

## Development of User-Friendly Modeling Software and Its Application in Processed Meat Products

Heeyoung Lee<sup>1</sup>, Panho Lee<sup>2</sup>, Soomin Lee<sup>1</sup>, Sejeong Kim<sup>1,3</sup>, Jeeyeon Lee<sup>1,3</sup>, Jimyeong Ha<sup>1,3</sup>, Yukyung Choi<sup>1,3</sup>, Hyemin Oh<sup>1,3</sup>, and Yohan Yoon<sup>1,3\*</sup>

<sup>1</sup>*Risk Analysis Research Center, Sookmyung Women's University, Seoul, Korea*

<sup>2</sup>*TNH, Seongnam, Korea*

<sup>3</sup>*Department of Food and Nutrition, Sookmyung Women's University, Seoul, Korea*

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**ABSTRACT** - The objective of this study was to develop software to predict the kinetic behavior and the probability of foodborne bacterial growth on processed meat products. It is designed for rapid application by non-specialists in predictive microbiology. The software, named Foodborne bacteria Animal product Modeling Equipment (FAME), was developed using Javascript and HTML. FAME consists of a kinetic model and a probabilistic model, and it can be used to predict bacterial growth pattern and probability. In addition, validation and editing of model equation are available in FAME. The data used by the software were constructed with 5,400 frankfurter samples for the kinetic model and 345,600 samples for the probabilistic model using a variety of combinations including atmospheric conditions, temperature, NaCl concentrations and NaNO<sub>2</sub> concentrations. Using FAME, users can select the concentrations of NaCl and NaNO<sub>2</sub> meat products as well as storage conditions (atmosphere and temperature). The software displays bacterial growth patterns and growth probabilities, which facilitate the determination of optimal safety conditions for meat products. FAME is useful in predicting bacterial kinetic behavior and growth probability, especially for quick application, and is designed for use by non-specialists in predictive microbiology.

**Key words** : Meat product, Bacterial growth, Software, Kinetic model, Probabilistic model

Predictive models have been used to predict kinetic behavior and to calculate the growth probability of foodborne pathogens under various conditions<sup>1,2</sup>. For kinetic modeling, a primary model and a secondary model need to be developed to estimate kinetic parameters of foodborne pathogens such as lag phase duration and growth rate. A primary model describes kinetic behavior over time, and a secondary model describes the effect of environmental factors on the kinetic parameters<sup>3,4</sup>. In addition, a probabilistic model has been used to estimate the probabilities of bacterial growth under a variety of factor-combinations<sup>3,5</sup>.

Although many predictive models are developed, they are difficult for nonspecialists to understand, especially for industry applications. Thus, the applications of previously developed models have been limited. The advent of computer technology and associated advances in computational power have made it possible to perform complex mathematical calculations that would otherwise be too time-

consuming for useful applications in predictive microbiology<sup>6</sup>. Hence, computer software has been developed to simplify the prediction of growth or inactivation of foodborne pathogens under various conditions. However, this type of software is not considered user-friendly for those who are not specialized in predictive modeling. Thus, although predictive models are useful in processing meat products, this technology is not used in the industry. In addition, even for experts in predictive microbiological modelling, the development of a predictive model is time-consuming.

Therefore, the objective of this study was to develop a user-friendly modeling software, which is equipped to handle both kinetic and probabilistic models, in order to predict bacterial growth and growth probability by simulating simple meat-product-related conditions.

## Materials and Methods

### Data collection

All the data were collected from our previous research<sup>7-13</sup>. A kinetic model was constructed with 5,400 samples of frankfurters for *Pseudomonas* spp., *Listeria monocytogenes*

\*Correspondence to: Yohan Yoon, Department of Food and Nutrition, Sookmyung Women's University, Seoul 04310, Korea  
Tel: 82-2-2077-7585, Fax: 82-2-710-9479  
E-mail: [yoon@sookmyung.ac.kr](mailto:yoon@sookmyung.ac.kr)

and *Salmonella*, and probabilistic models was constructed with 345,600 samples in broth for *L. monocytogenes*, *Staphylococcus aureus*, and *Salmonella*.

### Mathematical base

Kinetic models such as primary and secondary models can estimate kinetic parameters. Primary models describe the kinetic behavior of bacteria over time, and secondary models describe the effect of environmental factors on the kinetic parameters<sup>3,5</sup>. The primary model was based on a modified Gompertz model<sup>3,14</sup>, and the model equation was as follows:

$$N_t = A + C \times \exp\{-\exp[-B(t - M)]\}, \quad (1)$$

where  $N_t$  is the cell number at any time  $t$ ,  $A$  is the lower asymptotic line of the growth curve as  $t$  decreases to zero,  $C$  is the difference between the upper asymptotic line of the growth curve and the lower asymptotic line,  $B$  is the relative growth rate at time  $M$ , and  $M$  is the time at which the growth rate is at a maximum (h).  $\mu_{\max}$ , LPD, and  $N_{\max}$  can be calculated by the equations:

$$\mu_{\max} = BC/e \quad (e = 2.7182), \quad (2)$$

$$\text{LPD} = M - (1/B), \text{ and} \quad (3)$$

$$N_{\max} = A + C. \quad (4)$$

In the validation function, the bias factor ( $Bf$ ), the accuracy factor ( $Af$ ), and the root mean square error (RMSE) could be calculated. The equations for these calculations are as follows:

$$Bf = 10^{[\sum \log(\text{predicted values} - \text{observed value})/n]}, \text{ and} \quad (5)$$

$$\text{RMSE} = \text{square root } [\sum (\text{observed values} - \text{predicted values})^2/n], \quad (6)$$

where  $n$  represents the number of data points.

Probabilistic models can estimate the probabilities of bacterial growth under various environmental conditions such as temperature,  $\text{NaNO}_2$  concentrations, and  $\text{NaCl}$  concentrations<sup>15</sup>. The probabilistic model equation is based on logistic regression analysis, and the equation is as follows<sup>3,5</sup>:

$$\begin{aligned} \text{Logit (P)} = & a_0 + a_1 \cdot \text{NaCl} + a_2 \cdot \text{NaNO}_2 + a_3 \cdot \text{Time} + a_4 \cdot \text{NaCl}^2 \\ & + a_5 \cdot \text{NaNO}_2^2 + a_6 \cdot \text{Time}^2 + a_7 \cdot \text{NaCl} \cdot \text{NaNO}_2 + a_8 \cdot \\ & \text{NaCl} \cdot \text{Time} + a_9 \cdot \text{NaNO}_2 \cdot \text{Time}, \end{aligned} \quad (7)$$

where  $\text{Logit (P)}$  is an abbreviation of  $\ln[P/(1 - P)]$ ,  $P$  is the bacterial growth probability in the range of 0 to 1,  $a_i$  are estimates,  $\text{NaCl}$  is sodium chloride concentration,  $\text{NaNO}_2$  is sodium nitrite concentration, and  $\text{Time}$  is storage time.

### Development of predictive modeling software

The predictive modeling software, named FAME (Food-borne bacteria Animal product Modeling Equipment), was developed for predicting bacterial growth on meat products. FAME can calculate bacterial concentrations and bacterial growth probabilities of meat product processing in advance. The software was programmed using Javascript and HTML, and the software was developed for two distinct model types, kinetic models and probabilistic models.

In kinetic models, the cell counts of *L. monocytogenes*, *Pseudomonas* spp., and *Salmonella* spp., can be predicted by entering atmospheric conditions (aerobic or anaerobic), storage temperatures (0-40°C),  $\text{NaNO}_2$  concentrations (0 or 10 ppm), and  $\text{NaCl}$  concentrations (0-4.0%). In addition, a validation function was incorporated into FAME to compare experimental data and predicted bacterial concentrations.

In probabilistic models, bacterial growth probability (*L. monocytogenes*, *Salmonella* spp., *S. aureus*) can be predicted based on atmospheric conditions (aerobic or anaerobic), temperatures (0-15°C),  $\text{NaCl}$  concentrations (0, 0.25, 0.50, 0.75, 1.00, 1.25, 1.50, or 1.75),  $\text{NaNO}_2$  concentrations (0-150 ppm) and especially at 4°C, 7°C, 10°C, 12°C, and 15°C. The formulation for the validation of the predicted value

**Table 1.** Scenarios for application on meat products, and calculated bacterial concentrations and growth probabilities based on the scenarios using FAME

Scenario	Packaging	Temperature (°C)	$\text{NaNO}_2$ concentration (ppm)	$\text{NaCl}$ concentration (%)	Time for 1 Log CFU/g growth
1	Anaerobic	7	0	1.5	288 h
2	Anaerobic	15	0	1.5	54 h
3	Anaerobic	7	0	0.5	160 h
4	Anaerobic	15	0	0.5	38 h
5	Aerobic	7	0	1.5	510 h
6	Aerobic	15	0	1.5	35 h
7	Aerobic	7	0	0.5	165 h
8	Aerobic	15	0	0.5	20 h

with experimental data was incorporated into the software. In addition, in both the kinetic and the probabilistic models, all model equations can be edited by a user, and new model equations can be uploaded by a user.

**Application on meat products**

In the application of FAME, eight scenarios for *Salmonella* spp. on meat products according to atmospheric conditions, storage temperatures, and NaCl concentrations were compared using the kinetic model (Table 1). In addition, growth probabilities of *Salmonella* spp. were calculated, using the probabilistic model, based on the scenarios.

**Results and Discussion**

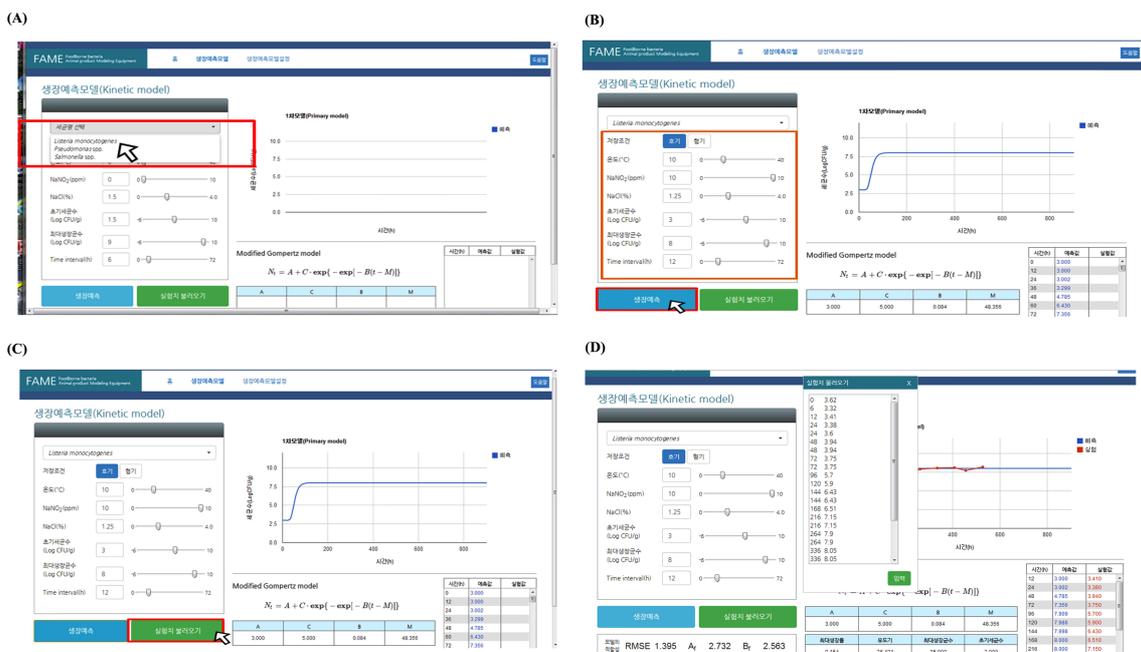
The user interface developed for FAME is shown Figs. 1-3. In the kinetic model, the user can choose bacteria (Fig. 1(A)), and then select food atmospheric conditions (aerobic or anaerobic), NaNO<sub>2</sub> concentrations, NaCl concentrations, assumed initial cell concentrations, maximum cell concentrations, and time intervals (Fig. 1(B)). Users can select ‘growth prediction’ to display the graph and value of predicted cell concentrations according to the database. In addition, if users want to validate their own laboratory data, users can input their experimental data by a simple copy-and-paste from Microsoft® Excel into FAME. Then, B<sub>f</sub>, A<sub>f</sub>, and RMSE values are calculated by comparing experimental

data and predicted data.

The probabilistic model also allows users to select the name of the bacteria (Fig. 2(A)), as well as variables such as packaging condition, growth probability (10%, 50%, and 90% interfaces), temperature, and NaCl concentration (Fig. 2(B)). When users click ‘growth probability prediction’, the graph of bacterial growth probability is displayed according to the strength of the probability, using blue (10% growth probability), red (50% growth probability), and/or yellow lines (90% growth probability). Users can estimate bacterial growth probability under selected environmental conditions, and the data can be used for determining the best conditions for the safety of meat products.

If users want to change the calculating equation, they can click the ‘setting’ button to edit, and users also can add new equations from their own data (Fig. 3). When editing an equation or adding a new equation, users can immediately confirm the growth prediction graph and cell concentration under certain conditions for both kinetic and probabilistic models.

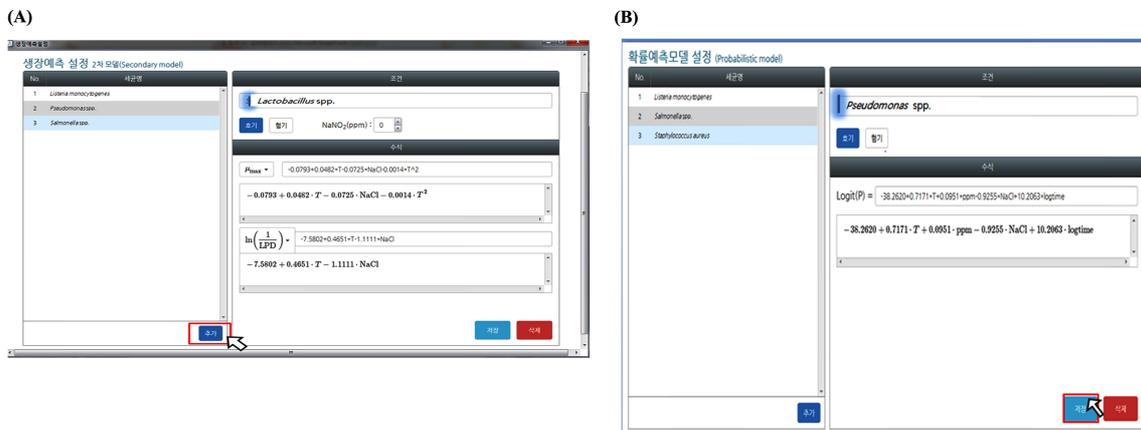
Using FAME software, users can predict bacterial concentrations in advance and can thus, determine the best conditions for the safety of meat products with specific bacterial concentrations as set in FAME. Table 1 provides data on simple scenarios for the application of FAME for meat products. When users select environmental conditions based on these scenarios, the bacterial growth curve and concentrations according to time are presented. According



**Fig. 1.** Kinetic model part in FAME. A user selects (A) the name of bacteria and (B) conditions such as atmospheric condition, temperature, NaCl concentration, NaNO<sub>2</sub> concentration, initial and maximum cell concentration, and time interval. This is followed by (C) entering observed data and (D) the resulting data validation.



**Fig. 2.** Probabilistic modeling in FAME. A user selects (A) bacteria and (B) conditions such as packaging condition, growth probability (10, 50, 90% interface), temperature and NaCl concentration.



**Fig. 3.** Editing (A) kinetic and (B) probabilistic models in FAME.

to the scenarios, the times for 1 Log CFU/g growth on meat products, relative to initial concentrations, are predicted by the kinetic model as 288 h, 54 h, 160 h, 38 h, 510 h, 35 h, 165 h, and 20 h, respectively. Comparing scenarios 1 and 2, when the temperature is increased from 7°C to 15°C, time for 1 Log CFU/g *Salmonella* spp. growth is decreased from 288 h to 54 h in an anaerobic atmosphere. Also, when NaCl concentrations decreased 1.5% to 0.5%, time for 1 Log CFU/g *Salmonella* spp. growth is decreased from 288 h to 160 h at 7°C (scenarios 1 and 3), and from 54 h to 38 h at 15°C in an anaerobic atmosphere (scenarios 2 and 4). In addition, when meat products were packaged aerobically, time for 1 Log CFU/g *Salmonella* spp. growth is increased, compared to an aerobic packaging (scenarios 5-8). With these results, users can predict bacterial growth and determine appropriate plans for food safety for meat products.

**Conclusion**

In conclusion, FAME can be useful in the meat processing industry for food safety, especially in terms of its rapid

application. In addition, because of its user-friendly interface, even non specialists in predictive modeling can use the software to predict both bacterial concentrations from kinetic models and growth probabilities from probabilistic models.

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**Disclosure Statement**

No competing financial interests exist.

**국문요약**

본 연구에서는 육제품의 다양한 조건(포장, 저장온도, 염농도, 아질산염농도)에서의 식중독세균의 성장을 예측하는 소프트웨어를 예측미생물학에 대한 지식이 부족한 비전문

가도 손쉽게 이용할 수 있도록 개발하였다. 육제품에서의 식중독세균예측소프트웨어(FAME: Foodborne bacteria Animal product Modeling Equipment)는 Javascript와 HTML을 이용하여 개발하였으며, 육제품에 대한 카이네틱모델과 확률모델을 포함하고있다. FAME에서는 검증(validation) 기능을 포함하고 있으며, FAME에 탑재 되어있는 예측모델의 수식을 자유롭게 수정할 수 있도록 고안 하였다. FAME에는 포장조건, 온도, 염농도, 아질산염농도 조합에 따라 실험한 데이터를 카이네틱모델(5,400 데이터)과 확률모델(345,600 데이터)에 탑재하였다. 사용자가 FAME을 이용하여 육제품의 제조 조건을 소프트웨어에 입력하면, 시간에 따른 식중독세균의 생장패턴과 생장확률이 즉시 계산 되어진다. 따라서 예측 미생물학에 대한 전문 지식이 없는 비전문가라고 하더라도 FAME을 이용하여 직접 실험을 하지 않고도 육제품에서의 식중독세균의 생장을 쉽고 빠르게 예측할 수 있어, 육가공분야에서 매우 유용하게 사용되어 질 수 있을 것으로 판단된다.

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