One-step dynamic inverse analysis and Markov Chain Monte Carlo simulation of microbial growth in foods

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Abstract

Predictive microbiology is an area of research applying mathematical models to describe the changes in microbial population in foods during storage and distribution. It has been applied in product development, microbial shelf life prediction, and food safety risk management and decision-making. Conventionally, models are constructed for isothermal conditions to determine kinetic parameters using a two-step process, which is very time-consuming and always accumulates and propagates errors in each step and experiment. One-step dynamic inverse analysis (OSDIA) is a new method used for extracting useful information from dynamic microbial growth and survival curves for determination of kinetic parameters.

OSDIA is performed by analyzing the data collected from food samples exposed to dynamic temperature profiles designed for observation in changes in the microbial population in response to variations in temperature. Numerical analysis and optimization are then used to solve differential equations describing microbial growth and survival in combination with secondary models to determine the kinetic parameters. With Bayesian analysis, posterior distribution of kinetic parameters can be constructed and sampled in Markov Chain Monte Carlo (MCMC) simulation to predict the growth and survival of microorganisms in foods.

One-step dynamic analysis and MCMC simulation has been experimented for studying the dynamic growth of *Clostridium perfringens* and *Salmonella* spp. The validation studies have shown that accurate prediction of microbial growth can be obtained, with the root mean square error (RMSE) within ± 0.25 log CFU/g, suggesting the usefulness of One-step dynamic analysis and Bayesian for inverse analysis and predictive modeling in food safety applications.