



A strategy to establish Food Safety Model Repositories



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ABSTRACT

Transferring the knowledge of predictive microbiology into real world food manufacturing applications is still a major challenge for the whole food safety modelling community. To facilitate this process, a strategy for creating open, community driven and web-based predictive microbial model repositories is proposed. These collaborative model resources could significantly improve the transfer of knowledge from research into commercial and governmental applications and also increase efficiency, transparency and usability of predictive models. To demonstrate the feasibility, predictive models of *Salmonella* in beef previously published in the scientific literature were re-implemented using an open source software tool called PMM-Lab. The models were made publicly available in a Food Safety Model Repository within the *OpenML for Predictive Modelling in Food* community project. Three different approaches were used to create new models in the model repositories: (1) all information relevant for model re-implementation is available in a scientific publication, (2) model parameters can be imported from tabular parameter collections and (3) models have to be generated from experimental data or primary model parameters. All three approaches were demonstrated in the paper. The sample Food Safety Model Repository is available via: <http://sourceforge.net/projects/microbialmodelingexchange/files/models> and the PMM-Lab software can be downloaded from <http://sourceforge.net/projects/pmmmlab/>. This work also illustrates that a standardized information exchange format for predictive microbial models, as the key component of this strategy, could be established by adoption of resources from the Systems Biology domain.

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1. Introduction

International efforts to improve the quality and safety of food products have led to an increased interest in predictive microbial modelling among food manufacturers (Buchanan, 1993b; McMeekin et al., 2002) and regulatory agencies (Manfreda and De Cesare, 2014). As predictive microbiology can be used to predict the behaviour of microorganisms in various stages of processing, storage and distribution (McMeekin et al., 2002; Nauta, 2002), Regulation (EC), 2073/2005 (and all amendments) contemplates the use of predictive microbial models in the food industry for demonstrating compliance with established microbiological criteria. In that sense, the quantitative estimates generated by predictive microbial models can provide additional information useful in decision making during HACCP planning, process design and product reformulation (Halder et al., 2010; McMeekin et al., 2006; Nauta, 2002).

For example predictive models on growth and inactivation of *Salmonella* in beef products have a high practical relevance and a large amount of them have been generated (Hwang et al., 2009; Juneja et al., 2003, 2009). This development has been driven by the fact that *Salmonella* is considered as a major causative agent of gastrointestinal diseases (CDC, 2013; EFSA, 2010, 2012; Guillier et al., 2013; Juneja et al., 2003, 2009) and meat is highly favourable for growth of *Salmonella* (de Oliveira et al., 2013). Although the number of salmonellosis cases attributed to beef products is considered to be lower than those attributed to products derived from poultry, pork or eggs (David, 2009), some studies identified *Salmonella* as one of the most significant hazards linked to beef consumption (Fosse et al., 2008; Greig and Ravel, 2009). Additionally, in the U.S. many disease outbreaks could be directly linked to *Salmonella* contaminations in beef (CDC, 2011, 2012, 2013; McLaughlin et al., 2006; Robinson, 2013).

However, despite the fact that existing predictive models could potentially help the meat sector to reliably predict and estimate potential growth, inactivation or survival of *Salmonella* during processing and storage, the application of models into the day-to-day operations of the food industry is limited. Potential reasons for this are:

1. Models are frequently only published in scientific journals or implemented in stand-alone software solutions.

Abbreviations: DOI, Digital Object Identifier; EC, European Commission; FSMR, Food Safety Model Repository; HACCP, Hazard Analysis and Critical Control Points; ICPMF, International Conference on Predictive Modelling in Food; ICRA, Interactive Catalogue on Risk Assessment; MIRIAM, Minimal Information Required In the Annotation of Models; RMSE, Root-Mean-Square Error; SBML, Systems Biology Markup Language; PMF-ML, Predictive Modelling in Food-Markup Language

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- Free and open databases containing predictive microbial models are not widely accepted or utilized.
- No standardized data format for description of predictive models exists.

In order to facilitate the discussions on harmonized data formats an open community forum called *OpenML for Predictive Modelling in Food* (<http://sourceforge.net/projects/microbialmodelingexchange/>) has been launched recently. Such harmonized data formats would facilitate the exchange of modelling information between different software tools and also allow the creation of model repositories. A publicly available model repository hosting predictive microbial models in a standardized format would support easy access and wider application of predictive models within the research community as well as the food industry.

During the past few years, numerous software solutions in the domain of predictive microbiology have been developed (Baranyi and Tamplin, 2004; Buchanan, 1993a; ComBase, 2013; Huang, 2014; Koseki, 2009; Leporq et al., 2005) for which Table 1 provides an overview. Many of these software tools were built around models for specific microorganisms in specific food matrices (*FISHMAP*, *Prediction of Microbial safety in Meat Products*, *FSSP*, *Dairy product Safety Predictor*, *Sym'Previus*, *GroPIN*, *Listeria Meat Model*). Other tools are designed to accomplish specific tasks such as risk prioritization (*FDA-iRISK*), evaluation of microbial growth/no growth boundaries (*Microbial Responses Viewer*) or model generation (*GlnaFIT*, *FILTREX*, *PMM-Lab*).

Regarding those software tools which contain a type of database for predictive models, the stand-alone software *Pathogen Modeling Program* (*PMP*) and the on-line software *ComBase Predictor* can be considered as the pioneering software solutions. They make unpublished and published models available by incorporating them into their web based software solution (Perez-Rodríguez and Valero, 2013). However, end users cannot implement new models in these systems themselves, as only the software owners can accomplish this task. Moreover, predictive microbial models themselves cannot be exported, only the predictions made by the web-based software tools.

New web-based prediction tools for microbial growth and inactivation have been launched recently. *MicroHibro* and *Baseline* (Manfreda and De Cesare, 2014; Posada-Izquierdo et al., 2012) allow incorporation

of user defined models for any microorganisms and food of interest, enabling the user to obtain predictions for growth and inactivation. However, the type of model equation that can be used within these systems is currently restricted, especially due to the restriction to a predefined set of primary models. As in the case of *ComBase Predictor* and *PMP*, there is no functionality allowing users to export models implemented in *MicroHibro* or *Baseline* to be used for prediction by other predictive modelling tools.

Another new solution developed recently is *GroPIN*, which already contains a predictive microbial model database with more than 400 published models, including spoilage and mycotoxigenic fungi, bacteria and yeasts in several food matrices. However, *GroPIN* is not open sourced, and it does not provide the user with a feature to exchange model information with other software tools, either. Moreover, it is also focused on the model application and does not provide any functionality to integrate real experimental data or to carry out a model generation process.

Finally there is *PMM-Lab* which can be used to create new models based on microbial data and which includes a database capable of storing experimental data, predictive microbial models as well as model generation workflows. It is primarily intended to support domain experts in their efforts to create, document and share predictive microbial models in a transparent fashion (Filter et al., 2013). This tool is freely available as open source software and provides many valuable features for model generation, model import and export as well as for re-implementation of models published in scientific literature. As *PMM-Lab* also provides a prototype implementation of a module that allows exporting models into the proposed standardized data exchange format, it has been selected as the tool to create sample models for the new Food Safety Model Repository (FSMR). Additionally, the workflow-based approach creates transparency on data processing and facilitates collaboration and quality control among different researchers.

The aim of this study was to propose and illustrate a strategy for creation of FSMR for predictive microbial models of growth, inactivation and survival of microorganisms (Fig. 1). The strategy was demonstrated using models for *Salmonella* in beef re-implemented or generated within *PMM-Lab*. Three possible approaches related to the implementation process and the available data are presented.

Table 1
Software solutions available in the domain of predictive microbiology and quantitative microbial risk assessment.

Software	Link (accessed 11/27/2014)
A swift Quantitative Microbiological Risk Assessment (sQMRA) tool	http://foodrisk.org/exclusives/sqmr/
Baseline	www.baselineapp.com
ComBase	http://www.combase.cc
Dairy Product Safety Predictor	www.aqr.maisondu lait.fr
DMFit	http://www.ifr.ac.uk/safety/dmfit/
FDA-iRISK	https://irisk.foodrisk.org
FILTREX	http://w3.jouy.inra.fr/unites/miaj/public/logiciels/filtrex/
FISHMAP	http://www.azti.es/fishmap
Food Spoilage and Safety Predictor (FSSP)	http://fssp.food.dtu.dk
FoodProcess-Lab	http://sourceforge.net/projects/foodprocesslab/
FRISBEE	http://frisbee-wp2.chemeng.ntua.gr/coldchaindb/
GlnaFIT	http://cit.kuleuven.be/biotec/downloads.php
GroPIN	www.aua.gr/psomas/gropin
Interactive online Catalogue on Risk Assessment (ICRA)	http://icra.foodrisk.org/
IPMP	http://www.ars.usda.gov/Services/Docs.htm?docid=23355
Listeria Meat Model	http://www.cpmf2.be/software.php
MicroHibro	www.microhibro.com
MRV, Microbial Responses Viewer	http://mrviewer.info/
OptiPa	https://perswww.kuleuven.be/~u0040603/optipa/optipamain.htm
PMM-Lab	https://sourceforge.net/projects/pmmlab/
Prediction of Microbial Safety in Meat Products	http://dmripredict.dk
PredOxyPack	http://predoxypack.be/
Shelf Stability Predictor	http://www.meathaccp.wisc.edu/ST_calc.html
Sym'Previus	www.symprevius.org
Therm 2.0	http://www.meathaccp.wisc.edu/pathogen_modeling/therm.html

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