PSYCHOLOGY

An Application of Univariate Bootstrapping to DeFries-Fulker Regression Models

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Thesis under the direction of Professor Joseph Lee Rodgers

The univariate bootstrap is a relatively recently developed version of the bootstrap (Lee & Rodgers, 1998). Currently, research on the univariate bootstrap has largely focused on individual, bivariate correlations. DeFries-Fulker (DF) analysis is a regression model used to estimate parameters in behavioral genetic models (DeFries & Fulker, 1985). It is appealing for its simplicity; however, it violates certain regression assumptions such as homogeneity of variance and independence of errors that make calculation of standard errors and confidence intervals problematic. Methods have been developed to account for these issues (Kohler & Rodgers, 2001), however the univariate bootstrap represents a unique means of doing so that is presaged by suggestions from previous DF research (e.g., Cherny, Cardon, Fulker, & DeFries, 1992). DF analysis also presents an ideal area for application of univariate bootstrapping in that DF analysis primarily relies on a bivariate (intraclass) correlation, however it provides a convenient stepping off point for potential future applications of univariate bootstrapping to more complex models.

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Table of Contents

List of Tables

Appendix

Introduction

The purpose of this project is to evaluate the application of several bootstrap resampling approaches, including the standard and the univariate bootstrap, to DeFries-Fulker behavioral genetic models (DF models). The goal is to provide a relatively simple way to get accurate confidence intervals for DF model parameter estimates, particularly in DF models applied to non-normal data. Current options for DF model confidence interval (CI) creation are limited to CI's formed using a sandwich estimator, which may not be implemented in most software systems, or the standard regression CI's, which are guaranteed to be inaccurate. In contrast, the standard bootstrap is widely available and the univariate bootstrap is relatively simple to implement. Currently there are few applications of the univariate bootstrap in the literature, despite some advantages over the standard bootstrap. Thus, this project may provide a stepping off point for the application of univariate bootstrapping to broader multiple regression and more advanced models.

Bootstrapping

Bootstrapping in general is a resampling procedure for obtaining accurate confidence intervals for model parameters (e.g., Efron & Tibshirani, 1986). The bootstrap procedure can also be used to create a sampling distribution to support standard hypothesis testing. The basic bootstrap takes a data set and samples observations of that data set with replacement to create another resampled data set. In the taxonomy of Rodgers (1999), bootstrapping is sampling with replacement to form a full data set. A model is then fit to the new resampled data set and the model parameters are recorded. This process is repeated thousands of times, each time with a new resampled data set. Other versions of the bootstrap exist, but each is based on the core idea of resampling with replacement from some given set of observations or distributions to create new resample data sets to refit the model being tested. If the original data being bootstrapped are representative of the population, bootstrapping provides a way to approximate the results researchers would get if they replicated their study thousands of times in the population. This approach allows the researcher to create a confidence interval around the observed parameter estimates. For a given sample there are 2n-1 choose n possible bootstrap samples (where n is the number of unique observations), from which to calculate the parameter estimate of interest. For example, for ten observations there are 92,378 unique samples.

Permutation

The permutation resampling procedure is similar to bootstrapping in that it takes an original sample and creates thousands of new data sets, estimates parameters in each one, and creates a distribution of parameter estimates. In a permutation resampling procedure (also known as a randomization test; see Edgington, 1987) the researcher permutes the data thousands of different ways (potentially all possible ways if the number of possible permutations is low enough) by resampling observations without replacement from individual variables of the data set. In essence each variable is shuffled like a deck of cards, randomizing the relationship between all the variables (hence a randomization test). In the taxonomy of Rodgers (1999) the permutation (randomization) test is resampling without replacement to form a full sample. This resampling framework allows researchers to create intervals around the null hypothesis of no relationship to use for null hypothesis significance testing. For a given sample there are $n!^{k-1}$ possible combinations (where k is the number of variables). For example, for ten observations with two variables there are 3,628,800 unique samples.

Univariate bootstrapping

The univariate bootstrap resamples with replacement, like the traditional bootstrap, but from each variable independently as in permutation analysis (Lee & Rodgers, 1998). This procedure gives a distribution of parameter estimates under the null hypothesis, as in the permutation analysis. Alternatively, the univariate bootstrap data set can have a correlation imposed on it using a diagonalization technique (Beasley et al., 2007). The correlation imposed can either be a hypothesis imposed (HI) or observed imposed (OI) null hypothesis about the correlation. When a correlation is imposed the resulting bootstrap provides a distribution of parameter estimates that would occur if the imposed correlation were the population correlation (Rodgers & Beasley, 2012). When the observed correlations are imposed on the data set this will result in a confidence interval around the observed parameter estimates, as in standard bootstrapping. The number of unique samples in a univariate bootstrap is $\binom{n^k + n - 1}{n}$ unique samples. For example, for ten observations and two variables there are 42.6 trillion possible unique data sets.

The diagonalization technique used in past research on the univariate bootstrap was first developed by Kaiser and Dickman (1962). In the original Kaiser-Dickman method the data to be diagonalized are standardized (and are assumed to be uncorrelated in the population), and then matrix multiplied by a square-root type decomposition of the desired correlation matrix; the Cholesky decomposition has performed best in univariate bootstrapping applications. For the univariate bootstrap the Kaiser-Dickman procedure needs to be slightly altered. Because the goal is a sampling frame with a given correlation structure, the sampling frame needs to be standardized, not the raw data. If the raw data were standardized it would involve dividing the data by the sample standard deviation, however the sampling frame standard deviation of that variable is based on many repetitions of that variable (n^{k-1}, where k is the number of variables and n is the number of observations). This means that the sampling frame estimate of the variance is equal to $\frac{n^{(k-1)}\sum(x-\bar{x})^2}{n^k-1}$, instead of the original sample estimate of the variance, $\frac{\sum(x-\bar{x})^2}{n-1}$. If the correct variance is used in the standardization, the normal Kaiser-Dickman procedure can then be followed and will result in a sampling frame with the correct correlation structure. If the original sample estimate of the variance is used, the correlation structure will not match the desired correlation structure. The discrepancy between the two variances should go to 0 as n gets large, because both equations will, in the limit, be equivalent to the sum of squares over n. For small n cases, the difference can be quite important.

Although the typical bootstrap is conceptually simple, in practice some bias is present in where the interval in centered; the estimate needs to be corrected for this bias, because the interval may not be wide enough. Bias corrected and accelerated intervals (BCa) were created to help manage bias and width issues in standard bootstrapping (Efron, 1982). In contrast, the univariate bootstrap has generally low bias, both in its null and HI and OI forms, although the OI form performs somewhat better than the HI form with regards to alpha control (Beasley et al., 2007). In addition, a bootstrap can (with low probability) return a data set that has a single constant resampled value for one of the variables (because the samples are with replacement the same observation could be selected every time). In the typical bootstrap that will happen with probability n/(n+n-1 choose n). For ten unique observations that occurs about .01% of the time. In the univariate bootstrap it occurs with probability (n+n-1 choose n)*k/(n^k + n – 1 choose n). For ten observations that occurs approximately .0000004% of the time. Although these probabilities are low, when sampling from a data set with ten bivariate observations, for 10,000 bootstrap samples there is a 66.13% chance of at least one invalid sample in the typical bootstrap procedure; with the univariate bootstrap there is only a .004% chance of an invalid sample.

The univariate bootstrap has some significant limitations (at least as currently implemented). The univariate bootstrap eliminates heteroscedasticity in regression residuals entirely, similar to residual bootstrapping (Stine, 1989). Heteroscedasticity occurs when the variance of the residuals changes across levels of the independent variable. Some authors have suggested that failure to use a bootstrapping method that replicates heteroscedasticity can result in an unrepresentative bootstrap parameter distribution and potential bias (e.g., Stine 1989; Wu 1986). The univariate bootstrap creates a grid of points that is uniformly variable across the whole length of every axis, and as a result there is no heteroscedasticity in the base univariate sampling frame. Diagonalization reintroduces linear relationships, but it does not reintroduce heteroscedasticity. In addition to heteroscedasticity, if higher order relationships are of substantive importance the univariate bootstrap is inadequate. Finally, the univariate bootstrap has not been adequately extended beyond bivariate correlations (but see Rodgers & Beasley, 2012, for an introductory effort at using the univariate bootstrap for regression). Although these are all weaknesses that need to be addressed, they are not the focus of the present study.

DF Analysis

DeFries-Fulker (DF) analysis is a regression method to estimate biometrical parameters from behavioral genetic/kinship data (DeFries & Fulker, 1985). The typical goal in any biometric analysis is to partition the total variance of a given outcome into the proportion that is genetic variance (h^2), the proportion that is shared environmental variance (c^2), and the proportion that is nonshared environmental variance (e^2). The DF model does this using a regression formula that is easy to use and that can allow for the easy inclusion of additional explanatory variables (e.g., to further partition environmental variance into known and unknown environmental factors).

In their original formulation DeFries and Fulker (1985) intended their model to be used in cases where one member of a kinship pair had a selected condition (e.g., a reading disability, or schizophrenia). This member of the kinship pair would be the focal member, or proband. The proband's score on the outcome variable would be the IV in the regression model. Using the score of the other kin pair member (K), and the known average genetic relatedness of kin (R; 1 for monozygotic twins, .5 for full siblings and dizygotic twins, etc.) DeFries and Fulker's regression model can partition the overall phenotypic variance into a genetic component, a shared environment component, and a non-shared environment and error component (the error component and the non-shared environmental component are combined in the residual term in most DF models). Table 1 shows an example of the kind of data that might be used for a DF model. This data set has four MZ twin pairs (R = 1) and two full sibling or dizygotic twin pair (R = .5). The higher scores correspond to the proband and form variable K_2 for the regression analysis.

Table 1: Example of kinship data.

K_1	K_2	R
9	20	1
8	18	1
21	16	1
7	19	1
19	17	.5
7	21	.5

The original formulation of the DF model follows:

$$K_1 = B_0 + B_1K_2 + B_2R + B_3K_2R + e$$

In their formulation K_2 is the proband outcome score, K_1 is the co-kin outcome score, and R is the proportion of (segregating) genes shared on average. The coefficients can be directly interpreted in behavioral genetic terms (see Rodgers & McGue, 1994): B_1 is the proportion of variance caused by shared environmental effects (genetic effects have been controlled for by the other regression terms, and non-shared environmental effects lead to differences, not similarities, and go into the residual term). B_3 is a direct estimate of the proportion of variability associated with genetic processes. Rodgers and Kohler (2005), also pointed out that the model contains a second (hidden) estimate of these two biometrical parameters, because $E(B_0) = (1 - c^2) * \overline{K}$ and $E(B_2) = -h^2 * \overline{K}$; note that the two estimates of h^2 and of c^2 are not in general equal to one another. Although the original DF model is simple to implement, it has two notable shortcomings. First, when kinship pairs are not selected such that one member is clearly the proband and the other is not, the decision about which member provides the IV and which provides the DV is arbitrary. Second, the ability to estimate h^2 and c^2 in more than one way causes some ambiguity about which estimate to use.

In order to address the first shortcoming of the DF model, i.e., arbitrariness in unselected settings of which score is the IV, double entry of data was introduced. Double entry of the data allows each member of a kinship pair to take a turn as both the IV and the DV, resolving this issue (e.g., Kohler & Rodgers, 2001; Rodgers & McGue, 1994). Double entry also results in the kinship correlations being equivalent to the intraclass correlation coefficient. Table 2 shows the data from Table 1 in double entered form.

Table 2: Example of double entered kinship data.

K_1	K_2	R
9	20	1
8	18	1
21	16	1
7	19	1
19	17	.5
7	21	.5
20	9	1
18	8	1
16	21	1
19	7	1
17	19	.5
21	7	.5

Finally, the DF model has been simplified to provide an equivalent, but easier to interpret, model (Rodgers & Kohler, 2005). The simplified model, which will be used in this project, resolves the ambiguity of which estimate to use for h^2 and c^2 by providing a single estimate of each. The model follows.

$$(K_1 - K_m) = b_1(K_2 - K_m) + b_2(R * (K_2 - K_m)) + e$$

In the simplified DF model, K_m is the mean of K_1 and K_2 (it is identical in double entry settings), b_1 estimates the proportion of variation attributable to shared environment factors (when model assumptions are met), b_2 estimates the proportion of variation due to shared genetic factors (i.e., heritability), and e is the residual of the model; the proportion of variation due to non-shared environment can be estimated from the identity $h^2 + c^2 + e^2 = 1.0$. The model has no intercept because both sides of the equation are mean centered using K_m, which ensures that the true intercept of the model is 0.

The DF model is conceptually similar to an ANCOVA model. The outcome/predictor variable, *K* can (and arguably should) be a quantitative variable. *R* is theoretically quantitative as a ratio scale variable. In using kinship pairs, we assume an outcome variable has been measured for both members of a kinship pair. The level of genetic relatedness needs to be known (although in large samples some ambiguity can potentially be supported; cf NLSYlinks), and there need to be at least two kinship groups (e.g., monozygotic twins and dizygotic twins; full siblings and half siblings) to identify estimation of both c2 and h2.

It makes statistical and logical sense to double enter the data (Kohler & Rodgers, 2001; Rodgers & McGue, 1994). Without double entry the decision about which member of the kin pair is the predictor and which is the predicted is entirely arbitrary. Furthermore, without double entry the centering of the variables and fitting of a no-intercept model is a questionable practice when using unselected samples given that the “proband” group will in general have a different mean from the co-kin group (although because there is not a true “proband” in unselected cases this difference would be due to random chance). However, double entry artificially doubles the sample size, meaning standard errors that are produced by typical regression output are too small (Kohler & Rodgers, 2001). A sandwich estimator approach has been proposed to correct this deflation; however some have suggested that the sandwich estimator may not be entirely appropriate in this case (Mike Hunter, personal communication) because the sandwich estimator is for model misspecification, not incorrect sample sizes. Other authors have suggested a permutation technique for estimating the standard errors although they did not actually utilize that method (Cherny et al., 1992). Interestingly, both the Kohler and Rodgers (2001) paper and the Cherny et al. (1992) paper foreshadow the current study. Kohler and Rodgers (2001) used bootstrapping as a test for their estimator, and Cherny et al.’s (1992) suggestion of permutation is immediately relevant to univariate bootstrapping.

In addition to the issue of double entry, heteroscedasticity across the groups may also be a concern (Kohler & Rodgers, 2001). If there is a genetic effect it implies that more genetically related individuals will be more similar to each other (presuming that the equal environments assumption holds). Although the effects of genetics and the environment will be equal across groups, our ability to accurately predict an individual's score based on their co-kin score will increase as their genetic relatedness increases. This increase in predictive ability will decrease the residual term for genetically more higly related groups, particularly as genetic effects increase. This increase has the effect of guaranteeing heteroscedasticity in the model, an obvious violation of regression assumptions involved in hypothesis testing. Resampling procedures can help us account for such violations, although results from bootstrapping techniques can vary depending on how heteroscedasticity is managed (e.g., Stine, 1989; Wu 1986).

At a minimum, a well conducted DF analysis has violated two of the fundamental assumptions of regression. The errors will not be independent because of double entry, and the errors will be heteroskedastic (assuming that any genetic heritability is present). Furthermore, double entry results in a doubling of the *n* term in any equations used, which will result in overly narrow confidence intervals. Determining what methods (if any) are appropriate for correcting for these regression violations is the purpose of this project.

Current application

The DF model is a perfect case for the application of the univariate bootstrap, despite heteroscedasticity. There are only two variables of interest, which is a case where the univariate bootstrap is known to work well (e.g., Beasley et al., 2007; Beasley & Rodgers, 2012; Lee & Rodgers, 1998). The calculation of standard errors in DF analysis is not straightforward, which is a case where bootstrapping methods generally are advised. Lastly, it is nearly impossible to conceive of a case with non-selected twins where the DF analysis would contain a nonlinear effect (because items are double entered it is unlikely to make sense to say that someone's score would be a quadratic or other nonlinear function of their co-kin's score). Nonlinear effects are currently difficult to model using univariate bootstrapping, so their nearly guaranteed absence is a good safeguard. Heteroscedasticity would typically be an issue for the univariate bootstrap, however DF analysis is a special case where the logical resampling framework obviates the issue.

The procedure to be used in this study is to calculate sample correlations for each of the kinship groups (e.g., monozygotic twins, siblings and half siblings). A sampling frame using all possible pairs of the observed outcomes is created for each group, with the observed correlation for each group imposed on their sampling frame. Because diagonalization is imposed for a different sampling frame for each group, the natural heteroscedasticity is retained. This occurs because each kinship group (e.g., all identical twins as a group) is diagonalized separately from the other kinship groups. For each group, the number of pairs of data, equal to the number of original pairs in the group, are then randomly selected with replacement from each sampling frame. The DF analysis is conducted on this sample. Unlike traditional DF analysis, double entry is unnecessary in this case because the repeated sampling of the bootstrap gives each co-kin an equal probability of being the predictor or the predicted. The standard errors are then formed using bootstrap confidence intervals. These intervals will typically be wider than those normally achieved using single-entry DF analysis because of the reduced sample sizes used in the bootstrap analysis, but narrower than those from double-entry settings. This method should also provide all of the typical advantages of bootstrapping (e.g., minimal distributional assumptions) that are not specific to the DF case.

Methods

A study was designed with 96 potential conditions. These were formed by crossing four factors: distribution, sample size, MZ:DZ balance and effect sizes. The distributions selected were normal, χ_1^2 and χ_{10}^2. The rationale behind these three distributions is that they provided a "best case" scenario (the normal distribution) a moderately skewed case (χ_{10}^2) and a "worst case" highly skewed distribution (χ_1^2). There were 2 sample sizes, 48 and 498 twin pairs, split between MZ and DZ twins. Forty eight twin pairs was chosen as being what might be expected from a convenience sample of twins, while 498 was chosen as what might be expected from a larger, more focused, twin study. A balanced and unbalanced twin design was used, with the unbalanced twin design having an exactly 2:1 DZ:MZ ratio. The 2:1 ratio was chosen as being approximately equal to the ratio of MZ to DZ twins in the general population. Finally, 0, 0.3 and 0.69 were used as the effect sizes for a^2 and c^2, representing no effect, a medium effect and a large effect. There were 8 allowable a^2 and c^2 effect size combinations (0, 0; 0, 0.3; 0, 0.69; 0.3, 0; 0.3, 0.3; 0.3, 0.69; 0.69, 0; 0.69, 0.3; note that 0.69, 0.69 cannot occur, because that combination is larger than 1). Unfortunately in the small sample size and high correlation conditions (0.69, 0.3 and 0.3, 0.69) the simulations using a χ_1^2 distribution had many invalid cases where the correlation for MZ twins was equal to one. The univariate bootstrap uses a Cholesky decomposition which requires the use of positive definite matrices and the MZ twin matrices were not positive definite in cases where their correlation was one. Alternative matrix decompositions could be used in this case, however such alternatives (i.e., the spectral decomposition) have been found to have unacceptably high Type I error rates. Rather than use a worse version of the univariate bootstrap these four conditions were dropped. The χ_1^2 with MZ correlations of .99 and large samples sizes were not problematic and were retained. No other conditions caused additional problems. As a result, only 92 conditions out of the potential 96 are represented in the current study.

Code for the univariate bootstrap was written in R. To test that it was performing as expected, full univariate sampling frames were created using the software and checked against what would be expected (i.e., variable means, variances and correlations were as expected), and a brief simulation study examining the univariate bootstrap CI properties was conducted. To examine the CI properties 10,000 simulations were run. For each simulation, 100 bivariate normal observations were selected with a population correlation of .3, and 1,000 bootstrap samples were taken and a CI created. The proportion of CI's that contained the true population value of .3 was not statistically significantly different from the nominal rate of .95. From these tests it was concluded that the software was behaving as expected.

Six R scripts were run simultaneously (in different windows) on a personal laptop so that multiple conditions could run simultaneously. Each R script used a random number generator seeded with a unique number. The simulations took approximately four days to run. For each condition all of the confidence interval methods under consideration were conducted 1,000 times; for bootstrap methods 1,000 bootstrap resamples were used.

There were multiple plausible ways to conduct the bootstrap analyses. For the standard bootstrap it was possible to bootstrap prior to double entry, or after double entry. For cases after double entry it seemed worthwhile to examine the effects of taking a bootstrap sample equal to the double entered sample size (twice the number of twin pairs) versus taking a sample equal to the original number of twin pairs. For univariate bootstrapping all the possibilities for the standard bootstrap existed. Additionally there was the possibility of using the entire sample (both MZ and DZ twins) as the source for each group and then diagonalizing afterwards (i.e., sampling within groups, and sampling ignoring group membership). The thought was that, because we are already assuming the same mean and variance for MZ and DZ twins on the focal variable, and the correlation is imposed after resampling, it should make little difference if observations were actually from an MZ or DZ twin. These considerations resulted in three standard bootstrapping schemes and six univariate bootstrapping schemes. For all bootstrapping schemes, both a standard 95% CI was created as well as a BCa 95% CI using a jackknife estimate for the acceleration parameter (DiCiccio & Efron, 1996).

Ultimately there were 21 different confidence interval methods tested. The standard regression CI, the standard regression CI but with the interval width multiplied by the square root of two (to account for the doubling of the sample size due to double entry), the Kohler-Rodgers sandwich CI, six standard bootstrap CI's (half were standard intervals, half BCa intervals), and 12 univariate bootstrap CI's (half were standard intervals, half BCa intervals).

Results

The results are organized into sections as follows. First Type I error rates of the various methods are presented and tested for deviations from the nominal Type I error rates. After considering the general Type I error rate the proportions of Type I errors that occur due to the confidence interval being too high or being too low are considered. Next the power of each method is presented and compared with other methods. Finally, a follow up simulation that helps illuminate some of the main results, and further confirms the reliability of the programming, is presented.

First, Type I errors will be addressed. A binomial distribution with p = .95 produces cutoffs of .936 and .963 as the lower and upper bounds of a 95% CI. If a confidence interval method is used we would expect on average 95% of simulations using that method to capture the true population value at least 93.6% of the time and no more than 96.3% of the time. Given that we might allow for conservatism but not liberalism in a confidence interval I also evaluated the confidence interval methods using a cutoff of 93.8%, which is equivalent to a 1-tailed cutoff. After dropping the 4 conditions with frequent invalid solutions there were 92 conditions overall, each with 2 parameters. This resulted in 184 tests for each confidence interval. Table 3 summarizes how often each confidence interval either properly captured the true population value or was not overly liberal (i.e., either proper or conservative).

Based on table 3, it appears that no confidence interval method was ideal in controlling for Type I errors; however, if conservatism is allowed there were several promising methods. In particular, every method that double entered prior to bootstrapping and then used bootstrap resamples half the size of the double entered data set had adequate or conservative coverage in at least 89% of cases. The univariate versions of that method had adequate or conservative coverage for all cases. Table 4 shows marginal Type I error rates across conditions (i.e., the average type I error rate for each interval across parameter type, parameter value, MZ sample size, and population distribution separately). A version of this table that shows the results of all crossings of all conditions (i.e., the 92 simulated conditions and both regression parameters) can be found in Appendix A. Most confidence interval methods were overly liberal, and significantly so. Only bootstrapping methods where double entry occurred before bootstrapping and the bootstrap sample size was half the size of the double entered data set performed well by this metric across all conditions.

Table 3: Proportion of confidence intervals with expected Type I error rates or non-liberal Type I error rates.

	Proportion with expected Type I error*	**Proportion with non-liberal Type I error***
Robust CI	0.42	0.38
Typical CI	0.02	0.08
Typical CI Corrected by $\sqrt{2}$	0.65	0.88
Standard DEA Bootstrap standard CI	0.47	0.41
Standard DEA Bootstrap BCa CI	0.45	0.39
Univariate DEA WGS Bootstrap standard CI	0.18	0.13
Univariate DEA WGS Bootstrap BCa CI	0.16	0.10
Univariate DEA UGS Bootstrap standard CI	0.24	0.16
Univariate DEA UGS Bootstrap BCa CI	0.24	0.13
Standard DEB .5 Bootstrap standard CI	0.33	0.97
Standard DEB .5 Bootstrap BCa CI	0.29	0.85
Standard DEB 1 Bootstrap standard CI	0.08	0.11
Standard DEB 1 Bootstrap BCa CI	0.03	0.11
Univariate DEB .5 WGS Bootstrap standard CI	0.31	1.00
Univariate DEB .5 WGS Bootstrap BCa CI	0.39	1.00
Univariate DEB 1 WGS Bootstrap standard CI	0.09	0.10
Univariate DEB 1 WGS Bootstrap BCa CI	0.08	0.11
Univariate DEB .5 UGS Bootstrap standard CI	0.31	0.98
Univariate DEB .5 UGS Bootstrap BCa CI	0.31	1.00
Univariate DEB 1 UGS Bootstrap standard CI	0.10	0.11
Univariate DEB 1 UGS Bootstrap BCa CI	0.06	0.11

Note: DEA: Double entry after bootstrapping; DEB: Double entry before bootstrapping; .5: bootstrap resample size was half the (double entered) sample size; 1: bootstrap resample size was equal to the size of the (double entered) sample size; WGS: within group sampling was used for the univariate bootstrap; UGS: ungrouped sampling, or sampling without regard to class membership was used for the univariate bootstrap.

*Test for proper cases was two-tailed, test for non-liberal was one tailed. This resulted in some intervals faring poorer in the non-liberal Type I error case than in the expected Type I error test.

Table 4: Table of Type I error rates (in %) marginalized across different simulation settings.

	Population Beta Weights			**MZ:DZ Twin Pair Sample Size**				**Parameter**		**Population**		
	0	0.3	0.69	16:32	24:24	166:332	249:249	a2	c2	χ^2_1	χ^2_{10}	normal
Robust CI*	7.63	8.09	8.23	9.72	10.87	5.84	5.74	7.88	8.01	7.49	8.14	8.14
Typical CI*	16.25	15.01	11.33	12.70	15.39	13.91	16.37	13.19	16.04	15.10	14.40	14.40
Typical CI Corrected by $\sqrt{2}$	4.94	4.64	3.03	3.40	4.89	4.07	5.09	3.85	4.90	4.53	4.30	4.30
Standard DEA Bootstrap standard coverage CI*	6.45	6.52	6.93	7.38	7.91	5.76	5.49	6.58	6.61	6.46	6.65	6.65
Standard DEA Bootstrap coverage BCa CI*	7.03	6.97	7.29	8.39	8.88	5.78	5.49	7.14	7.00	7.00	7.10	7.10
Univariate DEA WGS Bootstrap standard coverage CI*	6.87	8.79	10.11	8.37	8.96	8.28	7.85	8.50	8.20	8.00	8.51	8.51
Univariate DEA WGS Bootstrap coverage BCa CI*	7.22	8.55	9.63	8.42	9.06	8.11	7.63	8.53	8.04	8.13	8.35	8.35
Univariate DEA UGS Bootstrap standard coverage CI*	6.70	8.29	9.49	7.67	8.26	8.28	7.61	8.12	7.79	7.71	8.06	8.06
Univariate DEA UGS Bootstrap coverage BCa CI*	7.00	8.10	9.35	8.21	8.16	8.16	7.38	8.26	7.68	7.85	8.02	8.02
Standard DEB .5 Bootstrap standard	4.14	2.95	1.50	3.00	3.72	2.79	2.81	2.85	3.28	3.24	2.99	2.99

coverage CI												
Standard DEB .5 Bootstrap coverage BCa CI	4.82	3.43	1.88	3.93	4.80	2.94	2.87	3.47	3.73	3.81	3.52	3.52
Standard DEB 1 Bootstrap standard coverage CI*	15.41	12.02	8.26	13.24	14.68	11.16	10.98	12.15	12.75	12.99	12.21	12.21
Standard DEB 1 Bootstrap coverage BCa CI*	16.05	12.33	8.53	14.06	15.41	11.30	11.05	12.55	13.20	13.47	12.62	12.62
Univariate DEB .5 WGS Bootstrap standard coverage CI	3.82	2.83	1.72	2.85	3.45	2.77	2.77	2.84	3.06	3.09	2.89	2.89
Univariate DEB .5 WGS Bootstrap coverage BCa CI	4.15	3.15	1.81	3.28	4.09	2.79	2.79	3.16	3.27	3.38	3.15	3.15
Univariate DEB 1 WGS Bootstrap standard coverage CI*	14.58	11.83	8.83	12.93	13.89	11.11	11.03	11.98	12.39	12.60	12.01	12.01
Univariate DEB 1 WGS Bootstrap coverage BCa CI*	14.72	11.86	8.65	12.93	14.11	11.07	10.96	12.00	12.42	12.67	12.01	12.01
Univariate DEB .5 UGS Bootstrap standard	3.68	2.73	1.48	2.66	3.19	2.61	2.78	2.63	2.98	2.94	2.74	2.74

coverage CI												
Univariate DEB .5 UGS Bootstrap coverage BCa CI	3.65	2.67	1.37	2.63	3.08	2.57	2.70	2.58	2.90	2.89	2.68	2.68
Univariate DEB 1 UGS Bootstrap standard coverage CI*	14.29	11.63	8.31	12.47	13.34	11.09	10.79	11.55	12.21	12.32	11.69	11.69
Univariate DEB 1 UGS Bootstrap standard coverage CI*	13.81	10.97	7.50	11.46	12.08	10.93	10.62	10.91	11.59	11.76	11.03	11.03

*Significantly greater Type I error rate than expected at $p < .05$ across all conditions. Note: The highest admissible Type I error rate varies slightly across conditions, however in any given cell the highest admissible rate possible is 5.17%. All numbers are percentages.

Next I examined the probability of missing to the left or right. I was primarily concerned with too many misses to the left or right. I used a 1-tailed test for left and right misses (and treated missing left and right as separate events with separate tests). With 1,000 simulations and an expected miss rate of .025 for both left and right, it gave a cutoff of 33, that is, simulations in which there were more than 33 misses left or more than 33; misses right were considered statistically significantly different from expected. Surprisingly, there did not appear to be much of a pattern, except that confidence intervals that performed poorly tended to have a high miss rate both right and left. Table 5 shows this.

Table 5: Number of simulations out of 184 (with proportion in parentheses) that had significantly many misses

	Miss Low	**Miss High**
Robust CI	89 (.48)	107 (.58)
Typical CI	170 (.92)	169 (.92)
Typical CI Corrected by $\sqrt{2}$	20 (.11)	11 (.06)
Standard DEA Bootstrap standard CI	97 (.53)	73 (.40)
Standard DEA Bootstrap BCa CI	103 (.56)	97 (.53)
Univariate DEA WGS Bootstrap standard CI	118 (.64)	121 (.66)
Univariate DEA WGS Bootstrap BCa CI	137 (.74)	133 (.72)
Univariate DEA UGS Bootstrap standard CI	127 (.69)	127 (.69)
Univariate DEA UGS Bootstrap BCa CI	117 (.64)	125 (.68)
Standard DEB .5 Bootstrap standard CI	9 (.05)	6 (.03)
Standard DEB .5 Bootstrap BCa CI	24 (.13)	9 (.05)
Standard DEB 1 Bootstrap standard CI	161 (.88)	159 (.86)
Standard DEB 1 Bootstrap BCa CI	161 (.88)	161 (.88)
Univariate DEB .5 WGS Bootstrap standard CI	6 (.03)	3 (.02)
Univariate DEB .5 WGS Bootstrap BCa CI	3 (.02)	3 (.02)
Univariate DEB 1 WGS Bootstrap standard CI	158 (.86)	155 (.84)
Univariate DEB 1 WGS Bootstrap BCa CI	161 (.88)	158 (.86)
Univariate DEB .5 UGS Bootstrap standard CI	3 (.02)	3 (.02)
Univariate DEB .5 UGS Bootstrap BCa CI	3 (.02)	3 (.02)
Univariate DEB 1 UGS Bootstrap standard CI	155 (.84)	152 (.83)
Univariate DEB 1 UGS Bootstrap BCa CI	149 (.81)	149 (.81)

Note: using this method we would expect each CI method to have approximately nine (0.05) cases in which the method was found to have too many misses due to chance [i.e., the expected value of each cell under perfect conditions is nine (0.05)].

The next consideration was power. The number of times 0 was outside the lower bounds of the confidence interval was calculated for each condition for each confidence interval method for which the null hypothesis was incorrect and should be rejected (i.e., excluding conditions where the population value was 0). The following table shows the power of all confidence interval methods marginalized across the simulation conditions as a proportion of times that zero was outside the confidence intervals. An additional table in Appendix A shows the same calculations for power in each simulation and for each CI method. Lower numbers indicate lower power. Overall, the highest power was found in the bootstrapping methods that used bootstrap samples equal in size to the sample being bootstrapped and the typical regression confidence interval. The bootstrap intervals that performed well in terms of their Type I error rate (i.e., those that double entered and took bootstrap sample sizes half the size of the double entered sample) and the square root of two corrected typical CI perform poorer in terms of power. This is exactly in line with the Type I error rate results given the typical tradeoffs between power and Type I errors.

Table 6: Power to detect population deviation from zero for each method marginalized across simulation conditions.

	Population Beta Weight		**MZ:DZ Twin Pair Sample Size**				**Parameter**		**Population**		
	0.3	0.69	16: 32	24: 24	166: 332	249: 249	a2	c2	χ_1^2	χ_{10}^2	normal
Robust CI	0.48	0.86	0.43	0.41	0.81	0.79	0.61	0.65	0.61	0.63	0.63
Typical CI	0.56	0.87	0.42	0.46	0.90	0.89	0.63	0.73	0.69	0.68	0.68
Typical CI Corrected by $\sqrt{2}$	**0.41**	**0.77**	**0.24**	**0.28**	**0.81**	**0.81**	**0.49**	**0.62**	**0.58**	**0.54**	**0.54**
Standard DEA Bootstrap standard CI	0.46	0.84	0.39	0.39	0.81	0.79	0.61	0.61	0.59	0.62	0.62
Standard DEA Bootstrap BCa CI	0.47	0.84	0.41	0.40	0.81	0.79	0.62	0.61	0.60	0.62	0.62
Univariate DEA WGS Bootstrap standard CI	0.49	0.85	0.41	0.41	0.83	0.82	0.63	0.63	0.61	0.64	0.64
Univariate DEA WGS Bootstrap BCa CI	0.49	0.86	0.42	0.41	0.83	0.82	0.63	0.63	0.61	0.64	0.64
Univariate DEA UGS Bootstrap standard CI	0.49	0.85	0.41	0.40	0.83	0.82	0.62	0.63	0.61	0.64	0.64
Univariate DEA UGS Bootstrap BCa CI	0.48	0.85	0.41	0.39	0.83	0.81	0.63	0.62	0.61	0.63	0.63
Standard DEB .5 Bootstrap standard CI	**0.37**	**0.76**	**0.25**	**0.23**	**0.77**	**0.76**	**0.48**	**0.56**	**0.54**	**0.51**	**0.51**
Standard DEB .5 Bootstrap BCa CI	**0.37**	**0.77**	**0.26**	**0.25**	**0.77**	**0.76**	**0.49**	**0.56**	**0.55**	**0.52**	**0.52**
Standard DEB 1 Bootstrap standard CI	0.54	0.87	0.45	0.43	0.88	0.87	0.64	0.71	0.68	0.67	0.67
Standard DEB 1 Bootstrap BCa CI	0.55	0.87	0.46	0.44	0.88	0.86	0.64	0.71	0.68	0.67	0.67
Univariate DEB .5 WGS Bootstrap standard CI	**0.37**	**0.76**	**0.25**	**0.23**	**0.78**	**0.76**	**0.48**	**0.56**	**0.54**	**0.51**	**0.51**

Univariate DEB .5 WGS Bootstrap BCa CI	**0.37**	**0.77**	**0.26**	**0.24**	**0.78**	**0.76**	**0.49**	**0.57**	**0.55**	**0.52**	**0.52**
Univariate DEB 1 WGS Bootstrap standard CI	0.54	0.87	0.45	0.43	0.88	0.87	0.63	0.71	0.68	0.67	0.67
Univariate DEB 1 WGS Bootstrap BCa CI	0.54	0.87	0.46	0.43	0.88	0.87	0.64	0.71	0.68	0.67	0.67
Univariate DEB .5 UGS Bootstrap standard CI	**0.36**	**0.75**	**0.24**	**0.22**	**0.77**	**0.75**	**0.47**	**0.55**	**0.54**	**0.50**	**0.50**
Univariate DEB .5 UGS Bootstrap BCa CI	**0.36**	**0.75**	**0.24**	**0.22**	**0.77**	**0.76**	**0.47**	**0.56**	**0.54**	**0.51**	**0.51**
Univariate DEB 1 UGS Bootstrap standard CI	0.53	0.86	0.44	0.41	0.88	0.86	0.63	0.70	0.67	0.66	0.66
Univariate DEB 1 UGS Bootstrap standard CI	0.53	0.87	0.44	0.41	0.88	0.87	0.63	0.70	0.67	0.66	0.66
Average	0.46	0.83	0.37	0.36	0.83	0.81	0.58	0.63	0.61	0.61	0.61

Note: CIs with acceptable marginalized Type I error rates (table 4) are presented in **bold** typeface in this table, and also presented in Table 7 below for ease of comparison.

Table 7: Selected entries from table 6

	Population Beta Weight		**MZ:DZ Twin Pair Sample Size**				**Parameter**		**Population**		
Typical CI Corrected by $\sqrt{2}$	0.41	0.77	0.24	0.28	0.81	0.81	0.49	0.62	0.58	0.54	0.54
Standard DEB .5 Bootstrap standard CI	0.37	0.76	0.25	0.23	0.77	0.76	0.48	0.56	0.54	0.51	0.51
Standard DEB .5 Bootstrap BCa CI	0.37	0.77	0.26	0.25	0.77	0.76	0.49	0.56	0.55	0.52	0.52
Univariate DEB .5 WGS Bootstrap standard CI	0.37	0.76	0.25	0.23	0.78	0.76	0.48	0.56	0.54	0.51	0.51
Univariate DEB .5 WGS Bootstrap BCa CI	0.37	0.77	0.26	0.24	0.78	0.76	0.49	0.57	0.55	0.52	0.52
Univariate DEB .5 UGS Bootstrap standard CI	0.36	0.75	0.24	0.22	0.77	0.75	0.47	0.55	0.54	0.50	0.50
Univariate DEB .5 UGS Bootstrap BCa CI	0.36	0.75	0.24	0.22	0.77	0.76	0.47	0.56	0.54	0.51	0.51

Table 8: Type I error rates for various confidence interval methods using bivariate normal data with a correlation of .3.

Confidence Interval Method	Type I error rate
Standard Confidence interval	4.5%
Univariate Bootstrap NDE k=1	4.4%
Standard Bootstrap NDE k=1	5.5%
Univariate Bootstrap NDE k=2*	18.5%
Standard Bootstrap NDE k=2*	19.2%
Univariate Bootstrap DE k=1*	17.8%
Standard Bootstrap DE k=1*	19.2%
Univariate Bootstrap DE k=.5	5.1%
Standard Bootstrap DE k=.5	5.7%

* Significantly greater Type I error rate than expected $p < .05$. Note: (N)DE: (Not) Double Entered; k: Bootstrap resample size is that multiple of input data size (e.g., if not double entered, and k =1, bootstrap resample size is n, if double entered 2n).

The fact that the bootstraps that double entered and then took bootstrap samples half the size of double entered data set did much better than all the other methods was quite surprising. In order to make sure that this was not due to a coding error, I tried one small simulation to confirm the behavior outside of DF models. For this simulation 100 bivariate normal observations with standard deviations of 1, means of 5, and correlations of .3 were generated. The cor.test function in the *R stats* package (R Core Team, 2015) was used to obtain the standard confidence intervals. A univariate bootstrap and typical bootstrap confidence interval were constructed, followed by a univariate and typical bootstrap that used bootstrap resamples twice the size of the original sample. Then the data were double entered and univariate bootstraps, typical bootstraps using both the full double entered data sample size and a sample size equal to half that were used to obtain four more confidence intervals. This simulation was repeated 1,000 times. The results match the results above and provide some insight into the process underlying the results. When the bootstrap sample size is greater than the actual effective sample size it reduces the variability of the bootstrap resamples' parameter estimates around the sample parameter estimate, producing confidence intervals that are too narrow and that have an alpha level far higher than the nominal rate. Table 7 shows the actual alpha rate for the various confidence interval methods. The highest alpha rate expected with 1,000 simulations is 6.2%.

Discussion

Overall it would appear that, if more weight is given to avoiding Type I errors than Type II errors/power, bootstrapping or a correction using the square root of two should be the preferred method of users of DF analysis. In particular, when bootstrapping, data should be double entered and then a bootstrap sampling scheme that takes samples half the size of the double entered data should be used. This method had slightly lower power and slightly wider confidence intervals, however it captured the true population value at a far higher rate than other methods across all conditions. The square root of two correction might actually be preferable, however, as it had slightly higher power in general, while still maintaining a favorable Type I error rate. Neither the univariate bootstrap nor the standard bootstrap appeared to radically outperform the other in this study. However previous work by Beasley et al. (2007) would suggest that the univariate bootstrap might be preferred because of the potential for superior performance in other settings, particularly when the data have multiple variables with skewed distributions.

The final simulation illuminates why the most effective bootstrap method was double entry followed by a bootstrap half the size of the double entered sample size (an $m < n$ bootstrap). When the sample size is inflated, either by using a bootstrap resample that is larger than the original sample size, or using a sample that is double entered, the bootstrap appears to lack the necessary variability; as a result, overly narrow confidence intervals are obtained, which then have Type I error rates that are substantially lower than expected. In DF models it appears that, although heteroscedasticity and non-independence of errors exists, the primary driver of CI inaccuracy is the doubling of the sample size with double entry. Although the Type I error rate was substantially better in the $m < n$ bootstraps, the power was lower. Researchers may be tempted to use the other methods for the sake of improved power, but that cannot be recommended here, with the exception of the square-root-of-two correction. Although power could be increased to virtually one with increasing sample size, nothing can be done to reduce Type I error rates if the method itself is flawed. This study shows that several methods are flawed with regards to Type I error rates and only correcting for the sample size can resolve this. If scientists want credible results they must use methods that provide the advertised Type I error rate.

Overall the univariate bootstrap lived up to expectations, generally performing identically to the standard bootstrap. Given that this represents our first full-scale application of the univariate bootstrap beyond bivariate correlations this finding is encouraging for future research regarding the application of the univariate bootstrap to more advanced applications. With regards to DF models specifically, researchers can reasonably use a square root of two correction, or a sample size corrected bootstrap.

Works Cited

Beasley, W. H., DeShea, L., Toothaker, L. E., Mendoza, J. L., Bard, D. E., & Rodgers, J. L. (2007). Bootstrapping to test for nonzero population correlation coefficients using univariate sampling. *Psychological Methods*, *12*(4), 414–433. https://doi.org/10.1037/1082-989X.12.4.414

Beasley, W. H., & Rodgers, J. L. (2012). Bootstrapping and Monte Carlo methods. *APA Handbook of Research Methods in Psychology*, *2*, 407–425.

Cherny, S. S., Cardon, L. R., Fulker, D. W., & DeFries, J. C. (1992). Differential heritability across levels of cognitive ability. *Behavior Genetics*, *22*(2), 153–162.

DeFries, J. C., & Fulker, D. W. (1985). Multiple regression analysis of twin data. *Behavior Genetics*, *15*(5), 467–473.

DiCiccio, T. J., & Efron, B. (1996). Bootstrap confidence intervals. *Statistical science*, 189-212.

Edgington, E. S. (1987). *Randomization tests*. New York: Marcel Dekker.

Efron, B. (1982). The jackknife, the bootstrap, and other resampling plans. Philadelphia: Society for Industrial and Applied Mathematics.

Efron, B. (1987). Better Bootstrap Confidence Intervals. *Journal of the American Statistical Association*, *82*(397), 171. https://doi.org/10.2307/2289144

Efron, B., & Tibshirani, R. (1986). Bootstrap methods for standard errors, confidence intervals, and other measures of statistical accuracy. *Statistical Science*, 54–75.

Kaiser, H. F., & Dickman, K. (1962). Sample and population score matrices and sample correlation matrices from an arbitrary population correlation matrix. *Psychometrika, 27*(2), 179–182.

Kohler, H.-P., & Rodgers, J. L. (2001). DF-analyses of heritability with double-entry twin data: Asymptotic standard errors and efficient estimation. *Behavior Genetics*, *31*(2), 179–191.

Lee, W.-C., & Rodgers, J. L. (1998). Bootstrapping correlation coefficients using univariate and bivariate sampling. *Psychological Methods*, *3*(1), 91.

Rodgers, J. L. (1999). The Bootstrap, the Jackknife, and the Randomization Test: A Sampling Taxonomy. *Multivariate Behavioral Research*, *34*(4), 441–456. https://doi.org/10.1207/S15327906MBR3404_2

Rodgers, J. L., & Beasley, W. H. (2012). Fisher, Gosset, and Alternative Hypothesis Significance Testing (AHST): Using the Bootstrap to Test Scientific Hypotheses about the Multiple Correlation. In M. C. Edwards & R. C. MacCallum (Eds.), *Current topics in the theory and application of latent variable models* (pp. 217–239). Routledge.

Rodgers, J. L., & Kohler, H.-P. (2005). Reformulating and simplifying the DF analysis model. *Behavior Genetics*, *35*(2), 211–217.

R Core Team (2015). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL http://www.R-project.org/.Stine, R. (1989).

An Introduction to Bootstrap Methods: Examples and Ideas. *Sociological Methods and Research*, *18*(2 & 3), 243–291.

Tibshirani, R. (1985). *How many bootstraps?* Stanford University CA Department of Statistics.

Wu, C. F. J. (1986). Jackknife, bootstrap and other resampling methods in regression analysis. *the Annals of Statistics*, 1261-1295.

Appendix A

This appendix includes tables that would be unwieldly in the text. There are two tables presented. The first (Tables 9-13) show the proportion of confidence intervals (out of 1,000) that correctly included the population parameter value. Proportions less than .936 or greater than .963 are statistically different from the nominal .95 rate at $p < .05$. Proportions less than .938 would be considered significantly liberal if doing a 1-tailed test for liberalism at $p < .05$ (i.e., if allowing for conservatism but not liberalism in confidence intervals).

The second set of tables (Tables 14-18) show the proportion of confidence intervals (out of 1,000) that excluded zero at the low end (i.e., the entire CI was positive) when the population value was greater than 0 for that parameter.

Table 9: Proportion of Confidence Intervals that captured the true population value. Part A.

Univariate DEB .5 UGS Bootstrap BCa CI	Univariate DEB 1 UGS Bootstrap standard CI	Univariate DEB 1 UGS Bootstrap BCa CI	Standard Adjusted by root 2	Standard Adjusted by root 2	Population Parameter Value	MZ ns	Distribution	parameter
0.949	0.828	0.833	0.948	0.948	0	24	χ^2_1	a2
0.952	0.831	0.826	0.957	0.957	0	24	χ^2_1	c2
0.959	0.844	0.857	0.948	0.948	0	24	χ^2_1	a2
0.966	0.848	0.863	0.955	0.955	0.3	24	χ^2_1	c2
0.983	0.881	0.905	0.954	0.954	0	24	χ^2_1	a2
0.982	0.893	0.912	0.961	0.961	0.69	24	χ^2_1	c2
0.958	0.847	0.847	0.946	0.946	0.3	24	χ^2_1	a2
0.949	0.849	0.846	0.939	0.939	0	24	χ^2_1	c2
0.974	0.867	0.884	0.953	0.953	0.3	24	χ^2_1	a2
0.979	0.85	0.87	0.944	0.944	0.3	24	χ^2_1	c2
0.969	0.87	0.885	0.956	0.956	0.69	24	χ^2_1	a2
0.967	0.847	0.868	0.935	0.935	0	24	χ^2_1	c2
0.962	0.854	0.862	0.965	0.965	0	249	χ^2_1	a2
0.957	0.857	0.861	0.96	0.96	0	249	χ^2_1	c2
0.969	0.839	0.846	0.952	0.952	0	249	χ^2_1	a2
0.964	0.847	0.846	0.943	0.943	0.3	249	χ^2_1	c2
0.987	0.936	0.936	0.96	0.96	0	249	χ^2_1	a2
0.988	0.926	0.931	0.965	0.965	0.69	249	χ^2_1	c2
0.941	0.839	0.839	0.926	0.926	0.3	249	χ^2_1	a2
0.941	0.824	0.826	0.927	0.927	0	249	χ^2_1	c2
0.981	0.906	0.902	0.951	0.951	0.3	249	χ^2_1	a2
0.969	0.892	0.89	0.938	0.938	0.3	249	χ^2_1	c2
0.996	0.96	0.965	0.989	0.989	0.3	249	χ^2_1	a2
0.997	0.956	0.958	0.954	0.954	0.69	249	χ^2_1	c2
0.97	0.901	0.898	0.952	0.952	0.69	249	χ^2_1	a2
0.968	0.871	0.875	0.93	0.93	0	249	χ^2_1	c2
0.989	0.933	0.931	0.958	0.958	0.69	249	χ^2_1	a2
0.989	0.932	0.935	0.915	0.915	0.3	249	χ^2_1	c2
0.955	0.853	0.848	0.951	0.951	0	16	χ^2_1	a2

0.958	0.837	0.831	0.956	0.956	0	16	χ_1^2	c2
0.971	0.857	0.868	0.957	0.957	0	16	χ_1^2	a2
0.96	0.825	0.846	0.948	0.948	0.3	16	χ_1^2	c2
0.989	0.911	0.93	0.978	0.978	0	16	χ_1^2	a2
0.985	0.909	0.93	0.975	0.975	0.69	16	χ_1^2	c2
0.96	0.823	0.839	0.958	0.958	0.3	16	χ_1^2	a2
0.955	0.832	0.841	0.952	0.952	0	16	χ_1^2	c2
0.976	0.888	0.889	0.968	0.968	0.3	16	χ_1^2	a2
0.972	0.873	0.881	0.96	0.96	0.3	16	χ_1^2	c2
0.981	0.876	0.896	0.975	0.975	0.69	16	χ_1^2	a2
0.976	0.861	0.868	0.954	0.954	0	16	χ_1^2	c2
0.953	0.84	0.835	0.955	0.955	0	166	χ_1^2	a2
0.944	0.84	0.841	0.947	0.947	0	166	χ_1^2	c2
0.968	0.857	0.861	0.937	0.937	0	166	χ_1^2	a2
0.957	0.86	0.865	0.94	0.94	0.3	166	χ_1^2	c2
0.992	0.918	0.921	0.962	0.962	0	166	χ_1^2	a2
0.993	0.93	0.932	0.962	0.962	0.69	166	χ_1^2	c2
0.952	0.835	0.84	0.94	0.94	0.3	166	χ_1^2	a2
0.947	0.822	0.822	0.94	0.94	0	166	χ_1^2	c2
0.976	0.89	0.887	0.954	0.954	0.3	166	χ_1^2	a2
0.97	0.885	0.887	0.945	0.945	0.3	166	χ_1^2	c2
0.997	0.966	0.969	0.999	0.999	0.3	166	χ_1^2	a2
0.996	0.958	0.956	0.991	0.991	0.69	166	χ_1^2	c2
0.987	0.896	0.901	0.966	0.966	0.69	166	χ_1^2	a2
0.974	0.881	0.879	0.951	0.951	0	166	χ_1^2	c2
0.993	0.924	0.93	0.997	0.997	0.69	166	χ_1^2	a2
0.99	0.924	0.925	0.963	0.963	0.3	166	χ_1^2	c2
0.949	0.828	0.833	0.948	0.948	0	24	χ_{10}^2	a2
0.952	0.831	0.826	0.957	0.957	0	24	χ_{10}^2	c2
0.959	0.844	0.857	0.948	0.948	0	24	χ_{10}^2	a2
0.966	0.848	0.863	0.955	0.955	0.3	24	χ_{10}^2	c2
0.983	0.881	0.905	0.954	0.954	0	24	χ_{10}^2	a2
0.982	0.893	0.912	0.961	0.961	0.69	24	χ_{10}^2	c2
0.958	0.847	0.847	0.946	0.946	0.3	24	χ_{10}^2	a2
0.949	0.849	0.846	0.939	0.939	0	24	χ_{10}^2	c2
0.974	0.867	0.884	0.953	0.953	0.3	24	χ_{10}^2	a2
0.979	0.85	0.87	0.944	0.944	0.3	24	χ_{10}^2	c2
0.996	0.953	0.967	0.992	0.992	0.3	24	χ_{10}^2	a2
0.994	0.947	0.963	0.97	0.97	0.69	24	χ_{10}^2	c2
0.969	0.87	0.885	0.956	0.956	0.69	24	χ_{10}^2	a2
0.967	0.847	0.868	0.935	0.935	0	24	χ_{10}^2	c2
0.976	0.895	0.911	0.961	0.961	0.69	24	χ_{10}^2	a2
0.975	0.888	0.908	0.908	0.908	0.3	24	χ_{10}^2	c2
0.962	0.854	0.862	0.965	0.965	0	249	χ_{10}^2	a2
0.957	0.857	0.861	0.96	0.96	0	249	χ_{10}^2	c2
0.969	0.839	0.846	0.952	0.952	0	249	χ_{10}^2	a2

0.964	0.847	0.846	0.943	0.943	0.3	249	χ^2_{10}	c2
0.987	0.936	0.936	0.96	0.96	0	249	χ^2_{10}	a2
0.988	0.926	0.931	0.965	0.965	0.69	249	χ^2_{10}	c2
0.941	0.839	0.839	0.926	0.926	0.3	249	χ^2_{10}	a2
0.941	0.824	0.826	0.927	0.927	0	249	χ^2_{10}	c2
0.981	0.906	0.902	0.951	0.951	0.3	249	χ^2_{10}	a2
0.969	0.892	0.89	0.938	0.938	0.3	249	χ^2_{10}	c2
0.996	0.96	0.965	0.989	0.989	0.3	249	χ^2_{10}	a2
0.997	0.956	0.958	0.954	0.954	0.69	249	χ^2_{10}	c2
0.97	0.901	0.898	0.952	0.952	0.69	249	χ^2_{10}	a2
0.968	0.871	0.875	0.93	0.93	0	249	χ^2_{10}	c2
0.989	0.933	0.931	0.958	0.958	0.69	249	χ^2_{10}	a2
0.989	0.932	0.935	0.915	0.915	0.3	249	χ^2_{10}	c2
0.955	0.853	0.848	0.951	0.951	0	16	χ^2_{10}	a2
0.958	0.837	0.831	0.956	0.956	0	16	χ^2_{10}	c2
0.971	0.857	0.868	0.957	0.957	0	16	χ^2_{10}	a2
0.96	0.825	0.846	0.948	0.948	0.3	16	χ^2_{10}	c2
0.989	0.911	0.93	0.978	0.978	0	16	χ^2_{10}	a2
0.985	0.909	0.93	0.975	0.975	0.69	16	χ^2_{10}	c2
0.96	0.823	0.839	0.958	0.958	0.3	16	χ^2_{10}	a2
0.955	0.832	0.841	0.952	0.952	0	16	χ^2_{10}	c2
0.976	0.888	0.889	0.968	0.968	0.3	16	χ^2_{10}	a2
0.972	0.873	0.881	0.96	0.96	0.3	16	χ^2_{10}	c2
0.997	0.965	0.971	1	1	0.3	16	χ^2_{10}	a2
0.995	0.955	0.96	0.99	0.99	0.69	16	χ^2_{10}	c2
0.981	0.876	0.896	0.975	0.975	0.69	16	χ^2_{10}	a2
0.976	0.861	0.868	0.954	0.954	0	16	χ^2_{10}	c2
0.988	0.916	0.927	0.994	0.994	0.69	16	χ^2_{10}	a2
0.985	0.903	0.92	0.969	0.969	0.3	16	χ^2_{10}	c2
0.953	0.84	0.835	0.955	0.955	0	166	χ^2_{10}	a2
0.944	0.84	0.841	0.947	0.947	0	166	χ^2_{10}	c2
0.968	0.857	0.861	0.937	0.937	0	166	χ^2_{10}	a2
0.957	0.86	0.865	0.94	0.94	0.3	166	χ^2_{10}	c2
0.992	0.918	0.921	0.962	0.962	0	166	χ^2_{10}	a2
0.993	0.93	0.932	0.962	0.962	0.69	166	χ^2_{10}	c2
0.952	0.835	0.84	0.94	0.94	0.3	166	χ^2_{10}	a2
0.947	0.822	0.822	0.94	0.94	0	166	χ^2_{10}	c2
0.976	0.89	0.887	0.954	0.954	0.3	166	χ^2_{10}	a2
0.97	0.885	0.887	0.945	0.945	0.3	166	χ^2_{10}	c2
0.997	0.966	0.969	0.999	0.999	0.3	166	χ^2_{10}	a2
0.996	0.958	0.956	0.991	0.991	0.69	166	χ^2_{10}	c2
0.987	0.896	0.901	0.966	0.966	0.69	166	χ^2_{10}	a2
0.974	0.881	0.879	0.951	0.951	0	166	χ^2_{10}	c2
0.993	0.924	0.93	0.997	0.997	0.69	166	χ^2_{10}	a2
0.99	0.924	0.925	0.963	0.963	0.3	166	χ^2_{10}	c2
0.949	0.828	0.833	0.948	0.948	0	24	normal	a2

0.952	0.831	0.826	0.957	0.957	0	24	normal	c2
0.959	0.844	0.857	0.948	0.948	0	24	normal	a2
0.966	0.848	0.863	0.955	0.955	0.3	24	normal	c2
0.983	0.881	0.905	0.954	0.954	0	24	normal	a2
0.982	0.893	0.912	0.961	0.961	0.69	24	normal	c2
0.958	0.847	0.847	0.946	0.946	0.3	24	normal	a2
0.949	0.849	0.846	0.939	0.939	0	24	normal	c2
0.974	0.867	0.884	0.953	0.953	0.3	24	normal	a2
0.979	0.85	0.87	0.944	0.944	0.3	24	normal	c2
0.996	0.953	0.967	0.992	0.992	0.3	24	normal	a2
0.994	0.947	0.963	0.97	0.97	0.69	24	normal	c2
0.969	0.87	0.885	0.956	0.956	0.69	24	normal	a2
0.967	0.847	0.868	0.935	0.935	0	24	normal	c2
0.976	0.895	0.911	0.961	0.961	0.69	24	normal	a2
0.975	0.888	0.908	0.908	0.908	0.3	24	normal	c2
0.962	0.854	0.862	0.965	0.965	0	249	normal	a2
0.957	0.857	0.861	0.96	0.96	0	249	normal	c2
0.969	0.839	0.846	0.952	0.952	0	249	normal	a2
0.964	0.847	0.846	0.943	0.943	0.3	249	normal	c2
0.987	0.936	0.936	0.96	0.96	0	249	normal	a2
0.988	0.926	0.931	0.965	0.965	0.69	249	normal	c2
0.941	0.839	0.839	0.926	0.926	0.3	249	normal	a2
0.941	0.824	0.826	0.927	0.927	0	249	normal	c2
0.981	0.906	0.902	0.951	0.951	0.3	249	normal	a2
0.969	0.892	0.89	0.938	0.938	0.3	249	normal	c2
0.996	0.96	0.965	0.989	0.989	0.3	249	normal	a2
0.997	0.956	0.958	0.954	0.954	0.69	249	normal	c2
0.97	0.901	0.898	0.952	0.952	0.69	249	normal	a2
0.968	0.871	0.875	0.93	0.93	0	249	normal	c2
0.989	0.933	0.931	0.958	0.958	0.69	249	normal	a2
0.989	0.932	0.935	0.915	0.915	0.3	249	normal	c2
0.955	0.853	0.848	0.951	0.951	0	16	normal	a2
0.958	0.837	0.831	0.956	0.956	0	16	normal	c2
0.971	0.857	0.868	0.957	0.957	0	16	normal	a2
0.96	0.825	0.846	0.948	0.948	0.3	16	normal	c2
0.989	0.911	0.93	0.978	0.978	0	16	normal	a2
0.985	0.909	0.93	0.975	0.975	0.69	16	normal	c2
0.96	0.823	0.839	0.958	0.958	0.3	16	normal	a2
0.955	0.832	0.841	0.952	0.952	0	16	normal	c2
0.976	0.888	0.889	0.968	0.968	0.3	16	normal	a2
0.972	0.873	0.881	0.96	0.96	0.3	16	normal	c2
0.997	0.965	0.971	1	1	0.3	16	normal	a2
0.995	0.955	0.96	0.99	0.99	0.69	16	normal	c2
0.981	0.876	0.896	0.975	0.975	0.69	16	normal	a2
0.976	0.861	0.868	0.954	0.954	0	16	normal	c2
0.988	0.916	0.927	0.994	0.994	0.69	16	normal	a2

0.985	0.903	0.92	0.969	0.969	0.3	16	normal	c2
0.953	0.84	0.835	0.955	0.955	0	166	normal	a2
0.944	0.84	0.841	0.947	0.947	0	166	normal	c2
0.968	0.857	0.861	0.937	0.937	0	166	normal	a2
0.957	0.86	0.865	0.94	0.94	0.3	166	normal	c2
0.992	0.918	0.921	0.962	0.962	0	166	normal	a2
0.993	0.93	0.932	0.962	0.962	0.69	166	normal	c2
0.952	0.835	0.84	0.94	0.94	0.3	166	normal	a2
0.947	0.822	0.822	0.94	0.94	0	166	normal	c2
0.976	0.89	0.887	0.954	0.954	0.3	166	normal	a2
0.97	0.885	0.887	0.945	0.945	0.3	166	normal	c2
0.997	0.966	0.969	0.999	0.999	0.3	166	normal	a2
0.996	0.958	0.956	0.991	0.991	0.69	166	normal	c2
0.987	0.896	0.901	0.966	0.966	0.69	166	normal	a2
0.974	0.881	0.879	0.951	0.951	0	166	normal	c2
0.993	0.924	0.93	0.997	0.997	0.69	166	normal	a2
0.99	0.924	0.925	0.963	0.963	0.3	166	normal	c2

Table 10: Proportion of Confidence Intervals that captured the true population value. Part B.

Univariate DEB .5 WGS Bootstrap standard CI	Univariate DEB .5 WGS Bootstrap BCa CI	Univariate DEB 1 WGS Bootstrap standard CI	Univariate DEB 1 WGS Bootstrap BCa CI	Univariate DEB .5 UGS Bootstrap standard CI	Population Parameter Value	MZ ns	Distribution	parameter
0.955	0.941	0.825	0.818	0.959	0	24	χ_1^2	a2
0.955	0.939	0.825	0.818	0.953	0	24	χ_1^2	c2
0.957	0.95	0.842	0.834	0.954	0	24	χ_1^2	a2
0.963	0.954	0.85	0.849	0.964	0.3	24	χ_1^2	c2
0.971	0.968	0.869	0.863	0.982	0	24	χ_1^2	a2
0.971	0.967	0.881	0.881	0.977	0.69	24	χ_1^2	c2
0.954	0.944	0.841	0.844	0.96	0.3	24	χ_1^2	a2
0.945	0.943	0.848	0.844	0.946	0	24	χ_1^2	c2
0.974	0.958	0.851	0.846	0.975	0.3	24	χ_1^2	a2
0.975	0.97	0.853	0.849	0.971	0.3	24	χ_1^2	c2
0.966	0.961	0.862	0.861	0.97	0.69	24	χ_1^2	a2
0.958	0.953	0.848	0.843	0.964	0	24	χ_1^2	c2
0.96	0.96	0.85	0.86	0.962	0	249	χ_1^2	a2
0.963	0.959	0.856	0.86	0.961	0	249	χ_1^2	c2
0.967	0.966	0.841	0.836	0.97	0	249	χ_1^2	a2
0.963	0.965	0.845	0.845	0.961	0.3	249	χ_1^2	c2
0.984	0.984	0.925	0.928	0.987	0	249	χ_1^2	a2
0.989	0.99	0.92	0.926	0.989	0.69	249	χ_1^2	c2
0.942	0.94	0.843	0.841	0.943	0.3	249	χ_1^2	a2
0.944	0.942	0.829	0.826	0.938	0	249	χ_1^2	c2
0.976	0.981	0.901	0.9	0.978	0.3	249	χ_1^2	a2
0.968	0.966	0.888	0.886	0.966	0.3	249	χ_1^2	c2
0.996	0.996	0.959	0.962	0.996	0.3	249	χ_1^2	a2
0.996	0.996	0.954	0.96	0.995	0.69	249	χ_1^2	c2
0.971	0.968	0.894	0.897	0.967	0.69	249	χ_1^2	a2
0.967	0.969	0.868	0.865	0.965	0	249	χ_1^2	c2
0.986	0.986	0.933	0.927	0.99	0.69	249	χ_1^2	a2
0.985	0.986	0.93	0.928	0.988	0.3	249	χ_1^2	c2
0.955	0.952	0.85	0.849	0.953	0	16	χ_1^2	a2
0.959	0.95	0.843	0.834	0.955	0	16	χ_1^2	c2
0.97	0.966	0.852	0.853	0.971	0	16	χ_1^2	a2
0.962	0.958	0.836	0.83	0.959	0.3	16	χ_1^2	c2
0.988	0.983	0.895	0.889	0.99	0	16	χ_1^2	a2
0.987	0.983	0.905	0.909	0.989	0.69	16	χ_1^2	c2
0.963	0.948	0.823	0.823	0.963	0.3	16	χ_1^2	a2
0.958	0.952	0.836	0.837	0.958	0	16	χ_1^2	c2
0.971	0.965	0.871	0.871	0.974	0.3	16	χ_1^2	a2
0.971	0.963	0.863	0.862	0.976	0.3	16	χ_1^2	c2
0.967	0.968	0.866	0.865	0.979	0.69	16	χ_1^2	a2

0.963	0.963	0.849	0.855	0.973	0	16	χ_1^2	c2
0.953	0.948	0.834	0.831	0.954	0	166	χ_1^2	a2
0.948	0.945	0.838	0.841	0.948	0	166	χ_1^2	c2
0.961	0.962	0.856	0.863	0.968	0	166	χ_1^2	a2
0.958	0.959	0.854	0.86	0.961	0.3	166	χ_1^2	c2
0.988	0.989	0.919	0.926	0.99	0	166	χ_1^2	a2
0.99	0.992	0.926	0.923	0.994	0.69	166	χ_1^2	c2
0.948	0.948	0.844	0.846	0.95	0.3	166	χ_1^2	a2
0.942	0.947	0.82	0.816	0.943	0	166	χ_1^2	c2
0.975	0.971	0.887	0.881	0.975	0.3	166	χ_1^2	a2
0.972	0.972	0.89	0.886	0.971	0.3	166	χ_1^2	c2
0.995	0.996	0.965	0.968	0.997	0.3	166	χ_1^2	a2
0.995	0.996	0.955	0.96	0.997	0.69	166	χ_1^2	c2
0.983	0.981	0.895	0.896	0.983	0.69	166	χ_1^2	a2
0.973	0.974	0.882	0.878	0.973	0	166	χ_1^2	c2
0.988	0.987	0.929	0.929	0.989	0.69	166	χ_1^2	a2
0.988	0.986	0.928	0.925	0.99	0.3	166	χ_1^2	c2
0.955	0.941	0.825	0.818	0.959	0	24	χ_{10}^2	a2
0.955	0.939	0.825	0.818	0.953	0	24	χ_{10}^2	c2
0.957	0.95	0.842	0.834	0.954	0	24	χ_{10}^2	a2
0.963	0.954	0.85	0.849	0.964	0.3	24	χ_{10}^2	c2
0.971	0.968	0.869	0.863	0.982	0	24	χ_{10}^2	a2
0.971	0.967	0.881	0.881	0.977	0.69	24	χ_{10}^2	c2
0.954	0.944	0.841	0.844	0.96	0.3	24	χ_{10}^2	a2
0.945	0.943	0.848	0.844	0.946	0	24	χ_{10}^2	c2
0.974	0.958	0.851	0.846	0.975	0.3	24	χ_{10}^2	a2
0.975	0.97	0.853	0.849	0.971	0.3	24	χ_{10}^2	c2
0.991	0.994	0.945	0.952	0.991	0.3	24	χ_{10}^2	a2
0.988	0.993	0.938	0.942	0.99	0.69	24	χ_{10}^2	c2
0.966	0.961	0.862	0.861	0.97	0.69	24	χ_{10}^2	a2
0.958	0.953	0.848	0.843	0.964	0	24	χ_{10}^2	c2
0.972	0.971	0.886	0.891	0.978	0.69	24	χ_{10}^2	a2
0.973	0.97	0.883	0.885	0.976	0.3	24	χ_{10}^2	c2
0.96	0.96	0.85	0.86	0.962	0	249	χ_{10}^2	a2
0.963	0.959	0.856	0.86	0.961	0	249	χ_{10}^2	c2
0.967	0.966	0.841	0.836	0.97	0	249	χ_{10}^2	a2
0.963	0.965	0.845	0.845	0.961	0.3	249	χ_{10}^2	c2
0.984	0.984	0.925	0.928	0.987	0	249	χ_{10}^2	a2
0.989	0.99	0.92	0.926	0.989	0.69	249	χ_{10}^2	c2
0.942	0.94	0.843	0.841	0.943	0.3	249	χ_{10}^2	a2
0.944	0.942	0.829	0.826	0.938	0	249	χ_{10}^2	c2
0.976	0.981	0.901	0.9	0.978	0.3	249	χ_{10}^2	a2
0.968	0.966	0.888	0.886	0.966	0.3	249	χ_{10}^2	c2
0.996	0.996	0.959	0.962	0.996	0.3	249	χ_{10}^2	a2
0.996	0.996	0.954	0.96	0.995	0.69	249	χ_{10}^2	c2
0.971	0.968	0.894	0.897	0.967	0.69	249	χ_{10}^2	a2

0.967	0.969	0.868	0.865	0.965	0	249	χ^2_{10}	c2
0.986	0.986	0.933	0.927	0.99	0.69	249	χ^2_{10}	a2
0.985	0.986	0.93	0.928	0.988	0.3	249	χ^2_{10}	c2
0.955	0.952	0.85	0.849	0.953	0	16	χ^2_{10}	a2
0.959	0.95	0.843	0.834	0.955	0	16	χ^2_{10}	c2
0.97	0.966	0.852	0.853	0.971	0	16	χ^2_{10}	a2
0.962	0.958	0.836	0.83	0.959	0.3	16	χ^2_{10}	c2
0.988	0.983	0.895	0.889	0.99	0	16	χ^2_{10}	a2
0.987	0.983	0.905	0.909	0.989	0.69	16	χ^2_{10}	c2
0.963	0.948	0.823	0.823	0.963	0.3	16	χ^2_{10}	a2
0.958	0.952	0.836	0.837	0.958	0	16	χ^2_{10}	c2
0.971	0.965	0.871	0.871	0.974	0.3	16	χ^2_{10}	a2
0.971	0.963	0.863	0.862	0.976	0.3	16	χ^2_{10}	c2
0.994	0.993	0.962	0.963	0.996	0.3	16	χ^2_{10}	a2
0.99	0.989	0.943	0.949	0.993	0.69	16	χ^2_{10}	c2
0.967	0.968	0.866	0.865	0.979	0.69	16	χ^2_{10}	a2
0.963	0.963	0.849	0.855	0.973	0	16	χ^2_{10}	c2
0.989	0.987	0.911	0.914	0.984	0.69	16	χ^2_{10}	a2
0.98	0.983	0.906	0.915	0.982	0.3	16	χ^2_{10}	c2
0.953	0.948	0.834	0.831	0.954	0	166	χ^2_{10}	a2
0.948	0.945	0.838	0.841	0.948	0	166	χ^2_{10}	c2
0.961	0.962	0.856	0.863	0.968	0	166	χ^2_{10}	a2
0.958	0.959	0.854	0.86	0.961	0.3	166	χ^2_{10}	c2
0.988	0.989	0.919	0.926	0.99	0	166	χ^2_{10}	a2
0.99	0.992	0.926	0.923	0.994	0.69	166	χ^2_{10}	c2
0.948	0.948	0.844	0.846	0.95	0.3	166	χ^2_{10}	a2
0.942	0.947	0.82	0.816	0.943	0	166	χ^2_{10}	c2
0.975	0.971	0.887	0.881	0.975	0.3	166	χ^2_{10}	a2
0.972	0.972	0.89	0.886	0.971	0.3	166	χ^2_{10}	c2
0.995	0.996	0.965	0.968	0.997	0.3	166	χ^2_{10}	a2
0.995	0.996	0.955	0.96	0.997	0.69	166	χ^2_{10}	c2
0.983	0.981	0.895	0.896	0.983	0.69	166	χ^2_{10}	a2
0.973	0.974	0.882	0.878	0.973	0	166	χ^2_{10}	c2
0.988	0.987	0.929	0.929	0.989	0.69	166	χ^2_{10}	a2
0.988	0.986	0.928	0.925	0.99	0.3	166	χ^2_{10}	c2
0.955	0.941	0.825	0.818	0.959	0	24	normal	a2
0.955	0.939	0.825	0.818	0.953	0	24	normal	c2
0.957	0.95	0.842	0.834	0.954	0	24	normal	a2
0.963	0.954	0.85	0.849	0.964	0.3	24	normal	c2
0.971	0.968	0.869	0.863	0.982	0	24	normal	a2
0.971	0.967	0.881	0.881	0.977	0.69	24	normal	c2
0.954	0.944	0.841	0.844	0.96	0.3	24	normal	a2
0.945	0.943	0.848	0.844	0.946	0	24	normal	c2
0.974	0.958	0.851	0.846	0.975	0.3	24	normal	a2
0.975	0.97	0.853	0.849	0.971	0.3	24	normal	c2
0.991	0.994	0.945	0.952	0.991	0.3	24	normal	a2

0.988	0.993	0.938	0.942	0.99	0.69	24	normal	c2
0.966	0.961	0.862	0.861	0.97	0.69	24	normal	a2
0.958	0.953	0.848	0.843	0.964	0	24	normal	c2
0.972	0.971	0.886	0.891	0.978	0.69	24	normal	a2
0.973	0.97	0.883	0.885	0.976	0.3	24	normal	c2
0.96	0.96	0.85	0.86	0.962	0	249	normal	a2
0.963	0.959	0.856	0.86	0.961	0	249	normal	c2
0.967	0.966	0.841	0.836	0.97	0	249	normal	a2
0.963	0.965	0.845	0.845	0.961	0.3	249	normal	c2
0.984	0.984	0.925	0.928	0.987	0	249	normal	a2
0.989	0.99	0.92	0.926	0.989	0.69	249	normal	c2
0.942	0.94	0.843	0.841	0.943	0.3	249	normal	a2
0.944	0.942	0.829	0.826	0.938	0	249	normal	c2
0.976	0.981	0.901	0.9	0.978	0.3	249	normal	a2
0.968	0.966	0.888	0.886	0.966	0.3	249	normal	c2
0.996	0.996	0.959	0.962	0.996	0.3	249	normal	a2
0.996	0.996	0.954	0.96	0.995	0.69	249	normal	c2
0.971	0.968	0.894	0.897	0.967	0.69	249	normal	a2
0.967	0.969	0.868	0.865	0.965	0	249	normal	c2
0.986	0.986	0.933	0.927	0.99	0.69	249	normal	a2
0.985	0.986	0.93	0.928	0.988	0.3	249	normal	c2
0.955	0.952	0.85	0.849	0.953	0	16	normal	a2
0.959	0.95	0.843	0.834	0.955	0	16	normal	c2
0.97	0.966	0.852	0.853	0.971	0	16	normal	a2
0.962	0.958	0.836	0.83	0.959	0.3	16	normal	c2
0.988	0.983	0.895	0.889	0.99	0	16	normal	a2
0.987	0.983	0.905	0.909	0.989	0.69	16	normal	c2
0.963	0.948	0.823	0.823	0.963	0.3	16	normal	a2
0.958	0.952	0.836	0.837	0.958	0	16	normal	c2
0.971	0.965	0.871	0.871	0.974	0.3	16	normal	a2
0.971	0.963	0.863	0.862	0.976	0.3	16	normal	c2
0.994	0.993	0.962	0.963	0.996	0.3	16	normal	a2
0.99	0.989	0.943	0.949	0.993	0.69	16	normal	c2
0.967	0.968	0.866	0.865	0.979	0.69	16	normal	a2
0.963	0.963	0.849	0.855	0.973	0	16	normal	c2
0.989	0.987	0.911	0.914	0.984	0.69	16	normal	a2
0.98	0.983	0.906	0.915	0.982	0.3	16	normal	c2
0.953	0.948	0.834	0.831	0.954	0	166	normal	a2
0.948	0.945	0.838	0.841	0.948	0	166	normal	c2
0.961	0.962	0.856	0.863	0.968	0	166	normal	a2
0.958	0.959	0.854	0.86	0.961	0.3	166	normal	c2
0.988	0.989	0.919	0.926	0.99	0	166	normal	a2
0.99	0.992	0.926	0.923	0.994	0.69	166	normal	c2
0.948	0.948	0.844	0.846	0.95	0.3	166	normal	a2
0.942	0.947	0.82	0.816	0.943	0	166	normal	c2
0.975	0.971	0.887	0.881	0.975	0.3	166	normal	a2

0.972	0.972	0.89	0.886	0.971	0.3	166	normal	c2
0.995	0.996	0.965	0.968	0.997	0.3	166	normal	a2
0.995	0.996	0.955	0.96	0.997	0.69	166	normal	c2
0.983	0.981	0.895	0.896	0.983	0.69	166	normal	a2
0.973	0.974	0.882	0.878	0.973	0	166	normal	c2
0.988	0.987	0.929	0.929	0.989	0.69	166	normal	a2
0.988	0.986	0.928	0.925	0.99	0.3	166	normal	c2

Table 11: Proportion of Confidence Intervals that captured the true population value. Part C.

Univariate DEA UGS Bootstrap BCa CI	Standard DEB .5 Bootstrap standard CI	Standard DEB .5 Bootstrap BCa CI	Standard DEB 1 Bootstrap standard CI	Standard DEB 1 Bootstrap BCa CI	Population Parameter Value	MZ ns	Distribution	parameter
0.932	0.942	0.931	0.787	0.774	0	24	χ^2_1	a2
0.939	0.928	0.919	0.781	0.769	0	24	χ^2_1	c2
0.929	0.958	0.938	0.836	0.822	0	24	χ^2_1	a2
0.938	0.956	0.947	0.834	0.82	0.3	24	χ^2_1	c2
0.863	0.978	0.968	0.895	0.889	0	24	χ^2_1	a2
0.886	0.981	0.969	0.902	0.894	0.69	24	χ^2_1	c2
0.925	0.949	0.937	0.827	0.819	0.3	24	χ^2_1	a2
0.935	0.939	0.924	0.81	0.805	0	24	χ^2_1	c2
0.913	0.971	0.955	0.85	0.84	0.3	24	χ^2_1	a2
0.938	0.974	0.96	0.843	0.832	0.3	24	χ^2_1	c2
0.914	0.971	0.954	0.863	0.858	0.69	24	χ^2_1	a2
0.937	0.954	0.943	0.823	0.819	0	24	χ^2_1	c2
0.959	0.966	0.963	0.848	0.845	0	249	χ^2_1	a2
0.956	0.958	0.958	0.853	0.846	0	249	χ^2_1	c2
0.944	0.966	0.963	0.851	0.857	0	249	χ^2_1	a2
0.941	0.966	0.966	0.849	0.853	0.3	249	χ^2_1	c2
0.909	0.983	0.982	0.919	0.92	0	249	χ^2_1	a2
0.904	0.987	0.988	0.924	0.92	0.69	249	χ^2_1	c2
0.922	0.943	0.941	0.838	0.839	0.3	249	χ^2_1	a2
0.936	0.937	0.938	0.829	0.834	0	249	χ^2_1	c2
0.931	0.976	0.977	0.895	0.895	0.3	249	χ^2_1	a2
0.93	0.967	0.966	0.884	0.883	0.3	249	χ^2_1	c2
0.877	0.996	0.996	0.962	0.965	0.3	249	χ^2_1	a2
0.877	0.994	0.995	0.962	0.964	0.69	249	χ^2_1	c2
0.937	0.972	0.97	0.901	0.893	0.69	249	χ^2_1	a2
0.94	0.969	0.967	0.874	0.863	0	249	χ^2_1	c2
0.928	0.986	0.986	0.928	0.928	0.69	249	χ^2_1	a2
0.928	0.985	0.985	0.927	0.927	0.3	249	χ^2_1	c2
0.937	0.944	0.933	0.805	0.801	0	16	χ^2_1	a2
0.936	0.949	0.932	0.804	0.79	0	16	χ^2_1	c2
0.935	0.961	0.947	0.835	0.817	0	16	χ^2_1	a2
0.929	0.948	0.935	0.828	0.823	0.3	16	χ^2_1	c2
0.901	0.996	0.985	0.91	0.898	0	16	χ^2_1	a2
0.906	0.991	0.985	0.912	0.907	0.69	16	χ^2_1	c2
0.928	0.954	0.94	0.814	0.806	0.3	16	χ^2_1	a2
0.935	0.945	0.939	0.831	0.817	0	16	χ^2_1	c2
0.892	0.977	0.963	0.883	0.875	0.3	16	χ^2_1	a2
0.912	0.971	0.963	0.854	0.846	0.3	16	χ^2_1	c2
0.905	0.977	0.968	0.88	0.869	0.69	16	χ^2_1	a2
0.923	0.969	0.963	0.862	0.843	0	16	χ^2_1	c2

0.946	0.945	0.945	0.823	0.826	0	166	χ_1^2	a2
0.942	0.941	0.941	0.84	0.836	0	166	χ_1^2	c2
0.93	0.964	0.961	0.867	0.86	0	166	χ_1^2	a2
0.93	0.959	0.964	0.859	0.855	0.3	166	χ_1^2	c2
0.9	0.993	0.99	0.911	0.916	0	166	χ_1^2	a2
0.903	0.992	0.989	0.923	0.922	0.69	166	χ_1^2	c2
0.934	0.953	0.951	0.853	0.852	0.3	166	χ_1^2	a2
0.925	0.947	0.944	0.832	0.826	0	166	χ_1^2	c2
0.912	0.973	0.969	0.885	0.877	0.3	166	χ_1^2	a2
0.92	0.972	0.971	0.888	0.886	0.3	166	χ_1^2	c2
0.881	0.997	0.996	0.969	0.97	0.3	166	χ_1^2	a2
0.884	0.996	0.995	0.961	0.965	0.69	166	χ_1^2	c2
0.916	0.981	0.98	0.892	0.893	0.69	166	χ_1^2	a2
0.932	0.975	0.969	0.875	0.875	0	166	χ_1^2	c2
0.915	0.985	0.984	0.919	0.919	0.69	166	χ_1^2	a2
0.925	0.98	0.981	0.917	0.914	0.3	166	χ_1^2	c2
0.932	0.942	0.931	0.787	0.774	0	24	χ_{10}^2	a2
0.939	0.928	0.919	0.781	0.769	0	24	χ_{10}^2	c2
0.929	0.958	0.938	0.836	0.822	0	24	χ_{10}^2	a2
0.938	0.956	0.947	0.834	0.82	0.3	24	χ_{10}^2	c2
0.863	0.978	0.968	0.895	0.889	0	24	χ_{10}^2	a2
0.886	0.981	0.969	0.902	0.894	0.69	24	χ_{10}^2	c2
0.925	0.949	0.937	0.827	0.819	0.3	24	χ_{10}^2	a2
0.935	0.939	0.924	0.81	0.805	0	24	χ_{10}^2	c2
0.913	0.971	0.955	0.85	0.84	0.3	24	χ_{10}^2	a2
0.938	0.974	0.96	0.843	0.832	0.3	24	χ_{10}^2	c2
0.889	0.991	0.992	0.958	0.958	0.3	24	χ_{10}^2	a2
0.893	0.99	0.991	0.956	0.956	0.69	24	χ_{10}^2	c2
0.914	0.971	0.954	0.863	0.858	0.69	24	χ_{10}^2	a2
0.937	0.954	0.943	0.823	0.819	0	24	χ_{10}^2	c2
0.923	0.977	0.972	0.894	0.891	0.69	24	χ_{10}^2	a2
0.926	0.973	0.971	0.887	0.893	0.3	24	χ_{10}^2	c2
0.959	0.966	0.963	0.848	0.845	0	249	χ_{10}^2	a2
0.956	0.958	0.958	0.853	0.846	0	249	χ_{10}^2	c2
0.944	0.966	0.963	0.851	0.857	0	249	χ_{10}^2	a2
0.941	0.966	0.966	0.849	0.853	0.3	249	χ_{10}^2	c2
0.909	0.983	0.982	0.919	0.92	0	249	χ_{10}^2	a2
0.904	0.987	0.988	0.924	0.92	0.69	249	χ_{10}^2	c2
0.922	0.943	0.941	0.838	0.839	0.3	249	χ_{10}^2	a2
0.936	0.937	0.938	0.829	0.834	0	249	χ_{10}^2	c2
0.931	0.976	0.977	0.895	0.895	0.3	249	χ_{10}^2	a2
0.93	0.967	0.966	0.884	0.883	0.3	249	χ_{10}^2	c2
0.877	0.996	0.996	0.962	0.965	0.3	249	χ_{10}^2	a2
0.877	0.994	0.995	0.962	0.964	0.69	249	χ_{10}^2	c2
0.937	0.972	0.97	0.901	0.893	0.69	249	χ_{10}^2	a2
0.94	0.969	0.967	0.874	0.863	0	249	χ_{10}^2	c2

0.928	0.986	0.986	0.928	0.928	0.69	249	χ^2_{10}	a2
0.928	0.985	0.985	0.927	0.927	0.3	249	χ^2_{10}	c2
0.937	0.944	0.933	0.805	0.801	0	16	χ^2_{10}	a2
0.936	0.949	0.932	0.804	0.79	0	16	χ^2_{10}	c2
0.935	0.961	0.947	0.835	0.817	0	16	χ^2_{10}	a2
0.929	0.948	0.935	0.828	0.823	0.3	16	χ^2_{10}	c2
0.901	0.996	0.985	0.91	0.898	0	16	χ^2_{10}	a2
0.906	0.991	0.985	0.912	0.907	0.69	16	χ^2_{10}	c2
0.928	0.954	0.94	0.814	0.806	0.3	16	χ^2_{10}	a2
0.935	0.945	0.939	0.831	0.817	0	16	χ^2_{10}	c2
0.892	0.977	0.963	0.883	0.875	0.3	16	χ^2_{10}	a2
0.912	0.971	0.963	0.854	0.846	0.3	16	χ^2_{10}	c2
0.886	0.998	0.995	0.964	0.969	0.3	16	χ^2_{10}	a2
0.882	0.996	0.994	0.954	0.955	0.69	16	χ^2_{10}	c2
0.905	0.977	0.968	0.88	0.869	0.69	16	χ^2_{10}	a2
0.923	0.969	0.963	0.862	0.843	0	16	χ^2_{10}	c2
0.932	0.987	0.984	0.928	0.923	0.69	16	χ^2_{10}	a2
0.935	0.985	0.982	0.915	0.921	0.3	16	χ^2_{10}	c2
0.946	0.945	0.945	0.823	0.826	0	166	χ^2_{10}	a2
0.942	0.941	0.941	0.84	0.836	0	166	χ^2_{10}	c2
0.93	0.964	0.961	0.867	0.86	0	166	χ^2_{10}	a2
0.93	0.959	0.964	0.859	0.855	0.3	166	χ^2_{10}	c2
0.9	0.993	0.99	0.911	0.916	0	166	χ^2_{10}	a2
0.903	0.992	0.989	0.923	0.922	0.69	166	χ^2_{10}	c2
0.934	0.953	0.951	0.853	0.852	0.3	166	χ^2_{10}	a2
0.925	0.947	0.944	0.832	0.826	0	166	χ^2_{10}	c2
0.912	0.973	0.969	0.885	0.877	0.3	166	χ^2_{10}	a2
0.92	0.972	0.971	0.888	0.886	0.3	166	χ^2_{10}	c2
0.881	0.997	0.996	0.969	0.97	0.3	166	χ^2_{10}	a2
0.884	0.996	0.995	0.961	0.965	0.69	166	χ^2_{10}	c2
0.916	0.981	0.98	0.892	0.893	0.69	166	χ^2_{10}	a2
0.932	0.975	0.969	0.875	0.875	0	166	χ^2_{10}	c2
0.915	0.985	0.984	0.919	0.919	0.69	166	χ^2_{10}	a2
0.925	0.98	0.981	0.917	0.914	0.3	166	χ^2_{10}	c2
0.932	0.942	0.931	0.787	0.774	0	24	normal	a2
0.939	0.928	0.919	0.781	0.769	0	24	normal	c2
0.929	0.958	0.938	0.836	0.822	0	24	normal	a2
0.938	0.956	0.947	0.834	0.82	0.3	24	normal	c2
0.863	0.978	0.968	0.895	0.889	0	24	normal	a2
0.886	0.981	0.969	0.902	0.894	0.69	24	normal	c2
0.925	0.949	0.937	0.827	0.819	0.3	24	normal	a2
0.935	0.939	0.924	0.81	0.805	0	24	normal	c2
0.913	0.971	0.955	0.85	0.84	0.3	24	normal	a2
0.938	0.974	0.96	0.843	0.832	0.3	24	normal	c2
0.889	0.991	0.992	0.958	0.958	0.3	24	normal	a2
0.893	0.99	0.991	0.956	0.956	0.69	24	normal	c2

0.914	0.971	0.954	0.863	0.858	0.69	24	normal	a2
0.937	0.954	0.943	0.823	0.819	0	24	normal	c2
0.923	0.977	0.972	0.894	0.891	0.69	24	normal	a2
0.926	0.973	0.971	0.887	0.893	0.3	24	normal	c2
0.959	0.966	0.963	0.848	0.845	0	249	normal	a2
0.956	0.958	0.958	0.853	0.846	0	249	normal	c2
0.944	0.966	0.963	0.851	0.857	0	249	normal	a2
0.941	0.966	0.966	0.849	0.853	0.3	249	normal	c2
0.909	0.983	0.982	0.919	0.92	0	249	normal	a2
0.904	0.987	0.988	0.924	0.92	0.69	249	normal	c2
0.922	0.943	0.941	0.838	0.839	0.3	249	normal	a2
0.936	0.937	0.938	0.829	0.834	0	249	normal	c2
0.931	0.976	0.977	0.895	0.895	0.3	249	normal	a2
0.93	0.967	0.966	0.884	0.883	0.3	249	normal	c2
0.877	0.996	0.996	0.962	0.965	0.3	249	normal	a2
0.877	0.994	0.995	0.962	0.964	0.69	249	normal	c2
0.937	0.972	0.97	0.901	0.893	0.69	249	normal	a2
0.94	0.969	0.967	0.874	0.863	0	249	normal	c2
0.928	0.986	0.986	0.928	0.928	0.69	249	normal	a2
0.928	0.985	0.985	0.927	0.927	0.3	249	normal	c2
0.937	0.944	0.933	0.805	0.801	0	16	normal	a2
0.936	0.949	0.932	0.804	0.79	0	16	normal	c2
0.935	0.961	0.947	0.835	0.817	0	16	normal	a2
0.929	0.948	0.935	0.828	0.823	0.3	16	normal	c2
0.901	0.996	0.985	0.91	0.898	0	16	normal	a2
0.906	0.991	0.985	0.912	0.907	0.69	16	normal	c2
0.928	0.954	0.94	0.814	0.806	0.3	16	normal	a2
0.935	0.945	0.939	0.831	0.817	0	16	normal	c2
0.892	0.977	0.963	0.883	0.875	0.3	16	normal	a2
0.912	0.971	0.963	0.854	0.846	0.3	16	normal	c2
0.886	0.998	0.995	0.964	0.969	0.3	16	normal	a2
0.882	0.996	0.994	0.954	0.955	0.69	16	normal	c2
0.905	0.977	0.968	0.88	0.869	0.69	16	normal	a2
0.923	0.969	0.963	0.862	0.843	0	16	normal	c2
0.932	0.987	0.984	0.928	0.923	0.69	16	normal	a2
0.935	0.985	0.982	0.915	0.921	0.3	16	normal	c2
0.946	0.945	0.945	0.823	0.826	0	166	normal	a2
0.942	0.941	0.941	0.84	0.836	0	166	normal	c2
0.93	0.964	0.961	0.867	0.86	0	166	normal	a2
0.93	0.959	0.964	0.859	0.855	0.3	166	normal	c2
0.9	0.993	0.99	0.911	0.916	0	166	normal	a2
0.903	0.992	0.989	0.923	0.922	0.69	166	normal	c2
0.934	0.953	0.951	0.853	0.852	0.3	166	normal	a2
0.925	0.947	0.944	0.832	0.826	0	166	normal	c2
0.912	0.973	0.969	0.885	0.877	0.3	166	normal	a2
0.92	0.972	0.971	0.888	0.886	0.3	166	normal	c2

0.881	0.997	0.996	0.969	0.97	0.3	166	normal	a2
0.884	0.996	0.995	0.961	0.965	0.69	166	normal	c2
0.916	0.981	0.98	0.892	0.893	0.69	166	normal	a2
0.932	0.975	0.969	0.875	0.875	0	166	normal	c2
0.915	0.985	0.984	0.919	0.919	0.69	166	normal	a2
0.925	0.98	0.981	0.917	0.914	0.3	166	normal	c2

Table 12: Proportion of Confidence Intervals that captured the true population value. Part D.

Standard DEA Bootstrap standard CI	Standard DEA Bootstrap BCa CI	Univariate DEA WGS Bootstrap standard CI	Univariate DEA WGS Bootstrap BCa CI	Univariate DEA UGS Bootstrap standard CI	Population Parameter Value	MZ ns	Distribution	parameter
0.932	0.918	0.938	0.923	0.941	0	24	χ_1^2	a2
0.921	0.904	0.941	0.933	0.941	0	24	χ_1^2	c2
0.934	0.922	0.935	0.919	0.936	0	24	χ_1^2	a2
0.941	0.928	0.941	0.935	0.944	0.3	24	χ_1^2	c2
0.902	0.895	0.87	0.866	0.893	0	24	χ_1^2	a2
0.911	0.895	0.871	0.876	0.897	0.69	24	χ_1^2	c2
0.921	0.909	0.931	0.917	0.929	0.3	24	χ_1^2	a2
0.919	0.913	0.935	0.925	0.933	0	24	χ_1^2	c2
0.92	0.905	0.901	0.9	0.906	0.3	24	χ_1^2	a2
0.923	0.917	0.915	0.918	0.915	0.3	24	χ_1^2	c2
0.918	0.902	0.918	0.909	0.913	0.69	24	χ_1^2	a2
0.918	0.913	0.924	0.922	0.925	0	24	χ_1^2	c2
0.961	0.96	0.963	0.962	0.959	0	249	χ_1^2	a2
0.954	0.953	0.96	0.955	0.959	0	249	χ_1^2	c2
0.958	0.956	0.938	0.937	0.939	0	249	χ_1^2	a2
0.95	0.951	0.935	0.938	0.937	0.3	249	χ_1^2	c2
0.937	0.933	0.903	0.908	0.915	0	249	χ_1^2	a2
0.94	0.939	0.905	0.907	0.904	0.69	249	χ_1^2	c2
0.938	0.935	0.919	0.92	0.917	0.3	249	χ_1^2	a2
0.931	0.931	0.925	0.929	0.926	0	249	χ_1^2	c2
0.954	0.948	0.93	0.927	0.929	0.3	249	χ_1^2	a2
0.944	0.946	0.925	0.93	0.931	0.3	249	χ_1^2	c2
0.934	0.94	0.862	0.869	0.867	0.3	249	χ_1^2	a2
0.929	0.936	0.861	0.872	0.875	0.69	249	χ_1^2	c2
0.949	0.947	0.934	0.936	0.934	0.69	249	χ_1^2	a2
0.95	0.954	0.933	0.939	0.937	0	249	χ_1^2	c2
0.946	0.945	0.926	0.926	0.926	0.69	249	χ_1^2	a2
0.947	0.948	0.925	0.925	0.928	0.3	249	χ_1^2	c2
0.929	0.914	0.95	0.933	0.944	0	16	χ_1^2	a2
0.935	0.923	0.949	0.939	0.944	0	16	χ_1^2	c2
0.94	0.927	0.938	0.93	0.938	0	16	χ_1^2	a2
0.924	0.908	0.921	0.921	0.934	0.3	16	χ_1^2	c2
0.913	0.897	0.895	0.889	0.911	0	16	χ_1^2	a2
0.922	0.906	0.904	0.9	0.915	0.69	16	χ_1^2	c2
0.927	0.913	0.934	0.92	0.936	0.3	16	χ_1^2	a2
0.927	0.913	0.938	0.928	0.935	0	16	χ_1^2	c2
0.926	0.911	0.909	0.91	0.922	0.3	16	χ_1^2	a2
0.921	0.908	0.915	0.915	0.929	0.3	16	χ_1^2	c2
0.925	0.913	0.906	0.909	0.912	0.69	16	χ_1^2	a2

0.932	0.93	0.924	0.926	0.931	0	16	χ_1^2	c2
0.943	0.941	0.95	0.951	0.947	0	166	χ_1^2	a2
0.937	0.936	0.948	0.948	0.941	0	166	χ_1^2	c2
0.952	0.952	0.929	0.938	0.931	0	166	χ_1^2	a2
0.951	0.951	0.931	0.929	0.93	0.3	166	χ_1^2	c2
0.93	0.931	0.903	0.908	0.906	0	166	χ_1^2	a2
0.939	0.932	0.905	0.903	0.907	0.69	166	χ_1^2	c2
0.948	0.947	0.933	0.931	0.93	0.3	166	χ_1^2	a2
0.948	0.944	0.932	0.93	0.926	0	166	χ_1^2	c2
0.935	0.932	0.908	0.905	0.91	0.3	166	χ_1^2	a2
0.946	0.943	0.917	0.92	0.92	0.3	166	χ_1^2	c2
0.937	0.94	0.861	0.869	0.866	0.3	166	χ_1^2	a2
0.939	0.944	0.872	0.88	0.87	0.69	166	χ_1^2	c2
0.94	0.943	0.92	0.915	0.919	0.69	166	χ_1^2	a2
0.95	0.952	0.931	0.93	0.934	0	166	χ_1^2	c2
0.942	0.943	0.916	0.918	0.916	0.69	166	χ_1^2	a2
0.941	0.944	0.919	0.927	0.922	0.3	166	χ_1^2	c2
0.932	0.918	0.938	0.923	0.941	0	24	χ_{10}^2	a2
0.921	0.904	0.941	0.933	0.941	0	24	χ_{10}^2	c2
0.934	0.922	0.935	0.919	0.936	0	24	χ_{10}^2	a2
0.941	0.928	0.941	0.935	0.944	0.3	24	χ_{10}^2	c2
0.902	0.895	0.87	0.866	0.893	0	24	χ_{10}^2	a2
0.911	0.895	0.871	0.876	0.897	0.69	24	χ_{10}^2	c2
0.921	0.909	0.931	0.917	0.929	0.3	24	χ_{10}^2	a2
0.919	0.913	0.935	0.925	0.933	0	24	χ_{10}^2	c2
0.92	0.905	0.901	0.9	0.906	0.3	24	χ_{10}^2	a2
0.923	0.917	0.915	0.918	0.915	0.3	24	χ_{10}^2	c2
0.923	0.923	0.85	0.882	0.878	0.3	24	χ_{10}^2	a2
0.916	0.918	0.855	0.877	0.879	0.69	24	χ_{10}^2	c2
0.918	0.902	0.918	0.909	0.913	0.69	24	χ_{10}^2	a2
0.918	0.913	0.924	0.922	0.925	0	24	χ_{10}^2	c2
0.914	0.909	0.896	0.918	0.908	0.69	24	χ_{10}^2	a2
0.916	0.914	0.897	0.915	0.908	0.3	24	χ_{10}^2	c2
0.961	0.96	0.963	0.962	0.959	0	249	χ_{10}^2	a2
0.954	0.953	0.96	0.955	0.959	0	249	χ_{10}^2	c2
0.958	0.956	0.938	0.937	0.939	0	249	χ_{10}^2	a2
0.95	0.951	0.935	0.938	0.937	0.3	249	χ_{10}^2	c2
0.937	0.933	0.903	0.908	0.915	0	249	χ_{10}^2	a2
0.94	0.939	0.905	0.907	0.904	0.69	249	χ_{10}^2	c2
0.938	0.935	0.919	0.92	0.917	0.3	249	χ_{10}^2	a2
0.931	0.931	0.925	0.929	0.926	0	249	χ_{10}^2	c2
0.954	0.948	0.93	0.927	0.929	0.3	249	χ_{10}^2	a2
0.944	0.946	0.925	0.93	0.931	0.3	249	χ_{10}^2	c2
0.934	0.94	0.862	0.869	0.867	0.3	249	χ_{10}^2	a2
0.929	0.936	0.861	0.872	0.875	0.69	249	χ_{10}^2	c2
0.949	0.947	0.934	0.936	0.934	0.69	249	χ_{10}^2	a2

0.95	0.954	0.933	0.939	0.937	0	249	χ^2_{10}	c2
0.946	0.945	0.926	0.926	0.926	0.69	249	χ^2_{10}	a2
0.947	0.948	0.925	0.925	0.928	0.3	249	χ^2_{10}	c2
0.929	0.914	0.95	0.933	0.944	0	16	χ^2_{10}	a2
0.935	0.923	0.949	0.939	0.944	0	16	χ^2_{10}	c2
0.94	0.927	0.938	0.93	0.938	0	16	χ^2_{10}	a2
0.924	0.908	0.921	0.921	0.934	0.3	16	χ^2_{10}	c2
0.913	0.897	0.895	0.889	0.911	0	16	χ^2_{10}	a2
0.922	0.906	0.904	0.9	0.915	0.69	16	χ^2_{10}	c2
0.927	0.913	0.934	0.92	0.936	0.3	16	χ^2_{10}	a2
0.927	0.913	0.938	0.928	0.935	0	16	χ^2_{10}	c2
0.926	0.911	0.909	0.91	0.922	0.3	16	χ^2_{10}	a2
0.921	0.908	0.915	0.915	0.929	0.3	16	χ^2_{10}	c2
0.918	0.92	0.855	0.876	0.875	0.3	16	χ^2_{10}	a2
0.911	0.916	0.86	0.879	0.876	0.69	16	χ^2_{10}	c2
0.925	0.913	0.906	0.909	0.912	0.69	16	χ^2_{10}	a2
0.932	0.93	0.924	0.926	0.931	0	16	χ^2_{10}	c2
0.934	0.936	0.908	0.931	0.918	0.69	16	χ^2_{10}	a2
0.933	0.938	0.912	0.931	0.918	0.3	16	χ^2_{10}	c2
0.943	0.941	0.95	0.951	0.947	0	166	χ^2_{10}	a2
0.937	0.936	0.948	0.948	0.941	0	166	χ^2_{10}	c2
0.952	0.952	0.929	0.938	0.931	0	166	χ^2_{10}	a2
0.951	0.951	0.931	0.929	0.93	0.3	166	χ^2_{10}	c2
0.93	0.931	0.903	0.908	0.906	0	166	χ^2_{10}	a2
0.939	0.932	0.905	0.903	0.907	0.69	166	χ^2_{10}	c2
0.948	0.947	0.933	0.931	0.93	0.3	166	χ^2_{10}	a2
0.948	0.944	0.932	0.93	0.926	0	166	χ^2_{10}	c2
0.935	0.932	0.908	0.905	0.91	0.3	166	χ^2_{10}	a2
0.946	0.943	0.917	0.92	0.92	0.3	166	χ^2_{10}	c2
0.937	0.94	0.861	0.869	0.866	0.3	166	χ^2_{10}	a2
0.939	0.944	0.872	0.88	0.87	0.69	166	χ^2_{10}	c2
0.94	0.943	0.92	0.915	0.919	0.69	166	χ^2_{10}	a2
0.95	0.952	0.931	0.93	0.934	0	166	χ^2_{10}	c2
0.942	0.943	0.916	0.918	0.916	0.69	166	χ^2_{10}	a2
0.941	0.944	0.919	0.927	0.922	0.3	166	χ^2_{10}	c2
0.932	0.918	0.938	0.923	0.941	0	24	normal	a2
0.921	0.904	0.941	0.933	0.941	0	24	normal	c2
0.934	0.922	0.935	0.919	0.936	0	24	normal	a2
0.941	0.928	0.941	0.935	0.944	0.3	24	normal	c2
0.902	0.895	0.87	0.866	0.893	0	24	normal	a2
0.911	0.895	0.871	0.876	0.897	0.69	24	normal	c2
0.921	0.909	0.931	0.917	0.929	0.3	24	normal	a2
0.919	0.913	0.935	0.925	0.933	0	24	normal	c2
0.92	0.905	0.901	0.9	0.906	0.3	24	normal	a2
0.923	0.917	0.915	0.918	0.915	0.3	24	normal	c2
0.923	0.923	0.85	0.882	0.878	0.3	24	normal	a2

0.916	0.918	0.855	0.877	0.879	0.69	24	normal	c2
0.918	0.902	0.918	0.909	0.913	0.69	24	normal	a2
0.918	0.913	0.924	0.922	0.925	0	24	normal	c2
0.914	0.909	0.896	0.918	0.908	0.69	24	normal	a2
0.916	0.914	0.897	0.915	0.908	0.3	24	normal	c2
0.961	0.96	0.963	0.962	0.959	0	249	normal	a2
0.954	0.953	0.96	0.955	0.959	0	249	normal	c2
0.958	0.956	0.938	0.937	0.939	0	249	normal	a2
0.95	0.951	0.935	0.938	0.937	0.3	249	normal	c2
0.937	0.933	0.903	0.908	0.915	0	249	normal	a2
0.94	0.939	0.905	0.907	0.904	0.69	249	normal	c2
0.938	0.935	0.919	0.92	0.917	0.3	249	normal	a2
0.931	0.931	0.925	0.929	0.926	0	249	normal	c2
0.954	0.948	0.93	0.927	0.929	0.3	249	normal	a2
0.944	0.946	0.925	0.93	0.931	0.3	249	normal	c2
0.934	0.94	0.862	0.869	0.867	0.3	249	normal	a2
0.929	0.936	0.861	0.872	0.875	0.69	249	normal	c2
0.949	0.947	0.934	0.936	0.934	0.69	249	normal	a2
0.95	0.954	0.933	0.939	0.937	0	249	normal	c2
0.946	0.945	0.926	0.926	0.926	0.69	249	normal	a2
0.947	0.948	0.925	0.925	0.928	0.3	249	normal	c2
0.929	0.914	0.95	0.933	0.944	0	16	normal	a2
0.935	0.923	0.949	0.939	0.944	0	16	normal	c2
0.94	0.927	0.938	0.93	0.938	0	16	normal	a2
0.924	0.908	0.921	0.921	0.934	0.3	16	normal	c2
0.913	0.897	0.895	0.889	0.911	0	16	normal	a2
0.922	0.906	0.904	0.9	0.915	0.69	16	normal	c2
0.927	0.913	0.934	0.92	0.936	0.3	16	normal	a2
0.927	0.913	0.938	0.928	0.935	0	16	normal	c2
0.926	0.911	0.909	0.91	0.922	0.3	16	normal	a2
0.921	0.908	0.915	0.915	0.929	0.3	16	normal	c2
0.918	0.92	0.855	0.876	0.875	0.3	16	normal	a2
0.911	0.916	0.86	0.879	0.876	0.69	16	normal	c2
0.925	0.913	0.906	0.909	0.912	0.69	16	normal	a2
0.932	0.93	0.924	0.926	0.931	0	16	normal	c2
0.934	0.936	0.908	0.931	0.918	0.69	16	normal	a2
0.933	0.938	0.912	0.931	0.918	0.3	16	normal	c2
0.943	0.941	0.95	0.951	0.947	0	166	normal	a2
0.937	0.936	0.948	0.948	0.941	0	166	normal	c2
0.952	0.952	0.929	0.938	0.931	0	166	normal	a2
0.951	0.951	0.931	0.929	0.93	0.3	166	normal	c2
0.93	0.931	0.903	0.908	0.906	0	166	normal	a2
0.939	0.932	0.905	0.903	0.907	0.69	166	normal	c2
0.948	0.947	0.933	0.931	0.93	0.3	166	normal	a2
0.948	0.944	0.932	0.93	0.926	0	166	normal	c2
0.935	0.932	0.908	0.905	0.91	0.3	166	normal	a2

0.946	0.943	0.917	0.92	0.92	0.3	166	normal	c2
0.937	0.94	0.861	0.869	0.866	0.3	166	normal	a2
0.939	0.944	0.872	0.88	0.87	0.69	166	normal	c2
0.94	0.943	0.92	0.915	0.919	0.69	166	normal	a2
0.95	0.952	0.931	0.93	0.934	0	166	normal	c2
0.942	0.943	0.916	0.918	0.916	0.69	166	normal	a2
0.941	0.944	0.919	0.927	0.922	0.3	166	normal	c2

Table 13: Proportion of Confidence Intervals that captured the true population value. Part E.

Robust Upper CI	Typical Upper CI	Population Parameter Value	MZ ns	Distribution	parameter
0.906	0.832	0	24	χ_1^2	a2
0.894	0.837	0	24	χ_1^2	c2
0.913	0.835	0	24	χ_1^2	a2
0.906	0.843	0.3	24	χ_1^2	c2
0.901	0.862	0	24	χ_1^2	a2
0.893	0.881	0.69	24	χ_1^2	c2
0.901	0.851	0.3	24	χ_1^2	a2
0.889	0.84	0	24	χ_1^2	c2
0.9	0.839	0.3	24	χ_1^2	a2
0.894	0.825	0.3	24	χ_1^2	c2
0.904	0.858	0.69	24	χ_1^2	a2
0.885	0.804	0	24	χ_1^2	c2
0.961	0.857	0	249	χ_1^2	a2
0.954	0.859	0	249	χ_1^2	c2
0.951	0.805	0	249	χ_1^2	a2
0.954	0.814	0.3	249	χ_1^2	c2
0.937	0.856	0	249	χ_1^2	a2
0.941	0.859	0.69	249	χ_1^2	c2
0.937	0.819	0.3	249	χ_1^2	a2
0.933	0.812	0	249	χ_1^2	c2
0.945	0.848	0.3	249	χ_1^2	a2
0.941	0.823	0.3	249	χ_1^2	c2
0.926	0.922	0.3	249	χ_1^2	a2
0.92	0.84	0.69	249	χ_1^2	c2
0.951	0.847	0.69	249	χ_1^2	a2
0.952	0.787	0	249	χ_1^2	c2
0.94	0.873	0.69	249	χ_1^2	a2
0.939	0.76	0.3	249	χ_1^2	c2
0.905	0.854	0	16	χ_1^2	a2
0.916	0.849	0	16	χ_1^2	c2
0.899	0.845	0	16	χ_1^2	a2
0.897	0.826	0.3	16	χ_1^2	c2
0.905	0.893	0	16	χ_1^2	a2
0.923	0.886	0.69	16	χ_1^2	c2
0.896	0.83	0.3	16	χ_1^2	a2
0.906	0.833	0	16	χ_1^2	c2
0.912	0.874	0.3	16	χ_1^2	a2
0.901	0.848	0.3	16	χ_1^2	c2
0.906	0.897	0.69	16	χ_1^2	a2
0.907	0.847	0	16	χ_1^2	c2
0.947	0.839	0	166	χ_1^2	a2
0.94	0.842	0	166	χ_1^2	c2

0.946	0.824	0	166	χ_1^2	a2
0.952	0.812	0.3	166	χ_1^2	c2
0.931	0.862	0	166	χ_1^2	a2
0.94	0.866	0.69	166	χ_1^2	c2
0.943	0.818	0.3	166	χ_1^2	a2
0.941	0.8	0	166	χ_1^2	c2
0.938	0.845	0.3	166	χ_1^2	a2
0.945	0.831	0.3	166	χ_1^2	c2
0.934	0.987	0.3	166	χ_1^2	a2
0.934	0.922	0.69	166	χ_1^2	c2
0.942	0.879	0.69	166	χ_1^2	a2
0.951	0.826	0	166	χ_1^2	c2
0.942	0.964	0.69	166	χ_1^2	a2
0.94	0.857	0.3	166	χ_1^2	c2
0.906	0.832	0	24	χ_{10}^2	a2
0.894	0.837	0	24	χ_{10}^2	c2
0.913	0.835	0	24	χ_{10}^2	a2
0.906	0.843	0.3	24	χ_{10}^2	c2
0.901	0.862	0	24	χ_{10}^2	a2
0.893	0.881	0.69	24	χ_{10}^2	c2
0.901	0.851	0.3	24	χ_{10}^2	a2
0.889	0.84	0	24	χ_{10}^2	c2
0.9	0.839	0.3	24	χ_{10}^2	a2
0.894	0.825	0.3	24	χ_{10}^2	c2
0.858	0.944	0.3	24	χ_{10}^2	a2
0.849	0.877	0.69	24	χ_{10}^2	c2
0.904	0.858	0.69	24	χ_{10}^2	a2
0.885	0.804	0	24	χ_{10}^2	c2
0.861	0.86	0.69	24	χ_{10}^2	a2
0.862	0.773	0.3	24	χ_{10}^2	c2
0.961	0.857	0	249	χ_{10}^2	a2
0.954	0.859	0	249	χ_{10}^2	c2
0.951	0.805	0	249	χ_{10}^2	a2
0.954	0.814	0.3	249	χ_{10}^2	c2
0.937	0.856	0	249	χ_{10}^2	a2
0.941	0.859	0.69	249	χ_{10}^2	c2
0.937	0.819	0.3	249	χ_{10}^2	a2
0.933	0.812	0	249	χ_{10}^2	c2
0.945	0.848	0.3	249	χ_{10}^2	a2
0.941	0.823	0.3	249	χ_{10}^2	c2
0.926	0.922	0.3	249	χ_{10}^2	a2
0.92	0.84	0.69	249	χ_{10}^2	c2
0.951	0.847	0.69	249	χ_{10}^2	a2
0.952	0.787	0	249	χ_{10}^2	c2
0.94	0.873	0.69	249	χ_{10}^2	a2
0.939	0.76	0.3	249	χ_{10}^2	c2

0.905	0.854	0	16	χ^2_{10}	a2
0.916	0.849	0	16	χ^2_{10}	c2
0.899	0.845	0	16	χ^2_{10}	a2
0.897	0.826	0.3	16	χ^2_{10}	c2
0.905	0.893	0	16	χ^2_{10}	a2
0.923	0.886	0.69	16	χ^2_{10}	c2
0.896	0.83	0.3	16	χ^2_{10}	a2
0.906	0.833	0	16	χ^2_{10}	c2
0.912	0.874	0.3	16	χ^2_{10}	a2
0.901	0.848	0.3	16	χ^2_{10}	c2
0.878	0.988	0.3	16	χ^2_{10}	a2
0.874	0.943	0.69	16	χ^2_{10}	c2
0.906	0.897	0.69	16	χ^2_{10}	a2
0.907	0.847	0	16	χ^2_{10}	c2
0.901	0.97	0.69	16	χ^2_{10}	a2
0.9	0.883	0.3	16	χ^2_{10}	c2
0.947	0.839	0	166	χ^2_{10}	a2
0.94	0.842	0	166	χ^2_{10}	c2
0.946	0.824	0	166	χ^2_{10}	a2
0.952	0.812	0.3	166	χ^2_{10}	c2
0.931	0.862	0	166	χ^2_{10}	a2
0.94	0.866	0.69	166	χ^2_{10}	c2
0.943	0.818	0.3	166	χ^2_{10}	a2
0.941	0.8	0	166	χ^2_{10}	c2
0.938	0.845	0.3	166	χ^2_{10}	a2
0.945	0.831	0.3	166	χ^2_{10}	c2
0.934	0.987	0.3	166	χ^2_{10}	a2
0.934	0.922	0.69	166	χ^2_{10}	c2
0.942	0.879	0.69	166	χ^2_{10}	a2
0.951	0.826	0	166	χ^2_{10}	c2
0.942	0.964	0.69	166	χ^2_{10}	a2
0.94	0.857	0.3	166	χ^2_{10}	c2
0.906	0.832	0	24	normal	a2
0.894	0.837	0	24	normal	c2
0.913	0.835	0	24	normal	a2
0.906	0.843	0.3	24	normal	c2
0.901	0.862	0	24	normal	a2
0.893	0.881	0.69	24	normal	c2
0.901	0.851	0.3	24	normal	a2
0.889	0.84	0	24	normal	c2
0.9	0.839	0.3	24	normal	a2
0.894	0.825	0.3	24	normal	c2
0.858	0.944	0.3	24	normal	a2
0.849	0.877	0.69	24	normal	c2
0.904	0.858	0.69	24	normal	a2
0.885	0.804	0	24	normal	c2

0.861	0.86	0.69	24	normal	a2
0.862	0.773	0.3	24	normal	c2
0.961	0.857	0	249	normal	a2
0.954	0.859	0	249	normal	c2
0.951	0.805	0	249	normal	a2
0.954	0.814	0.3	249	normal	c2
0.937	0.856	0	249	normal	a2
0.941	0.859	0.69	249	normal	c2
0.937	0.819	0.3	249	normal	a2
0.933	0.812	0	249	normal	c2
0.945	0.848	0.3	249	normal	a2
0.941	0.823	0.3	249	normal	c2
0.926	0.922	0.3	249	normal	a2
0.92	0.84	0.69	249	normal	c2
0.951	0.847	0.69	249	normal	a2
0.952	0.787	0	249	normal	c2
0.94	0.873	0.69	249	normal	a2
0.939	0.76	0.3	249	normal	c2
0.905	0.854	0	16	normal	a2
0.916	0.849	0	16	normal	c2
0.899	0.845	0	16	normal	a2
0.897	0.826	0.3	16	normal	c2
0.905	0.893	0	16	normal	a2
0.923	0.886	0.69	16	normal	c2
0.896	0.83	0.3	16	normal	a2
0.906	0.833	0	16	normal	c2
0.912	0.874	0.3	16	normal	a2
0.901	0.848	0.3	16	normal	c2
0.878	0.988	0.3	16	normal	a2
0.874	0.943	0.69	16	normal	c2
0.906	0.897	0.69	16	normal	a2
0.907	0.847	0	16	normal	c2
0.901	0.97	0.69	16	normal	a2
0.9	0.883	0.3	16	normal	c2
0.947	0.839	0	166	normal	a2
0.94	0.842	0	166	normal	c2
0.946	0.824	0	166	normal	a2
0.952	0.812	0.3	166	normal	c2
0.931	0.862	0	166	normal	a2
0.94	0.866	0.69	166	normal	c2
0.943	0.818	0.3	166	normal	a2
0.941	0.8	0	166	normal	c2
0.938	0.845	0.3	166	normal	a2
0.945	0.831	0.3	166	normal	c2
0.934	0.987	0.3	166	normal	a2
0.934	0.922	0.69	166	normal	c2

0.942	0.879	0.69	166	normal	a2
0.951	0.826	0	166	normal	c2
0.942	0.964	0.69	166	normal	a2
0.94	0.857	0.3	166	normal	c2

Table 14: Power to exclude zero at the lower end of the confidence interval. Part A.

Univariate DEB .5 UGS Bootstrap standard CI	Univariate DEB .5 UGS Bootstrap BCa CI	Univariate DEB 1 UGS Bootstrap standard CI	Univariate DEB 1 UGS Bootstrap BCa CI	Standard Adjusted by root 2	Population Parameter Value	MZ ns	Distribution	parameter
0.084	0.095	0.241	0.249	0.112	0.3	24	χ_1^2	c2
0.452	0.471	0.676	0.705	0.531	0.69	24	χ_1^2	c2
0.054	0.061	0.192	0.189	0.065	0.3	24	χ_1^2	a2
0.067	0.06	0.184	0.178	0.086	0.3	24	χ_1^2	a2
0.094	0.097	0.25	0.234	0.122	0.3	24	χ_1^2	c2
0.221	0.231	0.456	0.453	0.281	0.69	24	χ_1^2	a2
0.555	0.562	0.747	0.754	0.59	0.3	249	χ_1^2	c2
1	1	1	1	1	0.69	249	χ_1^2	c2
0.361	0.356	0.574	0.575	0.384	0.3	249	χ_1^2	a2
0.361	0.356	0.621	0.624	0.508	0.3	249	χ_1^2	a2
0.549	0.557	0.79	0.796	0.7	0.3	249	χ_1^2	c2
1	1	1	1	1	0.3	249	χ_1^2	a2
1	1	1	1	1	0.69	249	χ_1^2	c2
0.982	0.983	0.994	0.994	0.99	0.69	249	χ_1^2	a2
1	1	1	1	1	0.69	249	χ_1^2	a2
0.733	0.74	0.903	0.911	0.918	0.3	249	χ_1^2	c2
0.084	0.078	0.263	0.243	0.097	0.3	16	χ_1^2	c2
0.459	0.439	0.728	0.713	0.549	0.69	16	χ_1^2	c2
0.071	0.084	0.199	0.204	0.081	0.3	16	χ_1^2	a2
0.052	0.061	0.175	0.192	0.062	0.3	16	χ_1^2	a2
0.093	0.084	0.268	0.246	0.119	0.3	16	χ_1^2	c2
0.201	0.245	0.439	0.467	0.215	0.69	16	χ_1^2	a2
0.588	0.581	0.796	0.794	0.63	0.3	166	χ_1^2	c2
1	1	1	1	1	0.69	166	χ_1^2	c2
0.345	0.349	0.574	0.585	0.368	0.3	166	χ_1^2	a2
0.321	0.334	0.593	0.602	0.442	0.3	166	χ_1^2	a2
0.619	0.623	0.837	0.838	0.739	0.3	166	χ_1^2	c2
1	1	1	1	0.999	0.3	166	χ_1^2	a2
1	1	1	1	1	0.69	166	χ_1^2	c2
0.97	0.97	0.996	0.997	0.988	0.69	166	χ_1^2	a2
1	1	1	1	1	0.69	166	χ_1^2	a2
0.841	0.838	0.955	0.955	0.923	0.3	166	χ_1^2	c2
0.084	0.095	0.241	0.249	0.112	0.3	24	χ_{10}^2	c2
0.452	0.471	0.676	0.705	0.531	0.69	24	χ_{10}^2	c2
0.054	0.061	0.192	0.189	0.065	0.3	24	χ_{10}^2	a2
0.067	0.06	0.184	0.178	0.086	0.3	24	χ_{10}^2	a2
0.094	0.097	0.25	0.234	0.122	0.3	24	χ_{10}^2	c2
0.072	0.046	0.325	0.266	0.114	0.3	24	χ_{10}^2	a2
0.725	0.747	0.869	0.889	0.871	0.69	24	χ_{10}^2	c2

0.221	0.231	0.456	0.453	0.281	0.69	24	χ^2_{10}	a2
0.435	0.396	0.826	0.802	0.595	0.69	24	χ^2_{10}	a2
0.127	0.131	0.291	0.305	0.272	0.3	24	χ^2_{10}	c2
0.555	0.562	0.747	0.754	0.59	0.3	249	χ^2_{10}	c2
1	1	1	1	1	0.69	249	χ^2_{10}	c2
0.361	0.356	0.574	0.575	0.384	0.3	249	χ^2_{10}	a2
0.361	0.356	0.621	0.624	0.508	0.3	249	χ^2_{10}	a2
0.549	0.557	0.79	0.796	0.7	0.3	249	χ^2_{10}	c2
1	1	1	1	1	0.3	249	χ^2_{10}	a2
1	1	1	1	1	0.69	249	χ^2_{10}	c2
0.982	0.983	0.994	0.994	0.99	0.69	249	χ^2_{10}	a2
1	1	1	1	1	0.69	249	χ^2_{10}	a2
0.733	0.74	0.903	0.911	0.918	0.3	249	χ^2_{10}	c2
0.084	0.078	0.263	0.243	0.097	0.3	16	χ^2_{10}	c2
0.459	0.439	0.728	0.713	0.549	0.69	16	χ^2_{10}	c2
0.071	0.084	0.199	0.204	0.081	0.3	16	χ^2_{10}	a2
0.052	0.061	0.175	0.192	0.062	0.3	16	χ^2_{10}	a2
0.093	0.084	0.268	0.246	0.119	0.3	16	χ^2_{10}	c2
0.102	0.088	0.468	0.426	0.025	0.3	16	χ^2_{10}	a2
0.825	0.831	0.932	0.942	0.875	0.69	16	χ^2_{10}	c2
0.201	0.245	0.439	0.467	0.215	0.69	16	χ^2_{10}	a2
0.584	0.604	0.902	0.916	0.349	0.69	16	χ^2_{10}	a2
0.117	0.109	0.273	0.285	0.164	0.3	16	χ^2_{10}	c2
0.588	0.581	0.796	0.794	0.63	0.3	166	χ^2_{10}	c2
1	1	1	1	1	0.69	166	χ^2_{10}	c2
0.345	0.349	0.574	0.585	0.368	0.3	166	χ^2_{10}	a2
0.321	0.334	0.593	0.602	0.442	0.3	166	χ^2_{10}	a2
0.619	0.623	0.837	0.838	0.739	0.3	166	χ^2_{10}	c2
1	1	1	1	0.999	0.3	166	χ^2_{10}	a2
1	1	1	1	1	0.69	166	χ^2_{10}	c2
0.97	0.97	0.996	0.997	0.988	0.69	166	χ^2_{10}	a2
1	1	1	1	1	0.69	166	χ^2_{10}	a2
0.841	0.838	0.955	0.955	0.923	0.3	166	χ^2_{10}	c2
0.084	0.095	0.241	0.249	0.112	0.3	24	normal	c2
0.452	0.471	0.676	0.705	0.531	0.69	24	normal	c2
0.054	0.061	0.192	0.189	0.065	0.3	24	normal	a2
0.067	0.06	0.184	0.178	0.086	0.3	24	normal	a2
0.094	0.097	0.25	0.234	0.122	0.3	24	normal	c2
0.072	0.046	0.325	0.266	0.114	0.3	24	normal	a2
0.725	0.747	0.869	0.889	0.871	0.69	24	normal	c2
0.221	0.231	0.456	0.453	0.281	0.69	24	normal	a2
0.435	0.396	0.826	0.802	0.595	0.69	24	normal	a2
0.127	0.131	0.291	0.305	0.272	0.3	24	normal	c2
0.555	0.562	0.747	0.754	0.59	0.3	249	normal	c2
1	1	1	1	1	0.69	249	normal	c2
0.361	0.356	0.574	0.575	0.384	0.3	249	normal	a2

0.361	0.356	0.621	0.624	0.508	0.3	249	normal	a2
0.549	0.557	0.79	0.796	0.7	0.3	249	normal	c2
1	1	1	1	1	0.3	249	normal	a2
1	1	1	1	1	0.69	249	normal	c2
0.982	0.983	0.994	0.994	0.99	0.69	249	normal	a2
1	1	1	1	1	0.69	249	normal	a2
0.733	0.74	0.903	0.911	0.918	0.3	249	normal	c2
0.084	0.078	0.263	0.243	0.097	0.3	16	normal	c2
0.459	0.439	0.728	0.713	0.549	0.69	16	normal	c2
0.071	0.084	0.199	0.204	0.081	0.3	16	normal	a2
0.052	0.061	0.175	0.192	0.062	0.3	16	normal	a2
0.093	0.084	0.268	0.246	0.119	0.3	16	normal	c2
0.102	0.088	0.468	0.426	0.025	0.3	16	normal	a2
0.825	0.831	0.932	0.942	0.875	0.69	16	normal	c2
0.201	0.245	0.439	0.467	0.215	0.69	16	normal	a2
0.584	0.604	0.902	0.916	0.349	0.69	16	normal	a2
0.117	0.109	0.273	0.285	0.164	0.3	16	normal	c2
0.588	0.581	0.796	0.794	0.63	0.3	166	normal	c2
1	1	1	1	1	0.69	166	normal	c2
0.345	0.349	0.574	0.585	0.368	0.3	166	normal	a2
0.321	0.334	0.593	0.602	0.442	0.3	166	normal	a2
0.619	0.623	0.837	0.838	0.739	0.3	166	normal	c2
1	1	1	1	0.999	0.3	166	normal	a2
1	1	1	1	1	0.69	166	normal	c2
0.97	0.97	0.996	0.997	0.988	0.69	166	normal	a2
1	1	1	1	1	0.69	166	normal	a2
0.841	0.838	0.955	0.955	0.923	0.3	166	normal	c2

Table 15: Power to exclude zero at the lower end of the confidence interval. Part B.

Standard DEB 1 Bootstrap BCa CI	Univariate DEB .5 WGS Bootstrap standard CI	Univariate DEB .5 WGS Bootstrap BCa CI	Univariate DEB 1 WGS Bootstrap standard CI	Univariate DEB 1 WGS Bootstrap BCa CI	Population Parameter Value	MZ ns	Distribution	parameter
0.263	0.089	0.1	0.255	0.261	0.3	24	χ_1^2	c2
0.717	0.488	0.493	0.709	0.712	0.69	24	χ_1^2	c2
0.222	0.057	0.064	0.191	0.202	0.3	24	χ_1^2	a2
0.203	0.071	0.082	0.185	0.194	0.3	24	χ_1^2	a2
0.272	0.107	0.107	0.259	0.262	0.3	24	χ_1^2	c2
0.481	0.226	0.264	0.474	0.486	0.69	24	χ_1^2	a2
0.744	0.554	0.558	0.762	0.758	0.3	249	χ_1^2	c2
1	1	1	1	1	0.69	249	χ_1^2	c2
0.563	0.359	0.362	0.572	0.578	0.3	249	χ_1^2	a2
0.644	0.369	0.369	0.634	0.633	0.3	249	χ_1^2	a2
0.793	0.558	0.555	0.798	0.793	0.3	249	χ_1^2	c2
1	1	1	1	1	0.3	249	χ_1^2	a2
1	1	1	1	1	0.69	249	χ_1^2	c2
0.996	0.982	0.982	0.995	0.994	0.69	249	χ_1^2	a2
1	1	1	1	1	0.69	249	χ_1^2	a2
0.906	0.758	0.754	0.911	0.914	0.3	249	χ_1^2	c2
0.291	0.084	0.095	0.269	0.278	0.3	16	χ_1^2	c2
0.724	0.486	0.49	0.746	0.738	0.69	16	χ_1^2	c2
0.238	0.069	0.084	0.207	0.223	0.3	16	χ_1^2	a2
0.213	0.064	0.076	0.188	0.198	0.3	16	χ_1^2	a2
0.283	0.096	0.103	0.288	0.285	0.3	16	χ_1^2	c2
0.486	0.23	0.264	0.462	0.48	0.69	16	χ_1^2	a2
0.787	0.594	0.595	0.789	0.79	0.3	166	χ_1^2	c2
1	1	1	1	1	0.69	166	χ_1^2	c2
0.563	0.356	0.353	0.581	0.585	0.3	166	χ_1^2	a2
0.628	0.343	0.346	0.613	0.616	0.3	166	χ_1^2	a2
0.842	0.629	0.629	0.838	0.839	0.3	166	χ_1^2	c2
1	0.999	1	1	1	0.3	166	χ_1^2	a2
1	1	1	1	1	0.69	166	χ_1^2	c2
0.997	0.978	0.981	0.997	0.997	0.69	166	χ_1^2	a2
1	1	1	1	1	0.69	166	χ_1^2	a2
0.956	0.853	0.846	0.959	0.957	0.3	166	χ_1^2	c2
0.263	0.089	0.1	0.255	0.261	0.3	24	χ_{10}^2	c2
0.717	0.488	0.493	0.709	0.712	0.69	24	χ_{10}^2	c2
0.222	0.057	0.064	0.191	0.202	0.3	24	χ_{10}^2	a2
0.203	0.071	0.082	0.185	0.194	0.3	24	χ_{10}^2	a2
0.272	0.107	0.107	0.259	0.262	0.3	24	χ_{10}^2	c2
0.376	0.078	0.076	0.38	0.37	0.3	24	χ_{10}^2	a2
0.887	0.759	0.75	0.895	0.9	0.69	24	χ_{10}^2	c2

0.481	0.226	0.264	0.474	0.486	0.69	24	χ^2_{10}	a2
0.851	0.508	0.524	0.841	0.854	0.69	24	χ^2_{10}	a2
0.325	0.142	0.131	0.332	0.315	0.3	24	χ^2_{10}	c2
0.744	0.554	0.558	0.762	0.758	0.3	249	χ^2_{10}	c2
1	1	1	1	1	0.69	249	χ^2_{10}	c2
0.563	0.359	0.362	0.572	0.578	0.3	249	χ^2_{10}	a2
0.644	0.369	0.369	0.634	0.633	0.3	249	χ^2_{10}	a2
0.793	0.558	0.555	0.798	0.793	0.3	249	χ^2_{10}	c2
1	1	1	1	1	0.3	249	χ^2_{10}	a2
1	1	1	1	1	0.69	249	χ^2_{10}	c2
0.996	0.982	0.982	0.995	0.994	0.69	249	χ^2_{10}	a2
1	1	1	1	1	0.69	249	χ^2_{10}	a2
0.906	0.758	0.754	0.911	0.914	0.3	249	χ^2_{10}	c2
0.291	0.084	0.095	0.269	0.278	0.3	16	χ^2_{10}	c2
0.724	0.486	0.49	0.746	0.738	0.69	16	χ^2_{10}	c2
0.238	0.069	0.084	0.207	0.223	0.3	16	χ^2_{10}	a2
0.213	0.064	0.076	0.188	0.198	0.3	16	χ^2_{10}	a2
0.283	0.096	0.103	0.288	0.285	0.3	16	χ^2_{10}	c2
0.491	0.118	0.121	0.492	0.486	0.3	16	χ^2_{10}	a2
0.932	0.839	0.842	0.939	0.945	0.69	16	χ^2_{10}	c2
0.486	0.23	0.264	0.462	0.48	0.69	16	χ^2_{10}	a2
0.931	0.61	0.668	0.917	0.93	0.69	16	χ^2_{10}	a2
0.293	0.132	0.113	0.315	0.289	0.3	16	χ^2_{10}	c2
0.787	0.594	0.595	0.789	0.79	0.3	166	χ^2_{10}	c2
1	1	1	1	1	0.69	166	χ^2_{10}	c2
0.563	0.356	0.353	0.581	0.585	0.3	166	χ^2_{10}	a2
0.628	0.343	0.346	0.613	0.616	0.3	166	χ^2_{10}	a2
0.842	0.629	0.629	0.838	0.839	0.3	166	χ^2_{10}	c2
1	0.999	1	1	1	0.3	166	χ^2_{10}	a2
1	1	1	1	1	0.69	166	χ^2_{10}	c2
0.997	0.978	0.981	0.997	0.997	0.69	166	χ^2_{10}	a2
1	1	1	1	1	0.69	166	χ^2_{10}	a2
0.956	0.853	0.846	0.959	0.957	0.3	166	χ^2_{10}	c2
0.263	0.089	0.1	0.255	0.261	0.3	24	normal	c2
0.717	0.488	0.493	0.709	0.712	0.69	24	normal	c2
0.222	0.057	0.064	0.191	0.202	0.3	24	normal	a2
0.203	0.071	0.082	0.185	0.194	0.3	24	normal	a2
0.272	0.107	0.107	0.259	0.262	0.3	24	normal	c2
0.376	0.078	0.076	0.38	0.37	0.3	24	normal	a2
0.887	0.759	0.75	0.895	0.9	0.69	24	normal	c2
0.481	0.226	0.264	0.474	0.486	0.69	24	normal	a2
0.851	0.508	0.524	0.841	0.854	0.69	24	normal	a2
0.325	0.142	0.131	0.332	0.315	0.3	24	normal	c2
0.744	0.554	0.558	0.762	0.758	0.3	249	normal	c2
1	1	1	1	1	0.69	249	normal	c2
0.563	0.359	0.362	0.572	0.578	0.3	249	normal	a2

0.644	0.369	0.369	0.634	0.633	0.3	249	normal	a2
0.793	0.558	0.555	0.798	0.793	0.3	249	normal	c2
1	1	1	1	1	0.3	249	normal	a2
1	1	1	1	1	0.69	249	normal	c2
0.996	0.982	0.982	0.995	0.994	0.69	249	normal	a2
1	1	1	1	1	0.69	249	normal	a2
0.906	0.758	0.754	0.911	0.914	0.3	249	normal	c2
0.291	0.084	0.095	0.269	0.278	0.3	16	normal	c2
0.724	0.486	0.49	0.746	0.738	0.69	16	normal	c2
0.238	0.069	0.084	0.207	0.223	0.3	16	normal	a2
0.213	0.064	0.076	0.188	0.198	0.3	16	normal	a2
0.283	0.096	0.103	0.288	0.285	0.3	16	normal	c2
0.491	0.118	0.121	0.492	0.486	0.3	16	normal	a2
0.932	0.839	0.842	0.939	0.945	0.69	16	normal	c2
0.486	0.23	0.264	0.462	0.48	0.69	16	normal	a2
0.931	0.61	0.668	0.917	0.93	0.69	16	normal	a2
0.293	0.132	0.113	0.315	0.289	0.3	16	normal	c2
0.787	0.594	0.595	0.789	0.79	0.3	166	normal	c2
1	1	1	1	1	0.69	166	normal	c2
0.563	0.356	0.353	0.581	0.585	0.3	166	normal	a2
0.628	0.343	0.346	0.613	0.616	0.3	166	normal	a2
0.842	0.629	0.629	0.838	0.839	0.3	166	normal	c2
1	0.999	1	1	1	0.3	166	normal	a2
1	1	1	1	1	0.69	166	normal	c2
0.997	0.978	0.981	0.997	0.997	0.69	166	normal	a2
1	1	1	1	1	0.69	166	normal	a2
0.956	0.853	0.846	0.959	0.957	0.3	166	normal	c2

Table 16: Power to exclude zero at the lower end of the confidence interval. Part C.

Univariate DEA UGS Bootstrap standard CI	Univariate DEA UGS Bootstrap BCa CI	Standard DEB .5 Bootstrap standard CI	Standard DEB .5 Bootstrap BCa CI	Standard DEB 1 Bootstrap standard CI	Population Parameter Value	MZ ns	Distribution	parameter
0.126	0.118	0.094	0.114	0.261	0.3	24	χ^2_1	c2
0.594	0.562	0.486	0.49	0.707	0.69	24	χ^2_1	c2
0.084	0.09	0.07	0.075	0.204	0.3	24	χ^2_1	a2
0.133	0.153	0.062	0.082	0.194	0.3	24	χ^2_1	a2
0.15	0.13	0.111	0.124	0.264	0.3	24	χ^2_1	c2
0.383	0.423	0.231	0.28	0.471	0.69	24	χ^2_1	a2
0.605	0.606	0.537	0.528	0.746	0.3	249	χ^2_1	c2
1	1	1	1	1	0.69	249	χ^2_1	c2
0.399	0.392	0.339	0.341	0.57	0.3	249	χ^2_1	a2
0.576	0.585	0.384	0.393	0.639	0.3	249	χ^2_1	a2
0.706	0.69	0.572	0.567	0.792	0.3	249	χ^2_1	c2
1	1	0.997	0.998	1	0.3	249	χ^2_1	a2
1	1	1	1	1	0.69	249	χ^2_1	c2
0.993	0.995	0.985	0.984	0.997	0.69	249	χ^2_1	a2
1	1	1	1	1	0.69	249	χ^2_1	a2
0.874	0.868	0.753	0.744	0.906	0.3	249	χ^2_1	c2
0.121	0.131	0.087	0.096	0.278	0.3	16	χ^2_1	c2
0.645	0.644	0.459	0.477	0.723	0.69	16	χ^2_1	c2
0.104	0.1	0.074	0.095	0.22	0.3	16	χ^2_1	a2
0.13	0.142	0.057	0.072	0.201	0.3	16	χ^2_1	a2
0.176	0.177	0.092	0.104	0.28	0.3	16	χ^2_1	c2
0.343	0.385	0.224	0.258	0.465	0.69	16	χ^2_1	a2
0.65	0.656	0.578	0.562	0.791	0.3	166	χ^2_1	c2
1	1	1	1	1	0.69	166	χ^2_1	c2
0.399	0.394	0.33	0.332	0.565	0.3	166	χ^2_1	a2
0.539	0.539	0.344	0.359	0.617	0.3	166	χ^2_1	a2
0.777	0.771	0.638	0.636	0.85	0.3	166	χ^2_1	c2
1	1	0.998	0.999	0.999	0.3	166	χ^2_1	a2
1	1	1	1	1	0.69	166	χ^2_1	c2
0.995	0.995	0.974	0.973	0.996	0.69	166	χ^2_1	a2
1	1	1	1	1	0.69	166	χ^2_1	a2
0.934	0.931	0.857	0.861	0.956	0.3	166	χ^2_1	c2
0.126	0.118	0.094	0.114	0.261	0.3	24	χ^2_{10}	c2
0.594	0.562	0.486	0.49	0.707	0.69	24	χ^2_{10}	c2
0.084	0.09	0.07	0.075	0.204	0.3	24	χ^2_{10}	a2
0.133	0.153	0.062	0.082	0.194	0.3	24	χ^2_{10}	a2
0.15	0.13	0.111	0.124	0.264	0.3	24	χ^2_{10}	c2
0.933	0.951	0.066	0.084	0.375	0.3	24	χ^2_{10}	a2
0.829	0.791	0.744	0.736	0.886	0.69	24	χ^2_{10}	c2

0.383	0.423	0.231	0.28	0.471	0.69	24	χ^2_{10}	a2
0.977	0.986	0.502	0.55	0.85	0.69	24	χ^2_{10}	a2
0.213	0.169	0.152	0.145	0.328	0.3	24	χ^2_{10}	c2
0.605	0.606	0.537	0.528	0.746	0.3	249	χ^2_{10}	c2
1	1	1	1	1	0.69	249	χ^2_{10}	c2
0.399	0.392	0.339	0.341	0.57	0.3	249	χ^2_{10}	a2
0.576	0.585	0.384	0.393	0.639	0.3	249	χ^2_{10}	a2
0.706	0.69	0.572	0.567	0.792	0.3	249	χ^2_{10}	c2
1	1	0.997	0.998	1	0.3	249	χ^2_{10}	a2
1	1	1	1	1	0.69	249	χ^2_{10}	c2
0.993	0.995	0.985	0.984	0.997	0.69	249	χ^2_{10}	a2
1	1	1	1	1	0.69	249	χ^2_{10}	a2
0.874	0.868	0.753	0.744	0.906	0.3	249	χ^2_{10}	c2
0.121	0.131	0.087	0.096	0.278	0.3	16	χ^2_{10}	c2
0.645	0.644	0.459	0.477	0.723	0.69	16	χ^2_{10}	c2
0.104	0.1	0.074	0.095	0.22	0.3	16	χ^2_{10}	a2
0.13	0.142	0.057	0.072	0.201	0.3	16	χ^2_{10}	a2
0.176	0.177	0.092	0.104	0.28	0.3	16	χ^2_{10}	c2
0.92	0.941	0.113	0.147	0.492	0.3	16	χ^2_{10}	a2
0.899	0.891	0.823	0.808	0.928	0.69	16	χ^2_{10}	c2
0.343	0.385	0.224	0.258	0.465	0.69	16	χ^2_{10}	a2
0.982	0.989	0.638	0.683	0.923	0.69	16	χ^2_{10}	a2
0.22	0.172	0.135	0.13	0.309	0.3	16	χ^2_{10}	c2
0.65	0.656	0.578	0.562	0.791	0.3	166	χ^2_{10}	c2
1	1	1	1	1	0.69	166	χ^2_{10}	c2
0.399	0.394	0.33	0.332	0.565	0.3	166	χ^2_{10}	a2
0.539	0.539	0.344	0.359	0.617	0.3	166	χ^2_{10}	a2
0.777	0.771	0.638	0.636	0.85	0.3	166	χ^2_{10}	c2
1	1	0.998	0.999	0.999	0.3	166	χ^2_{10}	a2
1	1	1	1	1	0.69	166	χ^2_{10}	c2
0.995	0.995	0.974	0.973	0.996	0.69	166	χ^2_{10}	a2
1	1	1	1	1	0.69	166	χ^2_{10}	a2
0.934	0.931	0.857	0.861	0.956	0.3	166	χ^2_{10}	c2
0.126	0.118	0.094	0.114	0.261	0.3	24	normal	c2
0.594	0.562	0.486	0.49	0.707	0.69	24	normal	c2
0.084	0.09	0.07	0.075	0.204	0.3	24	normal	a2
0.133	0.153	0.062	0.082	0.194	0.3	24	normal	a2
0.15	0.13	0.111	0.124	0.264	0.3	24	normal	c2
0.933	0.951	0.066	0.084	0.375	0.3	24	normal	a2
0.829	0.791	0.744	0.736	0.886	0.69	24	normal	c2
0.383	0.423	0.231	0.28	0.471	0.69	24	normal	a2
0.977	0.986	0.502	0.55	0.85	0.69	24	normal	a2
0.213	0.169	0.152	0.145	0.328	0.3	24	normal	c2
0.605	0.606	0.537	0.528	0.746	0.3	249	normal	c2
1	1	1	1	1	0.69	249	normal	c2
0.399	0.392	0.339	0.341	0.57	0.3	249	normal	a2

0.576	0.585	0.384	0.393	0.639	0.3	249	normal	a2
0.706	0.69	0.572	0.567	0.792	0.3	249	normal	c2
1	1	0.997	0.998	1	0.3	249	normal	a2
1	1	1	1	1	0.69	249	normal	c2
0.993	0.995	0.985	0.984	0.997	0.69	249	normal	a2
1	1	1	1	1	0.69	249	normal	a2
0.874	0.868	0.753	0.744	0.906	0.3	249	normal	c2
0.121	0.131	0.087	0.096	0.278	0.3	16	normal	c2
0.645	0.644	0.459	0.477	0.723	0.69	16	normal	c2
0.104	0.1	0.074	0.095	0.22	0.3	16	normal	a2
0.13	0.142	0.057	0.072	0.201	0.3	16	normal	a2
0.176	0.177	0.092	0.104	0.28	0.3	16	normal	c2
0.92	0.941	0.113	0.147	0.492	0.3	16	normal	a2
0.899	0.891	0.823	0.808	0.928	0.69	16	normal	c2
0.343	0.385	0.224	0.258	0.465	0.69	16	normal	a2
0.982	0.989	0.638	0.683	0.923	0.69	16	normal	a2
0.22	0.172	0.135	0.13	0.309	0.3	16	normal	c2
0.65	0.656	0.578	0.562	0.791	0.3	166	normal	c2
1	1	1	1	1	0.69	166	normal	c2
0.399	0.394	0.33	0.332	0.565	0.3	166	normal	a2
0.539	0.539	0.344	0.359	0.617	0.3	166	normal	a2
0.777	0.771	0.638	0.636	0.85	0.3	166	normal	c2
1	1	0.998	0.999	0.999	0.3	166	normal	a2
1	1	1	1	1	0.69	166	normal	c2
0.995	0.995	0.974	0.973	0.996	0.69	166	normal	a2
1	1	1	1	1	0.69	166	normal	a2
0.934	0.931	0.857	0.861	0.956	0.3	166	normal	c2

Table 17: Power to exclude zero at the lower end of the confidence interval. Part D.

Standard DEA Bootstrap standard CI	Standard DEA Bootstrap BCa CI	Univariate DEA WGS Bootstrap standard CI	Univariate DEA WGS Bootstrap BCa CI	Univariate DEA UGS Bootstrap standard CI	Population Parameter Value	MZ ns	Distribution	parameter
0.12	0.128	0.134	0.136	0.126	0.3	24	χ^2_1	c2
0.577	0.575	0.616	0.589	0.594	0.69	24	χ^2_1	c2
0.099	0.11	0.082	0.098	0.084	0.3	24	χ^2_1	a2
0.135	0.153	0.143	0.158	0.133	0.3	24	χ^2_1	a2
0.153	0.158	0.151	0.143	0.15	0.3	24	χ^2_1	c2
0.382	0.407	0.412	0.432	0.383	0.69	24	χ^2_1	a2
0.559	0.553	0.609	0.613	0.605	0.3	249	χ^2_1	c2
1	1	1	1	1	0.69	249	χ^2_1	c2
0.356	0.361	0.403	0.407	0.399	0.3	249	χ^2_1	a2
0.524	0.534	0.573	0.582	0.576	0.3	249	χ^2_1	a2
0.627	0.614	0.709	0.698	0.706	0.3	249	χ^2_1	c2
1	1	1	1	1	0.3	249	χ^2_1	a2
1	1	1	1	1	0.69	249	χ^2_1	c2
0.989	0.989	0.993	0.996	0.993	0.69	249	χ^2_1	a2
1	1	1	1	1	0.69	249	χ^2_1	a2
0.831	0.832	0.874	0.879	0.874	0.3	249	χ^2_1	c2
0.12	0.14	0.121	0.143	0.121	0.3	16	χ^2_1	c2
0.607	0.602	0.653	0.652	0.645	0.69	16	χ^2_1	c2
0.102	0.115	0.101	0.114	0.104	0.3	16	χ^2_1	a2
0.138	0.159	0.142	0.152	0.13	0.3	16	χ^2_1	a2
0.162	0.17	0.178	0.183	0.176	0.3	16	χ^2_1	c2
0.354	0.383	0.375	0.395	0.343	0.69	16	χ^2_1	a2
0.605	0.614	0.653	0.648	0.65	0.3	166	χ^2_1	c2
1	1	1	1	1	0.69	166	χ^2_1	c2
0.353	0.356	0.395	0.387	0.399	0.3	166	χ^2_1	a2
0.485	0.484	0.554	0.551	0.539	0.3	166	χ^2_1	a2
0.731	0.72	0.774	0.773	0.777	0.3	166	χ^2_1	c2
1	1	1	1	1	0.3	166	χ^2_1	a2
1	1	1	1	1	0.69	166	χ^2_1	c2
0.991	0.991	0.995	0.995	0.995	0.69	166	χ^2_1	a2
1	1	1	1	1	0.69	166	χ^2_1	a2
0.909	0.909	0.936	0.94	0.934	0.3	166	χ^2_1	c2
0.12	0.128	0.134	0.136	0.126	0.3	24	χ^2_{10}	c2
0.577	0.575	0.616	0.589	0.594	0.69	24	χ^2_{10}	c2
0.099	0.11	0.082	0.098	0.084	0.3	24	χ^2_{10}	a2
0.135	0.153	0.143	0.158	0.133	0.3	24	χ^2_{10}	a2
0.153	0.158	0.151	0.143	0.15	0.3	24	χ^2_{10}	c2
0.904	0.904	0.948	0.951	0.933	0.3	24	χ^2_{10}	a2
0.797	0.796	0.836	0.845	0.829	0.69	24	χ^2_{10}	c2

0.382	0.407	0.412	0.432	0.383	0.69	24	χ^2_{10}	a2
0.974	0.972	0.984	0.986	0.977	0.69	24	χ^2_{10}	a2
0.216	0.216	0.218	0.222	0.213	0.3	24	χ^2_{10}	c2
0.559	0.553	0.609	0.613	0.605	0.3	249	χ^2_{10}	c2
1	1	1	1	1	0.69	249	χ^2_{10}	c2
0.356	0.361	0.403	0.407	0.399	0.3	249	χ^2_{10}	a2
0.524	0.534	0.573	0.582	0.576	0.3	249	χ^2_{10}	a2
0.627	0.614	0.709	0.698	0.706	0.3	249	χ^2_{10}	c2
1	1	1	1	1	0.3	249	χ^2_{10}	a2
1	1	1	1	1	0.69	249	χ^2_{10}	c2
0.989	0.989	0.993	0.996	0.993	0.69	249	χ^2_{10}	a2
1	1	1	1	1	0.69	249	χ^2_{10}	a2
0.831	0.832	0.874	0.879	0.874	0.3	249	χ^2_{10}	c2
0.12	0.14	0.121	0.143	0.121	0.3	16	χ^2_{10}	c2
0.607	0.602	0.653	0.652	0.645	0.69	16	χ^2_{10}	c2
0.102	0.115	0.101	0.114	0.104	0.3	16	χ^2_{10}	a2
0.138	0.159	0.142	0.152	0.13	0.3	16	χ^2_{10}	a2
0.162	0.17	0.178	0.183	0.176	0.3	16	χ^2_{10}	c2
0.891	0.886	0.937	0.944	0.92	0.3	16	χ^2_{10}	a2
0.858	0.859	0.903	0.908	0.899	0.69	16	χ^2_{10}	c2
0.354	0.383	0.375	0.395	0.343	0.69	16	χ^2_{10}	a2
0.974	0.975	0.989	0.991	0.982	0.69	16	χ^2_{10}	a2
0.177	0.195	0.208	0.204	0.22	0.3	16	χ^2_{10}	c2
0.605	0.614	0.653	0.648	0.65	0.3	166	χ^2_{10}	c2
1	1	1	1	1	0.69	166	χ^2_{10}	c2
0.353	0.356	0.395	0.387	0.399	0.3	166	χ^2_{10}	a2
0.485	0.484	0.554	0.551	0.539	0.3	166	χ^2_{10}	a2
0.731	0.72	0.774	0.773	0.777	0.3	166	χ^2_{10}	c2
1	1	1	1	1	0.3	166	χ^2_{10}	a2
1	1	1	1	1	0.69	166	χ^2_{10}	c2
0.991	0.991	0.995	0.995	0.995	0.69	166	χ^2_{10}	a2
1	1	1	1	1	0.69	166	χ^2_{10}	a2
0.909	0.909	0.936	0.94	0.934	0.3	166	χ^2_{10}	c2
0.12	0.128	0.134	0.136	0.126	0.3	24	normal	c2
0.577	0.575	0.616	0.589	0.594	0.69	24	normal	c2
0.099	0.11	0.082	0.098	0.084	0.3	24	normal	a2
0.135	0.153	0.143	0.158	0.133	0.3	24	normal	a2
0.153	0.158	0.151	0.143	0.15	0.3	24	normal	c2
0.904	0.904	0.948	0.951	0.933	0.3	24	normal	a2
0.797	0.796	0.836	0.845	0.829	0.69	24	normal	c2
0.382	0.407	0.412	0.432	0.383	0.69	24	normal	a2
0.974	0.972	0.984	0.986	0.977	0.69	24	normal	a2
0.216	0.216	0.218	0.222	0.213	0.3	24	normal	c2
0.559	0.553	0.609	0.613	0.605	0.3	249	normal	c2
1	1	1	1	1	0.69	249	normal	c2
0.356	0.361	0.403	0.407	0.399	0.3	249	normal	a2

0.524	0.534	0.573	0.582	0.576	0.3	249	normal	a2
0.627	0.614	0.709	0.698	0.706	0.3	249	normal	c2
1	1	1	1	1	0.3	249	normal	a2
1	1	1	1	1	0.69	249	normal	c2
0.989	0.989	0.993	0.996	0.993	0.69	249	normal	a2
1	1	1	1	1	0.69	249	normal	a2
0.831	0.832	0.874	0.879	0.874	0.3	249	normal	c2
0.12	0.14	0.121	0.143	0.121	0.3	16	normal	c2
0.607	0.602	0.653	0.652	0.645	0.69	16	normal	c2
0.102	0.115	0.101	0.114	0.104	0.3	16	normal	a2
0.138	0.159	0.142	0.152	0.13	0.3	16	normal	a2
0.162	0.17	0.178	0.183	0.176	0.3	16	normal	c2
0.891	0.886	0.937	0.944	0.92	0.3	16	normal	a2
0.858	0.859	0.903	0.908	0.899	0.69	16	normal	c2
0.354	0.383	0.375	0.395	0.343	0.69	16	normal	a2
0.974	0.975	0.989	0.991	0.982	0.69	16	normal	a2
0.177	0.195	0.208	0.204	0.22	0.3	16	normal	c2
0.605	0.614	0.653	0.648	0.65	0.3	166	normal	c2
1	1	1	1	1	0.69	166	normal	c2
0.353	0.356	0.395	0.387	0.399	0.3	166	normal	a2
0.485	0.484	0.554	0.551	0.539	0.3	166	normal	a2
0.731	0.72	0.774	0.773	0.777	0.3	166	normal	c2
1	1	1	1	1	0.3	166	normal	a2
1	1	1	1	1	0.69	166	normal	c2
0.991	0.991	0.995	0.995	0.995	0.69	166	normal	a2
1	1	1	1	1	0.69	166	normal	a2
0.909	0.909	0.936	0.94	0.934	0.3	166	normal	c2

Table 18: Power to exclude zero at the lower end of the confidence interval. Part E.

Robust Upper CI	Typical Upper CI	Population Parameter Value	MZ ns	Distribution	parameter
0.177	0.254	0.3	24	χ_1^2	c2
0.671	0.742	0.69	24	χ_1^2	c2
0.118	0.194	0.3	24	χ_1^2	a2
0.15	0.209	0.3	24	χ_1^2	a2
0.221	0.295	0.3	24	χ_1^2	c2
0.405	0.49	0.69	24	χ_1^2	a2
0.568	0.777	0.3	249	χ_1^2	c2
1	1	0.69	249	χ_1^2	c2
0.36	0.601	0.3	249	χ_1^2	a2
0.516	0.73	0.3	249	χ_1^2	a2
0.655	0.853	0.3	249	χ_1^2	c2
1	1	0.3	249	χ_1^2	a2
1	1	0.69	249	χ_1^2	c2
0.989	0.997	0.69	249	χ_1^2	a2
1	1	0.69	249	χ_1^2	a2
0.855	0.977	0.3	249	χ_1^2	c2
0.151	0.265	0.3	16	χ_1^2	c2
0.685	0.75	0.69	16	χ_1^2	c2
0.146	0.201	0.3	16	χ_1^2	a2
0.175	0.181	0.3	16	χ_1^2	a2
0.221	0.288	0.3	16	χ_1^2	c2
0.408	0.423	0.69	16	χ_1^2	a2
0.612	0.826	0.3	166	χ_1^2	c2
1	1	0.69	166	χ_1^2	c2
0.357	0.598	0.3	166	χ_1^2	a2
0.496	0.68	0.3	166	χ_1^2	a2
0.741	0.882	0.3	166	χ_1^2	c2
1	1	0.3	166	χ_1^2	a2
1	1	0.69	166	χ_1^2	c2
0.989	0.998	0.69	166	χ_1^2	a2
1	1	0.69	166	χ_1^2	a2
0.928	0.975	0.3	166	χ_1^2	c2
0.177	0.254	0.3	24	χ_{10}^2	c2
0.671	0.742	0.69	24	χ_{10}^2	c2
0.118	0.194	0.3	24	χ_{10}^2	a2
0.15	0.209	0.3	24	χ_{10}^2	a2
0.221	0.295	0.3	24	χ_{10}^2	c2
0.643	0.403	0.3	24	χ_{10}^2	a2
0.881	0.944	0.69	24	χ_{10}^2	c2
0.405	0.49	0.69	24	χ_{10}^2	a2
0.922	0.873	0.69	24	χ_{10}^2	a2

0.333	0.44	0.3	24	χ^2_{10}	c2
0.568	0.777	0.3	249	χ^2_{10}	c2
1	1	0.69	249	χ^2_{10}	c2
0.36	0.601	0.3	249	χ^2_{10}	a2
0.516	0.73	0.3	249	χ^2_{10}	a2
0.655	0.853	0.3	249	χ^2_{10}	c2
1	1	0.3	249	χ^2_{10}	a2
1	1	0.69	249	χ^2_{10}	c2
0.989	0.997	0.69	249	χ^2_{10}	a2
1	1	0.69	249	χ^2_{10}	a2
0.855	0.977	0.3	249	χ^2_{10}	c2
0.151	0.265	0.3	16	χ^2_{10}	c2
0.685	0.75	0.69	16	χ^2_{10}	c2
0.146	0.201	0.3	16	χ^2_{10}	a2
0.175	0.181	0.3	16	χ^2_{10}	a2
0.221	0.288	0.3	16	χ^2_{10}	c2
0.754	0.224	0.3	16	χ^2_{10}	a2
0.912	0.953	0.69	16	χ^2_{10}	c2
0.408	0.423	0.69	16	χ^2_{10}	a2
0.958	0.757	0.69	16	χ^2_{10}	a2
0.315	0.336	0.3	16	χ^2_{10}	c2
0.612	0.826	0.3	166	χ^2_{10}	c2
1	1	0.69	166	χ^2_{10}	c2
0.357	0.598	0.3	166	χ^2_{10}	a2
0.496	0.68	0.3	166	χ^2_{10}	a2
0.741	0.882	0.3	166	χ^2_{10}	c2
1	1	0.3	166	χ^2_{10}	a2
1	1	0.69	166	χ^2_{10}	c2
0.989	0.998	0.69	166	χ^2_{10}	a2
1	1	0.69	166	χ^2_{10}	a2
0.928	0.975	0.3	166	χ^2_{10}	c2
0.177	0.254	0.3	24	normal	c2
0.671	0.742	0.69	24	normal	c2
0.118	0.194	0.3	24	normal	a2
0.15	0.209	0.3	24	normal	a2
0.221	0.295	0.3	24	normal	c2
0.643	0.403	0.3	24	normal	a2
0.881	0.944	0.69	24	normal	c2
0.405	0.49	0.69	24	normal	a2
0.922	0.873	0.69	24	normal	a2
0.333	0.44	0.3	24	normal	c2
0.568	0.777	0.3	249	normal	c2
1	1	0.69	249	normal	c2
0.36	0.601	0.3	249	normal	a2
0.516	0.73	0.3	249	normal	a2
0.655	0.853	0.3	249	normal	c2

1	1	0.3	249	normal	a2
1	1	0.69	249	normal	c2
0.989	0.997	0.69	249	normal	a2
1	1	0.69	249	normal	a2
0.855	0.977	0.3	249	normal	c2
0.151	0.265	0.3	16	normal	c2
0.685	0.75	0.69	16	normal	c2
0.146	0.201	0.3	16	normal	a2
0.175	0.181	0.3	16	normal	a2
0.221	0.288	0.3	16	normal	c2
0.754	0.224	0.3	16	normal	a2
0.912	0.953	0.69	16	normal	c2
0.408	0.423	0.69	16	normal	a2
0.958	0.757	0.69	16	normal	a2
0.315	0.336	0.3	16	normal	c2
0.612	0.826	0.3	166	normal	c2
1	1	0.69	166	normal	c2
0.357	0.598	0.3	166	normal	a2
0.496	0.68	0.3	166	normal	a2
0.741	0.882	0.3	166	normal	c2
1	1	0.3	166	normal	a2
1	1	0.69	166	normal	c2
0.989	0.998	0.69	166	normal	a2
1	1	0.69	166	normal	a2
0.928	0.975	0.3	166	normal	c2