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Article

A Robust Method for Calculating Precision for Interlaboratory Studies with a Staggered-Nested Design

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Abstract: Outlier testing and elimination can be avoided via application of robust estimators. Amongst robust estimators, the Q/Hampel method displays the best performance (in terms of breakdown point and efficiency). While the formulas and correction factors for Q/Hampel in the case of the design with two variance components (e.g. within- and between-laboratory variance) have already been made available, corresponding formulas for other designs have not. A case in point is the staggered-nested design, which is a highly efficient design for e.g. the estimation of intermediate precision in method validation studies. Accordingly, the formulas and correction factors for the use of Q/Hampel in the staggered-nested design are provided here.

Keywords: interlaboratory study; staggered-nested design; reproducibility precision; intermediate precision; reproducibility precision; robust estimator

1. Introduction

In the case of quantitative methods, the aim of interlaboratory validation studies is to characterize method performance in terms of trueness and precision. ISO 5725-2/-3/-4 (1, 2, 3) provide a number of different designs allowing the evaluation of these two performance characteristics.

A particularly powerful design is the staggered-nested design described in ISO 5725-3 2. The simplest such design is the two-factor staggered-nested design, where each laboratory obtains three test results. For laboratory i , test results y_{i1} and y_{i2} are obtained under repeatability conditions, and y_{i3} under intermediate conditions, e.g. on a different day.

The standard calculation method for precision is analysis of variance (ANOVA), preceded by outlier testing. While ANOVA, under the normal distribution assumption, is very efficient in the case of balanced designs, in the case of unbalanced designs, such as the staggered-nested design, the usual ANOVA does not use all the information available in the data. This is related to the fact that the reproducibility standard deviation is not calculated directly, but rather from the laboratory and intermediate standard deviation values; while the latter, in turn, is calculated from the standard deviation under intermediate conditions and the repeatability standard deviation. Another disadvantage of ANOVA and other conventional methods is that they very much depend on the data following a normal distribution and are thus highly sensitive to outliers. This can only be partially offset via outlier tests, since even if conspicuous values are not yet statistically significant outliers, considerable deviations can result in the determined precision data.

The advantage of robust estimators is that no outlier testing is required. For the estimation of means and standard deviation values, different robust estimators exist. The performance of a given robust estimators can be characterized via breakdown point (proportion of data that can be outliers without the estimate being affected) and efficiency (ratio of the statistical uncertainty of the estimate to that of the classical estimator under the normal distribution assumption). An overview of different breakdown point and efficiency values is provided in ISO 13528 4.

The Q/Hampel and Q_n methods have both the highest breakdown point and the best efficiency.

The Q/Hampel method uses the Q method for the calculation of the robust reproducibility standard deviation s_R and repeatability standard deviation s_r together with the Hampel estimator for the calculation of the location parameter x^* as described in ISO 13528 4. The theoretical basis for the Q method, including asymptotic performance and finite sample breakdown, is described in Müller et al. 5 and Uhlig 6.

The Q method is not only robust against outlying results, but also against a situation where many test results are identical, e.g. due to quantitative data on a discontinuous scale or due to rounding distortions. In such a situation other Q-like methods (e.g. the Q_n method originally introduced by Rousseeuw et al. 8 for univariate data) can fail because many pairwise differences are zero.

The Q method was introduced for the one-way random effect model and later modified – for ISO 13528 4 – to deal with the situation that there are many equal data, e.g., for the case where the number of significant digits is too small.

The Q/Hampel method is typically used for conventional designs, but it can also be applied for the staggered-nested design with two factors according to ISO 5725-3 2 – in particular for estimating the intermediate standard deviation in addition to the reproducibility and repeatability standard deviation.

2. Robust Statistical Analysis of Results by Means of the Q/Hampel Method in a Staggered-Nested Design with Two Factors

For each level, the data obtained in the experiment are denoted y_{ikl} (with i representing factor 0, i.e. laboratory, $i = 1, \dots, p$; k representing factor 1, $k = 1, 2$; and l representing the replicate, with l ranging from 1 to $n(k)$, with $n(1) = 2$ and $n(2) = 1$), i.e. for laboratory i there are three measurement results y_{i11} , y_{i12} , y_{i21} .

In summary, test results, grouped by laboratory, are denoted as follows:

$$\underbrace{y_{111}, y_{112}, y_{121}}_{\text{Lab 1}}, \underbrace{y_{211}, y_{212}, y_{221}}_{\text{Lab 2}}, \dots, \underbrace{y_{p11}, y_{p12}, y_{p21}}_{\text{Lab } p} \quad (1)$$

2.1. Determination of the Robust Reproducibility Standard Deviation s_R Using the Q Method

The calculation relies on the use of pairwise differences within the data set and, thus, does not depend on the estimate of the mean or median.

The algorithm can be described as follows.

Based on the measurement results as structured in equation (1), the cumulative distribution function of all absolute between-laboratory differences is calculated as follows:

$$H_1(x) = \frac{2}{9p(p-1)} \sum_{1 \leq i < j \leq p} (\mathbf{I}\{|y_{i11} - y_{j11}| \leq x\} + \mathbf{I}\{|y_{i11} - y_{j12}| \leq x\} + \mathbf{I}\{|y_{i11} - y_{j21}| \leq x\} + \mathbf{I}\{|y_{i12} - y_{j11}| \leq x\} + \mathbf{I}\{|y_{i12} - y_{j12}| \leq x\} + \mathbf{I}\{|y_{i12} - y_{j21}| \leq x\} + \mathbf{I}\{|y_{i21} - y_{j11}| \leq x\} + \mathbf{I}\{|y_{i21} - y_{j12}| \leq x\} + \mathbf{I}\{|y_{i21} - y_{j21}| \leq x\}) \quad (2)$$

where $\mathbf{I}\{|y_{ikl} - y_{jkl}| \leq x\} = \begin{cases} 1 & \text{if } |y_{ikl} - y_{jkl}| \leq x \\ 0 & \text{otherwise} \end{cases}$ denotes the indicator function.

Discontinuity points of $H_1(x)$ are denoted

x_1, \dots, x_m , where $x_1 < x_2 < \dots < x_m$.

For each positive discontinuity points x_1, \dots, x_m , define

$$G_1(x_i) = \begin{cases} 0,5 \cdot (H_1(x_i) + H_1(x_{i-1})) & \text{if } i \geq 2 \\ 0,5 \cdot H_1(x_1) & \text{if } i = 1; x_1 > 0 \end{cases} \quad (3)$$

and let

$G_1(0) = 0$

For each x within the interval $[0, x_m]$, $G_1(x)$ is obtained by linear interpolation between discontinuity points $0 < x_1 < x_2 < \dots < x_m$.

Finally, the robust reproducibility standard deviation s_R is obtained as

$$s_R = \frac{G_1^{-1}(0,25 + 0,75 \cdot H_1(0))}{\sqrt{2}\Phi^{-1}(0,625 + 0,375 \cdot H_1(0))} \cdot b_p \tag{4}$$

where $H_1(0)$ is calculated as in equation (2) and is set equal to zero unless there are identical values in the data set.

In Equation (4), $\Phi^{-1}(q)$ denotes the q^{th} quantile of the standard normal distribution and b_p denotes the correction factor corresponding to the number of laboratories p .

The correction factors b_p were obtained via a simulation study, which will now be briefly described. In each simulation step, normally ($N(0,1)$) distributed data corresponding to p laboratories were generated and the robust reproducibility standard deviation s_R was calculated in accordance with the Q method from the formulas given above. Taking the mean value across 10^6 simulation steps – separately for each p – it was possible to calculate the expected value for the reproducibility standard deviation s_R . For a given p , the correction factor b_p was then obtained by taking the reciprocal of the expected value. For each value p between 4 and 100, Table 1 provides the expected value for the reproducibility standard deviation s_R along with the corresponding relative standard error and correction factor b_p .

Table 1. Simulation results for each value of p : Expected value and relative standard error for s_R as well as the correction factor b_p .

p	s_R	Rel. se(s_R)	b_p	p	s_R	Rel. se(s_R)	b_p	p	s_R	Rel. se(s_R)	b_p
4	1.3212	0.058%	0.7569	37	1.0163	0.014%	0.9839	70	1.0084	0.010%	0.9917
5	1.1864	0.054%	0.8429	38	1.0158	0.014%	0.9845	71	1.0082	0.010%	0.9919
6	1.1490	0.044%	0.8703	39	1.0154	0.014%	0.9848	72	1.0080	0.010%	0.9921
7	1.1173	0.041%	0.8950	40	1.0149	0.013%	0.9853	73	1.0079	0.010%	0.9922
8	1.1001	0.036%	0.9090	41	1.0147	0.013%	0.9855	74	1.0078	0.009%	0.9922
9	1.0857	0.034%	0.9211	42	1.0140	0.013%	0.9861	75	1.0077	0.009%	0.9924
10	1.0737	0.032%	0.9313	43	1.0139	0.013%	0.9863	76	1.0075	0.009%	0.9925
11	1.0657	0.030%	0.9384	44	1.0138	0.013%	0.9864	77	1.0077	0.009%	0.9924
12	1.0586	0.028%	0.9446	45	1.0133	0.013%	0.9869	78	1.0075	0.009%	0.9925
13	1.0538	0.027%	0.9490	46	1.0130	0.012%	0.9872	79	1.0073	0.009%	0.9928
14	1.0494	0.026%	0.9529	47	1.0125	0.012%	0.9876	80	1.0071	0.009%	0.9930
15	1.0452	0.024%	0.9568	48	1.0124	0.012%	0.9877	81	1.0072	0.009%	0.9928
16	1.0417	0.023%	0.9600	49	1.0119	0.012%	0.9882	82	1.0071	0.009%	0.9929
17	1.0391	0.022%	0.9624	50	1.0119	0.012%	0.9883	83	1.0069	0.009%	0.9931
18	1.0365	0.022%	0.9648	51	1.0117	0.012%	0.9885	84	1.0069	0.009%	0.9931
19	1.0342	0.021%	0.9669	52	1.0115	0.012%	0.9886	85	1.0068	0.009%	0.9932
20	1.0322	0.020%	0.9688	53	1.0112	0.011%	0.9889	86	1.0067	0.009%	0.9933
21	1.0304	0.020%	0.9705	54	1.0109	0.011%	0.9892	87	1.0065	0.009%	0.9936
22	1.0292	0.019%	0.9716	55	1.0107	0.011%	0.9894	88	1.0066	0.009%	0.9935

23	1.0278	0.019%	0.9730	56	1.0105	0.011%	0.9896	89	1.0067	0.009%	0.9933
24	1.0261	0.018%	0.9746	57	1.0104	0.011%	0.9897	90	1.0065	0.009%	0.9935
25	1.0252	0.018%	0.9754	58	1.0102	0.011%	0.9899	91	1.0063	0.008%	0.9938
26	1.0238	0.017%	0.9768	59	1.0099	0.011%	0.9902	92	1.0062	0.008%	0.9938
27	1.0231	0.017%	0.9774	60	1.0096	0.011%	0.9905	93	1.0061	0.008%	0.9939
28	1.0221	0.017%	0.9784	61	1.0096	0.011%	0.9905	94	1.0061	0.008%	0.9939
29	1.0214	0.016%	0.9791	62	1.0095	0.010%	0.9905	95	1.0061	0.008%	0.9939
30	1.0203	0.016%	0.9801	63	1.0096	0.010%	0.9905	96	1.0059	0.008%	0.9941
31	1.0200	0.016%	0.9804	64	1.0092	0.010%	0.9909	97	1.0058	0.008%	0.9942
32	1.0192	0.015%	0.9812	65	1.0090	0.010%	0.9911	98	1.0058	0.008%	0.9942
33	1.0185	0.015%	0.9818	66	1.0088	0.010%	0.9913	99	1.0058	0.008%	0.9943
34	1.0180	0.015%	0.9823	67	1.0087	0.010%	0.9914	100	1.0058	0.008%	0.9942
35	1.0172	0.014%	0.9830	68	1.0086	0.010%	0.9915				
36	1.0168	0.014%	0.9835	69	1.0084	0.010%	0.9917				

For $p > 12$, it was possible to derive a functional relationship between p and the correction factor b_p via nonlinear optimization. This functional relationship is given in equation (5) and presented in Figure 1 for $12 < p \leq 100$.

$$b_p = \left(0,2680 \frac{1}{p^{2,3363}} + 0,5810 \frac{1}{p} + 0,9998 \right)^{-1}$$

(5)

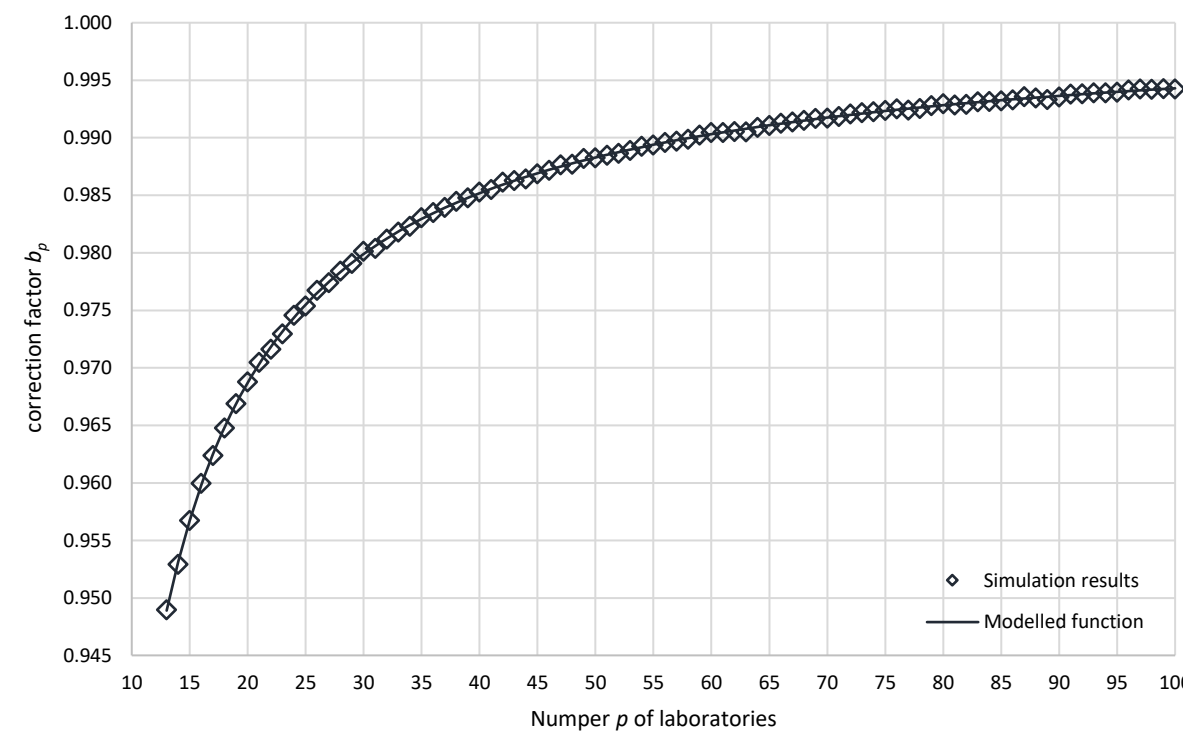


Figure 1. Functional relationship between the number p of laboratories and the correction factor b_p for S_R .

2.2. Determination of the Robust Intermediate Standard Deviation $s_{I(1)}$ Using the Q Method

Take the case that factor 1 is day. As explained above, in the two-factor staggered-nested design, there are two results for day 1, and one for day 2. For a given laboratory, there are thus two within-laboratory differences corresponding to factor 1. Accordingly, the cumulative distribution function corresponding to factor 1 is calculated as follows:

$$H_{2,I(1)}(x) = \frac{1}{2p} \sum_{i=1}^p (\mathbf{I}\{|y_{i11} - y_{i21}| \leq x\} + \mathbf{I}\{|y_{i12} - y_{i21}| \leq x\}) \tag{6}$$

where $\mathbf{I}\{|y_{i1l} - y_{i21}| \leq x\} = \begin{cases} 1 & \text{if } |y_{i1l} - y_{i21}| \leq x \\ 0 & \text{otherwise} \end{cases}$ ($l = 1,2$) denotes the indicator function.

As above, the discontinuity points of $H_{2,I(1)}(x)$ are denoted

$$x_1, \dots, x_m, \text{ where } x_1 < x_2 < \dots < x_m.$$

For each positive discontinuity points x_1, \dots, x_m , define

$$G_{2,I(1)}(x_i) = \begin{cases} 0,5 \cdot (H_{2,I(1)}(x_i) + H_{2,I(1)}(x_{i-1})) & \text{if } i \geq 2 \\ 0,5 \cdot H_{2,I(1)}(x_1) & \text{if } i = 1; x_1 > 0 \end{cases} \tag{7}$$

and let

$$G_{2,I(1)}(0) = 0$$

For each x within the interval $[0, x_m]$, $G_{2,I(1)}(x)$ is obtained via linear interpolation between discontinuity points $0 < x_1 < x_2 < \dots < x_m$.

Finally, the robust intermediate standard deviation $s_{I(1)}$ is obtained as

$$s_{I(1)} = \frac{G_{2,I(1)}^{-1}(0,5 + 0,5 \cdot H_{2,I(1)}(0))}{\sqrt{2}\Phi^{-1}(0,75 + 0,25 \cdot H_{2,I(1)}(0))} \cdot c_p \tag{8}$$

where $H_{2,I(1)}(0)$ is calculated as in equation (6) and is set equal to zero unless there are identical values in the data set.

As above, $\Phi^{-1}(q)$ denotes the q^{th} quantile of the standard normal distribution.

Similarly to b_p in the previous section, for a given number of laboratories p , the correction factor c_p was calculated via a simulation study.

For each value p between 4 and 100, Table 2 provides the expected value for the intermediate standard deviation $s_{I(1)}$ along with the corresponding relative standard error and correction factor c_p .

Table 2. Simulation results for each value of p : Expected value and relative standard error for $s_{I(1)}$ as well as the correction factor c_p .

p	s_R	Rel. se($s_{I(1)}$)	c_p	p	s_R	Rel. se($s_{I(1)}$)	c_p	p	s_R	Rel. se($s_{I(1)}$)	c_p
4	1.0855	0.046%	0.9212	37	1.0081	0.019%	0.9920	70	1.0043	0.014%	0.9957
5	1.0561	0.046%	0.9469	38	1.0080	0.018%	0.9920	71	1.0041	0.014%	0.9959
6	1.0550	0.040%	0.9479	39	1.0077	0.018%	0.9924	72	1.0043	0.014%	0.9957
7	1.0409	0.040%	0.9607	40	1.0077	0.018%	0.9923	73	1.0040	0.014%	0.9960
8	1.0410	0.036%	0.9606	41	1.0074	0.018%	0.9927	74	1.0041	0.013%	0.9959
9	1.0324	0.036%	0.9686	42	1.0073	0.018%	0.9928	75	1.0039	0.013%	0.9961
10	1.0321	0.033%	0.9689	43	1.0072	0.017%	0.9929	76	1.0040	0.013%	0.9960
11	1.0272	0.033%	0.9735	44	1.0068	0.017%	0.9932	77	1.0038	0.013%	0.9963
12	1.0270	0.031%	0.9737	45	1.0064	0.017%	0.9936	78	1.0040	0.013%	0.9960
13	1.0233	0.031%	0.9772	46	1.0068	0.017%	0.9933	79	1.0039	0.013%	0.9961
14	1.0231	0.029%	0.9774	47	1.0066	0.017%	0.9935	80	1.0038	0.013%	0.9962

15	1.0206	0.029%	0.9798	48	1.0064	0.016%	0.9937	81	1.0039	0.013%	0.9962
16	1.0200	0.027%	0.9804	49	1.0064	0.016%	0.9937	82	1.0034	0.013%	0.9966
17	1.0178	0.027%	0.9825	50	1.0063	0.016%	0.9937	83	1.0035	0.013%	0.9965
18	1.0173	0.026%	0.9830	51	1.0057	0.016%	0.9943	84	1.0037	0.013%	0.9963
19	1.0157	0.026%	0.9846	52	1.0059	0.016%	0.9941	85	1.0035	0.013%	0.9965
20	1.0157	0.025%	0.9845	53	1.0058	0.016%	0.9942	86	1.0036	0.012%	0.9964
21	1.0147	0.025%	0.9855	54	1.0055	0.016%	0.9946	87	1.0034	0.012%	0.9966
22	1.0140	0.024%	0.9862	55	1.0053	0.016%	0.9947	88	1.0036	0.012%	0.9964
23	1.0131	0.024%	0.9870	56	1.0055	0.015%	0.9946	89	1.0035	0.012%	0.9965
24	1.0134	0.023%	0.9867	57	1.0052	0.015%	0.9948	90	1.0036	0.012%	0.9964
25	1.0122	0.023%	0.9880	58	1.0054	0.015%	0.9946	91	1.0033	0.012%	0.9967
26	1.0121	0.022%	0.9880	59	1.0050	0.015%	0.9950	92	1.0034	0.012%	0.9966
27	1.0109	0.022%	0.9893	60	1.0051	0.015%	0.9949	93	1.0031	0.012%	0.9969
28	1.0112	0.021%	0.9889	61	1.0052	0.015%	0.9948	94	1.0032	0.012%	0.9968
29	1.0102	0.021%	0.9899	62	1.0050	0.015%	0.9950	95	1.0031	0.012%	0.9969
30	1.0102	0.021%	0.9899	63	1.0048	0.015%	0.9952	96	1.0031	0.012%	0.9969
31	1.0099	0.020%	0.9902	64	1.0051	0.014%	0.9949	97	1.0031	0.012%	0.9969
32	1.0095	0.020%	0.9906	65	1.0046	0.014%	0.9954	98	1.0031	0.012%	0.9969
33	1.0091	0.020%	0.9909	66	1.0048	0.014%	0.9952	99	1.0029	0.012%	0.9971
34	1.0092	0.019%	0.9909	67	1.0046	0.014%	0.9954	100	1.0032	0.012%	0.9968
35	1.0084	0.019%	0.9917	68	1.0044	0.014%	0.9956				
36	1.0088	0.019%	0.9913	69	1.0043	0.014%	0.9958				

For $p > 12$, it was possible to derive a functional relationship between the number p of laboratories and the correction factor c_p via nonlinear optimization. The functional relationship for $12 < p \leq 100$ is given in equation (9) and shown in Figure 2.

$$c_p = \begin{cases} \left(2,1251 \frac{1}{p^{11,3592}} + 0,3051 \frac{1}{p} + 0,9999\right)^{-1} & p \text{ odd} \\ \left(2,9723 \frac{1}{p^{4,6860}} + 0,3199 \frac{1}{p} + 0,9998\right)^{-1} & p \text{ even} \end{cases} \tag{9}$$

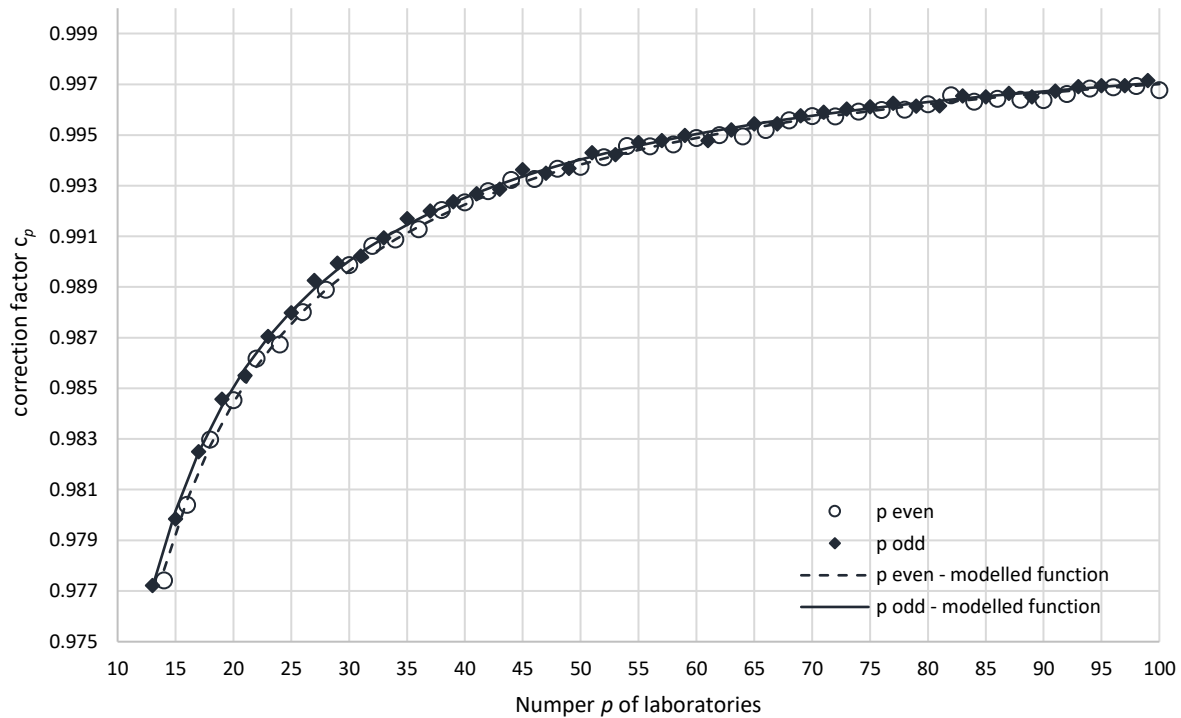


Figure 2. Functional relationship between the number p of laboratories and the correction factor c_p for $s_{I(1)}$.

If $s_{I(1)}$ results in a value greater than s_R , then $s_{I(1)}$ is set to s_R .

2.3. Determination of the Robust Repeatability Standard Deviation s_r Using the Q Method

As far as repeatability is concerned, there is only one difference which can be calculated per laboratory in the two-factor staggered-nested design: namely, that corresponding to the this first level of factor 1 (e.g. the two results obtained on day 1, if factor 1 is day). Accordingly, the cumulative distribution function corresponding to repeatability precision is calculated as follows::

$$H_{2,r}(x) = \frac{1}{p} \sum_{i=1}^p \mathbf{I}\{|y_{i11} - y_{i12}| \leq x\} \quad (10)$$

where $\mathbf{I}\{|y_{i11} - y_{i12}| \leq x\} = \begin{cases} 1 & \text{if } |y_{i11} - y_{i12}| \leq x \\ 0 & \text{otherwise} \end{cases}$ denotes the indicator function.

As above, the discontinuity points, the discontinuity points of $H_{2,r}(x)$ are denoted

x_1, \dots, x_m , where $x_1 < x_2 < \dots < x_m$.

For each positive discontinuity points x_1, \dots, x_m , define

$$G_{2,r}(x_i) = \begin{cases} 0,5 \cdot (H_{2,r}(x_i) + H_{2,r}(x_{i-1})) & \text{if } i \geq 2 \\ 0,5 \cdot H_{2,r}(x_1) & \text{if } i = 1; x_1 > 0 \end{cases} \quad (11)$$

and let

$$G_{2,r}(0) = 0$$

For each x within the interval $[0, x_m]$, the function $G_{2,r}(x)$ is calculated via linear interpolation between discontinuity points $0 < x_1 < x_2 < \dots < x_m$.

Finally, the robust repeatability standard deviation s_r is obtained as

$$s_r = \frac{G_{2,r}^{-1}(0,5 + 0,5 \cdot H_{2,r}(0))}{\sqrt{2}\Phi^{-1}(0,75 + 0,25 \cdot H_{2,r}(0))} \cdot c_p \quad (12)$$

where $H_{2,r}(0)$ is calculated as in equation (10) and is equal to zero unless there are identical values in the data set.

As above, $\Phi^{-1}(q)$ denotes the q^{th} quantile of the standard normal distribution.

The correction factor c_p is the same as in the previous section, see Table 2 and equation (9).

If s_r is greater than $s_{I(1)}$, then s_r is set equal to $s_{I(1)}$.

2.4. Determination of the Robust Mean x^* Using the Hampel Estimator

Calculate the weighted means for each laboratory, denoted y_1, \dots, y_p , i.e.

$$y_i = \frac{1}{4}(y_{i11} + y_{i12} + 2y_{i21}) \quad (13)$$

Calculate the robust mean, x^* , by solving the equation

$$\sum_{i=1}^p \psi\left(\frac{y_i - x^*}{s^*}\right) = 0 \quad (14)$$

where

$$\psi(q) = \begin{cases} 0, & q \leq -4,5 \\ -4,5 - q, & -4,5 < q \leq -3 \\ -1,5, & -3 < q \leq 1,5 \\ q, & -1,5 < q \leq 1,5 \\ 1,5, & 1,5 < q \leq 3 \\ 4,5 - q, & 3 < q \leq 4,5 \\ 0, & q > 4,5 \end{cases} \quad (15)$$

and

$$s^* = \sqrt{s_R^2 - \frac{1}{2}s_{I(1)}^2 - \frac{1}{8}s_r^2} \quad (16)$$

where s_R , $s_{I(1)}$ and s_r denote the robust reproducibility, intermediate and repeatability standard deviations obtained in accordance with the Q method (as described in 0, 0 and 0), respectively.

The exact solution may be obtained in a finite number of steps (not iteratively) using the property that Ψ is partially linear in x^* and by means of the interpolation nodes of the left side of equation (14) (interpreted here as a function of x^*).

The interpolation nodes are obtained as follows

- for the first value y_1 :

$$d_1 = y_1 - 4,5 \cdot s^*, d_2 = y_1 - 3 \cdot s^*, d_3 = y_1 - 1,5 \cdot s^*, d_4 = y_1 + 1,5 \cdot s^*, d_5 = y_1 + 3 \cdot s^*,$$

$$d_6 = y_1 + 4,5 \cdot s^*$$

- for the first value y_2 :

$$d_1 = y_2 - 4,5 \cdot s^*, d_2 = y_2 - 3 \cdot s^*, d_3 = y_2 - 1,5 \cdot s^*, d_4 = y_2 + 1,5 \cdot s^*, d_5 = y_2 + 3 \cdot s^*,$$

$$d_6 = y_2 + 4,5 \cdot s^*$$

- and so on for all values y_3, \dots, y_p .

The notes $d_1, d_2, d_3, \dots, d_{6,p}$ are sorted in ascending order: $d_{\{1\}}, d_{\{2\}}, d_{\{3\}}, \dots, d_{\{6,p\}}$.

For each $m = 1, \dots, (6 \cdot p - 1)$, the following quantity is then calculated:

$$p_m = \sum_{i=1}^p \psi\left(\frac{y_i - d_{\{m\}}}{s^*}\right) \quad (17)$$

It is then checked whether

- (i) $p_m = 0$. If so, $d_{\{m\}}$ is a solution of equation (14).
- (ii) $p_{m+1} = 0$. If so, $d_{\{m+1\}}$ is a solution of equation (14).
- (iii) $p_m \cdot p_{m+1} < 0$. If so, $x_m = d_{\{m\}} - \frac{p_m}{d_{\{m+1\}} - d_{\{m\}}}$ is a solution of equation (14).

Let S denote the set of all solutions of equation (14).

The solution $x^* \in S$ nearest to the median is taken as the location parameter x^* , i.e

$$|x^* - \text{median}(y_1, y_2, \dots, y_p)| = \min\{|x - \text{median}(y_1, y_2, \dots, y_p)|; x \in S\} \quad (18)$$

Several solutions may exist. If there are two solutions nearest the median, or if there is no solution at all, the median itself is taken as the location parameter x^* .

This implementation of Hampel's estimator has approximately 96 % efficiency for normally distributed data.

If this estimation method is used, laboratory results differing from the mean by more than 4,5 times the reproducibility standard deviation no longer have any effect on the calculation result, i.e. they are treated as outliers.

3. Conclusion

The Q/Hampel procedure described in this paper extends the range of robust statistical methods to staggered-nested designs, providing for the first time an adequate approach for handling outliers in such complex experimental formats. In conventional ISO 5725 approaches, especially under unbalanced conditions, the absence of a straightforward outlier identification process at the intermediate stage often necessitates the exclusion of all results from a laboratory, resulting in significant information loss. By contrast, the robust approach presented here allows the retention of valuable data from all laboratories, maximizing the information available for the estimation of precision parameters and means. Thus, the introduction of robust estimators in staggered-nested designs ensures both the integrity of statistical analysis and the efficient use of all available data in method validation studies.

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