Probabilistic Inversion for Chicken Processing Lines

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Abstract: We introduce probabilistic inversion techniques as applied in a recent example of Campylobacter transmission. Such techniques are indicated when we wish to quantify a model whose parameters cannot be directly measured. In this a (partially specified) uncertainty distribution over measurable quantities predicted by the model can be "pulled-back" onto the parameter space of the model. If a probabilistic inversion is feasible, the solution is seldom unique and we require a method of selecting a preferred solution. If a problem is not feasible, we require a best fitting distribution. This study illustrates two such techniques, Iterative Proportional Fitting (IPF) (Kruithof 1937) and PARmeter Fitting for Uncertain Models (PARFUM) (Cooke 1994). In addition, we illustrate how expert judgement on predicted observable quantities in combination with probabilistic inversion may be used for model validation and/or model criticism.

Key words: Probabilistic inversion, IPF, PARFUM, Campylobacter, transport models, expert judgment, entropy, information.

1. INTRODUCTION

"Probabilistic inversion" denotes a family of techniques which have recently been introduced into the field of risk and environmental modelling. They enable quantification of non-measurable model parameters in terms of distributions over measurable quantities. This is particularly useful when expert judgement is used: experts are queried about outcomes of possible measurements, and their uncertainty distributions are pulled back onto the parameter space of a model which predicts the measured outcomes. Recent applications may be found in (Kraan and Cooke, 2000a,b), for a discussion see (Kraan 2002, Kurowicka and Cooke 2002). A complete mathematical discussion of the techniques employed here is found in (Du et al 2003).

The ‘pull-back’ distribution on model parameters may be pushed through the model to re-predict the quantities assessed by the decision maker. This provides an opportunity for model validation and/or criticism. If the re-predicted distributions agree with the original decision maker’s distributions, then the model provides a suitable vehicle for capturing the decision maker’s uncertainty. If these distributions do not agree, then the model is not suitable to represent the decision maker’s uncertainty. In this case the model must be re-evaluated and possibly revised. For more discussion and examples of this aspect see (Kraan and Cooke 2000b).

This paper gives an informal introduction to probabilistic inversion techniques, illustrated with a recent application to campylobacter transmission. This is a relatively

simple environmental transport model and illustrates nicely how probabilistic inversion applied to structured expert judgment can play a constructive role in model evaluation.

2. CAMPYLOBACTER TRANSMISSION

Campylobacter contamination of chicken meat may be responsible for up to 40% of the annual 100,000 cases of Campylobacter-associated gastroenteritis in The Netherlands, and a similar proportion of an estimated 30 deaths. A recent effort to rank various control options for Campylobacter contamination of chicken carcasses has led to the development of a mathematical model of a typical chicken processing line (Nauta et al in preparation). This model has been quantified in an expert judgment study involving 12 experts (van der Fels et al 2003). Key parameters in the model are transfer coefficients from the chickens' skin and intestines to the processing environment, and from the environment back to the chickens' skin. Experimental data on such transfer coefficients are not available, and experts are unable to quantify their uncertainty on the values of these coefficients. Hence, the model must be quantified by asking the experts about other quantities which, under specific circumstances, can be predicted by the model. These quantities typically involve aggregate phenomena with which experts are sufficiently familiar to render a judgment. The experts need not endorse, or even know the model. Their uncertainty distributions are combined to form a "decision maker's" distribution, as described in (van der Fels et al 2003).

A schematic representation of a typical broiler chicken processing line is given in Fig. 1.

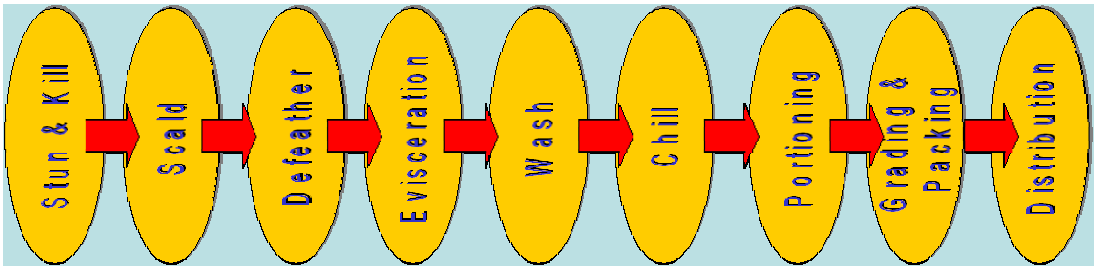

Figure 1. Broiler Chicken Processing line

For campylobacter transmission, the relevant phases are scalding, defeathering, evisceration, washing, and chilling. Two types of scalding processes are considered, namely low and intermediate temperature, as two types of chilling, namely air and spray chilling. Each phase is modelled as a physical transport process. A typical phase in the processing line is illustrated in Fig. 2.

N_{env} represents the number of campylobacter in the physical environment of the chicken in a processing phase (expressed in cfu, colony forming units). N_{ext} is the number on the exterior of the chicken, and C_{int} is the concentration in the intestines, containing the feces. The transfer coefficients are explained in Fig. 2 below, and depend on the processing phase S. Mass balance equations are formulated which say, eg, that the cfu's at the end of phase S on the exterior equals the number at the beginning, minus what is

transferred to the environment or inactivated/removed entirely, plus what moves onto the exterior during phase S:

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

In equilibrium we have $N_{env,S}(i) = N_{env,S}(i-1)$, so that:

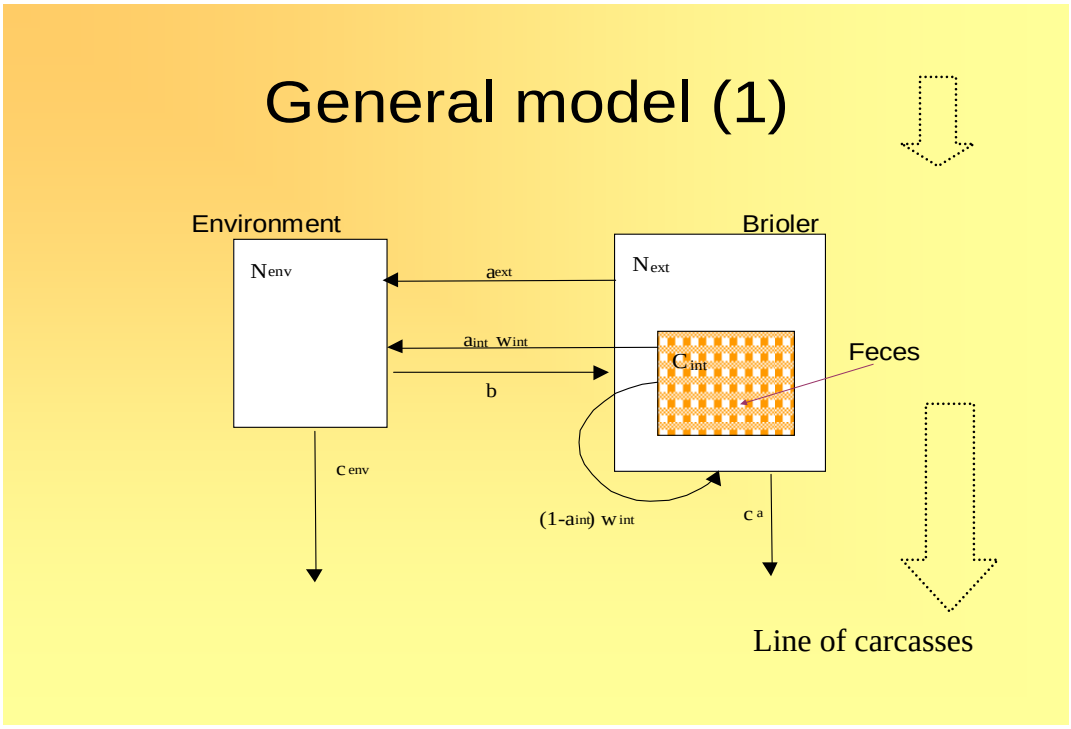

Figure 2. A typical phase in the chicken processing model

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

For more detail, see (Nauta et al in preparation). Ideally, we would like to have numerical values for the coefficients in Fig. 2. However, experimental data yielding these values are not available. Failing that, we would like to quantify the uncertainty in the transfer coefficients. Expert judgment could be applied for this purpose, if the experts had detailed knowledge of the interactions in each processing phase. Unfortunately, that is not the case. Experts are however able to quantify their uncertainty regarding the number of cfu's on a broiler in the situations described below taken from the elicitation protocol:

At the beginning of a new slaughtering day a thinned-flock is slaughtered in a "typical large broiler chicken slaughterhouse". Suppose each chicken of this flock to be infected with Campylobacter, both externally and internally. We suppose every chicken to be externally infected with 10^5 campylobacters per carcass and internally with 10^8 campylobacters per gram of caecal content *at the beginning of each slaughtering stage* (a hypothetical situation). So at the beginning of scalding, plucking etc., each chicken has this (identical) external and internal contamination rate.

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?

Experts respond to these questions, for each phase, by stating the 5, 50 and 95% quantiles of their uncertainty distributions. If distributions on the transfer coefficients in Fig. 2 are given, then a distribution, per processing phase, for the elicited variables can be computed from the mass balance equations by a Monte Carlo simulation. Thus, the elicited quantities may be expressed as (the processing phase S is suppressed in the notation):

$$
\begin{aligned}
&A1 = 10\text{^}5 \times (1-a_{ext,}) \times (1-c_a)+10\text{^}8 \times (1-a_{int}) \times w_{int} \times (1-ca);\\
&A2 = A1+b \times (a_{ext} \times 10\text{^}5 + (a_{int}) \times w_{int} \times 10\text{^}8)/(b + c_{env} - b \times c_{env});\\
&B1 = 10\text{^}4 \times (1 - a_{exr} - c_a + a_{exr} \times c_a);\\
&B2= B1 + b \times a_{exr} \times 10\text{^}4/(b + c_e - b*c_e);\\
&C= (1 - b - c_e + b \times c_e)\text{^}99 * b \times (a_{ext} * 10\text{^}5 + (a_{int}) \times w_{int} \times 10\text{^}8)/(b + c_{env} - b \times c_{env});\\
&W_{int} = W_{int}. \qquad (1)
\end{aligned}
$$

The variables A1, A2,… w_{int} are the variables assessed by the experts. Question A2 is similar to A1, but concerns the *last* chicken in the flock. Questions B1 and B2 are similar to A1 and A2, but refer to a flock in which the birds are externally contaminated, but not colonized (internally). Question C asks for the infection on the 100^{th} broiler of an uninfected flock which is processed after an internally and externally infected flock. W_{int} was queried directly. It is included here to indicate that its distribution must conform to the decision maker's quantile assessments. For the first 3 processing phases, we have 6 equations; for later phases the intestines are removed and the variable W_{int} is not defined. In total we have 39 such equations, counting the alternative processes for scalding and chilling[1]. The number of equations is equal to the number of transfer coefficients for the whole line.

Assuming distributions for coefficients on the right hand sides in (1) are known, we could sample from these distributions and build up distributions for the quantities on the left hand side. These quantities are assessed by the experts. We would like these distributions to comply with the quantiles given by the decision maker. The probabilistic inversion problem may now be expressed as follows: find a joint distribution over the

[1] The decision maker considered variable C for washing degenerate, i.e. zero with probability 1. Removing this would give 38 equations.

transfer coefficients, such that the quantiles of the quantities on left hand sides of the above equations agree with the decision maker's quantiles. If more than one such joint distribution exists, pick the least informative of these. If no such joint distribution exists, pick a "best fitting" distribution.

3. PROBABILISTIC INVERSION

Let X and Y be n- and m-dimensional random vectors, respectively, and let G be a function from $\Re^n$ to $\Re^m$. We call $x \in \Re^n$ an inverse of $y \in \Re^m$ under G if $G(x) = y$. Similarly we call X a probabilistic inverse of Y under G if $G(X) \sim Y$, where "~" means "has the same distribution as". If $\{Y \mid Y \in C\}$ is the set of random vectors satisfying constraints C, then we say that X is an element of the probabilistic inverse of $\{Y \mid Y \in C\}$ under G if $G(X) \in C$. Equivalently, and more conveniently, if the distribution of Y is partially specified, then we say that X is a probabilistic inverse of Y under G if $G(X)$ satisfies the partial specification of Y. In the current context, the transfer coefficients in Fig. 2 play the role of X, and the left hand sides of equations (1) play the role of Y. That is:

$Y = (A_{1,1},\ldots\ W_{int,1},\ldots\ A_{1,2}.\ldots..W_{int},5);$ (39 components in total) .

The joint distribution of these variables is partially specified by the decision maker, namely by given 5, 50 and 95% quantiles. The right hand sides of (1) constitute the function G.

If the function G could be inverted analytically, then it would be a simple matter to compute X as $G^{-1}(Y)$. Of course this is generally not possible, and we must devise other ways to find X. A number of approaches could be considered. A thorough discussion of this problem is found in (Du et al, 2003), and a shorter discussion in (Kurowicka and Cooke, 2002). By far most satisfactory to date are techniques based on *sample re-weighting*, and these have been applied to the chicken line model. We first choose an initial distribution for the transfer coefficients (X) such that, when we sample it a large number of times and compute Y via (1), some samples fall within each interquantile interval for each variable in Y, and all samples are physically possible. The choice of initial distribution is not further constrained, but it should cover the range of realistic values. We take N samples from X and compute N samples for Y, yielding N samples for (X,Y). When drawn from the initial distribution, each of the N samples has probability $1/N$. We now wish to re-weight these N samples such that, if we re-sample this distribution, drawing each sample (with replacement) with probability given by its weight, then the quantile constraints on Y are satisfied in the re-sampled distribution.

We describe two strategies for finding the weights, namely Iterative Proportional Fitting (IPF) and PARameter Fitting for Uncertain Models (PARFUM). These involve iteratively re-adjusting an initial set of weights so as to satisfy the constraints. For convenience, we describe this for one processing phase with 6 elicitation variables (Y is restricted to 6 components).

Since each sample contains a value for (A_1, A_2, B_1, B_2, C, W_{int}), and each component falls in one of 4 interquantile intervals, we may represent this sample as a 6-vector of components, each component taking values in {1, 2, 3, 4}. There are $4^6 = 4096$ possible vectors of this type, and we may think of each such vector as an *interquantile cell* containing a number of samples. Not all cells will be physically possible. It is easy to see from (1) that $A_1 \leq A_2$, and $B_1 \leq B_2$. Thus, if the 50% quantile for A_1 is above the 5% quantile for A_2, then it is impossible that A_1 could be above its median while A_2 is below its 5% quantile. Fortunately it is not necessary to figure out which combinations of interquantile intervals are feasible; sampling *X* and computing *Y* via (1) does that automatically. It is well to realize, however, that a large number of mathematically possible interquantile cells may actually be unfeasible under the function *G*. In a typical example for a processing phase, we would draw 65,000 samples and find that 150 – 300 of the 4096 interquantile cells were occupied. The weight assigned to each interquantile cell is simply the total weight of the samples falling in that cell. In our iterative algorithms, two samples falling in the same cell will be treated in the same way; therefore we can restrict our problem to that of finding weights for the non-empty interquantile cells. When these weights are found, we just distribute the cell weight uniformly over the samples in the cell to get the sample weights.

Rather than describe the IPF and PARFUM algorithms formally, it is appropriate here simply to illustrate them on a simple example and report the relevant mathematical facts. Details can be retrieved from the cited literature. For purposes of illustration, we consider only 2 elicitation variables, each with 4 interquantile intervals corresponding to the 5, 50 and 95% quantiles. The interquantile cells can be represented as a 4 × 4 matrix; where, for example, a sample is said to fall in cell (3,2) if it is between the 50 and 95% quantiles for variable 1 and between the 5 and 50% quantiles for variable 2.

We start with an initial distribution over *X* and generate an initial distribution over the interquantile cells, which we represent in Table 2. Note that 6 cells are empty. The marginals are shown in boldface.

0.1966	0.0006	0	0	**0.1972**
0.0407	0.1642	0.005	0	**0.2099**
0	0.0094	0.1196	0.0155	**0.1445**
0	0	0.0008	0.4476	**0.4484**
0.2373	**0.1742**	**0.1254**	**0.4631**	

Table 2. Initial distribution over interquantile cells.

The problem is now to adjust the non-empty cells in table 2 such that the margins equal 0.05, 0.45, 0.45, 0.05; which are the probabilities associated with the decision maker's interquantile intervals.

The IPF algorithm was introduced by (Kruithof 1937) and rediscovered by (Deming and Stefan 1942). Its convergence properties were studied by many, including (Fienberg, 1970, Csiszar, 1975). Simply stated, we first multiply each row by constant, so that the

column sums agree with the target. For the first row this constant is *target / row sum =0.05 / (0.1966+0.0006).* Then we multiply each column by the constant *(target / column sum)* to make the column sums agree with the target, then again the rows are multiplied by a constant, etc. Figure 4 illustrates the procedure. The target margins are shown by the starting distribution.

Csiszar (1975) showed that this algorithm converges if and only if there is a distribution with exactly the same zero's as the initial distribution which satisfies the target margins. In that case IPF converges to the distribution which has minimum information relative to the starting distribution, in the set of distributions with the target margins. This distribution may have zeros in cells where the starting distribution is non-zero. The result holds for arbitrary finite dimensions, and arbitrary finite numbers of cells per dimension. The target marginal distributions need not be the same on each dimension. It is evident that the criterion for convergence becomes more difficult to satisfy as the number of zero's increases. When the criterion is not met the probabilistic inversion problem is infeasible and IPF does not converge. In otherwords, there is *no* distribution over the non-zero cells in the starting matrix which has the target margins. In the case of two dimensions, it is known that IPF oscillates between 2 distributions, in case of non convergence (Csiszar and Tusnady 1983). Nothing is known about the behavior of IPF in higher dimensions when the condition for convergence is not satisfied.

The PARFUM algorithm (Cooke 1994, Du et al 2003) differs from IPF in the following way. Instead of first fitting the row sums, then the column sums, then again the row sums, etc; PARFUM successively averages the row and column sum fits. It is schematized in Fig. 4.

Unlike IPF, PARFUM *always* converges. If the problem is feasible, then it converges to a distribution P which minimizes the following functional:

$$F(P) = I(P^{row\ fit} \mid P) + I(P^{column\ fit} \mid P);$$

relative to the starting distribution. Here, $I(Q \mid P)$ denotes the relative information of Q with respect to P. If P is a solution, that is, if P's row- and column fits agree with the target, then $P^{row\ fit} = P = P^{column\ fit}$, so that $F(P) = 0$. Most importantly, if the problem is feasible, then PARFUM converges to a P with $F(P) = 0$, that is, it converges to a solution (see Du et al. 2003). If the problem is feasible then IPF is generally preferred. If infeasible, then IPF tends to distribute the lack of fit quite unevenly and tends to concentrate weight on a small number of samples. In such cases PARFUM often gives better results. Of course, if IPF does not cycle, we have no way of knowing on a finite number of iterations whether it is converging. Appeal to common sense is appropriate. These algorithms have several advantages relative to other methods. First, they are 'dumb' in the sense that they do not require intelligent steering. Second they avoid computationally expensive matrix manipulations, but simply loop repeatedly through the interquantile cells. Finally, since rows and columns are altered one at a time, the whole sample need not be stored in memory, and there is effectively no limit on the size of problems which can be tackled. There are disadvantages as well. Most significantly,

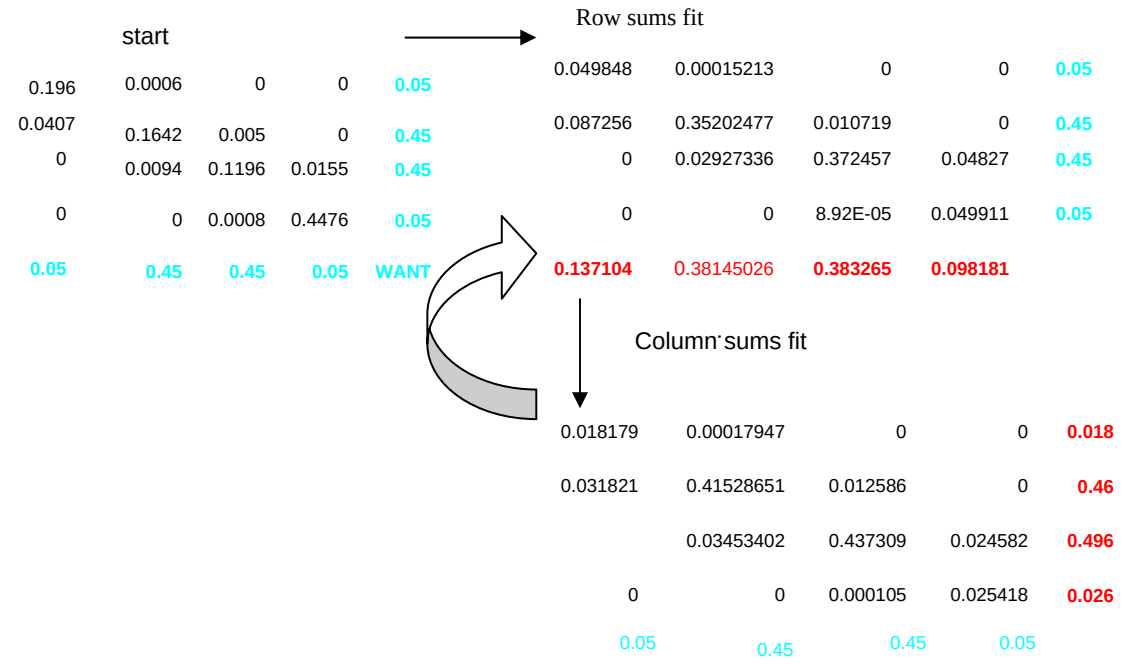

Figure 3. Iterative proportional fitting

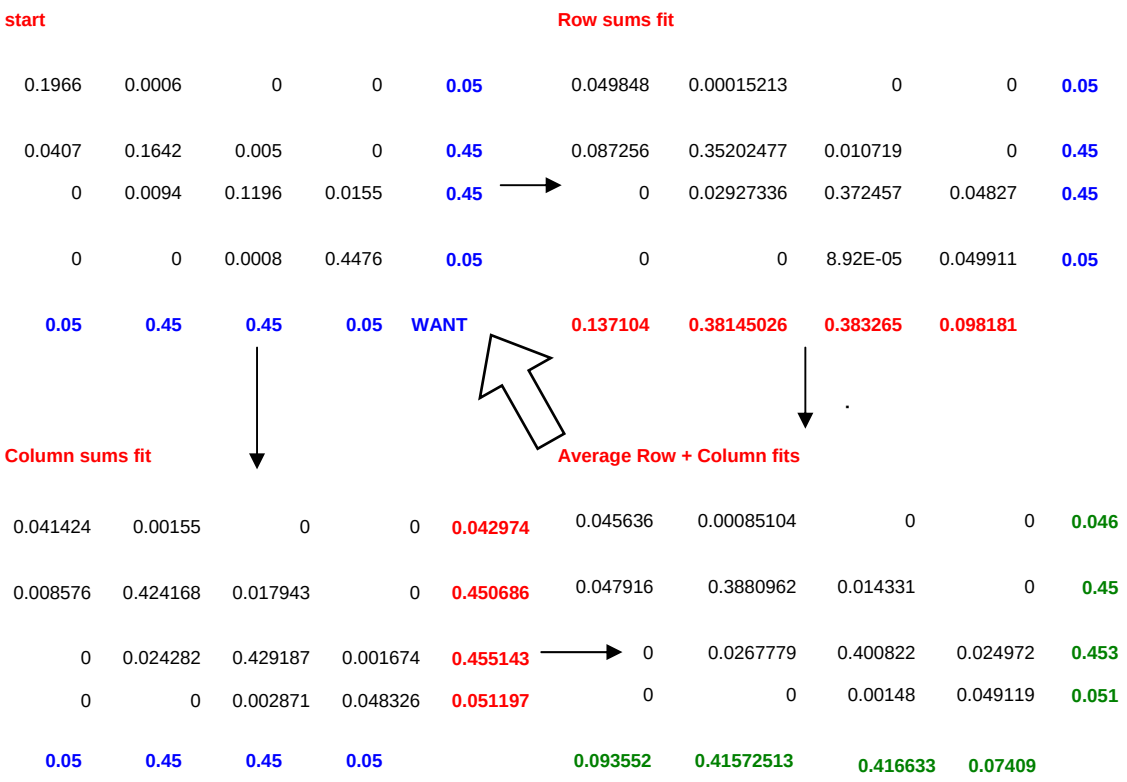

Figure 4. The PARFUM algorithm

it is impossible in practice to know if IPF is converging without verifying the condition for convergence, and this is just as hard as finding the solution. PARFUM has a distinct advantage in this regard. In case of infeasibility, neither algorithm yields information on how the original sample might be extended to yield better solutions.

4. RESULTS

The results with the model described above yielded a very poor fit between the re-predicted and decision maker distributions for some variables. Table 3 shows the results for defeathering. Especially bad fits are circled.

		DEFEATHERING	
elicitation variable	Quantile	PARFUM	IPF
A1	*5%*	0.053	0.014
	50%	0.424	0.175
	95%	0.871	0.719
A2	*5%*	0.030	0.033
	50%	0.256	0.151
	95%	0.543	0.654

Table 3. Re-predicted results of probabilistic inversion defeathering, showing the proportion of samples falling below the corresponding quantile.

Inspection of the experts' rationales revealed that the experts distinguished two transfer mechanisms from the exterior to the environment. Campylobactor in the pores of the skin would be difficult to remove, but on the feathers or skin surface they would come off more easily. It therefore 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. These two different situations had been the starting point of questions A and B. The processing model was therefore altered to include this second transport pathway. The coefficient a_{ext} is replaced by two coefficients, a_{xa} and a_{xb}. The equations for the elicited quantities now become:

$$A1 = 10\text{^}5 \times (1-a_{xa,}) \times (1-c_a)+10\text{^}8 \times (1-a_{int}) \times w_{int} \times (1-c_a);$$
$$A2 = A1+b \times (a_{xa} \times 10\text{^}5 + (a_{int}) \times w_{int} \times 10\text{^}8)/(b + c_{env} - b \times c_{env});$$
$$B1 = 10\text{^}4 \times (1-a_{xb}-c_a+a_{xb} \times c_a);$$
$$B2= B1 + b \times a_{x\ b} \times 10\text{^}4/(b + c_e – b \times c_e);$$
$$C= (1 – b - c_e + b \times c_e)\text{^}99 \times b \times (a_{xa} \times 10\text{^}5 + (a_{int}) \times w_{int} \times 10\text{^}8)/(b + c_{env} - b \times c_{env});$$
$$W_{int} = W_{int}. \qquad (2)$$

With the second model, the probabilistic inversion yielded better fits; partial results are shown in Table 4.

	Quantile	Scalding low IPF	Scalding low PARFUM	Scalding Intermediate IPF	Scalding Intermediate PARFUM	Defeathering IPF	Defeathering PARFUM
variable A_1	0.05	**0.05**	0.05	**0.04**	0.04	0.02	**0.05**
	0.5	**0.50**	0.53	**0.42**	0.45	0.78	**0.49**
	0.95	**0.95**	0.95	**0.81**	0.86	0.97	**0.94**
variable A_2	0.05	**0.05**	0.04	**0.07**	0.07	0.00	**0.04**
	0.5	**0.50**	0.41	**0.70**	0.65	0.14	**0.38**
	0.95	**0.95**	0.93	**0.95**	0.97	0.91	**0.72**

Table 4. Re-predictions with Model(2).

The bold values indicate the solution chosen. The PARFUM solution was chosen in 3 of the seven cases. There is still lack of fit, in particular for defeathering. However, overall, the model revision has produced a better fit. It is a truism that no model is fully adequate to reality. Information regarding the degree and locus of misfit is extremely valuable. The methods discussed here provide such information. The alternative is to search for compliant experts who will assess model parameters directly (and often anonymously); this cannot lead to model improvement.

5. CONCLUSIONS

Iterative sample re-weighting methods are available to solve probabilistic inversion problems, as illustrated in the model of chicken processing lines. IPF and PARFUM are easy to implement and have a solid theoretical foundation. They provide useful tools for the practicing risk modeller. The present study illustrates a fruitful interaction between the modellers and the experts made possible by querying experts on observable quantities and applying probabilistic inversion.

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