$ is a model that takes as an input the amount of bacteria $x$ on a chicken and returns the output $y$, which indicates the amount of bacteria on this chicken after a processing stage. The distribution of $\theta$, denoted as $f_\theta$ is given in a form of $N$ samples obtained through the probabilistic inversion technique from experts assessments on some observable quantities predicted by $M$. $f_\theta$ will be considered as the prior distribution of $\theta$. We get that

$$y = M(x; \theta).$$

We consider first situation when one is given data containing information about amount of bacteria on each chicken before and after the processing stage. Then one can apply the standard Bayesian inference technique to update the distribution of $\theta$. [3]

The data is of the form: $D$, $(x_i, y_i), i = 1, .., k$, where $x_i, y_i$ denote the amount of bacteria on $i$th observed chicken before and after the processing stage, respectively. The standard Bayesian inference technique requires the likelihood function of the data under the model. Observations are assumed to be independent.

Knowing the amount of bacteria on the $i$th chicken $x_i$ before the processing stage, the model determines the distribution of the output $h(.|x_i, \theta)$. Hence the probability of observing $y_i$ can be found as $h(y_i; \theta)$. (Since the distribution of $\theta$ is given only in a form of samples we would have a problem applying this technique as there can be no samples of $\theta$ such that $y_i = M(x_i, \theta)$)

The likelihood function gives us the probability of observing pairs of $(x_i, y_i)$ under this model. Hence

$$L(D|\theta = t) = \prod_{i=1}^{k} h_i(y_i; x_i, \theta = t)$$

Using Bayes theorem the posterior distribution of $\theta$ can be obtained as:

$$f(\theta|D) = \frac{L(D|\theta = t) f_\theta(t)}{\int_t L(D|\theta = t) f_\theta(t) dt}.$$

In our situation the observations differ from the case presented above. We only know that the amount of bacteria on an average chicken before and after the processing stage are the realizations of $f$ and $g$, respectively. Hence the likelihood is now given as :

$$g\left(\int_x M(x|\theta = t)dx\right)$$

where $x \sim f$.

From the above and Bayes theorem the posterior distribution of $\theta$ is

$$P(\theta') = \frac{g\left(\int_x M(x|\theta = t)dx\right) f_\theta(t)}{\int_t g\left(\int_x M(x|\theta = t)dx\right) f_\theta(t)dt}.$$

For $k$ flocks considered together, the likelihood function is obtain in the following way

$$\prod_{i=1}^{k} g_i\left(\int_x M(x|\theta = t)dx\right)$$

where $g_i$ are the likelihood functions for flock $i$, $i = 1, ..., k$. Thus, the posterior distribution of $\theta$ is

$$P(\theta') = \frac{\left(\prod_{i=1}^{k} g_i\left(\int_x M(x|\theta = t)dx\right)\right) f_\theta(t)}{\int_t \left(\prod_{i=1}^{k} g_i\left(\int_x M(x|\theta = t)dx\right)\right) f_\theta(x)}$$

# Application of the Bayesian inference

We apply this method of updating the model to each flock separately and to all flocks considered together.

First, we show our results for all flocks considered together. In figure (3.8) we observe that the uncertainty is wide for the defeathering stage and almost all values given by data fall into the 90% confidence interval. The confidence interval for the first stage is more narrow and contains two data points, but for evisceration, washing and chilling it contains only one value given by data.

We also implement this method to each flock observed separately. The results are presented below. We show the medians of the number of *Camylobacter* on

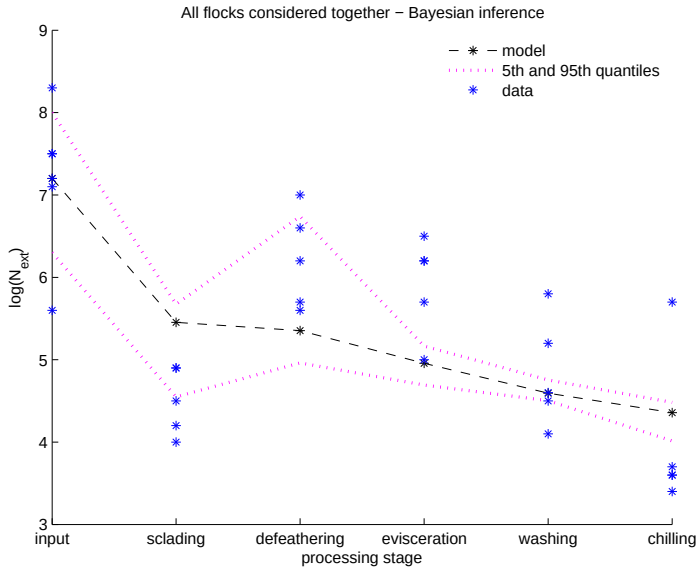


*Figure 3.8: The effect of processing on log(Next) for all flocks after updating and the uncertainty of the log(Next).*

the exterior of the chicken after each processing stage.

*Table 3.9: Distribution of log(Next) in the baseline of the processing model before and after updating for **FLOCK 2**.*

| | | before updating | | | after updating | | |
|---|---|---|---|---|---|---|---|
| | data | 5% | 50% | 95% | 5% | 50% | 95% |
| scalding | 4.5 | 5.3797 | 6.1214 | 6.4419 | 4.5105 | 5.0503 | 5.3826 |
| defeathering | 5.7 | 4.9207 | 5.6377 | 6.5000 | 4.8518 | 5.7500 | 6.1031 |
| evisceration | 5.7 | 5.0328 | 5.2948 | 5.5286 | 5.1114 | 5.3735 | 5.6061 |
| washing | 4.6 | 4.8813 | 4.9721 | 5.1317 | 4.8614 | 4.9890 | 5.0590 |
| chilling | 3.7 | 4.3765 | 4.7203 | 4.8440 | 4.3505 | 4.5745 | 4.7515 |

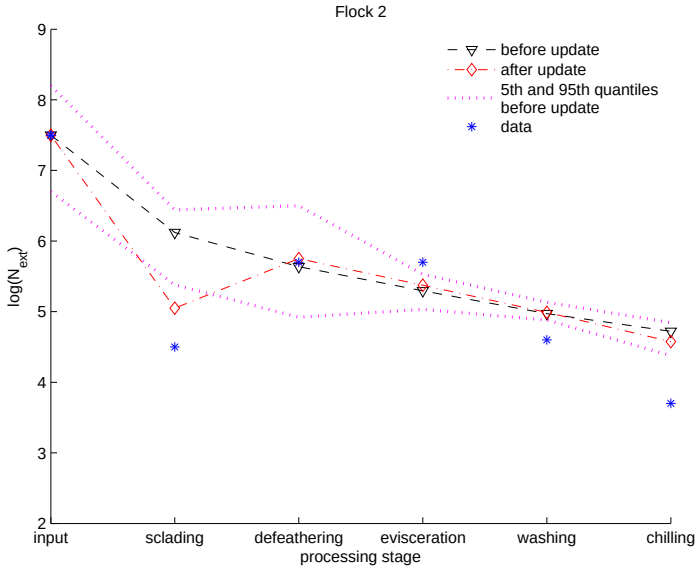


*Figure 3.9: The effect of processing on log(Next) for **FLOCK 2**, before and after updating and the uncertainty of the log(Next) using initial model.*

For flock 2, for defeathering stage, the median of the $\log(N_{ext})$ is almost equal to the observed median.

*Table 3.10: Distribution of log(Next) in the baseline of the processing model before and after updating for* ***FLOCK 3****.*

| | | before updating | | | after updating | | |
|---|---|---|---|---|---|---|---|
| | data | 5% | 50% | 95% | 5% | 50% | 95% |
| scalding | 4.2 | 5.4065 | 6.1479 | 6.4692 | 4.4795 | 4.9569 | 5.2728 |
| defeathering | 7 | 4.9158 | 5.6401 | 6.4756 | 5.9879 | 6.0974 | 6.9248 |
| evisceration | 6.2 | 5.0152 | 5.2775 | 5.5074 | 5.7018 | 5.8594 | 5.9360 |
| washing | 5.8 | 4.7953 | 4.8861 | 5.0457 | 5.5168 | 5.6158 | 5.6883 |
| chilling | 3.6 | 4.3245 | 4.6683 | 4.7920 | 4.9431 | 5.1535 | 5.1963 |

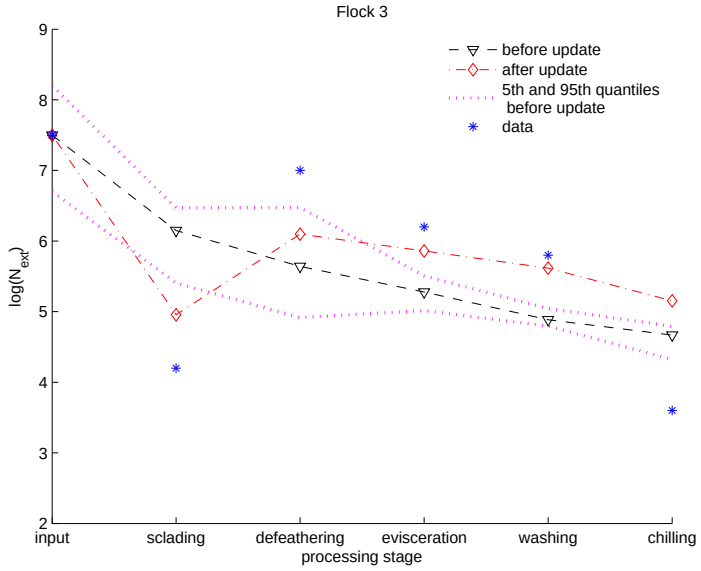


*Figure 3.10: The effect of processing on log(Next) for* ***FLOCK 3****, before and after updating and the uncertainty of the log(Next) using initial model.*

For flock 3, when we update the model using the information only about this group of chickens, we have good results for four stages, scalding, defeathering, evisceration and washing.

*Table 3.11: Distribution of log(Next) in the baseline of the processing model before and after updating for* ***FLOCK 4****.*

| | | before updating | | | after updating | | |
|---|---|---|---|---|---|---|---|
| | data | 5% | 50% | 95% | 5% | 50% | 95% |
| scalding | 4.9 | 3.6041 | 4.2814 | 4.6665 | 4.2857 | 4.4097 | 4.7527 |
| defeathering | 5.6 | 3.8767 | 4.2192 | 5.1317 | 5.5825 | 5.8914 | 6.1456 |
| evisceration | 5 | 3.9486 | 4.1831 | 4.3513 | 5.2356 | 5.3071 | 5.4966 |
| washing | 4.5 | 3.7933 | 3.8841 | 4.0437 | 4.7569 | 4.8810 | 4.9575 |
| chilling | 3.4 | 3.2745 | 3.6183 | 3.7420 | 4.1951 | 4.4055 | 4.4541 |

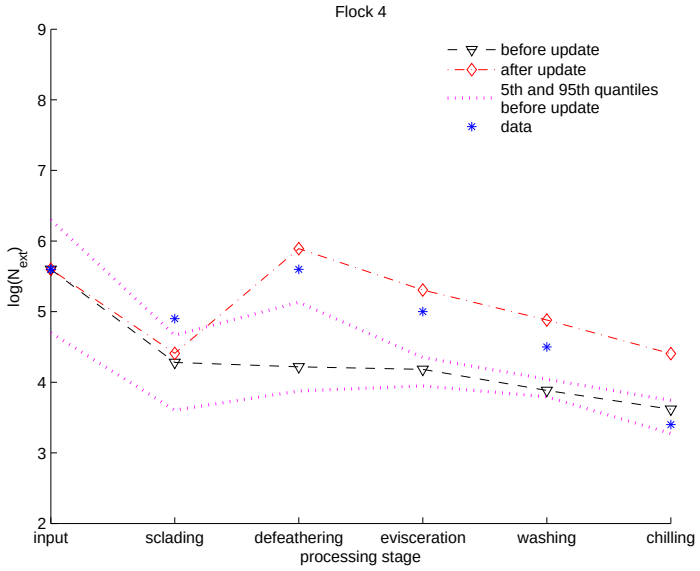


*Figure 3.11: The effect of processing on log(Next) for* ***FLOCK 4****, before and after updating and the uncertainty of the log(Next) using initial model.*

For flock 4, when we observe only this one flock than the updated model gives good results for almost all stages. The medians of the number of bacteria on the chicken after scalding, defeathering, evisceration and washing are close to the values given by data.

*Table 3.12: Distribution of log(Next) in the baseline of the processing model before and after updating for* ***FLOCK 5****.*

| | | before updating | | | after updating | | |
|---|---|---|---|---|---|---|---|
| | data | 5% | 50% | 95% | 5% | 50% | 95% |
| scalding | 4.9 | 6.2279 | 6.9703 | 7.2891 | 5.3240 | 5.7465 | 6.0822 |
| defeathering | 6.6 | 5.6432 | 6.4810 | 7.0262 | 6.4521 | 6.7340 | 6.7340 |
| evisceration | 6.5 | 5.8273 | 6.0910 | 6.3434 | 6.3107 | 6.4563 | 6.5797 |
| washing | 4.1 | 5.6773 | 5.7681 | 5.9277 | 5.8995 | 6.0350 | 6.0793 |
| chilling | 5.7 | 5.1905 | 5.5343 | 5.6580 | 5.5715 | 5.7605 | 5.8595 |

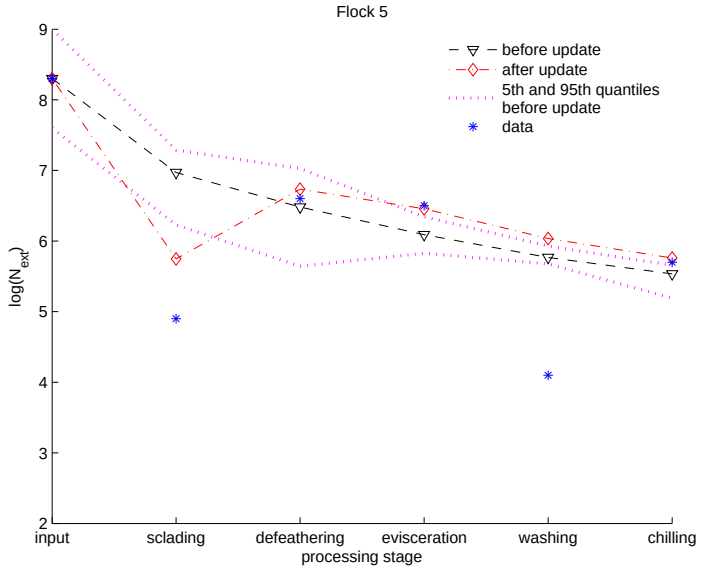


*Figure 3.12: The effect of processing on log(Next) for* ***FLOCK 5****, before and after updating and the uncertainty of the log(Next) using initial model.*

For flock 5, the results are not so good for scalding and washing stages, but the medians of the $\log(N_{ext})$ after defeathering, evisceration and chilling are close to the observed medians of the $\log(N_{ext})$.

*Table 3.13: Distribution of log(Next) in the baseline of the processing model before and after updating for* ***FLOCK 6****.*

| | | before updating | | | after updating | | |
|---|---|---|---|---|---|---|---|
| | data | 5% | 50% | 95% | 5% | 50% | 95% |
| scalding | 4 | 5.0597 | 5.7940 | 6.1183 | 4.0624 | 4.5891 | 4.9117 |
| defeathering | 6.2 | 4.6418 | 5.2984 | 6.2925 | 5.6582 | 5.9660 | 6.8602 |
| evisceration | 6.2 | 4.6916 | 4.9567 | 5.1685 | 5.2842 | 5.5455 | 5.7878 |
| washing | 5.2 | 4.5433 | 4.6341 | 4.7937 | 5.1272 | 5.1608 | 5.2815 |
| chilling | 3.6 | 4.0385 | 4.3823 | 4.5060 | 4.4931 | 4.7035 | 4.7488 |

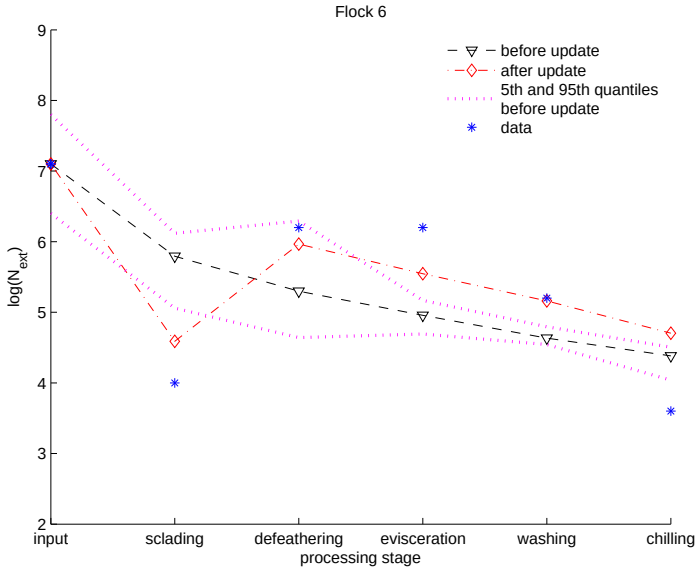


*Figure 3.13: The effect of processing on log(Next) for* ***FLOCK 6****, before and after updating and the uncertainty of the log(Next) using initial model.*

For flock 6, the updated model gives good results for defeathering, evisceration and washing phases.

## 3.4 Summary

Having quantitative data on *Campylobacter* during poultry processing in the slaughterhouse, we can update the chicken processing line model. We have applied two methods: probabilistic inversion and Bayesian inference techniques. We implement these methods to five flocks separately and then to all flocks considered together.

When we apply PI and Bayesian inference to each flock, we usually get good results for almost all stages. Medians of the average amount of bacteria on the exterior of the randomly chosen chicken are really close to the medians of this number given by data.

When we compare probabilistic inversion and Bayesian inference techniques, we observe that these methods give similar results when we observe only one flock (figure 3.14). It happens, because both these methods put weights on the samples and find new model parameters through the technique based on sample re-weighting. However, when we observe all flocks together, probabilistic inversion gives better results. Using this method, the uncertainty of the model is bigger than after the Bayesian inference is applied. Moreover, when we computed the posterior functions, very often the values of these functions are almost equal to zero.

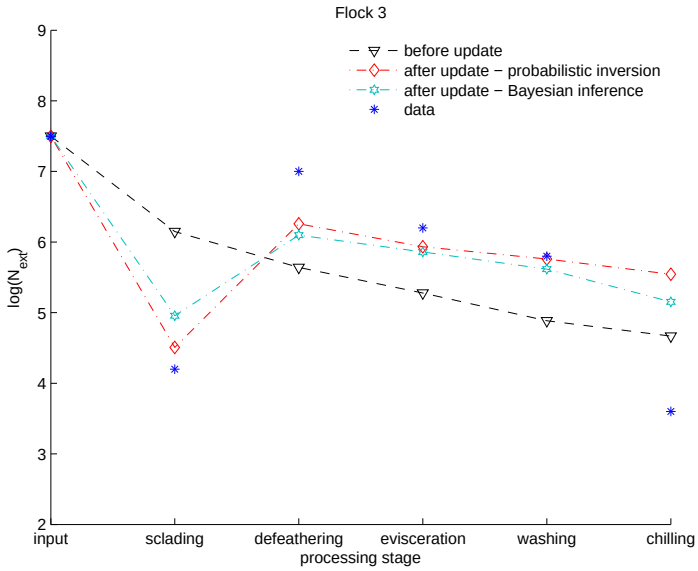


*Figure 3.14: The effect of processing on log(Next) for flock 2, before and after updating using two methods (in a case when we consider each flock separately).*

# Chapter 4

# Conclusions

Chicken processing line model, which describes the transmission of *Campylobacter* through the broiler meat production chain was presented in [1]. The processing data were not available and Expert Judgement Study was used for model parameter estimation, e.i. transfer coefficients. Experts having extensive knowledge and experience on broiler chicken processing in the Netherlands as well as behavior of pathogens, in particular *Campylobacter*, during the various processing stages were interviewed. They respond to the questions about their contamination with bacteria during the different stages (scalding, defeathering, evisceration, washing, chilling) of this process. Using experts opinion, the non-parametric distributions of the parameters were obtained with the probabilistic inversion method, in particular IPF and PARFUM algorithms were used.

Finally, the quantitative data on *Campylobacter* during poultry processing have been collected. Therefore, this model can be updated.

Using data collected by Berrang and Dickens during the poultry processing in the USA, we implemented two updating methods. We find new parameters of the model applying probabilistic inversion and Bayesian inference techniques.

We implemented these methods to each group of chickens separately and to all flocks considered together. In the first case, both probabilistic inversion and Bayesian inference usually gave really good results for almost all stages. If we assume that all flocks were observed together, the probabilistic inversion gives better results. Using this method, the uncertainty of the model is bigger than after the Bayesian inference is applied. Moreover, in the second method the posterior function may be almost equal to zero.

# Appendices

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# Appendix A

# Query variables

The assumptions:

- "Typical large broiler chicken slaughterhouse" in the Netherlands.
- Average day of the year (all seasons).
- At the beginning of the new slaughtering day *Campylobacter* is absent in the slaughterhouse.
- All machines are functioning well.
- Thinned-flocks of 10,000 chickens each.
- The chickens of the flocks are uniform in size and weight.
- The broiler-house might have been clean (dry) or dirty (wet).
- Time of fasting is 6 hours, travelling time 3 to 4 hours and waiting time is around 2 hours.
- In the scalding tank the principle of counter current is used.
- Low scalding temperature is 50-52$^o$C and intermediate scalding temperature is 55-56$^o$ C.

The query variables were grouped into four sections, which are explained below.

**Part A - A positive flock**

The experts were asked to assess the number of *Campylobacter* (cfu per carcass) on the exterior of specific broiler chicken carcasses after passed each of the processing stages of scalding, defeathering, evisceration, washing and chilling.

We supposed that it was the first flock processed that day and all carcasses of the flock were colonized by $10^8$ cfu *Campylobacter* per gram caecal content and contaminated by $10^5$ *Campylobacter* per carcass at the beginning of the particular processing stage. Query variable $A1$ related to the first carcass of the flock and query variable $A2$ to the last one.

*Question A1:*

*All chickens of the particular flock are passing successively each slaughtering stage. How many campylobacters (per carcass) will be found after each of the mentioned stages of the slaughtering process, each time on the first chicken of the flock?*

*Question A2:*

*All chickens of the particular flock are passing successively each slaughtering stage. How many campylobacters (per carcass) are found* ***after*** *each of the mentioned slaughtering stages, each time on the* ***last*** *chicken of this flock?*

**Part B - An externally infected flock**

The query variables of this section were similar to the variables of section A, but here all carcasses of the flock were contaminated by $10^4$ cfu *Campylobacter* per carcass and were not internally colonized by *Campylobacter* at the beginning of each processing stage. Variables $B1$ and $B2$ referred to the first and the last carcass, respectively.

*Question B1:*

*All chickens of the particular flock are passing successively each slaughtering stage. How many campylobacters (per carcass) are found* ***after*** *each of the mentioned slaughtering stages, each time on the* ***first*** *chicken of this flock?*

*Question B2:*

*All chickens of the particular flock are passing successively each slaughtering stage. How many campylobacters (per carcass) are found* ***after*** *each of the mentioned slaughtering stages, each time on the* ***last*** *chicken of this flock?*

**Part C - A negative flock after a positive flock**

The query variables of this section were similar to the variables of section A. First, the positive flock were processed and after this flock, the negative one were slaughtered. Query variable $C1$ related to the number of *Campylobacter* (cfu per carcass) on the exterior of the $100^{th}$ carcass of the second flock, query variable

$C2$ related to this number on the $1000^{th}$ carcass, and query variable $C3$ related to this number on the last carcass. Query variable $C4$ related to the number of carcasses that passed the particular processing stage until the increase of the external contamination of the carcasses of the second flock was neglectably low.

*Question C1:*

*How many campylobacters (per carcass) are found **after** each of the mentioned stages of the slaughtering process, each time **on** the **100th** chicken of this second (initially negative) flock?*

*Question C2:*

*How many campylobacters (per carcass) are found **after** each of the mentioned stages of the slaughtering process, each time **on** the **1000th** chicken of this second (initially negative) flock?*

*Question C3:*

*How many campylobacters (per carcass) are found **after** each of the mentioned stages of the slaughtering process, each time on the last chicken of this second (initially negative) flock?*

*Question C4:*

*In relation to the questions C1 t/m C3 in each slaughtering stage, a decrease in external contamination rate of the (initially negative) chickens of the second flock is possible. How many chickens of this second flock have passed the particular slaughtering stage until the increase of external infection is neglectably low (¡ detection-limit of used analytical method)?*

**Part D - The leaking of manure**

The query variables referred to the leaking of manure during the slaughtering process (scalding, plucking, evisceration) of the flock. We supposed that the chickens did not completely fast, i.e. there was still manure in their intestines. The leaking of manure occurred without disruption of the intestines (or before possible) intervention measures were taken. In the variables a difference was made between full and half-full intestines. Query variable $D1$ related to the number of chickens from which the manure was leaking in each stages. Query variable $D2$ related to the amount of feces leaked from a chicken and $D3$ to the average quantity of manure (gram per chicken) that leaked from the flock in each slaughtering stage. Query $D4$ related to the percentage of the leaked manure would contaminate the particular chicken. Those variables referred to the chicken with half-full intestines and the next variables are similar but referred to the chicken

with full intestines.

*Question D1:*

*From how many chickens out of one thinned-flock of 10,000 chickens with* ***half full*** *intestines is manure leaking in each of the mentioned slaughtering stages?*

*Question D2:*

*When manure is leaking from a chicken with* ***half-full*** *intestines during a certain slaughtering stage: how much manure is leaking (gram)?*

*Question D3:*

*What is the average quantity of manure (gram per chicken) that leaks from a thinned-flock of 10,0000 broiler chickens with* ***half-full*** *intestines in each slaughtering stage*

*Question D4:*

*During a certain slaughtering stage manure is leaking from a chicken with* ***half-full*** *intestines. What percentage (%) of the leaked manure will contaminate the particular chicken (before possible interventions are taken)?*

*Question D5:*

*From how many chickens out of one thinned-flock of 10,000 chickens with* ***full*** *intestines is manure leaking in each of the mentioned slaughtering stages?*

*Question D6:*

*In case manure is leaking from a chicken with* ***full*** *intestines during a certain slaughtering stage: how much manure is leaking (gram)?*

*Question D7:*

*What is the average quantity of manure (gram per chicken) that leaks from a thinned-flock of 10,0000 chickens with* ***full*** *intestines in each slaughtering stage?*

*Question D8:*

*During a certain slaughtering stage manure is leaking from a chicken with* ***full*** *intestines. What percentage (%) of leaked manure will contaminate the particular chicken (before possible interventions are taken)?*

**Part E - Correlation internal and external contamination of a chicken**

As a case we consider a thinned-flock just before transport. All broiler chickens of this flock are infected with Campylobacter, both externally and internally.

Assume that the concentration of campylobacters in the intestines (internal infection) of one particular chicken is higher than the median internal concentration of all chickens of the flock. In that case, what is the chance (%) that the number of campylobacters on this particular chicken (external infection) is also higher than the median of all chickens of the flock?
N.B.: In case there is no correlation, i.e. the internal and external Campylobacter contamination are independent, this chance is 50 %.

# Appendix B

# Seed variables

The 12 seed variables were grouped and numbered according to the experiment. These groups are described below.

**Part A**

Consider a flock of broiler chickens in 1995 just before they are prepared for transportation to the processing plant. The flock became colonized with *Campylobacter* during rearing and all birds are carrying the organism both internally and externally. A random broiler chicken sampled from this flock and number of *Campylobacter* of this chicken, both in its caecum and on its exterior is numerated.

*Seed variable A1*:
*How many campylobacters (number per gram) are found in the caecal content just before the chicken would have been transferred to a transport crate?*

*Seed variable A2*:
*How many campylobacters (number per carcass) are found on the outside of the carcass just before the chicken would have been transferred to a transport crate?*

*Seed variable A3*:
*How many campylobacters (number per gram) are found in the caecal content after transport for 3 to 4 hours?*

*Seed variable A4*:
*How many campylobacters (number per carcass) are found on the outside of the carcass after transport for 3 to 4 hours?*

*Seed variable A5*:

*How many campylobacters (number per gram) are found in the faecal samples from the crates after transporting the birds for 3 to 4 hours?*

**Part B**

In September 1995, a large broiler chicken processing plant was visited and the final products from 17 flocks (involving 14 different farms) were sampled and analyzed for *Camylobacter*. Based on a presence/absence test on caecal content, all flocks were colonized with *Camylobacter*. The processing operation used complete air-chilling. For each flock, 3 composite neck-skin samples were obtained, both before and after chilling, as well as 3 composite samples of breast fillet following portioning. The total sample size was 25 grams (skin/fillet). The number of *Camylobacter* in each composite sample was determined using the standard method. The samples were also analyzed by enrichment.

*Seed variable B1*:

*Before chilling, the number of campylobacters is 1300 per gram of skin (median of 51 composite samples). How many campylobacters (number per gram of skin) are found after chilling on the neck-skin?*

*Seed variable B2*:

*Campylobacters were found in all 51 composite neck-skin samples before chilling and all but 1 sample after chilling. In how many of the 51 composite fillet samples was Campylobacter detectable by plating and/or by enrichment?*

**Part C**

In five different broiler chicken processing plants, the final products (breast-skin and fillet) of 22 randomly selected flocks were analyzed for *Camylobacter*. The samples were taken in the last quarters of 2001 and 2002. For each flock, 3 to 5 composite samples were taken, totaling 25 grams, both from breast-skin and fillet. *Camylobacter* counts (quantitative) were obtained by the standard method. The breast-skin samples and fillet samples were also analyzed by various enrichment methods (qualitative). During processing, caecal content from 11 flocks was obtained and analyzed for *Camylobacter* (qualitative).

*Seed Variable C1*:

*How many of the 11 randomly selected flocks were carrying Campylobacter*

*on the basis testing caecal contents? Give the number of positive flocks.*

*Seed variable C2*:

*What percentage of composite breast-skin samples was positive for Campylobacter on the basis of the various enrichment methods?*

*Seed variable C3*:

*What percentage of composite fillet samples was positive for Campylobacter on the basis of the various enrichment methods?*

*Seed variable C4*:

*How many campylobacters (number per gram of breast-skin) were found on a positive breast-skin (based on composite samples of 25 grams of skin)?*

*Seed variable C5*:

*How many campylobacters (number per gram skin) were found on a positive fillet (based on composite samples of 25 grams of fillet)?*

# Appendix C

# Updating methods

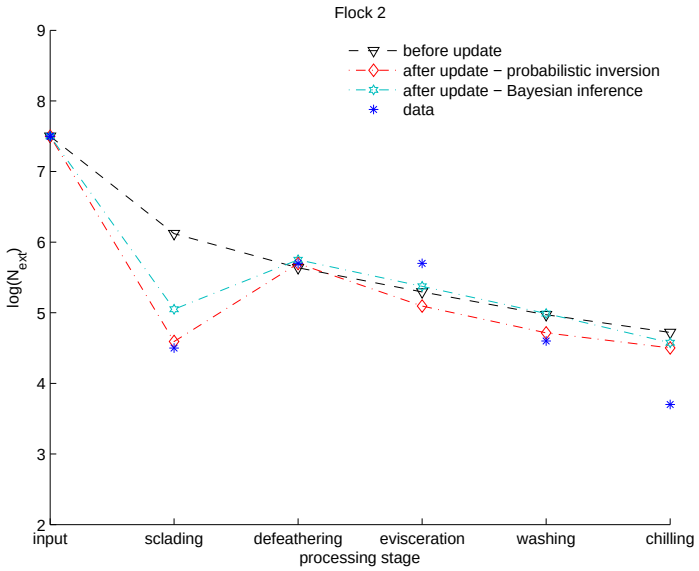


*Figure C.1: The effect of processing on log(Next) for flock 2, before and after updating using two methods (in a case when we consider each flock separately).*

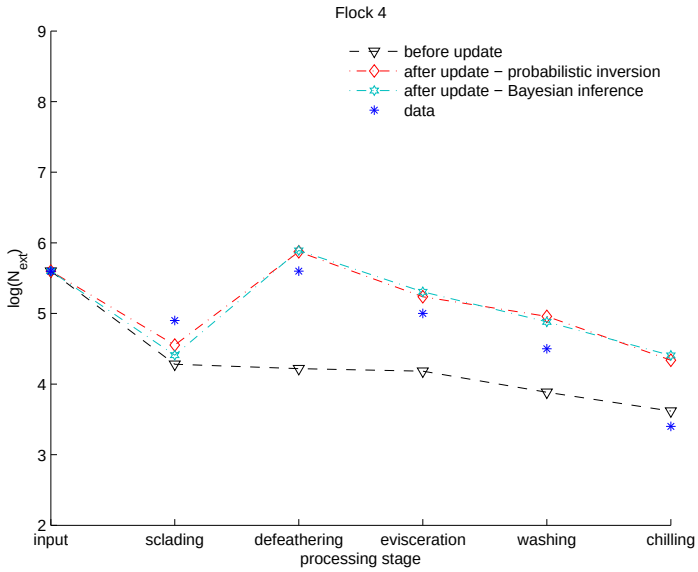


*Figure C.2: The effect of processing on log(Next) for flock 2, before and after updating using two methods (in a case when we consider each flock separately).*

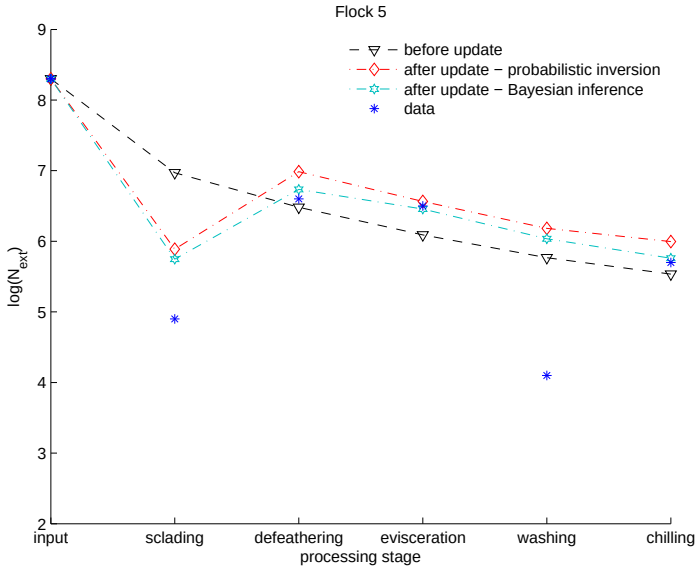


*Figure C.3: The effect of processing on log(Next) for flock 2, before and after updating using two methods (in a case when we consider each flock separately).*

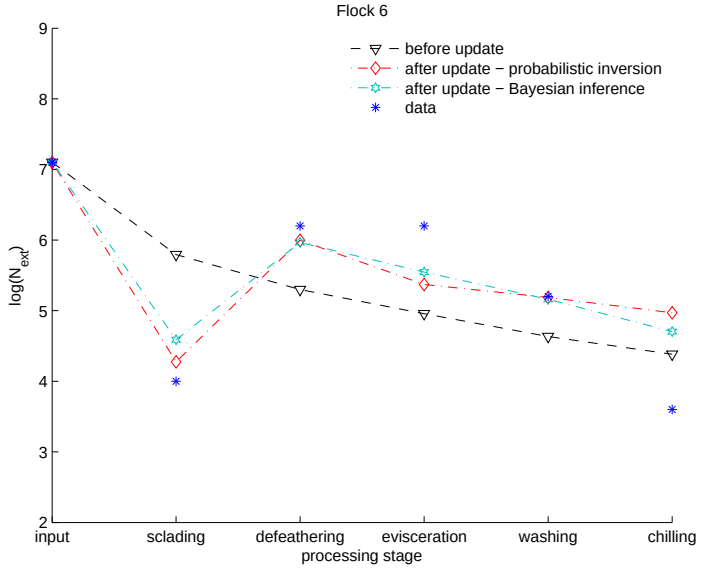


*Figure C.4: The effect of processing on log(Next) for flock 2, before and after updating using two methods (in a case when we consider each flock separately).*

# Appendix D

# Decision maker and model parameters distributions

Table D.1: Decision makers distributions.

| | Low Scalding | | | Intermediate Scalding | | |
|---|---|---|---|---|---|---|
| | 5% | 50% | 95% | 5% | 50% | 95% |
| B1 | 316 | 1585 | 3160 | 20 | 200 | 500 |
| B2 | 316 | 1585 | 3160 | 20 | 200 | 500 |
| A1 | 1000 | 5000 | 10000 | 150 | 1000 | 3000 |
| A2 | 5000 | 7500 | 50000 | 1000 | 5000 | 10000 |
| C1 | 100 | 316 | 1000 | 32 | 100 | 316 |
| W | 0.2 | 1 | 1.5 | 0.2 | 1 | 1.5 |
| | Defeathering | | | Evisceration | | |
| | 5% | 50% | 95% | 5% | 50% | 95% |
| B1 | 316 | 1000 | 3160 | 9330 | 9550 | 9770 |
| B2 | 3980 | 6310 | 7080 | 9330 | 9550 | 9770 |
| A1 | 3200 | 10000 | 30000 | 160000 | 320000 | 63000 |
| A2 | 200000 | 500000 | 100000 | 160000 | 320000 | 63000 |
| C1 | 1.3 | 1.6 | 2 | 1.3 | 1.6 | 2 |
| W | 0.2 | 1 | 1.5 | 0.2 | 1 | 1.5 |
| | Washing | | | Air Chilling | | |
| | 5% | 50% | 95% | 5% | 50% | 95% |
| B1 | 6310 | 7080 | 7940 | 3160 | 6310 | 9770 |
| B2 | 6310 | 7080 | 7940 | 3160 | 6310 | 9770 |
| A1 | 32000 | 50000 | 63000 | 32000 | 63000 | 98000 |
| A2 | 32000 | 50000 | 98000 | 79000 | 91000 | 98000 |
| C1 | 9e-13 | 1e-12 | 1.1e-12 | 1.3 | 1.6 | 2 |
| | Spray Chilling | | | | | |
| | 5% | 50% | 95% | | | |
| B1 | 316 | 1000 | 3160 | | | |
| B2 | 3980 | 6310 | 7080 | | | |
| A1 | 3200 | 10000 | 30000 | | | |
| A2 | 200000 | 500000 | 1000000 | | | |
| C1 | 1.3 | 1.6 | 2 | | | |

Table D.2: The mean, $5\%th$, $50\%th$ and $95\%th$ quantiles of the initial model parameters.

| | | $axa$ | $a_{xb}$ | $c_{ext}$ | $b$ | $c_{env}$ | $1-a_{int}$ | $w_{int}$ |
|---|---|---|---|---|---|---|---|---|
| Low Scalding | mean | 0.7746 | 0.4397 | 0.7197 | 1.55e-05 | 0.0271 | 4.44e-07 | 1.3255 |
| | 5% | 0.4699 | 0.3135 | 0.5148 | 1.04e-07 | 6.36e-03 | 2.55e-08 | 0.2356 |
| | 50% | 0.816 | 0.4397 | 0.7084 | 9.33e-07 | 0.0237 | 2.06e-07 | 1 |
| | 95% | 0.9645 | 0.5805 | 0.9434 | 7.28e-05 | 0.0599 | 1.64e-06 | 4.11 |
| Int Scalding | mean | 0.6257 | 0.6156 | 0.9356 | 1.23e-07 | 0.0184 | 1.07e-07 | 1.2089 |
| | 5% | 0.4248 | 0.423 | 0.8187 | 5.28e-08 | 3.185e-03 | 4.82e-08 | 0.2 |
| | 50% | 0.6361 | 0.6209 | 0.9539 | 1.1e-07 | 0.0181 | 9.77e-08 | 1.01 |
| | 95% | 0.7889 | 0.7826 | 0.9948 | 2.35e-07 | 0.031 | 2.04e-07 | 1.5 |
| Defeathering | mean | 0.8488 | 0.7865 | 0.0549 | 0.0415 | 0.0916 | 1.03e-05 | 1.0165 |
| | 5% | 0.6783 | 0.445 | 0.0111 | 8e-04 | 0.0417 | 5.45e-06 | 0.005 |
| | 50% | 0.9093 | 0.892 | 0.0569 | 4.543e-03 | 0.115 | 9.44e-06 | 0.45 |
| | 95% | 0.9729 | 0.9652 | 0.0956 | 0.109 | 0.1252 | 1.81e-05 | 1.49 |
| Evisceration | mean | 0.584 | 0.004 | 0.042 | 1.09e-05 | 0.0826 | 0.0043 | 0.9652 |
| | 5% | 0.3108 | 8.27e-04 | 0.0154 | 5.46e-06 | 0.0633 | 1.93e-03 | 0.218 |
| | 50% | 0.6208 | 3.45e-03 | 0.0407 | 1.01e-05 | 0.0832 | 3.46e-03 | 0.9645 |
| | 95% | 0.7952 | 7.781e-03 | 0.0628 | 2.06e-05 | 0.0952 | 9.332e-03 | 2.053 |
| Washing | mean | 0.4709 | 0.1141 | 0.1924 | 0.0088 | 0.0559 | - | - |
| | 5% | 0.188 | 0.0126 | 0.0879 | 4.722e-03 | 0.023 | - | - |
| | 50% | 0.4735 | 0.1238 | 0.1922 | 7.945e-03 | 0.0576 | - | - |
| | 95% | 0.7 | 0.1863 | 0.3179 | 0.0167 | 0.0973 | - | - |
| Air Chilling | mean | 0.0949 | 0.0580 | 0.2345 | 1.06-05 | 0.0118 | | |
| | 5% | 9.52e-03 | 7.2e-03 | 0.1063 | 5.36e-06 | 4.24e-03 | - | - |
| | 50% | 0.0783 | 0.0653 | 0.1874 | 9.69e-06 | 0.0108 | - | - |
| | 95% | 0.1834 | 0.0935 | 0.4306 | 2e-05 | 0.0213 | - | - |
| Spray Chilling | mean | 0.4267 | 0.5224 | 0.6721 | 0.0741 | 0.0211 | - | - |
| | 5% | 0.1755 | 0.2989 | 0.2925 | 0.0372 | 3.4e-03 | - | - |
| | 50% | 0.408 | 0.5474 | 0.7942 | 0.0748 | 0.0226 | - | - |
| | 95% | 0.5945 | 0.6453 | 0.9467 | 0.0937 | 0.536 | - | - |

Table D.3: The mean, 5%$th$, 50%$th$ and 95%$th$ quantiles of the model parameters after updating (probabilistic inversion).

| | | $axa$ | $a_{xb}$ | $c_{ext}$ | $b$ | $c_{env}$ | $1 - a_{int}$ | $w_{int}$ |
|---|---|---|---|---|---|---|---|---|
| Low Scalding | mean | 0.8629 | 0.4415 | 0.7518 | 9.8755e-06 | 0.0270 | 4.3917e-07 | 1.2372 |
| | 5% | 0.5313 | 0.3222 | 0.5212 | 1e-07 | 0.0043 | 2.6e-08 | 0.2533 |
| | 50% | 0.8822 | 0.4356 | 0.7426 | 1.54e-06 | 0.0263 | 3.23e-07 | 0.9467 |
| | 95% | 0.9978 | 0.5708 | 0.9950 | 6.19e-05 | 0.0449 | 1.345e-06 | 6.0685 |
| Defeathering | mean | 0.7923 | 0.8348 | 0.0562 | 0.0726 | 0.0810 | 1.0068e-05 | 4.2097 |
| | 5% | 0.6100 | 0.4975 | 0.0129 | 0.0010 | 0.0417 | 6.28e-06 | 0.0050 |
| | 50% | 0.7408 | 0.8920 | 0.0668 | 0.0777 | 0.0781 | 9.46e-06 | 1.3220 |
| | 95% | 0.9729 | 0.9679 | 0.0911 | 0.1172 | 0.1405 | 1.67e-05 | 11.3500 |
| Evisceration | mean | 0.7096 | 0.0021 | 0.0316 | 8.1773e-06 | 0.0780 | 0.0043 | 0.6831 |
| | 5% | 0.3762 | 0.0008 | 0.0205 | 5.74e-06 | 0.0719 | 0.0021 | 0.2622 |
| | 50% | 0.7952 | 0.0008 | 0.0240 | 5.83e-06 | 0.0743 | 0.0043 | 0.4667 |
| | 95% | 0.7952 | 0.0066 | 0.0613 | 2.07e-05 | 0.0952 | 0.0079 | 1.4330 |
| Washing | mean | 0.5785 | 0.1144 | 0.2114 | 0.0080 | 0.0642 | - | - |
| | 5% | 0.2411 | 0.0211 | 0.1075 | 0.0050 | 0.0230 | - | - |
| | 50% | 0.6893 | 0.1271 | 0.2115 | 0.0070 | 0.0695 | - | - |
| | 95% | 0.7398 | 0.1844 | 0.3271 | 0.0131 | 0.0972 | - | - |
| Spray Chilling | mean | 0.4046 | 0.5238 | 0.6312 | 0.0854 | 0.0193 | - | - |
| | 5% | 0.1974 | 0.4325 | 0.3145 | 0.0518 | 0.0037 | - | - |
| | 50% | 0.3921 | 0.5255 | 0.6035 | 0.0933 | 0.0183 | - | - |
| | 95% | 0.5823 | 0.6217 | 0.9160 | 0.0937 | 0.0421 | - | - |

Table D.4: The mean, 5%$th$, 50%$th$ and 95%$th$ quantiles of the model parameters after updating (Bayesian inference).

| | | $axa$ | $a_{xb}$ | $c_{ext}$ | $b$ | $c_{env}$ | $1 - a_{int}$ | $w_{int}$ |
|---|---|---|---|---|---|---|---|---|
| Low Scalding | mean | 0.8455 | 0.4361 | 0.7728 | 1.3957e-05 | 0.0288 | 5.1354e-07 | 1.2648 |
| | 5% | 0.5124 | 0.3118 | 0.5153 | 1.6e-07 | 0.0075 | 3e-08 | 0.2533 |
| | 50% | 0.9117 | 0.4371 | 0.7909 | 1.35e-06 | 0.0279 | 2.3e-07 | 1 |
| | 95% | 0.9867 | 0.5768 | 0.9794 | 3.31e-05 | 0.0597 | 1.66e-06 | 6.3948 |
| Defeathering | mean | 0.8018 | 0.8292 | 0.0527 | 0.0692 | 0.0718 | 9.4366e-06 | 1.3388 |
| | 5% | 0.6485 | 0.4612 | 0.0129 | 0.0007 | 0.0409 | 5.45e-06 | 0.0050 |
| | 50% | 0.7440 | 0.8920 | 0.0441 | 0.0777 | 0.0660 | 8.39e-06 | 0.5733 |
| | 95% | 0.9720 | 0.9644 | 0.0911 | 0.1163 | 0.1242 | 1.501e-05 | 8.8890 |
| Evisceration | mean | 0.5840 | 0.0040 | 0.0420 | 1.0861e-05 | 0.0826 | 0.0043 | 0.9652 |
| | 5% | 0.3109 | 0.0008 | 0.0154 | 5.46e-06 | 0.0635 | 0.0019 | 0.2178 |
| | 50% | 0.6208 | 0.0035 | 0.0407 | 1.01e-05 | 0.0832 | 0.0035 | 0.9733 |
| | 95% | 0.7952 | 0.0079 | 0.0628 | 2.07e-05 | 0.0952 | 0.0093 | 2.0530 |
| Washing | mean | 0.4709 | 0.1141 | 0.1924 | 0.0089 | 0.0559 | - | - |
| | 5% | 0.1881 | 0.0126 | 0.0880 | 0.0047 | 0.0230 | - | - |
| | 50% | 0.4736 | 0.1239 | 0.1926 | 0.0079 | 0.0576 | - | - |
| | 95% | 0.7003 | 0.1864 | 0.3187 | 0.0167 | 0.0973 | - | - |
| Spray Chilling | mean | 0.4267 | 0.5224 | 0.6721 | 0.0741 | 0.0211 | - | - |
| | 5% | 0.1756 | 0.2989 | 0.2925 | 0.0372 | 0.0034 | - | - |
| | 50% | 0.4078 | 0.5474 | 0.7942 | 0.0748 | 0.0226 | - | - |
| | 95% | 0.5947 | 0.6453 | 0.9467 | 0.0937 | 0.0536 | - | - |