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Comparison of Monte Carlo Simulation and Fuzzy Math Computation for Validation of Summation in Quantitative Risk Assessment

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Abstract As the application of quantitative risk assessment (QRA) to food safety becomes widespread, it is now being questioned whether experimental results and simulated results coincide. Therefore, this paper comparatively analyzed experimental data and simulated data of the cross contamination, which needs summation of the simplest calculations in QRA, of chicken by Monte Carlo simulation and fuzzy math computation. In order to verify summation, the following basic operation was performed. For the experiment, thigh, breast, and a mixture of both parts were preserved for 24 hr at 20°C, and then the cell number of *Salmonella* spp. was measured. In order to examine the differences between experimental results and simulated results, we applied the descriptive statistics. The result was that mean value by fuzzy math computation was more similar to the experimental than that by Monte Carlo simulation, whereas other statistical descriptors by Monte Carlo simulation were more similar.

Keywords: quantitative risk assessment (QRA), Monte Carlo simulation, fuzzy math computation, summation, *Salmonella* spp.

Introduction

The incidence of food poisoning in Korea has recorded rapid growth, except for in the year 2002. Such phenomenon has caused people to pay more attention to the safety of food and, thus, the risk assessment of food has become a big concern among the public. Throughout the food chain, from raw materials to consumption, there is more research focusing on the growth of pathogenic bacteria. In particular, the importance of making predictions of pathogenic bacteria behavior has risen (1). Most of such prospective research on bacteria uses Monte Carlo simulation. However, studies on validation of the simulation by comparison with experimental results are minimal.

Quantitative risk assessment (QRA) analyzes the risks of possible food contamination in five steps: hazard identification, exposure assessment, dose response assessment, risk characterization, and risk management (2). Monte Carlo simulation is the most popular method of predicting growth or death of the organisms of interest in the form of probability distribution in the exposure assessment step. This is because experimental data used in the simulation have the attributes of uncertainty and variability (3). In particular, Monte Carlo simulation has been applied extensively to predictive microbiology (4-6). But there is still a weakness in the initial stage of risk assessment when there is not enough data; the inadequate data can be used in Monte Carlo simulations to provide reliability of probability distribution to estimate uncertain and variable parameters.

Fuzzy theory also has been applied as an analytical method of QRA, and an alternative to Monte Carlo simulation (7). Fuzzy sets are defined by membership functions assigned to the elements in the sets, and membership function defines weightings of all elements with real numbers from 0 and 1 (8-10). Membership function can be regarded as a kind of probability distribution indicating uncertainty of data. In other words, fuzzy sets can represent data with uncertainty and variability of microbes. According to these attributes, Davidson and Ryks (7) applied Monte Carlo simulation and fuzzy math simulation in the quantitative risk assessment of microbes. They argued that fuzzy computation is a more appropriate method to explain data uncertainty in the early stage of risk assessment. However, it is pointed out that the limit of uncertainty increased in the sequential calculations with fuzzy sets because they included all of the combinations.

As mentioned above, risk assessment is based on the basic data of microbes and its mathematical operation consists of summation/subtraction, multiplication/division, logarithm/exponential, etc. However, the accuracy of the calculation has never been proved experimentally. In general, materials, surface, and machines are conducive to cross contamination with microorganisms from one carcass transferring to other carcasses by summation. Also the summation was a basic calculation that various predicting bacterial growth model. As first trial, thus, summation was selected to confirm the accuracy, comparing with the experimental data of cross contamination. To recreate the cross contamination of microbes, two parts of the chicken were artificially mixed and the cell number of *Salmonella* spp. was measured before and after the cross contamination. As algorithms, Monte Carlo simulation and fuzzy math computation were applied and validity was statistically examined in comparison with experimental results.

Materials and Methods

Materials Chicken thigh and breast were purchased (manufactured by Maniker Co., Ltd., Korea). Three days

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had passed since the meat was processed and frozen. Then, separate portions (3 g) of each thigh and breast were taken. The samples of thigh, breast, and the mixture (thigh : breast = 1 : 1, w/w) were preserved for 24 hr at 20°C.

Measurement of number of *Salmonella* spp. Chicken thigh (3 g), breast meat (3 g), and the mixture (6 g) were mixed with 94 mL of sterilized buffered peptone water, respectively (11). Then, the samples were homogenized in a pulsifier (Microgen Bioproducts Ltd., Surrey, UK) for 45 sec. Each sample's crude liquid was diluted to 10E-07 and cultivated in XLD agar (Gellix TM; Ventech Bio. Co., Korea) in 10 petri dishes for 24 hr at 35°C, using incubators. Then, the number (CFU/g) of *Salmonella* spp. was measured according to the standard plate count method. Ten samples were tested for each of thigh, breast, and the mixture.

Monte Carlo simulation Monte Carlo simulation was conducted using @RISK 4.0 (12). First, cell number data were obtained through experiments, and then an appropriate probability distribution model was selected after trying to fit those data to various models (13). Then, two sets of probability distribution for thigh and breast, respectively, were summed up by Monte Carlo simulation. The chi-square statistical method, which is the best known goodness-of-fit statistics and the latin hypercube sampling type (14) were adopted in the simulation computation. The computation was reiterated 10,000 times.

Fuzzy math computation In order to represent the cell numbers with fuzzy sets, we applied the triangular function and α-cut method (7). Fuzzy set X has a triangular membership function and defined by Eq. 1.

$$X = < minimum,\ apex,\ maximum > \quad (1)$$

Membership grades of the minimum and maximum elements in the set are both 0 and that of apex is 1. The three elements were estimated from the triangular probability distribution by Monte Carlo simulation on the cell number data. The triangular fuzzy set (TFS) is re-expressed as continuous intervals by α-cut. A and B, which are two TFS by α-cut, are defined as follows:

$$\begin{aligned} A &\rightarrow < a_1,\ b_1,\ c_1 > \\ &\rightarrow \{(b_1-a_1)\ \alpha + a_1,\ (b_1-c_1)\ \alpha + c_1\}\ \forall\alpha \in [0,1] \\ B &< a_2,\ b_2,\ c_2 > \\ &\rightarrow \{(b_2-a_2)\ \alpha + a_2,\ (b_2-c_2)\ \alpha + c_2\}\ \forall\alpha \in [0,1] \end{aligned} \quad (2)$$

The summation of two fuzzy sets is calculated by adding up all combinations of element values (Eq. 3).

$$\begin{aligned} C &= A + B \\ &\rightarrow < a_1+a_2,\ b_1+b_2,\ c_1+c_2 > \\ &\rightarrow \{[(b_1+b_2)-(a_1+a_2)]\ \alpha + (a_1+a_2),\ [(b_1+b_2)-(c_1+c_2)]\ \alpha + (c_1+c_2)\} \end{aligned} \quad (3)$$

Statistics To evaluate the differences between experimental results and simulated results, both of which were in the form of cell number distribution, we have used the descriptive statistics. The experimental data and calculated results of the Monte Carlo simulation were statistically treated with @RISK in terms of standard deviation, variance, skewness, kurtosis, etc., whereas the results of fuzzy computation were treated with the MS Excel, using simple formulas in calculations.

Results and Discussion

The cell numbers of 10 samples for each of thigh, breast, and the mixture are shown in Table 1. When the cell numbers of each part of the chicken meat was compared, the number (CFU/g) of breast meat was 8 log which is 1 log higher than 7 log of thigh. Oscar (5) reported that the specific growth rate of *Salmonella typhimurium* at 20°C was 0.192 log/hr for breast and 0.186 log/hr for thigh. Gram-negative bacteria cell numbers of breast and leg transported on ice from a local chicken plant in Korea were reported to be 3.23 log and 3.69 log CFU/g, respectively (15). *Salmonella* spp. cell number of breast from the carcasses was 3.34 log CFU/g (16). In our samples stored for 24 hr at 20°C, therefore, the cell numbers might result from both effects of growth rate and initial contamination levels. In addition, both standard deviation and variance were higher in breast than in thigh, which indicates the experiment data of breast have more uncertainty (Table 2). The cell numbers in the mixture were higher as expected since they are effectively the summation of the total microbial load on the breast and thigh. We experienced similar results when the same experiment was repeated 3 times.

Analysis of Monte Carlo simulation The results are shown in Tables 3, 4, and 5 from the data-fitting of 10 values of cell numbers of different parts of chicken, applying 9 distribution functions. To figure out the level of fitting, results from chi-square test were compared such as p-value (level of the significance of the fit) and bin statistics parameters (probability values for each bin for both the input and the fitted distribution) (12). Bins are the groups that input data are divided into, similar to the classes used to draw a histogram. Number of bins is that of histogram intervals calculated across the range of a graph. The setting 'auto' on @RISK program calculated

Table 1. Experimental data of cell numbers (CFU/g) of *Salmonella* spp. for different parts of chicken meat

Thigh (A)	Breast (B)	Mixture (A:B = 1:1, w/w)
6.50×10^7	2.02×10^8	2.55×10^8
5.90×10^7	1.95×10^8	2.63×10^8
6.00×10^7	1.90×10^8	2.60×10^8
5.60×10^7	1.90×10^8	2.55×10^8
6.30×10^7	1.93×10^8	2.60×10^8
5.50×10^7	1.76×10^8	2.42×10^8
5.30×10^7	1.95×10^8	2.50×10^8
6.10×10^7	1.86×10^8	2.53×10^8
6.00×10^7	2.00×10^8	2.60×10^8
5.00×10^7	1.93×10^8	2.55×10^8

Table 2. The results of descriptive statistics on experimental data of cell numbers (CFU/g) of *Salmonella* spp. for different parts of chicken meat

Statistical descriptors	Thigh (A)	Breast (B)	Mixture (A:B = 1:1, w/w)
Mean	5.82×10^{7}	1.92×10^{8}	2.55×10^{8}
Standard error	1.47×10^{6}	2.30×10^{6}	1.92×10^{6}
Median	5.95×10^{7}	1.93×10^{8}	2.55×10^{8}
Mode	6.00×10^{7}	1.95×10^{8}	2.60×10^{8}
Standard deviation	4.64×10^{6}	7.26×10^{6}	6.06×10^{6}
Sample variance	2.15×10^{13}	5.28×10^{13}	3.68×10^{13}
Kurtosis	-5.03×10^{-1}	1.72×10	1.43×10
Skewness	-3.85×10^{-1}	-9.64×10^{-1}	-1.10×10
Range	1.50×10^{7}	2.55×10^{7}	2.05×10^{7}
Minimum	5.00×10^{7}	1.76×10^{8}	2.42×10^{8}
Maximum	6.50×10^{7}	2.02×10^{8}	2.63×10^{8}
Sum	5.82×10^{8}	1.92×10^{9}	2.55×10^{9}
Confidence level (95.0%)	3.32×10^{6}	5.20×10^{6}	4.34×10^{6}

the best number of bins. Minimum is the value where histogram bins start. Maximum is the value where histogram bins end. The distribution charts of all samples were divided into groups with 2 bins and the frequency (equivalent to probability value) of each bin was predicted. For breast meat, the Weibull function revealed that the input and fitted data of bin #1 and #2 were identical and that the goodness of fit was rated the highest since the *p*-value was the highest. Meanwhile, for thigh, *p*-value of six functions were identical; the input and fitted results of bin #1 frequency were 4 and 5, respectively; the input and fitted results of bin #2 were 6 and 5, respectively. Nevertheless, Extvalue function was selected as optimal distribution function by comparing the other information from further descriptive statistics on the fitted data, which are not stated in this paper though. Likewise, for the meat mixture, normal function was chosen as the most appropriate fitting function. Same kinds of the optimal fitting function for each sample resulted from three-time repeated experiments.

RiskWeibull function for breast and Extvalue function for thigh were used in the summation (Fig. 1). The results from summation are shown both in Fig. 2 and Table 7. The mean value of probability distribution summed up by Monte Carlo simulation was 2.50×10^{8} (CFU/g) near that of the cell numbers of meat mixture, 2.55×10^{8} (CFU/g); the summed probability distribution was very similar to normal distribution of the cell numbers of meat mixture. In Fig. 2, the graph of summed distribution is wider than that of the experimental data of meat mixture.

Analysis of fuzzy math computation First, the triangular membership function was determined from the triangular probability distribution by Monte Carlo simula-

Table 3. The results of the goodness-of-fit statistics by chi-square test on experimental data of cell numbers (CFU/g) of *Salmonella* spp. for chicken breast

Function	Weibull[1)]	Extvalue[2)]	Logistic[3)]	Normal[4)]	Triang[5)]	BetaGeneral[6)]	Pareto[7)]	Uniform[8)]	Expon[9)]
p-Value[10)]	1.00×10	5.27×10^{-1}	5.27×10^{-1}	5.27×10^{-1}	5.27×10^{-1}	3.17×10^{-1}	5.78×10^{-2}	5.78×10^{-2}	1.14×10^{-2}
# Bins[11)]	2.00×10	2.00×10	2.00×10	2.00×10	2.00×10	2.00×10	2.00×10	2.00×10	2.00×10
Bin #1 Min	1.48×10^{8}	-Infinity	-Infinity	-Infinity	1.72×10^{8}	1.76×10^{8}	1.76×10^{8}	1.73×10^{8}	1.74×10^{8}
Bin #1 Max	1.93×10^{8}	1.91×10^{8}	1.92×10^{8}	1.92×10^{8}	1.93×10^{8}	1.91×10^{8}	1.87×10^{8}	1.89×10^{8}	1.85×10^{8}
Bin #1 Input	5.00×10	4.00×10	4.00×10	4.00×10	6.00×10	3.00×10	2.00×10	2.00×10	1.00×10
Bin #1 Fit	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10
Bin #2 Min	1.93×10^{8}	1.91×10^{8}	1.92×10^{8}	1.92×10^{8}	1.93×10^{8}	1.91×10^{8}	1.87×10^{8}	1.89×10^{8}	1.85×10^{8}
Bin #2 Max	+Infinity	+Infinity	+Infinity	+Infinity	2.02×10^{8}	2.02×10^{8}	+Infinity	2.04×10^{8}	+Infinity
Bin #2 Input	5.00×10	6.00×10	6.00×10	6.00×10	4.00×10	6.00×10	8.00×10	8.00×10	9.00×10
Bin #2 Fit	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10

[1)]Weibull(alpha, beta) specifies a weibull distribution with the shape parameter alpha and a scale parameter beta. The weibull distribution is a continuous distribution whose shape and scale vary greatly depending on the argument values entered.
[2)]Extvalue(a, b) specifies an extreme value distribution with location parameter a and shape parameter b.
[3)]Logistic(alpha, beta) specifies a logistic distribution with the entered alpha and beta values.
[4)]Normal(mean, standard deviation) specifies a normal distribution with the entered mean and standard deviation. This is traditional 'bell shaped' curve applicable to distribution of outcomes in many data sets.
[5)]Triang(minimum, mist likely, maximum) specifies a triangular distribution with three points- a minimum, most likely, and maximum. The direction of the 'skew' of the triangular distribution is set by the size of the most likely value relative to the minimum and the maximum.
[6)]BetaGeneral(alpha1, alpha 2, minimum, maximum) specifies a beta distribution with the defined minimum and maximum using the shape parameters alpha1 and alpha 2.
[7)]Pareto(theta, a) specifies a pareto distribution with the entered theta and a values.
[8)]Uniform(minimum, maximum) specifies a uniform probability distribution with the entered minimum and maximum values. Every value across the range of the uniform distribution has an equal likelihood of occurrence.
[9)]Expon(beta) specifies an exponential distribution with the entered beta value.
[10)]Observed level of the significance of the fit.
[11)]Number of histogram intervals with the min and max of each bin plus the probability value for the bin both the input and the fitted distribution.

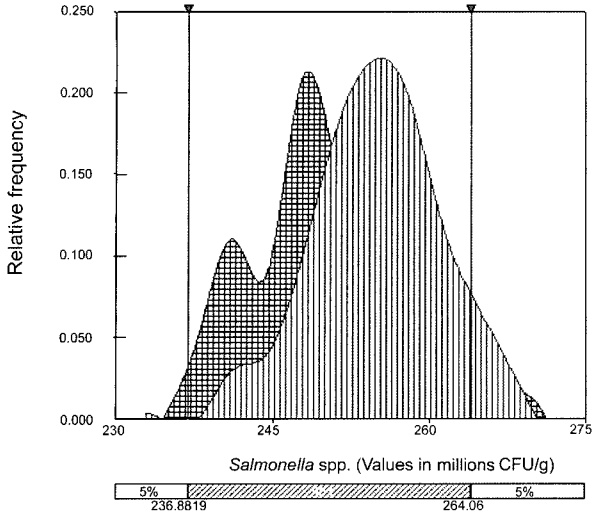

Fig. 1. Fitted distributions of *Salmonella* spp. cell number of chicken thigh (▦) and breast (▥).

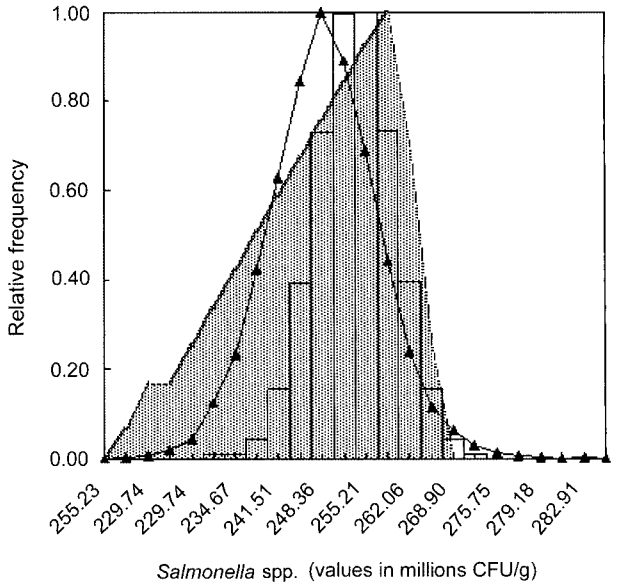

Fig. 2. Comparison between fitted data (□) of cell numbers of chicken mixture and mathematically summed distributions by Monte Carlo simulation (−▲−) and fuzzy computation (▦), respectively.

tion on the cell number data. For minimum, apex, and maximum elements, < 47473556, 60000000, 66909529 (CFU/g) > were estimated for thigh; < 171766865, 201436250, 201907632 (CFU/g) > were for breast. α-Cut was classified into six levels: 0, 0.2, 0.4, 0.6, 0.8, and 1. Right and left interval elements for a given α were calculated with Eq. 2. Then, summation was conducted using Eq. 3.

The membership function of fuzzy set after summation formed a triangular distribution (Fig. 2). To compare with Monte Carlo simulation, the membership grades were normalized between 0 and 1 by dividing membership grades by maximum grade. The dispersion of calculations by the two methods was similar.

The mean value of fuzzy set, 2.53×10^8 (CFU/g), was almost identical to that of the experimental data, 2.55×10^8 (CFU/g), compared with that of distribution by Monte Carlo simulation, 2.50×10^8 (CFU/g) (Table 7). However, the standard deviation and variance of fuzzy set were bigger than those of the experimental data and Monte Carlo simulation results. It indicates that the fuzzy set disperses more widely than the experimental data and even the distribution by Monte Carlo simulation, so its uncertainty may be the highest. Skewness and kurtosis of the fuzzy set had negative (-) sign, whereas those of the experimental data and Monte Carlo simulation results had positive (+) sign. Consequently, it represents that mean value by fuzzy math computation is more similar to the experimental than that by Monte Carlo simulation, whereas other statistical descriptors by Monte Carlo simulation are more similar. Davidson and Ryks (7) had reported that Monte Carlo simulation have a higher significance than fuzzy computation.

In conclusions, as food safety is becoming a major

Table 4. The results of the goodness-of-fit statistics by chi-square test on experimental data of cell numbers (CFU/g) of *Salmonella* spp. for chicken thigh

Function[1)]	Extvalue	Logistic	Normal	Triang	Uniform	Weibull	BetaGeneral	Pareto	Expon
p-Value[2)]	5.27×10^{-1}	5.27×10^{-1}	5.27×10^{-1}	5.27×10^{-1}	5.27×10^{-1}	5.27×10^{-1}	3.17×10^{-1}	2.06×10^{-1}	5.78×10^{-2}
# Bins[3)]	2.00×10	2.00×10	2.00×10	2.00×10	2.00×10	2.00×10	2.00×10	2.00×10	2.00×10
Bin #1 Min	-Infinity	-Infinity	-Infinity	4.75×10^7	4.83×10^7	4.18×10^7	5.00×10^7	5.00×10^7	4.92×10^7
Bin #1 Max	5.75×10^7	5.84×10^7	5.82×10^7	5.85×10^7	5.75×10^7	5.84×10^7	5.81×10^7	5.54×10^7	5.49×10^7
Bin #1 Input	4.00×10	4.00×10	4.00×10	4.00×10	4.00×10	4.00×10	3.00×10	3.00×10	2.00×10
Bin #1 Fit	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10
Bin #2 Min	5.75×10^7	5.84×10^7	5.82×10^7	5.85×10^7	5.75×10^7	5.84×10^7	5.81×10^7	5.54×10^7	5.49×10^7
Bin #2 Max	+Infinity	+Infinity	+Infinity	6.69×10^7	6.67×10^7	+Infinity	6.50×10^7	+Infinity	+Infinity
Bin #2 Input	6.00×10	6.00×10	6.00×10	6.00×10	6.00×10	6.00×10	6.00×10	7.00×10	8.00×10
Bin #2 Fit	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10

[1-3)]Refer to Table 3.

Table 5. The results of the goodness-of-fit statistics by chi-square test on experimental data of cell numbers (CFU/g) of *Salmonella* spp. for chicken mixture (thigh:breast = 1:1, w/w)

Function[1)]	Normal	Logistic	Triang	Weibull	Extvalue	BetaGeneral	Uniform	Pareto	Expon
p-Value[2)]	1.00×10	5.27×10^{-1}	5.27×10^{-1}	5.27×10^{-1}	2.06×10^{-1}	1.07×10^{-1}	5.78×10^{-2}	2.53×10^{-2}	1.14×10^{-2}
# Bins[3)]	2.00×10	2.00×10	2.00×10	2.00×10	2.00×10	2.00×10	2.00×10	2.00×10	2.00×10
Bin #1 Min	-Infinity	-Infinity	2.39×10^{8}	2.14×10^{8}	-Infinity	2.42×10^{8}	2.40×10^{8}	2.42×10^{8}	2.41×10^{8}
Bin #1 Max	2.55×10^{8}	2.56×10^{8}	2.56×10^{8}	2.56×10^{8}	2.55×10^{8}	2.55×10^{8}	2.52×10^{8}	2.51×10^{8}	2.50×10^{8}
Bin #1 Input	5.00×10	6.00×10	6.00×10	6.00×10	3.00×10	2.00×10	2.00×10	1.00×10	1.00×10
Bin #1 Fit	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10
Bin #2 Min	2.55×10^{8}	2.56×10^{8}	2.56×10^{8}	2.56×10^{8}	2.55×10^{8}	2.55×10^{8}	2.52×10^{8}	2.51×10^{8}	2.50×10^{8}
Bin #2 Max	+Infinity	+Infinity	2.63×10^{8}	+Infinity	+Infinity	2.63×10^{8}	2.65×10^{8}	+Infinity	+Infinity
Bin #2 Input	5.00×10	4.00×10	4.00×10	4.00×10	7.00×10	7.00×10	8.00×10	8.00×10	9.00×10
Bin #2 Fit	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10	5.00×10

[1-3)]Refer to Table 3.

Table 6. Alpha (α) cuts for fuzzy sets of experimental data of cell numbers (CFU/g) of *Salmonella* spp. for chicken thigh and breast and mathematically summed data for chicken mixture

α-Level	Thigh (A)		Breast (B)		Estimate (A+B)	
	Left	Right	Left	Right	Left	Right
0	4.75×10^{7}	6.69×10^{7}	1.72×10^{8}	2.02×10^{8}	2.19×10^{8}	2.69×10^{8}
0.2	5.00×10^{7}	6.55×10^{7}	1.78×10^{8}	2.02×10^{8}	2.28×10^{8}	2.67×10^{8}
0.4	5.25×10^{7}	6.41×10^{7}	1.84×10^{8}	2.02×10^{8}	2.36×10^{8}	2.66×10^{8}
0.6	5.50×10^{7}	6.28×10^{7}	1.90×10^{8}	2.02×10^{8}	2.45×10^{8}	2.64×10^{8}
0.8	5.75×10^{7}	6.14×10^{7}	1.96×10^{8}	2.02×10^{8}	2.53×10^{8}	2.63×10^{8}
1	6.00×10^{7}	6.00×10^{7}	2.01×10^{8}	2.01×10^{8}	2.61×10^{8}	2.61×10^{8}

Table 7. Comparison between experimental and predicted results by Monte Carlo simulation and fuzzy computation, respectively, in terms of descriptive statistics on *Salmonella* spp. cell numbers (CFU/g) of chicken mixture

Statistical descriptors	Cell number of chicken mixture	Predicted results	
		Monte Carlo	Fuzzy computation
Minimum	2.32×10^{8}	2.19×10^{8}	2.19×10^{8}
Mean	2.55×10^{8}	2.50×10^{8}	2.53×10^{8}
Maximum	2.79×10^{8}	2.91×10^{8}	2.69×10^{8}
Standard deviation	6.06×10^{6}	8.52×10^{6}	1.69×10^{7}
Sample variance	3.68×10^{13}	7.27×10^{13}	2.84×10^{14}
Skewness	6.50×10^{-4}	1.02×10^{-1}	-1.02×10
Kurtosis	3.00×10	3.43×10	-3.00×10^{-1}
Mode	2.55×10^{8}	2.40×10^{8}	2.61×10^{8}

concern in society, plenty of research on QRA is under way. Monte Carlo simulation has been considered the best method for being able to explain the uncertainty and variability of QRA. So, most studies have been conducted using Monte Carlo simulation. Currently, however, various methods other than Monte Carlo simulation in risk assessment are getting attention. Among them, fuzzy computation, which was mainly used in the artificial intelligence field, is becoming influential. Fuzzy computation alleviates uncertainty with every possible combination of inputs. Despite introductions of such diverse methods, the validation of the basic computation has been almost ignored. This paper is meaningful since it confirmed the significance of summation, the basic calculation of Monte Carlo simulation and fuzzy computation. In the future, other basic operations such as subtraction, division, multiplication, etc. also need to be validated. If the validity of those operations is confirmed, more effective risk assessment methods can be invented or developed. Furthermore, reliability and accuracy will be increasingly built up in predictive models of microbes, minimizing the uncertainty and variability of microbes.

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