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Bootstrap Inference for Choice-Based Conjoint Analysis

Eduardo C. Barbosa[1], Alice dos S. Ribeiro[1], Jhennifer dos S. Nascimento[1], Luciano G. Batista[1†], Carlos Henrique O. Silva[1], Suzana Maria Della Lucia[2], Valeria Paula R. Minim[3], Kamila A. de Oliveira[4], Paulo César Emiliano[1], Lucas P. Belo[1]

[1] *Department of Statistics, Federal University of Viçosa, Minas Gerais, Brazil.*
[2] *Agrarian Sciences Center, Federal University of Espirito Santo, Espirito Santo, Brazil.*
[3] *Food Technology Department, Federal University of Viçosa, Minas Gerais, Brazil.*
[4] *Agricultural engineering Department, Federal University of Maranhão, Maranhão, Brazil.*

Abstract: *This article aims to present an application of Choice-Based Conjoint Analysis (CBCA) with additional inferences for the Choice Probabilities of each treatment and for the Choice Ratios, made through their empirical distributions obtained via bootstrap. This study involved three attributes and eight treatments (light strawberry-flavored yogurt) in a full factorial design. By accessing the empirical distribution of the probabilities and choice ratios, it was possible to make inferences about such quantities, something that is not trivial in the frequentist context. Additionally, bias and standard error values were obtained for the Choice Probabilities and Choice Ratios, making it possible to assess the precision of these estimates, build confidence intervals, and conduct statistical comparisons on these.*

Keywords: *Paired bootstrap; Light yogurt; Free software R.*

Introduction

The Choice-Based Conjoint analysis (CBCA) originated from the studies of Louviere and Woodworth (1983), who combined the experimental concepts of traditional conjoint Analysis (LUCE & TUKEY, 1964) with the econometric models of discrete choice, more specifically, the Multinomial Logit model, initially derived by Luce (1959) and entirely specified by McFadden (1974). Afterward, in marketing – the field that predominantly uses it - other research studies were developed (KAMAKURA & SRIVASTAVA (1984), JOHNSON & OLBERTS (1991), KOELEMEIJER & OPPEWAL (1999), MOORE, LOUVIRE & VERMA (1999)), which disclosed and consolidated this methodology.

More specifically, the CBCA model use the choice of the individuals (or dependent variables) like a aproximation for the utility (benefit or satisfaction) assigned to a given treatment (product, service, and concept). The multinomial logit model divides this utility into partial utilities (independent variables) (MCFADDEN, 1974). Later, the parameters for this model are estimated and used to calculate the probabilities of choice within the set of treatments. Interpreting the estimated parameters is not trivial because the model employed in the treatment is not linear. Therefore, a significant result is the Ratio of Choice for each attribute, which shows how likely it is to choose a given attribute over the others (GREENE, 2017).

Additionally, beyond its traditional applications in marketing, CBCA has found use in various fields of knowledge, particularly in food technology. This methodology has evaluated consumer preferences towards new food products and product labels, and it is a more realistic and practical approach when it comes to real purchase scenarios because the consumer does not need to assign a rating to each treatment, which is far less tiresome (MOORE, 2004). The reader may check some of these applications in Lockshin *et al.* (2006), Della Lucia *et al.* (2010), Deliza *et al.* (2010), Tempesta *et al.* (2010), Szücs *et al.* (2014) and Meyerding (2016).

[†] Autor correspondente: luciano.batista@ufv.br
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Nevertheless, several researchers still adopt the Ratings-Based Conjoint Analysis (RBCA) to evaluate consumer preferences under the premise that this is the most informative approach since a set of ratings provides more information than a single choice (MOORE, GRAY-LEE, & LOUVIERE (1998), KARNIOUCHINA *et al.*, (2009) AND ASIOLI *et al.*, (2016)). In this sense, to try to make CBCA popular and improve the preference structure modeling, other frequentist approaches were proposed, such as the Dogit Multinomial model (GAUDRY & DAGENAIS, 1979), which allows the grouping of individuals who have made the same decision (individuals whose preference is independent of the treatments), and the Logit Sequential model (MCFADDEN, 1978), which makes possible for individuals to make decisions or choices hierarchically. Moreover, the latent class models (DESARBO, RAMASWAMY, & COHEN, 1995) and the Adjusted Heterogenous Logit Model (CHESHER & SANTOS SILVA, 2002) allow one to evaluate the influence of heterogeneity on the individuals' choices.

However, in none of these methods is it possible to infer about the probability of the choice alternatives or about the Ratio of Choice, that is, testing hypotheses or making statistical comparisons about such amounts, given that only their punctual estimations are known. Hence, the absence of such inferences, besides making CBCA less informative, may result in misleading conclusions since one must assess the variability of their respective estimators. More specifically, one may consider, wrongly, choice alternatives with equal statistically probabilities like different, only analysing the single-point estimations. Naturally, if the cost of each of these treatments is relatively different, a mistaken decision may cause unnecessary expenses to the manager.

Therefore, this work proposes applying the bootstrap method (EFRON, 1979) to CBCA. In addition to the traditional analysis, this approach will make it possible to explore the empirical distribution of the probabilities / Ratio of Choice and infer about such amounts, which by the frequentist approach is a very difficult task. To do so, the data used in this study come from an actual experiment (DELLA LUCIA *et al.*, 2010) conducted with 144 individuals and eight treatments.

Material and methods

Analyzed experimental data

This study comprised $N = 144$ individuals residing in the city of Viçosa (Minas Gerais, Brazil) and $R = 3$ attributes: information on sugar content ("Sugar"), information on Fat content ("Fat") and information on Protein content ("Protein") at the following levels: sugar ("0% sugar" and "with sweetener"), fat ("0% fat" and "low-fat") and protein ("enriched with whey protein" and "enriched with bioactive proteins"). The complete factorial design was employed in this study, with $J = 8$ treatments, as displayed in Table 1. Della Lucia et al. (2010) provides additional details on the experiment's methodology.

Table 1: Design of the treatments under study.

Treatment	Sugar	Fat	Protein
1	0% sugar	0% fat	Whey protein
2	Sweetener	0% fat	Whey protein
3	0% sugar	Low-fat	Whey protein
4	Sweetener	Low-fat	Whey protein
5	0% sugar	0% fat	Bioactive proteins
6	Sweetener	0% fat	Bioactive proteins
7	0% sugar	Low-fat	Bioactive proteins
8	Sweetener	Low-fat	Bioactive proteins

Source: from the authors (2024).

Choice-Based Conjoint Analysis (CBCA)

In CBCA, Equation (1) defines the model for random utility.

$$U = X\beta + \varepsilon, (1)$$

in which:

- $U = \left(U_{11} \ldots U_{1J} U_{21} \ldots U_{2J} \ldots U_{N1} \ldots U_{NJ}\right)'$ is the vector $(NJx1)$ of the random utilities (latente or not measured variables) associated with J treatments, as assigned by the N individuals.
- $X = \left[X_1 X_2 \ldots X_N\right]'$ in which $X_1 = X_2 = \ldots = X_N$ are matrices or submatrices of X with dimensions (J x R) that specify the coding of the s^{th} level of the r^{th} attribute in the j^{th} treatment. For $n = 1, 2, \ldots, N$ we have:

$$X_n = \left[X_1^1 X_2^1 \ldots X_R^1 X_1^2 X_2^2 \ldots X_R^2 \vdots \vdots \ldots \vdots X_1^J X_2^J \ldots X_R^J\right]$$

- $\beta = \left(\beta_1 \beta_2 \ldots \beta_R\right)'$ is the vector of unknown parameters (or preference coefficients) with dimensions (R x 1), in which $\beta_r$represents the effect of the r^{th} attribute on the mean random utility.

- $\varepsilon = \left(\varepsilon_{11} \ldots \varepsilon_{1J} \varepsilon_{21} \ldots \varepsilon_{2J} \ldots \varepsilon_{N1} \ldots \varepsilon_{NJ}\right)'$ is the vector (NJ x 1) of random, non-observable errors in the model, supposing that each ε_{nj} is independent, has a distribution of extreme type I values, or Gumbel, with a null mean and constant variance of $\frac{\pi^2}{6}$, constrain which is defined so the model may be identifiable[1] (TRAIN, 2009).

Model (2) or Multinomial Logit (MCFADDEN, 1974) is derived supposing that the n^{th} individual will choose the j^{th} treatment, if, and only if, $U_{nj} > U_{nk}$, $\forall_{j \neq k; j,k \in \{1,2,\ldots,J\}}$. Therefore:

$$P(X) = \frac{e^{X_j \beta}}{\sum_{k=1}^{J} e^{X_k \beta}}, (2)$$

1 A model is considered globally identifiable if there is a maximum value for likelihood for a single set of estimations. Otherwise, restrictions should be imposed on specific parameters so the model may become identifiable.

where, the probability $P(X)$ represents the probability of the n^{th} individual choosing the j^{th} treatment. Because the matrix $\boldsymbol{X}$ is the same for $n=1,2,\ldots,N$, $P(X)=P(X)$ (this occurs because the probability estimates for each treatment are considered approximately the same for all individuals in the sample, since the preference or taste of individuals is treated as homogeneous in this methodology). The parameter estimators of the model (2) are obtained by maximum likelihood, maximizing the natural log of $L(\beta)$ in (3), that is, $l(\beta)=\ln\left[L(\beta)\right]$, through the Netwon-Raphson method (GALLANT, 2009).

$$l(\beta)=\ln\left[\prod_{j=1}^{J}\left(\frac{e^{X_j\beta}}{\sum_{k=1}^{J}e^{X_k\beta}},(3)\right)^{\square}\right]$$

in which, n_j is the variable that shows the number of times that the j^{th} treatment was chosen. The contribution or effect of the levels of each attribute on the choice of individuals is assessed by the Choice Ratio (GREENE, 2017), a measure defined by the ratio between two distinct probabilities, as shown in (4)

$$RE_r(X_p,X_q)=\frac{P(X)}{P(X)}=e^{\left(X_r^p-X_r^q\right)\beta_r},\ \forall_{r=1,\ldots,R}(4)$$

in which treatment q is obtained from treatment p, fixating (r – 1) levels of r atributes or altering the level of a single characteristic only. Therefore, it is possible to interpret that if:

$$\{\ \mathcal{R}>1\quad P(X)>P(X)\ \mathcal{R}=1\quad P(X)=P(X)\ \mathcal{R}<1\quad P(X)<P(X)$$

Note that $C=(m2)$ Ratios of Choice will be estimated for an attribute with $m\geq 2$ levels, in which (.) indicates a simple combination. We also point out that *RE* is constant and depends solely on the characteristics of treatments p and q. Hence, removing or including other treatments does not alter its proportionality, which is particular to the Multinomial Logit Model, denominated by I.I.A. (Independence of Irrelevant Alternatives) and ensured by the independence of random errors (TRAIN, 2009).

Basic principles of Non-parametric Bootstrap

Consider $y=(y_1y_2\ldots y_n)'$ as the set of observed values which represents a realization of the random variable $Y=(Y_1Y_2\ldots Y_n)'$, arising from a population with unknown distribution and indexed by parameter θ, that is, $F(y,\theta)$. For simplicity, adopt θ as a scalar, although it can be represented as a vector. Admit the interest in knowing the sample distribution of statistics $\theta^{\square}t(y)$, used to estimate $\theta=t(Y)$. After applying the Bootstrap method, with repositioning, K new data sets are obtained: $y_k=(y_1y_2\ldots y_n)$, with $k=1,2,\ldots,K$. If for each k^{th} bootstrap re-sample or replica the statistics $\theta^{\square}t(y)$ is estimated, that is, $\theta_k^{\square}=t(y_k^{})$, then the Bootstrap distribution of $\theta^{\square}$ or the empirical distribution of $\theta^{\square}$ can be accessed. This distribution is considered an estimation of the sample distribution of $\theta^{\square}$ (FOX & WEISBERG, 2011). Therefore, histograms, position, and dispersion

measurements can be used to explore it, while confidence intervals and hypothesis tests can be elaborated or run to assess parameter θ. In general, the primary calculated measurements are Bootstrap mean (5), variance (6), mean standard deviation (7), and bias (8):

$$\theta_B^{\square} = \underline{\theta^{\square} = E^{\square}}$$
$$Var^{\square}$$
$$EP^{\square}$$
$$B^{\square}$$

There are several Bootstrap confidence intervals. The reader may check for further details in Efron and Tibshirani (1993) and Chernick and LaBudde (2014). In this work, we have only employed the Percentile Bootstrap interval, which uses the empirical quantiles of the distribution $\theta^{\square}$ to obtain the respective upper and lower limits. Therefore, let us consider that each $\theta_{(1)}^{\square}\theta_{(2)}^{\square}\ldots,\theta_{(K)}^{\square}$, so that $\theta_{(1)}^{\square}\theta_{(2)}^{\square}?<\ldots<\theta_{(K)}^{\square}$, represents the k[th] statistics of the order of distribution $\theta^{\square}$. Hence, the interval with $100(1-\alpha)\%$ of confidence for parameter θ is defined as shown in (9) (EFRON, 1981):

$$IC_{(1-\alpha)}(\theta) = ¿$$

in which $L = / \frac{(K+1)\alpha}{2} /$, $U = / (K+1)\left(1-\frac{\alpha}{2}\right) /$ and $/\ x\ /$ represents the highest whole number less than or equal to x.

Paired Bootstrap Method in CBCA

Assume the $y = (y_{11}\ldots y_{1J}\, y_{21}\ldots y_{2J}\ldots y_{N1}\ldots y_{NJ})'$ represents the vector comprised by NJ response variables (dependent variables) or observed choices (1 if the j[th] treatment was choose for the n[th] individual and 0 if not) and that $X_n^j = \left[X_1^j X_2^j \ldots X_R^j\right]$ represents the line vector in the design matrix $\boldsymbol{X}$, referring to the n[th] individual and consisting of the coding of the levels in the j[th] treatment. In the Paired Bootstrap method, resampling occurs in pairs $\left(X_{nj}^{\square}; y_{nj}^{\square}\right)$, and each of these pairs is considered to have come from a conjoint distribution or a bivariate probability distribution ($\boldsymbol{X}$; $\boldsymbol{Y}$). This approach is also known as Random-X Resampling or Cases Resampling (DAVISON & HINKLEY, 1997). The used algorithm is defined as follows (EFRON & TIBSHIRANI, 1993):

i. Randomly select with replacement the NJ pairs of values $\left(X_{nj}^{\square}; y_{nj}^{\square}\right)$ for $n = 1,2,\ldots,N$ and $j = 1,2,\ldots,J$, which will compose the first Bootstrap replica, according to the following rule;

$$\{ X_{nj}^{\square} = X_n^j \; y_{nj}^{\square} = y_{nj}$$

ii. Adjust the Multinomial Logit Model to the dataset obtained from step i., estimate its parameters, the treatment probabilities, and the Ratios of Choice of each attribute, as mentioned in section 2.2;

iii. Repeat steps i. and ii. K times to obtain the empirical distribution or Bootstrap of the statistics of interest.

Computational Aspects

In our statistical analyses, we leveraged the capabilities of the open-source R software (R CORE TEAM, 2017). The parameters of the Multinomial Logit Model were estimated using the *clogit* function from the *survival* package (THERNEAU, 2012). The treatment designs were crafted using the *expand.grid* and *caEncodedDesign* functions available in the *Conjoint* package (BAK & BARTLOMOWICZ, 2012). The Paired Boostrap was executed using the *boot* function from the *boot* package (DAVISON & HINKLEY, 1997). For deriving Bootstrap percentile confidence intervals, the *boot.ci* function from the same package was employed, utilizing the *perc* argument.

The Shapiro and Wilk test (1965) was applied with a significance level set at *5%* probability to evaluate hypotheses of normality on the empirical distributions of the treatment Probabilities and the Ratios of Choice for the attributes.

Results and discussion

In Table 2 are the estimations of mean, bias, and Bootstrap standard deviation for the parameters of the CBCA model. We used a total of K = 1999 replicas to build the empirical distribution of each estimator.

Table 2: Estimations and statistics[1] provided by the Paired Bootstrap method.

Attribute	β_B	$\hat{\mathrm{B}}\ (\hat{\beta}^*)$	$\hat{EP}(\hat{\beta})^*$
Sugar	-1.6759	-0.0156	0.2181 (0.2274)
Protein	1.5241	0.0115	0.2061 (0.2166)
Fat	-0.7918	-0.0033	0.1602 (0.1797)

Source: from the authors (2024).
Legend: Values in parentheses represent classical standard error estimates.

Note that the estimations for mean Bootstrap showed low bias and standard error, which is desirable because it demonstrates that we can use this measurement as an estimator for the effect of the attributes under study. Della Lúcia *et al.* (2010) found similar results when running CBCA on the same data when estimating the parameters of the Multinomial Logit model by Maximum Likelihood (ML). The bootstrap method provided standard error estimations quite close to the traditional ones; however, for non-linear models, the proposed approach is the most adequate to quantify the uncertainty of the estimations, given that the linear approximations (Delta Method), traditionally used, may be inadequate at the presence of outliers, significant dispersion of data or small samples.

In Table 3 are the Percentile Bootstrap intervals for the parameters of the CBCA model. In this Table, $\beta^{\square}_{(50)} e\, \beta^{\square}_{(1950)}$represent the order statistics of the empirical distribution of each $\beta^{\square}$, which accumulate 2.5% and 97.5% of probability, respectively. We also presented the traditional 95% confidence interval based on the Standard Normal distribution and determined the amplitude of these intervals *(A)* as a comparison criterion.

[1] In which ^B, B^^ and EP^^ represent the estimations for mean, bias, and standard error Bootstrap, respectively.

Table 3: Intervals based on the Standard Normal distribution and Percentile Bootstrap intervals.

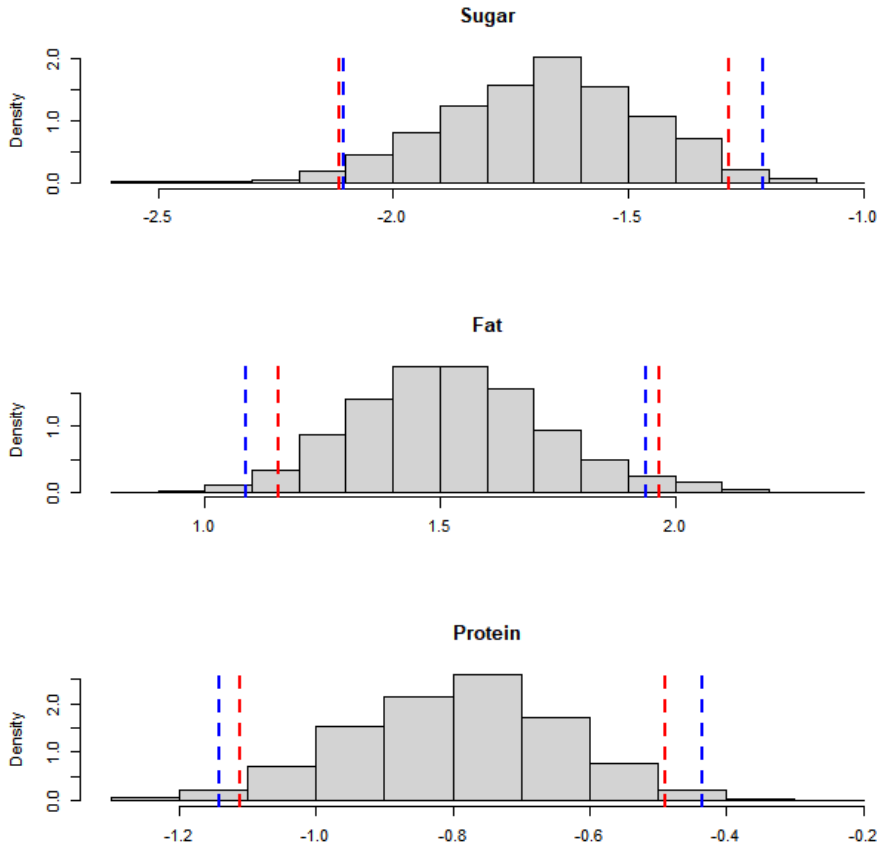
	Percentile *Bootstrap*			Standard Normal		
Attributes	$\hat{\beta}_{(50)}^{*}$	$\beta_{(1950)}^{*}$	*A*	*L*	*U*	*A*
Sugar	-2.1377	-1.2833	0.8544	-2.1061	-1.2144	0.8917
Protein	1.1514	1.9836	0.8322	1.0879	1.9372	0.8492
Fat	-1.1108	-0.4875	0.6233	-1.1408	-0.4360	0.7047

Source: from the authors (2024).

With the Percentile Bootstrap confidence intervals, it is possible to infer the statistical significance of the Sugar, Protein, and Fat attributes. We assess whether the zero value belongs to the respective intervals to obtain this decision. This result coincides with the one found by Della Lúcia *et al.* (2010) via the Wald test (1943), where its nullity statistical hypothesis $\left(H_0: \beta = 0\right)$ was rejected at 5% probability for all three attributes under study. So, it is possible to conclude that the sugar, protein, and fat content information presented in the light strawberry yogurt labels influences consumers' choices.

It is also possible to observe that the Percentile Bootstrap interval provided an amplitude very close to the traditional interval. We expected this, given that the sample distribution of the estimator of Maximum Likelihood converges asymptotically towards a normal distribution, that is, Np^−dN0,−H−1 in which *H* and (-*H*) represent the expected Hessian matrix and the expected Fisher information matrix, respectively (TRAIN, 2009). Therefore, it is hope that the empirical distributions behave likewise. However, the Shapiro-Wilk test rejected the hypothesis of normality for both Bootstrap distributions (p-value ≈ 0), and for this reason we observed some differences in the range of the percentile and normal intervals. Figure 1 displays the respective probability histograms. The red lines indicate the lower and upper limits of the Percentile Bootstrap intervals, and the blue lines represent the interval limits based on the Standard Normal distribution.

Figure 1: Histogram of the empirical distributions of the estimators of the CBCA model.



Source: from the authors (2024).

In Table 4 are the estimations for the Probabilities of Choice of the set of treatments under analysis and the other statistics provided by the Paired Bootstrap method.

Table 4: Estimations and Bootstrap statistics for the Probabilities of Choice.

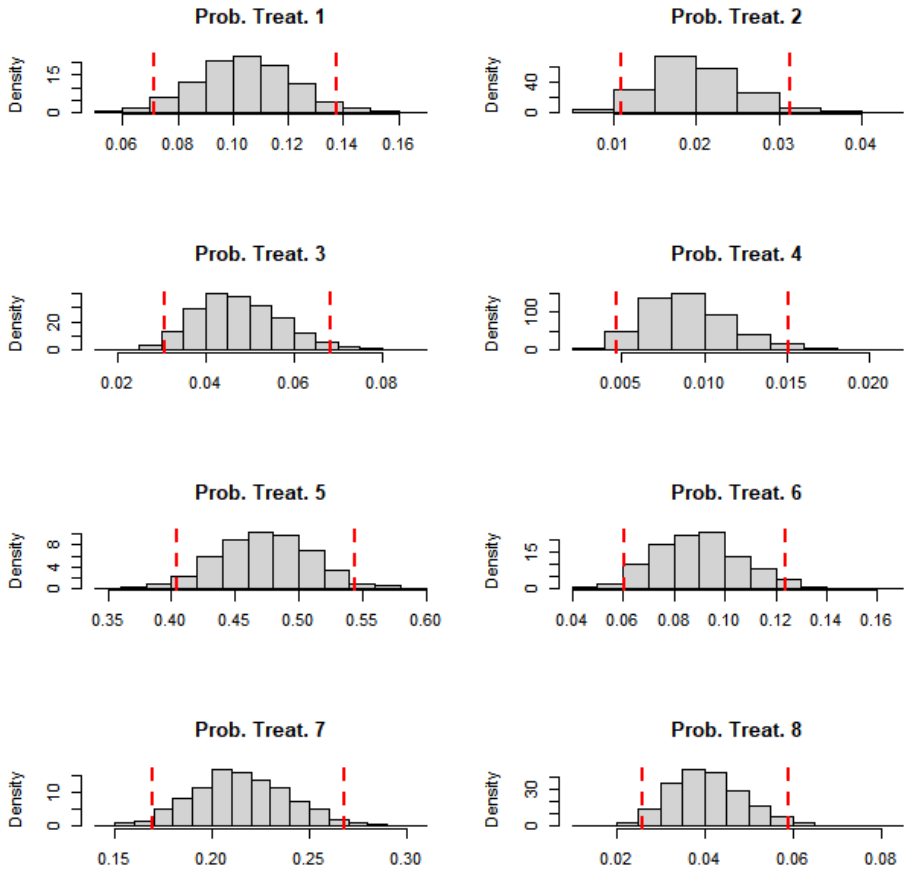
Treatment	p_B	$\hat{B}$	$EP(p^*_j)$	$\hat{P}_{j(50)}$	$\hat{P}_{j(1950)}$
1	0.1043	0.00001	0.0177	0.0687	0.1400
2	0.0199	0.00006	0.0052	0.0109	0.0316
3	0.0475	0.00012	0.0096	0.0295	0.0679
4	0.0091	0.00007	0.0026	0.0047	0.0149
5	0.4731	-0.00024	0.0354	0.4056	0.5421
6	0.0899	-0.00014	0.0165	0.0590	0.1230
7	0.2152	0.00006	0.0253	0.1681	0.2676
8	0.0409	0.00004	0.0087	0.0248	0.0593

Source: from the authors (2024).

It is possible to conclude that the highest Probability of Choice (0.4731) is associated with treatment 5, with the following characteristics: 0% sugar, 0% fat, and bioactive proteins. On the other hand, Treatment 4 (with sweetener, low-fat content, and whey protein) had the lowest Probability of Choice (0.0091). Della Lucia (2008) obtained the same result with Ratings-Based Conjoint Analysis, estimating positive coefficients of preference (which increased preference rate) for the levels present in treatment 5 and negative preference coefficients (which decreased preference rates) for the levels present in treatment 4.

In addition to low bias, the mean Bootstrap estimations for probabilities of choice also meet the probabilistic axioms of Kolmogorov (2018), which is fundamentally importance. Furthermore, with the Percentile Bootstrap intervals, it is possible to conclude, for example, that the Probability of Choice for treatment 5 and treatment 7 are statistically different because the limits of these intervals do not overlap. On the other hand, the Probability of Choice for treatment 1 and 6 are statistically equal. Note that 26 similar comparisons may still be made two by two. Therefore, in a corporate context, these additional inferences offer higher confidence to managers during decision-making processes or before investments, because the conclusions will not be based solely on mathematical differences but on probabilistic information. Figure 2 displays the histogram of probability with the respective empirical distributions. According to the Shapiro-Wilk test, only the distribution of the Probability of Choice for treatment 7 is considered approximately normal for 5% of signficance (p-value = 0.051).

Figure 2: Histogram of the empirical distributions of the Probabilities of Choice of treatments.



Source: from the authors (2024).

To infer about the effect of levels of each attribute on the consumer's choice, Table 5 shows the Ratio of Choice estimations and the results provided by the Paired Bootstrap method.

Regarding Sugar attribute, the mean Bootstrap estimation for the Ratio of Choice demonstrates that a treatment with "0% sugar" is 5.5217 times more likely to be chosen over a treatment "with sweetener". As for the Fat attribute, a treatment with "0% fat" is 2.2631 times more likely to be chosen over a "low-fat" treatment. Lastly, for the Protein attribute, the treatment with "bioactive proteins" is 4.7090 times more likely to be chosen over a treatment with "whey protein".

Table 5: Estimations and Bootstrap statistics of the Ratio of Choices for each attribute.

Attribute	$\hat{\Re}_B$	$\hat{B}(\hat{\Re})$	$\hat{EP}(\hat{\Re})$	$\hat{\Re}_{(50)}$	$\hat{\Re}_{(1950)}$
Sugar	5.5217	0.2608	1.3858	3.5609	8.8897
Fat	2.2631	0.0031	0.3749	1.6515	3.1034
Protein	4.7090	0.1705	1.0252	3.1670	7.2269

Source: from the authors (2024).

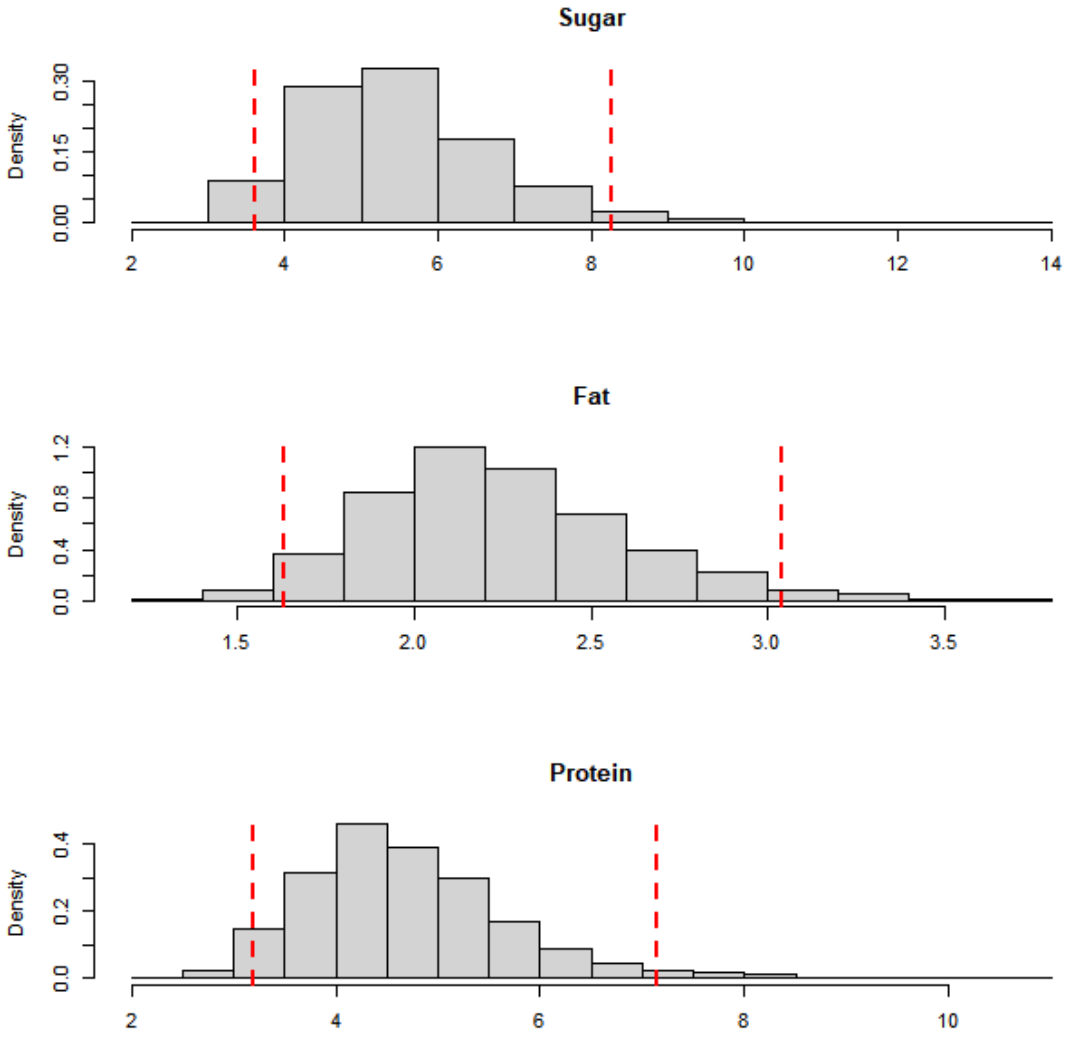
Reis (2007) observed, using Ratings-Based Conjoint Analysis, that the level "with sweetener" also harmed the consumer's preference rate as opposed to the level "No sugar". However, the interviewed consumers seem to prefer products with no fat. Della Lucia (2010) explained that the negative aspect associated with the term "whey protein" may be related to the not-so-pleasant sensory characteristics of this level, differently from the term "bioactive proteins", which is associated with a healthier food product, justifying its higher acceptance.

As observed before, the analysis of the Percentile Bootstrap intervals for the Ratio of Choice corroborates the statistical significance of the attributes since the unit value is not within the respective limits for each interval. In other words, it is as if we tested $H_0: RE_r = 1 \ \forall_r$ against $H_1: RE_r \neq 1 \ \forall_r$, deciding about the rejection of zero hypotheses for r = 1, 2, and 3. In addition, in studies in which at least one of the attributes consists of more than two levels, it will be possible to evaluate the ratios of choice in each attribute[1], given that statistical tests, such as Wald's (1943), traditionally applied in the frequentist analysis of CBCA, only inform whether the effect of an attribute is different from zero or not.

Figure 3 illustrates the probability histogram for the empirical distributions of these numbers. The Shapiro-Wilk test rejected the hypothesis of normality for both Ratios of Choice (p-value ≈ 0), given that such distributions are asymmetrical to the right.

[1] An attribute with *m* levels provides m 2 ratios of choice, in which (.) represents a simple combination. Therefore, if *m* = 2, we have a single *RE* that compares levels a1,a2 of an attribute *A*. However, if *m* = 3, then *RE* = 3, because the levels of attribute *A* will be compared 2 by 2, that is, (a1,a2),(a1,a3),(a2,a3).

Figure 3: Histogram of empirical distributions of Ratios of Choice for each attribute.



Source: From the authors (2024).

Conclusions

In addition to offering more precise punctual estimations, the Paired Bootstrap method allowed us to assess the empirical distribution of probabilities of choice alternatives and ratios of choice and to make statistical inferences about these quantities. Under the frequentist approach, similar results are very difficult to obtain, since deriving the standard error of the probability and choice ratio estimators or accessing the respective estimators' sample distribution is not a trivial task. Hence, it was possible to conclude the superiority and the statistical equivalence between the probabilities of choice for specific treatments. This conclusion may help managers determine which treatments should receive investment or be removed from the market during commercial decision-making.

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