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Modelling of Salmonella dynamics in the pig slaughterhouse

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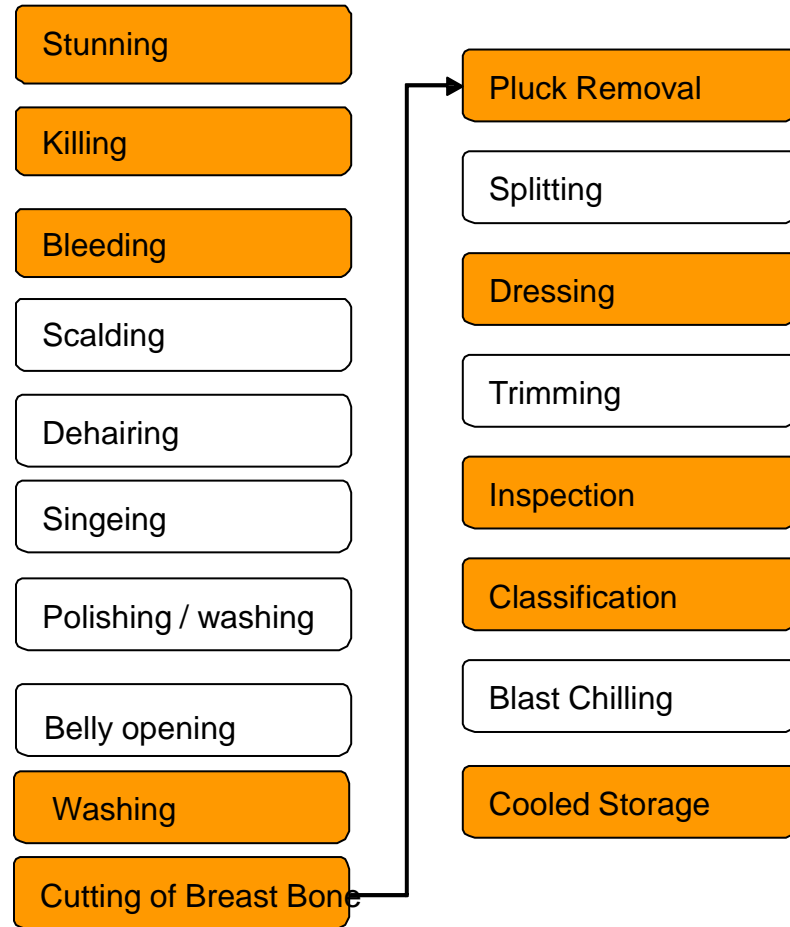


Introduction

- We developed a QMRA for *Salmonella* in the pig slaughterhouse
 - This model is part of the *EFSA QMRA on Salmonella in Slaughter and Breeder Pigs*
 - The full QMRA models the chain
 - > Farm
 - > Transport and Lairage
 - > Slaughter
 - > Cutting plant
 - > Consumer
 - > Dose response
 - > Nr. of *Salmonella* cases
 - For four representative EU member states



Slaughter Phases





Schematic Process

For each phase, we model

- Inactivation
- Growth
- Cross-contamination

And keep track of *Salmonella* numbers

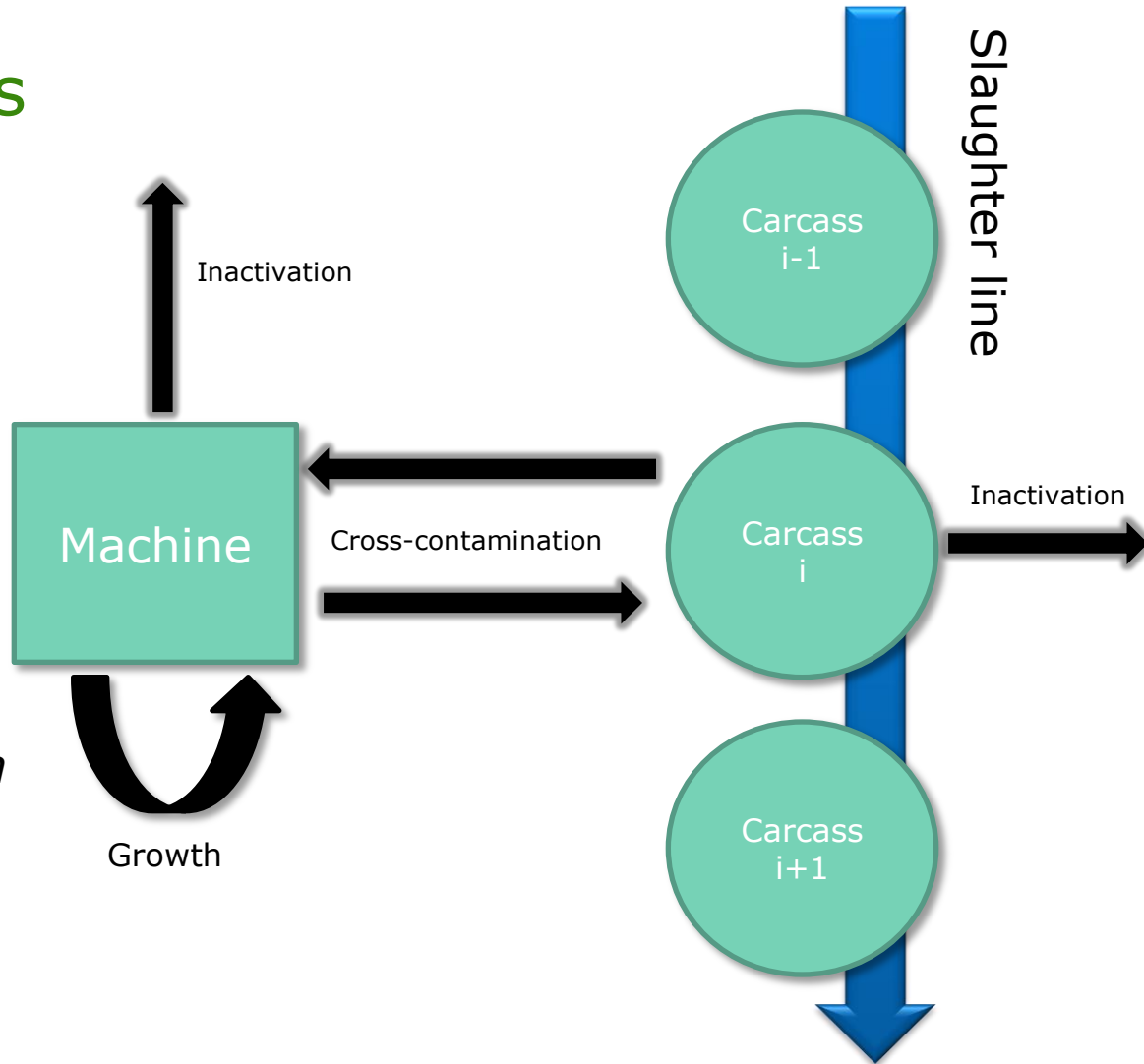




Illustration: the scalding phase

- Carcasses are dragged through the scalding bath
- Several inactivation and cross-contamination processes

| <i>Quantity</i> | <i>Domain</i> | <i>Unit</i> | <i>Description</i> |
|-----------------|----------------|--------------------|---|
| $N_{1,k}(t)$ | \mathbb{R}^+ | cfu | the number of <i>Salmonella</i> on P_k , at time $t \geq 0$ |
| $W_1(t)$ | \mathbb{R}^+ | cfu | the number of <i>Salmonella</i> in the environment W_1 , at time $t \geq 0$. |
| n | \mathbb{N} | - | the total number of pigs in the current batch |
| \mathcal{T}_1 | \mathbb{R}^+ | $^{\circ}\text{C}$ | the temperature of the scalding water |
| $\alpha_{1,k}$ | $[0, 1]$ | 1/min. | the fraction of bacteria moving from the water to the pig |
| β_1 | $[0, 1]$ | - | the fraction of bacteria moving from the pig to the water |
| τ_1 | $[0, 1]$ | 1/min | the fraction of pathogen inactivation on the pig |
| γ_1 | $[0, 1]$ | 1/min | the fraction of pathogen inactivation in the water |
| T_1 | \mathbb{R}^+ | min | the time spent in the scalding bath |



Variability

- Note that individual carcasses are modelled: captures variability over carcasses
- Variability over slaughterhouses is included by using distributions for parameters.
- Sampling from these distributions by means of Monte Carlo iterations

Example: *scalding water temperature*

| Cluster | Quantity | Source |
|---------|--|-----------------------------|
| MS1 | $\mathcal{T}_1 = \mathfrak{R}(U(58, 60))$ | European Guideline |
| MS2 | $\mathcal{T}_1 = \mathfrak{R}(BP(58, 60, 64))$ | Wilkin, Purnell et al. 2007 |
| MS3 | $\mathcal{T}_1 = \mathfrak{R}(U(58, 60))$ | European Guideline |
| MS4 | $\mathcal{T}_1 = \mathfrak{R}(U(58, 60))$ | European Guideline |



Model Equations

- α : Transfer water to carcass
- β : Transfer carcass to water (instantaneous)
- τ : Inactivation on carcass
- γ : Inactivation in the water

$$N'_{1,k}(t) = -\tau_1 N_{1,k}(t) + \alpha_k W(t), \quad t \in (t_k, t_{k+1}),$$

$$N_{1,k}(t_k) = (1 - \beta_1) N_{0,k},$$

$$W'(t) = -\gamma_1 (1 - \alpha_{1,k}) W(t), \quad t \in (t_k, t_{k+1}),$$

$$W(t_k) = \beta_1 N_{1,k}(t_k) + \lim_{t \rightarrow t_k} W(t),$$

$$W(0) = 0.$$



Results in recursion relations

Recursions:

$$W(t_{k+1}) = [\beta_1(1 - \beta_1)N_{0,k} + W(t_k)]e^{-\gamma_1(1 - \alpha_{1,k})T_1},$$

$$N_{1,k}(t_{k+1}) = W(t_{k+1}) \frac{\alpha_{1,k}}{\eta} (1 - e^{\eta T_1}) + (1 - \beta_1)N_{0,k} e^{-\tau_1 T_1}.$$

$$\eta = \gamma_1(1 - \alpha_{1,k}) - \tau_1$$

May solved iteratively

$W(t_0) \rightarrow W(t_1) \rightarrow \dots$, then $N(t_0) \rightarrow N(t_1) \rightarrow \dots$

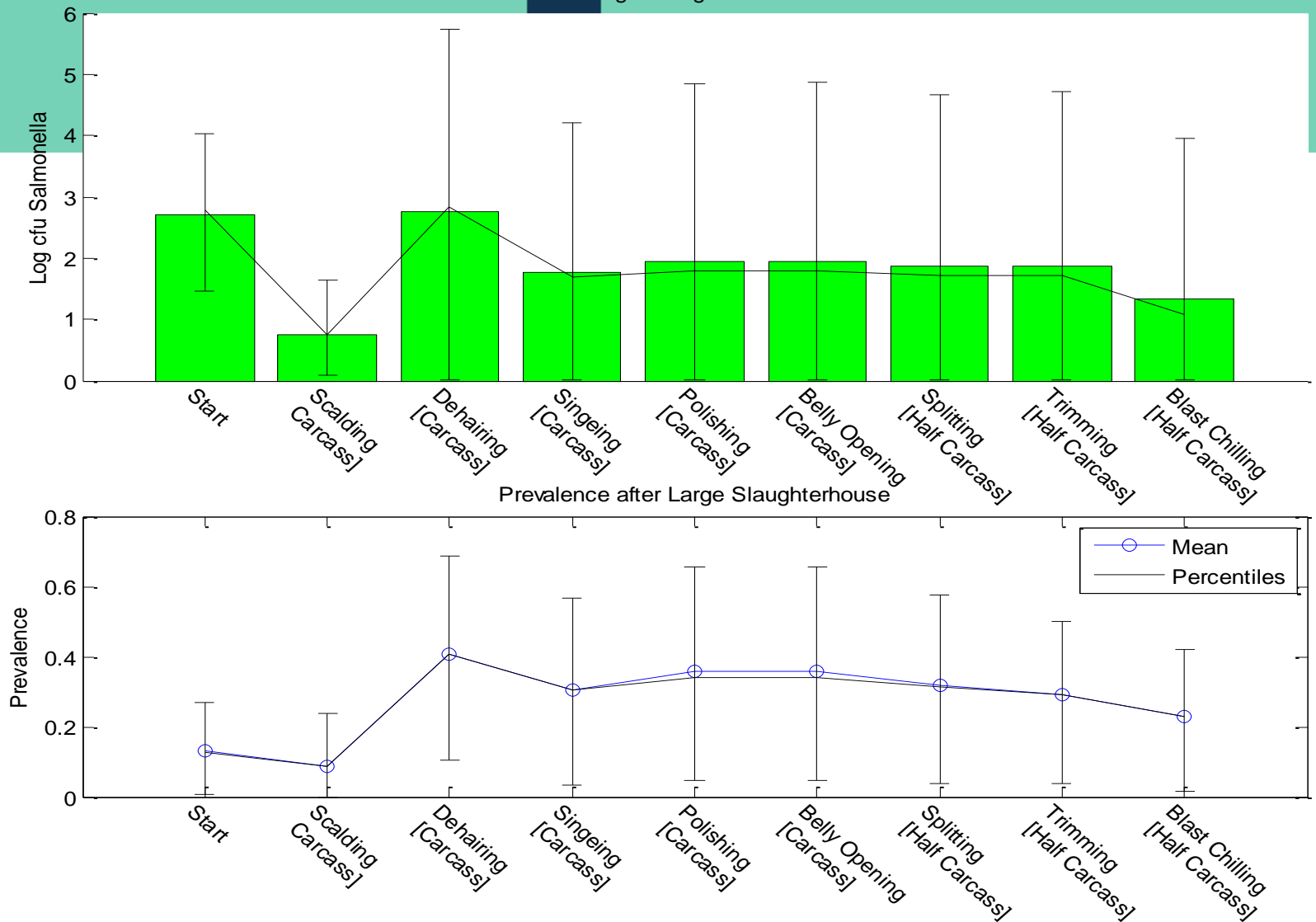
Allows for rapid calculation (in e.g. Matlab or Mathematica)



Interventions

- Due to the explicit handling of the microbial processes, several interventions can be modelled, e.g.,
 - Logistic slaughter [sort batches by infection]
 - Decontamination [apply a log-reduction]
 - Prevention of faecal leakage [set cont. of feces to zero]

Results

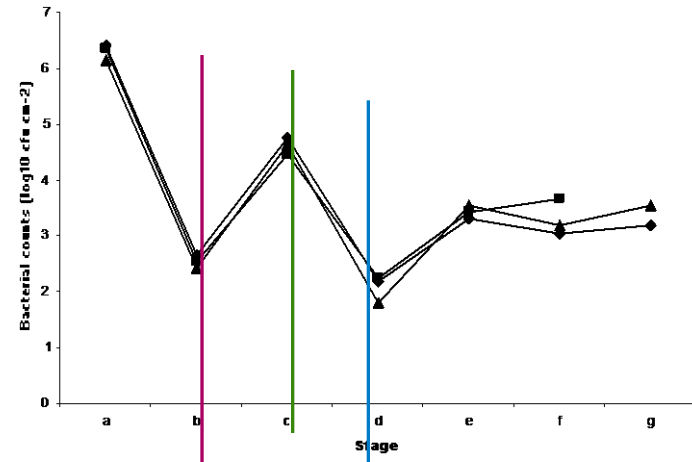
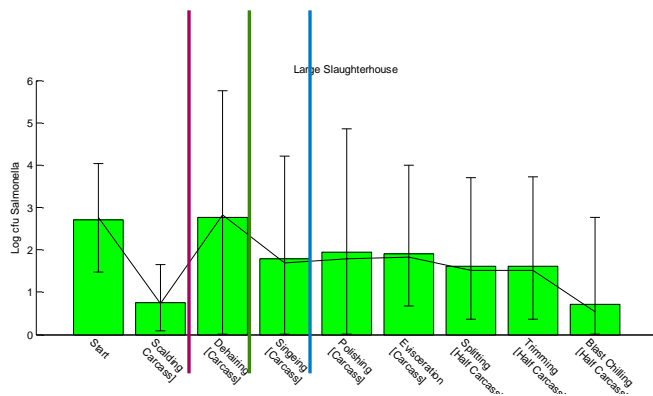


Includes prevalence and Salmonella numbers

Individual carcasses recorded (for later use in dose-response).



Qualitative Validation



Left: model result

Right: total counts (Richards and Dodd, 2009)

Purple = Scalding, Green = Dehairing, Blue = Singeing



Conclusion

- We have developed a quantitative QMRA for Salmonella in the pig slaughterhouse
- Including variability at several levels is feasible
- Individual carcasses are modelled for more realistic inclusion of cross-contamination
- The mechanistic setting allows for implementation of interventions
- Comparison to data or other QMRAs look reasonable

Drawbacks

- Such a QMRA is data hungry: many data gaps
- Uncertainties of parameter values

We believe that conclusions on *relative* effects are appropriate (e.g. % effect of interventions)