Sensitivity analysis of microbial growth parameter distributions with respect to data quality and quantity by using Monte Carlo analysis

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Abstract

Nowadays, most of the mathematical models used in predictive microbiology are deterministic, i.e. their model output is only one single value for the microbial load at a certain time instant. For more advanced exploitation of predictive microbiology in the context of hazard analysis and critical control points (HACCP) and risk analysis studies, stochastic models should be developed. Such models predict a probability mass function for the microbial load at a certain time instant. An excellent method to deal with stochastic variables is Monte Carlo analysis. In this research, the sensitivity of microbial growth model parameter distributions with respect to data quality and quantity is investigated using Monte Carlo analysis. The proposed approach is illustrated with experimental growth data. There appears to be a linear relation between data quality (expressed by means of the standard deviation of the normal distribution assumed on experimental data) and model parameter uncertainty (expressed by means of the standard deviation of the model parameter distribution). The quantity of data (expressed by means of the number of experimental data points) as well as the positioning of these data in time have a substantial influence on model parameter uncertainty. This has implications for optimal experiment design.

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1. Introduction

Mathematical models developed in the field of *predictive microbiology* are used to predict the growth, survival and inactivation responses of food-borne micro-organisms to different environmental conditions (e.g. temperature, pH) [11].

By consequence, predictive microbiology plays a key role when aiming at a *quantitative* implementation of the food safety management system (hazard analysis and critical control points (HACCP)), which is up till now more *qualitatively* implemented in the *food industry* [6]. HACCP has been developed as an alternative, proactive method for the time-consuming and laborious a posteriori analyses to assess the microbiological safety of the end product. In this method, the critical control points are determined in the whole production process. The specifications for the process parameters (more specifically, the admissible upper and/or lower limits) at those critical control points may be calculated by using predictive models.

Predictive microbiology is also a major component of risk analysis studies at *regulatory level*. Risk analysis is divided into three related, but distinct components: risk assessment, risk management and risk communication. Predictive microbiology, together with a dose–response relationship, should be the key element to perform quantitative microbial risk assessments of foods [3]. Currently, the FAO/WHO framework of risk analysis is world-wide being implemented [21].

At present, most of the models predicting the microbial load are *deterministic*: at a certain time instant, the model predicts a single value for the microbial load. However, the microbial quality and safety may be characterised by a high level of variation. Typical examples of variation are: variation in growth and pre-growth conditions (e.g. temperature, pH, water activity), measurement uncertainty, and variation among strains. There is an urgent need for *stochastic* predictive microbiology which encompasses model types incorporating *uncertainty* at the level of measurements and model parameters and predicts the microbial load by a probability mass function [16]. As such, stochastic predictive microbiology is a key element for performing statistically founded HACCP and risk analysis studies.

Monte Carlo analysis is a general method to deal with stochastic models, examples in the field of predictive microbiology can be found in [4,5,14,16,17].

The main goal of this paper is to investigate by means of a Monte Carlo analysis the influence of: (i) the quality of data, characterised by means of the standard deviation of the error distribution on the experimental data points; and (ii) the quantity and positioning of data in time, on the propagated model parameter uncertainty.

2. Materials and methods

2.1. Experimental data

A large set of experimental growth curves generated under various environmental conditions was available for this research. All experimental cultures were grown on brain heart infusion (BHI). Plate counting was done on plate count agar (PCA). Each experimental data point was based on one single plate count.

To illustrate the methodology and the results obtained for *all* growth curves available, the following two growth curves have been selected as typical examples.