

Bootstrap simulation for quantification of uncertainty in risk assessment

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Abstract : The choice of input distribution in quantitative risk assessments modeling is of great importance to get unbiased overall estimates, although it is difficult to characterize them in situations where data available are too sparse or small. The present study is particularly concerned with accommodation of uncertainties commonly encountered in the practice of modeling. The authors applied parametric and non-parametric bootstrap simulation methods which consist of re-sampling with replacement, in together with the classical Student-t statistics based on the normal distribution. The implications of these methods were demonstrated through an empirical analysis of trade volume from the amount of chicken and pork meat imported to Korea during the period of 1998-2005. The results of bootstrap method were comparable to the classical techniques, indicating that bootstrap can be an alternative approach in a specific context of trade volume. We also illustrated on what extent the bias corrected and accelerated non-parametric bootstrap method produces different estimate of interest, as compared by non-parametric bootstrap method.

Key words : bootstrap, risk analysis, simulation, uncertainty

Introduction

If all the information that is critical to any probabilistic model is obtainable, then the outputs would not be subject to uncertainty. Instead, some input parameters even in this model are typically assigned a probability with uncertainty. In fact, researchers often confront uncertainties in many phase of modeling works. These can be attributed to structural uncertainty such as the specific problems of interest and scenario specification and model uncertainty such as parameters in the model, lack of representativeness at the time where a given task is to be performed, lack of reliability of empirical data, disagreement of experts, an even non-existence, or a combination of these [11, 15]. Furthermore, some inputs in the model are estimated using relatively small sets of sampled data, resulting in uncertainty in the estimates due to sampling error. Consequently these uncertainties in the simulation model may result in unrealistic risk

estimates. In this situation, parametric statistical methods whose characteristics are defined by one or more parameters or non-parametric techniques that do not assume a particular family of probability distributions are commonly used.

In the absence of any accurate knowledge of a population's distribution of interest, the distribution of a random sample taken from that population can be a guide to the distribution in that population [8, 10, 11]. Quantification of sampling error in a sample may be done using classical statistical techniques or numerical simulation methods [19]. The bootstrap method belongs to latter category and essentially employs re-sampling to model the unknown variables. This technique is increasingly being employed in the medical literature such as disease surveillance and modeling [9, 14, 18], reproductive performance [4], vaccine potency testing [1], molecular biology [13] as well as in diverse fields including economics [12], geology [3], and engineering [2].

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Where extensive data are not available, researchers try to use a variety of different distributions to approximate their data, often leading to substantial discrepancy in estimates and subsequent choice of distribution. In this respect, the aim of this study was to employ bootstrap method to quantify uncertainty of risk especially when only limited information is available. The authors used trade volume of chicken and pork meats officially imported during a specified period as an uncertainty parameter. This statistic can be considered highly variable that may be associated with changes in disease factors in exporting country, animal, seasonal or factors regarding with trade.

Materials and Methods

Data

The total amount of chilled or frozen chicken and pork meat imported in Korea was obtained from the National Veterinary Research and Quarantine Services and is shown in Table 1.

Data fitting

A variety of different models were fitted for observed data. Of these, the best 3 models (model 1-3) were presented, and the goodness-of-fit was tested by Anderson-Darling (AD) or Kolmogorov-Smirnov (KS) test.

Bootstrap model

The details of the bootstrap simulation procedures have been well chronicled by Efron [5, 6] and others [7]. Trade volume (bootstrap sample) was generated by iteration from the observed data to construct distribution for the sample. Sampling from that constructed distribution is repeated a large number of times until a stable distribution can be obtained. Non-parametric bootstrap models with no assumptions (RiskDuniform distribution) about the parent distribution and parametric bootstrap models (RiskNormal distribution) were constructed using Microsoft Excel (Microsoft, USA) and its add-in software, @Risk (Palisade, USA). Classical mean statistics from an assumed normal distribution were also presented using a Student-t distribution with $n-1$ (n = sample size) degree of freedom (df): Student $(n-1) \times SD / \sqrt{n}$ (mean), where SD and sqrt means standard deviation and square root, respectively. To consider the bias between the estimates

and the unknown true value and to improve the performance of bootstrap by transforming the cumulative percentiles, bias corrected and accelerated (BCa) proposed by Efron and Tibshirani [7] was used. The bootstrap uncertainty distributions were obtained from 1,000 iterations. For BCa method, 3,000 and 5,000 iterations were run to estimate the mean trade volume for chicken and pork meat data, respectively.

Results

As shown in Table 1, total amounts of imported chicken and pork meat were found to be highly variable by year. By fitting the raw data using @Risk Bestfit module, extreme value and exponential distribution were found to be the best fit for chicken and pork meat data, respectively. Two other possible distributions are presented for comparison purpose (Table 2). All distributions were satisfied with goodness-of-fit assessed by AD or KS test. The skewness was ranged 0-1.14 for chicken meat and 2.0-18.9 for pork meat data. The kurtosis showed even wider range.

In comparison with the classical models (range: 1.13×10^8 for chicken and 2.15×10^8 for pork meat) both bootstrap methods provided a narrower range of mean trade volume for chicken (range: 6.01×10^7 and 6.43×10^7 for parametric and non-parametric, respectively) and pork meat data (range: 1.02×10^8 and 8.96×10^7 for parametric and non-parametric, respectively) (Fig. 1). The results from the non-parametric bootstrap and BCa models are shown in Fig. 2.

Table 1. Amount (kg) of chilled or frozen chicken and pork meat officially imported to Korea for human consumption, during the period of 1998-2005

Year	Chicken	Pork
1998	11,753,000	55,683,000
1999	45,977,000	142,256,000
2000	66,335,000	96,645,000
2001	83,738,000	51,098,000
2002	97,324,000	45,184,919
2003	81,920,000	60,789,627
2004	23,556,000	76,793,744
2005	52,766,000	173,598,000

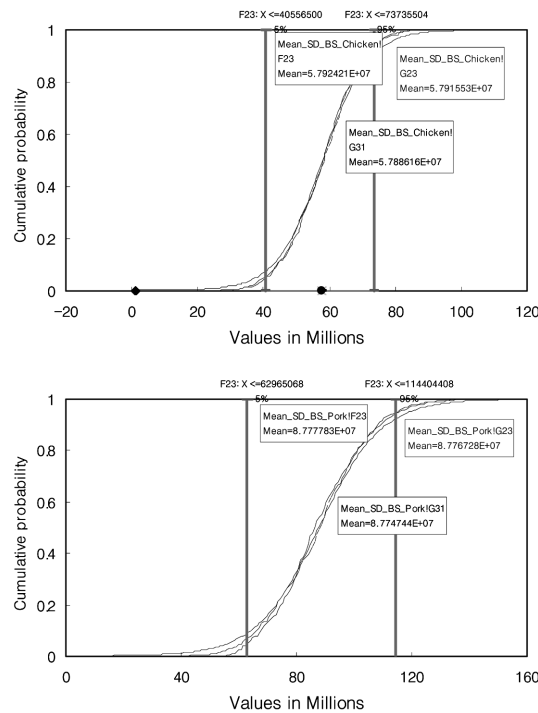
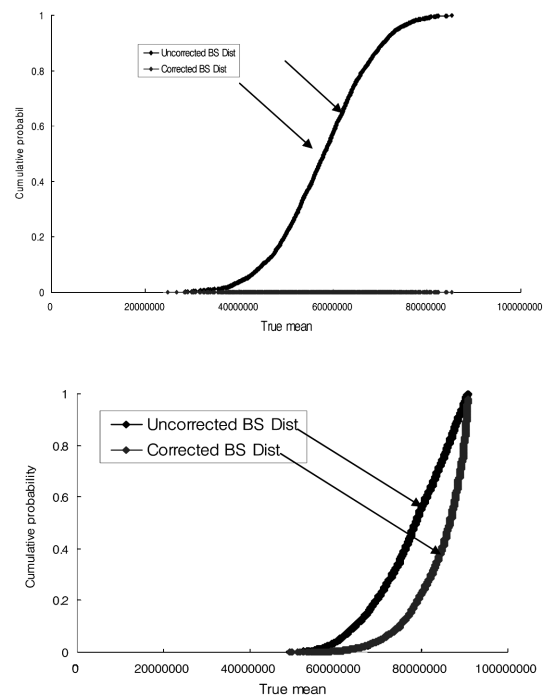
Table 2. Summary statistics fitted for chicken and pork meat data

Model ¹	Statistic				GOF ²	
	Mean	SD	Skewness	Kurtosis	S1	S2
[For chicken meat]						
Model 1	59,116,457	34,616,188	1.14	5.40	> 0.25	> 0.10
Model 2	59,151,954	30,927,538	0.00	4.20	> 0.25	> 0.10
Model 3	57,921,125	30,112,959	0.00	3.00	> 0.25	> 0.15
[For pork meat]						
Model 1	82,434,647	42,571,117	2.00	9.00	> 0.25	> 0.25
Model 2	87,756,036	63,064,005	3.97	29.3	NA ³	NA
Model 3	99,032,861	127,254,722	18.9	2141.7	NA	NA

¹For chicken data, model 1, 2, and 3 represent extreme value, logistic and normal distribution, respectively. For pork data, model 1, 2, and 3 represent exponential, inverse Gaussian, and lognormal distribution, respectively.

²GOF represents goodness-of-fit of the model, assessed by Anderson-Darling (S1) or Kolmogorov-Smirnov (S2) statistic.

³NA, not available.

**Fig. 1.** Results of mean statistics by the parametric and non-parametric bootstrap model and classical method for chicken (top) and pork meat (bottom) data.**Fig. 2.** Comparison of results from the non-parametric bootstrap (BS) and bias corrected and accelerated BS models for chicken (top) and pork meat (bottom) data.

Discussion

In a view of the fact that risk assessment is a tool aimed at predicting the probability of an outcome of a particular event by combining successive conditional

probability, the quantification of uncertainty of a true but unknown distribution of values has become an essential part in risk assessment modeling [11]. This is quite important in a model that some inputs are assigned a probability distribution with inherent

uncertainty. In addition, since the uncertain probability assigned to each step in a scenario pathway may have a large impact on the final estimate as a multiplicative effect and consequently on the conclusion drawn, it is essential to assure high credibility in it. As seen in our data, the degree of normality cannot be assumed in terms of the skewness and kurtosis, although three distributions were satisfied with goodness-of-fit by AD or KS test. Non-normality was particularly significant for pork meat data, indicating that classical approach could provide biased estimates and consequently over or under-estimate of final probability of interest. Where there are plentiful and representative data a probability distribution can be applied from either the parameters, which are derived by fitting empirical data to a theoretical distribution using parametric techniques, or directly from the data using non-parametric techniques [16]. In contrast, where data are very sparse the parameters used to specify a distribution is often subjected to be uncertain. In such cases the first choice is to use classical statistical techniques if the basic assumptions are correct.

However it is often difficult to appreciate the degree of inaccuracy even by using approximation. Thus, bootstrap simulation method could be applied as an alternative when other classical methods are not available. A key idea of this approach is that sampling with replacement should be repeated by randomly re-sampling a given set of data and computing the statistic of interest for each sample. The resulting set of values, bootstrap distribution provides an approximate sampling distribution for the statistic. This method was known to be useful especially when the data is small or non-Gaussian, and the confidence intervals calculated by using the bootstrap re-sampling technique are not subject to a restriction of symmetry, as is the Student-t distribution, making them much more versatile [10, 17, 19].

The result of parametric bootstrap approach together with that from applying the classical statistics method looks incidentally very similar to the non-parametric distribution (Fig. 1). Because of very small set of data in this study it is not easy to evaluate relative utility of these methods. However, bootstrap method was found to have narrower range compared to the classical method which was based on an assumed normal distribution to estimate mean trade volume. This result may suggest that bootstrap method provides an

alternative technique to assess the uncertainty about a parameter where classical statistics is not appropriate without recourse to determining a prior [20]. On the other hand, the bias defined as difference between the estimate using the original data and the estimate using the bootstrap sample is inevitable in predicting works. Like many other methods, the bootstrap also tends to underestimate the uncertainty and thus bias corrective measures such as BCa were proposed by Efron and Tibshirani [7]. This method is essentially assumes that for some unknown transformation, bias correction and skewness correction, the transformed estimator is normally distributed. This method is known to be the best correction procedure for overcoming the weakness of the bootstrap [20]. As seen in Fig. 2, the difference between the uncorrected and corrected distributions was relatively small for chicken, while there are some differences for pork meat data. This is in part due to the mean illustrating in this analysis is the most stable statistic for a given amount of data, and in part because the range of raw data was wider in pork meat (128,413,081) than chicken meat (85,571,000), although coefficient of variation was not quite different (53.5% vs. 51.9%).

Based on the findings in this study the authors conclude that when quantifying uncertainty point estimates may be different depending on the methods employed, indicating that more attention should be paid to the data underlying distributional choices. The bootstrap techniques in together with the classical parametric methods can be an alternative means, where appropriate. As far as possible perspectives are concerned, it would be worth while to investigate to what extent our approaches apply to other data sets with different characteristics. Another interesting development concerns the comparison between estimations of BCa method with the corresponding ones derived by means of other classical procedures assuming different fitting distributions. Lastly Bayesian bootstrap models need to be developed to improve an estimate to characterize a distribution.

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References

1. **Barnett PV, Statham RJ, Vosloo W, Haydon DT.** Foot-and-mouth disease vaccine potency testing: determination and statistical validation of a model using a serological approach. *Vaccine* 2003, **21**, 3240-3248.
2. **Birsan M, Molnar P, Burlando P, Pfaundler M.** Streamflow trends in Switzerland. *J Hydrol* 2005, **314**, 312-329.
3. **Brühlhart M, Traeger R.** An account of geographic concentration patterns in Europe. *Reg Sci Urban Econ* 2005, **35**, 597-624.
4. **Dohoo IR, Tillard E, Stryhn H, Faye B.** The use of multilevel models to evaluate sources of variation in reproductive performance in dairy cattle in Reunion Island. *Prev Vet Med* 2001, **50**, 127-144.
5. **Efron B.** Bootstrap methods: another look at the jackknife. *Ann Stat* 1979, **7**, 1-26.
6. **Efron B.** Better bootstrap confidence intervals. *J Am Stat Assoc* 1987, **82**, 171-185.
7. **Efron B, Tibshirani RJ.** An Introduction to the Bootstrap. pp. 1-436, Chapman & Hall/CRC, New York, 1993.
8. **Gleason JR.** Algorithms for balanced bootstrap simulations. *Am Stat* 1988, **42**, 263-266.
9. **Heinze G, Schemper M.** Comparing the importance of prognostic factors in Cox and logistic regression using SAS. *Comput Methods Programs Biomed* 2003, **71**, 155-163.
10. **Henderson AR.** The bootstrap: a technique for data-driven statistics. Using computer-intensive analyses to explore experimental data. *Clin Chim Acta* 2005, **359**, 1-26.
11. **Hoffman FO, Hammonds JS.** Propagation of uncertainty in risk assessments: the need to distinguish between uncertainty due to lack of knowledge and uncertainty due to variability. *Risk Anal* 1994, **14**, 707-712.
12. **Lesnoff M, Lancelot R, Tillard E, Dohoo IR.** A steady-state approach of benefit-cost analysis with a periodic leslie-matrix model. Presentation and application to the evaluation of a sheep-disease preventive scheme in Kolda, Senegal. *Prev Vet Med* 2000, **46**, 113-128.
13. **Lew AE, Gale KR, Minchin CM, Shkap V, de Waal DT.** Phylogenetic analysis of the erythrocytic *Anaplasma* species based on 16S rDNA and GroEL (HSP60) sequences of *A. marginale*, *A. centrale*, and *A. ovis* and the specific detection of *A. centrale* vaccine strain. *Vet Microbiol* 2003, **92**, 145-160.
14. **Mannelli A, Mandola ML, Pedri P, Tripoli M, Nebbia P.** Associations between dogs that were serologically positive for *Rickettsia conorii* relative to the residences of two human cases of Mediterranean spotted fever in Piemonte (Italy). *Prev Vet Med* 2003, **60**, 13-26.
15. **Mokhtari A, Moore CM, Yang H, Jaykus LA, Morales R, Cates SC, Cowen P.** Consumer-phase *Salmonella enterica* serovar enteritidis risk assessment for egg-containing food products. *Risk Anal* 2006, **26**, 753-768.
16. **OIE (World Organisation for Animal Health).** Handbook on Import Risk Analysis for Animals and Animal Product: Quantitative risk analysis. Vol 2. pp. 67-73, OIE, Paris, 2004.
17. **Oviedo M, Muñoz MP, Domínguez A, Carmona G.** Estimated incidence of hepatitis A virus infection in Catalonia. *Ann Epidemiol* 2006, **16**, 812-819.
18. **Pawitan Y, Griffin JM, Collins JD.** Analysis and prediction of the BSE incidence in Ireland. *Prev Vet Md* 2004, **62**, 267-283.
19. **Rodgers JL.** The bootstrap, the jackknife, and the randomization test: a sampling taxonomy. *Multivariate Behav Res* 1999, **34**, 441-456.
20. **Vose D.** Risk Analysis: A Quantitative Guide. 2nd ed. pp. 181-200, John Wiley & Sons, New York, 2000.