Discrete and Smoothed Resampling Methods for Interval Numbers

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Abstract. The classical Efron's bootstrap is a widely used tool in statistical inference. However, because of its disadvantages, many other resampling algorithms were proposed in the literature, especially for the real-valued data. In this paper, we consider three resampling methods for the special case of the interval real-valued data. They were inspired by the smoothed bootstrap and special algorithms known for fuzzy numbers. Using numerical simulations and statistical tools, the introduced methods are compared with the Efron's bootstrap. It seems that these new algorithms produce samples that can be considered as "similar, but not exactly the same" as the initial data, which is an important aim in the case of resampling methods.

Keywords: Statistical simulations · Smoothed bootstrap · Non-parametric model · Bootstrap · Imprecise data.

1 Introduction

The classical Efron's bootstrap [6] is a very powerful tool in statistical inference [4]. However, due to its important shortcomings (like the repetitions of the same values especially seen for small samples), many other resampling algorithms were developed, like the smoothed bootstrap [22], wild bootstrap [3], etc. They are widely used in, e.g., estimation procedures, hypotheses testing, construction of confidence intervals, and regression analysis.

The resampling methods were also applied "outside the world of real numbers" and proved to be useful statistical techniques also in the case of fuzzy numbers [8–11, 13, 17, 19].

Inspired by the above-mentioned approaches, especially the smoothed bootstrap, d-method [19], and s-method [20], we propose three different resampling methods for the special case of the interval random numbers. Such a kind of statistical data is closely related to the imprecise information [15] and requires a special treatment taking into account its interval structure. To achieve greater flexibility and omit the unnecessary assumptions about the initial sample, we

focus on non- or semi-parametric algorithms based on increases of the intervals, non-informative distribution (the uniform distribution in this case), and the Gaussian kernel density estimators. Moreover, these introduced methods exploit the inner structure of the data, i.e. information about the ends of their intervals. Due to this, these approaches can be directly extended, e.g., for the triangular and trapezoidal fuzzy numbers which can be seen as a kind of unions of "points" or "intervals" (the cores of the triangular or trapezoidal fuzzy numbers, respectively), and additional "intervals" (given by the respective supports of these fuzzy numbers).

The proposed approaches were also numerically compared with the classical Efron's bootstrap directly adapted to the interval real numbers. During our analysis, the synthetic initial samples were simulated from various probability distributions. Then, both the statistical graphs and tests (including the goodness-of-fit and variance tests) were applied. It seems that these new resampling algorithms (especially the third one) lead to interesting results. The variability of the secondary (i.e. bootstrapped) samples was increased when compared with the outputs for the Efron's bootstrap. This is an important advantage. Moreover, the goodness-of-fit tests did not reject the hypotheses concerning agreement between the distributions of the initial and secondary samples regarding the ends and middles of the intervals. Therefore, we obtain the new samples that are "very similar, but not the same as initial values" – an important goal of other resampling approaches [11, 20].

The paper is organized as follows. In Sect. 2, the necessary notation is introduced, and some basic facts about the resampling methods are recalled. The new resampling algorithms for the interval numbers are described in Sect. 3. Their exhaustive numerical analysis is conducted in Sect. 4. Then, some final remarks are presented in Sect. 5.

2 Preliminaries

Let us start with the following definition:

Definition 1. *Let X^L and X^R be two random real-valued variables defined on the same sample space Ω such that $X^L(\omega) \leq X^R(\omega)$ for all $\omega \in \Omega$. Then $\boldsymbol{X} = \left[X^L, X^R\right]$ is called a random interval. A random sample $\mathbb{X} = (\boldsymbol{X}_1, \ldots, \boldsymbol{X}_n)$ consists of n* iid *random intervals.*

Now we recall some basic facts concerning the resampling methods considered further on. Let $\mathbb{x} = (x_1, \ldots, x_n)$ be a realization of a real-valued random sample of size n (so-called *the initial sample*). The Efron's bootstrap [6] generates the bootstrapped (secondary) sample $\mathbb{y} = (y_1, \ldots, y_m)$ using the values from $\mathbb{x}$ with repetitions and constant probabilities $\frac{1}{n}$, where usually $m = n$. The whole procedure can be repeated B times, so we get $\mathbb{y}^i = \left(y_1^i, \ldots, y_m^i\right)$ for $i = 1, \ldots, B$.

In the case of the smoothed bootstrap [22], the values in the bootstrapped sample $\mathbb{y}$ are also drawn from the initial sample $\mathbb{x}$, but then the random noise generated from some kernel density estimator is added to each of them. This

procedure leads to greater variability of the outputs which may be helpful especially when the initial data were modeled with some continuous probability distribution. Many different kernel densities were proposed in the literature, e.g., the Gaussian one [1].

The d-method [19] is a resampling approach for fuzzy numbers, especially useful for the triangular or trapezoidal ones (see, e.g., [2]). During its first step, the initial sample of fuzzy numbers is decomposed into four auxiliary sets, consisting of the left ends of cores of these fuzzy values, the width of their cores, left and right increases of their supports. Then, the secondary sample is created using these special sets. Each output fuzzy number is built from the randomly drawn (with repetitions and the constant probabilities) elements from the auxiliary sets, starting with its core and ending with its support.

This approach was extended for the interval fuzzy numbers in [20], where another algorithm, known as the s-method, was also proposed. Because of special features of the interval fuzzy numbers (see, e.g., [5]), the initial sample in the s-method is decomposed into auxiliary sets consisting of pairs related to the respective lower and upper fuzzy numbers. Then, during the building of a new value for the bootstrapped sample, two-dimensional variables from specially tailored normal densities are added to the left ends of the cores, their widths, etc. The underlying idea for this procedure is closely related to the smoothed bootstrap.

3 New resampling approaches

Let $\mathbb{x} = (\boldsymbol{x}_1, \ldots, \boldsymbol{x}_n)$ be a realization of a primary sample of real-valued interval numbers $\boldsymbol{x}_i = \left[x_i^L, x_i^R\right]$, where $i = 1, \ldots, n$. In this section, we discuss three resampling methods to create a bootstrapped (i.e., secondary) sample $\mathbb{y} = (\boldsymbol{y}_1, \ldots, \boldsymbol{y}_m)$, where $\boldsymbol{y}_i = \left[y_i^L, y_i^R\right]$ for $i = 1, \ldots, m$.

There are two steps in **method 1**, which is closely related to the d-method [19, 20] (see also Sect. 2). During the initialization step, two auxiliary sets $\mathcal{L}$ and $\mathcal{R}$ are created (see Algorithm 1). The first one consists of the left ends of the intervals from $\mathbb{x}$, namely $\mathcal{L} = \left\{x_1^L, \ldots, x_n^L\right\}$, and the second one contains the respective lengths of these intervals, so $\mathcal{R} = \left\{x_1^R - x_1^L, \ldots, x_n^R - x_n^L\right\}$.

Algorithm 1 Method 1 – Initialization step

Require: The initial sample $\mathbb{x} = (\boldsymbol{x}_1, \ldots, \boldsymbol{x}_n)$
Ensure: The auxiliary sets $\mathcal{L}$ and $\mathcal{R}$
1: **for** $i = 1, \ldots, n$ **do**
2: Append x_i^L to $\mathcal{L}$
3: Append $x_i^R - x_i^L$ to $\mathcal{R}$
4: **return** $\mathcal{L}, \mathcal{R}$

Then, for each $i = 1, \ldots, m$, a new interval value $\boldsymbol{y}_i$ is created (see Algorithm 2). Its left end y_i^L is randomly drawn from $\mathcal{L}$, and the respective length

d_i is generated using $\mathcal{R}$. In both cases, repetitions are possible and the constant probability $\frac{1}{n}$ is applied. The right end y_i^R of the new interval is calculated as a sum of its left end and length, namely $y_i^R = y_i^L + d_i$.

Algorithm 2 Method 1 – Resampling step

Require: The sets $\mathcal{L}, \mathcal{R}$
Ensure: The secondary sample $\mathbb{y} = (\boldsymbol{y}_1, \ldots, \boldsymbol{y}_m)$
1: **for** $i = 1, \ldots, m$ **do**
2: Randomly draw y_i^L from $\mathcal{L}$
3: Randomly draw d_i from $\mathcal{R}$
4: $y_i^R \leftarrow y_i^L + d_i$
5: $\boldsymbol{y}_i \leftarrow \left[y_i^L, y_i^R\right]$
6: **return** $\mathbb{y}$

When the smoothed approach (as in the case of the s-method [20], see also Sect. 2) is applied to the *method 1*, we obtain a more complex **method 2**. Its first, initialization step is the same as in the previous case (see Algorithm 1). During the second step, the Gaussian kernel density estimator $\hat{f}_{\mathcal{L}}$ is calculated based on the set $\mathcal{L}$ (see also [21, 22]), e.g., using the function *density* in R (see Algorithm 3). Next, the respective left end y_i^L of the new interval $\boldsymbol{y}_i$ is randomly drawn from this density $\hat{f}_{\mathcal{L}}$, and the length d_i is generated similarly as in the *method 1*, i.e., using $\mathcal{R}$ and the discrete probabilities $\frac{1}{n}$. As previously, the right end y_i^R is obtained as the sum $y_i^L + d_i$.

Algorithm 3 Method 2 – Resampling step

Require: The sets $\mathcal{L}, \mathcal{R}$
Ensure: The secondary sample $\mathbb{y} = (\boldsymbol{y}_1, \ldots, \boldsymbol{y}_m)$
1: Calculate the Gaussian kernel density estimator $\hat{f}_{\mathcal{L}}$ using $\mathcal{L}$
2: **for** $i = 1, \ldots, m$ **do**
3: Randomly draw y_i^L from $\hat{f}_{\mathcal{L}}$
4: Randomly draw d_i from $\mathcal{R}$
5: $y_i^R \leftarrow y_i^L + d_i$
6: $\boldsymbol{y}_i \leftarrow \left[y_i^L, y_i^R\right]$
7: **return** $\mathbb{y}$

The *method 2* may be criticized as being more parametric in its form, because of using the Gaussian kernel during the second step. Of course, other types of kernels can be applied, instead of the Gaussian one. However, we propose another approach aimed to be a more non-parametric one – the **method 3**.

Once again, the first step of the *method 3* is run as previously (see Algorithm 1). Next, two Gaussian kernel density estimators are calculated, $\hat{f}_{\mathcal{L}}$ using $\mathcal{L}$, and $\hat{f}_{\mathcal{R}}$ with $\mathcal{R}$, respectively (see Algorithm 4). Then, for each $i = 1, \ldots, m$,

a single interval $\boldsymbol{x}_* = \left[x_*^L, x_*^R\right]$ is randomly drawn from the initial sample $\mathbb{x}$ as in the classical bootstrap. The values from this interval are treated as quantiles to calculate their orders, $\hat{p}_L$ for the left end x_*^L using the cdf (cumulative distribution function) $F_{\hat{f}_\mathcal{L}}$ related to $\hat{f}_\mathcal{L}$, and $\hat{p}_L$ for the right end x_*^R with the cdf $F_{\hat{f}_\mathcal{R}}$ based on $\hat{f}_\mathcal{R}$, respectively.

To give us an additional level of "variability" for the output, the obtained orders of the quantiles are expanded to two intervals $[\hat{p}_L - r_q, \hat{p}_L + r_q]$ and $[\hat{p}_R - r_q, \hat{p}_R + r_q]$ for some $r_q > 0$. Afterward, these two intervals are transformed back to intervals of the quantiles using the respective inversions of the cdfs $F^{-1}_{\hat{f}_\mathcal{L}}$ and $F^{-1}_{\hat{f}_\mathcal{R}}$ with the formulas

$$\boldsymbol{q}_L = \left[\max\left(0, F^{-1}_{\hat{f}_\mathcal{L}}(\hat{p}_L - r_q)\right), \min\left(1, F^{-1}_{\hat{f}_\mathcal{L}}(\hat{p}_L + r_q)\right)\right], \tag{1}$$

$$\boldsymbol{q}_R = \left[\max\left(0, F^{-1}_{\hat{f}_\mathcal{R}}(\hat{p}_R - r_q)\right), \min\left(1, F^{-1}_{\hat{f}_\mathcal{R}}(\hat{p}_R + r_q)\right)\right]. \tag{2}$$

In this way, we can draw both ends y_i^L, y_i^R of the new output interval $\boldsymbol{y}_i$ from the uniform distributions on $\boldsymbol{q}_L$ (denoted further on by $U\left[\boldsymbol{q}_L\right]$, so $y_i^L \sim U\left[\boldsymbol{q}_L\right]$) and $\boldsymbol{q}_R$ (i.e. $y_i^R \sim U\left[\boldsymbol{q}_R\right]$), respectively. Using the non-informative distribution (i.e. the uniform density in this case) leads to a more non-parametric approach than for the *method 2*. Moreover, the extension parameter r_q gives us the possibility to control the "variability" of the output, if it should be smaller (for the low values of r_q) or bigger (otherwise).

The ends of the output interval obtained in this way should fulfill the obvious condition $y_i^L \leq y_i^R$. In the contrary case, they have to be generated once again.

Algorithm 4 Method 3 – Resampling step

Require: The sets $\mathcal{L}, \mathcal{R}$
Ensure: The secondary sample $\mathbb{y} = (\boldsymbol{y}_1, \ldots, \boldsymbol{y}_m)$
1: Calculate the Gaussian kernel density estimators $\hat{f}_\mathcal{L}$ for $\mathcal{L}$, and $\hat{f}_\mathcal{R}$ for $\mathcal{R}$
2: **for** $i = 1, \ldots, m$ **do**
3: Randomly draw $\boldsymbol{x}_* = \left[x_*^L, x_*^R\right]$ from $\mathbb{x}$
4: $\hat{p}_L \leftarrow F_{\hat{f}_\mathcal{L}}\left(x_*^L\right)$
5: $\boldsymbol{q}_L \leftarrow \left[\max\left(0, F^{-1}_{\hat{f}_\mathcal{L}}(\hat{p}_L - r_q)\right), \min\left(1, F^{-1}_{\hat{f}_\mathcal{L}}(\hat{p}_L + r_q)\right)\right]$
6: $\hat{p}_R \leftarrow F_{\hat{f}_\mathcal{R}}\left(x_*^R\right)$
7: $\boldsymbol{q}_R \leftarrow \left[\max\left(0, F^{-1}_{\hat{f}_\mathcal{R}}(\hat{p}_R - r_q)\right), \min\left(1, F^{-1}_{\hat{f}_\mathcal{R}}(\hat{p}_R + r_q)\right)\right]$
8: **repeat**
9: Randomly draw y_i^L from $U\left[\boldsymbol{q}_L\right]$
10: Randomly draw y_i^R from $U\left[\boldsymbol{q}_R\right]$
11: **until** $y_i^L \leq y_i^R$
12: $\boldsymbol{y}_i \leftarrow \left[y_i^L, y_i^R\right]$
13: **return** $\mathbb{y}$

4 Numerical analysis

We compared the three resampling methods proposed in Sect. 3 with their classical counterpart – the Efron's bootstrap directly adapted to the interval numbers (when each whole interval $\left[x^L, x^R\right]$ is randomly drawn from the initial sample $\mathbb{x}$ with the probability $\frac{1}{n}$ and possible repetitions). In our analysis, synthetic samples consisting of interval real-valued numbers generated from different probability distributions were created. To obtain the initial sample $\mathbb{x} = (\boldsymbol{x}_1, \ldots, \boldsymbol{x}_n)$, realizations of two independent random variables were necessary. The first variable X^L was used for the left ends of $\mathbb{x}$, i.e., $\mathbb{x}^L = \left(x_1^L, \ldots, x_n^L\right)$, and the second one X^R – for their right-hand side counterparts $\mathbb{x}^R = \left(x_1^R, \ldots, x_n^R\right)$ (see, e.g., [11, 18, 19] for similar approaches). Their distributions are summarized in Table 1, where $U(a, b)$ stands for the uniform distribution on the interval $[a, b]$, $N(\mu, \sigma)$ denotes the normal distribution with the expected value μ and standard deviation σ, $\Gamma(\alpha, \beta)$ – the gamma distribution with the shape parameter α and scale parameter β. It should be noted that the probability distribution for the right ends of Γ/NN is the most interesting one, as a composition of two normal distributions with rather distant modes.

Table 1. Probability distributions of the types of synthetic samples.

Type	Left end	Right end
U/U$_1$	$U(0, 100)$	$U(0, 100)$
U/U$_2$	$U(0, 1)$	$U(0, 1)$
N/U$_1$	$N(0.24, 0.5)$	$U(0, 0.25)$
N/U$_2$	$N(1, 1)$	$U(0, 1)$
Γ/Γ_1	$\Gamma(0.08, 2.5)$	$\Gamma(0.08, 2.5)$
Γ/Γ_2	$\Gamma(0.5, 2.5)$	$\Gamma(0.5, 2.5)$
Γ/NN	$\Gamma(2, 1)$	$\frac{1}{2}N(5, 2) + \frac{1}{2}N(20, 3)$

To shorten the length of this paper, only some of the obtained numerical results are presented in the following. Others are available upon request.

4.1 Convergence to the means

We started from analysis of the convergence of the means $\bar{y}^L(m), \bar{y}^R(m)$ for the left and right ends, respectively, together with the middles $\bar{\dot{y}}(m)$ of the intervals for the bootstrapped sample $\mathbb{y} = (\boldsymbol{y}_1, \ldots, \boldsymbol{y}_m)$ as the function of its size m, to their counterparts $\bar{x}^L, \bar{x}^R, \bar{\dot{x}}$ based on the initial sample $\mathbb{x}$, where

$$\bar{y}^L(m) = \frac{1}{m}\sum_{i=1}^{m} y_i^L, \qquad \bar{y}^R(m) = \frac{1}{m}\sum_{i=1}^{m} y_i^R \qquad \bar{\dot{y}}(m) = \frac{1}{m}\sum_{i=1}^{m} \frac{y_i^L + y_i^R}{2} \tag{3}$$

$$\bar{x}^L = \frac{1}{n}\sum_{i=1}^{n} x_i^L, \qquad \bar{x}^R = \frac{1}{n}\sum_{i=1}^{n} x_i^R \qquad \bar{\dot{x}} = \frac{1}{n}\sum_{i=1}^{n} \frac{x_i^L + x_i^R}{2}. \tag{4}$$

In our experiments, the rather small samples U/U_1, N/U_1, Γ/Γ_1, Γ/NN with $n = 20$ elements were considered. For some exemplary results, see Figs. 1–2.

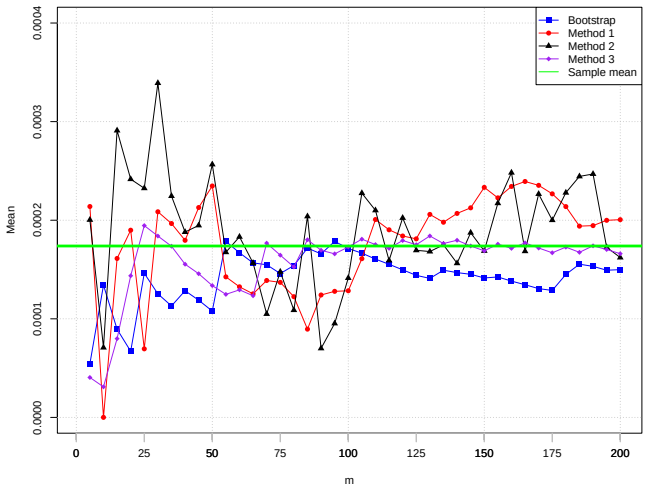


Fig. 1. Convergence of the means for the left ends of the intervals for Γ/Γ_1.

The resampling means converged to their counterparts related to the initial sample in all cases. It seems that the variability for the *method 2* was rather big during the initial steps, but then its trajectory stabilized. The *method 3* had the fastest convergence speed and rather stable trajectory. However, in the case of Γ/Γ_1, it led to values of the means that are bigger than for other methods.

4.2 Behavior of the ends of intervals

We also compared the plots of the sorted values for the left and right ends of the intervals. To do this, the initial samples consisting of $n = 20$ elements of the same types as in Sect. 4.1 were generated. Then, after their resampling, the outputs for the secondary samples (with $m = 100$) were sorted and compared with the initial values. Some exemplary results can be found in Fig. 3, where the horizontal axes are related to the indexes of observations, and the vertical axes – to their sorted values.

The *method 1* gave outputs that are very similar to the classical bootstrap – it directly follows from its construction. Both the *method 2* and *method 3* reproduced exactly the initial sample, even with some of its discontinuities. Moreover, this last approach resulted in an almost linear approximation of some "missing values" that can be observed in the initial sample (compare Figs. 3a and 3d).

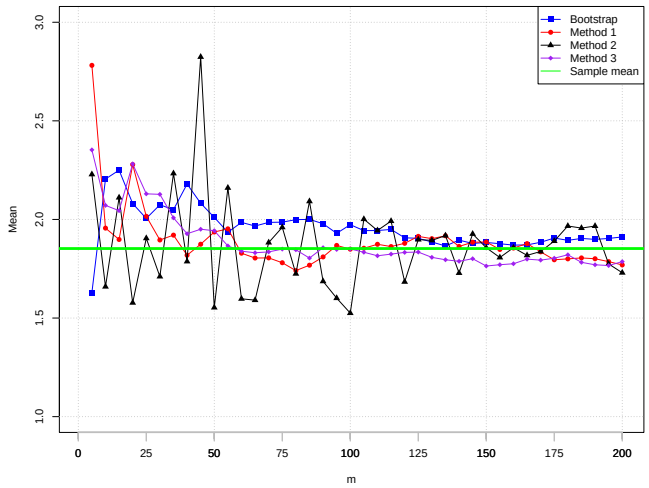


Fig. 2. Convergence of the means for the left ends of the intervals for Γ/NN.

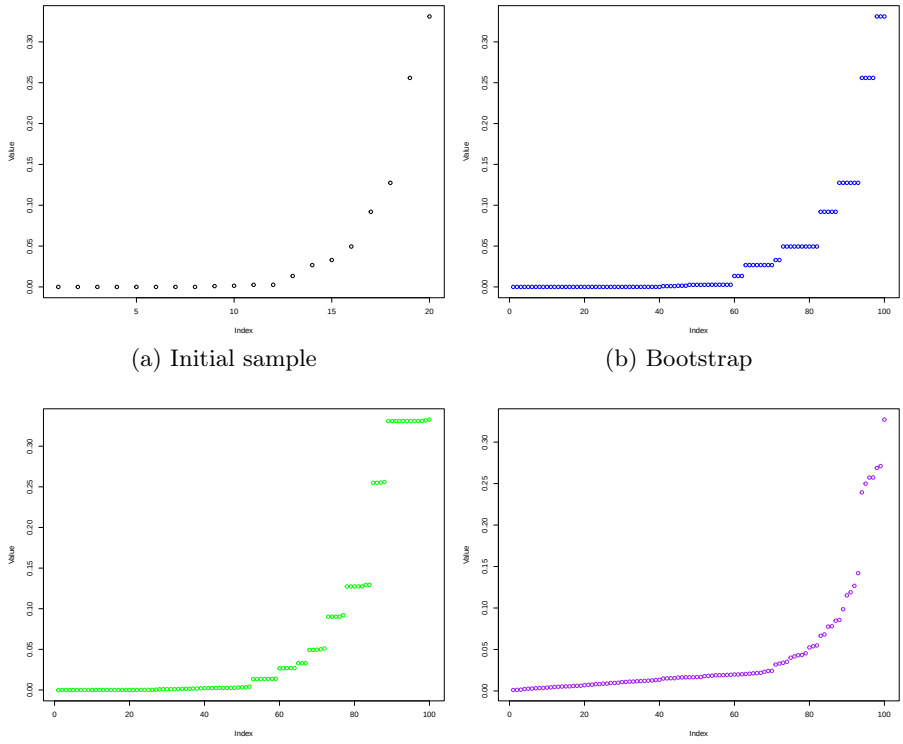
4.3 Statistical tests

Next, the resampling methods were compared with the help of statistical tests. For each initial sample of the size $n = 20$, the new secondary sample with $m = 100$ elements was created, and then various tests were conducted. To minimize the randomness of their outputs, each experiment was repeated $l = 100$ times, and the obtained p-values were averaged then (see also, e.g., [11, 12] for the similar approaches).

Firstly, the two-sample goodness-of-fit Kolmogorov-Smirnov test (abbreviated further as the KS test [16]) and Mann-Whitney U test (denoted by the U test [14]) were applied. We checked if the probability distributions of the left ends of the intervals for the initial sample $\mathbb{x}^L$ and secondary one $\mathbb{y}^L = \left(y_1^L, \ldots, y_m^L\right)$ can be considered as the same, just as the probability distributions of the right ends for the initial sample $\mathbb{x}^R$ and its resampled counterpart $\mathbb{y}^R = \left(y_1^L, \ldots, y_m^R\right)$, and the middles of the intervals $\dot{\mathbb{x}} = (\dot{\boldsymbol{x}}_1, \ldots, \dot{\boldsymbol{x}}_n)$ versus $\dot{\mathbb{y}} = (\dot{\boldsymbol{y}}_1, \ldots, \dot{\boldsymbol{y}}_m)$, respectively. Exemplary results for the estimated p-values of the KS test are given in Table 2.

For all of these considered cases, the null hypotheses about the same distributions were not rejected, even for high significance levels like 0.45. But it seems that the *method 3* (together with the classical bootstrap, which is rather unsurprising) gave the highest p-values. This is especially seen in the KS test.

Then, we compared the variances of the left ends of the intervals for the initial and secondary samples, and also the variances of their right counterparts, with the help of the Levene's test (e.g., [7]). The obtained averaged p-values are given in Table 3. The null hypotheses about the equality of the variances could not be rejected for the classical significance level of 0.05. However, the proposed resampling methods led to the relatively high p-values, even about 0.7–0.8. On



(a) Initial sample (b) Bootstrap

(c) Method 2 (d) Method 3

Fig. 3. Sorted values for Γ/Γ_1.

the contrary, the classical bootstrap behaved in a very unstable manner, and for N/U_2 and Γ/Γ_2 the obtained p-values were much closer to 0.15.

5 Conclusion

In this paper, we presented three different resampling methods for the interval real-valued numbers. They were inspired by the smoothed bootstrap (developed for real numbers), together with the *d*- and *s*-methods (introduced for fuzzy numbers). After conducting numerical comparisons based on simulations, it seems that especially the third method leads to interesting results. We achieved greater variability than for the Efron's bootstrap without the rejection of the null hypothesis in the goodness-of-fit tests. Therefore, the obtained secondary samples can be seen as "similar, but not the same" when compared with the initial data.

We are aware of the fact that for the interval-valued random numbers, the most important is the joint distribution of the two ends of these intervals. However, in the case of the *method 1* and *method 2*, we consider a simpler resampling

Table 2. Averaged p-values for the KS test

Type	U/U_2	N/U_2	Γ/Γ_2	Γ/NN
Left ends				
Bootstrap	0.98273	0.97170	0.97571	0.97208
Method 1	0.57936	0.86509	0.79504	0.69609
Method 2	0.49309	0.84862	0.74592	0.66200
Method 3	0.92678	0.91202	0.80107	0.87577
Right ends				
Bootstrap	0.98273	0.97170	0.97571	0.97208
Method 1	0.57936	0.86509	0.79504	0.69609
Method 2	0.49309	0.84862	0.74592	0.66200
Method 3	0.92678	0.91202	0.80107	0.87577
Middles				
Bootstrap	0.98273	0.97170	0.97571	0.97208
Method 1	0.57936	0.86509	0.79504	0.69609
Method 2	0.49309	0.84862	0.74592	0.66200
Method 3	0.92678	0.91202	0.80107	0.87577

Table 3. Averaged p-values for the Levene's test

Type	U/U_2	N/U_2	Γ/Γ_2	Γ/NN
Left ends				
Bootstrap	0.73318	0.75163	0.65573	0.74148
Method 1	0.74165	0.72858	0.63140	0.76282
Method 2	0.74268	0.79654	0.68247	0.72330
Method 3	0.75259	0.75990	0.63444	0.74392
Right ends				
Bootstrap	0.79805	0.17125	0.13193	0.80441
Method 1	0.80816	0.71755	0.63669	0.78242
Method 2	0.82147	0.72449	0.78333	0.73931
Method 3	0.80648	0.78606	0.73810	0.81620

approach when the left end of the interval and its respective diameter are generated independently. Such an idea is similar to the one represented by the d-method for fuzzy numbers and leads to greater numerical efficiency of these algorithms. Nevertheless, in the case of the *method 3*, some properties of the joint distribution are taken into account with the additional level of "variability" of the obtained results due to using non-informative uniform distributions for both ends of the resampled intervals.

Of course, there are still other ideas that can be used to develop new resampling methods, e.g., the correlation coefficient between the ends of the intervals can be useful in further exploiting the inner structure of the interval data [20].

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