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an overview and a practical application

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Predictive Microbiology: an overview and a practical application

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DTU Food
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Outline:

• Definition
• Challenges
• Applications
• Example (Eg)
  ✓ Introduction
  ✓ Objectives of the study
  ✓ Summarizing the performed work
  ✓ Process to build up the developed models
  ✓ Results
  ✓ Remarks and future perspectives
Definition:

New area

Development due to emergence of powerful computational resources and statistics

Predictive Microbiology

Responses of microorganisms in foods to environmental factors

Assurance of: food safety and food quality

Challenges:

• Many different researchers have developed models for the behaviour of particular microorganisms in laboratory media and different food matrices, and made them available in the public domain through peer reviewed publications (Ross and Dalgaard, 2004).

• From an industry perspective, the utility of these public-domain models is often somewhat limited:
  ✓ In many cases, models have been developed under laboratory conditions,
  ✓ are based on specific combinations of parameters that might not be appropriate for the particular food products of an industry,
  ✓ and have not always been validated or even used in real food systems.

• Despite that, such models can be useful as long as their limitations are recognised and considered in their application (Membré and Lambert, 2008).
Applications:

Current applications of predictive microbiology in an industrial context are wide and according to Membré and Lambert (2008) can be summarised into three groups of activities:

1. **Product innovation**, where new products and process are developed, existing products are reformulated, storage conditions and shelf-life are determined, by assessment of speed of microbial proliferation, growth limits, or inactivation rate associated with particular food formulations and/or process conditions;

2. **Operational support**, where predictive models are used as support decision tools to implement or run a food manufacturing operation, such as designing in-factory heating regimes, setting Critical Control Points (CCPs) in Hazard Analysis and Critical Control Points (HACCP), assessing impact of process deviations on microbiological safety and quality of food products;

3. **Incident support**, where the impact on consumer safety or product quality are estimated in case of problems with products on the market.
Modelling transfer of *Salmonella* Typhimurium DT104 during grinding of pork

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Introduction

- *Salmonella* is a critical pathogen (CDC, 2011; EFSA, 2010).

- Pork still is an important source of salmonellosis (EFSA, 2010; van Hoek *et al.*, 2012; Wegener *et al.*, 2003).

- Ground meat is frequently associated with outbreaks of salmonellosis (Stock and Stolle, 2001).

- Up to 70% of foodborne illnesses are estimated to be linked to catered food (Filion and Powell, 2011; Hensen *et al.*, 2006; Jones *et al.*, 2004; Lee and Middleton, 2003).

- In Denmark, 61 of 86 reported outbreaks in 2011 were associated with outside-the-home settings (anonymous, 2012).

- To model the distribution of pathogens during the processing operation are of major relevance to risk analysts (Flores, 2006).
Objective

The aim of this study was to develop a model able to predict cross contamination of *Salmonella* in pork grinding.
Experimental work

Transfer study

Eg

S. Typhimurium DT104

37°C, overnight + 5°C, 1-3 days
Ca.10^9 Salmonella/g

Matrix

Salmonella

Up to 100 slices

Distribution of Salmonella

- Analysis performed
- Build up the model
- Validation

Transfer Modelling

37°C, 24h

22°C, 3d
Describing the transfer rates of *Salmonella* during pork grinding
Modelling cross-contamination during pork grinding

Nauta et al. (2005) Model

\[ \text{Grinder surfaces} \ | \text{meat} \]

- **a:** transfer of *Salmonella* from met to grinder
- **b:** transfer of *Salmonella* from grinder to meat
- **c\(_1\):** *Salmonella* inactivated on grinder during the process
- **c\(_2\):** *Salmonella* inactivated on the ground meat
Describing the transfer rates of *Salmonella* during pork grinding

Transfer rates of *Salmonella* DT104 based on cell count data fitted to the suggested model
Modelling cross-contamination during pork grinding

Suggested Model

- **Environment 1 (E1)**
- **Environment 2 (E2)**
- **Grinder surfaces**

**Salmonella**

- $a_1$ - transfer from meat slice to E1
- $a_2$ - transfer from meat slice to E2
- $b_1$ - transfer from E1 to ground meat
- $b_2$ - transfer from E2 to ground meat
- $c_1$ - inactivation in E1
- $c_2$ - inactivation in E2
- $c_3$ - inactivation in meat

- grinder surfaces
- grinding process
Describing the transfer rates of *Salmonella* during pork grinding

Transfer rates of *Salmonella* DT104 based on cell count data fitted to the suggested model.
Challenges in cross-contamination during pork grinding

- **Graph**
  - **X-axis**: Portion number
  - **Y-axis**: Salmonella counts (log CFU/portion)
  - **Data points**: Black dots
  - **Suggested model**: Red line
  - **Legend**:
    - Black dots: data from challenge test
    - Red line: Suggested model

- **Text**
  - "Eg Transfer study"
Remarks and future perspectives

Modelling transfer of *Salmonella* Typhimurium DT104 during simulation of grinding of pork

C.O.A. Möller¹, M.J. Nauta¹, B.B. Christensen², P. Dalgaard³ and T.B. Hansen¹

- Tail phenomenon
  - Food processors
    - Control measures
    - Cleaning and sanitization
- Observed transfer successfully modelled
- Model can describe different processes
- Tool to support risk assessors

- To be investigated:
  - Food matrices
  - Pathogens
  - Inoculum levels
  - Processings
## Available pathogen modeling programs

[http://ucfoodsafety.ucdavis.edu/Food_Safety_Links/Pathogen_Modeling_Programs/](http://ucfoodsafety.ucdavis.edu/Food_Safety_Links/Pathogen_Modeling_Programs/)

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Available pathogen modeling programs

http://ucfoodsafety.ucdavis.edu/Food_Safety_Links/Pathogen_Modeling_Programs/#

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<td>3) DMRI - predictive models for meat</td>
<td><a href="http://dmripredict.dk/Default.aspx?ReturnUrl=%2fModels%2fMeatSafety%2fDefault.aspx">http://dmripredict.dk/Default.aspx?ReturnUrl=%2fModels%2fMeatSafety%2fDefault.aspx</a></td>
<td>Can be used to predict aspects of food safety and also food quality. All of the prediction tools from DMRI are based on data obtained from experiments with meat products.</td>
</tr>
<tr>
<td>4) Isothermal-Based Prediction Tool, IBPT</td>
<td><a href="http://www.meathaccp.wisc.edu/pathogen_modeling/therm.html">http://www.meathaccp.wisc.edu/pathogen_modeling/therm.html</a></td>
<td>can predict whether Salmonella, E. coli O157:H7, or S. aureus will grow to a “level of concern” in raw beef and pork products.</td>
</tr>
</tbody>
</table>
### Available pathogen modeling programs

**Model name** | **URL** | **Applicability**
--- | --- | ---
5) OptiForm *Listeria* Control Model 2007 | http://www.purac.com/EN/Food/Brands/OptiForm.aspx | Help to calculate the level of lactate and diacetate needed to control *Listeria* in cured and uncured cooked meat and poultry products for their required shelf life.

6) Risk Management Tool for the Control of *Campylobacter* and *Salmonella* in Chicken Meat (Version 1.0) | http://www.mramodels.org/poultryRMTTool/ | To be used in conjunction with the Codex Guidelines for the Control of *Campylobacter* and *Salmonella* in chicken meat.
### Available pathogen modeling programs

Visit [UC Food Safety](http://ucfoodsafety.ucdavis.edu/Food_Safety_Links/Pathogen_Modeling_Programs/#) for more information.

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<td>7) Seafood Safety and Spoilage Predictor, SSSP v 3.0</td>
<td><a href="http://sssp.dtuaqua.dk/">http://sssp.dtuaqua.dk/</a></td>
<td>To predict the simultaneous growth of <em>Listeria monocytogenes</em> and lactic acid bacteria in lightly preserved seafood.</td>
</tr>
<tr>
<td>8) USDA Pathogen Modeling Program</td>
<td><a href="http://ars.usda.gov/Services/docs.htm?docid=11550">http://ars.usda.gov/Services/docs.htm?docid=11550</a></td>
<td>Estimates the effects of multiple variables on the growth, inactivation or survival of foodborne pathogens. Most of the models are based on experimental data of microbial behavior in liquid microbiological media.</td>
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Maarten Nauta
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