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Quantification of the environmental structural risk with spoiling ties: Is randomization worth?

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ABSTRACT¹

Many recent works show that copulas turn out to be useful in a variety of different applications, especially in environmental sciences. Here the variables of interest are usually continuous, being times, lengths, weights, and so on. Unfortunately, the corresponding observations may suffer from (instrumental) rounding and adjustments, and eventually they may show several repeated values (i.e., ties). In turn, on the one hand, a tricky issue of identifiability of the model arises, and, on the other hand, the assessment of the risk may be adversely affected. A possible remedy is to introduce suitable randomization procedures: here three different jittering strategies are outlined. The target of the work

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is to carry out a simulation study in order to evaluate the effects of the randomization of multivariate observations when ties are present. In particular, it will be investigated whether, how, and to what extent, the randomization may change the estimation of the structural risk: for this purpose, a coastal engineering example will be used, as archetypical of a broad class of models and problems in engineering practice. Practical advices and warnings about the use of randomization techniques are hence given.

KEYWORDS: Copula, Risk Management, Randomization, Jittering, Structural Risk

1. Introduction

Copulas have proved to be useful in a variety of different applications, especially in environmental sciences (see, e.g., Genest and Favre (2007); Salvadori et al. (2007); AghaKouchak et al. (2013)), where they contribute to quantify the risk in a suitable way. In fact, it is well known that the description of the joint probability law of a vector of random variables can be conveniently represented (via Sklar’s Theorem Sklar (1959)) as the composition of a copula and one-dimensional marginals ruling the phenomenon of interest. In particular, both the copula and the marginal laws are chosen and fitted on a set of available data, considered as an i.i.d. (sometimes, also stationary) sample from an unknown *continuous* joint distribution.

The emphasis on the adjective “continuous” is extremely important in the present context. In fact, if the marginals are continuous, then

- the observations assume (with probability 1) distinct values ranging in the support of the underlying distribution, and no *ties* (i.e., repeated observations) occur in the dataset;
- the copula associated with a random vector can be uniquely determined.

Conversely, when the marginals are not continuous, the data typically contain ties, and a tricky issue of identifiability of the model arises. For an overview about possible problems using copulas with non-continuous data, we refer to the excellent survey by Genest and Nešlehová (2007) (see also Marshall (1996)).

In many applications of environmental sciences, however, the situation is somehow mixed. While it is not questionable (for physical reasons) that the random variables of interest can be viewed as continuous, the available measurements suffer from (instrumental) adjustments and rounding procedures, so that they may show several repeated observations. Now, as documented e.g. in Genest et al. (2011); Bücher and Kojadinovic (2014), the presence of such repetitions may have a non-negligible impact on the rank-based inference of copulas. For instance, the performances of popular goodness-of-fit procedures for copula models cannot be guaranteed anymore.

As stressed in Bücher and Kojadinovic (2014), when ties are present, the “copula-oriented” practitioner has (at least) two possibilities — excluding the limiting case of stopping any further statistical analysis: (i) discard the ties; (ii) randomize the data, by adding a suitable, continuous white noise to all observations. Since the former case was already discussed in Genest et al. (2011), we focus here on the latter methodology, which is known in literature as *randomization*, sometimes also called *jittering* or *rounding*.

The target of this note is to carry out a simulation study in order to evaluate the effects of the randomization of multivariate observations when ties are present. In particular, we will investigate whether, how, and to what extent, the randomization may change the estimation of the structural risk, using a coastal engineering example representing an archetype of a broad class of models and problems in engineering practice. To this end, we use with a practical illustration involving a realistic simulation study tailored to a dataset previously investigated in other works. Despite the peculiar situation, the results shown may provide practical advices and warnings about the use of randomization techniques.

2. The illustration

We consider an application in coastal engineering related to the design of a rubble mound breakwater as described in Salvadori et al. (2014) (see also Pappadà et al. (2015); Salvadori et al. (2015)). The target is to compute the quantiles associated to the weight W of a concrete cube element forming the breakwater structure, assuming that the environmental load is given by the pair of non-independent random variables (H, D) , where H represents the significant wave height (in meters), and D the sea storm duration (in hours). For this purpose, we use a structural model Ψ that expresses W as a function of (H, D) by means of the formula

$$\begin{aligned} W &= \Psi(H, D) \\ &= \rho_S \cdot \left[H \left(\frac{2 \pi H}{g [4.597 \cdot H^{0.328}]^2} \right)^{0.1} \right]^3 \\ &\quad \cdot \left[\left(\frac{\rho_S}{\rho_W} - 1 \right) \cdot \left(1 + \frac{6.7 \cdot N_d^{0.4}}{(3600 D / [4.597 \cdot H^{0.328}])^{0.3}} \right) \right]^{-3}. \end{aligned} \quad (1)$$

The values of the structural parameters in Eq. (1) are calibrated for the buoy of Alghero (Sardinia, Italy), previously investigated in Salvadori et al. (2014). Following a copula approach to the structural risk (see, for instance, Straub (2014)), in order to estimate the quantiles associated with W we can proceed as follows:

- First, determine the univariate distribution functions associated with H and D , respectively;
- Then, fix the copula associated with (H, D) ;
- Finally, calculate the quantile of W either analytically (if possible), or by resampling from the distribution of (H, D) previously obtained via Sklar's Theorem.

It is important to realize that, in principle, both H and D describe continuous phenomena (viz., a length and a time). Unfortunately, due to a limited instrumental resolution, the available measurements may be a discretized version of the actual continuous values of these variables. This is, for instance, the case of the data presented in Salvadori et al. (2014). Thus, ties may occur, and adversely affect the statistical analysis of the data both at the marginal level and at the copula level — see, e.g., (De Michele et al., 2013, Sec. 3 and Fig. 2) for a different hydrological case study. Concerning this latter aspect, the situation is particularly problematic, since copula-based procedures are grounded on the possibility of uniquely determining the ranks of the observations.

A practical way to circumvent the problem could consist in adding independent random components to the coordinates of each observed pair (X_i, Y_i) — here, the pair (H, D) — by setting

$$\tilde{X}_i = X_i + U_i \quad \text{and} \quad \tilde{Y}_i = Y_i + V_i, \quad i = 1, \dots, n,$$

where n is the available sample size, and U_1, \dots, U_n and V_1, \dots, V_n are independent random samples from the Uniform distribution on a suitable interval I_X and I_Y , respectively.

In De Michele et al. (2013); Salvadori et al. (2014), for instance, the specification of these intervals is determined by the known resolution of the measurements of the corresponding variables. We will refer to such a procedure as the *independent randomization*. Here, two other types of randomization will also be considered:

- the *co-monotone randomization*, which assumes that U_i and V_i are coupled by the Fréchet–Hoeffding upper bound copula $M_2(u, v) = \min\{u, v\}$;
- the *mixed randomization*, which assumes that U_i and V_i are coupled by a convex mixture C of M_2 and the independence copula $\Pi_2(u, v) = uv$ (i.e., $C = \lambda M_2 + (1 - \lambda)\Pi_2$, with $\lambda \in (0, 1)$). Here, the mixing coefficient λ is related to degree of association of the observations (X_i, Y_i) , as estimated via the available data (note that λ coincides with the Kendall's τ associated with the mixing copula C) — see below.

Roughly speaking, if (X_i, Y_i) are positively associated, then the independent randomization tends to produce pairs $(\tilde{X}_i, \tilde{Y}_i)$'s featuring a positive dependence weaker than that of (X_i, Y_i) , whereas co-monotone and mixed randomization tend to put a remedy to such an inconvenience. In particular, these two latter methods are likely to yield more conservative estimates (from the risk manager's viewpoint) than the independent randomization.

Remark 2.1 *At a formal level, in the presence of ties, a pair of random variables is uniquely associated to a sub-copula, not to a copula (see, for instance, Durante and Sempi (2015)). Thus, every type of randomization can be thought of as a specific way to extend a sub-copula to a copula (see, e.g., de Amo et al. (2012)). In particular, the independent randomization is related to the multilinear extension of Genest et al. (2014) (see also Durante et al. (2015)), while the co-monotone and mixed randomizations are associated with extensions that distribute the probability mass according to, respectively, M_2 and the convex linear combination C of M_2 with Π_2 .*

Remark 2.2 *In recognition of the fact that the sample $(\tilde{X}_i, \tilde{Y}_i)$'s is generated via a randomization process, a possible strategy could be to perform a large number of independent randomizations, and average the results. However, as shown in Genest and Nešlehová (2007), this procedure does not seem to mitigate the bias produced by the randomization.*

As mentioned in the Introduction, while it is arguable whether the randomization procedures may provide valuable indications for statistical inference procedures for copulas (like parameter estimation, goodness-of-fit tests, etc.), it is unclear whether the risk quantification (in a given situation) can be severely biased by randomizing as well. In the present study, starting with the practical application described above, we would like to shed light on this latter aspect.

In order to focus on those features that characterize the practical problem we are addressing, we make the following assumptions.

- Without loss of generality, both H and D follow the Generalized Weibull distributions F_H and F_D , with the same parameters as those estimated in Salvadori et al. (2014) for a specific dataset.

- We assume that the pair (H, D) is modeled by a Frank copula C^{Frank} with a specified parameter. Note that, according to the results shown in Salvadori et al. (2014), the Frank family may represent a convenient one-parameter dependence structure for the analyzed dataset.

3. The simulation study

The simulation study proposed in the following will reproduce the main features outlined above. Specifically, we proceed as follows.

- We generate a set of i.i.d. observations for the random pair (H, D) , according to a joint distribution function $C^{\text{Frank}}(F_H, F_D)$ as previously described.
- We round (loosely speaking, “discretize”) the simulated observations according to a predefined level. More specifically,
 - the measurements of H may have a basic resolution equal to $\Delta_H \in \{0.5m, 0.1m, 0.01m\}$;
 - the measurements of D may have a basic resolution equal to $\Delta_D \in \{3h, 1h, 0.5h\}$.

Note that the discretization levels given above roughly correspond to the actual ones for real buoy data. The resulting dataset generally presents several ties, and may reproduce conveniently some features observed in practice.

- Then, we apply a randomization procedure to the discretized dataset in order to carry out the “jittering”.

Given the randomized data, two questions will be considered.

- Is a goodness-of-fit test able to correctly identify the copula C^{Frank} that generates the data? Viz., is it able to reject the assumption that the dependence structure of the data belongs to another family such as the Gumbel, the Clayton, etc.?
- If the dependence structure is correctly identified, does the copula estimated using the randomized data help to provide valuable guesses of the risk associated with the random variable W defined via Eq. (1)?

The answer to these questions will depend on three aspects, namely:

- the sample size n , which is set equal to 150 or 300 — as in Kojadinovic et al. (2011);
- the degree of association between H and D , which is expressed in terms of the Kendall’s τ and takes on values in $\{0.25, 0.5, 0.75\}$ — as in Kojadinovic et al. (2011);
- the jittering strategy, viz. the independent, co-monotone, or mixed randomization, where the mixing coefficient λ is set equal to the sample Kendall’s τ associated with the discretized pairs (H, D) ’s.

First, we investigate how the presence of ties may affect the performance of rank-invariant procedures for the identification of the copula of (H, D) .

For $i \in \{1, \dots, B\}$, the following steps are repeated.

- i. Simulate n pairs from the model described above (based on Frank copulas), with three levels of dependence as given by $\tau \in \{0.25, 0.5, 0.75\}$, and apply the rounding with resolutions $(\Delta_H, \Delta_D) \in \{(0.01, 0.5), (0.1, 1), (0.5, 3)\}$.
- ii. Randomize the dataset obtained at the previous step (which typically contains ties) according to the three randomization strategies previously outlined.
- iii. Carry out the Crámer–von Mises goodness-of-fit test — here at a 5% significance level, using the multiplier variant proposed in Kojadinovic et al. (2011); Kojadinovic and Yan (2011) — of the null hypothesis \mathcal{H}_0 that the copula of the data belongs to a given family \mathcal{F} against the alternative that it does not belong to \mathcal{F} .

The results are reported in Tables 1 and 2. As can be noticed, for a sample size $n = 150$, in the case of weak/moderate discretization of the data, the goodness-of-fit test procedures tend to attain the nominal level (5%) for the null hypothesis that the copula comes from the Frank family (in particular the results are comparable with the ones obtained in Kojadinovic et al. (2011)). However, for strong discretizations, the test tends to reject the null hypothesis too often: apparently, in this latter case, the mixed randomization seems to produce the less biased results.

In testing the null hypothesis that the data comes from another fixed copula family different from the Frank one, the results seem overall quite reasonable. However, it should be noticed that, in case of weak dependence, the test applied to the randomized data does not seem to be able to distinguish between the Frank copula and the Gaussian one. In all cases, the performance improves using a larger sample size $n = 300$.

In case the goodness-of-fit test correctly identifies the true copula model (i.e., it does not reject, at the given significance level, the null hypothesis that the copula belongs to the Frank family), it could also be convenient to check how the parameter estimation varies with respect to the true value. Such results are illustrated in Figs. 1–2. As can be seen, the true parameter’s values are roughly identified (on average) in all cases and for all the randomization procedures, with the exception of a strong discretization with large dependence. In this latter case the true value of the parameter is generally underestimated and, consequently, a weaker degree of dependence is incorrectly perceived.

More interestingly, it is also useful to investigate how the randomization procedures may affect the estimation of the structural risk, as represented by a suitable quantile of the structural random variable W . We recall that, given the information about the model, the estimation of the structural risk can be easily computed via Monte Carlo simulation (by using the formula $W = \psi(H, D)$). The quantiles of order $q = 0.9, 0.95, 0.99$ of W — the ones usually of interest in applications — with fixed marginals for H and D , are computed, under different parameters as estimated from the Frank family (see Figs. 3–8).

As a result, in general the design quantiles are approximated in a reasonable way, except for the case when a strong discretization is present. Moreover, the co-monotone randomization yields a more conservative procedure (from a risk manager perspective) with respect to the independent jittering. To a smaller extent, the same conclusions hold for the mixed approach.

4. Conclusions

From the partial (yet realistic) simulation results presented above, it seems sensible to conclude that, as soon as the level of discretization of the data is weak or moderate, the randomization procedures outlined in this work can be adopted to achieve a practically reliable approximation to the structural risk. However, if a strong discretization is at play, then the jittering procedures overall tend to underestimate the true risk. In such a case, a partial remedy could be the use of the co-monotone randomization.

Of course, it must be borne in mind that the results may depend upon the particular structure function considered here, and the associated risk function. As a suggestion, the practitioner should repeat the procedures outlined above, properly calibrated on the case study under investigation.

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TABLE 1. Probability of rejection of the null hypothesis that the copula belongs to the Frank (F) family (respectively, Clayton (C), Gumbel (G), Normal (N), Student- t (t) with $\nu = 4$ degrees of freedom) for a random sample of size $n = 150$ generated from a Frank copula, with $\tau = 0.25, 0.5, 0.75$ (nominal level 5%) obtained from $B = 10000$ repetitions of the discretization and randomization procedures — see text.

Δ_H	Δ_D	F (True)	C	G	N	t
Independent randomization						
$\tau = 0.25$						
0.01	0.50	0.05124	0.79127	0.38351	0.13594	0.26872
0.10	1.00	0.04945	0.79477	0.39801	0.14384	0.27942
0.50	3.00	0.07014	0.85656	0.37201	0.21383	0.34402
$\tau = 0.5$						
0.01	0.50	0.05024	0.99835	0.79057	0.42781	0.70698
0.10	1.00	0.05244	0.99865	0.78977	0.45780	0.73238
0.50	3.00	0.13344	0.99985	0.78817	0.68108	0.88006
$\tau = 0.75$						
0.01	0.50	0.04695	0.99995	0.94936	0.87446	0.95415
0.10	1.00	0.05314	0.99995	0.95485	0.90776	0.96545
0.50	3.00	0.48510	0.99995	0.96105	0.98595	0.99805
Co-monotone randomization						
$\tau = 0.25$						
.01	0.50	0.05414	0.78937	0.38831	0.14044	0.27842
.10	1.00	0.05454	0.77127	0.39981	0.13644	0.26362
.50	3.00	0.11154	0.65968	0.51110	0.17803	0.23263
$\tau = 0.5$						
.01	0.50	0.05104	0.99755	0.79537	0.43281	0.71168
.10	1.00	0.05124	0.99655	0.79307	0.43211	0.68258
.50	3.00	0.14354	0.98635	0.86526	0.50110	0.63939
$\tau = 0.75$						
.01	0.50	0.04485	0.99995	0.94456	0.87906	0.95015
.10	1.00	0.04625	0.99965	0.95305	0.86916	0.93116
.50	3.00	0.37711	0.99995	0.98645	0.94596	0.97625
Mixed randomization						
$\tau = 0.25$						
0.01	0.50	0.05624	0.78357	0.40301	0.14954	0.28982
0.10	1.00	0.04865	0.78467	0.39181	0.14284	0.27142
0.50	3.00	0.06284	0.80867	0.36471	0.17653	0.28032
$\tau = 0.5$						
0.01	0.50	0.05134	0.99745	0.78987	0.43161	0.70758
0.10	1.00	0.05074	0.99705	0.79227	0.43841	0.70018
0.50	3.00	0.08604	0.99775	0.77617	0.53160	0.71798
$\tau = 0.75$						
0.01	0.50	0.04665	0.99995	0.95155	0.87826	0.95105
0.10	1.00	0.05044	0.99995	0.95225	0.87116	0.94086
0.50	3.00	0.26952	0.99995	0.96675	0.94256	0.97885

TABLE 2. Same as Table 1, for the case $n = 300$.

Δ_H	Δ_D	F (True)	C	G	N	t
Independent randomization						
$\tau = 0.25$						
0.01	0.50	0.04465	0.96075	0.72028	0.25282	0.58729
0.10	1.00	0.04515	0.96545	0.72578	0.25852	0.58699
0.50	3.00	0.07664	0.98395	0.71198	0.40311	0.69888
$\tau = 0.50$						
0.01	0.50	0.04155	0.99995	0.98875	0.79937	0.96845
0.10	1.00	0.04305	0.99995	0.98985	0.82347	0.97525
0.50	3.00	0.19843	0.99995	0.99185	0.95615	0.99695
$\tau = 0.75$						
0.01	0.50	0.03545	0.99995	0.99995	0.99725	0.99965
0.10	1.00	0.04265	0.99995	0.99985	0.99835	0.99975
0.50	3.00	0.78647	0.99995	0.99985	0.99995	0.99995
Co-monotone randomization						
$\tau = 0.25$						
0.01	0.50	0.04485	0.96405	0.71368	0.25312	0.58819
0.10	1.00	0.04225	0.94796	0.71128	0.24493	0.55539
0.50	3.00	0.14684	0.87166	0.84107	0.31142	0.47770
$\tau = 0.50$						
0.01	0.50	0.04465	0.99995	0.98875	0.79737	0.96805
0.10	1.00	0.04775	0.99985	0.99025	0.78527	0.95415
0.50	3.00	0.24703	0.99995	0.99655	0.86776	0.93476
$\tau = 0.75$						
0.01	0.50	0.03445	0.99995	0.99985	0.99605	0.99985
0.10	1.00	0.04525	0.99995	0.99965	0.99475	0.99885
0.50	3.00	0.71128	0.99995	0.99995	0.99975	0.99995
Mixed randomization						
$\tau = 0.25$						
0.01	0.50	0.04675	0.96225	0.72508	0.25832	0.58509
0.10	1.00	0.04595	0.95625	0.71688	0.26052	0.58359
0.50	3.00	0.06414	0.96565	0.69228	0.32792	0.59529
$\tau = 0.50$						
0.01	0.50	0.04275	0.99995	0.98915	0.80207	0.96975
0.10	1.00	0.04675	0.99995	0.99055	0.80187	0.96585
0.50	3.00	0.10064	0.99995	0.98765	0.87986	0.96985
$\tau = 0.75$						
0.01	0.50	0.03345	0.99995	0.99995	0.99535	0.99995
0.10	1.00	0.03945	0.99995	0.99965	0.99645	0.99935
0.50	3.00	0.46760	0.99995	0.99995	0.99955	0.99985

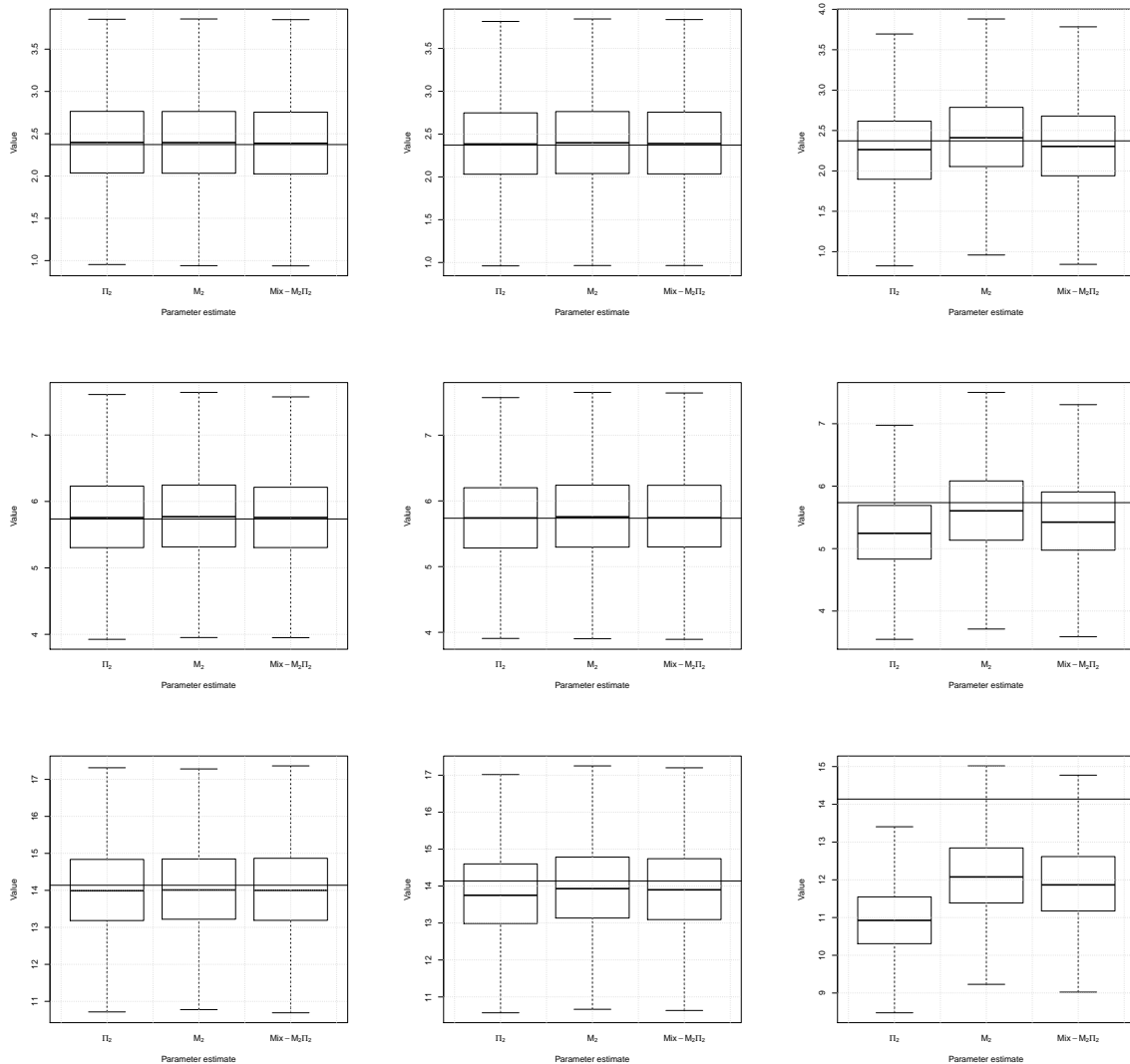


FIG. 1. Boxplots of the copula parameter estimates for $n = 150$; the horizontal thick lines indicate the true values — see text. From top to bottom, the rows correspond, respectively, to the values of the Kendall $\tau = 0.25, 0.5, 0.75$. From left to right, the columns correspond, respectively, to the following pairs of height and duration resolutions: $(\Delta_H, \Delta_D) \in \{(0.01, 0.5), (0.1, 1), (0.5, 3)\}$. The labels Π_2 , M_2 , and $Mix-M_2\Pi_2$ denote the use of an independent, a co-monotone, and a mixed randomization, respectively.

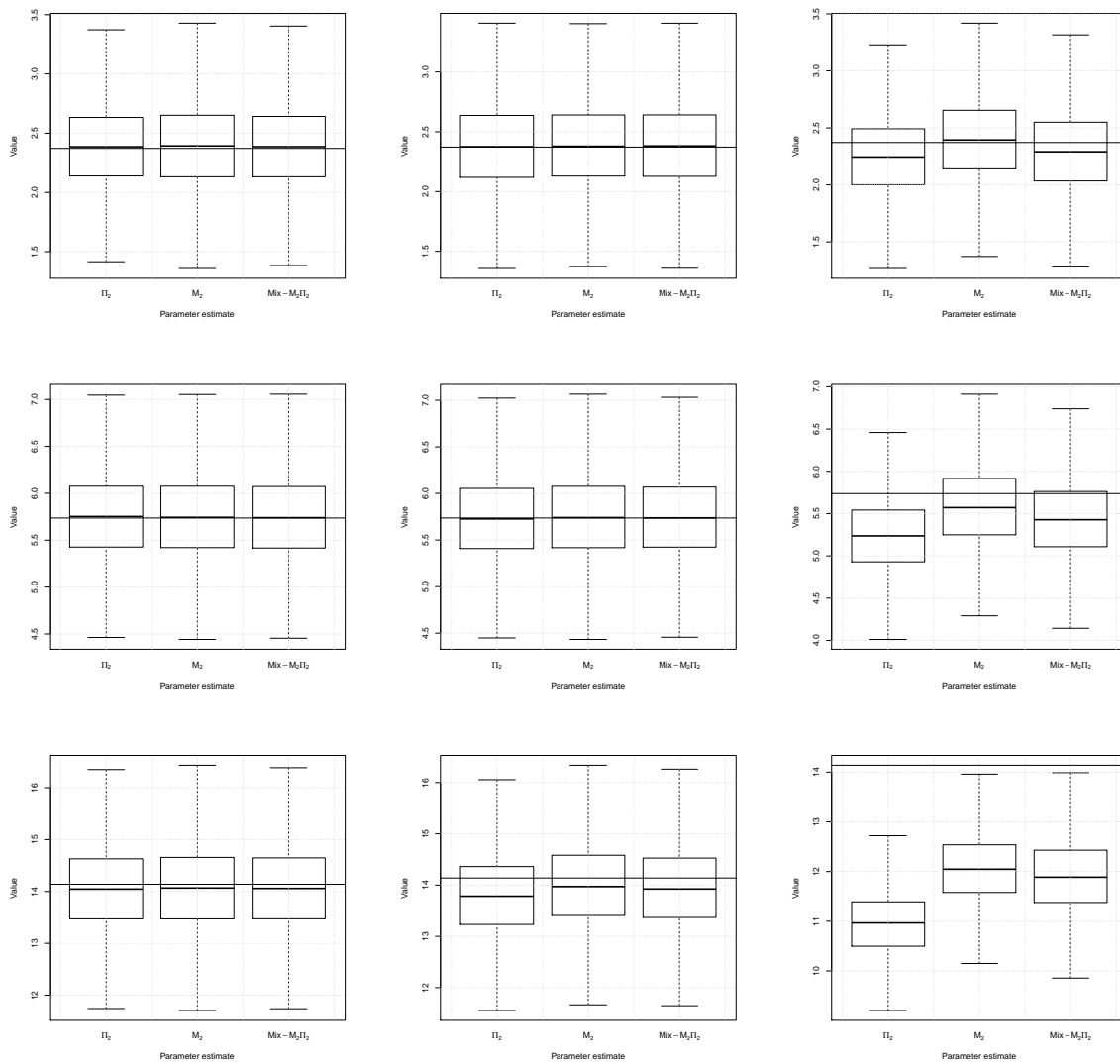


FIG. 2. Same as Fig. 1, for the case $n = 300$.

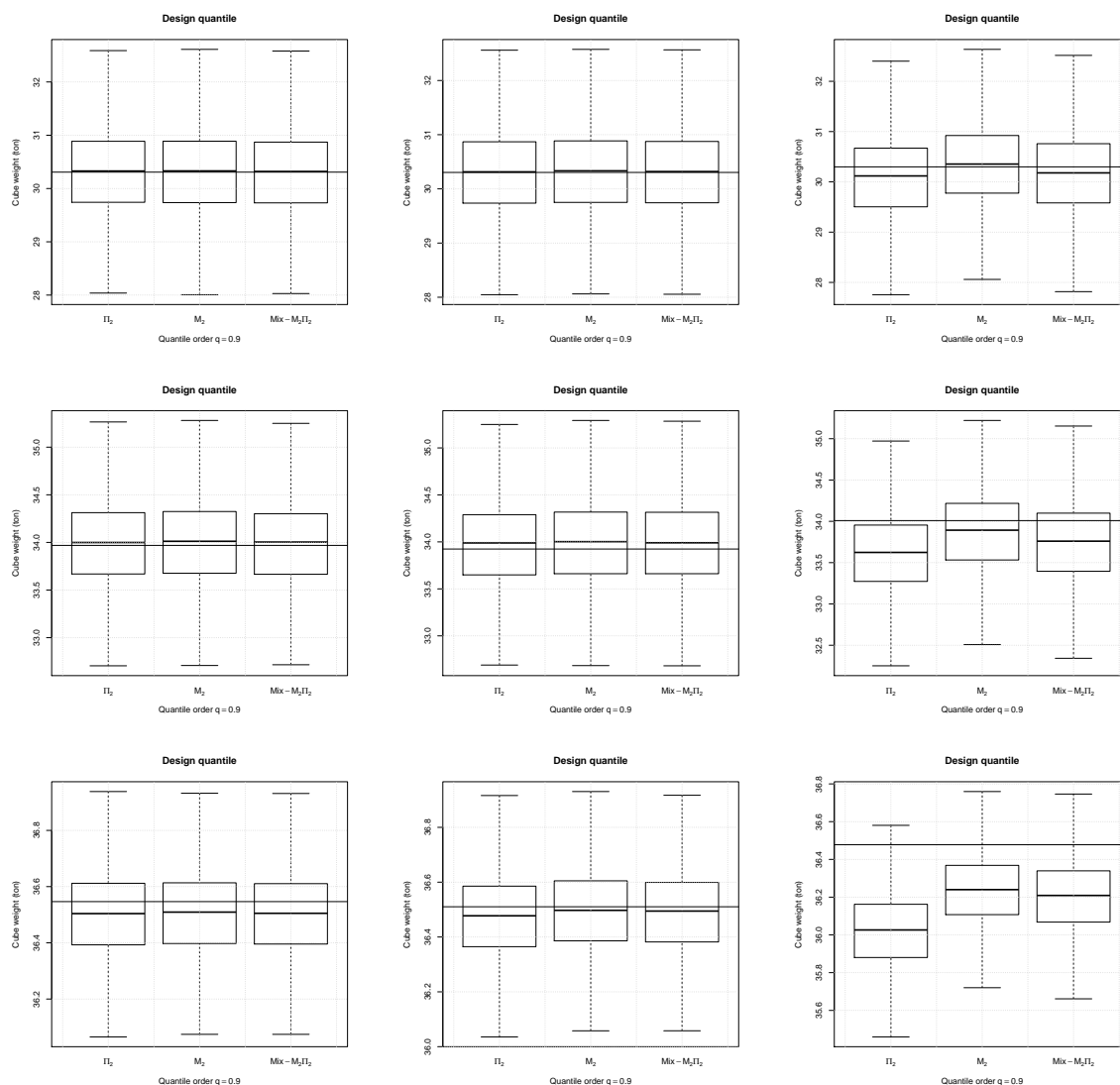


FIG. 3. Boxplots of the Cube Weight design quantiles estimates for $q = 0.90$ and $n = 150$; the horizontal thick lines indicate the true values — see text. From top to bottom, the rows correspond, respectively, to the values of the Kendall $\tau = 0.25, 0.5, 0.75$. From left to right, the columns correspond, respectively, to the following pairs of height and duration resolutions: $(\Delta_H, \Delta_D) \in \{(0.01, 0.5), (0.1, 1), (0.5, 3)\}$. The labels Π_2 , M_2 , and $\text{Mix-}M_2\Pi_2$ denote the use of an independent, a co-monotone, and a mixed randomization, respectively.

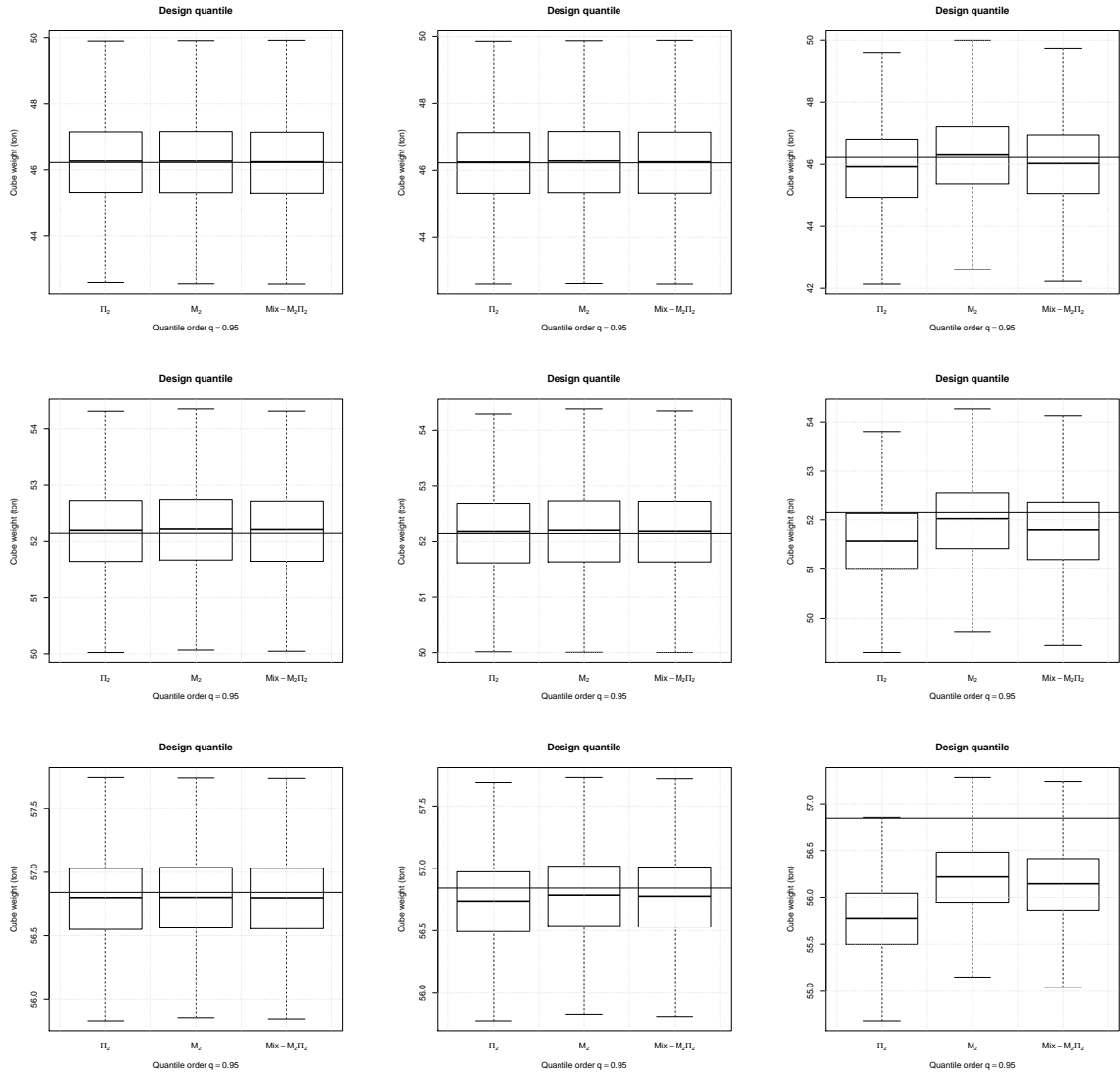


FIG. 4. Same as Fig. 3, for the design quantile $q = 0.95$.

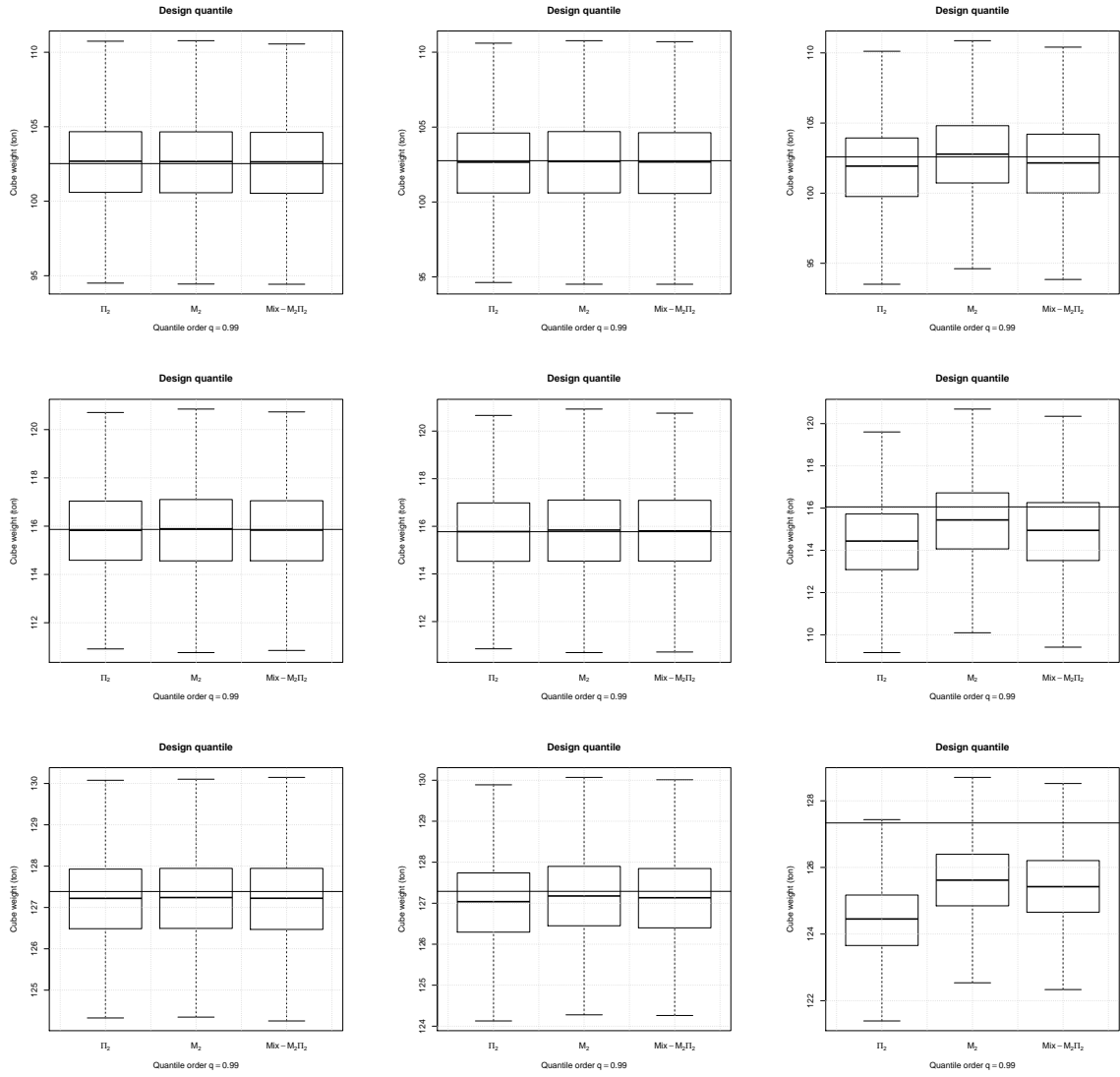


FIG. 5. Same as Fig. 3, for the design quantile $q = 0.99$.

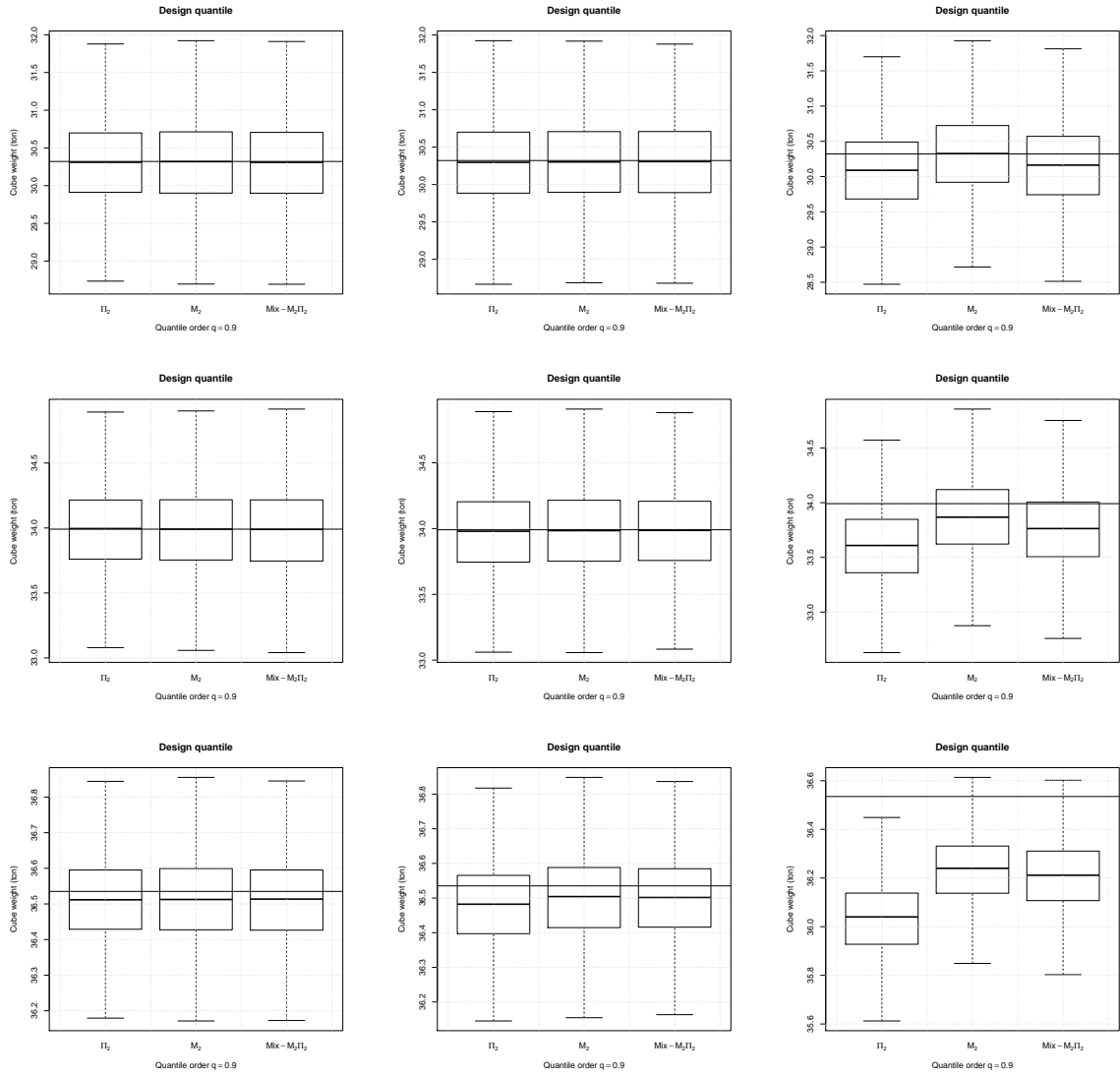


FIG. 6. Same as Fig. 3, for the case $n = 300$.

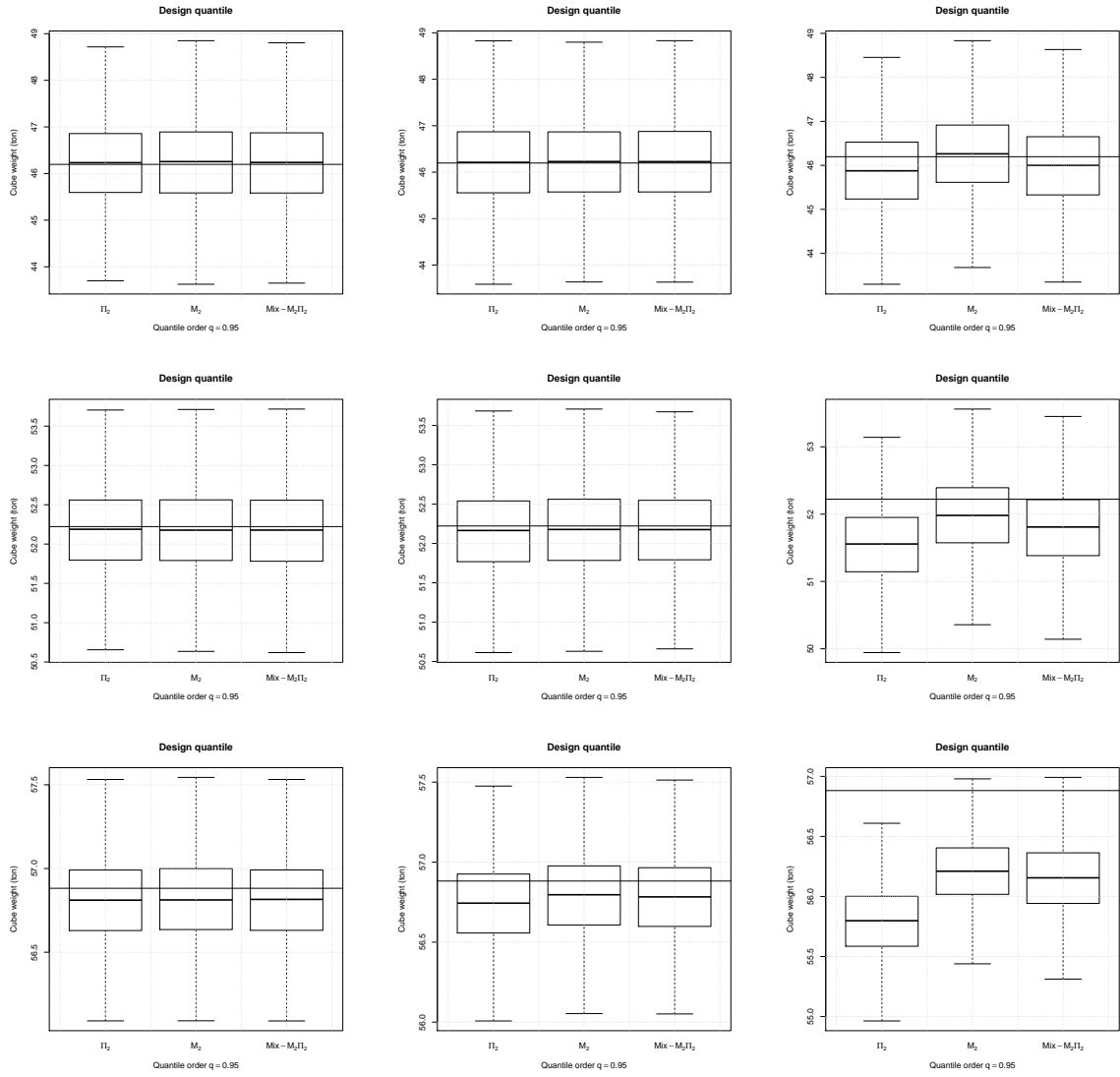


FIG. 7. Same as Fig. 4, for the case $n = 300$.

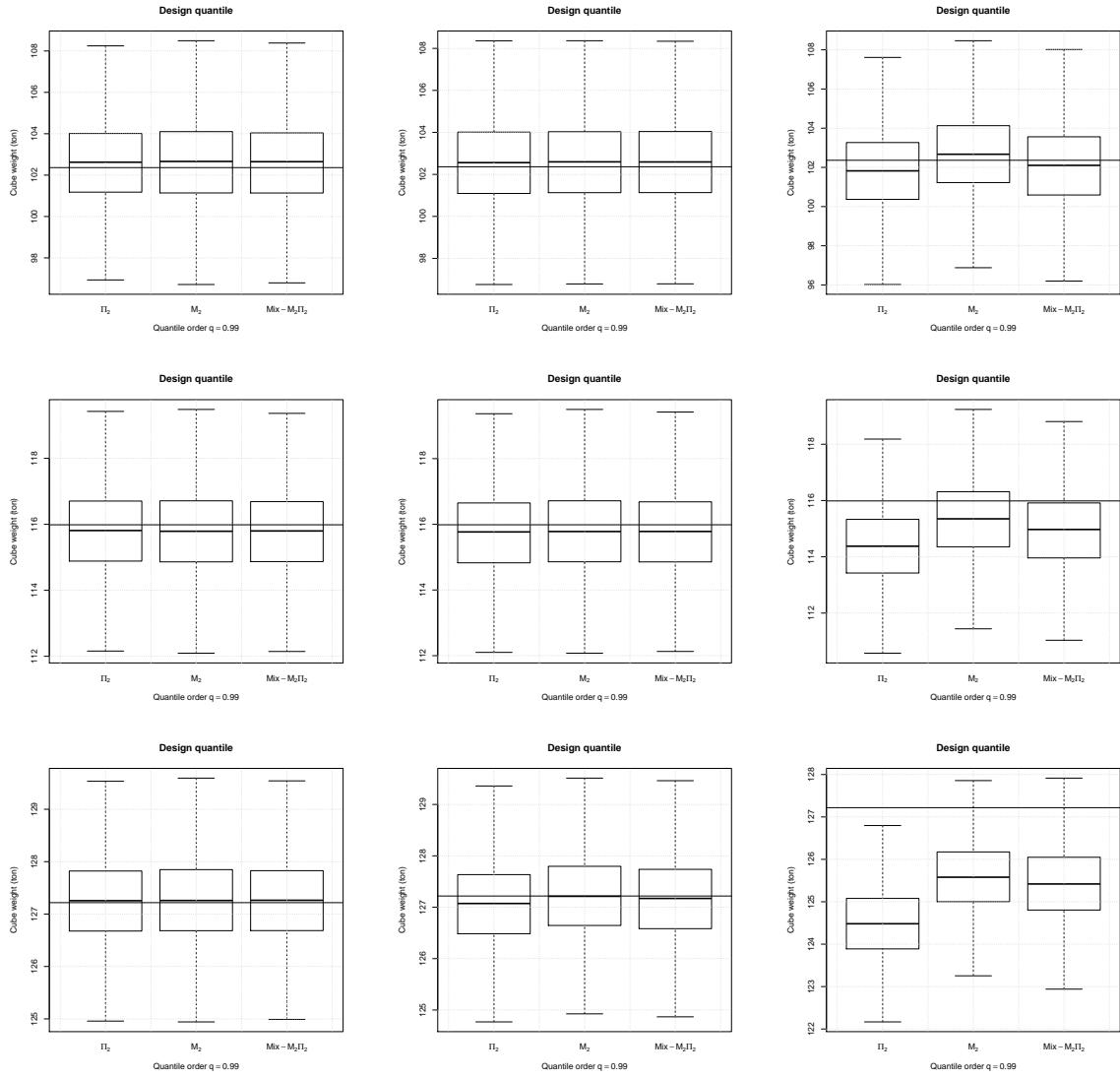


FIG. 8. Same as Fig. 5, for the case $n = 300$.

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