

Methodology for answering BioTraceability questions

“Salmonella in the pork chain”

Introduction

WP1 is a **framework** package that serves as a backbone for integrative research between the Modelling and Experimental WP's within BioTracer-IP. This includes a methodology for answering BioTraceability questions with links to current and future research. In this poster we present a methodology that makes use of Bayesian Networks illustrated with the “Salmonella in pork chain”.

General BioTraceability questions, Salmonella in the Slaughter Chain

What is the source of contamination based on observations at the end of the chain?

Which steps in the chain are critical (cause of deviations)?

Which sampling strategies will account for which results?

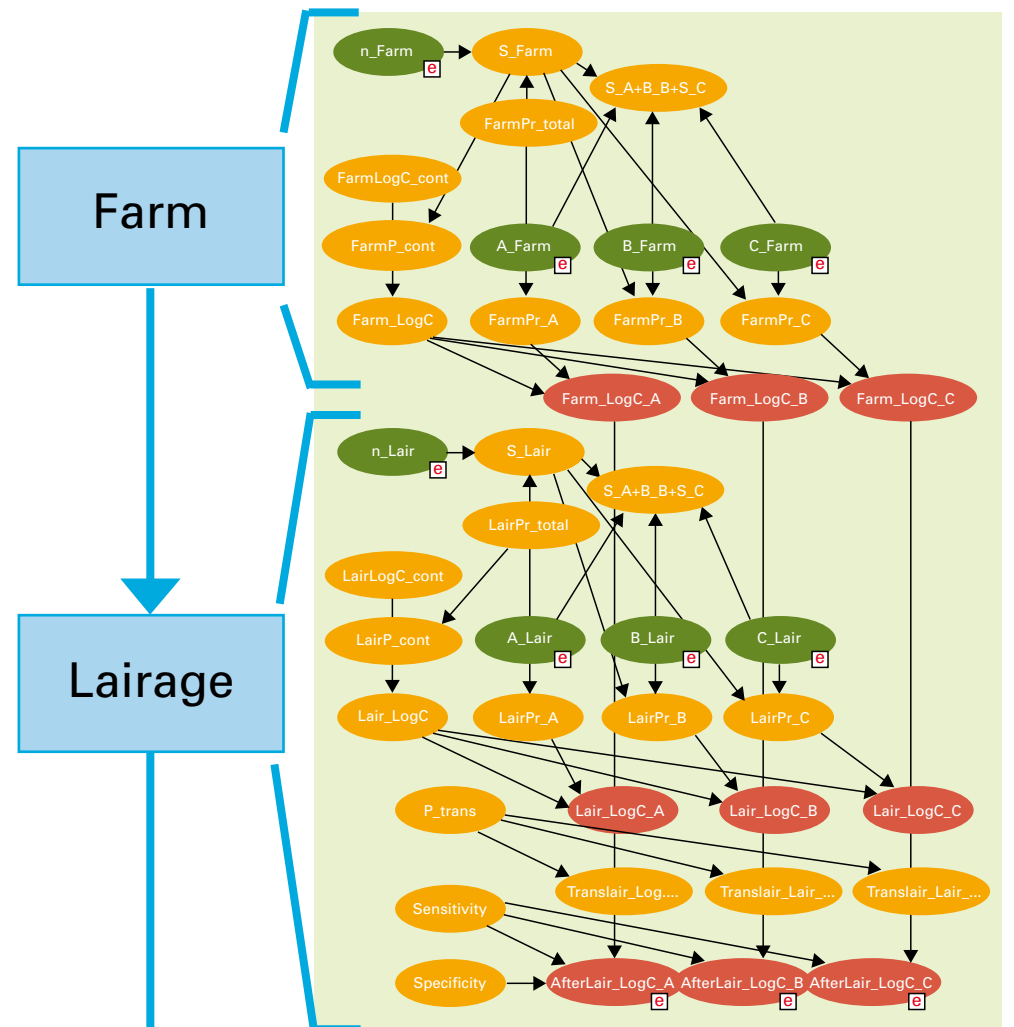
Methodology

1. Assess the relevant processing steps of the chain with micro biological dynamics (*domain model*) (WP3, 4, 5)
2. Define begin and end point of the process model (*boundary conditions*) (WP3, 5)
3. Formulate the extent of simplifications of both the process and microbiological dynamics (*assumptions*) (WP1, 3)
4. Gather process & microbiological data
 - Data describing natural *variability* in the system (e.g. a *distribution* of numbers of Salmonella at the farm) (WP2,11)
 - Data concerning different *strain types* is essential for tracing (WP2,11,13)
5. Implement the data distributions into the biological process model (parameter estimation) (WP5)
 - Using *prior knowledge*
 - Account for *uncertainty* in the parameter estimate due to lack of knowledge (e.g. in the growth rate)
 - Update the parameter values in a *Bayesian* way regarding the data
6. Implement the *domain model* into a *Bayesian Belief Network* (BBN) (WP 5)
7. Start *Tracing* through observations
 - At particular steps in the chain (e.g. measure number and type of *Salmonella* after lairage)
 - On environmental factors

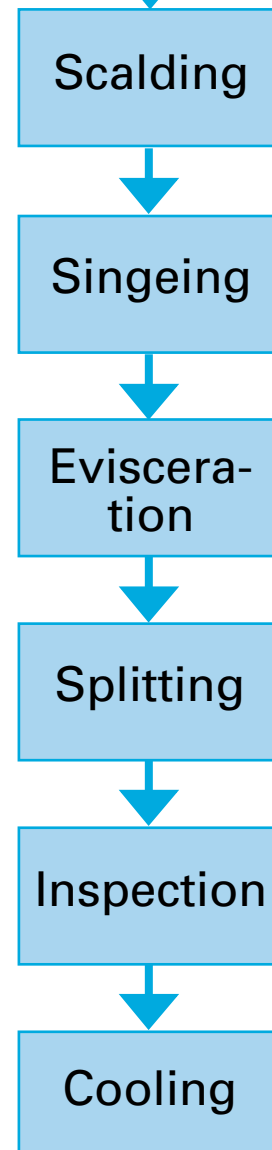
Conclusions

Minimal requirements for BioTracing with respect to a Public Health Risk are:

- Prevalence, Concentration and Typing data at relevant steps in the chain
- Sensitivity, Specificity of measurement data
- Detection limits and recovery rates



Bayesian Belief Network of the Farm and Lairage parts of the *domain*, including *boundary conditions*. In the green ovals, data has been inserted that defines *distributions* of three types of *Salmonella* (A, B and C) at the farm, in the lairage environment and in pigs after lairage (red ovals).



Farm_LogC_A	Farm_LogC_B	Farm_LogC_C
100.00	100.00	99.24
-2.5	-2.5	-2.5
-2	-1.5	-1.5
0.00	0.00	0.43
-1.5	-1.5	-1.5
-1	-1	-1
-0.5	-0.5	0.08
0	0	-0.5
0.5	0.5	0.03
1	1	6.24E-3
1.5	1.5	0.07
2	2	0.00
2.5	2.5	0.00
3	3	0.00
3.5	3.5	0.00
4	4	0.00
4.5	4.5	0.00
5	5	0.00

Lair_LogC_A	Lair_LogC_B	Lair_LogC_C
0.06	0.06	0.00
-2.5	-2.5	-2.5
-2	-1.5	-1.5
-1.5	-1	-1
-1	-0.5	0.02
-0.5	0	-0.5
0	0.5	0.01
0.5	1	0.05
1	1.5	99.88
1.5	2	0.00
2	2.5	0.00
2.5	3	0.00
3	3.5	0.00
3.5	4	0.00
4	4.5	0.00
4.5	5	0.00

AfterLair_LogC_A	AfterLair_LogC_B	AfterLair_LogC_C
100.00	100.00	0.00
-2.5	-2.5	-2.5
-2	-1.5	-1.5
-1.5	-1	-1
-1	-0.5	-0.5
-0.5	0	0.00
0	0.5	0.00
0.5	1	0.00
1	1.5	100.00
1.5	2	0.00
2	2.5	0.00
2.5	3	0.00
3	3.5	0.00
3.5	4	0.00
4	4.5	0.00
4.5	5	0.00

By observations on the state of pigs after lairage we can *trace* the source of contamination. Since a high concentration of *Salmonella* C-type was found and no *Salmonella* A and B types, the probable source was the lairage environment.