



Article Comparing the Robustness of Statistical Estimators of Proficiency Testing Schemes for a Limited Number of Participants

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Abstract: This study aims at developing models in analyzing the results of proficiency testing (PT) schemes for a limited number of participants. The models can determine the best estimators of location and dispersion using unsatisfactory results as a criterion by combining: (a) robust and classical estimators; (b) kernel density plots; (c) Z-factors; (d) Monte Carlo simulations; (e) distributions derived from the addition of one or two contaminating distributions and one main Gaussian. The standards ISO 13258:2015, ISO 5725:2:1994, and EN ISO/IEC 17043:2010 are the basis of the analysis. The study describes an algorithm solving the optimization problem for (a) Gaussian, bimodal or trimodal distributions; (b) participating labs from 10 to 30; (c) fraction of the contaminating population up to 0.10; (d) variation coefficient of the main distribution equal to 2; (e) equal standard deviations of all the distributions, and provide figures with the optimal estimators. We also developed a generalized algorithm using kernel density plots and the previous algorithm, which is not subject to restrictions (b)–(e) and implemented in the results of a PT for the 28-day strength of cement with 12–13 participants. Optimal estimators' figures and the generalized algorithm are helpful for a PT expert in choosing robust estimators.

Keywords: proficiency testing; robust estimator; kernel; Monte Carlo; optimization



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1. Introduction

In an interlaboratory test, different laboratories measure one or more characteristics of one or various homogenous samples, following the corresponding standards and documented procedures. The evaluation of participant performance against pre-established criteria through interlaboratory comparisons is called proficiency testing (PT) [1] (p. 2). The PT is a means in verifying and improving the technical competence of labs, and it is one of the accreditation requirements according to ISO/IEC 17025: 2017 [2] (p. 14). Z-score usually expresses the performance of each participant. The value of Z depends on both assigned value and standard deviation for proficiency assessment [1] (p. 30). These two values are frequently affected by results appearing inconsistent with the remainder dataset, called outliers. ISO/IEC 17043:2010 requires the use of robust statistical methods or appropriate tests to detect statistical outliers, where such statistical methods are defined as being insensitive to small departures from underlying assumptions surrounding a probabilistic model [1] (pp. 2–3). The vulnerability of the most common statistical estimators to the data contamination by noise or outliers led to this research and motivated the use of robust statistical estimation. The robustness measure of the first statistical estimators was the influence function, and they were robust to small changes of a single measurement. Later, the focus of robust estimation became methods with a high breakdown point [3]. In connection to the above, the finite sample breakdown point of an estimator is the minimum proportion of observations that, when altered sufficiently, can render the statistic beyond all bounds [4,5]. A systematic treatment of robust statistics is provided by Hampel et al. [6], Huber et al. [7], and Maronna et al. [8]. A series of researchers focused on specific areas of robust statistics, such as the kernel density estimation [9–11] and the robust estimates of

location and standard deviation in control charts [12,13]. Annex C of ISO 13258:2015 [14] describes a series of robust estimators for the population mean and standard deviation widely used in PT schemes as an alternative to the classical method analyzed in 5725–2:1994 [15]. The estimators of the population mean are the median value, *MED*; the average according to algorithm A with iterated scale, Ax^* ; the Hampel estimator for mean, Hx^* . The corresponding estimates of the standard deviation are the scaled median absolute deviation, *MADe*; the normalized interquartile range, *nIQR*; the estimator according to algorithm A with iterated scale, As^* ; the estimator according to the Q method, Hs^* . ISO 13253:2015 [14] (p. 53) notifies that the *MADe* estimator shows appreciable negative bias for participants less than 30, which may adversely affect the Z values. Rosseeuw et al. [16] constructed alternative estimators to the *MADe* by studying their influence functions, their bias curves, and their finite sample performance. These methods rely on applying univariate algorithms to results of one measurand or test material at a time. A multivariate approach is necessary if the participants provide measurements of a characteristic in several test materials. Various researchers have faced and successfully solved the multivariate problem [17–20].

Although there is widespread development and implementation of PT schemes worldwide for a variety of types of analyzes, tests, and laboratories, the number of studies comparing these estimators for their optimality is limited. Rosario et al. [21] evaluated one round of data of a PT scheme on precious alloys by comparing four statistical methods: (a) ISO 5725-2 to calculate the grand mean and reproducibility; (b) MED and MADe; (c) algorithm A of ISO 13528 for the robust average and standard deviation; (d) fit-forpurpose criterion [22] using the robust average and a target reproducibility derived from past tests. They comment on the results of each method without coming up with an optimal one for these results. Srnková et al. [23] investigated 953 datasets of chemical analyzes performed in soils, sludge and sediments, and other materials of various PT schemes. The processing using the average and standard deviation calculated according to algorithm A with iterated scale [14] was found to be the most suitable for matrices and levels of measurands. Tripathy et al. [24] compared a series of statistical methods for outliers' detection in PT data of lead analysis in an aqueous solution. They used typical outliers' tests described in ISO 5725-2 and the Z-score derived from robust methods like MED-nIQR and method A with an iterated scale. They also utilized a procedure provided by the National Association of Testing Authorities (NATA) of Australia, concluding that it seems more suitable in outliers' detection for the evaluated dataset. Daszykoswki et al. [25], in an excellent review of robust statistics in data analysis, note that the Q estimator shows higher efficiency than MADe at Gaussian distributions. De Oliveira et al. [26] compare different statistical approaches, classical and robust, to evaluate the participants' performance in a PT program for lead in blood determination. One of their main conclusions is that a PT provider should conduct studies using different statistical approaches to obtain the best standard deviation estimate since there is no consensus on which method is more suitable for the experimental data. All the reported comparative studies between the procedures described in the international standards refer to individual PT schemes. A more generalized and practical approach to the robustness and optimal use of these methods remains challenging. Kojima et al. [27] attempted such generalization using a Monte Carlo approach by adding a contaminating Gauss distribution to the main one. They also discuss an actual PT for a dioxin isomer compared with the simulation results. They restricted their study to the next set of parameters: (a) The number of participants is 200; (b) the standard deviation of the main population is 5% of the mean value; (c) the secondary population is 20% of the total. They concluded that the robustness to outliers of the *MED-nIQR* is more significant than the algorithm A with iterated scale and the Q-Hampel method. However, they noticed that the *MED-nIQR* does not always provide the best conclusion in the actual PT due to its reduced degrees of freedom.

ISO 13528:2015 dedicates a part of the informative annex D to describe procedures for a small number of participants [14] (pp. 63–64). Belli et al. [28] and Kuselman et al. [29] studied the implementation of PT schemes for a limited number of participants and the

comparability of their results. Hund et al. [30] report the importance of the labs' number to determine repeatability and reproducibility. The PT organizer usually performs the test several times a year because the participating labs must regularly demonstrate their technical competence.

This study uses the Monte Carlo approach to investigate the optimal use of the robust methods mentioned above by taking as initial point the idea of the addition of a Gaussian distribution and one or two contaminating ones and considering participants ranging from 10 to 30. The ISO guide 98-3 [31], referred to the expression of the uncertainty in measurement, also utilizes the same Monte Carlo approach to investigate the propagation of distributions. The simulation cooperates with the kernel density plots created following ISO 13528:2015 [14] (pp. 32–33). Actual results of the 28-day cement strength measured according to EN 196-1 [32] are also processed, belonging to a PT scheme of cement organized by Eurocert S.A. This company is the provider for several accredited and fully conforming with ISO/IEC 17043:2010 PT schemes in construction materials, one of which is the PT of cement. The organizer performs the cement scheme nine rounds a year with 11–14 participants per round, including all the tests defined by the standard EN 197-1 [33]. All tests performed on all PT schemes follow international test standards of the respective materials to minimize the uncertainty due to the measurement method. For all the PT schemes, the organizer shows special care for the homogeneity and stability of the distributed samples by strictly applying the corresponding sections of the standards ([1] pp. 8–9, [14] pp. 44–51). Note that this is not an easy task for samples of some building materials. Examples include preparing cubic specimens of fresh concrete and obtaining hardened concrete cores. Participants pass their results on specialized software forms to avoid numerical errors as much as possible. The organization has a committee to assess the results of all schemes and a technical expert who developed the software for evaluating the results. This software computes all estimators for location, standard deviation, and repeatability provided in [14,15], including uncertainties for assigned value and repeatability. The algorithm calculates the Z-factors per participant and each test result, using the respecting values of Hx^* and Hs^* . The report of each round comprises, except the numerical results, various charts assisting in evaluating the performance of each lab: Control charts of Z-score; Grubbs' test; Cochran's test; Kernel density plots; plots of repeatability standard deviation. The central evaluating indicator is the Z-score, while the others are informative.

The structure of the paper is as follows. Section 2 presents the kernel density plots as a possibility to estimate the results' distribution and shows that the sum of two or three normal distributions of adjustable parameters can adequately approximate an actual kernel density plot. The section also describes the Monte Carlo-based model and its inputs and outputs. Section 3 compares the population means and standard deviations of all the methods reported in [14,15] for selected distributions. It also provides an algorithm in determining the best estimators for a small number of laboratories when the contaminating populations are up to 10% of the total. Section 4 implements this algorithm concluding in some tables of optimal estimators if the model assumptions are valid or nearly valid. Additionally, it provides a generalized algorithm taking into account the findings of Sections 2 and 3, which, finally, is applied to 18 datasets of actual PT results. The author developed all software in C#.

2. Model Development

One of the main goals of a PT scheme is to enable the participating laboratories to have a unimodal distribution of results through the corrective actions taken in each round of tests. However, the distribution of most data sets is not symmetrical or includes a proportion of results that are distant from the rest. One of the tasks of this research is the effective modeling of these density functions in a form convenient to apply the estimators of the location and variance referred to the statistical standards related to the PT schemes and to calculate the respecting Z-factors. The probabilistic assumption used in modeling

the density distribution of the PT results is that it comes from the addition of Gaussian distributions of different mean values and equal or unequal variations. The model assumes up to three distributions, one of which is the main one and the others are contaminating ones. The resulting sum of such distributions fits well with the actual ones, as one can see in Section 2.1.

2.1. Kernel Density Plots and Initial Simulations

ISO 13258-2015 [14] (p. 10, Note 1) refers that a kernel density plot is functional in identifying bimodalities or lack of symmetry. This standard describes the algorithm to develop these plots in paragraph 10.3 [14] (pp. 32–33), and Figure 1 shows two examples of kernels plots of two 28-day strength tests performed during 2020. The software utilizes normal distributions and the nIQR as the standard deviation estimator to derive the kernels, as the standard recommends [14] (p. 32).





The results of each test belong to distributions that are difficult to disclose for participating laboratories, 11 to 13 per round. However, the results of all yearly tests are a population large enough to estimate the distribution. The algorithm achieves normalization by using the difference of the assigned value from the mean value of each participant, $D_{ij} = x_{ij} - x_{pt,j}$, where *i* is the participant and *j* is the round. Figure 2 depicts the kernel functions and the actual 28-day strength results for the 2019 and 2020 rounds.



Figure 2. Actual distributions, kernel plots, and calculated distributions for all the yearly results.

The addition of one or two contaminating normal distributions to the main distribution effectively simulates such situations. The best-fitting mix of normal distributions, having the minimum distance from the kernel distribution, is also presented in Figure 2. The fraction of the surface of each distribution and the corresponding parameters have been computed using the Generalized Reduced Gradient non-linear regression technique, and their values are shown in Table 1.

Table 1. Parameters of the normal distributions.

Parameter	2019	2020
Main distribution mean value, m_1 , MPa	0.00	0.04
Main distribution standard deviation, <i>s</i> ₁ , MPa	1.24	1.46
Second distribution mean value, m_2 , MPa	2.51	4.00
Second distribution standard deviation, s ₂ , MPa	0.90	0.70
Third distribution mean value, m_3 , MPa	-4.30	-3.60
Third distribution standard deviation, s ₃ , MPa	0.90	0.70
Fraction of the main distribution, fr_1	0.812	0.925
Fraction of the second distribution, fr_2	0.107	0.019
Fraction of the third distribution, fr_3	0.081	0.057
Distance of m_1 and m_2 , $ m_2 - m_1 /s_1$	2.0	2.7
Distance of m_1 and m_3 , $ m_3 - m_1 /s_1$	3.5	2.5

Using the subsequent two simple simulations, one can observe the impact of the secondary contaminating distributions on the main one:

- (i) The main normal distribution with $m_1 = 0$ and $s_1 = 1$ represents 90% of the population, while a secondary group representing the rest 10% has $m_2 = 2s_1$, $4s_1$, $6s_1$, and $s_2 = s_1$. The sum of the two populations results in a bimodal distribution.
- (ii) The main distribution with $m_1 = 0$ and $s_1 = 1$ represents 90% of the population, a second one the 5% with $m_2 = 4s_1$, while a third distribution the rest 5% with $m_3 = -4s_1$, $-2s_1$, $2s_1$. All the standard deviations are equal to one, and the derived distribution is trimodal.
- (iii) Figures 3 and 4 demonstrate the results of these initial simulations, and one can recognize a lot of actual distributions obtained in proficiency testing.

2.2. Monte Carlo Simulations

The model developed utilizes the Monte Carlo approach to investigate and compare the robust methods used in the PT schemes. It assumes a default normal distribution of mean m_1 and standard deviation s_1 , contaminated with one or two secondary distributions with mean values m_2 and m_3 , respectively, and standard deviations equal to s_1 . The following data are inputs and independent variables of the algorithm:

- Number of participating laboratories, *N*_{lab};
- Number of replicate analyses per laboratory, *N_{rep}*;
- Repeatability standard deviation, *s_r*;
- Mean of the main normal distribution, *m*₁;
- Standard deviation of the main normal distribution, *s*₁;
- Mean and standard deviation of the second distribution, *m*₂, *s*₂;
- Population fraction of second distribution, *fr*₂;
- Mean and standard deviation of the third distribution, *m*₃, *s*₃;
- Population fraction of third distribution, *fr*₃;
- Number of iterations, *N*_{iter};
- Number of simulations, N_s;
- Number of buckets to create histograms, *N*_b.



Figure 3. Distribution of populations consisting of a main and secondary distribution. Dashed lines; main and secondary groups, and solid line; total population.



Figure 4. Distribution of populations consisting of a main and two secondary distribution. Dashed lines; main and secondary groups, and solid line; total population.

The Monte Carlo simulation initially selects a main normal distribution with mean value m_1 and standard deviation s_1 and adds two distributions contaminating the first one. The mean values of these two added populations are m_2 and m_3 , their standard deviation $s_2 = s_3 = s_1$, the repeatability of each result is equal to s_r , and their fractions fr_2 and fr_3 correspondingly. Consequently, the fraction of the main population is $fr_1 = 1 - fr_2 - fr_3$. This approach manages to create three types of distributions: (a) if $fr_2 = fr_3 = 0$, a single normal distribution; (b) if $fr_2 > 0$ and $fr_3 = 0$, a bimodal population; (c) if $fr_2 > 0$ and $fr_3 > 0$, a trimodal population. The simulation assumes N_{lab} participating laboratories and selects for each laboratory's result a random number, Rnd, between 0 and 1. If $Rnd < fr_3$, the result belongs to the third population. If $fr_3 \leq Rnd < fr_3 + fr_2$, it belongs to the second population. If $fr_3 \leq Rnd < fr_3 + fr_2$, it belongs to the second population.

$$X_i = Norm.Inv(m_k, s_k, Rnd_1) \tag{1}$$

where X_i is the mean value of the laboratory *i*, *Norm.Inv* is the inverse of the cumulative function of the normal distribution with mean value m_k , standard deviation s_k , and probability Rnd_1 which is a random number between 0 and 1. The index *k* is 1, 2, or 3 depending on the value of Rnd. The number of replicate analyses per laboratory is assumed to be always two. The same formula (1) applies to computing the value of each analysis by replacing: (a) m_k with X_i ; (b) s_k with s_r ; (c) Rnd_1 with Rnd_2 and $1-Rnd_2$ for each calculation where Rnd_2 represents a random number between 0 and 1. Each simulation includes $N_{iter} = 1000$ iterations, and for each dataset, the software performs $N_s = 25$ simulations to compute the statistics of the randomly generated populations. The developed algorithm calculates the mean values, standard deviations, and the performance statistics shown in Table 2, according to the analysis of ISO 13258-2015 [14] (pp. 52–62), ISO 5725-2:1994 [15]

(pp. 10–14), and EN ISO/IEC 17043:2010 [1] (pp. 30–33). This table demonstrates the respecting clause of the standard applied as well as the variable name.

Table 2. Classical and robust statistics.

Statistic	Applied Standard	Variable Name
Mean values		
General mean		GM^{1}
Median value	ISO 13528:2015, C. 2.1	MED
Robust mean—Algorithm A with iterated scale	ISO 13528:2015, C. 3.1	Ax^*
Hampel estimator for mean	ISO 13528:2015, C. 5.3.2	Hx^*
Standard deviations		
Scaled median absolute deviation		MADe
Normalized interquartile range	ISO 13528:2015, C. 2.3	nIQR
Reproducibility standard deviation without outliers	ISO 5725-2:1994, 7.4	sRep
Robust standard deviation—Algorithm A with iterated scale	ISO 13528:2015, C. 3.1	As^*
Robust standard deviation—Q method	ISO 13528:2015, C. 5.2.2	Hs^*
Absolute Z factors		
Z using MED, MADe	_	Z_MADe
Z using MED, nIQR		Z_nIQR
Z using GM, sRep	17043:2010. B3.1.3	Z_sRep
Z using Ax^* , As^*		Z_A
Z using Q/Hampel, Hx^* , Hs^*		Z_Hamp

¹ The abbreviation GM, used for general mean, should not be confused with that commonly used for GMestimators (generalized M-estimators) described in [34].

The outliers in the application of ISO 5725-2 for mean and reproducibility were determined using the Cochran's and Grubbs' tests: The first test was applied once, while the second one for the highest and lowest values. Tables 4 and 5 of ISO 5725-2 have critical values of the two outliers' tests, up to a maximum number of participating laboratories $N_{lab} = 40$ [15] (pp. 21–22). The software used the following Equations (2) and (3) to compute the 1% critical values for any N_{lab} [35,36], which were also verified in case $N_{lab} \leq 40$:

$$C_{crit} = \frac{1}{\left(1 + \frac{N_{lab} - 1}{1 + F.Inv\left(\frac{a}{N_{lab}}, N_{rep} - 1, (N_{lab} - 1) \cdot (N_{rep} - 1)\right)}\right)}$$
(2)

$$G_{crit} = \frac{(N_{lab} - 1) \cdot t.Inv\left(\frac{a}{N_{lab}}, N_{lab} - 2\right)}{\sqrt{N_{lab}}} \cdot \sqrt{\frac{1}{N_{lab} - 2 + t.Inv\left(\frac{a}{N_{lab}}, N_{lab} - 2\right)^2}}$$
(3)

where C_{crit} , G_{crit} are the critical values of Cochran's and Grubbs' tests, correspondingly, for $\alpha = 0.01$, and *t.Inv*, *F.Inv* are the inverse functions of the Student and Fisher distributions. The software applied the robust algorithms described in Annex C of ISO 13528:2015 to calculate the population means and standard deviations provided in Table 2. The *Z*-factor for laboratory value X_i , assigned value x_{PT} , and population standard deviation σ_{PT} is determined using Equation (4) according to 17043:2010 [1] (p. 30):

$$Z = \frac{X_i - x_{PT}}{\sigma_{PT}} \tag{4}$$

3. Comparisons of Population Mean Values and Standard Deviations

3.1. Initial Implementation of Simulations

The Monte Carlo simulation was first applied to a wide range of participating laboratories and a narrow range for the other independent variables presented in Section 2.2. In Section 2.1, one can see kernel density plots of actual 28-day strength results and computed parameters of the mix of three Gaussian distributions. The initial implementation of the simulation uses long-term 28-day strength data for the mean value and the variance of the normally distributed main population. Afterwards, the simulator adds a contaminating population following the same distribution with the main one and differing in mean value from it. The settings used were: *N*_{*lab*} = 15, 20, 30, 40, 60, 80, 100, 150, 200, 300, 400; *N*_{*rep*} = 2; $s_r = 0.40, 0.01$ MPa; $m_1 = 50.8$ MPa; $s_1 = 1.76$ MPa; $m_2 = 52.6, 54.4, 56.2$ MPa; $s_2 = 1.76$ MPa; $fr_2 = 0, 0.05, 0.10; fr_3 = 0; N_{iter} = 1000; N_s = 25; N_b = 20;$ The mean value $m_1 = 50.8$ MPa is the average of the population means of 81 rounds the PT scheme performed from 2012 to 2020 using the Hampel estimator. The $s_1 = 1.76$ and $s_r = 0.4$ represent the average between laboratories' standard deviation, s_L , and the repeatability for the same rounds. Q-method uses all the results of each laboratory, while the other robust methods use the mean value of each participant. By applying two s_r values, the simulation investigates the possible impact of the repeatability on the Q-method results. The settings selected correspond to bimodal distributions, where the mean of the second population m_2 is in distances of 1.02 (=1.8/1.76), 2.05, and 3.07 from the mean m_1 in s_1 units. Table 3 presents the average values and standard deviations of mean values of the population, m_{av} and s_{av} , correspondingly, calculated from Equations (5) and (6), for $fr_2 = 0.10$:

$$m_{j} = \sum_{i=1}^{N_{iter}} m_{ij} / N_{iter}, \ sm_{j} = \sqrt{\frac{\sum_{i=1}^{N_{iter}} (m_{ij} - m_{j})^{2}}{N_{iter} - 1}} \ j = 1 \ to \ N_{s}$$
(5)

$$m_{av} = \sum_{j=1}^{N_s} m_j / N_s, \ s_{av} = \sum_{j=1}^{N_s} sm_j / N_s$$
 (6)

where m_{ij} are the mean values of each N_{lab} , m_j is the mean value, and sm_j is the standard deviation of m_{ij} for the simulation j.

Table 3. Average and standard deviation of the mean values.

	GM	MED	Ax^*	Hx^*	GM	MED	Ax^*	Hx^*	GM	MED	Ax^*	Hx^*	GM	MED	Ax^*	Hx^*
N _{lab}	Ν	vlean va	lues, m _a	v	Star	ndard de	viation	s, s _{av}	Ν	vlean va	lues, ma	υ	Star	ndard de	viation	s, s _{av}
		$m_2 = \frac{1}{2}$	52.6 MP	a, $m_{tot} =$	50.98 N	/IPa, fr ₂ =	= 0.10			$m_2 = 1$	54.4 MP	a, m_{tot} =	51.16 N	/IPa, fr ₂ =	= 0.10	
15	50.98	50.96	50.97	50.97	0.48	0.59	0.50	0.50	51.16	51.05	51.09	51.09	0.54	0.63	0.55	0.55
20	50.98	50.96	50.97	50.97	0.41	0.50	0.42	0.42	51.15	51.04	51.09	51.09	0.47	0.53	0.47	0.47
30	50.97	50.96	50.97	50.97	0.33	0.41	0.34	0.34	51.15	51.04	51.09	51.09	0.38	0.44	0.38	0.38
40	50.98	50.96	50.97	50.97	0.28	0.34	0.28	0.28	51.15	51.03	51.08	51.08	0.31	0.36	0.31	0.31
60	50.98	50.96	50.97	50.97	0.23	0.28	0.23	0.23	51.15	51.03	51.09	51.09	0.26	0.30	0.26	0.26
80	50.98	50.96	50.97	50.97	0.21	0.25	0.21	0.21	51.16	51.03	51.09	51.09	0.23	0.27	0.23	0.23
100	50.98	50.96	50.97	50.97	0.18	0.23	0.19	0.19	51.16	51.03	51.09	51.09	0.21	0.24	0.21	0.21
150	50.98	50.96	50.97	50.97	0.15	0.19	0.15	0.15	51.16	51.04	51.09	51.09	0.17	0.20	0.17	0.17
200	50.98	50.96	50.97	50.97	0.13	0.16	0.13	0.13	51.16	51.03	51.09	51.09	0.15	0.17	0.15	0.15
300	50.98	50.96	50.97	50.97	0.11	0.13	0.11	0.11	51.16	51.03	51.09	51.09	0.12	0.14	0.12	0.12
400	50.98	50.96	50.97	50.97	0.09	0.11	0.09	0.09	51.16	51.03	51.09	51.09	0.10	0.12	0.10	0.10
		$m_2 = \frac{1}{2}$	56.2 MP	a, $m_{tot} =$	51.34 N	/IPa, fr ₂ =	= 0.10		_							
15	51.31	51.06	51.15	51.15	0.63	0.64	0.59	0.59	_							
20	51.31	51.06	51.16	51.15	0.55	0.54	0.51	0.51								
30	51.32	51.05	51.15	51.15	0.45	0.44	0.41	0.41								
40	51.32	51.05	51.15	51.15	0.38	0.37	0.34	0.34								
60	51.33	51.05	51.14	51.14	0.31	0.31	0.28	0.28								
80	51.33	51.05	51.14	51.14	0.27	0.27	0.25	0.25								
100	51.33	51.05	51.14	51.14	0.24	0.25	0.23	0.23								
150	51.33	51.05	51.14	51.14	0.20	0.20	0.18	0.18								
200	51.34	51.05	51.14	51.14	0.17	0.17	0.16	0.16								
300	51.34	51.05	51.14	51.14	0.14	0.14	0.13	0.13								
400	51.34	51.05	51.14	51.14	0.12	0.12	0.11	0.11								

For comparison reasons, the mean value of the bimodal distribution is provided, computed from Equation (7):

$$m_{tot} = (1 - fr_2) \cdot m_1 + fr_2 \cdot m_2 \tag{7}$$

The four estimators of the mean population value are approximately equal for $m_2 = 52.6$ MPa and close to m_1 . For larger values of m_2 , the *GM* estimator starts to be higher than the others and approaches the m_{tot} value, meaning that when $m_2 > m_1 + s_1$, *GM* is not a robust estimator. The three robust estimators provide a good approximation of m_1 , but the median value shows a higher variance, especially for smaller N_{lab} .

The average values and standard deviations of the population standard deviations are computed by Equations (8) and (9):

$$s_{j} = \sum_{i=1}^{N_{iter}} s_{ij} / N_{iter}, \ ss_{j} = \sqrt{\frac{\sum_{i=1}^{N_{iter}} (s_{ij} - s_{j})^{2}}{N_{iter} - 1}} \ j = 1 \ to \ N_{s}$$
(8)

$$m_{std} = \sum_{j=1}^{N_s} s_j / N_s, \ s_{std} = \sum_{j=1}^{N_s} s_s / N_s \tag{9}$$

where s_{ij} is the standard deviation of each N_{lab} , s_j is the mean value, and ss_j is the standard deviation of s_{ij} for the simulation j. Figures 5 and 6 show the average values and standard deviations of the population standard deviation for $fr_2 = 0$ and 0.10, from which one can conclude the following:

- (i) For a large number of laboratories, $N_{lab} \ge 200$, the mean values of the estimators converge to different values. *MADe*, *nIQR*, and *As*^{*} approach approximately the same value, while the convergence value of Hs^* is higher for both repeatability values. The *sRep* is between these values for $fr_2 = 0$ and $m_2 = m_1 + s_1$ and becomes higher from both for $m_2 \ge m_1 + 2s_1$. The above proves that this estimator is not resistant to outliers. The high value of *sRep* for high m_2 can underestimate the number of laboratories with |Z| > 3.
- (ii) All functions between estimators and N_{lab} are monotonic. Those of *MADe*, *sRep*, and *As** are increasing and those of *nIQR* and *Hs** are decreasing. The *MADe* and *As** low values for small N_{lab} may overestimate |Z| values. The current analysis shows *MADe* and *As** are the lowest among robust estimators for small N_{lab} .
- (i) Increasing the m_2 value, the average value and standard deviation of the population standard deviation also increase.
- (ii) The standard deviation of the population standard deviation of *MADe* and *nIQR* is continuously higher than the respecting values of the other three estimators. The above is in good agreement with paragraph 6.5.2 of ISO 13253:2015 [14] (p. 12), which further notes that more sophisticated robust estimators provide better performance for approximately normally distributed data, while retaining much of the resistance to outliers offered by *MADe* and *nIQR*.
- (iii) The average standard deviation of the Q method with $s_r = 0.40$ is a little higher than that with negligible repeatability, $s_r = 0.01$. Further simulations will utilize only $s_r = 0.01$ for the Q method to be comparable with the other robust methods.

Figure 7 depicts the distributions of the population standard deviations for one simulation with $N_{iter} = 10000$, $N_s = 1$, $s_r = 0.01$, $m_2 = 52.6$ MPa, 56.2 MPa, $fr_2 = 0.10$, $N_b = 20$, and $N_{lab} = 20$, 40, from where one can observe:

- (i) All distributions are approximately symmetric around their mean;
- (ii) The variance of *MADe* and *nIQR* is greater than that of other estimators, especially for lower values of *m*₂.



Figure 5. Average values of the population standard deviations. *MADe*: scaled median absolute deviation; *nIQR*: normalized interquartile range; *sRep*: reproducibility standard deviation without outliers; *As**: standard deviation—Algorithm A; *Hs**, 0.40: standard deviation using Q method and $s_r = 0.40$; *Hs**, 0.01: standard deviation using the Q method and $s_r = 0.01$.



Figure 6. Standard deviations of the population standard deviations. *MADe*: scaled median absolute deviation; *nIQR*: normalized interquartile range; *sRep*: reproducibility standard deviation without outliers; *As**: standard deviation—Algorithm A; *Hs**, 0.40: standard deviation using Q method and $s_r = 0.40$; *Hs**, 0.01: standard deviation using Q method and $s_r = 0.01$.



Figure 7. Distribution of the population standard deviations.

3.2. Determining the Best Estimators for a Small Number of Laboratories

As proved in Section 3.1, the estimators *GM* and *sRep* are not resistant to outliers. The problem needing a solution is the determination of the best robust estimators based on the number of participants and the actual distribution of the results. The proposed method uses the absolute value of the Z-factor given by Equation (4). According to EN ISO/IEC 17043:2010 [1] (p. 32), if |Z|>3, the laboratory performance is unsatisfactory, and the result is an outlier. Using robust estimators to detect the outliers indicates that the approach is nonparametric. Supposing that a distribution of a large number of results, actual or simulated, contains *Zu*% non-satisfactory results, the question is which robust estimators best approach these values when the number of labs is N_{lab} . The developed algorithm applies the Monte Carlo simulation presented in Section 2.2 and follows the subsequent steps:

- (i) It creates a main normal distribution D_1 with mean value m_1 and standard deviation s_1 and two contaminating distributions D_2 , D_3 with mean values m_2 , m_3 , and standard deviations $s_2 = s_3 = s_1$.
- (ii) The fractions of the contaminating distributions are fr_2 and fr_3 , and, depending on these two values, the total distribution can be unimodal, bimodal, or trimodal.
- (iii) The mean values m_2 and m_3 differ by an integer number of standard deviations s_1 from m_1 , n_2 and n_3 , shown in Equation (10). In the case of trimodal distribution, if $n_2 \cdot n_3 > 0$, then D_2 and D_3 are both to the same side of the D_1 . Otherwise, one is to the left and the other to the right of D_1 . Figure 4 of Section 2.1 depicts such distributions:

$$m_2 = m_1 + n_2 \cdot s_1$$
, $m_3 = m_1 + n_3 \cdot s_1$ with $n_2 \ge 0$ and $n_3 \ge 0$ or $n_3 < 0$ (10)

- (iv) According to the values of fr_2 , fr_3 , n_2 , and n_3 , the software calculates the values of Zu%, which are unsatisfactory, compared to the normal distribution function with mean and standard deviation m_1 and s_1 , correspondingly. These values are the initial values. For example, if $fr_2 = 0.1$, $fr_3 = 0$, and $n_2 = 3$, then Zu% = 0.24 (from D_1) + 5.0 (from D_2) = 5.24.
- (v) The algorithm calculates all the estimators for the mean and standard deviation shown in Table 1 and the Zu% for the absolute values of the five Z-factors presented in the same table using a $N_{lab} = 400$. Afterwards, it calculates the average of Zu% for $N_{iter} = 400$ and $N_s = 4$. The other settings are the ones shown in Table 4. For this

number of participants, all estimators converge to their final value. Figure 8 illustrates the procedure.

 Table 4. Simulation settings.

Setting	Value
N _{lab}	10, 15, 20, 30 and 400 ¹
N _{rep}	2
s_r , MPa	0.01
m_1 , MPa	50
<i>s</i> ₁ , MPa	1
<i>m</i> ₂ , MPa	$m_2 = m_1 + n_2 \cdot s_1, n_2 = 1$ to 8 and step 1
fr_2	0, 0.025, 0.05, 0.075, 0.1 ²
<i>m</i> ₃ , MPa	$m_3 = m_1 + n_3 \cdot s_1, n_3 = -8$ to 8 and step 1
fr_3	0, 0.025, 0.05
<i>s</i> ₂ , <i>s</i> ₃ , MPa	1
N _{iter}	1000
N_s	25

¹ If $N_{lab} = 400$, then the $N_s = 4$. ² If $fr_3 = 0$, then the maximum value of fr_2 is 0.1. Otherwise $fr_{2Max} = 0.075$ and $fr_2 + fr_3 \le 0.1$.



Figure 8. Function between Zu% and number of standard deviations n_2 , n_3 , and $N_{lab} = 400$. Calculation of initial values using step (iv) of Section 3.2.

- (vi) The Zu% of each of the five Z-factors are compared with the initial results of step (iv). Those results closest to the initial ones are the reference values and represent the best estimation of the robust methods in approaching the unsatisfactory results calculated using the main distribution.
- (vii) The simulations implemented all the settings shown in Table 4 for participants up to 30. The populations correspond to unimodal, bimodal, and trimodal distributions with a maximum total fraction of secondary distributions up to 0.1. The coefficient of variation of the main distribution is 2% (= $1/50 \times 100$).
- (viii) The software performs N_{iter} iterations and N_s simulations for each N_{lab} . For all these results, the average of each one of the five Zu% is calculated. These results are compared with each other and with reference values. The estimator providing the closest value to the reference value for each parameter set is optimal.

Figure 8 proves that the calculation of Zu% using Z_sRep results leads to a severe underestimation of the percentage of the unacceptable Z-factors, compared to all the other estimators. The Zu% values derived from the robust estimators are close to each other and not far from the initial values computed using the main normal distribution. The Zu% values calculated by Z_Hamp are slightly worse than the values calculated by Z_MADe , Z_nIQR , and Z_A . The simulator compared all Zu% for $N_{lab} = 400$ and all the other settings of Table 4. It found that the closest estimator of unacceptable Z-factors to the estimation based on the main normal distribution is the Z_MADe in 95% of cases. For this reason, it uses the values of this estimator as a reference in further calculations. However, this does not mean that the *Z_MADe* is consistently the optimal estimator for a small number of participants.

Figures 9 and 10 depict the Zu% for the reference values and all the robust estimators for selected bimodal and trimodal distributions of the results' population. In both figures, the number of labs is from 10 to 30.



Figure 9. Functions between Zu% and number of standard deviations n_2 , for the reference values and robust estimators, and $N_{lab} = 10, 15, 20, 30$.



Figure 10. Functions between Zu% and number of standard deviations n_3 , for the reference values and robust estimators, and $N_{lab} = 10, 15, 20, 30$.

One can observe that the optimal estimator is a function of both the number of deviations and the number of labs. In bimodal distribution and for the given f_2 , Z_Hamp is optimal for $n_2 \le 2$ and $n_2 \ge 6$, depending on the N_{lab} value. Z_MADe is more efficient for $N_{lab} \ge 20$ and $n_2 = 4$, while for the other values of n_2 and N_{lab} , the optimal estimators are Z_nIQR and Z_A . The trimodal distributions of Figure 10 contain two bimodal distributions in the case $n_3 = 0$ and 8. For the given value of n_2 , Z_Hamp is more efficient in the center for $-2 \le n_3 \le 2$. Z_A and Z_nIQR are optimal in the two side zones for $n_3 \le -6$ and

 $n_3 \ge 7$ and $n_3 = -3$, $n_3 = 3$. Finally, Z_MAde is the closest estimator to the reference values in the two intermediate zones for $-5 \le n_3 \le -4$ and $4 \le n_3 \le 6$. The conclusion from the processing so far is that there is no generally optimal robust estimator, but its choice depends on the type of population distribution and its variance.

4. Optimal Robust Estimators for a Limited Number of Participants

4.1. Use of a Normal Distribution Mix

The application of steps (i)–(viii) of 3.2 for the full range of N_{lab} , n_2 , n_3 , fr_2 , and fr_3 of Table 4 leads to a complete and exhaustive evaluation of the optimal robust estimator of the percentage of unacceptable results for each set of the mentioned settings and guides a PT scheme expert on which estimator to choose. The core of such an option for an actual PT is to disclose the distribution of results using the kernel plots and to fit a mixture of normal distributions into it, as described in Section 2.1. If the PT scheme organizer executes the test several times a year, selecting the results of the last and several recent rounds to generate the kernel plots is preferable. The last results have a significant probability of belonging to a population similar to the recent results' population, especially if the same or almost the same laboratories participate. On the contrary, if the PT scheme expert would use only the last round to build the distribution, the parameters could have severe uncertainty due to the small number of participants.

Figure 11 shows the optimal robust estimators of Zu% for the bimodal distributions and the settings of Table 4. For $f_2 = 0.025$, the Q/Hampel estimator is predominant for most of the n_2 values, and only for $n_2 = 4$ method A and *MED-nIQR* are optimal. By increasing f_2 , Q/Hampel remains optimal for $n_2 \le 2$, and its performance gradually decreases to high values of n_2 . For $f_2 = 0.05$, method A and *MED-nIQR* predominate for $3 \le n_2 \le 6$. As f_2 increases, *MED-MADe* becomes optimal near the mid-range of n_2 , while the optimal Z_A move to the right, replacing Z_nIQR and Z_Hamp .

							n2				
f2	f3	Nlab	0	1	2	3	4	5	6	7	8
0.025	0	10	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp
		15	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp
		20	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp
		30	Z_Hamp	Z_Hamp	Z_Hamp	Z_A	Z_A	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp
0.05	0	10	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_A	Z_A	Z_nIQR	Z_nlQR	Z_Hamp
		15	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_A	Z_A	Z_nIQR	Z_Hamp	Z_Hamp
		20	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_A	Z_A	Z_nIQR	Z_Hamp	Z_Hamp
		30	Z_Hamp	Z_Hamp	Z_Hamp	Z_A	Z_MADe	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp
0.075	0	10	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_MADe	Z_MADe	Z_A	Z_A	Z_A
		15	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_MADe	Z_MADe	Z_A	Z_nIQR	Z_nIQR
		20	Z_Hamp	Z_Hamp	Z_Hamp	Z_A	Z_MADe	Z_MADe	Z_A	Z_nIQR	Z_Hamp
		30	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_MADe	Z_MADe	Z_MADe	Z_Hamp	Z_Hamp
0.10	0	10	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_MADe	Z_MADe	Z_MADe	Z_MADe	Z_A
		15	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_MADe	Z_MADe	Z_MADe	Z_A	Z_A
		20	Z_Hamp	Z_Hamp	Z_Hamp	Z_A	Z_MADe	Z_MADe	Z_MADe	Z_A	Z_A
		30	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_MADe	Z_MADe	Z_MADe	Z_MADe	Z_A

Figure 11. Optimal robust estimators of Zu% for number of standard deviations $n_2 = 0$ to 8, $f_2 = 0.025$ to 0.10 and $N_{lab} = 10, 15, 20, 30$.

Figures 12–15 depict the optimal estimators of Zu% for the trimodal distributions and all the combinations of f_2 and f_3 with $f_2 + f_3 \le 0.10$. For $f_2 + f_3 = 0.05$, Q/Hampel is optimal in the center ($-3 \le n_3 \le 3$) and in the two sides ($n_3 \le -6$, $n_3 \ge 6$) for low and high n_2 values. Method A and *MED-nIQR* are highly performing in the remaining area of n_2 , n_3 . These results agree with those of Figure 11. For $f_2 + f_3 = 0.075$, Q/Hampel is optimal mainly in the center ($-2 \le n_3 \le 2$) for low and high n_2 values. *MED-MADe* shows the higher performance for the two mid-ranges of n_3 ($n_3 = -4$, -5, and $n_3 = 4$, 5) while method A and *MED-nIQR* remain optimal in the remaining area. For $f_2 + f_3 = 0.10$, the area covered by optimal *Z_MADe* is larger, replacing *Z_A* and *Z_nIQR*. Especially for $f_2 = 0.05$ and $f_3 = 0.05$, the region of optimal *Z_Hamp* becomes narrower, replaced mainly by *Z_nIQR*. Figures 11–15 are suitable for practical reasons because they allow the PT scheme expert to select the proper robust estimator to evaluate the unsatisfactory results when the number of participants is between 10 and 30 with the underlying assumption that the main distribution presents a coefficient of variation ~2. Rounding to the values given in these figures is necessary for the number of labs and the f_2 and f_3 fractions calculated from the actual distribution.

												n3							
f2 f3	Nlab	n2	-8	-7	-6	-5	-4	-3	-2	-1	0	1	2	3	4	5	6	7	8
0.025 0.02	5 10	8	Z_Hamp	Z_Hamp	Z_nlQR	Z_nlQR	Z_nIQR	Z_Hamp	Z_nlQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_Hamp						
	15	8	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_nlQR	Z_Hamp	Z_nIQR	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp						
	20	8	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_nlQR	Z_Hamp	Z_nIQR	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp						
	30	8	Z_Hamp	Z_Hamp	Z_Hamp	Z_A	Z_A	Z_A	Z_A	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_A	Z_A	Z_A	Z_Hamp	Z_Hamp	Z_Hamp
0.025 0.02	5 10	7		Z_Hamp	Z_nlQR	Z_nIQR	Z_nIQR	Z_nlQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_nIQR	Z_nIQR	Z_nlQR	Z_nlQR	
	15	7		Z_Hamp	Z_Hamp	Z_nIQR	Z_nlQR	Z_nlQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_nlQR	Z_nIQR	Z_nIQR	Z_Hamp	
	20	7		Z_Hamp	Z_Hamp	Z_nIQR	Z_nIQR	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_Hamp	
	30	7		Z_Hamp	Z_Hamp	Z_A	Z_A	Z_A	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_A	Z_A	Z_A	Z_A	Z_Hamp	
0.025 0.02	5 10	6			Z_nIQR	Z_nlQR	Z_nIQR	Z_nlQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nlQR	Z_A	Z_A	Z_nlQR		
	15	6			Z_nIQR	Z_nIQR	Z_nIQR	Z_nlQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_A	Z_nIQR	Z_nIQR		
	20	6			Z_Hamp	Z_nIQR	Z_nIQR	Z_nlQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_A	Z_nIQR	Z_nIQR		
	30	6			Z_Hamp	Z_A	Z_A	Z_A	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_A	Z_A	Z_A	Z_Hamp		
0.025 0.02	5 10	5				Z_nIQR	Z_A	Z_nlQR	Z_nlQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_A	Z_A			
	15	5				Z_nIQR	Z_A	Z_nlQR	Z_Hamp	Z_nIQR	Z_Hamp	Z_Hamp	Z_nIQR	Z_nIQR	Z_A	Z_A			
	20	5				Z_nIQR	Z_A	Z_nlQR	Z_nlQR	Z_nIQR	Z_Hamp	Z_Hamp	Z_nIQR	Z_nIQR	Z_A	Z_A			
	30	5				Z_A	Z_A	Z_A	Z_Hamp	Z_A	Z_Hamp	Z_Hamp	Z_A	Z_nIQR	Z_MADe	Z_nIQR			
0.025 0.02	5 10	4					Z_A	Z_nlQR	Z_nlQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_A				
	15	4					Z_A	Z_nlQR	Z_nlQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_A				
	20	4					Z_A	Z_A	Z_nlQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_A	Z_MADe				
	30	4					Z_A	Z_nIQR	Z_MADe										
0.025 0.02	5 10	3						Z_nlQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR					
	15	3						Z_nlQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR					
	20	3						Z_nIQR	Z_nlQR	Z_Hamp	Z_nlQR	Z_Hamp	Z_nIQR	Z_nIQR					
	30	3						Z_A	Z_A	Z_A	Z_A	Z_Hamp	Z_A	Z_A					
0.025 0.02	5 10	2							Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp						
	15	2							Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp						
	20	2							Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp						
	30	2							Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp						
0.025 0.02	5 10	1								Z_Hamp	Z_Hamp	Z_Hamp							
	15	1								Z_Hamp	Z_Hamp	Z_Hamp							
	20	1								Z_Hamp	Z_Hamp	Z_Hamp							
	30	1								Z Hamp	Z Hamp	Z Hamp							

Figure 12. Optimal robust estimators of Zu% for trimodal distributions, $f_2 = 0.025$ and $f_3 = 0.025$.

												n ₃							
f2 f3	Nlab	n2	-8	-7	-6	-5	-4	-3	-2	-1	0	1	2	3	4	5	6	7	8
0.025 0.050	10	8	Z_nIQR	Z_nIQR	Z_A	Z_A	Z_A	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_A	Z_A	Z_A	Z_A	Z_A
	15	8	Z_nIQR	Z_nIQR	Z_nIQR	Z_A	Z_A	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_A	Z_MADe	Z_A	Z_nIQR	Z_nIQR
	20	8	Z_Hamp	Z_Hamp	Z_nIQR	Z_A	Z_MADe	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_MADe	Z_MADe	Z_A	Z_nIQR	Z_Hamp
	30	8	Z_Hamp	Z_A	Z_A	Z_MADe	Z_MADe	Z_A	Z_A	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_A	Z_MADe	Z_MADe	Z_nlQR	Z_Hamp	Z_Hamp
0.025 0.050	10	7		Z_nIQR	Z_A	Z_A	Z_A	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_A	Z_MADe	Z_A	Z_A	
	15	7		Z_nIQR	Z_nIQR	Z_A	Z_A	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_A	Z_MADe	Z_A	Z_nlQR	
	20	7		Z_Hamp	Z_nIQR	Z_A	Z_MADe	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_MADe	Z_MADe	Z_A	Z_nlQR	
	30	7		Z_Hamp	Z_A	Z_nIQR	Z_MADe	Z_A	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_A	Z_MADe	Z_MADe	Z_A	Z_Hamp	
0.025 0.050	10	6			Z_A	Z_MADe	Z_A	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nlQR	Z_A	Z_MADe	Z_MADe	Z_A		
	15	6			Z_A	Z_MADe	Z_MADe	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nlQR	Z_A	Z_MADe	Z_MADe	Z_A		
	20	6			Z_nIQR	Z_MADe	Z_MADe	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nlQR	Z_A	Z_MADe	Z_MADe	Z_A		
	30	6			Z_A	Z_MADe	Z_MADe	Z_A	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_MADe	Z_MADe	Z_MADe		
0.025 0.050	10	5				Z_MADe	Z_MADe	Z_A	Z_nIQR	Z_nIQR	Z_nIQR	Z_nlQR	Z_nlQR	Z_A	Z_MADe	Z_MADe			
	15	5				Z_MADe	Z_MADe	Z_A	Z_nIQR	Z_Hamp	Z_Hamp	Z_nIQR	Z_nlQR	Z_A	Z_MADe	Z_MADe			
	20	5				Z_MADe	Z_MADe	Z_A	Z_nIQR	Z_nIQR	Z_Hamp	Z_nIQR	Z_nIQR	Z_A	Z_MADe	Z_MADe			
	30	5				Z_MADe	Z_MADe	Z_A	Z_Hamp	Z_A	Z_Hamp	Z_Hamp	Z_A	Z_MADe	Z_MADe	Z_MADe			
0.025 0.050	10	4					Z_MADe	Z_A	Z_nIQR	Z_nIQR	Z_nlQR	Z_nlQR	Z_nlQR	Z_A	Z_MADe				
	15	4					Z_MADe	Z_A	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_A	Z_MADe				
	20	4					Z_MADe	Z_A	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_A	Z_MADe				
	30	4					Z_MADe	Z_MADe	Z_A	Z_A	Z_A	Z_A	Z_A	Z_MADe	Z_MADe				
0.025 0.050	10	3						Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR					
	15	3						Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR					
	20	3						Z_A	Z_nIQR	Z_Hamp	Z_nIQR	Z_nlQR	Z_nIQR	Z_A					
	30	3						Z_MADe	Z_A	Z_Hamp	Z_A	Z_A	Z_A	Z_nIQR					
0.025 0.050	10	2							Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp						
	15	2							Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp						
	20	2							Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp						
	30	2							Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp						
0.025 0.050	10	1								Z_Hamp	Z_Hamp	Z_Hamp							
	15	1								Z_Hamp	Z_Hamp	Z_Hamp							
	20	1								Z_Hamp	Z_Hamp	Z_Hamp							
	30	1								Z_Hamp	Z_Hamp	Z_Hamp							

Figure 13. Optimal robust estimators of Zu% for trimodal distributions, $f_2 = 0.025$ and $f_3 = 0.05$.

												n3							
f2 f3	Nlab	n2	-8	-7	-6	-5	-4	-3	-2	-1	0	1	2	3	4	5	6	7	8
0.025 0.075	10	8	Z_A	Z_A	Z_MADe	Z_MADe	Z_MADe	Z_nlQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_MADe	Z_MADe	Z_MADe	Z_MADe	Z_A
	15	8	Z_nIQR	Z_A	Z_MADe	Z_MADe	Z_MADe	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_MADe	Z_MADe	Z_MADe	Z_MADe	Z_A
	20	8	Z_nIQR	Z_A	Z_MADe	Z_MADe	Z_MADe	Z_A	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_A	Z_MADe	Z_MADe	Z_MADe	Z_MADe	Z_A
	30	8	Z_Hamp	Z_A	Z_MADe	Z_MADe	Z_MADe	Z_nlQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_MADe	Z_MADe	Z_MADe	Z_MADe	Z_A
0.025 0.075	10	7		Z_A	Z_MADe	Z_MADe	Z_MADe	Z_A	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_A	Z_MADe	Z_MADe	Z_MADe	Z_MADe	
	15	7		Z_A	Z_MADe	Z_MADe	Z_MADe	Z_A	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_A	Z_MADe	Z_MADe	Z_MADe	Z_A	
	20	7		Z_A	Z_MADe	Z_MADe	Z_MADe	Z_A	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_A	Z_MADe	Z_MADe	Z_MADe	Z_A	
	30	7		Z_A	Z_nlQR	Z_MADe	Z_MADe	Z_MADe	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_MADe	Z_MADe	Z_MADe	Z_MADe	
0.025 0.075	10	6			Z_MADe	Z_MADe	Z_MADe	Z_A	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_A	Z_MADe	Z_MADe	Z_MADe		
	15	6			Z_MADe	Z_MADe	Z_MADe	Z_nIQR	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_A	Z_MADe	Z_MADe	Z_MADe		
	20	6			Z_MADe	Z_MADe	Z_MADe	Z_A	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_A	Z_MADe	Z_MADe	Z_MADe		
	30	6			Z_MADe	Z_MADe	Z_MADe	Z_nIQR	Z_A	Z_Hamp	Z_Hamp	Z_Hamp	Z_A	Z_nIQR	Z_MADe	Z_MADe	Z_MADe		
0.025 0.075	10	5				Z_MADe	Z_MADe	Z_A	Z_nIQR	Z_nlQR	Z_nIQR	Z_Hamp	Z_nIQR	Z_A	Z_MADe	Z_MADe			
	15	5				Z_MADe	Z_MADe	Z_A	Z_nIQR	Z_nIQR	Z_Hamp	Z_Hamp	Z_nIQR	Z_A	Z_MADe	Z_MADe			
	20	5				Z_MADe	Z_MADe	Z_A	Z_nIQR	Z_nIQR	Z_Hamp	Z_Hamp	Z_nIQR	Z_A	Z_MADe	Z_MADe			
	30	5				Z_MADe	Z_MADe	Z_MADe	Z_A	Z_A	Z_Hamp	Z_Hamp	Z_A	Z_nIQR	Z_MADe	Z_MADe			
0.025 0.075	10	4					Z_MADe	Z_A	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_A	Z_MADe				
	15	4					Z_MADe	Z_A	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_A	Z_MADe				
	20	4					Z_MADe	Z_A	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_MADe	Z_MADe				
	30	4					Z_MADe	Z_nIQR	Z_A	Z_A	Z_A	Z_A	Z_A	Z_MADe	Z_MADe				
0.025 0.075	10	3						Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR					
	15	3						Z_nIQR	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_nIQR					
	20	3						Z_A	Z_nIQR	Z_Hamp	Z_nIQR	Z_Hamp	Z_nIQR	Z_A					
	30	3						Z_nIQR	Z_A	Z_A	Z_A	Z_Hamp	Z_A	Z_nIQR					
0.025 0.075	10	2							Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp						
	15	2							Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp						
	20	2							Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp						
	30	2							Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp						
0.025 0.075	10	1								Z_Hamp	Z_Hamp	Z_Hamp							
	15	1								Z_Hamp	Z_Hamp	Z_Hamp							
	20	1								Z_Hamp	Z_Hamp	Z_Hamp							
	30	1								Z_Hamp	Z_Hamp	Z_Hamp							

Figure 14. Optimal robust estimators of Zu% for trimodal distributions, $f_2 = 0.025$ and $f_3 = 0.075$.

													n3							
f2	f3	Nlab	n2	-8	-7	-6	-5	-4	-3	-2	-1	0	1	2	3	4	5	6	7	8
0.050	0.050	10	8	Z_A	Z_A	Z_A	Z_MADe	Z_MADe	Z_A	Z_nlQR	Z_Hamp	Z_Hamp	Z_nIQR	Z_nIQR	Z_A	Z_MADe	Z_MADe	Z_MADe	Z_MADe	Z_A
		15	8	Z_nIQR	Z_nIQR	Z_A	Z_MADe	Z_MADe	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_MADe	Z_MADe	Z_MADe	Z_A	Z_A
		20	8	Z_nIQR	Z_nlQR	Z_A	Z_MADe	Z_MADe	Z_A	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_nIQR	Z_MADe	Z_MADe	Z_MADe	Z_A	Z_A
		30	8	Z_A	Z_A	Z_nlQR	Z_MADe	Z_MADe	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_A	Z_Hamp	Z_A	Z_MADe	Z_MADe	Z_MADe	Z_nIQR	Z_A
0.050	0.050	10	7		Z_A	Z_MADe	e Z_MADe	Z_MADe	Z_A	Z_nlQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_A	Z_MADe	Z_MADe	Z_MADe	Z_MADe	
		15	7		Z_A	Z_MADe	e Z_MADe	Z_MADe	Z_nIQR	Z_nIQR	Z_nIQR	Z_Hamp	Z_Hamp	Z_nIQR	Z_A	Z_MADe	Z_MADe	Z_MADe	Z_A	
		20	7		Z_nIQR	Z_MADe	e Z_MADe	Z_MADe	Z_A	Z_nIQR	Z_nIQR	Z_Hamp	Z_Hamp	Z_Hamp	Z_A	Z_MADe	Z_MADe	Z_MADe	Z_A	
		30	7		Z_A	Z_MADe	Z_MADe	Z_MADe	Z_A	Z_A	Z_A	Z_Hamp	Z_Hamp	Z_A	Z_nlQR	Z_MADe	Z_MADe	Z_MADe	Z_A	
0.050	0.050	10	6			Z_MADe	e Z_MADe	Z_MADe	Z_A	Z_A	Z_nIQR	Z_nIQR	Z_A	Z_A	Z_A	Z_MADe	Z_MADe	Z_MADe		
		15	6			Z_MADe	e Z_MADe	Z_MADe	Z_A	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_A	Z_MADe	Z_MADe	Z_MADe		
		20	6			Z_MADe	Z_MADe	Z_MADe	Z_A	Z_nlQR	Z_nIQR	Z_nlQR	Z_A	Z_A	Z_MADe	Z_MADe	Z_MADe	Z_MADe		
		30	6			Z_nlQR	Z_MADe	Z_MADe	Z_nIQR	Z_A	Z_A	Z_A	Z_A	Z_A	Z_MADe	Z_MADe	Z_MADe	Z_MADe		
0.050	0.050	10	5				Z_MADe	Z_MADe	Z_MADe	Z_A	Z_A	Z_A	Z_A	Z_A	Z_MADe	Z_MADe	Z_MADe			
		15	5				Z_MADe	Z_MADe	Z_MADe	Z_A	Z_A	Z_A	Z_A	Z_A	Z_MADe	Z_MADe	Z_MADe			
		20	5				Z_MADe	Z_MADe	Z_MADe	Z_MADe	Z_A	Z_A	Z_MADe	Z_MADe	Z_MADe	Z_MADe	Z_MADe			
		30	5				Z_MADe	Z_MADe	Z_MADe	Z_MADe	Z_nIQR	Z_nlQR	Z_nlQR	Z_MADe	Z_MADe	Z_MADe	Z_MADe			
0.050	0.050	10	4					Z_MADe	Z_MADe	Z_A	Z_A	Z_A	Z_A	Z_A	Z_A	Z_MADe				
		15	4					Z_MADe	Z_MADe	Z_A	Z_A	Z_A	Z_A	Z_A	Z_MADe	Z_MADe				
		20	4					Z_MADe	Z_MADe	Z_MADe	Z_A	Z_MADe	Z_MADe	Z_A	Z_MADe	Z_MADe				
		30	4					Z_MADe												
0.050	0.050	10	3						Z_A	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nlQR					
		15	3						Z_A	Z_nlQR	Z_nIQR	Z_nlQR	Z_nlQR	Z_nlQR	Z_A					
		20	3						Z_A	Z_nlQR	Z_nIQR	Z_nlQR	Z_nlQR	Z_nlQR	Z_A					
		30	3						Z_nIQR	Z_A	Z_A	Z_A	Z_A	Z_A	Z_nlQR					
0.050	0.050	10	2							Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp						
		15	2							Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp						
		20	2							Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp						
		30	2							Z_A	Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp						
0.050	0.050	10	1								Z_Hamp	Z_Hamp	Z_Hamp							
		15	1								Z_Hamp	Z_Hamp	Z_Hamp							
		20	1								Z_Hamp	Z_Hamp	Z_Hamp							
1		30	1								7 Hamn	7 Hamn	Z Hamp							

Figure 15. Optimal robust estimators of Zu% for trimodal distributions, $f_2 = 0.05$ and $f_3 = 0.05$.

4.2. Use of Kernel Density Plots

Using the methods described in Sections 2.1 and 3.2, we provide a generalized algorithm in determining the optimal robust estimators using actual results. The description of the algorithm follows using the practical example of the mentioned EUROCERT PT scheme. In that particular PT example, the organizer performs the 28-day strength test 9 times a year. The proposed algorithm implements the kernel density plot of each round, including the last test and the previous eight. For a small number of participants and several repeats of the test during the year, the estimated distribution using moving time horizon results should be closer to the real one than taking into account the limited number of the last round's results. The algorithm performs normalization using the formula $D_{ij} = x_{ij} - x_{pt,j}$,

described already in Section 2.1, before building the kernel density plot. It then assumes a main normal distribution. The addition of one or two contaminating normal distributions to the main follows, and the best-fitting mix of them, having the minimum distance from the kernel plot, is computed via non-linear regression. The values of m_1 , m_2 , m_3 , s_2 , s_3 , f_2 , and f_3 are the outputs of this process. Afterwards, the algorithm applies steps (i) to (viii) of Section 3.2 and determines the optimal estimator.

Table 5 shows the parameters of the distributions for 18 consecutive 28-day strength tests, along with the average N_{lab} and the optimal robust estimators of Zu% using the mentioned algorithm. If a second estimator differs from the reference value less than 5% from the respecting distance of the optimal one, the estimator is also optimal. If $f_2 + f_3$ is lower than or close to 0.1, the algorithm compares the optimal estimator with the one predicted in Figures 11–15. In the case of a positive check, the table indicates the values of N_{lab} , n_2 , and n_3 of the corresponding figure. In 8 out of the 9 cases where f_2 and f_3 meet the conditions of Figures 11–15, the prediction of these figures is correct, although the standard deviations are not equal and $s_1 \approx 1.5$ MPa. The long-term average of the populations' means is around 50 MPa, as reported in 3.1, concluding that the coefficient of variation of D_1 is about 3%. That means that the results of Figures 11–15 obtained for a variation coefficient of 2% are robust for values up to 3%. Table 5 shows that the algorithm is suitable for an expanded range of the secondary populations' fractions and unequal standard deviations s_1 , s_2 , and s_3 .

Table 5. Normal distribution parameters and optimum robust estimators for 18 consecutive 28-day strength tests.

					Code				
	012019	022019	032019	042019	052019	062019	092019	102019	112019
Count	1	2	3	4	5	6	7	8	9
N _{lab} average	12	12	13	13	13	13	12	13	13
m_1 , MPa	0.12	0.09	0.03	0.05	0.12	0.07	0.12	0.1	-0.02
s_1 , MPa	1.48	1.56	1.59	1.64	1.51	1.37	1.46	1.48	1.23
f_2	0.024	0.015	0.019	0.017	0.015	0.036	0.015	0.033	0.105
<i>m</i> ₂ , MPa	4.55	4.5	5.19	5.28	5.36	3.75	5.34	4	2.46
<i>s</i> ₂ , MPa	0.67	0.82	0.74	0.63	0.52	1.45	0.49	1.36	0.85
f3	0.101	0.08	0.044	0.053	0.08	0.074	0.06	0.056	0.081
<i>m</i> ₃ , MPa	-3.52	-3.51	-4.14	-4.31	-3.9	-3.96	-4.16	-4.5	-4.32
<i>s</i> ₃ , MPa	1.15	1.13	0.8	0.88	1.01	0.93	0.96	0.88	0.99
$(m_2 - m_1)/s_1$	2.99	2.83	3.25	3.19	3.47	2.69	3.58	2.64	2.02
$(m_3 - m_1)/s_1$	-2.46	-2.31	-2.62	-2.66	-2.66	-2.94	-2.93	-3.11	-3.50
$f_2 + f_3$	0.125	0.095	0.063	0.070	0.095	0.110	0.075	0.089	0.186
Optimal	Z_Hamp	Z_Hamp	Z_nIQR, Z_Hamp	Z_nIQR, Z_Hamp	Z_nIQR	Z_nIQR	Z_nIQR, Z_A	Z_nIQR	Z_nIQR
Status	N/A	OK	OK	ОК	OK	OK	ОК	OK	N/A
Figure		14	13	13	14	14	13	13	
N_{lab}, n_2, n_3		10, -2, 3	15, -3, 3	15, -3, 3	15, -3, 3	15, -3, 3	10, -3, 4	15, -3, 3	
					Code				
	012020	022020	032020	042020	052020	062020	092020	102020	112020
Count	11	12	13	14	15	16	17	18	19
N _{lab} average	12	12	12	12	12	12	12	12	12
m_1 , MPa	-0.14	0.43	-0.28	-0.3	-0.37	-0.41	0.08	0.16	0.04
s_1 , MPa	1.28	1.51	0.73	0.71	0.71	0.78	1.26	1.43	1.5
f_2	0.142	0.154	0.171	0.196	0.367	0.375	0.08	0.045	0.015
<i>m</i> ₂ , MPa	2.31	-0.58	1.47	1.42	1.25	1.34	2.94	1.43	4.7
s ₂ , MPa	0.84	0.6	0.62	0.61	0.9	0.9	1.3	2.63	0.8
f ₃	0.059	0.068	0.383	0.389	0.166	0.151	0.081	0.061	0.041
<i>m</i> ₃ , MPa	-4.27	-4.04	-0.16	-0.23	-2.63	-3.03	-3.54	-3.61	-3.69

<i>s</i> ₃ , MPa	1.01	1.1	2.49	2.46	1.52	1.29	0.82	0.69	0.53
$(m_2 - m_1)/s_1$	1.91	-0.67	2.40	2.42	2.28	2.24	2.27	0.89	3.11
$(m_3 - m_1)/s_1$	-3.23	-2.96	0.16	0.10	-3.18	-3.36	-2.87	-2.64	-2.49
$f_2 + f_3$	0.201	0.222	0.554	0.585	0.533	0.526	0.161	0.106	0.056
Optimal	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR	Z_nIQR, Z_Hamp	Z_Hamp	Z_Hamp	Z_Hamp
Status	N/A	N/A	N/A	N/A	N/A	N/A	N/A	Not OK	OK
Table									13
N_{lab}, n_2, n_3									10, -2, 3

Table 5. Cont.

Figure 16 depicts all the Zu% results, including the optimal ones, Z_Optim , leading to the following conclusions for $N_{lab} = 12-13$:

- The best estimator provided by the generalized algorithm depends on the distribution parameters.
- *Z_sRep* is always much lower than the reference values, *Z_Ref*, proving that it is not a robust estimator and verifying the findings of Section 3.2.
- For the given levels of N_{lab} and distribution parameters, Z_MADe is always much higher than Z_Ref and never optimum, verifying paragraph C. 2.3 of 13253:2015 [14] (p. 53). Z_A is closer to Z_Ref than Z_MADe but continuously overestimates Zu%.
- For the given range of m_1 , m_2 , m_3 , and s_1 , Z_nIQR and Z_Hamp are the best estimators: the first is 13 times, while the second is 8 times optimal. The results show that Z_Hamp is optimum for lower values of Zu% and Z_nIQR for higher Zu% values.



Figure 16. Estimators of Zu% for 18 rounds of the 28-day strength test.

5. Conclusions

This study developed efficient models in analyzing the results of PT schemes by combining: (a) robust and classical estimators of the population mean and standard deviation; (b) kernel density plots; (c) distributions derived from the addition of two or three Gaussians; (d) Monte Carlo simulations; and (e) Z-factors.

The analysis shows that the sum of two or three normal distributions of adjustable parameters can adequately approximate an actual kernel density plot, so it is a good approximation of the results' distribution. The one distribution is the main while the others contaminate it. Monte Carlo simulations implemented to such sums of distributions are effective in studying the characteristics of location and dispersion estimators based on ISO 13258:2015 and ISO 5725:2:1994. Assuming a distribution of a large number of results contain Zu% unsatisfactory results according to EN ISO/IEC 17043:2010, the simulator can

find the estimators providing non-satisfactory results close to this percentage when the number of labs is limited. The study describes an algorithm solving the above optimization problem with the following constraints: (a) Gaussian, bimodal or trimodal distributions; (b) participants from 10 to 30; (c) fraction of the contaminating population up to 0.10 of the total; (d) variation coefficient of the main distribution equal to 2; (e) equal standard deviations of all the distributions. The analysis proves that using the robust estimators of location and variance is necessary because the classical estimators based on ISO 5725-2:1994 lead to a severe underestimation of the percentage of outliers. The answer to which is the best robust estimator is by no means categoric because the selection depends on the fraction of the contaminating populations and the distances of the mean values of the distributions. The corresponding figures showing the optimal estimators for the constraints (a)–(e) are helpful for a PT expert to decide which estimator to choose if the Gaussian distributions approximating the actual kernel density plot fulfill these constraints. Generally, if the fraction of the contaminating population is ≤ 0.05 of the total, the selection of *MED-MADe* is not suitable.

By extending the above, we provided a generalized algorithm, using actual kernel density plots and the previous algorithm, which is not subject to restrictions (b)–(e) and implemented to the results of 18 consecutive rounds of a PT for the 28-day strength of cement with 12–13 participants in average per round. The optimal estimators in the cases studied in this particular test were the *MED-nIQR* and Q/Hampel methods. The generalized algorithm is suitable for various PT schemes in selecting the optimal robust estimators because it covers an expanded range of the secondary populations' fractions and unequal standard deviations.

Based on the above arguments, the novelty of this study is the combination of actual kernel density plots and robust estimators through Gaussian distributions and Monte Carlo simulations, helping to select the best robust estimator for the correct calculation of outliers. The investigation of the optimal estimators can continue in the following directions:

- The impact of assigned value and standard deviation uncertainty on the Z-factors;
- Type I and Type II errors of the estimators;
- Comparison of the statistic estimators (a) for a medium and large number of participants; (b) for a range of variation coefficient of results' distribution;
- Direct use of the kernel density plots, by taking into account our generalized algorithm, in determining the best estimator;
- Estimators' comparisons for Z-factors of absolute value between two and three.

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