Predictive models for the growth of *Bacillus cereus*

Eunhee Kim, Gun-Young Lee[1], Munsin Kim, Hyeon Jeong Kim, Junghoon Jang,
In-Gyun Hwang[1], Ki-Sung Kwon[1], Dongdeuk Jang[2], Bong Hyun Nam

Department of Biostatistics, National Institute of Toxicological Research, Korea
[1]Department of Food Microbiology, Korea Food and Drug Administration, Korea
[2]Division of Risk Assessment Research, National Institute of Toxicological Research, Korea

This study illustrated the statistical inference process for establishing the predictive models for the growth of microbial pathogens, using the general primary models and the secondary models which are used in the fields of Quantitative Microbial Risk Assessment (QMRA). The modeling processes for microbial growth consist of three steps. First one is to estimate the parameters that represent the growth of bacteria in process of time in the primary model. Second one is to estimate the effects of environmental factors such as temperature on the growth of bacteria through the secondary model. Finally the predictive models for the growth of bacteria are obtained from combining two models. Several issues from the combination of the two models were considered and the real data were applied to the predictive model for the growth of *Bacillus cereus* in ready-to-eat foods.