Estimation of a Measure of Skewness Taking the Median as the Axis of Symmetry

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Abstract: *Skewness is a property defining the shape of a distribution, with various methods available for its measurement. A recent proposal by Gunver, Senocak, and Vehid, denoted as g_{GSV}, utilizes the median as the axis of symmetry. The first objective of this article is to develop a script for point and interval estimation of g_{GSV} using the R program. Bootstrap confidence intervals are computed using percentile and bias-corrected and accelerated percentile methods. The script also includes skewness evaluation through bootstrap probability and visual examination of distribution via a box plot and histogram. To illustrate, the script is applied to a random sample conforming to a logistic distribution. The second objective is to establish interpretive symmetry rules for g_{GSV}, accomplished by generating bootstrap confidence intervals at 90%, 95%, and 99% from 34 population-samples of various sizes following a standard normal distribution. A third objective is to analyze the relationship of g_{GSV} with quartile and percentile skewness coefficients, and jackknife acceleration. It is concluded that g_{GSV} can be interchanged with the percentile skewness coefficient. Moreover, if variable X adheres to a normal distribution or satisfies the conditions of the central limit theorem, the sampling distribution of $g_{GSV}(x)$ converges to normality.*

Keywords: shape measure, skewness, confidence interval, bootstrap, R program.

1. Introduction

The shape of the distribution is described by measures of skewness, peakedness, tailedness, and kurtosis. Skewness measures whether the two parts of the cumulative distribution function, when divided by a (symmetry) axis defined by a measure of central tendency (arithmetic mean, median, mid-range, interquartile mean or mode), are equal or dissimilar. If the part of the scores to the left of the symmetry axis is longer than the other part, there is left-tailed or negative skewness. Conversely, if the part of the scores to the right of the symmetry axis is longer than the other part, there is right-tailed or positive skewness. If both parts are equal, there is symmetry [1].

The measurement of skewness has traditionally been proposed for continuous random variables [2], which is the subject of the present article. However, it also applies to ordinal variables [3−4], and there is even an approach for measuring this property of the shape with variables measured on a nominal scale [5−6].

There are several approaches to the measurement of skewness [7−9]. One is the standardized distance between the mode and the arithmetic mean, $(m − mo) / sd$ [10], or between the median and the arithmetic mean, $(m − mdn) / sd$ [11]. Both measures take the arithmetic mean as their axis of symmetry. They are based on the relationship between the median and a single mode with the arithmetic mean. If there is symmetry, the three central tendency statistics coincide. If there is positive or right-tailed skewness, the arithmetic mean is greater than the median and mode. If there is negative or left-tailed skewness, the arithmetic mean is smaller than the median and mode [4]. A related proposal is Singh, Gewali, and Bativada's [12] area asymmetry or difference between the cumulative probability of the mean and the median.

On the other hand, there are measures based on Pearson's

standardized third central moment [11] and Fisher's standardized third cumulant [13]. These measures yield a value of zero when symmetry is present; they are positive when the right tail is greater than the left tail, and negative when the left tail exceeds the right tail. Moreover, the greater the disparity between the tails, the larger the absolute value of both coefficients.

Furthermore, we have Bowley's quartile skewness coefficient [14], Hinkley's percentile skewness coefficient [15], Groeneveld and Meeden's integrated quantile skewness coefficient [16], and Altinay's coefficient of skewness [17]. This set of statistics uses the median as the axis of symmetry, dividing the difference between two shoulder or parts of the distribution: (right quantile − median) − (median − left quantile) by its maximum: right quantile − left quantile, resulting in values ranging from −1 to 1. These measures are interpreted similarly to the previously mentioned skewness measures.

A similar approach is the measure developed by Eberl and Klar [18], which is based on expectiles instead of quantiles. The concept of expectile, or expected quantile, was introduced by Newey and Powell in 1987 within the context of least squares quantile regression, also known as asymmetric least squares regression [19]. The expectile of order p is denoted by e_p, where p represents the cumulative probability value up to that point. It is obtained by minimizing the asymmetric quadratic loss function given in Equation 1 [20].

$$y = \{y_i\}_{i=1}^n = \{y_1, y_2, \ldots y_n\} \in Y$$

$$\min_{\substack{e_p \in \mathbb{R} \\ p \in [0,1]}} \left\{ \sum_{i=1}^n w_i (y_i - e_p)^2 \right\} \quad (1)$$

$$w_i = \begin{cases} 1 - p & y_i < e_p \\ p & y_i \geq e_p \end{cases}$$

Linked to this third group are Kelley's [21−22] absolute

asymmetry index or distance between the mid-percentile range and the median, $q_{0.5} - (q_{0.1} + q_{0.9})$ /2, and Kelley's dimensionless asymmetry index. The latter is derived by dividing the absolute index by the median, resulting in $1 - (q_{0.1} + q_{0.9}) / q_{0.5}$. In these two indices, negative values correspond to right-tailed skewness, while positive values indicate left-tailed skewness, in contrast to the coefficients observed previously.

Another proposal is Hogg's [23] adaptive and robust measure of skewness, which relies on the interquartile mean (mean truncated at 25%) and the 5% averages of the data at each end of the cumulative distribution function. This measure is derived from the ratio of the difference between the mean of the top 5% of the data and the interquartile mean (numerator) to the difference between the interquartile mean and the mean of the bottom 5% of the data. A value of 1 indicates symmetry. The measure indicates greater asymmetry towards the left tail as it approaches 0, and greater asymmetry towards the right tail the further it deviates from 1.

There is also Bickel's [24] robust asymmetry measure, which requires a single mode and adopts the mode as the axis of symmetry. It is defined as the complement of twice the value in the cumulative distribution function of the mode. The mode is estimated using an iterative procedure of half-samples, and the cumulative probability of the mode is obtained through a quotient. The numerator of this quotient is the sum of the number of data points smaller than the mode and half the number of data points equal to the mode. The denominator is the sample size. Consequently, Bickel's coefficient of skewness is bounded between −1 and 1.

2. Gunver-Senocak-Vehid measure of skewness

Gunver, Senocak, and Vehid, professors at the Department of Biostatistics, Istanbul University, developed in 2018 a new robust measure of skewness for continuous variables, which can also be applied to ordinal variables [25]. These authors proposed to use the median as the axis of symmetry.

The proposed asymmetry statistic is calculated as the quotient between two sums of differential scores with respect to the median. In the numerator, sample data smaller than the median are included, resulting in negative differences with respect to the median. In the denominator, sample data greater than or equal to the median are included, resulting in positive differences with respect to the median. It is denoted by γ_{GSV} at the population level and g_{GSV} at the sample level, similar to Fisher's measure. Please refer to Equation 2 for further details.

$$x = \{x_1, x_2, \ldots, x_n\} \subseteq X$$
$$x_{(1)} \le x_{(2)} \le \cdots \le x_{(n)}$$
$$mdn(x) = \frac{x_{\left(\lfloor \frac{n}{2} \rfloor\right)} + x_{\left(\lfloor \frac{n}{2} \rfloor + 1\right)}}{2}$$
$$\hat{\gamma}(x) = g_{GSV}(x) \qquad (2)$$
$$= \frac{\sum_{i=1}^{\lfloor n/2 \rfloor} \left(x_{(i)} - mdn(x)\right)}{\sum_{i=\lfloor n/2 \rfloor + 1}^{n} \left(x_{(i)} - mdn(x)\right)}$$

The quotient is always negative, since the numerator is

negative and the denominator is positive. Its range extends over the interval $(-\infty, 0)$. When there is symmetry, as in the case of the normal distribution, its value is −1. When there is left-tailed skewness (left tail longer than the right tail), its value is less than −1. Since the numerator is larger than the denominator, the ratio tends to −∞. When there is asymmetry to the right tail (right tail longer than the left), its value is greater than −1. As the numerator is smaller than the denominator, the quotient tends to 0. In the situation of a constant random sample, the indeterminacy 0 / 0 appears and this can be resolved as −1, since it is the value that corresponds to a symmetric distribution, as is the case of the distribution of a constant. This distribution has only one peak and lacks (symmetrically) the two shoulders and the two tails.

3. Objectives and justification of the study

This methodological study aims to: 1) develop a script for the R program for point and interval estimation of skewness, using the γ_{GSV} coefficient; 2) provide interpretive symmetry rules for that coefficient, generating bootstrap confidence intervals at 90%, 95% and 99% from population-samples of various sizes with standard normal distribution; and 3) analyze the relationship of the g_{GSV} coefficient with three other measures of skewness, namely, Bowley's Quartile Skewness Coefficient (*QSC*) [14], Hinkley's Percentile Skewness Coefficient (*PSC*) [15], and jackknife acceleration (*a*) [26].

This article focuses on the Gunver-Senocak-Vehid coefficient of skewness [25], as it is considered to be an interesting proposal to measure asymmetry, little known and underutilized. It is relevant in that it proposes to compare the two parts of the distribution defined by the median through a quotient, so it uses all the information of the distribution and utilizes as symmetry axis the most robust measure of central tendency that exists, which is unique and can be defined with any type of distribution [27]. The R program is utilized to facilitate the implementation of this asymmetry measure. R was selected due to its status as a freely available statistical tool, developed by the mathematical community, and regarded as one of the most comprehensive options existing [28].

4. Method

For the first objective of point estimation of γ_{GSV}, the basic package of the R program [28] was used. Since the sampling distribution of the g_{GSV} was unknown, the interval estimation approach of γ_{GSV} was performed through bootstrap utilizing the bias-corrected and accelerated (BCa) percentile and percentile (PERC) methods, with the assistance of the "boot" package [29]. Additionally, the script was enhanced by evaluating skewness using bootstrap probability under the null hypothesis of symmetry: H_0: $\gamma_{GSV} = -1$ [30], and by visually inspecting the distribution through a box plot and a histogram with an overlaid density curve, generating high-definition plots with the "ggplot2" package [31].

As an illustrative example, the script was applied to a random sample of 35 data points generated from a logistic distribution with parameters: $\mu = 0$ and $\beta = 200 \times \sqrt{2}$. To

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provide context, the data represent the skill levels of 35 chess players, quantified by the Rating Difference (RD). This quantitative variable spans from −800 to 800, is employed by the International Chess Federation, and adheres to a logistic distribution [32].

For the second objective of providing interpretive symmetry rules for g_{GSV}, 34 population-samples of various sizes (ranging from 10 to 50 with increments of 5, from 60 to 100 with increments of 10, from 150 to 1000 with increments of 50, and from 1500 to 2000) were generated. These population-samples were perfectly symmetric, with a standard normal distribution. From each of these 34 population-samples, 1000 draws with replacement were taken, and bootstrap confidence intervals were defined at 90%, 95%, and 99% using the BCa percentile and PERC methods. Additionally, 95% confidence intervals were established using the normal or Gaussian (NORM) method for the 30 population-samples with sizes greater than or equal to 30 data points [29].

When one interval estimation method is more efficient than others, it tends to yield smaller width intervals [33−34]. To determine whether one of the three methods is more efficient, two approaches were taken. First, the average widths of the bootstrap confidence intervals obtained by the BCa percentile and PERC methods were compared using the Wilcoxon's test [35]. Second, the difference among average widths of the 95% bootstrap confidence intervals obtained by the BCa percentile, PERC, and NORM methods were tested using the Friedman's test [36−37]. Nonparametric tests were employed due to the violation of the normality assumption [38]. This assumption was assessed at the univariate level using the Shapiro-Wilk W-test [39] and at the bi- or multivariate level using Royston's H-test [40].

For the third objective of analyzing the relationship between g_{GSV} and the quartile and percentile skewness coefficients, along with jackknife acceleration, the 34 bootstrap distributions of 1000 data points obtained from the 34 normally distributed population-samples were utilized. The quantile coefficients of skewness were selected due to their higher affinity to g_{GSV} in measuring asymmetry, thus serving as validity criteria alongside jackknife acceleration. The correlations among the four measures of skewness were calculated using Spearman's rank-order correlation coefficient, as the data did not meet the assumption of normality [38, 41]. This assumption was assessed at the univariate level using the Shapiro-Wilk W-test [39] and at the bivariate level using Royston's H-test [40]. Comparisons between correlations were conducted using the Meng-Rosenthal-Rubin Z-test [42], with the Rosner-Glynn transformation [43] applied. Effect size was estimated using the statistic: $d = z / \sqrt{n}$, where z represents the Meng-Rosenthal-Rubin standardized test statistic and n denotes the sample size. Values of the d statistic less than 0.2 were interpreted as indicating a trivial effect size, those between 0.2 and 0.49 as small, between 0.5 and 0.79 as medium, and those greater than or equal to 0.8 as large [44].

5. Results

5.1 Point and interval estimation of γ_{GSV}

Since the sampling distribution of g_{GSV} is unknown, the calculation of its standard error can be approached using the technique of repetitive sampling with replacement from the original sample (nonparametric bootstrap). Additionally, its confidence interval can be estimated using the percentile (PERC) and bias-corrected and accelerated (BCa) percentile methods. This is the approach followed in the script. In the case of small bias and acceleration ($|bias| < 0.1$ and $|a| < 0.025$, respectively), both methods are suitable [26]. If bias and acceleration are not small, the BCa percentile method is preferable [30]. One thousand extractions with replacement from the original sample were utilized [29].

The script developed for the R program, which can be adapted to other data than those presented, is shown below. The aspects that could be changed for such adaptation were marked in blue. This script allows point and interval estimation at 90% and 95% confidence level of the γ_{GSV} coefficient. Prior to applying the bootstrap method, the script checks the randomness of the sample using the Wald-Wolfowitz runs test, available in the "DescTools" package [45]. Furthermore, the estimation of γ_{GSV} was enhanced with two plots depicting the original sample of variable X: a box plot and a histogram with an overlaid density curve. The number of bins for the histogram is determined by the Freedman-Diaconis rule [46], while the densities for the curve are estimated using the Epanechnikov's kernel function [47], with bandwidth established via the method of Sheather and Jones [48]. Given the significance of evaluating shape, visual inspection of the distribution is emphasized.

In the script, the calculation of the skewness of the bootstrap sampling distribution of g_{GSV} and the acceleration correction factor were also incorporated. Additionally, the R program automatically provides the bias and standard error of the bootstrap point estimate of γ_{GSV}, along with plots of the bootstrap sampling distribution of g_{GSV} (including a histogram and a quantile-normal quantile-quantile plot). Another enhancement included was the computation of the bootstrap probability for the null hypothesis of symmetry (H_0: $\gamma_{GSV} = -1$). This probability is twice the minimum of two ratios: the ratio of the number of g_{GSV} estimates less than −1 in the 1000 bootstrap samples to the total number of draws (# [$g_{GSV} < -1$] / 1000), and the ratio of the number of g_{GSV} estimates greater than −1 in the 1000 bootstrap samples to the total number of draws (# [$g_{GSV} > -1$] / 1000). If the probability value is less than or equal to the significance level (alpha <- 0.05), the null hypothesis of symmetry in a two-tailed test is upheld; if it is greater, it is rejected.

The results were rounded to three decimal places to enhance readability, except for the jackknife acceleration value, which necessitates more decimal places.

```
# Data vector definition
x <- c(-154, 9, -599, 242, 520, 228, -186, -264, -118, 625, -190, -408, 134, -54, 656, -337, 619, -188, -422, -373, 367, 90, 220, -248, -787, 276, 761, 536, -693, 453, 234, -83, 249, 150, 27)
# Histogram with overlaid density curve
library(ggplot2)
```

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```
n <- length(x)
h <- 2 * IQR(x) / (n^(1/3))
density <- density(x, kernel = "epanechnikov", bw = "SJ")
histogram <- ggplot(data = data.frame(x = x), aes(x = x)) +
geom_histogram(aes(y = ..density..), binwidth = h, fill =
"darkolivegreen2", color = "black") +
geom_line(data = data.frame(x = density$x, y = density$y),
aes(x = x, y = y), color = "black", size = 1.5) +
labs(x = "X = Rating difference", y = "Density") +
theme(panel.background = element_rect(fill = "white"),
axis.text.x.bottom = element_text(size = 8), axis.text.y =
element_text(size = 8), axis.title.x = element_text(size = 9),
axis.title.y = element_text(size = 9), axis.line =
element_line(color = "black")) + scale_y_continuous(labels
= scales::label_number(accuracy = 0.0001))
jpeg("histogram.jpeg", width = 800, height = 600, units =
"px", res = 300)
print(histogram)
dev.off()
histogram

# Box plot
boxplot <- ggplot(data = data.frame(x = x), aes(x = "", y =
x)) +
geom_boxplot(fill = "darkolivegreen2", color = "black") +
labs(x = NULL, y = "Rating difference") +
theme_minimal() +
theme(panel.background = element_rect(fill = "white"),
axis.line = element_line(colour = "black"),
axis.title.x = element_text(size = 9),
axis.text.x = element_text(size = 8)) +
scale_x_discrete(position = "top") +
coord_flip()
jpeg("box_plot.jpeg", width = 800, height = 600, units =
"px", res = 300)
print(boxplot)
dev.off()
boxplot

# Point estimate of the Gunver-Senocak-Vehid measure of
skewness
mdn <- median(x)
pdm <- x - mdn
g_GSV <- sum(pdm[pdm < 0]) / sum(pdm[pdm >= 0])
g_GSV <- ifelse(is.nan(g_GSV), -1, g_GSV)
cat("Sample size: n =", n, "\n")
cat("Median: mdn(x) =", mdn, "\n")
cat("Gunver-Senocak-Vehid measure of skewness:
g_GSV(x) =", round(g_GSV, 3), "\n")

# Testing the randomness of the sample by means of the
Wald-Wolfowitz runs test
library(DescTools)
RunsTest(x, alternative = "two.sided", exact = TRUE)

# Interval estimation of the Gunver-Senocak-Vehid measure
of skewness
library(boot)
set.seed(123)
b <- boot(x, function(x, i) {
pdm <- x[i] - median(x[i])
g <- sum(pdm[pdm < 0]) / sum(pdm[pdm >= 0])
g <- ifelse(is.nan(g), -1, g)
```

```
return(g)
}, R = 1000)
print(b)
plot(b)
boot.ci(b, conf = c(0.90, 0.95), type = c("perc", "bca"))
boot_g_GSV <- mean(b$t)
cat("Bootstrap estimate of gamma_GSV(X): m(bootstrap
distribution) =", round(boot_g_GSV, 3), "\n")

# Skewness in the bootstrap sampling distribution of g_GSV
mdn_boot <- median(b$t)
pdm_boot <- b$t - mdn_boot
g_GSV_boot <- sum(pdm_boot[pdm_boot < 0]) /
sum(pdm_boot[pdm_boot >= 0])
g_GSV_boot <- ifelse(is.nan(g_GSV_boot), -1,
g_GSV_boot)
cat("Skewness in the bootstrap sampling distribution of
g_GSV(x): g_GSV(bootstrap distribution) =",
round(g_GSV_boot, 3), "\n")

# Skew correction factor (acceleration) using jackknife
estimation
g_jackknife <- numeric(n)
for (i in 1:n) {
muestra_jackknife <- x[-i]
pdm <- muestra_jackknife - median(muestra_jackknife)
g_jackknife[i] <- sum(pdm[pdm < 0]) / sum(pdm[pdm >=
0])
}
media_g_jackknife <- sum(g_jackknife) / n
acel <- sum((media_g_jackknife - g_jackknife)^3) / (6 *
sum((media_g_jackknife - g_jackknife)^2)^(3/2))
cat("Skew correction factor (acceleration): a =", round(acel,
6), "\n")
p_boot_izq <- sum(b$t < -1) / length(b$t)
p_boot_der <- sum(b$t > -1) / length(b$t)
p_boot <- 2 * min(p_boot_izq, p_boot_der)
alpha <- 0.05
cat("Two-tailed bootstrap probability for the null hypothesis
of symmetry: p-value =", round(p_boot, 3), "\n")
if (p_boot >= alpha) {
cat("Since the p-value (", round(p_boot, 3), ") is greater than
or equal to alpha (", alpha, "), the null hypothesis of
symmetry is not rejected in a two-tailed test.\n")
} else {
cat("Since the p-value (", round(p_boot, 3), ") is less than
alpha (", alpha, "), the null hypothesis of symmetry is
rejected in a two-tailed test.\n")
}

# Creation of the JPEG file to save bootstrap graphics
conf_intervals <- boot.ci(b, conf = c(0.90, 0.95), type =
c("perc", "bca"))
jpeg("bootstrap_plots.jpeg", width = 800, height = 600,
quality = 100)
par(mfrow = c(1, 2))
plot(b)
plot(conf_intervals)
dev.off()
```

The script can be run online via https://rdrr.io/snippets/, but
it produces low-resolution graphics when exported.
Alternatively, users can run the script using either the R

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program [28] or RStudio [49] with the 'DescTools', 'boot', and 'ggplot2' packages installed on their personal computer. In the latter scenario, three high-definition *.jpeg files containing four plots are saved in the Documents directory: the box plot (Figure 1), the histogram with the overlaid density curve (Figure 2), and two plots representing the bootstrap sampling distribution of g_{GSV} (Figure 3). The results of executing the script are summarized in Table 1,

which includes the outputs of the ordinary nonparametric bootstrap analysis presented by R in two tables.

- Sample size: $n = 35$
- Median: $mdn(x) = 27$
- Gunver-Senocak-Vehid measure of skewness: $g_{GSV}(x) = -0.941$
- runs = 19, $n_0 = 18$, $n_1 = 17$, p-value = 0.862.

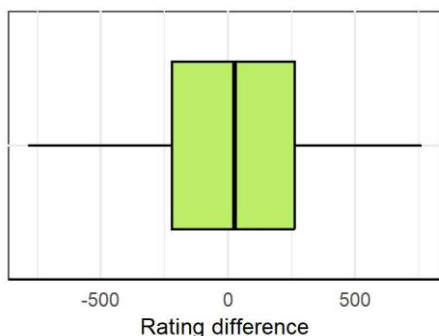**Table 1:** Point estimate and bootstrap confidence intervals of Gunver-Senocak-Vehid coefficient of skewness

| g_{GSV}	Bootstrap estimation		Bootstrap confidence interval			
			90%		95%	
	bias	se	PERC	BCa	PERC	BCa
-0.941	-0.195	0.523	(-2.143, -0.486)	(-1.821, -0.411)	(-2.332, -0.421)	(-2.065, -0.375)
Note. g_{GSV} = Gunver-Senocak-Vehid coefficient of skewness of the original sample, *bias* and *se* = standard error of bootstrap estimate, bootstrap confidence interval (drawing 1000 samples for repetitive sampling with replacement from original sample): PERC = percentile method and BCa = bias-corrected and accelerated percentile method.						

- Bootstrap estimate of gamma$_{GSV}$(X): m(bootstrap distribution) = −1.136.
- Skewness in the bootstrap sampling distribution of $g_{GSV}(x)$: g_{GSV}(bootstrap distribution) = −1.603.
- Skew correction factor (acceleration): $a = 0.000441$
- Two-tailed bootstrap probability for the null hypothesis of symmetry: p-value = 0.904.
- Since the p-value (0.904) is greater than or equal to alpha (0.05), the null hypothesis of symmetry is not rejected in a two-tailed test.

Figure 1: Box plot depicting the chess skill, measured by the rating difference, in a random sample of 35 chess players
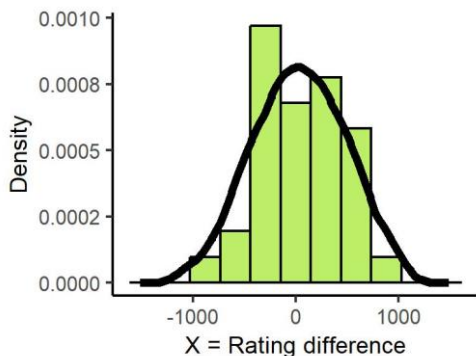
Figure 2: Histogram (uniform width of bins defined by the Freedman-Diaconis rule) with an overlaid density curve (using Epanechnikov's kernel with Sheather-Jones bandwidth), depicting chess skill as measured by the rating difference in a random sample of 35 chess players

In the sample of 35 data points outlined in the script, the median value is 27. The Gunver-Senocak-Vehid coefficient of skewness is −0.941, indicating a proximity to the symmetry value of −1. Both the box plot (Figure 1) and histogram (Figure 2) depict symmetry in the data distribution. Furthermore, the density curve clearly shows the logistic distribution underlying the dataset.

The sample can be considered random or as a sequence of independent data since the null hypothesis of randomness is not rejected by the Wald-Wolfowitz runs test in a two-tailed test with a significance level of 5%, using the median as the cut-off criterion and calculating the exact probability. In case n_0 (values less than the median) and n_1 (values greater than the median) are greater than 20, the asymptotic normal approximation (exact = FALSE) can be chosen. Consequently, we have a random sample, larger than 30 data points, and assume it to be representative of the population (generated from the theoretical model of the population distribution).

The value of the acceleration is tiny ($|a| = 0.0004 < 0.025$), but the bias of the bootstrap estimate in absolute value is larger than 0.1 ($|bias_{bootstrap}| = 0.195$), which is not a small value. The skewness of the bootstrap distribution, measured by the g_{GSV} coefficient, is away from −1 with a value of −1.603, suggesting left-tailed skewness. Precisely, the density plot of the bootstrap distribution (left plot in Figure 3) shows some asymmetry with the left tail longer than the right. The normal quantile-quantile plot (right in Figure 3) evidences departure from normality with a concave profile that is typical of left-tailed skewness [50]. Therefore, the bias-corrected and accelerated (BCa) percentile method is more suitable than the percentile (PERC) method to obtain the bootstrap confidence interval for the dataset. In addition, the bootstrap confidence interval widths (at 90% and 95%) obtained using the BCa percentile method are smaller than those obtained using the PERC method with this data.

Consistent with what the graphs depicting the Rating Difference scores in the sample of 35 participants reveal, the 90% and 95% bootstrap confidence intervals obtained by both methods include −1, thereby supporting the symmetry hypothesis. See Table 1.

The bootstrap probability for the null hypothesis of symmetry is greater than the significance level (H$_0$: γ$_{GSV}$ = −1; $p_{2-tailed}$ = 0.904 > α = 0.05), so the hypothesis of

symmetry is not rejected in a two-tailed test with a significance level of 5%, even 10%. Consequently, it can be inferred that the distribution from which the sample was

drawn exhibits symmetry. This conclusion is correct (true), since the dataset was generated from a logistic distribution.
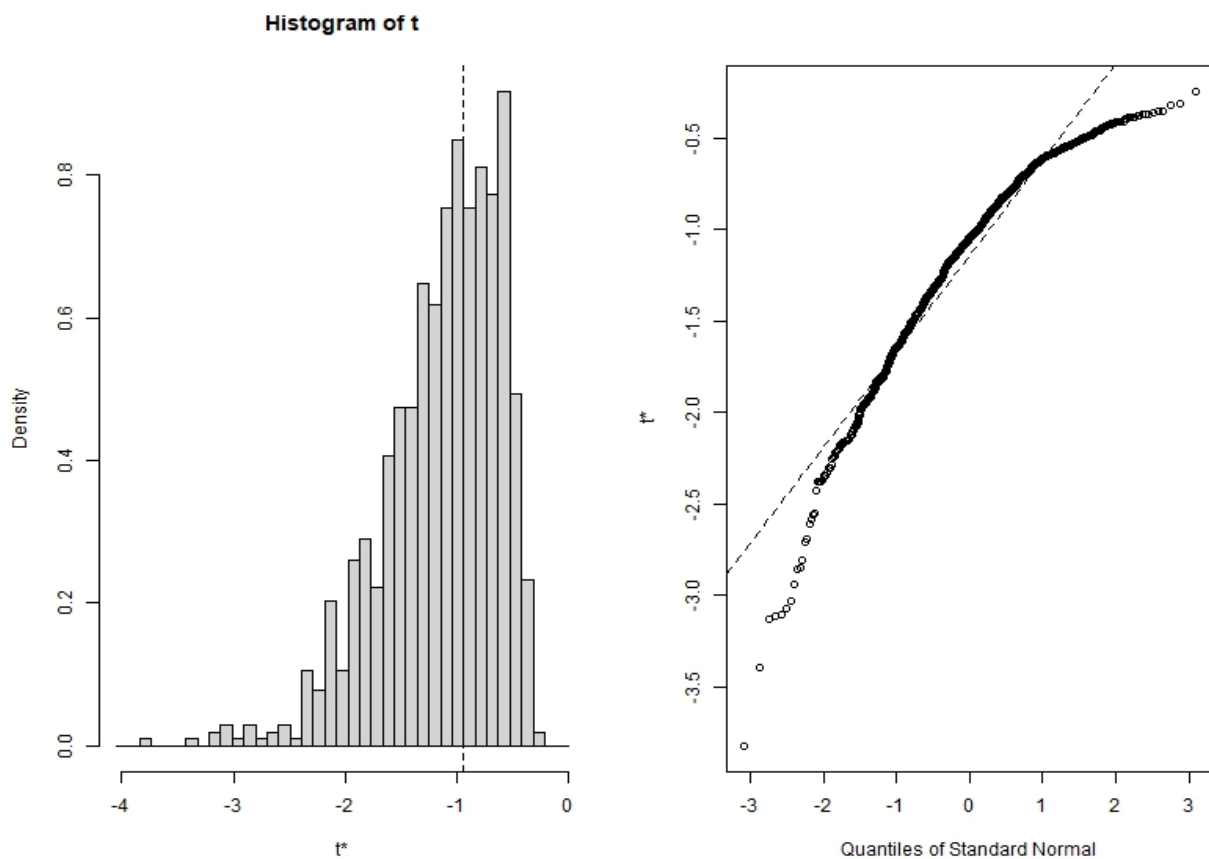

Figure 3: Bootstrap sampling distribution of g_{GSV}.
The histogram is shown on the left, and the normal quantile-quantile plot is displayed on the right

5.2 Reference bootstrap confidence intervals of symmetry for g_{GSV} modeled from population-samples following a standard normal distribution

The range of the 34 population-samples generated was bounded to the closed interval, comprised between $\Phi^{-1}(p = 0.001)$ or the quantile of order 0.001 of a standard normal distribution ($z_{0.001} \approx -3.090$) and $\Phi^{-1}(p = 0.999) = z_{0.999} \approx 3.090$. Samples were generated using the probit function with orders in an arithmetic sequence to ensure perfect symmetry and centering at 0. In each population-sample, the first datum was: $x_{(1)} = \Phi^{-1}(p = 0.001) \approx -3.090$. The incremental constant of the order of the quantile in each of the 34 sequences was obtained by dividing 0.998 (0.999 − 0.001) by the sample size decreased by one unit ($n - 1$). Adding the constant c to 0.001 and obtaining the quantile in that order with the probit function yielded the second datum for each sample: $x_{(2)} = \Phi^{-1}(p = 0.001 + c)$. Adding the constant c to the order of the second datum and obtaining the quantile in that order resulted in the third datum: $x_{(3)} = \Phi^{-1}(p = 0.001 + 2 \times c)$. Thus, the arithmetic sequence was continued in quantile order until the nth sample datum was reached ($\Phi^{-1}(p = 0.001 + (n-1) \times c) = z_{0.999} \approx 3.090$). From these 34 population-samples by resampling with replacement and fixing a seed (123), 1000 samples, called bootstrap samples, were randomly drawn. We proceeded in this way to generate perfectly reproducible confidence intervals. For each bootstrap sample, the g_{GSV} statistic was calculated, yielding

the bootstrap sampling distribution of g_{GSV} or bootstrap distribution.

For each bootstrap distribution of 1000 data, the bootstrap bias or difference between its mean (bootstrap estimate of γ_{GSV}) (Equation 3) and the point estimate of γ_{GSV} in the original sample of size n (Equation 4) was calculated. By inspecting Table 2, a value of 0.05 can be considered to represent a slight bias for small samples (30 to 100), 0.01 for medium samples (100 to 900), and 0.001 for large samples (greater than 1000).

$$\hat{\gamma}_{bootstrap} = E(\{\hat{\gamma}_i\}_{i=1}^B)$$
$$= \frac{\sum_{i=1}^B \hat{\gamma}_i}{B} = \frac{\sum_{i=1}^{1000} \hat{\gamma}_i}{1000} \quad (3)$$

$$bias(\hat{\gamma}_{bootstrap}) = E(\{\hat{\gamma}_i\}_{i=1}^B) - \hat{\gamma}$$
$$= \hat{\gamma}_{bootstrap} - g_{GSV} \quad (4)$$

The bootstrap standard error was also calculated, which is obtained through the sample standard deviation of g_{GSV} in the bootstrap distribution of 1000 data (Equation 5). See Table 2.

$$se_{boostrap} = s_{B-1}(\{\hat{\gamma}_i\}_{i=1}^B)$$
$$= \sqrt{\frac{\sum_{i=1}^B (\hat{\gamma}_i - \hat{\gamma}_{bootstrap})^2}{B-1}} \quad (5)$$
$$= \sqrt{\frac{\sum_{i=1}^{1000} (\hat{\gamma}_i - \hat{\gamma}_{bootstrap})^2}{999}}$$

In addition, the jackknife acceleration or skewness was calculated (Table 2). From the population-sample of size n, n samples were generated by eliminating one element in each population-sample, the g_{GSV} statistic was calculated in each of these n jackknife samples of size $n - 1$ and Equation 6 was applied to obtain the acceleration, denoted by a. Refer to Table 3 for details. This was supplemented with the skewness of the bootstrap distribution estimated by the Gunver-Senocak-Vehid coefficient, as well as the quartile and percentile skewness coefficients.

$$\hat{\gamma}_{jackknife} = E\left(\{\hat{\gamma}_{(-i)}\}_{i=1}^{n}\right) = \frac{\sum_{i=1}^{n} \hat{\gamma}_{(-i)}}{n}$$

$$a = \frac{1}{6} \times \frac{\sum_{i=1}^{n}\left(\hat{\gamma}_{jackknife} - \hat{\gamma}_{(-i)}\right)^3}{\left[\sum_{i=1}^{n}\left(\hat{\gamma}_{jackknife} - \hat{\gamma}_{(-i)}\right)^2\right]^{3/2}} \quad (6)$$

Confidence intervals were obtained using two methods: the bias-corrected and accelerated (BCa) percentile method, presented in Table 2, and the percentile (PERC) method, outlined in Table 3. Both methods fall under the category of nonparametric techniques [26]. Additionally, Table 3 includes the 95% confidence interval obtained through the normal or Gaussian (NORM) method, which is a parametric approach [26]. It is applied to population-samples of 30 or more data, which have low indices of estimation bias and distributional skewness.

Applying these reference tables to the provided example, the skewness value of the sample x falls within the reference intervals of symmetry for 90% confidence level (two-tailed 10% significance level) and 95% (two-tailed 5% significance level) obtained by the BCa percentil, PERC, and normal methods. In the bootstrap distribution of 1000 data derived from the population-sample of 35 normally distributed data in the interval [$z_{0.001}$, $z_{0.999}$], the values of estimation bias and distributional skewness are small ($|bias| = |0.052| < 0.1$, $|a| = 0.004 < 0.025$), so the PERC method, even the normal method are adequate. Consequently, the previously reached conclusion of symmetry holds. However, the bootstrap distribution (b) does exhibit left-tailed skewness ($g_{GSV} = -1.617$), as its skewness value falls outside the reference confidence intervals at 90% obtained by the three methods, and at 95% by the PERC and BCa percentile methods.

<div align="center">CI at 95% for n = 35</div>

- $g_{GVS}(\text{x}) = -0.941 \in$ and $g_{GVS}(\text{b}) = -1.603 \notin (-1.948, -0.505)$ by BCa percentile method, width = upper limit – lower limit: $w = UL - LL = -0.505 + 1.948 = 1.443$.
- $g_{GVS}(\text{x}) = -0.941 \in$ and $g_{GVS}(\text{b}) = -1.603 \notin (-1.938, -0.502)$ by PERC method, $w = UL - LL = 1.436$.
- $g_{GVS}(\text{x}) = -0.941 \in$ and $g_{GVS}(\text{b}) = -1.603 \notin (-1.684, -0.212)$ by NORM method, $w = UL - LL = 1.472$.

<div align="center">CI at 90% for n = 35</div>

- $g_{GVS}(\text{x}) = -0.941 \in$ and $g_{GVS}(\text{b}) = -1.603 \notin (-1.777, -0.564)$ by BCa percentile method, $w = UL - LL = 1.213$.
- $g_{GVS}(\text{x}) = -0.941 \in$ and $g_{GVS}(\text{b}) = -1.603 \notin (-1.766, -0.549)$ by PERC method, $w = UL - LL = 1.217$.
- $g_{GVS}(\text{x}) = -0.941$ and $g_{GVS}(\text{b}) = -1.603 \in (-1.566, -0.331)$ by NORM method, $w = UL - LL = 1.235$.

Table 2: Bias, standard error, acceleration, and reference bootstrap confidence intervals of symmetry obtained by the BCa percentile method

n	Bootstrap estimation			BCa bootstrap confidence interval		
	bias	se	a	90%	95%	99%
10	-0.226	0.988	0.03550	(-2.648, -0.328)	(-3.161, -0.257)	(-5.598, -0.119)
15	-0.195	0.769	0.02206	(-2.604, -0.429)	(-3.209, -0.345)	(-4.803, -0.249)
20	-0.111	0.524	0.01159	(-2.212, -0.498)	(-2.474, -0.430)	(-3.172, -0.302)
25	-0.091	0.474	0.00846	(-1.861, -0.482)	(-2.124, -0.439)	(-2.983, -0.326)
30	-0.079	0.390	0.00532	(-1.778, -0.563)	(-1.979, -0.503)	(-2.623, -0.416)
35	-0.052	0.375	0.00426	(-1.777, -0.564)	(-1.948, -0.505)	(-2.916, -0.415)
40	-0.051	0.329	0.00301	(-1.665, -0.607)	(-1.857, -0.533)	(-2.291, -0.447)
45	-0.046	0.310	0.00254	(-1.614, -0.608)	(-1.758, -0.550)	(-2.068, -0.432)
50	-0.037	0.298	0.00194	(-1.573, -0.643)	(-1.695, -0.582)	(-2.265, -0.495)
60	-0.021	0.252	0.00136	(-1.485, -0.678)	(-1.639, -0.615)	(-1.893, -0.488)
70	-0.027	0.235	0.00101	(-1.480, -0.689)	(-1.579, -0.648)	(-1.766, -0.560)
80	-0.028	0.221	0.00078	(-1.373, -0.677)	(-1.473, -0.623)	(-1.711, -0.559)
90	-0.012	0.205	0.00063	(-1.392, -0.711)	(-1.487, -0.667)	(-1.631, -0.590)
100	-0.011	0.193	0.00052	(-1.352, -0.736)	(-1.474, -0.696)	(-1.629, -0.616)
150	-0.014	0.162	0.00025	(-1.288, -0.766)	(-1.337, -0.725)	(-1.521, -0.650)
200	-0.009	0.133	0.00015	(-1.230, -0.810)	(-1.289, -0.773)	(-1.438, -0.713)
250	-0.011	0.120	0.00011	(-1.201, -0.823)	(-1.264, -0.783)	(-1.403, -0.709)
300	-0.005	0.112	0.00008	(-1.200, -0.836)	(-1.250, -0.805)	(-1.354, -0.733)
350	-0.004	0.104	0.00006	(-1.215, -0.856)	(-1.250, -0.828)	(-1.309, -0.779)
400	-0.002	0.096	0.00005	(-1.173, -0.855)	(-1.209, -0.835)	(-1.282, -0.788)
450	-0.003	0.091	0.00004	(-1.153, -0.860)	(-1.186, -0.831)	(-1.285, -0.788)
500	-0.001	0.086	0.00004	(-1.150, -0.869)	(-1.179, -0.847)	(-1.255, -0.812)
550	-0.003	0.084	0.00003	(-1.157, -0.882)	(-1.189, -0.859)	(-1.247, -0.815)
600	-0.003	0.078	0.00003	(-1.141, -0.887)	(-1.165, -0.863)	(-1.222, -0.821)
650	-0.007	0.076	0.00002	(-1.129, -0.886)	(-1.156, -0.867)	(-1.220, -0.822)
700	-0.006	0.073	0.00002	(-1.126, -0.881)	(-1.146, -0.854)	(-1.191, -0.815)
750	-0.004	0.068	0.00002	(-1.129, -0.899)	(-1.143, -0.887)	(-1.196, -0.858
800	-0.003	0.067	0.00002	(-1.111, -0.890)	(-1.142, -0.872)	(-1.214, -0.847)
850	-0.004	0.065	0.00002	(-1.110, -0.895)	(-1.130, -0.874)	(-1.175, -0.830)

900	<0.001	0.062	0.00001	(-1.101, -0.897)	(-1.122, -0.879)	(-1.183, -0.860)
950	-0.001	0.064	0.00001	(-1.109, -0.902)	(-1.136, -0.887)	(-1.210, -0.841)
1000	-0.003	0.060	0.00001	(-1.098, -0.906)	(-1.119, -0.892)	(-1.119, -0.892)
1500	<-.001	0.050	0.00001	(-1.088, -0.926)	(-1.102, -0.911)	(-1.139, -0.868)
2000	<-.001	0.043	0	(-1.076, -0.931)	(-1.087, -0.920)	(-1.118, -0.900)
m				0.651	0.796	1.185
m^*					0.586	

Note. n = sample size of the generating population-sample; bootstrap distribution consists of 1000 samples drawn by repetitive resampling with replacement, using a seed (123), from the a perfectly symmetric generating population-sample with n normally distributed data in the interval [$z_{0.001}$, $z_{0.999}$] with equispaced quantile orders (0. 998 / (n - 1)); bias = difference between the estimate in the original sample and the bootstrap estimate; se =bootstrap standard error; a = jackknife acceleration; bootstrap confidence intervals at 90%, 95%, and 99% calculated using the bias-corrected and accelerated (BCa) percentile method m = average width of the bootstrap confidence intervals in the 34 population-samples, and m^*= average width of the bootstrap confidence intervals in the 30 population-samples with sizes $n \geq 30$. For all bootstrap distributions, the value of g_{GSV} was -1.

Table 3: Skewness of bootstrap distribution, and reference bootstrap confidence intervals obtained by percentile and normal methods

n	Skewness			PERC			Normal
	g_{GSV}	QSC	PSC	90%	95%	99%	95%
10	-2.208	-0.177	-0.437	(-2.869, -0.350)	(-3.428, -0.268)	(-5.895, -0.154)	
15	-2.440	-0.257	-0.437	(-2.587, -0.427)	(-3.210, -0.345)	(-4.906, -0.251)	
20	-1.977	-0.274	-0.336	(-2.147, -0.479)	(-2.457, -0.420)	(-2.963, -0.298)	
25	-1.558	-0.097	-0.219	(-2.020, -0.497)	(-2.167, -0.448)	(-3.091, -0.331)	
30	-1.617	-0.148	-0.242	(-1.804, -0.575)	(-1.992, -0.510)	(-2.630, -0.422)	(-1.685, -0.158)
35	-1.560	-0.116	-0.194	(-1.766, -0.549)	(-1.938, -0.502)	(-2.890, -0.401)	(-1.684, -0.212)
40	-1.580	-0.161	-0.226	(-1.648, -0.604)	(-1.845, -0.528)	(-2.285, -0.442)	(-1.594, -0.304)
45	-1.431	-0.097	-0.196	(-1.618, -0.610)	(-1.762, -0.550)	(-2.069, -0.434)	(-1.563, -0.346)
50	-1.447	-0.110	-0.194	(-1.566, -0.640)	(-1.679, -0.580)	(-2.189, -0.486)	(-1.547, -0.379)
60	-1.289	-0.027	-0.112	(-1.483, -0.670)	(-1.630, -0.608)	(-1.892, -0.477)	(-1.472, -0.486)
70	-1.348	-0.097	-0.136	(-1.468, -0.687)	(-1.575, -0.647)	(-1.751, -0.560)	(-1.433, -0.514)
80	-1.170	-0.006	-0.088	(-1.421, -0.702)	(-1.508, -0.641)	(-1.756, -0.573)	(-1.404, -0.540)
90	-1.227	-0.038	-0.091	(-1.379, -0.707)	(-1.484, -0.668)	(-1.608, -0.582)	(-1.390, -0.587)
100	-1.256	-0.082	-0.092	(-1.337, -0.732)	(-1.464, -0.680)	(-1.628, -0.614)	(-1.367, -0.611)
150	-1.213	-0.019	-0.121	(-1.295, -0.769)	(-1.372, -0.731)	(-1.531, -0.651)	(-1.303, -0.668)
200	-1.210	-0.061	-0.074	(-1.229, -0.807)	(-1.288, -0.772)	(-1.432, -0.712)	(-1.252, -0.731)
250	-1.126	-0.012	-0.034	(-1.211, -0.828)	(-1.277, -0.791)	(-1.411, -0.714)	(-1.225, -0.754)
300	-1.135	-0.011	-0.077	(-1.199, -0.835)	(-1.250, -0.803)	(-1.349, -0.732)	(-1.215, -0.774)
350	-1.283	-0.106	-0.103	(-1.185, -0.839)	(-1.234, -0.819)	(-1.307, -0.763)	(-1.120, -0.792)
400	-1.146	-0.045	-0.059	(-1.169, -0.850)	(-1.206, -0.832)	(-1.263, -0.786)	(-1.186, -0.809)
450	-1.067	0.017	-0.057	(-1.153, -0.860)	(-1.187, -0.831)	(-1.288, -0.789)	(-1.175, -0.820)
500	-1.098	-0.023	-0.028	(-1.146, -0.867)	(-1.173, -0.845)	(-1.254, -0.812)	(-1.168, -0.830)
550	-1.318	-0.157	-0.146	(-1.148, -0.872)	(-1.181, -0.846)	(-1.231, -0.800)	(-1.161, -0.833)
600	-1.177	-0.065	-0.071	(-1.135, -0.882)	(-1.162, -0.858)	(-1.222, -0.813)	(-1.151, -0.844)
650	-1.102	0.025	-0.065	(-1.142, -0.891)	(-1.168, -0.872)	(-1.227, -0.827)	(-1.168, -0.872)
700	-1.058	0.020	-0.053	(-1.136, -0.891)	(-1.158, -0.868)	(-1.198, -0.824)	(-1.137, -0.850)
750	-1.209	-0.073	-0.121	(-1.126, -0.898)	(-1.143, -0.882)	(-1.193, -0.858)	(-1.130, -0.863)
800	-1.076	-0.005	0.012	(-1.116, -0.892)	(-1.156, -0.875)	(-1.216, -0.848)	(-1.129, -0.865)
850	-1.039	0.003	-0.022	(-1.118, -0.902)	(-1.135, -0.881)	(-1.186, -0.837)	(-1.123, -0.868)
900	-0.995	-0.013	0.026	(-1.101, -0.896)	(-1.122, -0.879)	(-1.183, -0.860)	(-1.121, -0.880)
950	-1.107	-0.067	-0.045	(-1.107, -0.901)	(-1.130, -0.882)	(-1.204, -0.839)	(-1.125, -0.873)
1000	-1.048	-0.019	-0.021	(-1.103, -0.912)	(-1.121, -0.894)	(-1.164, -0.866)	(-1.114, -0.880)
1500	-1.101	-0.025	-0.055	(-1.087, -0.925)	(-1.101, -0.908)	(-1.140, -0.866)	(-1.097, -0.902)
2000	-1.051	-0.011	-0.017	(-1.075, -0.931)	(-1.088, -0.918)	(-1.118, -0.898)	(-1.084, -0.915)
m				0.659	0.806	1.193	
m^*					0.588		0.585

Note. n = sample size of the generating population-sample; bootstrap distribution consists of 1000 samples drawn by repetitive resampling with replacement, using a seed (123), from the a perfectly symmetric generating population-sample with n normally distributed data in the interval [$z_{0.001}$, $z_{0.999}$] with equispaced quantile orders (0. 998 / (n - 1)); QSC =Bowley's quartile skewness coefficient; PSC = percentile skewness coefficient; PERC = bootstrap confidence intervals at 90%, 95%, and 99% calculated using the percentile (PERC) method; Normal = 95% bootstrap confidence interval obtained by the normal or Gaussian method; m = average width of the bootstrap confidence intervals in the 34 population-samples, and m^*= average width of the bootstrap confidence intervals in the 30 population-samples with sizes $n \geq 30$.

Although the average width of the bootstrap confidence intervals obtained by the BCa percentile method was the shortest, the differences in width were not statistically significant when making central tendency comparisons

between the two methods (BCa versus PERC) for 90%, 95%, and 99% confidence intervals (Table 4), or among the three methods for the 95% confidence interval (Table 5).

The distributions of bootstrap confidence interval widths deviated from normality at the univariate level (PERC_90: $z_W = 0.791$, $p_{right\text{-}tailed} < 0.001$; BCa_90: $z_W = 0.797$, $p_{right\text{-}tailed} < 0.001$; PERC_95: $z_W = 0.778$, $p_{right\text{-}tailed} < 0.001$; BCa_95: $z_W = 0.785$, $p_{right\text{-}tailed} < 0.001$; PERC_99: $z_W = 0.724$, $p_{right\text{-}}$

$_{tailed} < 0.001$; BCa_99: $z_W = 0.740$, $p_{right\text{-}tailed} < 0.001$) and bivariate (PERC_90 and BCa_90: $h = 18.545$, $p_{right\text{-}tailed} < 0.001$; PERC_95 and BCa_95: $h = 19.543$, $p_{right\text{-}tailed} < 0.001$; PERC_99 and BCA_99: $h = 23.831$, $p_{right\text{-}tailed} < 0.001$) in comparisons with 34 pairs of data, as well as at the univariate level (Normal_95: $z_W = 0.832$, $p_{right\text{-}tailed} < 0.001$; BCa_95: $z_W = 0.839$, $p_{right\text{-}tailed} < 0.001$; PERC_95: $z_W = 0.842$, $p_{right\text{-}tailed} < 0.001$) and multivariate ($h = 13.038$, $p_{right\text{-}tailed} < 0.001$) in comparisons with 30 data terns.

Table 4: Comparison of the average width of bootstrap confidence intervals between the PERC and BCa percentile methods

Level	Method	n	m	mdn	T	$p_{1\text{-}tailed}$	$p_{2\text{-}tailed}$	$|r_{rb}|$
0.90	PERC	34	0.659	0.374	253	0.335	0.670	0.088
	BCa		0.651	0.371				
0.95	PERC	34	0.806	0.467	199	0.249	0.497	0.144
	BCa		0.796	0.463				
0.99	PERC	34	1.193	0.657	249	0.290	0.580	0.112
	BCa		1.185	0.658				

Note. Level = confidence level of the interval estimate; method for defining bootstrap confidence intervals: BCa = bias-corrected and accelerated percentile and PERC = percentile; n = number of paired data, m = arithmetic mean, and mdn = median of the width of bootstrap confidence intervals; T = Wilcoxon's test statistic for paired samples, $p_{1\text{-}tailed}$ = exact probability at one tail, and $p_{2\text{-}tailed}$ = exact probability at two tails; $|r_{rb}|$ = the absolute value of the rank-biserial correlation coefficient as a measure of effect size.

Table 5: Comparison of the average width of 95% bootstrap confidence intervals by method

Method for defining CI	RM	Conover-Iman test		Friedman's test				Effect size
		t	$p_{2\text{-}tailed}$	F	df_1	df_2	$p_{right\text{-}tailed}$	w
Normal	1.967			0.165	2	58	0.848	0.006
BcA	1.950							
PERC	2.083							
NORM - BcA	0.017	0.066	0.948					
NORM - PERC	0.117	0.461	0.646					
BcA - PERC	0.133	0.527	0.600					

Note. Method for defining bootstrap confidence intervals (*CI*): BCa = bias-corrected and accelerated percentile, PERC = percentile, and NORM = normal or Gaussian. *MR* = mean rank of confidence interval width (three first rows) or of the difference between bootstrap confidence interval widths (last three rows), t = Conover-Iman test statistic for a posteriori comparisons by matched pairs of data [36], $p_{2\text{-}tailed}$ = two-tailed probability in a Student's t distribution with $(k\text{-}1) \times (n\text{-}1)$ degrees of freedom, where k is the number of methods and n is the number of bootstrap confidence interval width pairs, F = test statistic of the Friedman's test as modified by Iman and Davenport [37], $df_1 = k\text{-}1$ = degrees of freedom 1, whose value corresponds to the number of methods minus 1, $df_2 = (k\text{-}1) \times (n\text{-}1)$ = degrees of freedom 2, whose value corresponds to the product of the number of methods minus 1 and the number of bootstrap confidence interval width pairs minus 1, $p_{right\text{-}tailed}$ = right-tailed probability in a Snedecor-Fisher F distribution with df_1 and df_2 degrees of freedom, w = Kendall's coefficient of concordance as a measure of effect size.

5.3 Comparison of g_{GSV} with *QSC*, *PSC*, and *a*

The distribution of none of the four skewness measures conformed to normality by Shapiro-Wilk W-test (g_{GSV}: $w = 0.763$, $p_{right\text{-}tail} < 0.001$, *QSC*: $w = 0.884$, $p_{right\text{-}tail} = 0.002$, *PSC*; $w = 0.886$, $p_{right\text{-}tail} = 0.002$, jackknife *a*: $w = 0.502$, $p_{right\text{-}tail} < 0.001$) and their bivariate distributions also moved away from normality by Royston's H-test (g_{GSV} and *QSC*: $h = 22.277$, $p_{right\text{-}tail} < 0.001$; g_{GSV} and *PSC*: $h = 18.801$, $p_{right\text{-}tail} < 0.001$; *QSC* and *PSC*: $h = 16.377$, $p_{right\text{-}tail} < 0.001$; jackknife *a* and g_{GSV}: $h = 26.300$, $p_{right\text{-}tail} < 0.001$; jackknife *a* and *QSC*: $h = 37.844$, $p_{right\text{-}tail} < 0.001$; jackknife *a* and *PSC*: $h = 24.698$, $p_{right\text{-}tail} < 0.001$); hence correlations were calculated by Spearman's rank-order correlation coefficient [41] and comparisons were run by the Meng-Rosenthal-Rubin Z-test [42], applying the Rosner-Glynn transformation to convert Spearman's rank-order correlation coefficients to Pearson's product-moment correlation coefficients [43]. See Table 6.

The Gunver-Senocak-Vehid coefficient of skewness (g_{GSV}) exhibited a significantly higher correlation ($z = 3.549$, $p_{1\text{-}tailed} < 0.001$) with the percentile skewness coefficient ($r_S = 0.965$) than with the quartile skewness coefficient ($r_S = 0.881$). The effect size for the coefficient type (*QSC* versus *PSC*) on the strength of association with g_{GSV} was medium ($d = 0.609 < 0.8$). The correlation between the Gunver-Senocak-Vehid coefficient of skewness and jackknife acceleration ($r_S = -0.896$) was also significantly stronger in absolute value ($z = -3.959$, $p_{1\text{-}tailed} < 0.001$) than the correlation between the quartile skewness coefficient and jackknife acceleration ($r_S = -0.667$). The effect size for the coefficient type (g_{GSV} versus *QSC*) on the strength of association with acceleration was also medium ($d = 0.679 < 0.8$). However, the difference in correlation between the Gunver-Senocak-Vehid coefficient of skewness and jackknife acceleration ($r_S = -0.896$) compared to the correlation between the percentile skewness coefficient and jackknife acceleration ($r_S = -0.868$) was not statistically significant ($z = -0.579$, $p_{1\text{-}tailed} < 0.281$), with the effect size being trivial ($d = 0.099 < 0.1$). Refer to Table 6.

Table 6: Comparison of overlapping correlations in one-sample

Coefficients	Spearman	Transformed r	Meng et al.	Effect size

1	2	3	$r_S(1, 2)$	$r_S(1, 3)$	$r(1, 2)$	$r(1, 3)$	$r(2, 3)$	z	$p_{1\text{-}tailed}$	d	Interpretation
g_{GSV}	QSC	PSC	0.881	0.965	0.834	0.957	0.770	3.549	<.001	0.609	medium
a	g_{GSV}	QSC	-0.896	-0.667	-0.883	-0.654	0.834	-3.959	<.001	0.679	medium
a	g_{GSV}	PSC	-0.896	-0.868	-0.883	-0.869	0.957	-0.579	0.281	0.099	trivial

Note. g_{GSV} = Gunver-Senocak-Vehid coefficient of skewness, QSC = quartile skewness coefficient, PSC = percentile skewness coefficient, a = jackknife acceleration, r_S = Spearman rank-order correlation coefficient, r = Rosner-Glynn transformation to convert a Spearman rank-order correlation coefficient to a Pearson product-moment correlation coefficient [43], z = Meng-Rosenthal-Rubin z-test statistic for comparing overlapping correlations from the same sample [42], p = one-tailed probability value, Effect size: $d = z / \sqrt{n}$. Interpretation of d statistic: < 0.2 trivial, [0.20, 0.5) small, [0.5, 0.8) medium, and ≥ 0.8 large effect size [44].

6. Discussion

With respect to the first objective of the study, the script developed for the R program allows for the calculation of the g_{GSV} statistic and the obtaining of confidence intervals at 90% and 95%, with the possibility of adjusting the significance level. For instance, to require a 99% confidence interval, the following can be added: conf = c(0.90, 0.95, 0.99). The script also facilitates the testing of the randomness of the sample, a prerequisite assumption for bootstrap techniques when applied to statistics [26], and provides information on bootstrap estimation bias and acceleration, or skewness in the bootstrap distribution, to guide the choice of method. When the bias and skewness are minimal, both the BCa percentile and PERC methods are valid, producing very similar confidence intervals. It is noted that the BCa percentile method tends to yield slightly narrower intervals than the PERC method, though this difference is not statistically significant nor consistent across all sample sizes, as observed with the reference confidence intervals generated. However, when bias and skewness are substantial (|bias| > 0.1 and |a| > 0.025 with mean samples), the BCa percentile method is recommended over PERC [51]. The script can also include the calculation of the confidence interval by the normal or Gaussian method (type = c("perc", "bca", "norm")). This method necessitates a sample of at least 30 data points, symmetry, and a bell-shaped normal distribution in the histogram of the bootstrap distribution.

Additionally, the script enables us to assess skewness using the box plot, which offers a visual approximation of symmetry, and with the histogram using the Freedman-Diaconis rule, allowing us to determine an optimal bin width without assuming normality [46]. By adding a density curve to the histogram, calculated with Epanechnikov's kernel function [47] and the Sheather-Jones bandwidth [48], a very accurate estimate of the underlying distribution is achieved, which is particularly relevant at the inferential level [52].

Another inferential addition to the script is the calculation of the bootstrap probability for the null hypothesis of symmetry. This probability tends to be conservative towards the null hypothesis, so the significance level can be adjusted to 0.1, especially for samples smaller than 100 [53]. To this end, it is changed to: alpha <- 0.1.

With respect to the second objective of providing suggestive symmetry rules for g_{GSV}, bootstrap confidence intervals were generated at 90%, 95%, and 99%, which are the widths commonly considered, by the nonparametric methods BCa and PERC, chosen for the script as they are the most recommended [30]. These were generated from 34 non-random population-samples but defined from the probit function or quantile function of the normal distribution with an arithmetic sequence in the quantile orders, between 0.001 for the minimum sample value and 0.999 for the maximum sample value. Thus, perfectly symmetric and normally distributed population data were obtained, so that the (population) g_{GSV} statistic always resulted in −1. One seed (123) was used for random resampling, which makes the reference intervals perfectly reproducible. We opted for 1000 draws, as in the script, to minimize standard errors [26]. Additionally, 95% confidence intervals were generated by a parametric (normal) method for samples of at least 30 data. Since it is less recommended, only the most conventional width is reported.

With samples of 30 or more data, the bootstrap estimation bias and skewness of the bootstrap distribution are small, so all three methods for obtaining reference confidence intervals are valid. It should be noted that the sampling distribution of $g_{GSV}(x)$ converges to a normal distribution if the variable X follows a normal distribution, implying that this distributional convergence is also going to occur when the conditions of the central limit theorem are satisfied, namely, that the distribution of the variable has a finite mean and variance and that the random sample is large in size [54]. These reference intervals suggestive of symmetry are complementary to the interval obtained from the sample data by BCa or PERC methods and visual inspection of the plots. The reference intervals only go up to 2000 data. Since random samples of more than 2000 data are very precise in their estimates, no symmetry-suggestive norms were considered necessary from a standard normal distribution model for such sizes.

With respect to the third objective, concerning the relationship of g_{GSV} with three skewness criteria, namely, the quartile and percentile skewness coefficients, and jackknife acceleration, the correlations were high, greater than 0.88. The highest association was with the percentile skewness coefficient, with a shared variance of 93.2%. This correlation was significantly higher than the correlations of g_{GSV} with the quartile skewness coefficient and jackknife acceleration. The effect size of the coefficient type on the strength of association was medium, indicating that the findings have potential practical applications or are worth considering [55].

The percentile skewness coefficient, by defining the two parts of the distribution with a very wide range and using the median as the axis of symmetry, closely resembles the proposal of Gunver et al. [25]. Even the correlation of g_{GSV} and PSC with jackknife acceleration is statistically equivalent. Consequently, it is a valid measure of asymmetry, interchangeable with the percentile coefficient.

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It is probably also the case with respect to Altinay's measure of asymmetry [17], which uses the median as the axis of symmetry. It should be recalled that this author proposes the arithmetic mean and mode as other options for the axis of symmetry, although he finally recommends the median.

7. Conclusions

This article provides a practical and fairly comprehensive script for assessing symmetry with the Gunver-Senocak-Vehid coefficient of skewness, as well as suggestive interpretive rules for symmetry modeled after the normal distribution, which allow us to appreciate the behavior of this measure. The sampling distribution of the g_{GSV} coefficient converges to a normal distribution if the variable follows a normal distribution, or when the conditions of the central limit theorem are satisfied, that is, when the variable follows a distribution of finite mean and variance and the sample size is large. The g_{GSV} coefficient is interchangeable with the percentile skewness coefficient and has a high strength of association with the quartile skewness coefficient and the jackknife acceleration.

8. Future Scope

The use of the script is recommended for measuring asymmetry with random samples of at least 30 data and obtaining the confidence interval with the BCa method, either at 90% ($n \leq 100$) or 95% (in general) from the practical scope of this work. Considering the distributional convergence of g_{GSV}, it is suggested to use the delta method to obtain an asymptotic standard error and to be able to define a Wald-type asymptotic confidence interval [56].

The relationship of g_{GSV} [25] can be studied with Altinay's coefficient of skewness [17], Groeneveld and Meeden's integrated quantile skewness coefficient [16], Hogg's adaptive and robust measure of skewness [23], as well as asymmetry measures based on the standardized third central moment [11] or the standardized third cumulant [13]. Expectations are for high correlations (> 0.80) and very high (> 0.90) with the first two measures of skewness due to their greater affinity. It is also useful to analyze and discuss the nuances of unshared variation.

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