

WALD TYPE TESTS WITH THE WRONG DISPERSION MATRIX

by

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M.Sc., Southern Illinois University Carbondale, 2017

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A Dissertation

Submitted in Partial Fulfillment of the Requirements for the
Doctor of Philosophy Degree

Department of Mathematics
in the Graduate School
Southern Illinois University Carbondale
August, 2021

DISSERTATION APPROVAL

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June 18, 2021

AN ABSTRACT OF THE DISSERTATION OF

KOSMAN W.G.D.H. RAJAPAKSHA, for the Doctor of Philosophy degree in Mathematics, presented on June 18, 2021, at Southern Illinois University Carbondale.

TITLE: Wald Type Tests With the Wrong Dispersion Matrix

MAJOR PROFESSOR: Dr. David Olive

A Wald type test with the wrong dispersion matrix is used when the dispersion matrix is not a consistent estimator of the asymptotic covariance matrix of the test statistic. One class of such tests occurs when there are k groups and it is assumed that the population covariance matrices from the k groups are equal, but the common covariance matrix assumption does not hold. The pooled t test, one way AVOVA F test, and one way MANOVA F test are examples of this class. Two bootstrap confidence regions are modified to obtain large sample Wald type tests with the wrong dispersion matrix.

KEY WORDS: ANOVA, bootstrap, MANOVA, regularized covariance matrix estimator.

ACKNOWLEDGMENTS

I would first like to express my gratitude to my thesis adviser Dr. D. Olive at Southern Illinois University. Prof. D. Olive was helpful throughout my Master's and Ph.D. research work. Without his guidance and persistent help this dissertation would not been possible.

Also, I would like to thank Dr. Bhattacharya, Dr. Hughes, Dr. McSorley, and Dr. Jayasekara not only for serving as my committee members, but also they had important impact to develop my Statistical and Mathematical knowledge by several courses I had with them. I would like to thank Dr. Kanthi Perera who did encourage me to get into the higher studies.

Finally, I would like to thank my family mother, father, brother and specially my wife who gave me support and encouraged me to do my work.

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CHAPTER 1

INTRODUCTION

Consider testing $H_0 : \boldsymbol{\theta} = \boldsymbol{\theta}_0$ versus $H_1 : \boldsymbol{\theta} \neq \boldsymbol{\theta}_0$ where a $g \times 1$ statistic T_n satisfies $\sqrt{n}(T_n - \boldsymbol{\theta}) \xrightarrow{D} \mathbf{u} \sim N_g(\mathbf{0}, \boldsymbol{\Sigma})$. If $\hat{\boldsymbol{\Sigma}}^{-1} \xrightarrow{P} \boldsymbol{\Sigma}^{-1}$ and H_0 is true, then

$$D_n^2 = D_n^2(\hat{\boldsymbol{\Sigma}}) = D_{\boldsymbol{\theta}_0}^2(T_n, \hat{\boldsymbol{\Sigma}}/n) = n(T_n - \boldsymbol{\theta}_0)^T \hat{\boldsymbol{\Sigma}}^{-1} (T_n - \boldsymbol{\theta}_0) \xrightarrow{D} \mathbf{u}^T \boldsymbol{\Sigma}^{-1} \mathbf{u} \sim \chi_g^2$$

as $n \rightarrow \infty$. Then a Wald type test rejects H_0 if $D_n^2 > \chi_{g,1-\delta}^2$ where $P(X \leq \chi_{g,1-\delta}^2) = 1 - \delta$ if $X \sim \chi_g^2$, a chi-square distribution with g degrees of freedom. Note that $D_{\boldsymbol{\theta}_0}^2(T_n, \hat{\boldsymbol{\Sigma}}/n)$ is a squared Mahalanobis distance.

It is common to implement a Wald type test using

$$D_n^2 = D_n^2(\mathbf{C}_n) = D_{\boldsymbol{\theta}_0}^2(T_n, \mathbf{C}_n/n) = n(T_n - \boldsymbol{\theta}_0)^T \mathbf{C}_n^{-1} (T_n - \boldsymbol{\theta}_0) \xrightarrow{D} \mathbf{u}^T \mathbf{C}^{-1} \mathbf{u}$$

as $n \rightarrow \infty$ if H_0 is true, where the $g \times g$ symmetric positive definite matrix $\mathbf{C}_n \xrightarrow{P} \mathbf{C} \neq \boldsymbol{\Sigma}$. Hence \mathbf{C}_n is the wrong dispersion matrix, and $\mathbf{u}^T \mathbf{C}^{-1} \mathbf{u}$ does not have a χ_g^2 distribution when H_0 is true. Often \mathbf{C}_n is a regularized estimator of $\boldsymbol{\Sigma}$, or \mathbf{C}_n^{-1} is a regularized estimator of the precision matrix $\boldsymbol{\Sigma}^{-1}$, such as $\mathbf{C}_n = \mathbf{I}_g$ or $\mathbf{C}_n = \text{diag}(\hat{\boldsymbol{\Sigma}})$. Another example is $\mathbf{C}_n = \mathbf{S}_p$ where \mathbf{S}_p is a pooled covariance matrix, and it is assumed that k groups have the same covariance matrix $\boldsymbol{\Sigma}$. When this assumption is violated, \mathbf{C}_n is not a consistent estimator of $\boldsymbol{\Sigma}$. When the bootstrap is used, often $\mathbf{C}_n = n\mathbf{S}_T^*$ where \mathbf{S}_T^* is the sample covariance matrix of the bootstrap sample T_1^*, \dots, T_B^* . The assumption that $n\mathbf{S}_T^*$ is a consistent estimator of $\boldsymbol{\Sigma}$ is strong. See, for example, Machado and Parente (2005).

Some examples include the pooled t test and one way ANOVA test. Rupasinghe Arachchige Don and Pelawa Watagoda (2018) and Rupasinghe Arachchige Don and Olive (2019) gave Wald type tests for analogs of the two sample Hotelling's T^2 and one way MANOVA tests using a consistent estimator $\hat{\boldsymbol{\Sigma}}$ of $\boldsymbol{\Sigma}$. These tests could greatly outperform the classical tests that used the pooled covariance matrix when the sample sizes were

large enough to give good estimates of the covariance matrix of each group, but for small sample sizes, the classical tests (with the wrong dispersion matrix) often did better in the simulations.

If $\sqrt{n}(T_n - \boldsymbol{\theta}) \xrightarrow{D} \mathbf{u}$ and $\sqrt{n}(T_n^* - T_n) \xrightarrow{D} \mathbf{u}$, then the percentiles of $n(T_n - \boldsymbol{\theta}_0)^T \mathbf{C}_n^{-1}(T_n - \boldsymbol{\theta}_0)$ can be estimated with the sample percentiles of $n(T_n^* - T_n)^T \mathbf{C}_n^{-1}(T_n^* - T_n)$. Section 2 shows how to use this idea with bootstrap confidence regions. Sections 3 and 4 review large sample theory for one way MANOVA type tests, while Sections 5 to 11 illustrate special cases. Section 12 considers weighted least squares.

CHAPTER 2

THE BOOTSTRAP

This section follows Olive (2020, ch. 2) closely. There are several methods for obtaining a bootstrap sample T_1^*, \dots, T_B^* where the sample size n is suppressed: $T_i^* = T_{in}^*$. The nonparametric bootstrap will be discussed in this section. The wild bootstrap is discussed in Section 12.

When $g = 1$, a confidence interval (CI) is a special case of a confidence region. We often want the probability to converge to $1 - \delta$ if the confidence interval is based on a statistic with an asymptotic distribution that has a probability density function.

Definition 2.1. The interval $[L_n, U_n]$ is a large sample $100(1 - \delta)\%$ *confidence interval* for θ if $P(L_n \leq \theta \leq U_n)$ is eventually bounded below by $1 - \delta$ as $n \rightarrow \infty$.

If the data are Z_1, \dots, Z_n , let $Z_{(1)} \leq \dots \leq Z_{(n)}$ be the order statistics. Let $[x]$ denote the smallest integer greater than or equal to x (e.g., $[7.7] = 8$). Consider intervals that contain c cases $[Z_{(1)}, Z_{(c)}], [Z_{(2)}, Z_{(c+1)}], \dots, [Z_{(n-c+1)}, Z_{(n)}]$. Compute $Z_{(c)} - Z_{(1)}, Z_{(c+1)} - Z_{(2)}, \dots, Z_{(n)} - Z_{(n-c+1)}$. Then the estimator $\text{shorth}(c) = [Z_{(s)}, Z_{(s+c-1)}]$ is the interval with the shortest length.

Example 2.1. Given below were votes for preseason 1A basketball poll from Nov. 22, 2011 WSIL News where the 778 was a typo: the actual value was 78. As shown below, finding $\text{shorth}(3)$ from the ordered data is simple. If the outlier was corrected, $\text{shorth}(3) = [76, 78]$.

111 89 778 78 76

order data: 76 78 89 111 778

$$13 = 89 - 76$$

$$33 = 111 - 78$$

$$689 = 778 - 89$$

`shorth(3) = [76,89]`

Next we discuss two bootstrap confidence intervals (2.1) and (2.2) that are obtained by applying prediction intervals to the bootstrap sample. Two additional bootstrap CIs are obtained from bootstrap confidence regions from Section 2.2 when $g = 1$. See Efron (1982) and Chen (2016) for the percentile CI. Let T_n be an estimator of a parameter θ such as $T_n = \bar{Z} = \sum_{i=1}^n Z_i/n$ with $\theta = E(Z_1)$. Let T_1^*, \dots, T_B^* be a bootstrap sample for T_n . Let $T_{(1)}^*, \dots, T_{(B)}^*$ be the order statistics of the bootstrap sample.

Definition 2.2. The bootstrap large sample $100(1 - \delta)\%$ percentile confidence interval for θ is an interval $[T_{(k_L)}^*, T_{(K_U)}^*]$ containing $\approx [B(1 - \delta)]$ of the T_i^* . Let $k_1 = [B\delta/2]$ and $k_2 = [B(1 - \delta/2)]$. A common choice is

$$[T_{(k_1)}^*, T_{(k_2)}^*]. \quad (2.1)$$

Definition 2.3. The large sample $100(1 - \delta)\%$ *shorth(c) CI*

$$[T_{(s)}^*, T_{(s+c-1)}^*] \quad (2.2)$$

uses the interval $[T_{(1)}^*, T_{(c)}^*], [T_{(2)}^*, T_{(c+1)}^*], \dots, [T_{(B-c+1)}^*, T_{(B)}^*]$ of shortest length. Here

$$c = \min(B, [B[1 - \delta + 1.12\sqrt{\delta/B}]]). \quad (2.3)$$

The shorth CI is obtained by applying the Frey (2013) prediction interval to the bootstrap sample. The shorth CI is the shortest percentile CI covering c_n cases, and the shorth CI can be regarded as the shortest large sample $100(1 - \delta)\%$ percentile CI, asymptotically. Hence the shorth confidence interval is a practical implementation of the Hall (1988) shortest bootstrap interval based on all possible bootstrap samples. See Remark 2.1 for some theory for bootstrap CIs such as (2.1) and (2.2). Olive (2014: p. 283, 2017b: p. 168, 2018) recommended using the shorth CI for the percentile CI.

2.1 THE NONPARAMETRIC BOOTSTRAP

This subsection illustrates the nonparametric bootstrap with some examples. Suppose a statistic $T_n = t(Y_1, \dots, Y_n)$ is computed from a data set with n cases. The nonparametric bootstrap draws a sample of n cases $Y_{11}^*, \dots, Y_{1n}^*$ with replacement from that data set. Then $T_1^* = t(Y_{11}^*, \dots, Y_{1n}^*)$ is the statistic T_n computed from the sample. This process is repeated B times to produce the bootstrap sample T_1^*, \dots, T_B^* . Sampling cases with replacement uses the empirical distribution.

Definition 2.4. Suppose that data $\mathbf{x}_1, \dots, \mathbf{x}_n$ has been collected and observed. Often the \mathbf{x}_i are independent and identically distributed (iid) from a distribution with cumulative distribution function (cdf) F . The *empirical distribution* is a discrete distribution where the \mathbf{x}_i are the possible values, and each value is equally likely. If \mathbf{w} is a random variable having the empirical distribution, then $p_i = P(\mathbf{w} = \mathbf{x}_i) = 1/n$ for $i = 1, \dots, n$. The *cdf of the empirical distribution* is denoted by F_n .

Example 2.2. Let \mathbf{w} be a random variable having the empirical distribution given by Definition 2.4. Show that $E(\mathbf{w}) = \bar{\mathbf{x}} \equiv \bar{\mathbf{x}}_n$ and $\text{Cov}(\mathbf{w}) = \frac{n-1}{n} \mathbf{S} \equiv \frac{n-1}{n} \mathbf{S}_n$.

Solution: Recall that for a discrete random vector, the population expected value $E(\mathbf{w}) = \sum \mathbf{x}_i p_i$ where \mathbf{x}_i are the values that \mathbf{w} takes with positive probability p_i . Similarly, the population covariance matrix

$$\text{Cov}(\mathbf{w}) = E[(\mathbf{w} - E(\mathbf{w}))(\mathbf{w} - E(\mathbf{w}))^T] = \sum (\mathbf{x}_i - E(\mathbf{w}))(\mathbf{x}_i - E(\mathbf{w}))^T p_i.$$

Hence

$$E(\mathbf{w}) = \sum_{i=1}^n \mathbf{x}_i \frac{1}{n} = \bar{\mathbf{x}},$$

and

$$\text{Cov}(\mathbf{w}) = \sum_{i=1}^n (\mathbf{x}_i - \bar{\mathbf{x}})(\mathbf{x}_i - \bar{\mathbf{x}})^T \frac{1}{n} = \frac{n-1}{n} \mathbf{S}. \quad \square$$

Example 2.3. If W_1, \dots, W_n are iid from a distribution with cdf F_W , then the empirical cdf F_n corresponding to F_W is given by

$$F_n(y) = \frac{1}{n} \sum_{i=1}^n I(W_i \leq y)$$

where the indicator $I(W_i \leq y) = 1$ if $W_i \leq y$ and $I(W_i \leq y) = 0$ if $W_i > y$. Fix n and y . Then $nF_n(y) \sim \text{binomial}(n, F_W(y))$. Thus $E[F_n(y)] = F_W(y)$ and $V[F_n(y)] = F_W(y)[1 - F_W(y)]/n$. By the central limit theorem,

$$\sqrt{n}(F_n(y) - F_W(y)) \xrightarrow{D} N(0, F_W(y)[1 - F_W(y)]).$$

Thus $F_n(y) - F_W(y) = O_P(n^{-1/2})$, and F_n is a reasonable estimator of F_W if the sample size n is large.

Suppose there is data $\mathbf{w}_1, \dots, \mathbf{w}_n$ collected into an $n \times p$ matrix \mathbf{W} . Let the statistic $T_n = t(\mathbf{W}) = T(F_n)$ be computed from the data. Suppose the statistic estimates $\boldsymbol{\mu} = T(F)$, and let $t(\mathbf{W}^*) = t(F_n^*) = T_n^*$ indicate that t was computed from an iid sample from the empirical distribution F_n : a sample $\mathbf{w}_1^*, \dots, \mathbf{w}_n^*$ of size n was drawn with replacement from the observed sample $\mathbf{w}_1, \dots, \mathbf{w}_n$. This notation is used for von Mises differentiable statistical functions in large sample theory. See Serfling (1980, ch. 6). The *nonparametric bootstrap* draws B samples of size n from the rows of \mathbf{W} , e.g. from the empirical distribution of $\mathbf{w}_1, \dots, \mathbf{w}_n$. Then $T_{j_n}^*$ is computed from the j th sample for $j = 1, \dots, B$.

Example 2.4. Suppose the data is 1, 2, 3, 4, 5, 6, 7. Then $n = 7$ and the sample median T_n is 4. Using R , we drew $B = 2$ samples (of size n drawn with replacement from the original data) and computed the sample median $T_{1,n}^* = 3$ and $T_{2,n}^* = 4$.

```
b1 <- sample(1:7,replace=T)
```

```
b1
```

```
[1] 3 2 3 2 5 2 6
```

```
median(b1)
```

```
[1] 3
```

```
b2 <- sample(1:7,replace=T)
```

```
b2
```

```
[1] 3 5 3 4 3 5 7
```

median(b2)

[1] 4

The bootstrap has been widely used to estimate the population covariance matrix of the statistic $\text{Cov}(T_n)$, for testing hypotheses, and for obtaining confidence regions (often confidence intervals). An iid sample T_{1n}, \dots, T_{Bn} of size B of the statistic would be very useful for inference, but typically we only have one sample of data and one value $T_n = T_{1n}$ of the statistic, where n is often suppressed. Often $T_n = t(\mathbf{w}_1, \dots, \mathbf{w}_n)$, and the bootstrap sample $T_{1n}^*, \dots, T_{Bn}^*$ is formed where $T_{jn}^* = t(\mathbf{w}_{j1}^*, \dots, \mathbf{w}_{jn}^*)$. Note that $T_{1n}^* - T_n, \dots, T_{Bn}^* - T_n$ is pseudodata for $T_{1n} - \boldsymbol{\theta}, \dots, T_{Bn} - \boldsymbol{\theta}$ when n is large if $\sqrt{n}(T_n - \boldsymbol{\theta}) \xrightarrow{D} \mathbf{u}$ and $\sqrt{n}(T_n^* - T_n) \xrightarrow{D} \mathbf{u}$.

Suppose there is a statistic T_n that is a $g \times 1$ vector. Let

$$\bar{T}^* = \frac{1}{B} \sum_{i=1}^B T_i^* \quad \text{and} \quad \mathbf{S}_T^* = \frac{1}{B-1} \sum_{i=1}^B (T_i^* - \bar{T}^*)(T_i^* - \bar{T}^*)^T \quad (2.4)$$

be the sample mean and sample covariance matrix of the bootstrap sample T_1^*, \dots, T_B^* where $T_i^* = T_{i,n}^*$.

2.2 BOOTSTRAP CONFIDENCE REGION

Consider testing $H_0 : \boldsymbol{\theta} = \boldsymbol{\theta}_0$ versus $H_1 : \boldsymbol{\theta} \neq \boldsymbol{\theta}_0$ where $\boldsymbol{\theta}_0$ is a known $g \times 1$ vector. Then a large sample $100(1 - \delta)\%$ confidence region for $\boldsymbol{\theta}$ is a set \mathcal{A}_n such that $P(\boldsymbol{\theta} \in \mathcal{A}_n)$ is eventually bounded below by $1 - \delta$ as the sample size $n \rightarrow \infty$. Then reject H_0 if $\boldsymbol{\theta}_0$ is not in the confidence region \mathcal{A}_n .

For a confidence region, let the $g \times 1$ vector T_n be an estimator of the $g \times 1$ parameter vector $\boldsymbol{\theta}$. Let T_1^*, \dots, T_B^* be the bootstrap sample for T_n . Let \mathbf{A} be a full rank $g \times q$ constant matrix where $g \leq q$, and consider testing $H_0 : \mathbf{A}\boldsymbol{\mu} = \boldsymbol{\theta}_0$ versus $H_1 : \mathbf{A}\boldsymbol{\mu} \neq \boldsymbol{\theta}_0$ with $\boldsymbol{\theta} = \mathbf{A}\boldsymbol{\mu}$ where often $\boldsymbol{\theta}_0 = \mathbf{0}$. Then let $T_n = \mathbf{A}\hat{\boldsymbol{\mu}}$ and let $T_i^* = \mathbf{A}\hat{\boldsymbol{\mu}}^*$ for $i = 1, \dots, B$.

To bootstrap a confidence region, Mahalanobis distances will be useful. Let the $g \times 1$ column vector T be a multivariate location estimator, and let the $g \times g$ symmetric positive

definite matrix \mathbf{C} be a dispersion estimator. Then the i th *squared sample Mahalanobis distance* is the scalar

$$D_i^2 = D_i^2(T, \mathbf{C}) = D_{\mathbf{z}_i}^2(T, \mathbf{C}) = (\mathbf{z}_i - T)^T \mathbf{C}^{-1} (\mathbf{z}_i - T) \quad (2.5)$$

for each observation \mathbf{z}_i . Notice that the Euclidean distance of \mathbf{z}_i from the estimate of center T is $D_i(T, \mathbf{I}_g)$ where \mathbf{I}_g is the $g \times g$ identity matrix. The classical Mahalanobis distance D_i uses $(T, \mathbf{C}) = (\bar{\mathbf{z}}, \mathbf{S})$, the sample mean and sample covariance matrix where

$$\bar{\mathbf{z}} = \frac{1}{B} \sum_{i=1}^B \mathbf{z}_i \quad \text{and} \quad \mathbf{S} = \frac{1}{B-1} \sum_{i=1}^B (\mathbf{z}_i - \bar{\mathbf{z}})(\mathbf{z}_i - \bar{\mathbf{z}})^T. \quad (2.6)$$

Let $q_B = \min(1 - \delta + 0.05, 1 - \delta + d/B)$ for $\delta > 0.1$ and

$$q_B = \min(1 - \delta/2, 1 - \delta + 10\delta d/B), \quad \text{otherwise.} \quad (2.7)$$

If $1 - \delta < 0.999$ and $q_B < 1 - \delta + 0.001$, set $q_B = 1 - \delta$. We often use $d = g$ or $d = q$ if $\boldsymbol{\theta} = \mathbf{A}\boldsymbol{\mu}$ and $\boldsymbol{\mu}$ is a $q \times 1$ vector. Let $D_{(U_B)}$ be the $100q_B$ th sample quantile of the D_i . Equation (2.7) is often useful for getting good coverage when $B \geq 50d$. Undercoverage could occur without the correction factor. This result is useful because the bootstrap confidence regions can be slow to simulate. Hence we want to use small values of $B \geq 50d$.

For the following **two new confidence regions**, let a statistic T estimate $\boldsymbol{\theta}$. Assume $\sqrt{n}(T_n - \boldsymbol{\theta}) \xrightarrow{D} \mathbf{u}$ and $\sqrt{n}(T_n^* - T_n) \xrightarrow{D} \mathbf{u}$. Let the bootstrap sample be T_1^*, \dots, T_B^* . Let \bar{T}^* and \mathbf{S}_T^* be the sample mean and sample covariance matrix of the bootstrap sample. The first large sample $100(1 - \delta)\%$ confidence region is

$$\{\mathbf{w} : n(\mathbf{w} - T_n)^T \mathbf{C}_n^{-1} (\mathbf{w} - T_n) \leq D_{(U_B, T)}^2\} = \{\mathbf{w} : D_{\mathbf{w}}^2(T_n, \mathbf{C}_n/n) \leq D_{(U_B, T)}^2\} \quad (2.8)$$

where the cutoff $D_{(U_B, T)}^2$ is the $100q_B$ th sample quantile of the $D_i^2 = n(T_i^* - T_n)^T \mathbf{C}_n^{-1} (T_i^* - T_n)$. Note that the corresponding test for $H_0 : \boldsymbol{\theta} = \boldsymbol{\theta}_0$ rejects H_0 if $n(T_n - \boldsymbol{\theta}_0)^T \mathbf{C}_n^{-1} (T_n - \boldsymbol{\theta}_0) > D_{(U_B, T)}^2$. Note that q_B is found from (2.7) with $\mathbf{z}_i = T_i^*$.

The second large sample $100(1 - \delta)\%$ confidence region for $\boldsymbol{\theta}$ is

$$\{\mathbf{w} : n(\mathbf{w} - \bar{T}^*)^T \mathbf{C}_n^{-1} (\mathbf{w} - \bar{T}^*) \leq D_{(U_B)}^2\} = \{\mathbf{w} : D_{\mathbf{w}}^2(\bar{T}^*, \mathbf{C}_n/n) \leq D_{(U_B)}^2\} \quad (2.9)$$

where $D_{(U_B)}^2$ is computed from $D_i^2 = n(T_i^* - \bar{T}^*)^T \mathbf{C}_n^{-1} (T_i^* - \bar{T}^*)$ for $i = 1, \dots, B$. Note that the corresponding test for $H_0 : \boldsymbol{\theta} = \boldsymbol{\theta}_0$ rejects H_0 if $n(\bar{T}^* - \boldsymbol{\theta}_0)^T \mathbf{C}_n^{-1} (\bar{T}^* - \boldsymbol{\theta}_0) > D_{(U_B)}^2$.

If $n\mathbf{C}_n^{-1} = [\mathbf{S}_T^*]^{-1}$, then (2.8) and (2.9) are the modified Bickel and Ren (2001) and Olive (2017ab, 2018) prediction region method large sample $100(1 - \delta)\%$ confidence regions for $\boldsymbol{\theta}$. Under regularity conditions, Bickel and Ren (2001) and Olive (2017b, 2018) proved that (2.8) and (2.9) are large sample confidence regions when $n\mathbf{C}_n^{-1} = [\mathbf{S}_T^*]^{-1}$. Pelawa Watagoda and Olive (2019) gave simpler proofs.

The ratio of the volumes of regions (2.9) and (2.8) is

$$\left(\frac{D_{(U_B)}}{D_{(U_{B,T})}} \right)^g. \quad (2.10)$$

Hence region (2.9) has smaller volume than region (2.8) if $D_{(U_B)} < D_{(U_{B,T})}$.

Pelawa Watagoda and Olive (2021) showed that under reasonable regularity conditions, i) $\sqrt{n}(T_n - \boldsymbol{\theta}) \xrightarrow{D} \mathbf{u}$, ii) $\sqrt{n}(T_i^* - T_n) \xrightarrow{D} \mathbf{u}$, iii) $\sqrt{n}(\bar{T}^* - \boldsymbol{\theta}) \xrightarrow{D} \mathbf{u}$, and iv) $\sqrt{n}(T_i^* - \bar{T}^*) \xrightarrow{D} \mathbf{u}$. Then

$$D_1^2 = D_{T_i^*}^2(\bar{T}^*, \mathbf{C}_n/n) = \sqrt{n}(T_i^* - \bar{T}^*)^T \mathbf{C}_n^{-1} \sqrt{n}(T_i^* - \bar{T}^*),$$

$$D_2^2 = D_{\boldsymbol{\theta}}^2(T_n, \mathbf{C}_n/n) = \sqrt{n}(T_n - \boldsymbol{\theta})^T \mathbf{C}_n^{-1} \sqrt{n}(T_n - \boldsymbol{\theta}),$$

$$D_3^2 = D_{\boldsymbol{\theta}}^2(\bar{T}^*, \mathbf{C}_n/n) = \sqrt{n}(\bar{T}^* - \boldsymbol{\theta})^T \mathbf{C}_n^{-1} \sqrt{n}(\bar{T}^* - \boldsymbol{\theta}), \quad \text{and}$$

$$D_4^2 = D_{T_i^*}^2(T_n, \mathbf{C}_n/n) = \sqrt{n}(T_i^* - T_n)^T \mathbf{C}_n^{-1} \sqrt{n}(T_i^* - T_n),$$

are well behaved. If $\mathbf{C}_n^{-1} \xrightarrow{P} \mathbf{C}^{-1}$, then $D_j^2 \xrightarrow{D} D^2 = \mathbf{u}^T \mathbf{C}^{-1} \mathbf{u}$. If \mathbf{C}_n^{-1} is “not too ill conditioned” then $D_j^2 \approx \mathbf{u}^T \mathbf{C}_n^{-1} \mathbf{u}$ for large n , and the confidence regions (2.8) and (2.9) will have coverage near $1 - \delta$.

The basic idea is to use sample percentiles of D_1^2 or D_4^2 from a bootstrap sample to get better cutoffs for Wald type tests that use the wrong dispersion matrix.

If $g = 1$, then a hyperellipsoid is an interval, and confidence intervals are special cases of confidence regions. Suppose the parameter of interest is θ , and there is a bootstrap

sample T_1^*, \dots, T_B^* where the statistic T_n is an estimator of θ based on a sample of size n . A percentile CI contains $U_B \approx k_B = \lceil B(1 - \delta) \rceil$ of the T_i^* by Definition 2.2. Let $a_i = |T_i^* - \bar{T}^*|$. For $g = 1$, the CI corresponding to (2.9) is $[\bar{T}^* - a_{(U_B)}, \bar{T}^* + a_{(U_B)}]$, which is a percentile CI centered at \bar{T}^* just long enough to cover U_B of the T_i^* . Efron (2014) used a similar large sample $100(1 - \delta)\%$ confidence interval assuming that \bar{T}^* is asymptotically normal. The CI $[T_n - b_{(U_B, T)}, T_n + b_{(U_B, T)}]$ corresponding to (2.8) is a percentile CI centered at T_n just long enough to cover “ U_B, T ” of the T_i^* with $b_i = |T_i^* - T_n|$.

Note that the two CIs corresponding to (2.8) and (2.9) can be computed without finding \mathbf{C}_n , $D_{(U_B)}$, or $D_{(U_B, T)}$. Hence these CIs correspond to the prediction region method CI and the modified Bickel and Ren CI. Suppose $\sqrt{n}(\hat{\boldsymbol{\mu}} - \boldsymbol{\mu}) \xrightarrow{D} N_g(\mathbf{0}, \boldsymbol{\Sigma})$. Then confidence regions (2.8) and (2.9) do not depend on whether \mathbf{C}_n^{-1} or $d_n \mathbf{C}_n^{-1}$ is used if the scalar $d_n > 0$. Let $\theta = \mathbf{a}^T \boldsymbol{\mu}$ and $T_n = \mathbf{a}^T \hat{\boldsymbol{\mu}}$. Then $\mathbf{a}^T \mathbf{C}_n^{-1} \mathbf{a} = d_n \mathbf{a}^T \boldsymbol{\Sigma}^{-1} \mathbf{a}$ where $d_n = \mathbf{a} \mathbf{C}_n^{-1} \mathbf{a} / \mathbf{a}^T \boldsymbol{\Sigma}^{-1} \mathbf{a}$. Hence the confidence intervals do not depend on whether the wrong dispersion matrix is used.

Remark 2.1, Pelawa Watagoda and Olive (2021). If $g = 1$, if $\sqrt{n}(T_n - \theta) \xrightarrow{D} U$, and if $\sqrt{n}(T_i^* - T_n) \xrightarrow{D} U$ where U has a unimodal probability density function symmetric about zero with $E(U) = 0$, then the confidence intervals from the two confidence regions (2.8) and (2.9), the shorth confidence interval (2.2), and the “usual” percentile confidence interval (2.1) are asymptotically equivalent (use the central proportion of the bootstrap sample, asymptotically).

CHAPTER 3

THEORY AND METHODS

3.1 ONE WAY MANOVA TEST

This section follows Olive (2017b, § 10.3) closely. Using double subscripts will be useful for describing the one way MANOVA model. Suppose there are independent random samples of size n_i from p different populations (treatments), or n_i cases are randomly assigned to p treatment groups. Then $n = \sum_{i=1}^p n_i$ and the group sample sizes are n_i for $i = 1, \dots, p$. Assume that m response variables $\mathbf{y}_{ij} = (Y_{ij1}, \dots, Y_{ijm})^T$ are measured for the i th treatment group and the j th case (often an individual or thing) in the group. Hence $i = 1, \dots, p$ and $j = 1, \dots, n_i$. The Y_{ijk} follow different one way ANOVA models for $k = 1, \dots, m$. Assume $E(\mathbf{y}_{ij}) = \boldsymbol{\mu}_i$ and $\text{Cov}(\mathbf{y}_{ij}) = \boldsymbol{\Sigma}_\epsilon$. Hence the p treatments have different mean vectors $\boldsymbol{\mu}_i$, but common covariance matrix $\boldsymbol{\Sigma}_\epsilon$.

The one way MANOVA is used to test $H_0 : \boldsymbol{\mu}_1 = \boldsymbol{\mu}_2 = \dots = \boldsymbol{\mu}_p$. Often $\boldsymbol{\mu}_i = \boldsymbol{\mu} + \boldsymbol{\tau}_i$, so H_0 becomes $H_0 : \boldsymbol{\tau}_1 = \dots = \boldsymbol{\tau}_p$. If $m = 1$, the one way MANOVA model is the one way ANOVA model. MANOVA is useful since it takes into account the correlations between the m response variables. Performing m ANOVA tests fails to account for these correlations, but can be a useful diagnostic. The Hotelling's T^2 test that uses a common covariance matrix is a special case of the one way MANOVA model with $p = 2$.

Let $\boldsymbol{\mu}_i = \boldsymbol{\mu} + \boldsymbol{\tau}_i$ where $\sum_{i=1}^p n_i \boldsymbol{\tau}_i = \mathbf{0}$. The j th case from the i th population or treatment group is $\mathbf{y}_{ij} = \boldsymbol{\mu} + \boldsymbol{\tau}_i + \boldsymbol{\epsilon}_{ij}$ where $\boldsymbol{\epsilon}_{ij}$ is an error vector, $i = 1, \dots, p$ and $j = 1, \dots, n_i$. Let $\bar{\mathbf{y}} = \hat{\boldsymbol{\mu}} = \sum_{i=1}^p \sum_{j=1}^{n_i} \mathbf{y}_{ij} / n$ be the overall mean. Let $\bar{\mathbf{y}}_i = \sum_{j=1}^{n_i} \mathbf{y}_{ij} / n_i$ so $\hat{\boldsymbol{\tau}}_i = \bar{\mathbf{y}}_i - \bar{\mathbf{y}}$. Let the residual vector $\hat{\boldsymbol{\epsilon}}_{ij} = \mathbf{y}_{ij} - \bar{\mathbf{y}}_i = \mathbf{y}_{ij} - \hat{\boldsymbol{\mu}} - \hat{\boldsymbol{\tau}}_i$. Then $\mathbf{y}_{ij} = \bar{\mathbf{y}} + (\bar{\mathbf{y}}_i - \bar{\mathbf{y}}) + (\mathbf{y}_{ij} - \bar{\mathbf{y}}_i) = \hat{\boldsymbol{\mu}} + \hat{\boldsymbol{\tau}}_i + \hat{\boldsymbol{\epsilon}}_{ij}$.

Several $m \times m$ matrices will be useful. Let \mathbf{S}_i be the sample covariance matrix corresponding to the i th treatment group. Then the within sum of squares and cross products matrix is $\mathbf{W} = (n_1 - 1)\mathbf{S}_1 + \dots + (n_p - 1)\mathbf{S}_p = \sum_{i=1}^p \sum_{j=1}^{n_i} (\mathbf{y}_{ij} - \bar{\mathbf{y}}_i)(\mathbf{y}_{ij} - \bar{\mathbf{y}}_i)^T$.

Then $\hat{\Sigma}_{\epsilon} = \mathbf{W}/(n - p)$. The treatment or between sum of squares and cross products matrix is

$$\mathbf{B}_T = \sum_{i=1}^p n_i (\bar{\mathbf{y}}_i - \bar{\mathbf{y}})(\bar{\mathbf{y}}_i - \bar{\mathbf{y}})^T.$$

The total corrected (for the mean) sum of squares and cross products matrix is $\mathbf{T} = \mathbf{B}_T + \mathbf{W} = \sum_{i=1}^p \sum_{j=1}^{n_i} (\mathbf{y}_{ij} - \bar{\mathbf{y}})(\mathbf{y}_{ij} - \bar{\mathbf{y}})^T$. Note that $\mathbf{S} = \mathbf{T}/(n - 1)$ is the usual sample covariance matrix of the \mathbf{y}_{ij} if it is assumed that all n of the \mathbf{y}_{ij} are iid so that the $\boldsymbol{\mu}_i \equiv \boldsymbol{\mu}$ for $i = 1, \dots, p$.

The one way MANOVA model is $\mathbf{y}_{ij} = \boldsymbol{\mu} + \boldsymbol{\tau}_i + \boldsymbol{\epsilon}_{ij}$ where the $\boldsymbol{\epsilon}_{ij}$ are iid with $E(\boldsymbol{\epsilon}_{ij}) = \mathbf{0}$ and $\text{Cov}(\boldsymbol{\epsilon}_{ij}) = \Sigma_{\epsilon}$. The MANOVA table is shown below.

Summary One Way MANOVA Table

Source	matrix	df
Treatment or Between	\mathbf{B}_T	$p - 1$
Residual or Error or Within	\mathbf{W}	$n - p$
Total (corrected)	\mathbf{T}	$n - 1$

If all n of the \mathbf{y}_{ij} are iid with $E(\mathbf{y}_{ij}) = \boldsymbol{\mu}$ and $\text{Cov}(\mathbf{y}_{ij}) = \Sigma_{\epsilon}$, it can be shown that $\mathbf{A}/df \xrightarrow{P} \Sigma_{\epsilon}$ where $\mathbf{A} = \mathbf{W}, \mathbf{B}_T$, or \mathbf{T} , and df is the corresponding degrees of freedom. Let t_0 be the test statistic. Often Pillai's trace statistic, the Hotelling Lawley trace statistic, or Wilks' lambda are used. Wilks' lambda

$$\Lambda = \frac{|\mathbf{W}|}{|\mathbf{B}_T + \mathbf{W}|} = \frac{|\mathbf{W}|}{|\mathbf{T}|} = \frac{|\sum_{i=1}^p (n_i - 1)\mathbf{S}_i|}{|(n - 1)\mathbf{S}|} = \frac{|\sum_{i=1}^p \sum_{j=1}^{n_i} (\mathbf{y}_{ij} - \bar{\mathbf{y}}_i)(\mathbf{y}_{ij} - \bar{\mathbf{y}}_i)^T|}{|\sum_{i=1}^p \sum_{j=1}^{n_i} (\mathbf{y}_{ij} - \bar{\mathbf{y}})(\mathbf{y}_{ij} - \bar{\mathbf{y}})^T|}.$$

Then $t_o = -[n - 0.5(m + p - 2)] \log(\Lambda)$ and the estimated pvalue = pval = $P(\chi_{m(p-1)}^2 > t_o)$. Hence reject H_0 if $t_0 > \chi_{m(p-1)}^2(1 - \delta)$. See Johnson and Wichern (1988, p. 238).

The four steps of the one way MANOVA test follow.

i) State the hypotheses $H_0 : \boldsymbol{\mu}_1 = \dots = \boldsymbol{\mu}_p$ and $H_1 : \text{not } H_0$.

- ii) Get t_0 from output.
- iii) Get pval from output.
- iv) State whether you reject H_0 or fail to reject H_0 . If $\text{pval} \leq \delta$, reject H_0 and conclude that not all of the p treatment means are equal. If $\text{pval} > \delta$, fail to reject H_0 and conclude that all p treatment means are equal or that there is not enough evidence to conclude that not all of the p treatment means are equal. The value $\delta = 0.05$ is common.

Another way to perform the one way MANOVA test is to get R output. The default test is Pillai's test, but other tests can be obtained with the R output shown below.

```
library(MASS)
y <- iris[,1:4] #m = 4 = number of response variables
group <- iris[,5]
out <- manova(y~group)
summary(out$out) #default is Pillai's test
summary(out$out, test = "Wilks")
summary(out$out, test = "Hotelling-Lawley")
summary(out$out, test = "Roy")
```

Example 3.1. The R output for the famous iris data gives a Pillai's F statistic of 53.466 and $\text{pval} = 0$.

- i) $H_0 : \boldsymbol{\mu}_1 = \cdots = \boldsymbol{\mu}_4$ $H_1 : \text{not } H_0$
- ii) $F = 53.466$
- iii) $\text{pval} = 0$
- iv) Reject H_0 . The means for the three varieties of iris do differ.

Following Mardia et al. (1979, p. 335), let $\lambda_1 \geq \lambda_2 \cdots \geq \lambda_m$ be the eigenvalues of $\mathbf{W}^{-1}\mathbf{B}_T$. Then $1 + \lambda_i$ for $i = 1, \dots, m$ are the eigenvalues of $\mathbf{W}^{-1}\mathbf{T}$ and $\Lambda = \prod_{i=1}^m (1 + \lambda_i)^{-1}$.

Following Fujikoshi (2002), let the Hotelling Lawley trace statistic $U =$

$tr(\mathbf{B}_T \mathbf{W}^{-1}) = tr(\mathbf{W}^{-1} \mathbf{B}_T) = \sum_{i=1}^m \lambda_i$, and let Pillai's trace statistic $V = tr(\mathbf{B}_T \mathbf{T}^{-1}) = tr(\mathbf{T}^{-1} \mathbf{B}_T) = \sum_{i=1}^m \frac{\lambda_i}{1 + \lambda_i}$. If the $\mathbf{y}_{ij} - \boldsymbol{\mu}_j$ are iid with common covariance matrix $\boldsymbol{\Sigma}_\epsilon$, and if H_0 is true, then under regularity conditions $-[n - 0.5(m + p - 2)] \log(\Lambda) \xrightarrow{D} \chi_{m(p-1)}^2$, $(n - m - p - 1)U \xrightarrow{D} \chi_{m(p-1)}^2$, and $(n - 1)V \xrightarrow{D} \chi_{m(p-1)}^2$. Note that the common covariance matrix assumption implies that each of the p treatment groups or populations has the same covariance matrix $\boldsymbol{\Sigma}_i = \boldsymbol{\Sigma}_\epsilon$ for $i = 1, \dots, p$, an extremely strong assumption.

Remark 3.1. Another method for one way MANOVA is to use the model $\mathbf{Z} = \mathbf{X}\mathbf{B} + \mathbf{E}$ or

$$\begin{bmatrix}
 Y_{111} & Y_{112} & \cdots & Y_{11m} \\
 \vdots & \vdots & \cdots & \vdots \\
 Y_{1,n_1,1} & Y_{1,n_1,2} & \cdots & Y_{1,n_1,m} \\
 Y_{211} & Y_{212} & \cdots & Y_{21m} \\
 \vdots & \vdots & \cdots & \vdots \\
 Y_{2,n_2,1} & Y_{2,n_2,2} & \cdots & Y_{2,n_2,m} \\
 \vdots & \vdots & \cdots & \vdots \\
 Y_{p,11} & Y_{p,12} & \cdots & Y_{p,1m} \\
 \vdots & \vdots & \cdots & \vdots \\
 Y_{p,n_p,1} & Y_{p,n_p,2} & \cdots & Y_{p,n_p,m}
 \end{bmatrix}
 =
 \begin{bmatrix}
 1 & 1 & 0 & \cdots & 0 \\
 \vdots & \vdots & \vdots & & \vdots \\
 1 & 1 & 0 & \cdots & 0 \\
 1 & 0 & 1 & \cdots & 0 \\
 \vdots & \vdots & \vdots & & \vdots \\
 1 & 0 & 1 & \cdots & 0 \\
 \vdots & \vdots & \vdots & & \vdots \\
 1 & 0 & 0 & \cdots & 1 \\
 \vdots & \vdots & \vdots & & \vdots \\
 1 & 0 & 0 & \cdots & 1 \\
 1 & 0 & 0 & \cdots & 0 \\
 \vdots & \vdots & \vdots & & \vdots \\
 1 & 0 & 0 & \cdots & 0
 \end{bmatrix}
 \begin{bmatrix}
 \beta_{1,1} & \beta_{1,2} & \cdots & \beta_{1,m} \\
 \beta_{2,1} & \beta_{2,2} & \cdots & \beta_{2,m} \\
 \vdots & \vdots & \ddots & \vdots \\
 \beta_{p,1} & \beta_{p,2} & \cdots & \beta_{p,m}
 \end{bmatrix}
 + \mathbf{E}.$$

Then \mathbf{X} is full rank where the i th column of \mathbf{X} is an indicator for group $i - 1$ for

$i = 2, \dots, p$, $\hat{\beta}_{1k} = \bar{Y}_{pok} = \hat{\mu}_{pk}$ for $k = 1, \dots, m$, and

$$\hat{\beta}_{ik} = \bar{Y}_{i-1,ok} - \bar{Y}_{pok} = \hat{\mu}_{i-1,k} - \hat{\mu}_{pk}$$

for $k = 1, \dots, m$ and $i = 2, \dots, p$. Thus testing $H_0 : \boldsymbol{\mu}_1 = \dots = \boldsymbol{\mu}_p$ is equivalent to testing $H_0 : \mathbf{LB} = \mathbf{0}$ where $\mathbf{L} = [\mathbf{0} \ \mathbf{I}_{p-1}]$ using a multivariate linear regression model. Then $\mathbf{y}_{ij} = \boldsymbol{\mu}_i + \boldsymbol{\epsilon}_{ij}$ and

$$\mathbf{B} = \begin{bmatrix} \boldsymbol{\mu}_p^T \\ \boldsymbol{\mu}_1^T - \boldsymbol{\mu}_p^T \\ \boldsymbol{\mu}_2^T - \boldsymbol{\mu}_p^T \\ \vdots \\ \boldsymbol{\mu}_{p-2}^T - \boldsymbol{\mu}_p^T \\ \boldsymbol{\mu}_{p-1}^T - \boldsymbol{\mu}_p^T \end{bmatrix}. \quad (3.1)$$

The same \mathbf{X} can be used for one way ANOVA model with $m = 1$ as the \mathbf{X} used in the above one way MANOVA model. Then the multiple linear regression F test is the same as the one way ANOVA F test. See Section 6. Similarly, if $\mathbf{L} = (\mathbf{0} \ \mathbf{I}_{p-1})$ then the multivariate linear regression Hotelling Lawley test statistic for testing $H_0 : \mathbf{LB} = \mathbf{0}$ versus $H_1 : \mathbf{LB} \neq \mathbf{0}$ is $U = \text{tr}(\mathbf{W}^{-1}\mathbf{H})$, where $\mathbf{H} = \hat{\mathbf{B}}^T \mathbf{L}^T [\mathbf{L}(\mathbf{X}^T \mathbf{X})^{-1} \mathbf{L}^T]^{-1} \mathbf{L} \hat{\mathbf{B}}$, while the Hotelling Lawley test statistic for the one way MANOVA test with $H_0 : \boldsymbol{\mu}_1 = \boldsymbol{\mu}_2 = \dots = \boldsymbol{\mu}_p$ is $U = \text{tr}(\mathbf{W}^{-1}\mathbf{B}_T)$. Rupasinghe Arachchige Don (2018) showed that these two test statistics are the same for the above \mathbf{X} by showing that $\mathbf{B}_T = \mathbf{H}$. (End of Remark 3.1.)

3.2 AN ALTERNATIVE TEST BASED ON LARGE SAMPLE THEORY

Large sample theory can be also be used to derive a competing test. Let $\boldsymbol{\Sigma}_i$ be the nonsingular population covariance matrix of the i th treatment group or population. To simplify the large sample theory, assume $n_i = \pi_i n$ where $0 < \pi_i < 1$ and $\sum_{i=1}^p \pi_i = 1$. Let T_i be a multivariate location estimator such that $\sqrt{n_i}(T_i - \boldsymbol{\mu}_i) \xrightarrow{D} N_m(\mathbf{0}, \boldsymbol{\Sigma}_i)$, and

$\sqrt{n}(T_i - \boldsymbol{\mu}_i) \xrightarrow{D} N_m \left(\mathbf{0}, \frac{\boldsymbol{\Sigma}_i}{\pi_i} \right)$. Let $\mathbf{T} = (T_1^T, T_2^T, \dots, T_p^T)^T$, $\boldsymbol{\nu} = (\boldsymbol{\mu}_1^T, \boldsymbol{\mu}_2^T, \dots, \boldsymbol{\mu}_p^T)^T$, and \mathbf{A} be a full rank $r \times mp$ matrix with rank r , then a large sample test of the form $H_0 : \mathbf{A}\boldsymbol{\nu} = \boldsymbol{\theta}_0$ versus $H_1 : \mathbf{A}\boldsymbol{\nu} \neq \boldsymbol{\theta}_0$ uses

$$\mathbf{A}\sqrt{n}(\mathbf{T} - \boldsymbol{\nu}) \xrightarrow{D} \mathbf{u} \sim N_r \left(\mathbf{0}, \mathbf{A} \text{diag} \left(\frac{\boldsymbol{\Sigma}_1}{\pi_1}, \frac{\boldsymbol{\Sigma}_2}{\pi_2}, \dots, \frac{\boldsymbol{\Sigma}_p}{\pi_p} \right) \mathbf{A}^T \right). \quad (3.2)$$

Let the Wald-type statistic

$$t_0 = [\mathbf{A}\mathbf{T} - \boldsymbol{\theta}_0]^T \left[\mathbf{A} \text{diag} \left(\frac{\hat{\boldsymbol{\Sigma}}_1}{n_1}, \frac{\hat{\boldsymbol{\Sigma}}_2}{n_2}, \dots, \frac{\hat{\boldsymbol{\Sigma}}_p}{n_p} \right) \mathbf{A}^T \right]^{-1} [\mathbf{A}\mathbf{T} - \boldsymbol{\theta}_0]. \quad (3.3)$$

Let $F_0 = t_0/r$ and use Remark 3.2 below. These results prove the following theorem.

Theorem 3.1. Under the above conditions, $t_0 \xrightarrow{D} \chi_r^2$ if H_0 is true.

This test is due to Rupasinghe Arachchige Don and Olive (2019), and a special case was used by Zhang and Liu (2013) and Konietzschke et al. (2015) with $T_i = \bar{\mathbf{y}}_i$ and $\hat{\boldsymbol{\Sigma}}_i = \mathbf{S}_i$. The $p = 2$ case gives analogs to the two sample Hotelling's T^2 test. See Rupasinghe Arachchige Don and Pelawa Watagoda (2018). The $m = 1$ case gives analogs of the one way ANOVA test. If $m = 1$, see competing tests in Section 6, Brown and Forsythe (1974a,b), Olive (2017a, pp. 200-202), Pathiravasan (2019), and Welch (1947, 1951).

For the one way MANOVA type test, let \mathbf{A} be the block matrix

$$\mathbf{A} = \begin{bmatrix} \mathbf{I} & \mathbf{0} & \mathbf{0} & \dots & -\mathbf{I} \\ \mathbf{0} & \mathbf{I} & \mathbf{0} & \dots & -\mathbf{I} \\ \vdots & \vdots & \vdots & & \vdots \\ \mathbf{0} & \mathbf{0} & \dots & \mathbf{I} & -\mathbf{I} \end{bmatrix}.$$

Let $\boldsymbol{\mu}_i \equiv \boldsymbol{\mu}$, let $H_0 : \boldsymbol{\mu}_1 = \cdots = \boldsymbol{\mu}_p$ or, equivalently, $H_0 : \mathbf{A}\boldsymbol{\nu} = \mathbf{0}$, and let

$$\mathbf{w} = \mathbf{AT} = \begin{bmatrix} T_1 - T_p \\ T_2 - T_p \\ \vdots \\ T_{p-2} - T_p \\ T_{p-1} - T_p \end{bmatrix}. \quad (3.4)$$

Then $\sqrt{n}\mathbf{w} \xrightarrow{D} N_{m(p-1)}(\mathbf{0}, \boldsymbol{\Sigma}\mathbf{w})$ if H_0 is true with $\boldsymbol{\Sigma}\mathbf{w} = (\boldsymbol{\Sigma}_{ij})$ where $\boldsymbol{\Sigma}_{ij} = \frac{\boldsymbol{\Sigma}_p}{\pi_p}$ for $i \neq j$, and $\boldsymbol{\Sigma}_{ii} = \frac{\boldsymbol{\Sigma}_i}{\pi_i} + \frac{\boldsymbol{\Sigma}_p}{\pi_p}$ for $i = j$. Hence

$$t_0 = n\mathbf{w}^T \hat{\boldsymbol{\Sigma}}\mathbf{w} = \mathbf{w}^T \left(\frac{\hat{\boldsymbol{\Sigma}}\mathbf{w}}{n} \right)^{-1} \mathbf{w} \xrightarrow{D} \chi_{m(p-1)}^2$$

as the $n_i \rightarrow \infty$ if H_0 is true. Here

$$\frac{\hat{\boldsymbol{\Sigma}}\mathbf{w}}{n} = \begin{bmatrix} \frac{\hat{\boldsymbol{\Sigma}}_1}{n_1} + \frac{\hat{\boldsymbol{\Sigma}}_p}{n_p} & \frac{\hat{\boldsymbol{\Sigma}}_p}{n_p} & \frac{\hat{\boldsymbol{\Sigma}}_p}{n_p} & \cdots & \frac{\hat{\boldsymbol{\Sigma}}_p}{n_p} \\ \frac{\hat{\boldsymbol{\Sigma}}_p}{n_p} & \frac{\hat{\boldsymbol{\Sigma}}_2}{n_2} + \frac{\hat{\boldsymbol{\Sigma}}_p}{n_p} & \frac{\hat{\boldsymbol{\Sigma}}_p}{n_p} & \cdots & \frac{\hat{\boldsymbol{\Sigma}}_p}{n_p} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ \frac{\hat{\boldsymbol{\Sigma}}_p}{n_p} & \frac{\hat{\boldsymbol{\Sigma}}_p}{n_p} & \frac{\hat{\boldsymbol{\Sigma}}_p}{n_p} & \cdots & \frac{\hat{\boldsymbol{\Sigma}}_{p-1}}{n_{p-1}} + \frac{\hat{\boldsymbol{\Sigma}}_p}{n_p} \end{bmatrix} \quad (3.5)$$

is a block matrix where the off diagonal block entries equal $\hat{\boldsymbol{\Sigma}}_p/n_p$ and the i th diagonal block entry is $\frac{\hat{\boldsymbol{\Sigma}}_i}{n_i} + \frac{\hat{\boldsymbol{\Sigma}}_p}{n_p}$ for $i = 1, \dots, (p-1)$.

Reject H_0 if

$$t_0 > m(p-1)F_{m(p-1), d_n}(1-\delta) \quad (3.6)$$

where $d_n = \min(n_1, \dots, n_p)$. See Remark 3.2 below. It may make sense to relabel the groups so that n_p is the largest n_i or $\hat{\boldsymbol{\Sigma}}_p/n_p$ has the smallest generalized variance of the $\hat{\boldsymbol{\Sigma}}_i/n_i$. This test may start to outperform the one way MANOVA test if $n \geq (m+p)^2$ and $n_i \geq 40m$ for $i = 1, \dots, p$.

Remark 3.2. A useful fact for the F and chi-square distributions is $d_n F_{g,d_n,1-\delta} \rightarrow \chi_{g,1-\delta}^2$ as $d_n \rightarrow \infty$. Here $P(X \leq \chi_{g,1-\delta}^2) = 1 - \delta$ if $X \sim \chi_g^2$, and $P(X \leq F_{g,d_n,1-\delta}) = 1 - \delta$ if $X \sim F_{g,d_n}$.

If $\Sigma_i \equiv \Sigma$ and $\hat{\Sigma}_i$ is replaced by $\hat{\Sigma}$, we will show that for the one way MANOVA test that $t_0 = (n - p)U$ where U is the Hotelling Lawley statistic. For the proof, some results on the vec and Kronecker product will be useful. Following Henderson and Searle (1979), $\text{vec}(\mathbf{G})$ and $\text{vec}(\mathbf{G}^T)$ contain the same elements in different sequences. Let matrix $\mathbf{A} = [\mathbf{a}_1 \ \mathbf{a}_2 \ \dots \ \mathbf{a}_p]$. Then the vec operator stacks the columns of \mathbf{A} on top of one another so

$$\text{vec}(\mathbf{A}) = \begin{pmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \\ \vdots \\ \mathbf{a}_p \end{pmatrix}.$$

Let $\mathbf{A} = (a_{ij})$ be an $m \times n$ matrix and \mathbf{B} a $p \times q$ matrix. Then the Kronecker product of \mathbf{A} and \mathbf{B} is the $mp \times nq$ matrix

$$\mathbf{A} \otimes \mathbf{B} = \begin{bmatrix} a_{11}\mathbf{B} & a_{12}\mathbf{B} & \cdots & a_{1n}\mathbf{B} \\ a_{21}\mathbf{B} & a_{22}\mathbf{B} & \cdots & a_{2n}\mathbf{B} \\ \vdots & \vdots & \cdots & \vdots \\ a_{m1}\mathbf{B} & a_{m2}\mathbf{B} & \cdots & a_{mn}\mathbf{B} \end{bmatrix}.$$

An important fact is that if \mathbf{A} and \mathbf{B} are nonsingular square matrices, then $[\mathbf{A} \otimes \mathbf{B}]^{-1} = \mathbf{A}^{-1} \otimes \mathbf{B}^{-1}$. Following Henderson and Searle (1979), define the permutation matrix $\mathbf{P}_{r,m}$ such that

$$\text{vec}(\mathbf{G}) = \mathbf{P}_{r,m} \text{vec}(\mathbf{G}^T) \quad (3.7)$$

where \mathbf{G} is $r \times m$. Then $\mathbf{P}_{r,m}^T = \mathbf{P}_{m,r}$, and $\mathbf{P}_{r,m} \mathbf{P}_{m,r} = \mathbf{P}_{m,r} \mathbf{P}_{r,m} = \mathbf{I}_{rm}$. If \mathbf{C} is $s \times m$ and \mathbf{D} is $p \times r$, then

$$\mathbf{C} \otimes \mathbf{D} = \mathbf{P}_{p,s} (\mathbf{D} \otimes \mathbf{C}) \mathbf{P}_{m,q}. \quad (3.8)$$

Also

$$(\mathbf{C} \otimes \mathbf{D})\text{vec}(\mathbf{G}) = \text{vec}(\mathbf{DGC}^T) = \mathbf{P}_{p,s}(\mathbf{D} \otimes \mathbf{C})\text{vec}(\mathbf{G}^T). \quad (3.9)$$

If \mathbf{C} is $m \times m$ and \mathbf{D} is $r \times r$, then $\mathbf{C} \otimes \mathbf{D} = \mathbf{P}_{r,m}(\mathbf{D} \otimes \mathbf{C})\mathbf{P}_{m,r}$, and

$$[\text{vec}(\mathbf{G})]^T(\mathbf{C} \otimes \mathbf{D})\text{vec}(\mathbf{G}) = [\text{vec}(\mathbf{G}^T)]^T(\mathbf{D} \otimes \mathbf{C})\text{vec}(\mathbf{G}^T). \quad (3.10)$$

The two proofs of the following theorem are new.

Theorem 3.2. For the one way MANOVA test using $\boldsymbol{\theta}_0 = \mathbf{0}$, \mathbf{A} as defined below Theorem 3.1, and $T_i = \bar{\mathbf{y}}_i$, let the Hotelling Lawley trace statistic $U = \text{tr}(\mathbf{W}^{-1}\mathbf{B}_T)$. Let $\hat{\boldsymbol{\Sigma}}$ be the usual pooled covariance matrix estimator. Then

$$(n-p)U = t_0 = [\mathbf{AT}]^T \left[\mathbf{A} \text{diag} \left(\frac{\hat{\boldsymbol{\Sigma}}}{n_1}, \frac{\hat{\boldsymbol{\Sigma}}}{n_2}, \dots, \frac{\hat{\boldsymbol{\Sigma}}}{n_p} \right) \mathbf{A}^T \right]^{-1} [\mathbf{AT}].$$

Hence if the $\boldsymbol{\Sigma}_i \equiv \boldsymbol{\Sigma}$ and $H_0 : \boldsymbol{\mu}_1 = \dots = \boldsymbol{\mu}_p$ is true, then $(n-p)U = t_0 \xrightarrow{D} \chi_{m(p-1)}^2$.

Proof 1. Let \mathbf{B} and \mathbf{X} be as in Remark 3.1. Let $\mathbf{L} = [\mathbf{0} \ \mathbf{I}_{p-1}]$ be an $s \times p$ matrix with $s = p - 1$. For this choice of \mathbf{X} , $U = \text{tr}(\mathbf{W}^{-1}\mathbf{B}_T) = \text{tr}(\mathbf{W}^{-1}\mathbf{H})$ by Remark 3.1. By Olive (2017b, p. 341),

$$(n-p)U = [\text{vec}(\mathbf{L}\hat{\mathbf{B}})]^T [\hat{\boldsymbol{\Sigma}}_{\boldsymbol{\epsilon}}^{-1} \otimes (\mathbf{L}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{L}^T)^{-1}] [\text{vec}(\mathbf{L}\hat{\mathbf{B}})]. \quad (3.11)$$

Now $\text{vec}([\mathbf{L}\hat{\mathbf{B}}]^T) = \mathbf{w} = \mathbf{AT}$ of Equation (3.4) with $T_i = \bar{\mathbf{y}}_i$. Then

$$t_0 = \mathbf{w}^T \left(\frac{\hat{\boldsymbol{\Sigma}}\mathbf{w}}{n} \right)^{-1} \mathbf{w}$$

where

$$\frac{\hat{\boldsymbol{\Sigma}}\mathbf{w}}{n} = \mathbf{L}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{L}^T \otimes \hat{\boldsymbol{\Sigma}}$$

is given by Equation (3.5) with each $\hat{\boldsymbol{\Sigma}}_i$ replaced by $\hat{\boldsymbol{\Sigma}}$. Thus $t_0 =$

$$[\text{vec}([\mathbf{L}\hat{\mathbf{B}}]^T)]^T [(\mathbf{L}(\mathbf{X}^T\mathbf{X})^{-1}\mathbf{L}^T)^{-1} \otimes \hat{\boldsymbol{\Sigma}}_{\boldsymbol{\epsilon}}^{-1}] [\text{vec}([\mathbf{L}\hat{\mathbf{B}}]^T)]. \quad (3.12)$$

Then $t_0 = (n-p)U$ by Equation (3.10) with $\mathbf{G} = \mathbf{L}\hat{\mathbf{B}}$. \square

Proof 2. Let \mathbf{B} be a $p \times m$ vector, $\mathbf{L} = [\mathbf{0} \ \mathbf{I}_{p-1}]$ is an $s \times p$ matrix, $\mathbf{L}\hat{\mathbf{B}}$ is an $s \times m$ matrix where $s = p - 1$ then,

$$(n-p)U = [\text{vec}(\mathbf{L}\hat{\mathbf{B}})]^T [\hat{\Sigma}_{\boldsymbol{\epsilon}}^{-1} \otimes (\mathbf{L}(\mathbf{X}^T \mathbf{X})^{-1} \mathbf{L}^T)^{-1}] [\text{vec}(\mathbf{L}\hat{\mathbf{B}})].$$

By Equation (3.7),

$$\text{vec}(\mathbf{L}\hat{\mathbf{B}}) = \mathbf{P}_{s \times m} \text{vec}[(\mathbf{L}\hat{\mathbf{B}})^T].$$

By Equation (3.8)

$$\hat{\Sigma}^{-1} \otimes (\mathbf{L}(\mathbf{X}^T \mathbf{X})^{-1} \mathbf{L}^T) = \mathbf{P}_{s \times m} [(\mathbf{L}(\mathbf{X}^T \mathbf{X})^{-1} \mathbf{L}^T) \otimes \hat{\Sigma}_{\boldsymbol{\epsilon}}^{-1}] \mathbf{P}_{m \times s}.$$

Substitute the above two equations in Equation (3.11),

$$\begin{aligned} (n-p)U &= (\mathbf{P}_{s \times m} \text{vec}[(\mathbf{L}\hat{\mathbf{B}})^T])^T [\mathbf{P}_{s \times m} [(\mathbf{L}(\mathbf{X}^T \mathbf{X})^{-1} \mathbf{L}^T) \otimes \hat{\Sigma}_{\boldsymbol{\epsilon}}^{-1}] \mathbf{P}_{m \times s}] (\mathbf{P}_{s \times m} \text{vec}[(\mathbf{L}\hat{\mathbf{B}})^T]) \\ &= (\text{vec}[(\mathbf{L}\hat{\mathbf{B}})^T])^T (\mathbf{P}_{s \times m})^T (\mathbf{P}_{s \times m}) [(\mathbf{L}(\mathbf{X}^T \mathbf{X})^{-1} \mathbf{L}^T) \otimes \hat{\Sigma}_{\boldsymbol{\epsilon}}^{-1}] (\mathbf{P}_{m \times s}) (\mathbf{P}_{m \times s})^T \text{vec}[(\mathbf{L}\hat{\mathbf{B}})^T] \\ &= (\text{vec}[(\mathbf{L}\hat{\mathbf{B}})^T])^T [(\mathbf{L}(\mathbf{X}^T \mathbf{X})^{-1} \mathbf{L}^T) \otimes \hat{\Sigma}_{\boldsymbol{\epsilon}}^{-1}] \text{vec}[(\mathbf{L}\hat{\mathbf{B}})^T] \end{aligned}$$

. \square

Hence the one way MANOVA test is a special case of Equation (3.3) where $\boldsymbol{\theta}_0 = \mathbf{0}$ and $\hat{\Sigma}_i \equiv \hat{\Sigma}$, but then Theorem 3.1 only holds if H_0 is true and $\Sigma_i \equiv \Sigma$. Note that the large sample theory of Theorem 3.1 is trivial compared to the large sample theory of $(n-p)U$ given in Theorem 3.2. Fujikoshi (2002) showed $(n-m-p-1)U \xrightarrow{D} \chi_{m(p-1)}^2$ while $(n-p)U \xrightarrow{D} \chi_{m(p-1)}^2$ by Theorem 3.2 if H_0 is true under the common covariance matrix assumption. There is no contradiction since $(m+1)U \xrightarrow{P} 0$ as the $n_i \rightarrow \infty$. Note the \mathbf{A} is $m(p-1) \times mp$.

If $H_0 : \mathbf{A}\boldsymbol{\nu} = \boldsymbol{\theta}_0$ is true and if the $\Sigma_i \equiv \Sigma$ for $i = 1, \dots, p$, then

$$t_0 = [\mathbf{AT} - \boldsymbol{\theta}_0]^T \left[\mathbf{A} \text{diag} \left(\frac{\hat{\Sigma}}{n_1}, \frac{\hat{\Sigma}}{n_2}, \dots, \frac{\hat{\Sigma}}{n_p} \right) \mathbf{A}^T \right]^{-1} [\mathbf{AT} - \boldsymbol{\theta}_0] \xrightarrow{D} \chi_r^2.$$

If H_0 is true but the Σ_i are not equal, we get a bootstrap cutoff by using

$$t_{0i}^* = [\mathbf{AT}_i^* - \mathbf{AT}]^T \left[\mathbf{A} \text{diag} \left(\frac{\hat{\Sigma}}{n_1}, \frac{\hat{\Sigma}}{n_2}, \dots, \frac{\hat{\Sigma}}{n_p} \right) \mathbf{A}^T \right]^{-1} [\mathbf{AT}_i^* - \mathbf{AT}] =$$

$$D^2_{\mathbf{AT}_i^*} \left(\mathbf{AT}, \mathbf{A} \operatorname{diag} \left(\frac{\hat{\Sigma}}{n_1}, \frac{\hat{\Sigma}}{n_2}, \dots, \frac{\hat{\Sigma}}{n_p} \right) \mathbf{A}^T \right).$$

Let $F_0 = t_0/r$. Then we can get a bootstrap cutoff using $F_{0i}^* = t_{0i}^*/r$.

For the bootstrap, take a sample of size n_j with replacement from the n_j cases for each group for $j = 1, 2, \dots, p$ to obtain T_j^* and \mathbf{T}_1^* . Repeat B times to obtain $\mathbf{T}_1^*, \dots, \mathbf{T}_B^*$. Then form $\mathbf{w}_i^* = \mathbf{AT}_i^*$ for $i = 1, \dots, B$. If $\mathbf{w} = \mathbf{AT}$, then $\sqrt{n}(\mathbf{w} - \boldsymbol{\theta}) \xrightarrow{D} \mathbf{u}$ by (3.2), and we need $\sqrt{n}(\mathbf{w}_i^* - \mathbf{w}) \xrightarrow{D} \mathbf{u}$. This condition holds if $T_i^* = \bar{\mathbf{y}}_i^*$.

We may need $B \geq 50m(p-1)$, $n \geq (m+p)^2$, and $n_i \geq 40m$. If the n_i are not large, the one way MANOVA test can be regarded as a regularized estimator, and can perform better than the tests that do not assume equal population covariance matrices. See the simulations in Rupasinghe Arachchige Don and Olive (2019).

CHAPTER 4
DISTRIBUTION OF QUADRATIC FORMS

The distribution of $\mathbf{Y}^T \mathbf{G} \mathbf{Y}$ will be useful where \mathbf{G} is a symmetric matrix, $\mathbf{Y} \sim N_g(\boldsymbol{\mu}, \boldsymbol{\Sigma})$, and $\boldsymbol{\Sigma}$ is positive definite. Let $\mathbf{Z} \sim N_g(\boldsymbol{\mu}, \mathbf{I})$ where $\mathbf{Z}^T \mathbf{Z} \sim \chi^2(g, \delta)$, a noncentral chi-square distribution with g degrees of freedom and noncentrality parameter $\delta = \boldsymbol{\mu}^T \boldsymbol{\mu}$. Following Khuri (2010, pp. 94-101, 118),

$$\mathbf{Y}^T \mathbf{G} \mathbf{Y} \sim \sum_{i=1}^k \lambda_i W_i$$

where $\lambda_1, \dots, \lambda_k$ are the distinct nonzero eigenvalues of $\boldsymbol{\Sigma}^{1/2} \mathbf{G} \boldsymbol{\Sigma}^{1/2}$ (and of $\mathbf{G} \boldsymbol{\Sigma}$), with multiplicities ν_1, \dots, ν_k where the $W_i \sim \chi^2(\nu_i, \delta_i)$ with $\delta_i = \boldsymbol{\mu}^T \boldsymbol{\Sigma}^{-1/2} \mathbf{P}_i \mathbf{P}_i^T \boldsymbol{\Sigma}^{-1/2} \boldsymbol{\mu}$ where $\boldsymbol{\Sigma}^{1/2} \mathbf{G} \boldsymbol{\Sigma}^{1/2} = \mathbf{P} \boldsymbol{\Lambda} \mathbf{P}^T$ by the Spectral Decomposition Theorem, $\boldsymbol{\Lambda}$ is the diagonal matrix of the eigenvalues of $\boldsymbol{\Sigma}^{1/2} \mathbf{G} \boldsymbol{\Sigma}^{1/2}$, \mathbf{P} is the orthogonal matrix with columns equal to the corresponding eigenvectors, and \mathbf{P}_i is the $g \times \nu_i$ matrix with columns that are the eigenvectors corresponding to ν_i . Hence $\mathbf{P} \mathbf{P}^T = \mathbf{P}^T \mathbf{P} = \mathbf{I}_g$.

Davies (1980) shows how to find the percentiles of $\mathbf{Y}^T \mathbf{G} \mathbf{Y}$ when $\boldsymbol{\mu}$, $\boldsymbol{\Sigma}$, and \mathbf{G} are known. If $\boldsymbol{\mu} = \mathbf{0}$ or if \mathbf{Y} is replaced by $\mathbf{Y} - \boldsymbol{\mu}$, then $W_i \sim \chi^2(\nu_i)$, a (central) chi-square distribution with ν_i degrees of freedom. For more results on the distribution of $\mathbf{Y}^T \mathbf{G} \mathbf{Y}$, see Baldessari (1967), Imhof (1961), Liu, Tang, and Zhang (2009), Mathai and Provost (1992), and Singull and Koski (2012). The following argument uses ideas from an unpublished proof due to K.B. Halvorson.

$$\begin{aligned} \text{Let } \mathbf{Z} &= \boldsymbol{\Sigma}^{-1/2}(\mathbf{Y} - \boldsymbol{\mu}) \sim N_g(\mathbf{0}, \mathbf{I}). \text{ Then } \mathbf{Y} = \boldsymbol{\Sigma}^{1/2}(\mathbf{Z} + \boldsymbol{\Sigma}^{-1/2} \boldsymbol{\mu}), \text{ and } \mathbf{Y}^T \mathbf{G} \mathbf{Y} = \\ &(\mathbf{Z} + \boldsymbol{\Sigma}^{-1/2} \boldsymbol{\mu})^T \boldsymbol{\Sigma}^{1/2} \mathbf{G} \boldsymbol{\Sigma}^{1/2} (\mathbf{Z} + \boldsymbol{\Sigma}^{-1/2} \boldsymbol{\mu}) = (\mathbf{Z} + \boldsymbol{\Sigma}^{-1/2} \boldsymbol{\mu})^T \mathbf{P} \boldsymbol{\Lambda} \mathbf{P}^T (\mathbf{Z} + \boldsymbol{\Sigma}^{-1/2} \boldsymbol{\mu}) \\ &= (\mathbf{P}^T \mathbf{Z} + \mathbf{P}^T \boldsymbol{\Sigma}^{-1/2} \boldsymbol{\mu})^T \boldsymbol{\Lambda} (\mathbf{P}^T \mathbf{Z} + \mathbf{P}^T \boldsymbol{\Sigma}^{-1/2} \boldsymbol{\mu}) = (\mathbf{v} + \mathbf{b})^T \boldsymbol{\Lambda} (\mathbf{v} + \mathbf{b}) \end{aligned}$$

where $\mathbf{v} = \mathbf{P}^T \mathbf{Z} \sim N_g(\mathbf{0}, \mathbf{I})$ and $\mathbf{b} = \mathbf{P}^T \boldsymbol{\Sigma}^{-1/2} \boldsymbol{\mu}$. Hence $\mathbf{Y}^T \mathbf{G} \mathbf{Y} = \sum_{i=1}^g \lambda_i X_i$ where the independent $X_i = (v_i + b_i)^2 \sim \chi^2(1, b_i^2)$ with $b_i = \mathbf{p}_i^T \boldsymbol{\Sigma}^{-1/2} \boldsymbol{\mu}$ and \mathbf{p}_i is the i th column of \mathbf{P} . Note that $\sum_{i=1}^{\nu_i} X_i = W_i$.

CHAPTER 5
POOLED T TYPE TEST

Following DasGupta (2008, pp. 402-404) and Olive (2014, pp. 278-279, 290) consider the pooled t CI for $\mu_1 - \mu_2$. Let X_1, \dots, X_{n_1} be iid with mean μ_1 and variance σ_1^2 . Let Y_1, \dots, Y_{n_2} be iid with mean μ_2 and variance σ_2^2 . Assume that the two samples are independent and that $n_i \rightarrow \infty$ for $i = 1, 2$ in such a way that $\hat{\rho} = \frac{n_1}{n_1+n_2} \rightarrow \rho = \pi_1 \in (0, 1)$. Let $n_i/n \rightarrow \pi_i$ as $n \rightarrow \infty$, let $\gamma = \sigma_2^2/\sigma_1^2$, and let the pooled sample variance

$$S_p^2 = \frac{(n_1 - 1)S_1^2 + (n_2 - 1)S_2^2}{n_1 + n_2 - 2}.$$

Then

$$\begin{pmatrix} \sqrt{n_1}(\bar{X} - \mu_1) \\ \sqrt{n_2}(\bar{Y} - \mu_2) \end{pmatrix} \xrightarrow{D} N_2(\mathbf{0}, \mathbf{\Sigma})$$

where $\mathbf{\Sigma} = \text{diag}(\sigma_1^2, \sigma_2^2)$. Hence

$$\sqrt{n}[(\bar{X} - \bar{Y}) - (\mu_1 - \mu_2)] \xrightarrow{D} N(0, \frac{\sigma_1^2}{\pi_1} + \frac{\sigma_2^2}{\pi_2}).$$

So

$$\frac{\bar{X} - \bar{Y} - (\mu_1 - \mu_2)}{\sqrt{\frac{S_1^2}{n_1} + \frac{S_2^2}{n_2}}} \xrightarrow{D} N(0, 1).$$

Thus

$$\frac{\sqrt{\frac{S_1^2}{n_1} + \frac{S_2^2}{n_2}}}{S_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}} \frac{\bar{X} - \bar{Y} - (\mu_1 - \mu_2)}{\sqrt{\frac{S_1^2}{n_1} + \frac{S_2^2}{n_2}}} = \frac{\bar{X} - \bar{Y} - (\mu_1 - \mu_2)}{S_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}} \xrightarrow{D} N(0, \tau^2)$$

where

$$\begin{aligned} \frac{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}{(\frac{1}{n_1} + \frac{1}{n_2}) \frac{n_1 \sigma_1^2 + n_2 \sigma_2^2}{n_1 + n_2}} &= \frac{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}{\hat{\rho} \sigma_1^2 + (1 - \hat{\rho}) \sigma_2^2} \frac{1/\sigma_1^2}{1/\sigma_1^2} \frac{n_1 n_2}{n_1 + n_2} \\ &= \frac{\frac{1}{n_1} + \frac{\gamma}{n_2}}{\hat{\rho} + (1 - \hat{\rho})\gamma} \frac{n_1 n_2}{n_1 + n_2} \xrightarrow{D} \frac{1 - \rho + \rho\gamma}{\rho + (1 - \rho)\gamma} = \tau^2. \end{aligned}$$

Now let $\hat{\gamma} = S_2^2/S_1^2$ and

$$\hat{\tau}^2 = \frac{1 - \hat{\rho} + \hat{\rho} \hat{\gamma}}{\hat{\rho} + (1 - \hat{\rho}) \hat{\gamma}}.$$

Notice that $\hat{\tau} = 1$ if $\hat{\rho} = 1/2$, and $\hat{\tau} = 1$ if $\hat{\gamma} = 1$.

The usual large sample $(1 - \alpha)100\%$ pooled t CI for $(\mu_1 - \mu_2)$ is

$$\bar{X} - \bar{Y} \pm t_{n_1+n_2-2, 1-\alpha/2} S_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}. \quad (5.1)$$

The large sample theory says that this CI is valid if $\tau = 1$, and that

$$\frac{\bar{X} - \bar{Y} - (\mu_1 - \mu_2)}{\hat{\tau} S_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}} \xrightarrow{D} N(0, 1).$$

Hence a large sample $(1 - \alpha)100\%$ CI for $(\mu_1 - \mu_2)$ is

$$\bar{X} - \bar{Y} \pm z_{1-\alpha/2} \hat{\tau} S_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}.$$

Then the large sample $(1 - \alpha)100\%$ modified pooled t CI for $(\mu_1 - \mu_2)$ is

$$\bar{X} - \bar{Y} \pm t_{n_1+n_2-4, 1-\alpha/2} \hat{\tau} S_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}. \quad (5.2)$$

The large sample $(1 - \alpha)100\%$ Welch CI for $(\mu_1 - \mu_2)$ is

$$\bar{X} - \bar{Y} \pm t_{d, 1-\alpha/2} \sqrt{\frac{S_1^2}{n_1} + \frac{S_2^2}{n_2}} \quad (5.3)$$

where $d = n_1 + n_2 - 4$ or $d = \max(1, [d_0])$, and

$$d_0 = \frac{(\frac{S_1^2}{n_1} + \frac{S_2^2}{n_2})^2}{\frac{1}{n_1-1}(\frac{S_1^2}{n_1})^2 + \frac{1}{n_2-1}(\frac{S_2^2}{n_2})^2}.$$

Suppose $n_1/(n_1+n_2) \rightarrow \rho$. It can be shown that if the CI length is multiplied by $\sqrt{n_1}$, then the scaled length of the pooled t CI converges in probability to $2z_{1-\alpha/2}\sqrt{\frac{\rho}{1-\rho}\sigma_1^2 + \sigma_2^2}$ while the scaled lengths of the modified pooled t CI and Welch CI both converge in probability to $2z_{1-\alpha/2}\sqrt{\sigma_1^2 + \frac{\rho}{1-\rho}\sigma_2^2}$.

5.1 SIMULATION FOR POOLED T TYPE TEST

The simulations computed the shorth CI (2.2), the CIs corresponding to (2.8) and (2.9) with $d = 1$ in (2.7), the pooled CI (5.1), the modified pooled CI (5.2), and the

Welch CI (5.3). The bootstrap resampling scheme used samples with replacement from the X 's and from the Y 's. A competitor for (5.2) is the bootstrap pooled CI

$$\bar{X} - \bar{Y} \pm D_{(U_B)} S_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}} \quad (5.4)$$

where $D_{(U_B)}$ is the 100 U_B th percentile of the D_i where

$$D_i^2 = \frac{n[(\bar{X}_i^* - \bar{Y}_i^*) - (\bar{X} - \bar{Y})]^2}{S_p^2 \left(\frac{1}{n_1} + \frac{1}{n_2} \right)}.$$

The `lregpack` function `pcisim2` can be used to simulate and compare the tests. Each simulation used 5000 runs and used different $n_1, n_2, \sigma_1, \sigma_2$ with the Normal data for X and Y .

```
args(pcisim2)
```

```
function (nruns = 100, n1 = 10, n2 = 10, mu1 = 0, mu2 = 0, var1 = 1,
        var2 = 1, dist = 1, BB = 100, alph = 0.05)
```

From Table 5.1-5.3, when n_1 and n_2 are less than 50, the Welch test gives coverage near 0.95, while the other tests often give coverage lower than the nominal coverage.

In Table 5.6, the pooled t test performance was worst when the variance of the two groups are not equal. Sometimes the pooled t test gives higher coverages and sometime it gives lower coverages questioning the applicability of the method to the different variances situation. The bootstrap pooled CI worked well. Table 5.7 shows the situation where the n_1 and n_2 are equal to 100. In this situation all tests perform fairly good, resulting in coverages near the nominal coverage. CI lengths were similar and so not given.

Table 5.1. Coverage for seven Pooled t type CIs for Normal data when $n_1=10$ and $n_2=10$

n_1, n_2	BB	σ_1, σ_2	$pcov$	$bpcov$	$mpcov$	$wcov$	$shcov$	$prcov$	$brcov$
10,10	100	1,1	0.944	0.913	0.946	0.945	0.919	0.904	0.913
10,10	100	1,9	0.934	0.904	0.936	0.947	0.916	0.905	0.904
10,10	100	1,49	0.938	0.904	0.94	0.956	0.913	0.901	0.903
10,10	100	1,100	0.927	0.887	0.929	0.944	0.905	0.883	0.887
10,10	100	9,1	0.931	0.894	0.932	0.942	0.906	0.898	0.894
10,10	100	9,9	0.942	0.921	0.946	0.945	0.928	0.917	0.921
10,10	100	9,49	0.933	0.897	0.933	0.936	0.915	0.895	0.897
10,10	100	9,100	0.924	0.892	0.926	0.937	0.904	0.889	0.892
10,10	100	49,1	0.945	0.911	0.947	0.955	0.919	0.906	0.911
10,10	100	49,9	0.948	0.909	0.951	0.954	0.92	0.91	0.909
10,10	100	49,49	0.934	0.894	0.936	0.936	0.906	0.892	0.894
10,10	100	49,100	0.952	0.921	0.952	0.952	0.93	0.919	0.921
10,10	100	100,1	0.937	0.902	0.938	0.947	0.915	0.901	0.902
10,10	100	100,9	0.942	0.912	0.947	0.956	0.917	0.908	0.912
10,10	100	100,49	0.942	0.904	0.943	0.942	0.916	0.905	0.904
10,10	100	100,100	0.958	0.925	0.959	0.961	0.943	0.926	0.925

Table 5.2. Coverage for seven Pooled t type CIs for Normal data when $n_1=20$ and $n_2=20$

n_1, n_2	BB	σ_1, σ_2	$pcov$	$bpcov$	$mpcov$	$wcov$	$shcov$	$prcov$	$brcov$
20,20	100	1,1	0.945	0.935	0.946	0.946	0.93	0.93	0.935
20,20	100	1,9	0.949	0.93	0.95	0.952	0.938	0.928	0.93
20,20	100	1,49	0.947	0.918	0.948	0.953	0.929	0.915	0.917
20,20	100	1,100	0.934	0.903	0.935	0.943	0.918	0.902	0.903
20,20	100	9,1	0.939	0.919	0.939	0.946	0.934	0.917	0.919
20,20	100	9,9	0.951	0.937	0.951	0.951	0.936	0.928	0.935
20,20	100	9,49	0.953	0.937	0.953	0.955	0.949	0.932	0.937
20,20	100	9,100	0.949	0.935	0.949	0.954	0.949	0.935	0.935
20,20	100	49,1	0.948	0.941	0.949	0.955	0.943	0.934	0.941
20,20	100	49,9	0.945	0.92	0.945	0.947	0.929	0.91	0.92
20,20	100	49,49	0.948	0.935	0.949	0.949	0.936	0.929	0.934
20,20	100	49,100	0.954	0.936	0.956	0.956	0.944	0.937	0.935
20,20	100	100,1	0.941	0.918	0.941	0.946	0.938	0.915	0.918
20,20	100	100,9	0.952	0.937	0.952	0.961	0.941	0.935	0.937
20,20	100	100,49	0.942	0.923	0.942	0.943	0.935	0.925	0.923
20,20	100	100,100	0.946	0.935	0.946	0.947	0.935	0.93	0.935

Table 5.3. Coverage for seven Pooled t type CIs for Normal data when $n_1=20$ and $n_2=50$

n_1, n_2	BB	σ_1, σ_2	$pcov$	$bpcov$	$mpcov$	$wcov$	$shcov$	$prcov$	$brcov$
20,50	1000	1,1	0.941	0.93	0.944	0.946	0.938	0.93	0.93
20,50	1000	1,9	0.994	0.944	0.955	0.955	0.951	0.944	0.944
20,50	1000	1,49	0.998	0.947	0.952	0.952	0.947	0.945	0.947
20,50	1000	1,100	0.997	0.94	0.949	0.95	0.946	0.942	0.94
20,50	1000	9,1	0.819	0.921	0.931	0.938	0.923	0.922	0.921
20,50	1000	9,9	0.949	0.931	0.945	0.953	0.935	0.931	0.931
20,50	1000	9,49	0.991	0.936	0.944	0.943	0.938	0.935	0.936
20,50	1000	9,100	0.993	0.943	0.951	0.951	0.948	0.943	0.943
20,50	1000	49,1	0.794	0.929	0.934	0.945	0.931	0.926	0.929
20,50	1000	49,9	0.859	0.932	0.943	0.952	0.94	0.931	0.932
20,50	1000	49,49	0.952	0.939	0.951	0.957	0.942	0.938	0.939
20,50	1000	49,100	0.978	0.942	0.95	0.951	0.94	0.938	0.942
20,50	1000	100,1	0.773	0.938	0.947	0.958	0.938	0.937	0.938
20,50	1000	100,9	0.817	0.93	0.94	0.948	0.935	0.928	0.93
20,50	1000	100,49	0.899	0.927	0.938	0.946	0.929	0.927	0.927
20,50	1000	100,100	0.942	0.936	0.947	0.951	0.948	0.934	0.936

Table 5.4. Coverage for seven Pooled t type CIs for Normal data when $n_1=20$ and $n_2=50$

n_1, n_2	BB	σ_1, σ_2	$pcov$	$bpcov$	$mpcov$	$wcov$	$shcov$	$prcov$	$brcov$
50,50	400	1,1	0.95	0.939	0.95	0.95	0.949	0.937	0.939
50,50	400	1,9	0.951	0.945	0.951	0.953	0.953	0.945	0.945
50,50	400	1,49	0.934	0.924	0.934	0.936	0.934	0.926	0.924
50,50	400	1,100	0.945	0.935	0.945	0.949	0.945	0.933	0.935
50,50	400	9,1	0.941	0.937	0.941	0.941	0.943	0.934	0.937
50,50	400	9,9	0.942	0.935	0.942	0.942	0.943	0.935	0.935
50,50	400	9,49	0.938	0.935	0.938	0.938	0.935	0.932	0.935
50,50	400	9,100	0.954	0.948	0.954	0.958	0.957	0.947	0.948
50,50	400	49,1	0.956	0.947	0.956	0.961	0.958	0.948	0.947
50,50	400	49,9	0.941	0.934	0.941	0.943	0.938	0.93	0.934
50,50	400	49,49	0.957	0.943	0.957	0.957	0.95	0.94	0.943
50,50	400	49,100	0.939	0.93	0.939	0.94	0.936	0.931	0.93
50,50	400	100,1	0.947	0.937	0.947	0.95	0.944	0.938	0.937
50,50	400	100,9	0.958	0.951	0.958	0.961	0.955	0.949	0.951
50,50	400	100,49	0.937	0.929	0.937	0.937	0.937	0.929	0.929
50,50	400	100,100	0.959	0.951	0.959	0.959	0.955	0.951	0.951

Table 5.5. Coverage for seven Pooled t type CIs for Normal data when $n_1=50$ and $n_2=50$

n_1, n_2	BB	σ_1, σ_2	$pcov$	$bpcov$	$mpcov$	$wcov$	$shcov$	$prcov$	$brcov$
50,50	400	1,1	0.95	0.939	0.95	0.95	0.949	0.937	0.939
50,50	400	1,9	0.951	0.945	0.951	0.953	0.953	0.945	0.945
50,50	400	1,49	0.934	0.924	0.934	0.936	0.934	0.926	0.924
50,50	400	1,100	0.945	0.935	0.945	0.949	0.945	0.933	0.935
50,50	400	9,1	0.941	0.937	0.941	0.941	0.943	0.934	0.937
50,50	400	9,9	0.942	0.935	0.942	0.942	0.943	0.935	0.935
50,50	400	9,49	0.938	0.935	0.938	0.938	0.935	0.932	0.935
50,50	400	9,100	0.954	0.948	0.954	0.958	0.957	0.947	0.948
50,50	400	49,1	0.956	0.947	0.956	0.961	0.958	0.948	0.947
50,50	400	49,9	0.941	0.934	0.941	0.943	0.938	0.93	0.934
50,50	400	49,49	0.957	0.943	0.957	0.957	0.95	0.94	0.943
50,50	400	49,100	0.939	0.93	0.939	0.94	0.936	0.931	0.93
50,50	400	100,1	0.947	0.937	0.947	0.95	0.944	0.938	0.937
50,50	400	100,9	0.958	0.951	0.958	0.961	0.955	0.949	0.951
50,50	400	100,49	0.937	0.929	0.937	0.937	0.937	0.929	0.929
50,50	400	100,100	0.959	0.951	0.959	0.959	0.955	0.951	0.951

Table 5.6. Coverage for seven Pooled t type CIs for Normal data when $n_1=50$ and $n_2=100$

n_1, n_2	BB	σ_1, σ_2	$pcov$	$bpcov$	$mpcov$	$wcov$	$shcov$	$prcov$	$brcov$
50,100	100	1,1	0.953	0.95	0.953	0.953	0.953	0.948	0.95
50,100	100	1,9	0.989	0.955	0.959	0.959	0.96	0.953	0.955
50,100	100	1,49	0.993	0.94	0.945	0.947	0.95	0.939	0.94
50,100	100	1,100	0.992	0.944	0.951	0.951	0.951	0.944	0.944
50,100	100	9,1	0.868	0.948	0.958	0.959	0.954	0.943	0.948
50,100	100	9,9	0.947	0.937	0.95	0.95	0.947	0.936	0.937
50,100	100	9,49	0.99	0.954	0.958	0.958	0.957	0.946	0.954
50,100	100	9,100	0.994	0.951	0.956	0.956	0.957	0.944	0.951
50,100	100	49,1	0.844	0.948	0.951	0.954	0.955	0.946	0.947
50,100	100	49,9	0.893	0.953	0.957	0.959	0.953	0.95	0.953
50,100	100	49,49	0.946	0.943	0.948	0.95	0.953	0.939	0.943
50,100	100	49,100	0.98	0.951	0.96	0.96	0.96	0.953	0.951
50,100	100	100,1	0.824	0.926	0.939	0.947	0.932	0.926	0.926
50,100	100	100,9	0.872	0.963	0.965	0.97	0.962	0.958	0.963
50,100	100	100,49	0.918	0.947	0.953	0.957	0.947	0.942	0.947
50,100	100	100,100	0.953	0.945	0.954	0.954	0.954	0.942	0.945
50,50	400	100,100	0.959	0.951	0.959	0.959	0.955	0.951	0.951

Table 5.7. Coverage for seven Pooled t type CIs for Normal data when $n_1=100$ and $n_2=100$

n_1, n_2	BB	σ_1, σ_2	$pcov$	$bpcov$	$mpcov$	$wcov$	$shcov$	$prcov$	$brcov$
100,100	400	1,1	0.952	0.946	0.952	0.952	0.952	0.946	0.946
100,100	400	1,9	0.937	0.933	0.937	0.938	0.941	0.935	0.933
100,100	400	1,49	0.944	0.94	0.944	0.945	0.949	0.941	0.94
100,100	400	1,100	0.953	0.953	0.953	0.953	0.958	0.951	0.953
100,100	400	9,1	0.952	0.948	0.952	0.954	0.948	0.946	0.948
100,100	400	9,9	0.948	0.939	0.948	0.948	0.95	0.939	0.939
100,100	400	9,49	0.948	0.943	0.948	0.948	0.956	0.944	0.943
100,100	400	9,100	0.959	0.954	0.959	0.96	0.961	0.959	0.954
100,100	400	49,1	0.959	0.96	0.959	0.962	0.962	0.958	0.96
100,100	400	49,9	0.951	0.952	0.951	0.952	0.953	0.948	0.952
100,100	400	49,49	0.938	0.936	0.938	0.938	0.941	0.937	0.936
100,100	400	49,100	0.951	0.95	0.951	0.951	0.953	0.95	0.95
100,100	400	100,1	0.952	0.946	0.952	0.952	0.952	0.948	0.946
100,100	400	100,9	0.948	0.948	0.948	0.949	0.959	0.945	0.948
100,100	400	100,49	0.948	0.944	0.948	0.948	0.954	0.944	0.944
100,100	400	100,100	0.958	0.956	0.958	0.958	0.961	0.954	0.956

CHAPTER 6

ONE WAY ANOVA TYPE TEST

Models in which the response variable Y is quantitative, but all of the predictor variables are qualitative are called *analysis of variance* (ANOVA or Anova) models, *experimental design* models, or *design of experiments* (DOE) models. Each combination of the levels of the predictors gives a different distribution for Y . A predictor variable W is often called a factor and a factor level a_i is one of the categories W can take. This section follows Olive (2017a, § 5.2) closely.

The one way Anova model is used to compare p treatments. Usually there is replication and $H_0: \mu_1 = \mu_2 = \dots = \mu_p$ is a hypothesis of interest. Investigators may also want to rank the population means from smallest to largest.

Definition 6.1. Let $f_Z(z)$ be the pdf of Z . Then the family of pdfs $f_Y(y) = f_Z(y - \mu)$ indexed by the *location parameter* μ , $-\infty < \mu < \infty$, is the *location family* for the random variable $Y = \mu + Z$ with *standard pdf* $f_Z(z)$.

Definition 6.2. A *one way fixed effects Anova model* has a single qualitative predictor variable W with p categories a_1, \dots, a_p . There are p different distributions for Y , one for each category a_i . The distribution of

$$Y|(W = a_i) \sim f_Z(y - \mu_i)$$

where the location family has second moments. Hence all p distributions come from the same location family with different location parameter μ_i and the same variance σ^2 .

Definition 6.3. The *one way fixed effects normal Anova model* is the special case where

$$Y|(W = a_i) \sim N(\mu_i, \sigma^2).$$

Example 6.1. The pooled 2 sample t -test is a special case of a one way Anova model with $p = 2$. For example, one population could be ACT scores for men and the

second population ACT scores for women. Then $W = \textit{gender}$ and $Y = \textit{score}$.

Notation. It is convenient to relabel the response variable Y_1, \dots, Y_n as the vector $\mathbf{Y} = (Y_{11}, \dots, Y_{1,n_1}, Y_{21}, \dots, Y_{2,n_2}, \dots, Y_{p1}, \dots, Y_{p,n_p})^T$ where the Y_{ij} are independent and Y_{i1}, \dots, Y_{i,n_i} are iid. Here $j = 1, \dots, n_i$ where n_i is the number of cases from the i th level where $i = 1, \dots, p$. Thus $n_1 + \dots + n_p = n$. Similarly use double subscripts on the errors. Then there will be many equivalent parameterizations of the one way fixed effects Anova model.

Definition 6.4. The *cell means model* is the parameterization of the one way fixed effects Anova model such that

$$Y_{ij} = \mu_i + e_{ij}$$

where Y_{ij} is the value of the response variable for the j th trial of the i th factor level. The μ_i are the unknown means and $E(Y_{ij}) = \mu_i$. The e_{ij} are iid from the location family with pdf $f_Z(z)$ and unknown variance $\sigma^2 = \text{VAR}(Y_{ij}) = \text{VAR}(e_{ij})$. For the normal cell means model, the e_{ij} are iid $N(0, \sigma^2)$ for $i = 1, \dots, p$ and $j = 1, \dots, n_i$.

The cell means model is a linear model (without intercept) of the form

$$\mathbf{Y} = \mathbf{X}_c \boldsymbol{\beta}_c + \mathbf{e} =$$

$$\begin{bmatrix} Y_{11} \\ \vdots \\ Y_{1,n_1} \\ Y_{21} \\ \vdots \\ Y_{2,n_2} \\ \vdots \\ Y_{p,1} \\ \vdots \\ Y_{p,n_p} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 & \dots & 0 \\ \vdots & \vdots & \vdots & & \vdots \\ 1 & 0 & 0 & \dots & 0 \\ 0 & 1 & 0 & \dots & 0 \\ \vdots & \vdots & \vdots & & \vdots \\ 0 & 1 & 0 & \dots & 0 \\ \vdots & \vdots & \vdots & & \vdots \\ 0 & 0 & 0 & \dots & 1 \\ \vdots & \vdots & \vdots & & \vdots \\ 0 & 0 & 0 & \dots & 1 \end{bmatrix} \begin{bmatrix} \mu_1 \\ \mu_2 \\ \vdots \\ \mu_p \end{bmatrix} + \begin{bmatrix} e_{11} \\ \vdots \\ e_{1,n_1} \\ e_{21} \\ \vdots \\ e_{2,n_2} \\ \vdots \\ e_{p,1} \\ \vdots \\ e_{p,n_p} \end{bmatrix}. \quad (6.1)$$

Notation. Let $Y_{i0} = \sum_{j=1}^{n_i} Y_{ij}$ and let

$$\hat{\mu}_i = \bar{Y}_{i0} = Y_{i0}/n_i = \frac{1}{n_i} \sum_{j=1}^{n_i} Y_{ij}. \quad (6.2)$$

Hence the “dot notation” means sum over the subscript corresponding to the 0, e.g. j . Similarly, $Y_{00} = \sum_{i=1}^p \sum_{j=1}^{n_i} Y_{ij}$ is the sum of all of the Y_{ij} .

Let $\mathbf{X}_c = [\mathbf{v}_1 \ \mathbf{v}_2 \ \dots \ \mathbf{v}_p]$, and notice that the indicator variables used in the cell means model (6.1) are $\mathbf{v}_{hk} = x_{hk} = 1$ if the h th case has $W = a_k$, and $\mathbf{v}_{hk} = x_{hk} = 0$, otherwise, for $k = 1, \dots, p$ and $h = 1, \dots, n$. So Y_{ij} has $x_{hk} = 1$ only if $i = k$ and $j = 1, \dots, n_i$. The model can use p indicator variables for the factor instead of $p - 1$ indicator variables because the model does not contain an intercept. Also notice that $(\mathbf{X}_c^T \mathbf{X}_c) = \text{diag}(n_1, \dots, n_p)$,

$$E(\mathbf{Y}) = \mathbf{X}_c \boldsymbol{\beta}_c = (\mu_1, \dots, \mu_1, \mu_2, \dots, \mu_2, \dots, \mu_p, \dots, \mu_p)^T,$$

and $\mathbf{X}_c^T \mathbf{Y} = (Y_{10}, \dots, Y_{10}, Y_{20}, \dots, Y_{20}, \dots, Y_{p0}, \dots, Y_{p0})^T$. Hence

$(\mathbf{X}_c^T \mathbf{X}_c)^{-1} = \text{diag}(1/n_1, \dots, 1/n_p)$ and the least squares (OLS) estimator

$$\hat{\boldsymbol{\beta}}_c = (\mathbf{X}_c^T \mathbf{X}_c)^{-1} \mathbf{X}_c^T \mathbf{Y} = (\bar{Y}_{10}, \dots, \bar{Y}_{p0})^T = (\hat{\mu}_1, \dots, \hat{\mu}_p)^T.$$

Thus $\hat{\mathbf{Y}} = \mathbf{X}_c \hat{\boldsymbol{\beta}}_c = (\bar{Y}_{10}, \dots, \bar{Y}_{10}, \dots, \bar{Y}_{p0}, \dots, \bar{Y}_{p0})^T$. Hence the ij th fitted value is

$$\hat{Y}_{ij} = \bar{Y}_{i0} = \hat{\mu}_i \quad (6.3)$$

and the ij th residual is

$$r_{ij} = Y_{ij} - \hat{Y}_{ij} = Y_{ij} - \hat{\mu}_i. \quad (6.4)$$

Definition 6.5. Consider the one way fixed effects Anova model. The *response plot* is a plot of $\hat{Y}_{ij} \equiv \hat{\mu}_i$ versus Y_{ij} and the *residual plot* is a plot of $\hat{Y}_{ij} \equiv \hat{\mu}_i$ versus r_{ij} .

The points in the response plot scatter about the identity line and the points in the residual plot scatter about the $r = 0$ line, but the scatter need not be in an evenly populated band. A *dot plot* of Z_1, \dots, Z_m consists of an axis and m points each corresponding to the value of Z_i . The response plot consists of p dot plots, one for each value of $\hat{\mu}_i$. The dot plot corresponding to $\hat{\mu}_i$ is the dot plot of Y_{i1}, \dots, Y_{i,n_i} . The p dot plots should have roughly the same amount of spread, and each $\hat{\mu}_i$ corresponds to level a_i . If a new level a_f corresponding to \mathbf{x}_f was of interest, hopefully the points in the response plot corresponding to a_f would form a dot plot at $\hat{\mu}_f$ similar in spread to the other dot plots, but it may not be possible to predict the value of $\hat{\mu}_f$. Similarly, the residual plot consists of p dot plots, and the plot corresponding to $\hat{\mu}_i$ is the dot plot of r_{i1}, \dots, r_{i,n_i} .

Assume that each $n_i \geq 10$. Under the assumption that the Y_{ij} are from the same location family with different parameters μ_i , each of the p dot plots should have roughly the same shape and spread. This assumption is easier to judge with the residual plot. If the response plot looks like the residual plot, then a horizontal line fits the p dot plots about as well as the identity line, and there is not much difference in the μ_i . If the identity line is clearly superior to any horizontal line, then at least some of the means differ.

The plots contain a great deal of information. The response plot can be used to explain the model, check that the sample from each population (treatment) has roughly the same shape and spread, and to see which populations have similar means. If the

response plot closely resembles the residual plot, there may not be much difference in the p populations. Linearity seems reasonable if the samples scatter about the identity line. The residual plot makes the comparison of “similar shape” and “spread” easier.

Definition 6.6. a) The *total sum of squares*

$$SSTO = \sum_{i=1}^p \sum_{j=1}^{n_i} (Y_{ij} - \bar{Y}_{00})^2.$$

b) The *treatment sum of squares*

$$SSTR = \sum_{i=1}^p n_i (\bar{Y}_{i0} - \bar{Y}_{00})^2.$$

c) The residual sum of squares or *error sum of squares*

$$SSE = \sum_{i=1}^p \sum_{j=1}^{n_i} (Y_{ij} - \bar{Y}_{i0})^2.$$

Definition 6.7. Associated with each SS in Definition 6.6 is a *degrees of freedom* (df) and a *mean square* = SS/df . For SSTO, $df = n - 1$ and $MSTO = SSTO/(n - 1)$. For SSTR, $df = p - 1$ and $MSTR = SSTR/(p - 1)$. For SSE, $df = n - p$ and $MSE = SSE/(n - p)$.

Let $S_i^2 = \sum_{j=1}^{n_i} (Y_{ij} - \bar{Y}_{i0})^2 / (n_i - 1)$ be the sample variance of the i th group. Then the MSE is a weighted sum of the S_i^2 :

$$\begin{aligned} \hat{\sigma}^2 = MSE &= \frac{1}{n - p} \sum_{i=1}^p \sum_{j=1}^{n_i} r_{ij}^2 = \frac{1}{n - p} \sum_{i=1}^p \sum_{j=1}^{n_i} (Y_{ij} - \bar{Y}_{i0})^2 = \\ &= \frac{1}{n - p} \sum_{i=1}^p (n_i - 1) S_i^2 = S_{pool}^2 \end{aligned}$$

where S_{pool}^2 is known as the pooled variance estimator.

The ANOVA F test tests whether the p means are equal. If H_0 is not rejected and the means are equal, then it is possible that the factor is unimportant, but **it is also possible that the factor is important but the level is not**. For example, the factor might be type of catalyst. The yield may be equally good for each type of catalyst, but there would be no yield if no catalyst was used.

The ANOVA table is the same as that for multiple linear regression (MLR), except that SSTR replaces the regression sum of squares. The MSE is again an estimator of σ^2 . The ANOVA F test tests whether all p means μ_i are equal. Shown below is an ANOVA table given in symbols. Sometimes “Treatment” is replaced by “Between treatments,” “Between Groups,” “Model,” “Factor,” or “Groups.” Sometimes “Error” is replaced by “Residual,” or “Within Groups.” Sometimes “p-value” is replaced by “P”, “ $Pr(> F)$,” or “PR > F.” The “p-value” is nearly always an estimated p-value, denoted by pval.

Summary Analysis of Variance Table

Source	df	SS	MS	F	p-value
Treatment	p-1	SSTR	MSTR	$F_o = MSTR/MSE$	for Ho:
Error	n-p	SSE	MSE		$\mu_1 = \dots = \mu_p$

The 4 step fixed effects one way ANOVA F test of hypotheses:

- i) State the hypotheses Ho: $\mu_1 = \mu_2 = \dots = \mu_p$ and Ha: not Ho.
- ii) Find the test statistic $F_o = MSTR/MSE$ or obtain it from output.
- iii) Find the pval from output or use the F -table: pval =

$$P(F_{p-1, n-p} > F_o).$$

iv) State whether you reject Ho or fail to reject Ho. If the pval $\leq \delta$, reject Ho and conclude that the mean response depends on the factor level. (Hence not all of the treatment means are equal.) Otherwise fail to reject Ho and conclude that the mean response does not depend on the factor level. (Hence all of the treatment means are equal, or there is not enough evidence to conclude that the mean response depends on the factor level.)

Rule of thumb 6.1. If

$$\max(S_1, \dots, S_p) \leq 2 \min(S_1, \dots, S_p),$$

then the one way ANOVA F test results will be approximately correct if the response and residual plots suggest that the remaining one way Anova model assumptions are reasonable. See Moore (2007, p. 634). If all of the $n_i \geq 5$, replace the standard deviations by the ranges of the dot plots when examining the response and residual plots. The range $R_i = \max(Y_{i,1}, \dots, Y_{i,n_i}) - \min(Y_{i,1}, \dots, Y_{i,n_i}) = \text{length of the } i\text{th dot plot for } i = 1, \dots, p$. Harwell et al. (1992) suggest that the one way ANOVA F test is robust to the equal variance assumption if the sample sizes n_i are all equal to m where $pm = n$.

The assumption that the zero mean iid errors have constant variance $V(e_{ij}) \equiv \sigma^2$ is much stronger for the one way Anova model than for the multiple linear regression model. The assumption implies that the p population distributions have pdfs from the same location family with different means μ_1, \dots, μ_p but the same variances $\sigma_1^2 = \dots = \sigma_p^2 \equiv \sigma^2$. The one way ANOVA F test has some resistance to the constant variance assumption, but confidence intervals have much less resistance to the constant variance assumption. Consider confidence intervals for μ_i such as $\bar{Y}_{i0} \pm t_{n_i-1, 1-\delta/2} \sqrt{MSE} / \sqrt{n_i}$. MSE is a weighted average of the S_i^2 . Hence MSE overestimates small σ_i^2 and underestimates large σ_i^2 when the σ_i^2 are not equal. Hence using \sqrt{MSE} instead of S_i will make the CI too long or too short, and Rule of thumb 6.1 does not apply to confidence intervals based on MSE.

Remark 6.1. If the units are a representative sample of some population of interest, then randomization of units into groups makes the assumption that Y_{i1}, \dots, Y_{i,n_i} are iid hold to a useful approximation for large sample theory. Random sampling from populations also induces the iid assumption. Linearity can be checked with the response plot, and similar shape and spread of the location families can be checked with both the response and residual plots. Also check that outliers are not present. If the p dot plots in the response plot are approximately symmetric, then the sample sizes n_i can be smaller than if the dot plots are skewed. See Box et al. (2005, pp. 40, 73, 80, 93, 94, 142).

Remark 6.2. When the assumption that the p groups come from the same location

family with finite variance σ^2 is violated, the one way ANOVA F test may not make much sense because unequal means may not imply the superiority of one category over another. Suppose Y is the time in minutes until relief from a headache and that $Y_{1j} \sim N(60, 1)$ while $Y_{2j} \sim N(65, \sigma^2)$. If $\sigma^2 = 1$, then the type 1 medicine gives headache relief 5 minutes faster, on average, and is superior, all other things being equal. But if $\sigma^2 = 100$, then many patients taking medicine 2 experience much faster pain relief than those taking medicine 1, and many experience much longer time until pain relief. In this situation, predictor variables that would identify which medicine is faster for a given patient would be very useful.

Example 6.2. The output below represents grams of fat (minus 100 grams) absorbed by doughnuts using 4 types of fat. See Snedecor and Cochran (1967, p. 259). Let μ_i denote the mean amount of fat i absorbed by doughnuts, $i = 1, 2, 3$ and 4. a) Find $\hat{\mu}_1$. b) Perform a 4 step ANOVA F test.

Solution: a) $\hat{\beta}_{1c} = \hat{\mu}_1 = \bar{Y}_{10} = Y_{10}/n_1 = \sum_{j=1}^{n_1} Y_{1j}/n_1 = (64 + 72 + 68 + 77 + 56 + 95)/6 = 432/6 = 72$.

b) i) $H_0 : \mu_1 = \mu_2 = \mu_3 = \mu_4$ H_a : not H_0

ii) $F = 5.41$

iii) $pval = 0.0069$

iv) Reject H_0 , the mean amount of fat absorbed by doughnuts depends on the type of fat.

fat1	fat2	fat3	fat4
64	78	75	55
72	91	93	66
68	97	78	49
77	82	71	64
56	85	63	70
95	77	76	68

One way Anova for Fat1 Fat2 Fat3 Fat4					
Source	DF	SS	MS	F	P
treatment	3	1636.5	545.5	5.41	0.0069
error	20	2018.0	100.9		

Definition 6.8. A **contrast** $C = \sum_{i=1}^p k_i \mu_i$ where $\sum_{i=1}^p k_i = 0$. The estimated contrast is $\hat{C} = \sum_{i=1}^p k_i \bar{Y}_{i0}$.

If the null hypothesis of the fixed effects one way ANOVA test is not true, then not all of the means μ_i are equal. Researchers will often have hypotheses, before examining the data, that they desire to test. Often such a hypothesis can be put in the form of a contrast. For example, the contrast $C = \mu_i - \mu_j$ is used to compare the means of the i th and j th groups while the contrast $\mu_1 - (\mu_2 + \dots + \mu_p)/(p - 1)$ is used to compare the last $p - 1$ groups with the 1st group. This contrast is useful when the 1st group corresponds to a standard or control treatment while the remaining groups correspond to new treatments.

Assume that the normal cell means model is a useful approximation to the data. Then the $\bar{Y}_{i0} \sim N(\mu_i, \sigma^2/n_i)$ are independent, and

$$\hat{C} = \sum_{i=1}^p k_i \bar{Y}_{i0} \sim N \left(C, \sigma^2 \sum_{i=1}^p \frac{k_i^2}{n_i} \right).$$

Hence the standard error

$$SE(\hat{C}) = \sqrt{MSE \sum_{i=1}^p \frac{k_i^2}{n_i}}.$$

The degrees of freedom is equal to the MSE degrees of freedom $= n - p$.

Consider a family of null hypotheses for contrasts $\{H_0 : \sum_{i=1}^p k_i \mu_i = 0 \text{ where } \sum_{i=1}^p k_i = 0 \text{ and the } k_i \text{ may satisfy other constraints}\}$. Let δ_S denote the probability of a type I error for a single test from the family where a type I error is a false rejection. The **family level** δ_F is an upper bound on the (usually unknown) size δ_T . Note that $\delta_F \approx \delta_T = P(\text{of making at least one type I error among the family of contrasts})$.

Two important families of contrasts are the family of all possible contrasts and the family of pairwise differences $C_{ij} = \mu_i - \mu_j$ where $i \neq j$. The Scheffé multiple comparisons procedure has a δ_F for the family of all possible contrasts, while the Tukey multiple comparisons procedure has a δ_F for the family of all $\binom{p}{2}$ pairwise contrasts.

Remark 6.3. The response plot is also useful. If n is not too small, each $n_i \geq 5$, and the sample mean (where the dot plot crosses the identity line) for one dot plot is below or above another dot plot, then conclude that the population mean corresponding to the higher dot plot is greater than the sample mean corresponding to the lower dot plot. As the n_i increase, the sample mean of one dot plot only needs to be above or below most of the cases in the other dot plot. The p population means may or may not be equal if all p of the dot plots have lots of overlap. This will happen, for example, if the response plot looks like the residual plot. Then this graphical method is inconclusive. Remark 6.2 gives another situation where this graphical method can fail. An advantage of this graphical method is that the p populations do not need to come from populations with the same variance or from the same location scale family as long as OLS gives a consistent estimator of β , i.e., the sample means are consistent estimators of the population means.

Example 6.3. For the SAS Institute (1985, pp. 126-129) clover data, the mean nitrogen content of clover depends on the strain of clover (3dok1, 3dok5, 3dok7, compos, 3dok4, 3dok13). Figure 1 shows the response and residual plots for the data. The plots suggest the constant variance assumption is not reasonable. The population means may or may not differ for the groups with the two smallest sample means, but these two groups appear to have smaller population means than the other groups. Similarly, the population means may or may not differ for the two groups with sample means near 20, but these two groups appear to have population means that are smaller than the two groups with the largest sample means. The population means of these last two groups may or may not differ. Figure 1 was made with the following commands, using the Olive

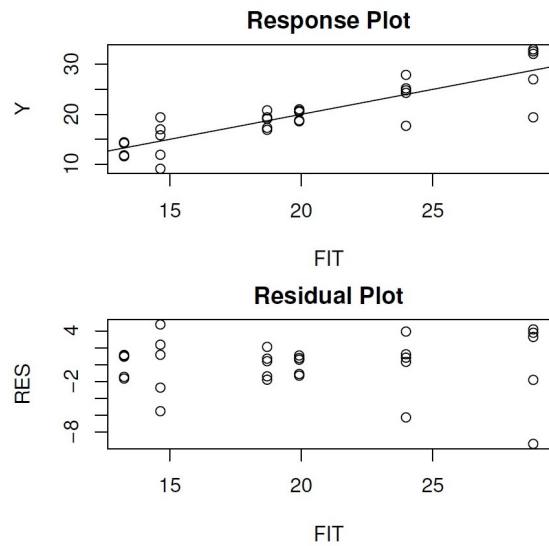


Figure 6.1. Response and Residual Plots for Clover Data

(2017a) *lregpack* function *aovplots*.

```
x<-c(1,1,1,1,1,2,2,2,2,2,3,3,3,3,3,4,4,4,4,4,5,5,5,5,
5,6,6,6,6,6)
```

```
y<-c(19.4,32.6,27.0,32.1,33.0,17.7,24.8,27.9,25.2,
24.3,17.0,19.4,9.1,11.9,15.8,20.7,21.0,20.5,18.8,
18.6,14.3,14.4,11.8,11.6,14.2,17.3,19.4,19.1,16.9,
20.8)
```

```
x <- factor(x)
z <- aov(y~x)
aovplots(Y=y,FIT=fitted(z),RES=resid(z))
#right click stop twice
```

All of the parameterizations of the one way fixed effects Anova model yield the

same predicted values, residuals, and ANOVA F test, but the interpretations of the parameters differ. The cell means model is a linear model (without intercept) of the form $\mathbf{Y} = \mathbf{X}_c \boldsymbol{\beta}_c + \mathbf{e}$ that can be fit using OLS. The OLS MLR output gives the correct fitted values and residuals but an incorrect ANOVA table. An equivalent linear model (with intercept) with correct OLS MLR ANOVA table as well as residuals and fitted values can be formed by replacing any column of the cell means model by a column of ones $\mathbf{1}$. Removing the last column of the cell means model and making the first column $\mathbf{1}$ gives the model $Y = \beta_0 + \beta_1 x_1 + \cdots + \beta_{p-1} x_{p-1} + e$ given in matrix form by (6.5) below. This model corresponds to the MANOVA model in Remark 3.1 with $m = 1$.

It can be shown that the OLS estimators corresponding to (6.5) are $\hat{\beta}_0 = \bar{Y}_{p0} = \hat{\mu}_p$, and $\hat{\beta}_i = \bar{Y}_{i0} - \bar{Y}_{p0} = \hat{\mu}_i - \hat{\mu}_p$ for $i = 1, \dots, p-1$. The cell means model has $\hat{\beta}_i = \hat{\mu}_i = \bar{Y}_{i0}$.

$$\begin{bmatrix} Y_{11} \\ \vdots \\ Y_{1,n_1} \\ Y_{21} \\ \vdots \\ Y_{2,n_2} \\ \vdots \\ Y_{p,1} \\ \vdots \\ Y_{p,n_p} \end{bmatrix} = \begin{bmatrix} 1 & 1 & 0 & \dots & 0 \\ \vdots & \vdots & \vdots & & \vdots \\ 1 & 1 & 0 & \dots & 0 \\ 1 & 0 & 1 & \dots & 0 \\ \vdots & \vdots & \vdots & & \vdots \\ 1 & 0 & 1 & \dots & 0 \\ \vdots & \vdots & \vdots & & \vdots \\ 1 & 0 & 0 & \dots & 1 \\ \vdots & \vdots & \vdots & & \vdots \\ 1 & 0 & 0 & \dots & 1 \\ \vdots & \vdots & \vdots & & \vdots \\ 1 & 0 & 0 & \dots & 0 \\ \vdots & \vdots & \vdots & & \vdots \\ 1 & 0 & 0 & \dots & 0 \end{bmatrix} \begin{bmatrix} \beta_0 \\ \beta_1 \\ \vdots \\ \beta_{p-1} \end{bmatrix} + \begin{bmatrix} e_{11} \\ \vdots \\ e_{1,n_1} \\ e_{21} \\ \vdots \\ e_{2,n_2} \\ \vdots \\ e_{p,1} \\ \vdots \\ e_{p,n_p} \end{bmatrix}. \quad (6.5)$$

Remark 6.4. The following result will be useful for alternative tests. By Graybill (1983, pp. 189-190), if $\mathbf{D} = \text{diag}(d_1, \dots, d_k) + \alpha \mathbf{a} \mathbf{b}^T$, then $\mathbf{D}^{-1} = \text{diag}(1/d_1, \dots, 1/d_k) + \gamma \mathbf{a}^* (\mathbf{b}^*)^T$ where $a_i^* = a_i/d_i, b_i^* = b_i/d_i$, and $\gamma = -\alpha [1 + \alpha \sum_{i=1}^k a_i b_i d_i^{-1}]^{-1}$.

Olive (2017a, pp. 201-202) describes four tests for $H_0 : \mu_1 = \dots = \mu_p$ that can be used if Rule of Thumb 6.1: $\max(S_1, \dots, S_p) \leq 2 \min(S_1, \dots, S_p)$ fails. Let $\mathbf{Y} = (Y_1, \dots, Y_n)^T$, and let $Y_{(1)} \leq Y_{(2)} \leq \dots \leq Y_{(n)}$ be the order statistics. Then the rank transformation of the response is $\mathbf{Z} = \text{rank}(\mathbf{Y})$ where $Z_i = j$ if $Y_i = Y_{(j)}$ is the j th order statistic. For example, if $\mathbf{Y} = (7.7, 4.9, 33.3, 6.6)^T$, then $\mathbf{Z} = (3, 1, 4, 2)^T$. The first test performs the one way ANOVA F test with \mathbf{Z} replacing \mathbf{Y} . (This test can be bad since the distributions of the ranks for each population need not have constant variance. Applying the Welch test to the ranks might work.) See Montgomery (1984, pp. 117-118). Two of the next three tests are described in Brown and Forsythe (1974b). Let $\lceil x \rceil$ be the smallest integer $\geq x$, e.g. $\lceil 7.7 \rceil = 8$. Then the Welch (1951) ANOVA F test uses test statistic

$$F_W = \frac{\sum_{i=1}^p w_i (\bar{Y}_{i0} - \tilde{Y}_{00})^2 / (p-1)}{1 + \frac{2(p-2)}{p^2-1} \sum_{i=1}^p (1 - \frac{w_i}{u})^2 / (n_i - 1)}$$

where $w_i = n_i/S_i^2, u = \sum_{i=1}^p w_i$ and $\tilde{Y}_{00} = \sum_{i=1}^p w_i \bar{Y}_{i0}/u$. Then the test statistic is compared to an F_{p-1, d_W} distribution where $d_W = \lceil f \rceil$ and

$$1/f = \frac{3}{p^2 - 1} \sum_{i=1}^p \left(1 - \frac{w_i}{u}\right)^2 / (n_i - 1).$$

For the modified Welch (1947) test, the test statistic is compared to an $F_{p-1, d_{MW}}$ distribution where $d_{MW} = \lceil f \rceil$ and

$$f = \frac{\sum_{i=1}^p (S_i^2/n_i)^2}{\sum_{i=1}^p \frac{1}{n_i-1} (S_i^2/n_i)^2} = \frac{\sum_{i=1}^p (1/w_i)^2}{\sum_{i=1}^p \frac{1}{n_i-1} (1/w_i)^2}.$$

Some software uses f instead of d_W or d_{MW} , and variants on the denominator degrees of freedom d_W or d_{MW} are common.

The modified ANOVA F test uses test statistic

$$F_M = \frac{\sum_{i=1}^p n_i (\bar{Y}_{i0} - \bar{Y}_{00})^2}{\sum_{i=1}^p (1 - \frac{n_i}{n}) S_i^2}.$$

The test statistic is compared to an F_{p-1, d_M} distribution where $d_M = [f]$ and

$$1/f = \sum_{i=1}^p c_i^2 / (n_i - 1)$$

where

$$c_i = \left(1 - \frac{n_i}{n}\right) S_i^2 / \left[\sum_{i=1}^p \left(1 - \frac{n_i}{n}\right) S_i^2 \right].$$

The new bootstrap test is the same as that given in Section 3.2 for the one way MANOVA model with $m = 1$. Then $F_0 = t_0 / (n - p)$ is equal to the one way ANOVA F statistic. Then

$$\mathbf{w} = \mathbf{AT} = \begin{bmatrix} \bar{Y}_1 - \bar{Y}_p \\ \bar{Y}_2 - \bar{Y}_p \\ \vdots \\ \bar{Y}_{p-2} - \bar{Y}_p \\ \bar{Y}_{p-1} - \bar{Y}_p \end{bmatrix} \quad \text{and} \quad \mathbf{w}^* = \mathbf{AT}^* = \begin{bmatrix} \bar{Y}_1^* - \bar{Y}_p^* \\ \bar{Y}_2^* - \bar{Y}_p^* \\ \vdots \\ \bar{Y}_{p-2}^* - \bar{Y}_p^* \\ \bar{Y}_{p-1}^* - \bar{Y}_p^* \end{bmatrix}. \quad (6.6)$$

Then $F_{0,i}^* = (\mathbf{w}_i^* - \mathbf{w})^T \mathbf{D}^{-1} (\mathbf{w}_i^* - \mathbf{w}) / [(p-1)S_p^2]$ where $S_p^2 = MSE$ and

$$\mathbf{D} = \mathbf{C} / MSE = \text{diag} \left(\frac{1}{n_1}, \dots, \frac{1}{n_{p-1}} \right) + \frac{1}{n_p} \mathbf{1}\mathbf{1}^T.$$

By Remark 6.4,

$$\mathbf{D}^{-1} = \text{diag}(n_1, \dots, n_{p-1}) - \frac{1}{n} (n_1, \dots, n_{p-1}) (n_1, \dots, n_{p-1})^T.$$

Let $F_{0, D(U_B)}$ be the $100U_B$ th percentile of the $F_{0,i}^*$ using with $g = p - 1$ in Equation (2.7).

The F test corresponding to (3.3) uses $F_L = F_0 = t_0 / (p-1)$ or $F_0 = \mathbf{w}^T \mathbf{C}^{-1} \mathbf{w} / (p-1)$

where

$$\mathbf{C} = \text{diag} \left(\frac{S_1^2}{n_1}, \dots, \frac{S_{p-1}^2}{n_{p-1}} \right) + \frac{S_p^2}{n_p} \mathbf{1}\mathbf{1}^T.$$

By Remark 6.4,

$$\mathbf{C}^{-1} = \text{diag} \left(\frac{n_1}{S_1^2}, \dots, \frac{n_{p-1}}{S_{p-1}^2} \right) + \gamma \left(\frac{n_1}{S_1^2}, \dots, \frac{n_{p-1}}{S_{p-1}^2} \right) \left(\frac{n_1}{S_1^2}, \dots, \frac{n_{p-1}}{S_{p-1}^2} \right)^T$$

where

$$\gamma = \frac{-S_p^2}{n_p} \left(1 + \frac{S_p^2}{n_p} \sum_{i=1}^{p-1} \frac{n_i}{S_i^2} \right)^{-1}.$$

This large sample theory test uses $F(n-p, \min(n_i), 1-\delta)$ as a cutoff and needs $\min(n_i)$ large for good power. A plot of F_W versus F_0 suggests that the two statistics are equal, but the two tests used different cutoffs.

6.1 SIMULATION FOR ONE WAY ANOVA

The `lregpack` function `anovasim2` can be used to simulate and compare the first four tests with the usual one way ANOVA test. Some simulation results are in Haenggi (2009). The `mpack` function `anovasim2` adds the new bootstrap test and the large sample theory test to the simulation.

```
args(anovasim2)
```

```
function (n1 = 20, n2 = 20, n3 = 20, n4 = 20, m1 = 0, m2 = 0,
         m3 = 0, m4 = 0, sd1 = 1, sd2 = 1, sd3 = 1, sd4 = 1, type = 1,
         B = 400, nruns = 100, alpha = 0.05)
```

Each simulation used 5000 runs and used different n_i, μ_i, σ_i where $i = 1, 2, 3,$ and 4 . Also $\alpha = 0.05$ and three type of data are used: Type 1(Normal data), Type 2(Exponential data), and Type 3(Mixture data).

It is expected to get the type 1 error coverage near 0.05 when $\mu_1, \mu_2, \mu_3, \mu_4$ are equal, otherwise want coverage near 1. In Tables 6.1, 6.2, and 6.3, for small sample size with equal variances, the bootstrap methods and large sample method gives poor coverages. When the sample size increases all methods work fine. Tables 6.4-6.9 show the coverages for exponential data with unequal variances. Then the Welch, Bootstrap method and Large sample method work best. Tabel 6.10 shows some interesting runs. In this table the Welch test is the best compared to other methods, especially for small sample sizes. The Bootstrap method and Large sample method works similar to Welch test when the sample size is large.

Table 6.1. $\sigma_1 = \sigma_2 = \sigma_3 = \sigma_4 = 1$, and for data type 1, F = proportion of times the ANOVA F test rejected H_0 with level .05, 5,000 runs

n_1, n_2, n_3, n_4	$\mu_1, \mu_2, \mu_3, \mu_4$	F	BT	F_M	F_W	F_{MW}	F_R	F_L
10,10,10,10	0,0,0,0	0.050	0.086	0.048	0.051	0.061	0.051	0.037
	1,0,0,0	0.561	0.656	0.553	0.521	0.559	0.542	0.459
	1,0,0,0.7	0.582	0.674	0.574	0.530	0.571	0.568	0.474
	5,0,0,0.5	1.000	1.000	1.000	1.000	1.000	1.000	1.000
20,20,20,20	0,0,0,0	0.053	0.064	0.053	0.054	0.059	0.051	0.045
	1,0,0,0	0.902	0.920	0.901	0.884	0.895	0.881	0.864
	1,0,0,0.7	0.909	0.926	0.908	0.900	0.906	0.897	0.883
	5,0,0,0.5	1.000	1.000	1.000	1.000	1.000	1.000	1.000
100,100,100,100	0,0,0,0	0.052	0.052	0.052	0.051	0.052	0.050	0.050
	1,0,0,0	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	1,0,0,0.7	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	5,0,0,0.5	1.000	1.000	1.000	1.000	1.000	1.000	1.000

Table 6.2. $\sigma_1 = \sigma_2 = \sigma_3 = \sigma_4 = 1$, and for data type 2, $F =$ proportion of times the ANOVA F test rejected H_0 with level .05, 5,000 runs

n_1, n_2, n_3, n_4	$\mu_1, \mu_2, \mu_3, \mu_4$	F	BT	F_M	F_W	F_{MW}	F_R	F_L
10,10,10,10	0,0,0,0	0.045	0.059	0.035	0.054	0.062	0.052	0.039
	1,0,0,0	0.598	0.662	0.575	0.693	0.719	0.817	0.630
	1,0,0,0.7	0.608	0.668	0.592	0.647	0.671	0.821	0.596
	5,0,0,0.5	1.000	1.000	1.000	1.000	1.000	1.000	1.000
20,20,20,20	0,0,0,0	0.046	0.050	0.044	0.058	0.064	0.047	0.047
	1,0,0,0	0.905	0.912	0.902	0.956	0.961	0.994	0.947
	1,0,0,0.7	0.905	0.910	0.902	0.919	0.925	0.989	0.905
	5,0,0,0.5	1.000	1.000	1.000	1.000	1.000	1.000	1.000
100,100,100,100	0,0,0,0	0.050	0.047	0.050	0.055	0.057	0.050	0.053
	1,0,0,0	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	1,0,0,0.7	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	5,0,0,0.5	1.000	1.000	1.000	1.000	1.000	1.000	1.000

Table 6.3. $\sigma_1 = \sigma_2 = \sigma_3 = \sigma_4 = 1$, and for data type 3, F = proportion of times the ANOVA F test rejected H_0 with level .05, 5,000 runs

n_1, n_2, n_3, n_4	$\mu_1, \mu_2, \mu_3, \mu_4$	F	BT	F_M	F_W	F_{MW}	F_R	F_L
10,10,10,10	0,0,0,0	0.051	0.076	0.047	0.068	0.077	0.063	0.053
	1,0,0,0	0.576	0.645	0.564	0.597	0.626	0.633	0.543
	1,0,0,0.7	0.595	0.662	0.583	0.590	0.615	0.670	0.527
	5,0,0,0.5	1.000	1.000	1.000	1.000	1.000	1.000	1.000
20,20,20,20	0,0,0,0	0.055	0.067	0.054	0.064	0.071	0.078	0.055
	1,0,0,0	0.887	0.902	0.885	0.903	0.912	0.943	0.887
	1,0,0,0.7	0.900	0.911	0.899	0.896	0.905	0.944	0.881
	5,0,0,0.5	1.000	1.000	1.000	1.000	1.000	1.000	1.000
100,100,100,100	0,0,0,0	0.052	0.052	0.052	0.053	0.054	0.178	0.052
	1,0,0,0	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	1,0,0,0.7	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	5,0,0,0.5	1.000	1.000	1.000	1.000	1.000	1.000	1.000

Table 6.4. $\sigma_1 = 1, \sigma_2 = 2, \sigma_3 = 2, \sigma_4 = 3$, and for data type 1, F = proportion of times the ANOVA F test rejected H_0 with level .05, 5,000 runs

n_1, n_2, n_3, n_4	$\mu_1, \mu_2, \mu_3, \mu_4$	F	BT	F_M	F_W	F_{MW}	F_R	F_L
10,10,10,10	0,0,0,0	0.063	0.083	0.058	0.056	0.064	0.064	0.041
	1.3,0,0,0	0.221	0.280	0.200	0.460	0.481	0.319	0.403
	0,0,0,1	0.174	0.206	0.160	0.113	0.123	0.139	0.088
	1,0,0,1	0.188	0.228	0.172	0.262	0.279	0.223	0.222
20,20,20,20	0,0,0,0	0.061	0.060	0.058	0.042	0.045	0.049	0.036
	1.3,0,0,0	0.481	0.483	0.470	0.825	0.835	0.658	0.807
	0,0,0,1	0.285	0.287	0.276	0.182	0.190	0.222	0.163
	1,0,0,1	0.360	0.360	0.347	0.542	0.557	0.440	0.513
100,100,100,100	0,0,0,0	0.058	0.049	0.057	0.046	0.048	0.060	0.045
	1.3,0,0,0	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	0,0,0,1	0.880	0.859	0.879	0.768	0.771	0.801	0.762
	1,0,0,1	0.992	0.988	0.992	1.000	1.000	0.998	1.000

Table 6.5. $\sigma_1 = 1, \sigma_2 = 2, \sigma_3 = 2, \sigma_4 = 3$, and for data type 2, F = proportion of times the ANOVA F test rejected H_0 with level .05, 5,000 runs

n_1, n_2, n_3, n_4	$\mu_1, \mu_2, \mu_3, \mu_4$	F	BT	F_M	F_W	F_{MW}	F_R	F_L
10,10,10,10	0,0,0,0	0.064	0.074	0.052	0.091	0.095	0.132	0.071
	1.3,0,0,0	0.318	0.361	0.289	0.666	0.682	0.658	0.627
	0,0,0,1	0.134	0.151	0.111	0.105	0.107	0.131	0.083
	1,0,0,1	0.214	0.248	0.185	0.428	0.441	0.450	0.389
20,20,20,20	0,0,0,0	0.064	0.063	0.061	0.084	0.085	0.232	0.073
	1.3,0,0,0	0.515	0.504	0.497	0.889	0.892	0.962	0.873
	0,0,0,1	0.247	0.237	0.236	0.156	0.162	0.218	0.138
	1,0,0,1	0.401	0.390	0.386	0.640	0.651	0.825	0.617
100,100,100,100	0,0,0,0	0.059	0.048	0.059	0.057	0.058	0.851	0.056
	1.3,0,0,0	0.999	0.999	0.999	1.000	1.000	1.000	1.000
	0,0,0,1	0.896	0.876	0.896	0.820	0.822	0.823	0.814
	1,0,0,1	0.992	0.988	0.992	0.999	0.999	1.000	0.999

Table 6.6. $\sigma_1 = 1, \sigma_2 = 2, \sigma_3 = 2, \sigma_4 = 3$, and for data type 3, F = proportion of times the ANOVA F test rejected H_0 with level .05, 5,000 runs

n_1, n_2, n_3, n_4	$\mu_1, \mu_2, \mu_3, \mu_4$	F	BT	F_M	F_W	F_{MW}	F_R	F_L
10,10,10,10	0,0,0,0	0.073	0.095	0.065	0.097	0.101	0.119	0.079
	1.3,0,0,0	0.304	0.351	0.280	0.598	0.613	0.543	0.546
	0,0,0,1	0.130	0.155	0.108	0.095	0.100	0.104	0.074
	1,0,0,1	0.199	0.241	0.174	0.369	0.383	0.328	0.320
20,20,20,20	0,0,0,0	0.074	0.073	0.069	0.085	0.088	0.186	0.075
	1.3,0,0,0	0.533	0.527	0.519	0.868	0.872	0.901	0.848
	0,0,0,1	0.252	0.240	0.238	0.143	0.148	0.151	0.122
	1,0,0,1	0.379	0.374	0.363	0.574	0.582	0.639	0.550
100,100,100,100	0,0,0,0	0.062	0.050	0.061	0.055	0.057	0.682	0.053
	1.3,0,0,0	1.000	0.999	0.999	1.000	1.000	1.000	1.000
	0,0,0,1	0.904	0.888	0.904	0.822	0.825	0.591	0.817
	1,0,0,1	0.993	0.991	0.993	0.999	0.999	1.000	0.999

Table 6.7. $\sigma_1 = \sigma_2 = \sigma_3 = 1, \sigma_4 = 9$, for Type 1 data, F = proportion of times the ANOVA F test rejected H_0 with level .05, 5,000 runs

$n1, n2, n3, n4$	$\mu_1, \mu_2, \mu_3, \mu_4$	F	BT	F_M	F_W	F_{MW}	F_R	F_L
10,10,10,10	0,0,0,0	0.116	0.097	0.084	0.050	0.032	0.093	0.038
	1.3,0,0,0	0.147	0.119	0.102	0.735	0.640	0.492	0.676
	0,0,0,1	0.131	0.111	0.098	0.057	0.035	0.094	0.040
	1,0,0,1	0.147	0.117	0.102	0.482	0.383	0.313	0.412
20,20,20,20	0,0,0,0	0.108	0.068	0.089	0.050	0.039	0.079	0.042
	1.3,0,0,0	0.144	0.097	0.121	0.977	0.970	0.895	0.972
	0,0,0,1	0.151	0.102	0.131	0.061	0.049	0.107	0.052
	1,0,0,1	0.148	0.096	0.122	0.836	0.799	0.639	0.809
100,100,100,100	0,0,0,0	0.107	0.054	0.103	0.051	0.049	0.085	0.049
	1.3,0,0,0	0.470	0.232	0.450	1.000	1.000	1.000	1.000
	0,0,0,1	0.291	0.187	0.285	0.132	0.127	0.198	0.129
	1,0,0,1	0.330	0.190	0.320	1.000	1.000	1.000	1.000

Table 6.8. $\sigma_1 = \sigma_2 = \sigma_3 = 1, \sigma_4 = 9$, for Type 2 data, F = proportion of times the ANOVA F test rejected H_0 with level .05, 5,000 runs

n_1, n_2, n_3, n_4	$\mu_1, \mu_2, \mu_3, \mu_4$	F	BT	F_M	F_W	F_{MW}	F_R	F_L
10,10,10,10	0,0,0,0	0.155	0.142	0.128	0.081	0.068	0.203	0.070
	1.3,0,0,0	0.210	0.189	0.171	0.843	0.785	0.759	0.805
	0,0,0,1	0.126	0.105	0.093	0.066	0.050	0.149	0.055
	1,0,0,1	0.146	0.129	0.113	0.616	0.529	0.540	0.559
20,20,20,20	0,0,0,0	0.140	0.103	0.119	0.075	0.065	0.308	0.067
	1.3,0,0,0	0.203	0.157	0.178	0.990	0.988	0.992	0.988
	0,0,0,1	0.120	0.078	0.102	0.058	0.048	0.187	0.051
	1,0,0,1	0.149	0.098	0.121	0.903	0.884	0.924	0.888
100,100,100,100	0,0,0,0	0.118	0.066	0.114	0.054	0.052	0.825	0.053
	1.3,0,0,0	0.458	0.265	0.442	1.000	1.000	1.000	1.000
	0,0,0,1	0.271	0.156	0.262	0.099	0.094	0.509	0.095
	1,0,0,1	0.327	0.166	0.316	1.000	1.000	1.000	1.000

Table 6.9. $\sigma_1 = \sigma_2 = \sigma_3 = 1, \sigma_4 = 9$, for Type 3 data, F = proportion of times the ANOVA F test rejected H_0 with level .05, 5,000 runs

$n1, n2, n3, n4$	$\mu_1, \mu_2, \mu_3, \mu_4$	F	BT	F_M	F_W	F_{MW}	F_R	F_L
10,10,10,10	0,0,0,0	0.160	0.142	0.130	0.096	0.074	0.209	0.078
	1.3,0,0,0	0.206	0.185	0.172	0.762	0.690	0.650	0.716
	0,0,0,1	0.131	0.112	0.100	0.074	0.054	0.139	0.059
	1,0,0,1	0.147	0.128	0.109	0.541	0.460	0.428	0.485
20,20,20,20	0,0,0,0	0.140	0.104	0.122	0.079	0.069	0.306	0.071
	1.3,0,0,0	0.208	0.161	0.186	0.979	0.972	0.963	0.974
	0,0,0,1	0.117	0.076	0.098	0.063	0.053	0.187	0.056
	1,0,0,1	0.129	0.086	0.110	0.859	0.831	0.798	0.840
100,100,100,100	0,0,0,0	0.114	0.064	0.110	0.060	0.058	0.837	0.058
	1.3,0,0,0	0.454	0.263	0.441	1.000	1.000	1.000	1.000
	0,0,0,1	0.273	0.154	0.264	0.096	0.090	0.543	0.091
	1,0,0,1	0.329	0.163	0.314	1.000	1.000	1.000	1.000

Table 6.10. $\mu_1 = \mu_2 = \mu_3 = \mu_4 = 0$, F = proportion of times the ANOVA F test rejected H_0 with level .05, 5,000 runs

n_1, n_2, n_3, n_4	$\sigma_1, \sigma_2, \sigma_3, \sigma_4$	Type	F	BT	F_M	F_W	F_{MW}	F_R	F_L
10,5,5,40	1,1,1,3	1	0.001	0.072	0.067	0.057	0.072	0.005	0.019
5,5,5,5	1,1,2,1	1	0.066	0.137	0.053	0.053	0.061	0.061	0.036
10,10,10,10	3,1,1,1	1	0.091	0.096	0.077	0.049	0.045	0.065	0.038
10,10,10,10	1,2,1,3	1	0.068	0.080	0.059	0.056	0.057	0.067	0.040
50,50,50,50	3,1,1,1	1	0.082	0.056	0.079	0.053	0.052	0.067	0.049
10,5,5,40	1,1,1,3	2	0.007	0.063	0.057	0.060	0.070	0.084	0.019
5,5,5,5	1,1,2,1	2	0.072	0.141	0.053	0.069	0.075	0.091	0.053
10,10,10,10	3,1,1,1	2	0.109	0.121	0.099	0.076	0.077	0.159	0.062
10,10,10,10	1,2,1,3	2	0.101	0.114	0.086	0.099	0.101	0.174	0.084
50,50,50,50	3,1,1,1	2	0.094	0.071	0.090	0.064	0.063	0.483	0.060
10,5,5,40	1,1,1,3	3	0.006	0.073	0.067	0.071	0.084	0.085	0.026
5,5,5,5	1,1,2,1	3	0.075	0.149	0.062	0.095	0.106	0.092	0.073
10,10,10,10	3,1,1,1	3	0.091	0.089	0.075	0.060	0.057	0.072	0.046
10,10,10,10	1,2,1,3	3	0.083	0.100	0.075	0.090	0.093	0.125	0.073
50,50,50,50	3,1,1,1	3	0.084	0.056	0.080	0.056	0.055	0.085	0.054

6.2 REAL DATA EXAMPLE FOR ANOVA

The data set contains information on 76 people who undertook one of three diets (referred to as diet A, B and C). There is background information such as age, gender, and height. The aim of the study was to see which diet was best for losing weight.

https://www.sheffield.ac.uk/polopoly_fs/1.570199!/file/stcp-Rdataset-Diet.csv

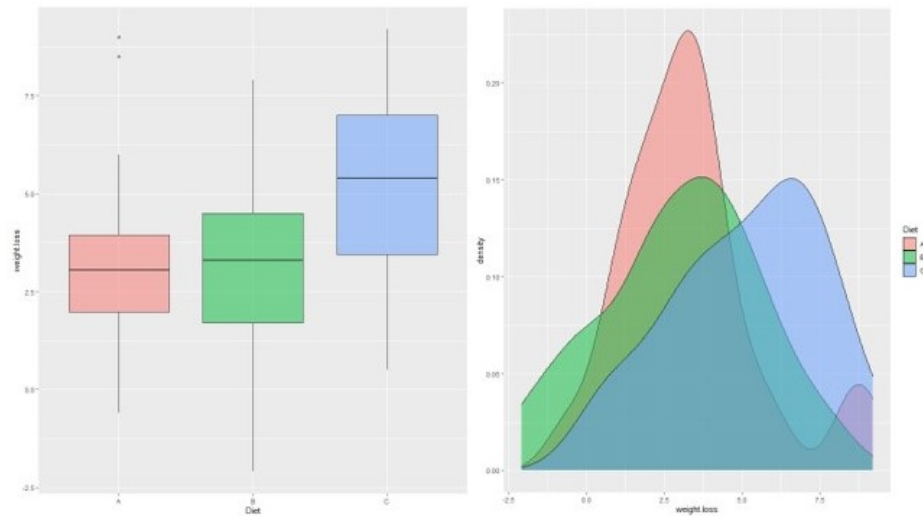


Figure 6.2. Box plot and Density curve for weights loss by Diet type

From Figure 6.2, it can be seen that weight loss has different mean and median for different diet plans. Specially diet C seems to have much higher affect on weight loss.

$$H_0 : \mu_1 = \mu_2 = \mu_3 \text{ vs } H_a : \text{not } H_0$$

For this data set we found the F value and cutoff value for: ANOVA F test, Modified F test, Welch F test, Modified Welch test, Rank F statistics, large sample F test, bootstrap F. In all tests, the F value is greater than the cutoff value. So reject the null and conclude that the some of the diet plans have more effect on weight loss.

Table 6.11. Seven F Tests

Test Type	F Value	Cutoff value
ANOVA F test	6.197447	3.118642
Modified F test	6.241915	3.118642
Welch F test	6.046653	3.18261
Modified Welch test	6.046653	3.18261
Rank F statistics	6.127447	3.402826
large sample F test	5.879764	3.118642
Bootstrap F	6.197447	3.145929

CHAPTER 7

HIGH DIMENSIONAL ONE SAMPLE HOTELLING'S T^2 TYPE TEST

Suppose there is a random sample from a population. A common multivariate one sample test of hypotheses is $H_0 : \boldsymbol{\mu} = \boldsymbol{\mu}_0$ versus $H_1 : \boldsymbol{\mu} \neq \boldsymbol{\mu}_0$ where $\boldsymbol{\mu}$ is a population location measure of the population. The one sample Hotelling's T^2 test is the classical method for the test.

Suppose there is a random sample $\mathbf{y}_1, \dots, \mathbf{y}_n$, and that it is desired to test $H_0 : \boldsymbol{\mu} = \boldsymbol{\mu}_0$ versus $H_1 : \boldsymbol{\mu} \neq \boldsymbol{\mu}_0$ where $\boldsymbol{\mu}$ is a $m \times 1$ vector. We will use $\boldsymbol{\mu} = E(\mathbf{y}_i)$. Let the test statistic $T_n = \bar{\mathbf{y}}$ and the bootstrapped test statistic $T^* = \bar{\mathbf{y}}^*$ where the nonparametric bootstrap is used. Hence n cases are drawn with replacement from the sample to form $\bar{\mathbf{y}}^*$. We will also use $T_n =$ the coordinatewise median where $\boldsymbol{\mu}$ is the population coordinatewise median. We will use $\mathbf{C}_n = \mathbf{C}_n^{-1} = \mathbf{I}_m$. Let $\boldsymbol{\theta} = \boldsymbol{\mu}_0 = \mathbf{0}$.

The first large sample $100(1 - \delta)\%$ confidence region is

$$\{\mathbf{w} : (\mathbf{w} - T_n)^T \mathbf{C}_n^{-1} (\mathbf{w} - T_n) \leq D_{(U_B, T)}^2\} = \{\mathbf{w} : D_{\mathbf{w}}^2(T_n, \mathbf{I}) \leq D_{(U_B, T)}^2\} \quad (7.1)$$

where the cutoff $D_{(U_B, T)}^2$ is the $100(1 - \alpha)$ th sample quantile of the squared Euclidean distance $D_i^2 = (T_i^* - T_n)^T (T_i^* - T_n)$. Note that the corresponding test for $H_0 : \boldsymbol{\theta} = \mathbf{0}$ rejects H_0 if $(T_n - \mathbf{0})^T (T_n - \mathbf{0}) > D_{(U_B, T)}^2$.

The second large sample $100(1 - \delta)\%$ confidence region for $\boldsymbol{\theta}$ is

$$\{\mathbf{w} : (\mathbf{w} - \bar{T}^*)^T \mathbf{C}_n^{-1} (\mathbf{w} - \bar{T}^*) \leq D_{(U_B)}^2\} = \{\mathbf{w} : D_{\mathbf{w}}^2(\bar{T}^*, \mathbf{I}) \leq D_{(U_B)}^2\} \quad (7.2)$$

where the cutoff $D_{(U_B)}^2$ is the $100(1 - \alpha)$ th sample quantile of the squared Euclidean distance $D_i^2 = (T_i^* - \bar{T}^*)^T (T_i^* - \bar{T}^*)$ for $i = 1, \dots, B$. Note that the corresponding test for $H_0 : \boldsymbol{\theta} = \mathbf{0}$ rejects H_0 if $(\bar{T}^* - \mathbf{0})^T (\bar{T}^* - \mathbf{0}) > D_{(U_B)}^2$.

The test uses the result that $\sqrt{n}(\bar{\mathbf{y}} - \boldsymbol{\mu}) \xrightarrow{D} N_m(\mathbf{0}, \boldsymbol{\Sigma}_{\mathbf{y}})$ and $\sqrt{n}(\bar{\mathbf{y}}^* - \bar{\mathbf{y}}) \xrightarrow{D} N_m(\mathbf{0}, \boldsymbol{\Sigma}_{\mathbf{y}})$. Since \mathbf{I} is independent of the bootstrap sample, correction factors for the

bootstrap cutoffs were not needed. Since the sample quantile is that of a random variable, B does not need to be large. If $\Sigma\mathbf{y} = \mathbf{I}$, then

$$(\bar{\mathbf{y}} - \boldsymbol{\mu})^T \mathbf{I}^{-1} (\bar{\mathbf{y}} - \boldsymbol{\mu}) \approx \frac{1}{n} \chi_m^2$$

since

$$n(\bar{\mathbf{y}} - \boldsymbol{\mu})^T \mathbf{I}^{-1} (\bar{\mathbf{y}} - \boldsymbol{\mu}) \xrightarrow{D} \chi_m^2$$

as $n \rightarrow \infty$. For high dimensional data with $m \geq n$, we still have $E(\bar{\mathbf{y}}) = \boldsymbol{\mu}$, $\text{Cov}(\bar{\mathbf{y}}) = \Sigma\mathbf{y}/n$, $E(\bar{\mathbf{y}}^*) = \bar{\mathbf{y}}$, and $\text{Cov}(\bar{\mathbf{y}}^*) = (n-1)\mathbf{S}/n^2$.

7.1 SIMULATIONS FOR HIGH DIMENSIONAL ONE SAMPLE HOTELLING'S T^2 TYPE TEST

The `mpack` function `hdhot1wsim` was used for the simulation. Some high dimensional one sample tests include Chen et al. (2011), Hyodo and Nishiyama (2017), Srivastava and Du (2008), and Wang, Peng, and Li (2015). $\mathbf{C}_n^{-1} = \mathbf{I}$ can be replaced by $\mathbf{C}_n^{-1} = \text{diag}(1/S_1^2, \dots, 1/S_m^2)$ where $S_i^2 = S_{ii}$ when the sample covariance matrix $\mathbf{S} = (S_{ij})$. Other choices of \mathbf{C}_n can be used as long as the computational complexity of \mathbf{C}_n^{-1} is not too high.

```
args(hdhot1wsim)
function (n = 100, p = 10, B = 100, nruns = 100, xtype = 1, eps = 0.4,
        dd = 4, delta = 0, covtyp = 1, psi = 0.1, alpha = 0.1)
```

The argument p is m , and the argument `xtype` gives the multivariate distribution of \mathbf{x} where $\mathbf{y} = \mathbf{A}\mathbf{x}$. Hence `xtype` = 1 for $\mathbf{x} \sim N_p(\mathbf{0}, \mathbf{I})$, `xtype` = 2 for a mixture distribution $\mathbf{x} \sim 0.6N_p(\mathbf{0}, \mathbf{I}) + 0.4N_p(\mathbf{0}, 25\mathbf{I})$ for the default argument `eps` = 0.4, `xtype` = 3 for a multivariate t_4 distribution for the default argument `dd` = 4, and `xtype` = 4 for a multivariate lognormal distribution where $\mathbf{x} = (x_1, \dots, x_p)$ with $w_i = \exp(Z)$ where $Z \sim N(0, 1)$ and $x_i = w_i - E(w_i)$ where $E(w_i) = \exp(0.5)$. The argument `covtyp` = 1 if

$\mathbf{A} = \mathbf{I}$ so, and `covtyp` = 2 if $\mathbf{A} = \text{diag}(\sqrt{1}, \dots, \sqrt{p})$. When `covtyp` = 3, $\text{cor}(Y_i, Y_j) = \rho$ where $\rho = 0$ if $\psi = 0$, $\rho \rightarrow 1/(c + 1)$ as $p \rightarrow \infty$ if $\psi = 1/\sqrt{cp}$ where $c > 0$, and $\rho \rightarrow 1$ as $p \rightarrow \infty$ if $\psi \in (0, 1)$ is a constant. $E(\mathbf{x}) = \delta \mathbf{1}$ where $\mathbf{1}$ is the $p \times 1$ vector of ones. Then the argument `delta` = δ .

The first three distributions have mean $\boldsymbol{\mu} = E(\mathbf{y})$ equal to the population coordinatewise median since the distributions are elliptically contoured distributions with center $\boldsymbol{\mu}$. The fourth distribution does not have $E(\mathbf{y}) =$ the population coordinatewise median. Hence if $H_0 : \boldsymbol{\mu} = \mathbf{0}$ is true for $\boldsymbol{\mu} = E(\mathbf{y})$, then H_0 is false if $\boldsymbol{\mu}$ is the population coordinatewise median.

The simulation used 5000 runs, $\alpha = 0.1$, 4 xtypes, and the 3 covtypes. We used $n = 100$ and $p = 10, 100, 200, 400$. For `covty`=3, we often used $\psi = 1/\sqrt{p}$. We used `delta` = 0 and `delta` = 1. For $\delta = 0$, expect coverage to be less than 0.1 as p increases.

Figures 7.1–7.2 show the type 1 error coverage changes with p . Columns of this plot show three covariences, and rows show the different data types. Figure 7.1 is coverage for the mean and shows how the type 1 error decreases as p increases. For Covtype 3 using $\psi = 0.33$, coverage gets close to nominal coverage 0.1 because when ψ is constant, $\rho \rightarrow 1$ as $p \rightarrow \infty$. But for Covtype 1 and 2 coverage decreases as p increases. Figure 7.2 is coverage for median, and the same results can be seen in the graph.

Table 7.1. HD One Sample Hotelling's T^2 Type Test, $p=10$, $n=100$, $\delta = 0$, $B=100$, and $\psi = 0.31$ (for $\text{covType} = 3$)

X	covType	prcv	brcv	prmedcv	brmedcv
N	1	0.121	0.1118	0.049	0.049
Mix	1	0.1004	0.0908	0.046	0.0438
t	1	0.1058	0.095	0.044	0.0478
LN	1	0.1048	0.0884	1	1
N	2	0.112	0.106	0.059	0.0598
Mix	2	0.1024	0.0922	0.0492	0.0506
t	2	0.1044	0.0954	0.0572	0.0586
LN	2	0.1054	0.0994	1	1
N	3	0.1156	0.1128	0.0896	0.0914
Mix	3	0.1132	0.11	0.0906	0.086
t	3	0.1182	0.1138	0.0902	0.089
LN	3	0.1258	0.121	0.7842	0.7848

Table 7.2. HD One Sample Hotelling's T^2 Type Test, $p=100$, $n=100$, $\delta = 0$, $B=100$, and $\psi = 0.31$ (for $\text{covType} = 3$)

X	covType	prcv	brcv	prmedcv	brmedcv
N	1	0.0714	0.0566	0.0026	0.0044
Mix	1	0.0232	0.0164	0.0016	0.0016
t	1	0.0258	0.0194	0.0024	0.0036
LN	1	0.0454	0.0312	1	1
N	2	0.0884	0.0684	0.006	0.0086
Mix	2	0.0328	0.024	0.0026	0.0038
t	2	0.039	0.0314	0.0048	0.0068
LN	2	0.0548	0.04	1	1
N	3	0.12	0.1162	0.1052	0.102
Mix	3	0.1172	0.1094	0.099	0.0972
t	3	0.125	0.1194	0.108	0.102
LN	3	0.1136	0.1074	0.214	0.213

Table 7.3. HD One Sample Hotelling's T^2 Type Test, $p=200$, $n=100$, $\delta = 0$, $B=100$, and $\psi = 0.31$ (for $\text{covType} = 3$)

X	covType	prcv	brcv	prmedcv	brmedcv
N	1	0.044	0.027	0	0.0006
Mix	1	0.0092	0.0044	0	0
t	1	0.0112	0.008	0	0.0008
LN	1	0.0252	0.0166	1	1
N	2	0.0554	0.0366	0.0002	0.0012
Mix	2	0.0122	0.0076	0.0004	0.0004
t	2	0.0178	0.0136	0.0004	0.0014
LN	2	0.0386	0.0266	1	1
N	3	0.1162	0.1132	0.1042	0.1014
Mix	3	0.1172	0.1136	0.1026	0.1
t	3	0.1208	0.1168	0.1106	0.1086
LN	3	0.1146	0.109	0.1686	0.1674

Table 7.4. HD One Sample Hotelling's T^2 Type Test, $p=400$, $n=100$, $\delta = 0$, $B=100$, and $\psi = 0.31$ (for $\text{covType} = 3$)

X	covType	prcv	brcv	prmedcv	brmedcv
N	1	0.0154	0.0072	0	0
Mix	1	0.0012	0.0012	0	0
t	1	0.0016	0.002	0	0
LN	1	0.013	0.006	1	1
N	2	0.0274	0.0136	0	0
Mix	2	0.0026	0.001	0	0
t	2	0.0034	0.0026	0	0
LN	2	0.021	0.0126	1	1
N	3	0.1226	0.12	0.1154	0.1112
Mix	3	0.1172	0.114	0.1024	0.1022
t	3	0.115	0.113	0.1084	0.107
LN	3	0.1232	0.1194	0.1504	0.1488

Table 7.5. HD One Sample Hotelling's T^2 Type Test, $p=10$, $n=100$, $\delta = 1$, $B=100$, and $\psi = 0.31$ (for $\text{covType} = 3$)

X	covType	prcv	brcv	prmedcv	brmedcv
N	1	1	1	1	1
Mix	1	1	1	1	1
t	1	1	1	1	1
LN	1	1	1	1	1
N	2	1	1	1	1
Mix	2	0.855	0.8526	1	0.9994
t	2	0.9998	0.9998	1	1
LN	2	0.9998	0.9996	0.98	0.9786
N	3	1	1	1	1
Mix	3	0.8052	0.8074	0.999	0.9986
t	3	0.9988	0.999	1	1
LN	3	0.995	0.9956	0.463	0.443

Table 7.6. HD One Sample Hotelling's T^2 Type Test, $p=100$, $n=100$, $\delta = 1$, $B=100$, and $\psi = 0.31$ (for $\text{covType} = 3$)

X	covType	prcv	brcv	prmedcv	brmedcv
N	1	1	1	1	1
Mix	1	1	1	1	1
t	1	1	1	1	1
LN	1	1	1	1	1
N	2	1	1	0.9994	0.999
Mix	2	0.2134	0.181	0.5968	0.5772
t	2	0.9782	0.9752	0.9918	0.9884
LN	2	0.7346	0.7006	1	1
N	3	0.921	0.9192	0.8268	0.823
Mix	3	0.271	0.2662	0.5522	0.5442
t	3	0.7378	0.7356	0.7882	0.781
LN	3	0.443	0.4362	0.149	0.146

Table 7.7. HD One Sample Hotelling's T^2 Type Test, $p=200$, $n=100$, $\delta = 1$, $B=100$, and $\psi = 0.31$ (for $\text{covType} = 3$)

X	covType	prcv	brcv	prmedcv	brmedcv
N	1	1	1	1	1
Mix	1	1	1	1	1
t	1	1	0.9998	1	1
LN	1	1	1	1	1
N	2	1	1	0.9132	0.9156
Mix	2	0.0692	0.0504	0.1232	0.1326
t	2	0.8546	0.8296	0.761	0.7662
LN	2	0.4314	0.3722	1	1
N	3	0.7326	0.7292	0.5832	0.577
Mix	3	0.2042	0.1992	0.3598	0.3504
t	3	0.5162	0.5098	0.5408	0.5348
LN	3	0.2716	0.269	0.121	0.1158

Table 7.8. HD One Sample Hotelling's T^2 Type Test, $p=400$, $n=100$, $\delta = 1$, $B=100$, and $\psi = 0.31$ (for $\text{covType} = 3$)

X	covType	prcv	brcv	prmedcv	brmedcv
N	1	1	1	1	1
Mix	1	1	1	1	1
t	1	1	1	1	1
LN	1	1	1	1	1
N	2	0.9986	0.998	0.2602	0.3334
Mix	2	0.0098	0.0064	0.0024	0.0042
t	2	0.45	0.3846	0.1206	0.1554
LN	2	0.1732	0.1204	1	1
N	3	0.484	0.4848	0.3768	0.3698
Mix	3	0.1618	0.1558	0.2366	0.23
t	3	0.3288	0.3258	0.3364	0.329
LN	3	0.2022	0.2	0.1216	0.1204

Table 7.9. HD One Sample Hotelling's T^2 Type Test, $n=100$, $\delta = 0$, $B=100$, and for $\text{covType} = 3$ with $\psi = 1/\sqrt{p}$

p	x	prcv	brcv	prmedcv	brmedcv
10	N	0.1186	0.1138	0.0908	0.0932
10	Mix	0.123	0.1204	0.0946	0.0902
10	t	0.1104	0.1044	0.0868	0.082
10	LN	0.1202	0.119	0.7876	0.7904
100	N	0.119	0.1154	0.087	0.0864
100	Mix	0.1172	0.1124	0.0784	0.0766
100	t	0.116	0.1098	0.0782	0.076
100	LN	0.1162	0.1092	0.5018	0.5068
200	N	0.1156	0.1086	0.0816	0.0832
200	Mix	0.1086	0.1082	0.0736	0.072
200	t	0.1148	0.1068	0.073	0.073
200	LN	0.1148	0.1098	0.422	0.4248
400	N	0.114	0.1114	0.0792	0.0806
400	Mix	0.1146	0.11	0.0752	0.0718
400	t	0.1116	0.1036	0.0744	0.0756
400	LN	0.1176	0.1118	0.3844	0.3896

Table 7.10. HD One Sample Hotelling's T^2 Type Test, $n=100$, $\delta = 1$, $B=100$, and for $\text{covType} = 3$ with $\psi = 1/\sqrt{p}$

p	x	prcv	brcv	prmedcv	brmedcv
10	N	1	1	1	1
10	Mix	0.8176	0.8148	0.9988	0.9988
10	t	0.9992	0.9992	1	1
10	LN	0.9962	0.9964	0.4682	0.4424
100	N	1	1	1	1
100	Mix	0.8818	0.881	0.9996	0.9996
100	t	0.9998	0.9998	1	1
100	LN	0.997	0.9966	0.7666	0.7586
200	N	1	1	1	1
200	Mix	0.8848	0.8828	0.9996	0.9996
200	t	0.9996	0.9996	1	1
200	LN	0.998	0.998	0.8112	0.8046
400	N	1	1	1	1
400	Mix	0.8984	0.9004	1	1
400	t	0.9998	0.9998	1	1
400	LN	0.998	0.9982	0.8388	0.8316

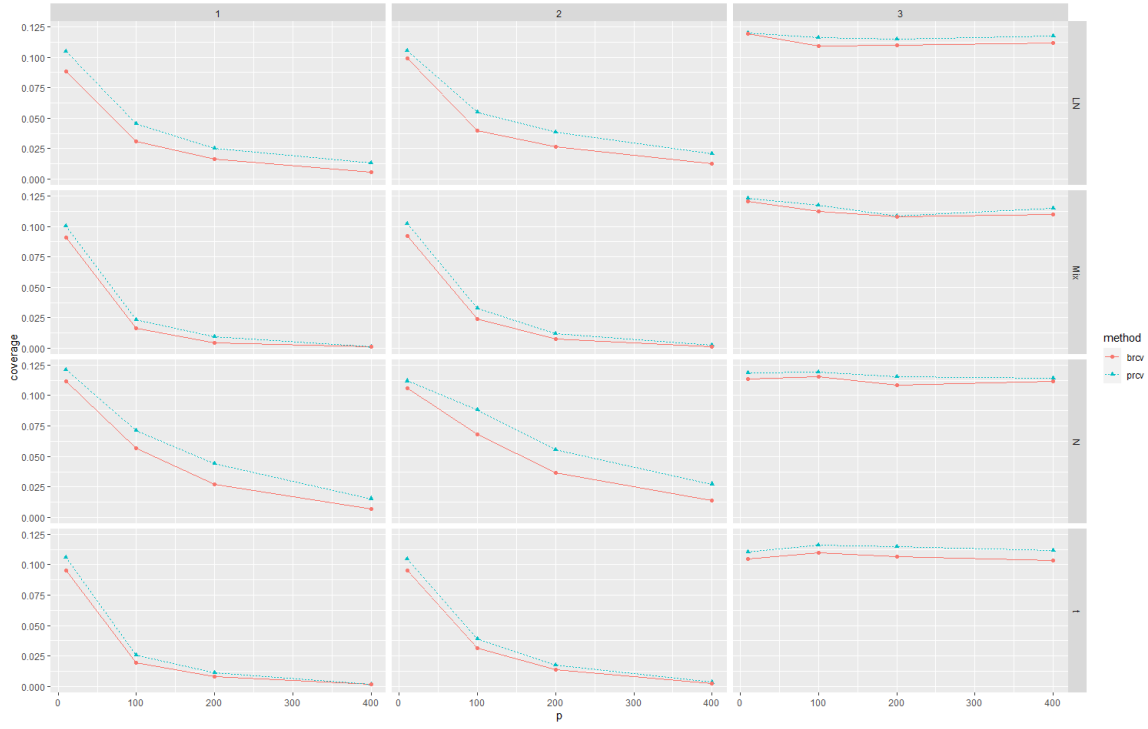


Figure 7.1. Line graph for type 1 error coverage for mean with data types, and covariance types

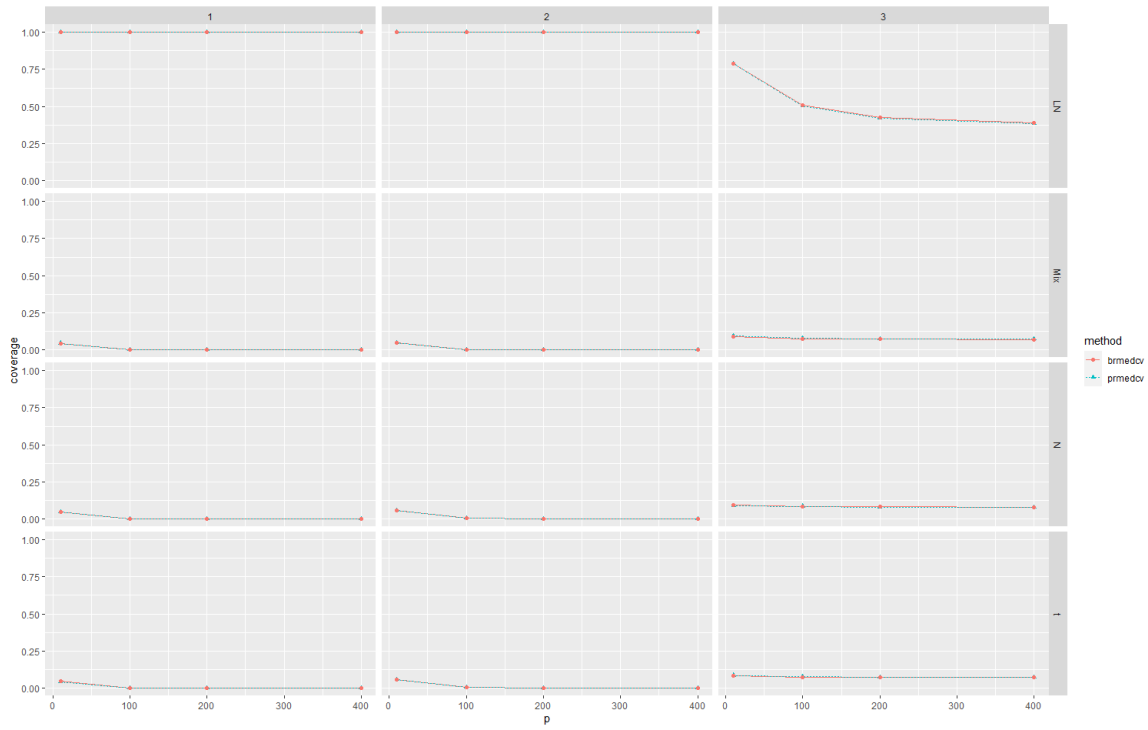


Figure 7.2. Line graph for type 1 error coverage for median with data types, and covariance types

CHAPTER 8

TWO SAMPLE HOTELLING'S T^2 TEST

Suppose there are two independent random samples from two populations or groups. A common multivariate two sample test of hypotheses is $H_0 : \boldsymbol{\mu}_1 = \boldsymbol{\mu}_2$ versus $H_1 : \boldsymbol{\mu}_1 \neq \boldsymbol{\mu}_2$ where $\boldsymbol{\mu}_i$ is a population location measure of the i th population for $i = 1, 2$. The two sample Hotelling's T^2 test is the classical method for the test.

Suppose there are two independent random samples $\boldsymbol{x}_{1,1}, \dots, \boldsymbol{x}_{n_1,1}$ and $\boldsymbol{x}_{1,2}, \dots, \boldsymbol{x}_{n_2,2}$ from two populations or groups, and that it is desired to test $H_0 : \boldsymbol{\mu}_1 = \boldsymbol{\mu}_2$ versus $H_1 : \boldsymbol{\mu}_1 \neq \boldsymbol{\mu}_2$ where $\boldsymbol{\mu}_i$ are $m \times 1$ vectors. Let $n = n_1 + n_2$.

The classical test uses

$$T_C^2 = (\bar{\boldsymbol{x}}_1 - \bar{\boldsymbol{x}}_2)^T \left[\left(\frac{1}{n_1} + \frac{1}{n_2} \right) \hat{\boldsymbol{\Sigma}}_{pool} \right]^{-1} (\bar{\boldsymbol{x}}_1 - \bar{\boldsymbol{x}}_2)$$

where

$$\hat{\boldsymbol{\Sigma}}_{pool} = \frac{(n_1 - 1)\boldsymbol{S}_1 + (n_2 - 1)\boldsymbol{S}_2}{n - 2}.$$

Then reject H_0 if $T_C^2 > mF_{m,n-2,1-\alpha}$.

The large sample test uses

$$T_L^2 = (\bar{\boldsymbol{x}}_1 - \bar{\boldsymbol{x}}_2)^T \left(\frac{\boldsymbol{S}_1}{n_1} + \frac{\boldsymbol{S}_2}{n_2} \right)^{-1} (\bar{\boldsymbol{x}}_1 - \bar{\boldsymbol{x}}_2).$$

Let $d_n = \min(n_1 - p, n_2 - p)$. Then reject H_0 if $T_L^2 > mF_{m,d_n,1-\alpha}$.

Note that $T_C^2 \approx T_L^2$ if $n_1 \approx n_2 \geq 20m$ and the two tests are asymptotically equivalent if $n_i/n \rightarrow 0.5$ as $n_1, n_2 \rightarrow \infty$. The BR bootstrap cutoff for the classical test uses

$$D_i^2 = (T_i^* - T_n)^T \left[\left(\frac{1}{n_1} + \frac{1}{n_2} \right) \hat{\boldsymbol{\Sigma}}_{pool} \right]^{-1} (T_i^* - T_n)$$

where $T_n = (\bar{\boldsymbol{x}}_1 - \bar{\boldsymbol{x}}_2)$ and $T_i^* = (\bar{\boldsymbol{x}}_{1i}^* - \bar{\boldsymbol{x}}_{2i}^*)$. We also use the PR and BR bootstrap tests for the test statistic

$$(\bar{\boldsymbol{x}}_1 - \bar{\boldsymbol{x}}_2)^T (\bar{\boldsymbol{x}}_1 - \bar{\boldsymbol{x}}_2)$$

that uses $C_n = \boldsymbol{I}$. These two tests are also used in Section 9.

8.1 SIMULATIONS FOR TWO SAMPLE HOTELLING'S T^2 TYPE TEST

The data distributions in the simulation are the same as those described in Section 9, but $n_i \geq 10m$. For the classical test, there are distributions where T_C^2 is too large compared to the cutoff, resulting small coverage, and there are distributions where T_C^2 is too small compared to the cutoff, resulting in large coverage. For highly skewed data, large n_i were often needed before the large sample test had coverage close to the nominal, but the coverage tended to be near 0.8805 when the nominal coverage was 0.95. The tests using $\mathbf{C}_n = I$ tended to have coverage close to the nominal, at the cost of producing a confidence region that has a large volume.

```
args(hot2sampsim)
```

```
function (n1 = 100, n2 = 100, p = 2, B = 100, nruns = 100, xtype = 1,  
        sig = 1, eps = 0.4, dd = 4, delta = 0, covtyp = 1, alpha = 0.05)
```

Figures 8.1 and 8.2 show the coverages for the multivariate normal distribution and multivariate t distribution for different delta levels. Here $\delta = \{0, 0.05, 0.1, 0.15, 0.2, 0.25, 0.3, 0.35, 0.4, 0.45\}$, When δ increases, the distance between mean vectors increases. In Figure 8.1, it can be clearly see that T_C^2 is too small compared to the cutoff, resulting in large coverage for classical test, while in Figure 8.2, T_C^2 is too large compared to the cutoff, resulting in small coverage for classical test compare to the other tests.

Figure 8.3 and Figure 8.4, use multivariate lognormal data which is skewed. The coverages for the to BR and PR methods are are near the nominal value, while the other coverages are lower than the nominal value. For skewed data, PR and BR methods work best compared to other methods.

8.2 REAL DATA EXAMPLE

A certain type of tropical disease is characterized by fever, low blood pressure and body aches. A pharmaceutical company is working on a new drug to treat this type

Table 8.1. Two Sample Hotelling's T^2 Type Test, $p=4$, $\alpha=0.05$, $\sigma = 4$, $B=100$, $\text{covType}=1$

xType	n1	n2	Ccov	LScov	bootcov	prcv	brcv
1	50	100	0.997	0.952	0.9445	0.932	0.934
1	100	100	0.937	0.9395	0.9445	0.924	0.9335
1	100	800	1	0.9615	0.9675	0.948	0.9475
1	200	100	0.7095	0.9405	0.948	0.936	0.9405
1	200	200	0.9535	0.957	0.96	0.9455	0.949
1	400	100	0.429	0.952	0.9535	0.934	0.937
1	1000	800	0.9005	0.946	0.9565	0.942	0.942
2	50	100	0.998	0.952	0.947	0.9315	0.936
2	100	100	0.943	0.9485	0.9545	0.943	0.949
2	100	800	1	0.951	0.9635	0.936	0.937
2	200	100	0.696	0.953	0.9575	0.937	0.944
2	200	200	0.959	0.9615	0.9645	0.946	0.95
2	400	100	0.4025	0.9555	0.962	0.948	0.9495
3	1000	800	0.9005	0.951	0.957	0.9335	0.9375
3	50	100	0.9985	0.957	0.955	0.94	0.946
3	100	100	0.9505	0.9565	0.9595	0.946	0.9515
3	100	800	1	0.9565	0.965	0.931	0.94
3	200	100	0.696	0.943	0.9495	0.9335	0.9395
3	200	200	0.9495	0.951	0.9575	0.9435	0.9485
3	400	100	0.4185	0.9495	0.959	0.9445	0.948
3	1000	800	0.8915	0.9445	0.9565	0.9315	0.938
4	50	100	0.9675	0.9105	0.8925	0.946	0.9475
4	100	100	0.8755	0.8805	0.8835	0.9455	0.95
4	100	800	1	0.9555	0.954	0.938	0.939
4	200	100	0.659	0.867	0.9015	0.947	0.95
4	200	200	0.9155	0.9165	0.925	0.949	0.952
4	400	100	0.379	0.853	0.9065	0.941	0.944

Table 8.2. Two Sample Hotelling's T^2 Type Test, $p=4$, $\alpha=0.05$, $\sigma = 4$, $B=100$, $\text{covType}=2$

xType	n1	n2	Ccov	LScov	bootcov	prev	brcv
1	50	100	0.999	0.9575	0.9535	0.937	0.939
1	100	100	0.9415	0.948	0.955	0.939	0.9425
1	100	800	1	0.9625	0.962	0.938	0.9415
1	200	100	0.7065	0.9465	0.9475	0.928	0.9315
1	200	200	0.9395	0.942	0.948	0.938	0.944
1	400	100	0.4165	0.942	0.9465	0.9315	0.9395
1	1000	800	0.8935	0.946	0.9545	0.935	0.939
2	50	100	0.9975	0.966	0.957	0.946	0.951
2	100	100	0.9385	0.9445	0.949	0.935	0.9405
2	100	800	1	0.9595	0.9645	0.935	0.9435
2	200	100	0.707	0.9485	0.955	0.9425	0.9485
2	200	200	0.951	0.952	0.9605	0.927	0.9355
2	400	100	0.401	0.952	0.962	0.9395	0.9455
2	1000	800	0.888	0.943	0.956	0.9365	0.9395
3	50	100	0.9975	0.961	0.957	0.9515	0.9525
3	100	100	0.949	0.952	0.9535	0.937	0.942
3	100	800	1	0.9535	0.9625	0.936	0.9395
3	200	100	0.7085	0.9495	0.9555	0.931	0.9345
3	200	200	0.9515	0.954	0.9625	0.938	0.945
3	400	100	0.4175	0.951	0.9555	0.93	0.9375
3	1000	800	0.9105	0.9575	0.9675	0.944	0.9475
4	50	100	0.9745	0.901	0.891	0.9335	0.936
4	100	100	0.866	0.8725	0.8905	0.935	0.9355
4	100	800	1	0.956	0.952	0.938	0.943
4	200	100	0.64	0.864	0.887	0.9395	0.943
4	200	200	0.895	0.8985	0.9145	0.929	0.9295
4	400	100	0.38	0.8505	0.9	0.931	0.934
4	1000	800	0.877	0.9345	0.9485	0.94	0.942

Table 8.3. Two Sample Hotelling's T^2 Type Test, $p=4$, $\alpha=0.05$, $\sigma = 4$, $B=100$, $\text{covType}=3$

xType	n1	n2	Ccov	LScov	bootcov	prev	brcv
1	50	100	0.997	0.9545	0.949	0.931	0.936
1	100	100	0.9385	0.945	0.945	0.9395	0.938
1	100	800	1	0.9615	0.967	0.9405	0.9435
1	200	100	0.7025	0.9475	0.9495	0.9385	0.9425
1	200	200	0.9505	0.9515	0.958	0.937	0.9375
1	400	100	0.393	0.9505	0.959	0.946	0.9475
1	1000	800	0.8905	0.9455	0.957	0.9295	0.939
2	50	100	0.999	0.9575	0.954	0.9375	0.9425
2	100	100	0.9405	0.9475	0.952	0.942	0.9445
2	100	800	1	0.9525	0.9545	0.941	0.9425
2	200	100	0.686	0.9485	0.9515	0.935	0.9365
2	200	200	0.9415	0.9435	0.953	0.933	0.94
2	400	100	0.3625	0.945	0.947	0.932	0.939
3	1000	800	0.898	0.9525	0.9585	0.9375	0.9345
3	50	100	0.999	0.953	0.9465	0.9365	0.939
3	100	100	0.9495	0.954	0.9585	0.9385	0.9425
3	100	800	1	0.956	0.96	0.9425	0.9465
3	200	100	0.6875	0.949	0.9515	0.9335	0.94
3	200	200	0.9535	0.955	0.9645	0.9495	0.949
3	400	100	0.3605	0.9525	0.9555	0.9375	0.941
3	1000	800	0.906	0.955	0.9695	0.9425	0.948
4	50	100	0.9765	0.888	0.8765	0.937	0.9405
4	100	100	0.8565	0.8625	0.876	0.9395	0.9445
4	100	800	1	0.951	0.9565	0.946	0.9505
4	200	100	0.6265	0.866	0.8865	0.9475	0.9535
4	200	200	0.887	0.89	0.901	0.9295	0.931
4	400	100	0.335	0.861	0.887	0.928	0.9315
4	1000	800	0.858	0.928	0.944	0.9415	0.9445

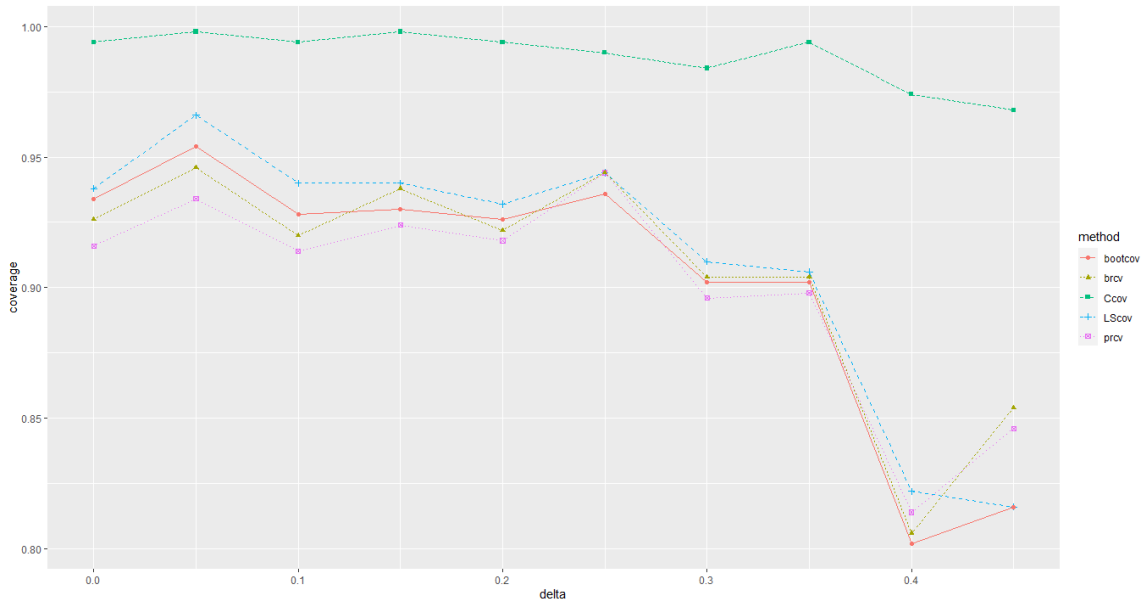


Figure 8.1. Coverage plot for $n_1=50$, $n_2=100$, $p=4$, $xtype=1$, $sig=4$, $covtyp=2$ according to delta values



Figure 8.2. Coverage plot for $n_1=200$, $n_2=100$, $p=4$, $xtype=2$, $sig=4$, $covtyp=2$ according to delta values

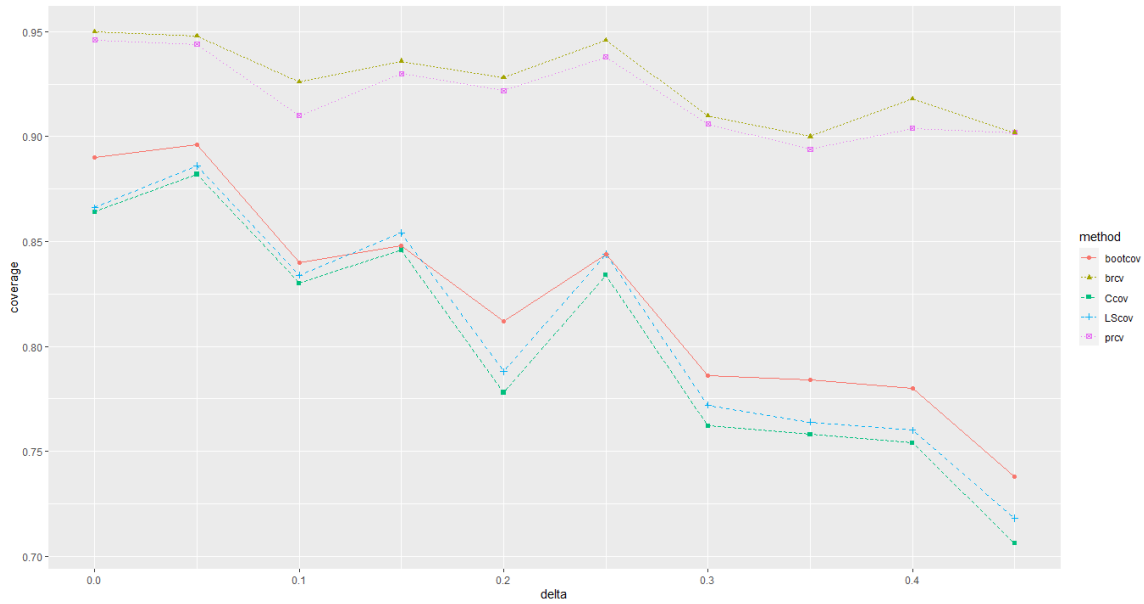


Figure 8.3. Coverage plot for $n_1=100$, $n_2=100$, $p=4$, $xtype=4$, $sig=4$, $covtyp=3$ according to delta values

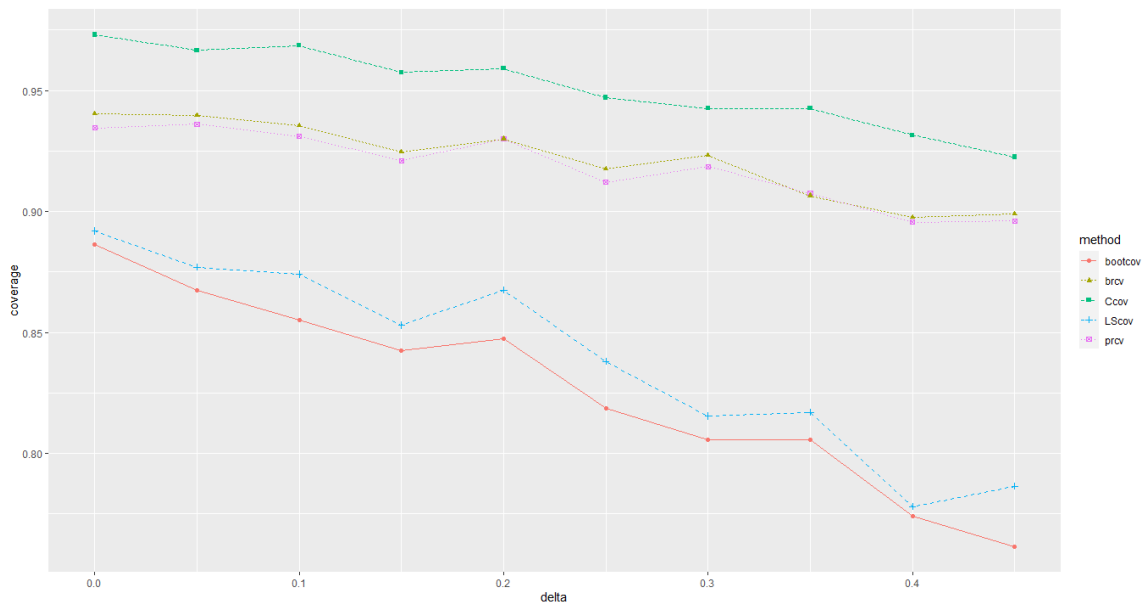


Figure 8.4. Coverage plot for $n_1=50$, $n_2=100$, $p=4$, $xtype=4$, $sig=4$, $covtyp=3$ according to delta values

of disease and wanted to determine whether the drug is effective. They took a random sample of 20 people with this type of disease and 18 with a placebo.

<https://www.real-statistics.com/multivariate-statistics/hotellings-t-square-re-statistic/hotellings-t-square-independent-samples/>

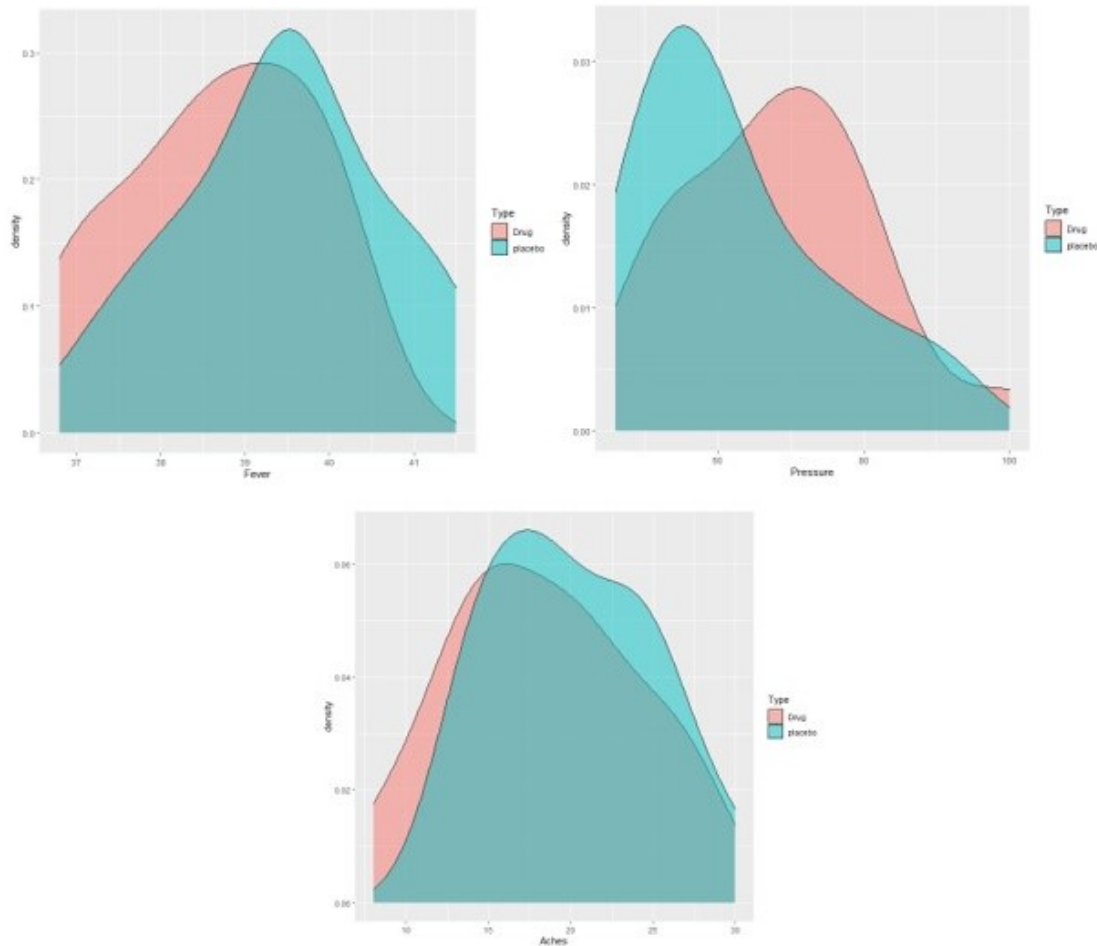


Figure 8.5. Density plots for Fever, low blood pressure, and body aches

$H_0 : \boldsymbol{\mu}_1 = \boldsymbol{\mu}_2$ vs $\boldsymbol{\mu}_1 \neq \boldsymbol{\mu}_2$ where now $\boldsymbol{\mu}_1$ and $\boldsymbol{\mu}_2$ are 3×1 vectors.

In this study we used the Classical test, Large Sample test, Bootstrap test, PR method test and BR method test. Table 8.4 shows the test value and the cutoff values for each test. All tests fail to reject the null hypothesis. It can be concluded that the drug has no effect. The PR and BR test values are closer to cut off values than the values

of the other three tests.

Table 8.4. Test value and the cutoff values for five F tests

Test Type	F Value	Cutoff value
Classical	4.116057	8.598797
Large Sample	4.126844	9.862146
Bootstrap	4.116057	7.979248
PR	6.763542	8.220848
BR	6.476545	8.497052

CHAPTER 9

HIGH DIMENSIONAL TWO SAMPLE HOTELLING'S T^2 TYPE TEST

Suppose there are two independent random samples from two populations or groups. A common multivariate two sample test of hypotheses is $H_0 : \boldsymbol{\mu}_1 = \boldsymbol{\mu}_2$ versus $H_1 : \boldsymbol{\mu}_1 \neq \boldsymbol{\mu}_2$ where $\boldsymbol{\mu}_i$ is a population location measure of the i th population for $i = 1, 2$. The two sample Hotelling's T^2 test is the classical method for the test.

Suppose there are two independent random samples $\mathbf{x}_{1,1}, \dots, \mathbf{x}_{n_1,1}$ and $\mathbf{x}_{1,2}, \dots, \mathbf{x}_{n_2,2}$ from two populations or groups, and that it is desired to test $H_0 : \boldsymbol{\mu}_1 = \boldsymbol{\mu}_2$ versus $H_1 : \boldsymbol{\mu}_1 \neq \boldsymbol{\mu}_2$ where $\boldsymbol{\mu}_i$ are $m \times 1$ vectors. We will use $\boldsymbol{\mu}_i = E(\mathbf{x}_i)$, and $p > n_i$ is possible. Let the test statistic $T_n = \bar{\mathbf{x}}_1 - \bar{\mathbf{x}}_2$ and the bootstrapped test statistic $T^* = \bar{\mathbf{x}}_1^* - \bar{\mathbf{x}}_2^*$ where the nonparametric bootstrap is used. Hence n_i cases are drawn with replacement from sample i to form $\bar{\mathbf{x}}_i^*$. We will use $\mathbf{C}_n = \mathbf{C}_n^{-1} = \mathbf{I}_m$. Let $\boldsymbol{\theta} = \boldsymbol{\mu}_1 - \boldsymbol{\mu}_2$.

The first large sample $100(1 - \delta)\%$ confidence region is

$$\{\mathbf{w} : (\mathbf{w} - T_n)^T \mathbf{C}_n^{-1} (\mathbf{w} - T_n) \leq D_{(U_B, T)}^2\} = \{\mathbf{w} : D_{\mathbf{w}}^2(T_n, \mathbf{I}) \leq D_{(U_B, T)}^2\} \quad (9.1)$$

where the cutoff $D_{(U_B, T)}^2$ is the $100(1 - \alpha)$ th sample quantile of the squared Euclidean distance $D_i^2 = (T_i^* - T_n)^T (T_i^* - T_n)$. Note that the corresponding test for $H_0 : \boldsymbol{\theta} = \mathbf{0}$ rejects H_0 if $(T_n - \mathbf{0})^T (T_n - \mathbf{0}) > D_{(U_B, T)}^2$.

The second large sample $100(1 - \delta)\%$ confidence region for $\boldsymbol{\theta}$ is

$$\{\mathbf{w} : (\mathbf{w} - \bar{T}^*)^T \mathbf{C}_n^{-1} (\mathbf{w} - \bar{T}^*) \leq D_{(U_B)}^2\} = \{\mathbf{w} : D_{\mathbf{w}}^2(\bar{T}^*, \mathbf{I}) \leq D_{(U_B)}^2\} \quad (9.2)$$

where the cutoff $D_{(U_B)}^2$ is the $100(1 - \alpha)$ th sample quantile of the squared Euclidean distance $D_i^2 = (T_i^* - \bar{T}^*)^T (T_i^* - \bar{T}^*)$ for $i = 1, \dots, B$. Note that the corresponding test for $H_0 : \boldsymbol{\theta} = \mathbf{0}$ rejects H_0 if $(\bar{T}^* - \mathbf{0})^T (\bar{T}^* - \mathbf{0}) > D_{(U_B)}^2$.

The test uses the result that $\sqrt{n}(\bar{\mathbf{x}} - \boldsymbol{\mu}) \xrightarrow{D} N_p(\mathbf{0}, \boldsymbol{\Sigma}_{\mathbf{x}})$ and $\sqrt{n}(\bar{\mathbf{x}}^* - \bar{\mathbf{x}}) \xrightarrow{D} N_p(\mathbf{0}, \boldsymbol{\Sigma}_{\mathbf{x}})$. Since \mathbf{I} is independent of the bootstrap sample, correction factors for the bootstrap cutoffs

were not needed. Since the sample quantile is that of a random variable, B does not need to be large. If $\boldsymbol{\mu}_1 = \boldsymbol{\mu}_2$, $\boldsymbol{\Sigma}_{\mathbf{x}_i} = \mathbf{I}$, and $n_1 = n_2 = k$, then

$$(\bar{\mathbf{x}}_1 - \bar{\mathbf{x}}_2)^T \mathbf{I}^{-1} (\bar{\mathbf{x}}_1 - \bar{\mathbf{x}}_2) \approx \frac{2}{k} \chi_m^2$$

since

$$(\bar{\mathbf{x}}_1 - \bar{\mathbf{x}}_2)^T (2\mathbf{I}/k)^{-1} (\bar{\mathbf{x}}_1 - \bar{\mathbf{x}}_2) \xrightarrow{D} \chi_m^2$$

as $k \rightarrow \infty$.

9.1 SIMULATION FOR HIGH DIMENSIONAL TWO SAMPLE HOTELLING'S T^2 TEST

Four types of data distributions \mathbf{w}_i were considered that were identical for $i = 1, 2$. Then $\mathbf{x}_1 = \mathbf{A}\mathbf{w}_1 + \delta\mathbf{1}$ and $\mathbf{x}_2 = \sigma\mathbf{B}\mathbf{w}_2$ where $\mathbf{1} = (1, \dots, 1)^T$ is a vector of ones. We used CovType 1 : $\mathbf{A} = \mathbf{B} = \mathbf{I}$, covType 2: $\mathbf{A} = \mathbf{B} = \text{diag}(1, \sqrt{2}, \dots, \sqrt{m})$, and covType 3: $\mathbf{A} = \mathbf{I}$ with $\mathbf{B} = \text{diag}(1, \sqrt{2}, \dots, \sqrt{m})$. The \mathbf{w}_i distributions were the multivariate normal distribution $N_p(\mathbf{0}, \mathbf{I})$, the mixture distribution $0.6N_m(\mathbf{0}, \mathbf{I}) + 0.4N_m(\mathbf{0}, 25\mathbf{I})$, the multivariate t distribution with 4 degrees of freedom, and the multivariate lognormal distribution shifted to have zero mean. Note that $\text{Cov}(\mathbf{x}_2) = \sigma^2 \text{Cov}(\mathbf{x}_1)$ when $\mathbf{A} = \mathbf{B}$, and $E(\mathbf{x}_i) = E(\mathbf{w}_i) = \mathbf{0}$ if $\delta = 0$.

The `mpack` function `hdhot2wsim` was used for the simulation. Some high dimensional two sample tests include Feng et al. (2015), Feng and Sun (2015), Gregory et al. (2015), Hu and Bai (2016), Tamatani and Naiti (2019), and Zhang et al. (2020) who use test statistic $n_1 n_2 T_n / n$ but assume $\boldsymbol{\Sigma}_{\mathbf{x}_1} = \boldsymbol{\Sigma}_{\mathbf{x}_2}$.

```
args(hdhot2wsim)
```

```
function (n1 = 100, n2 = 100, p = 10, B = 100, nruns = 100, xtype = 1,
        sig = 1, eps = 0.4, dd = 4, delta = 0, covtyp = 1, alpha = 0.05)
```

According to Tables 9.1 and 9.2 for Multivariate normal data with $\boldsymbol{\Sigma}_{x_1} = \boldsymbol{\Sigma}_{x_2}$, i.e. for covType 1 and 2, testing mean coverages gives type 1 error less than the nominal

value 0.1. As for the testing the median, coverages for Type 1 error are lower than the nominal coverage for both the PR and BR methods. In Table 9.3 when $\delta = 0.8$, means and medians of two groups are different so it is expected to get coverage near 1. For mixture data with covType 2 and 3, powers are poor, but for all other data types, the PR and BR methods provide good coverages.

Table 9.1. HD Two Sample Hotelling's T^2 Type Test, $p=100, n_1 < 100, n_2 < 100, \alpha=0.1, \delta = 0, B=100$

n1,n2	xtype	covType	prcv	brcv	prmedcv	brmedcv
50,50	1	1	0.077	0.058	0.0005	0.002
	1	2	0.111	0.0895	0.001	0.0055
	1	3	0.058	0.0455	0.002	0.0035
	2	1	0.0305	0.02	0	0
	2	2	0.0395	0.0335	0.001	0.002
	2	3	0.0155	0.01	0.0005	0.001
	3	1	0.0325	0.0225	0	0
	3	2	0.0465	0.0385	0.001	0.0045
	3	3	0.0285	0.0205	0.002	0.0025
	4	1	0.058	0.0445	0	0
	4	2	0.065	0.05	0.002	0.003
	4	3	0.0365	0.03	1	1
50,75	1	1	0.087	0.068	0.001	0.0035
	1	2	0.0915	0.076	0.003	0.0085
	1	3	0.076	0.0585	0.0005	0.0045
	2	1	0.0345	0.0205	0	0.0005
	2	2	0.041	0.0345	0.001	0.001
	2	3	0.0285	0.0205	0.001	0.0005
	3	1	0.0345	0.0275	0.0005	0.001
	3	2	0.045	0.033	0.001	0.0025

Table 9.2. HD Two Sample Hotelling's T^2 Type Test, $p=100$, $\alpha=0.1$, $\delta = 0$, $B=100$

n1,n2	xtype	covType	prcv	brcv	prmedcv	brmedcv
100,100	1	1	0.11	0.086	0.0045	0.0115
	1	2	0.1145	0.087	0.0055	0.0105
	1	3	0.083	0.0615	0.004	0.009
	2	1	0.0525	0.038	0.0015	0.0015
	2	2	0.0695	0.0535	0.0055	0.0065
	2	3	0.031	0.022	0.003	0.0045
	3	1	0.0555	0.043	0.003	0.0065
	3	2	0.063	0.0495	0.0085	0.0125
	3	3	0.041	0.034	0.0055	0.0075
	4	1	0.0695	0.0515	0.001	0.0025
	4	2	0.0735	0.061	0.003	0.0085
	4	3	0.0625	0.047	1	1
	1	1	0.103	0.0835	0.0045	0.0095
100,200	1	2	0.1035	0.082	0.0085	0.0165
	1	3	0.083	0.06	0.004	0.009
	2	1	0.0595	0.0475	0.003	0.004
	2	2	0.0655	0.0495	0.006	0.008
	2	3	0.0425	0.0325	0.0025	0.0035
	3	1	0.044	0.0315	0.003	0.005
	3	2	0.0575	0.0445	0.006	0.011
	3	3	0.0405	0.031	0.003	0.0035
	4	1	0.076	0.0585	0.0015	0.003
	4	2	0.0875	0.0645	0.007	0.0065
	4	3	0.06	0.0415	1	1

Table 9.3. HD Two Sample Hotelling's T^2 Type Test, $p=100$, $\alpha=0.1$, $\delta = 0.8$, $B=100$

n1,n2	xtype	covType	prcv	brcv	prmedcv	brmedcv
100,100	1	1	1	1	1	1
	1	2	0.9795	0.974	0.426	0.4485
	1	3	1	1	0.932	0.921
	2	1	1	1	1	1
	2	2	0.1105	0.0875	0.081	0.087
	2	3	0.1355	0.108	0.245	0.247
	3	1	0.9995	0.9995	1	1
	3	2	0.56	0.524	0.318	0.3325
	3	3	0.8925	0.874	0.817	0.7995
	4	1	1	1	1	1
	4	2	0.261	0.227	0.338	0.329
	4	3	0.462	0.4195	1	1
	1	1	1	1	1	1
	100,200	1	2	0.9985	0.9985	0.7115
1		3	1	1	0.9235	0.911
2		1	1	1	1	1
2		2	0.1545	0.1285	0.169	0.1695
2		3	0.125	0.1125	0.249	0.239
3		1	1	1	1	1
3		2	0.739	0.706	0.574	0.577
3		3	0.868	0.853	0.8385	0.8195
4		1	1	1	1	1
4		2	0.3635	0.3225	0.51	0.5575
4		3	0.472	0.4205	1	1

CHAPTER 10
ONE WAY MANOVA TYPE TEST

10.1 SIMULATION ONE WAY MANOVA TYPE TEST

We used 3 groups for the one way MANOVA type tests. Four types of data distributions \mathbf{w}_i were considered that were identical for $i = 1, 2$, and 3. Then $\mathbf{y}_1 = \sigma_1 \mathbf{C} \mathbf{w}_1 + \delta_1 \mathbf{1}$, $\mathbf{y}_2 = \sigma_2 \mathbf{C} \mathbf{w}_2 + \delta_2 \mathbf{1}$, and $\mathbf{y}_3 = \sigma_3 \mathbf{C} \mathbf{w}_3 + \delta_3 \mathbf{1}$ or $\mathbf{y}_3 = \mathbf{w}_3$ where $\mathbf{1} = (1, \dots, 1)^T$ is a vector of ones and $\mathbf{C} = \text{diag}(1, \sqrt{2}, \dots, \sqrt{m})$. The \mathbf{w}_i distributions were the multivariate normal distribution $N_m(\mathbf{0}, \mathbf{I})$, the mixture distribution $0.6N_m(\mathbf{0}, \mathbf{I}) + 0.4N_m(\mathbf{0}, 25\mathbf{I})$, the multivariate t distribution with 4 degrees of freedom, and the multivariate lognormal distribution shifted to have zero mean. If $\sigma_1 = 1$ and $\delta_i = 0$ for $i = 1, 2, 3$, note that $\text{Cov}(\mathbf{y}_2) = \sigma_2^2 \text{Cov}(\mathbf{y}_1)$, and $E(\mathbf{y}_i) = E(\mathbf{w}_i) = \mathbf{0}$. If $\mathbf{y}_3 = \mathbf{w}_3$ then $\text{Cov}(\mathbf{y}_3) = c\mathbf{I}_m$ for some constant $c > 0$. If $\sigma_1 = 1$ and $\mathbf{y}_3 = \sigma_3 \mathbf{C} \mathbf{w}_3 + \delta_3 \mathbf{1}$, then $\text{Cov}(\mathbf{y}_3) = \sigma_3^2 \text{Cov}(\mathbf{y}_1)$.

The classical test, bootstrapped classical test, large sample test, and bootstrap test with $\mathbf{C}_n = \mathbf{I}$ with BR and PR were used. For power, group i has mean $\boldsymbol{\mu}_i = \delta_i \mathbf{1}$ where $\delta_2 = 2 \delta_1$ and $\delta_3 = 3 \delta_1$. When δ_1 increases, the distance between the mean vectors increases.

All tables show that when the $\sigma_1, \sigma_2, \sigma_3$ differ from each other, the classical MANOVA test is poor, giving lower coverage when sample size is small and over coverage when sample size is large. In Table 10.2, it can be seen that the classical test, bootstrap test, and Large sample test gives lower coverage for skewed data while the PR and BR methods work well. In Table 10.6, lognormal data with the $\boldsymbol{\Sigma} = c\mathbf{I}$ shows the situation where the Large sample MANOVA test fails to get coverage near the nominal coverage due to skew and the unequal covariance matrices.

```
library(Matrix) #need to download the Matrix package
args(manovasim)
```

```
function (n1 = 100, n2 = 100, n3 = 100, m = 2, B = 100, nruns = 100,  
        ytype = 1, sig2 = 1, sig3 = 1, eps = 0.4, dd = 4, delta1 = 0,  
        delta2 = 0, delta3 = 0, cov3I = F, alpha = 0.05)  
#use 5000 runs
```

10.2 COVERAGE COMPARISON

10.2.1 Coverage comparison with respect to σ_3 levels

Figures 10.1 and 10.2 illustrate the coverage of several MANOVA type tests with the σ_3 levels. Here $\sigma_3 = \{1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5\}$. Figure 10.1 shows the coverage plot for Multivariate Normal data. For symmetric data when $\sigma_1 = \sigma_2 = \sigma_3 = 1$, all methods works well. As σ_3 increases, gradually the coverage of the classical test decreases but the all other methods work well because they gives the coverage near to the nominal coverage 0.95.

Figure 10.2 shows the coverage plot for Multivariate lognormal data. For skewed data when the σ_3 increases the coverages of classical method, large sample method and bootstrap cutoff for classical method all perform poorly, providing very low coverages. The PR and BR methods work better.

Table 10.1. One Way MANOVA Type Test, Coverage for MVN data with $\Sigma_3 \neq cI$

m	n1,n2,n3	B	σ_2, σ_3	mancov	bootcov	manLScov	prcv	brev
5	200,200,200	400	1,1	0.955	0.96	0.9535	0.946	0.9475
		1000	1,1	0.952	0.949	0.9475	0.9455	0.9465
		400	2,3	0.9315	0.959	0.952	0.946	0.9465
		1000	2,3	0.932	0.95	0.95	0.9415	0.943
5	200,400,600	400	1,1	0.958	0.9625	0.9545	0.949	0.949
		1000	1,1	0.954	0.9545	0.952	0.961	0.9605
		400	2,3	0.996	0.9585	0.9545	0.9505	0.9535
		1000	2,3	0.993	0.948	0.9465	0.957	0.957
10	400,400,400	800	1,1	0.953	0.9575	0.9485	0.948	0.9475
		2000	1,1	0.947	0.947	0.939	0.949	0.9475
		800	2,3	0.925	0.9525	0.9425	0.936	0.9375
		2000	2,3	0.931	0.9495	0.9535	0.949	0.95
10	400,800,1200	800	1,1	0.9555	0.9665	0.9525	0.9465	0.9485
		2000	1,1	0.961	0.9595	0.958	0.9525	0.952
		800	2,3	0.998	0.96	0.9565	0.9485	0.95
		2000	2,3	0.9985	0.9475	0.9575	0.949	0.9475
20	800,800,800	1600	1,1	0.9505	0.9545	0.947	0.9485	0.9505
		4000	1,1	0.9475	0.9475	0.943	0.9505	0.9505
		1600	2,3	0.9235	0.9545	0.937	0.949	0.951
		4000	2,3	0.93	0.9515	0.9495	0.949	0.9475
20	800,1600,2400	1600	1,1	0.952	0.962	0.9455	0.9505	0.9495
		4000	1,1	0.9575	0.9585	0.954	0.9565	0.9555
		1600	2,3	1	0.9585	0.9515	0.9485	0.9515
		4000	2,3	0.999	0.948	0.944	0.945	0.9445

Table 10.2. One Way MANOVA Type Test, Coverage for lognormal data with $\Sigma_3 \neq cI$

m	n1,n2,n3	B	σ_2, σ_3	mancov	bootcov	manLScov	prcv	brev
5	200,200,200	400	1,1	0.963	0.974	0.957	0.9635	0.965
		1000	1,1	0.957	0.962	0.941	0.948	0.951
		400	2,3	0.929	0.954	0.9095	0.9525	0.955
		1000	2,3	0.9255	0.945	0.9125	0.9595	0.96
5	200,400,600	400	1,1	0.952	0.9635	0.925	0.955	0.9555
		1000	1,1	0.956	0.9615	0.943	0.958	0.958
		400	2,3	0.995	0.964	0.956	0.956	0.9575
		1000	2,3	0.986	0.948	0.941	0.9505	0.9515
10	400,400,400	800	1,1	0.9515	0.966	0.9385	0.952	0.9525
		2000	1,1	0.952	0.957	0.9395	0.9545	0.9555
		800	2,3	0.9215	0.9555	0.92	0.9585	0.959
		2000	2,3	0.92	0.9375	0.908	0.9625	0.9625
10	400,800,1200	800	1,1	0.9425	0.957	0.928	0.9485	0.946
		2000	1,1	0.951	0.9525	0.9345	0.9565	0.9575
		800	2,3	0.997	0.9635	0.9495	0.957	0.958
		2000	2,3	0.996	0.9495	0.946	0.9435	0.9445
20	800,800,800	1600	1,1	0.946	0.9575	0.932	0.9465	0.947
		4000	1,1	0.9515	0.956	0.94	0.9515	0.953
		1600	2,3	0.92	0.949	0.8995	0.9525	0.9535
		4000	2,3	0.9175	0.9445	0.907	0.9535	0.954
20	800,1600,2400	1600	1,1	0.9585	0.9725	0.95	0.955	0.9565
		4000	1,1	0.9535	0.9585	0.937	0.9535	0.9535
		1600	2,3	0.9995	0.9645	0.9555	0.9565	0.956
		4000	2,3	0.9995	0.9445	0.9445	0.947	0.9475

Table 10.3. One Way MANOVA Type Test, Coverage for Mixture Normal data with $\Sigma_3 \neq c\mathbf{I}$

m	n1,n2,n3	B	σ_2, σ_3	mancov	bootcov	manLScov	prcv	brev
5	200,200,200	400	1,1	0.951	0.956	0.9505	0.948	0.9505
		1000	1,1	0.945	0.9445	0.945	0.9465	0.9485
		400	2,3	0.9445	0.961	0.9565	0.9485	0.949
		1000	2,3	0.9375	0.952	0.948	0.944	0.9455
5	200,400,600	400	1,1	0.958	0.961	0.9545	0.951	0.9495
		1000	1,1	0.953	0.951	0.951	0.949	0.949
		400	2,3	0.9945	0.964	0.961	0.9505	0.953
		1000	2,3	0.995	0.9505	0.9445	0.94	0.944
10	400,400,400	800	1,1	0.9505	0.9575	0.9445	0.953	0.9545
		2000	1,1	0.9495	0.95	0.9485	0.955	0.9555
		800	2,3	0.9265	0.9545	0.94	0.9515	0.9525
		2000	2,3	0.937	0.953	0.95	0.9535	0.9535
10	400,800,1200	800	1,1	0.955	0.965	0.949	0.9515	0.9535
		2000	1,1	0.953	0.954	0.9495	0.9515	0.9515
		800	2,3	0.998	0.955	0.9545	0.9445	0.9465
		2000	2,3	0.9955	0.945	0.9435	0.9415	0.9425
20	800,800,800	1600	1,1	0.939	0.949	0.938	0.9475	0.9475
		4000	1,1	0.9595	0.9605	0.952	0.9515	0.9525
		1600	2,3	0.935	0.958	0.9485	0.9615	0.9625
		4000	2,3	0.924	0.9465	0.9325	0.956	0.9555
20	800,1600,2400	1600	1,1	0.9565	0.962	0.952	0.9495	0.9515
		4000	1,1	0.948	0.949	0.947	0.956	0.9555
		1600	2,3	0.9995	0.9645	0.9465	0.951	0.9495
		4000	2,3	0.9985	0.9505	0.955	0.946	0.946

Table 10.4. One Way MANOVA Type Test, Coverage for Multivariate t data with $\Sigma_3 \neq c\mathbf{I}$

m	n1,n2,n3	B	σ_2, σ_3	mancov	bootcov	manLScov	prcv	brev
5	200,200,200	400	1,1	0.947	0.957	0.947	0.947	0.949
		1000	1,1	0.951	0.9515	0.9485	0.949	0.9495
		400	2,3	0.9315	0.956	0.951	0.949	0.952
		1000	2,3	0.942	0.9615	0.9525	0.947	0.9455
5	200,400,600	400	1,1	0.951	0.9595	0.953	0.954	0.956
		1000	1,1	0.96	0.961	0.9555	0.9525	0.9505
		400	2,3	0.994	0.956	0.9445	0.9435	0.944
		1000	2,3	0.996	0.9495	0.9545	0.953	0.9505
10	400,400,400	800	1,1	0.9555	0.962	0.949	0.954	0.9545
		2000	1,1	0.949	0.952	0.947	0.949	0.9495
		800	2,3	0.93	0.9585	0.9425	0.952	0.953
		2000	2,3	0.9305	0.955	0.952	0.948	0.95
10	400,800,1200	800	1,1	0.951	0.9585	0.9495	0.9505	0.9515
		2000	1,1	0.957	0.9585	0.956	0.9595	0.959
		800	2,3	0.9985	0.963	0.952	0.9495	0.951
		2000	2,3	0.9965	0.945	0.951	0.9395	0.9385
20	800,800,800	1600	1,1	0.9545	0.968	0.9545	0.954	0.9535
		4000	1,1	0.9495	0.952	0.946	0.9535	0.953
		1600	2,3	0.929	0.9595	0.946	0.9495	0.9485
		4000	2,3	0.9345	0.96	0.952	0.961	0.961
20	800,1600,2400	1600	1,1	0.9505	0.9665	0.9475	0.9545	0.955
		4000	1,1	0.952	0.9535	0.948	0.9575	0.9575
		1600	2,3	0.9995	0.9645	0.9545	0.9505	0.952
		4000	2,3	0.9995	0.948	0.9415	0.949	0.9495

Table 10.5. One Way MANOVA Type Test, Coverage for MVN data with $\Sigma_3 = cI$

m	n1,n2,n3	B	σ_2, σ_3	mancov	bootcov	manLScov	prcv	brev
5	200,200,200	400	1,1	0.9455	0.9525	0.9495	0.9485	0.949
		1000	1,1	0.941	0.945	0.953	0.9485	0.948
		400	2,3	0.928	0.952	0.948	0.947	0.947
		1000	2,3	0.927	0.943	0.949	0.948	0.9475
5	200,400,600	400	1,1	0.871	0.9595	0.9475	0.9505	0.953
		1000	1,1	0.8855	0.9565	0.953	0.9485	0.947
		400	2,3	0.9175	0.9625	0.9515	0.9465	0.9495
		1000	2,3	0.902	0.95	0.9535	0.9485	0.9475
10	400,400,400	800	1,1	0.9335	0.9485	0.9445	0.94	0.941
		2000	1,1	0.9495	0.955	0.954	0.9585	0.958
		800	2,3	0.9195	0.9545	0.945	0.942	0.943
		2000	2,3	0.9175	0.946	0.945	0.939	0.9405
10	400,800,1200	800	1,1	0.786	0.9585	0.9505	0.954	0.954
		2000	1,1	0.7615	0.9525	0.946	0.94	0.9415
		800	2,3	0.8685	0.956	0.9425	0.943	0.9445
		2000	2,3	0.875	0.9485	0.9465	0.9525	0.9525
20	800,800,800	1600	1,1	0.927	0.948	0.9375	0.951	0.9525
		4000	1,1	0.942	0.952	0.944	0.96	0.959
		1600	2,3	0.906	0.9465	0.934	0.9415	0.941
		4000	2,3	0.921	0.9545	0.9525	0.957	0.9585
20	800,1600,2400	1600	1,1	0.567	0.9635	0.945	0.952	0.9525
		4000	1,1	0.5775	0.946	0.9425	0.95	0.949
		1600	2,3	0.8305	0.962	0.95	0.949	0.949
		4000	2,3	0.8255	0.9515	0.94	0.951	0.9515

Table 10.6. One Way MANOVA Type Test, Coverage for lognormal data with $\Sigma_3 = cI$

m	n1,n2,n3	B	σ_2, σ_3	mancov	bootcov	manLScov	prcv	brev
5	200,200,200	400	1,1	0.9515	0.9665	0.936	0.963	0.963
		1000	1,1	0.9515	0.963	0.9295	0.963	0.9615
		400	2,3	0.903	0.9365	0.908	0.95	0.9505
		1000	2,3	0.904	0.9265	0.9125	0.9565	0.957
5	200,400,600	400	1,1	0.8895	0.9715	0.928	0.965	0.9665
		1000	1,1	0.8775	0.957	0.91	0.9585	0.958
		400	2,3	0.888	0.947	0.906	0.9535	0.9525
		1000	2,3	0.8975	0.9355	0.9095	0.959	0.9605
10	400,400,400	800	1,1	0.939	0.964	0.9145	0.9595	0.96
		2000	1,1	0.9385	0.954	0.912	0.957	0.9575
		800	2,3	0.8935	0.941	0.9005	0.951	0.952
		2000	2,3	0.907	0.94	0.9065	0.9685	0.969
10	400,800,1200	800	1,1	0.773	0.965	0.9215	0.961	0.9615
		2000	1,1	0.772	0.9655	0.9205	0.9705	0.9725
		800	2,3	0.856	0.9515	0.8975	0.9575	0.9585
		2000	2,3	0.831	0.9295	0.8905	0.9515	0.953
20	800,800,800	1600	1,1	0.935	0.965	0.9125	0.962	0.9625
		4000	1,1	0.9405	0.9525	0.9105	0.9605	0.961
		1600	2,3	0.8965	0.9375	0.909	0.96	0.959
		4000	2,3	0.885	0.9245	0.897	0.9545	0.9545
20	800,1600,2400	1600	1,1	0.5615	0.959	0.91	0.9565	0.9575
		4000	1,1	0.5855	0.948	0.8965	0.953	0.9535
		1600	2,3	0.7955	0.949	0.9095	0.955	0.9565
		4000	2,3	0.78	0.926	0.8985	0.9485	0.9485

Table 10.7. One Way MANOVA Type Test, Coverage for Mixture Normal data with $\Sigma_3 = c\mathbf{I}$

m	n1,n2,n3	B	σ_2, σ_3	mancov	bootcov	manLScov	prcv	brev
5	200,200,200	400	1,1	0.955	0.9655	0.9645	0.9565	0.958
		1000	1,1	0.9555	0.959	0.955	0.954	0.9545
		400	2,3	0.9235	0.955	0.9485	0.949	0.9495
		1000	2,3	0.93	0.95	0.958	0.955	0.9545
5	200,400,600	400	1,1	0.888	0.966	0.9635	0.9525	0.955
		1000	1,1	0.883	0.949	0.951	0.9435	0.944
		400	2,3	0.915	0.957	0.9515	0.949	0.951
		1000	2,3	0.914	0.9465	0.9475	0.953	0.9535
10	400,400,400	800	1,1	0.9365	0.9615	0.9375	0.9395	0.937
		2000	1,1	0.937	0.947	0.94	0.9465	0.9455
		800	2,3	0.9305	0.9655	0.9515	0.958	0.9565
		2000	2,3	0.921	0.9535	0.9495	0.9565	0.9545
10	400,800,1200	800	1,1	0.778	0.965	0.9565	0.959	0.962
		2000	1,1	0.7745	0.951	0.947	0.9475	0.9475
		800	2,3	0.8845	0.9615	0.9475	0.9475	0.949
		2000	2,3	0.8885	0.9575	0.9535	0.9495	0.949
20	800,800,800	1600	1,1	0.9345	0.9585	0.948	0.9565	0.956
		4000	1,1	0.9355	0.9505	0.9475	0.954	0.954
		1600	2,3	0.929	0.9585	0.9535	0.959	0.96
		4000	2,3	0.913	0.947	0.9425	0.9555	0.9535
20	800,1600,2400	1600	1,1	0.5835	0.96	0.944	0.95	0.953
		4000	1,1	0.5615	0.9545	0.948	0.9515	0.9515
		1600	2,3	0.819	0.9595	0.9515	0.955	0.9555
		4000	2,3	0.818	0.948	0.941	0.9535	0.954

Table 10.8. One Way MANOVA Type Test, Coverage for Multivariate t data with $\Sigma_3 = cI$

m	n1,n2,n3	B	σ_2, σ_3	mancov	bootcov	manLScov	prcv	brev
5	200,200,200	400	1,1	0.947	0.961	0.9525	0.9555	0.9535
		1000	1,1	0.9495	0.9515	0.957	0.9555	0.958
		400	2,3	0.9425	0.9705	0.96	0.959	0.9615
		1000	2,3	0.93	0.9475	0.944	0.9515	0.951
5	200,400,600	400	1,1	0.8735	0.9575	0.9475	0.943	0.9435
		1000	1,1	0.8775	0.9545	0.9575	0.95	0.952
		400	2,3	0.9015	0.961	0.9605	0.9575	0.9545
		1000	2,3	0.914	0.9625	0.959	0.9605	0.9595
10	400,400,400	800	1,1	0.943	0.964	0.9535	0.955	0.9595
		2000	1,1	0.9465	0.957	0.955	0.9555	0.9555
		800	2,3	0.92	0.9585	0.9515	0.952	0.953
		2000	2,3	0.9185	0.953	0.9485	0.9545	0.954
10	400,800,1200	800	1,1	0.79	0.959	0.946	0.9555	0.956
		2000	1,1	0.7685	0.954	0.9465	0.954	0.956
		800	2,3	0.8785	0.965	0.9515	0.948	0.9505
		2000	2,3	0.8775	0.952	0.946	0.9465	0.948
20	800,800,800	1600	1,1	0.938	0.959	0.938	0.962	0.963
		4000	1,1	0.936	0.951	0.9465	0.953	0.953
		1600	2,3	0.906	0.9475	0.935	0.9525	0.954
		4000	2,3	0.919	0.955	0.95	0.9585	0.957
20	800,1600,2400	1600	1,1	0.5625	0.9705	0.951	0.9635	0.964
		4000	1,1	0.5815	0.954	0.948	0.9495	0.9505
		1600	2,3	0.8185	0.957	0.939	0.9525	0.9535
		4000	2,3	0.8165	0.952	0.947	0.96	0.96

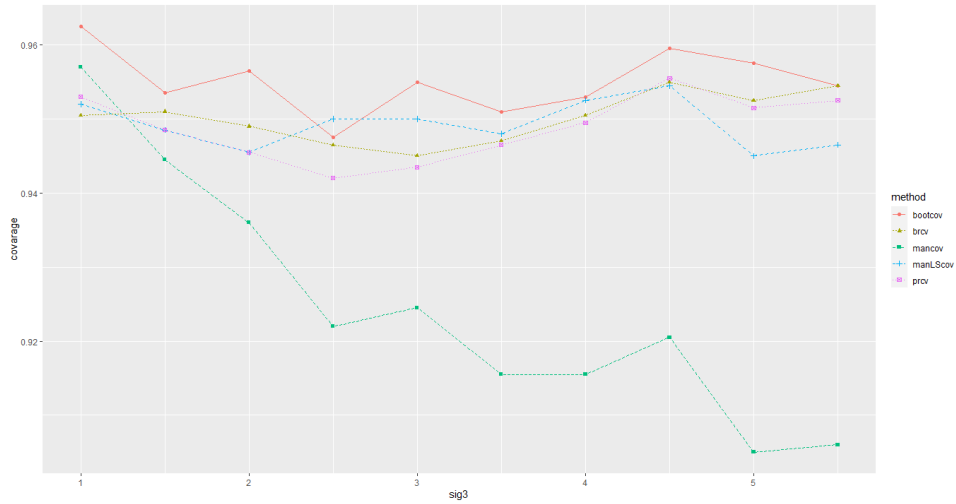


Figure 10.1. MANOVA Coverage graph for Normal data with $n1=200, n2=200, n3=200, m=5, B=400$ and $\sigma_1 = 1, \sigma_2 = 1$ and different σ_3 levels.

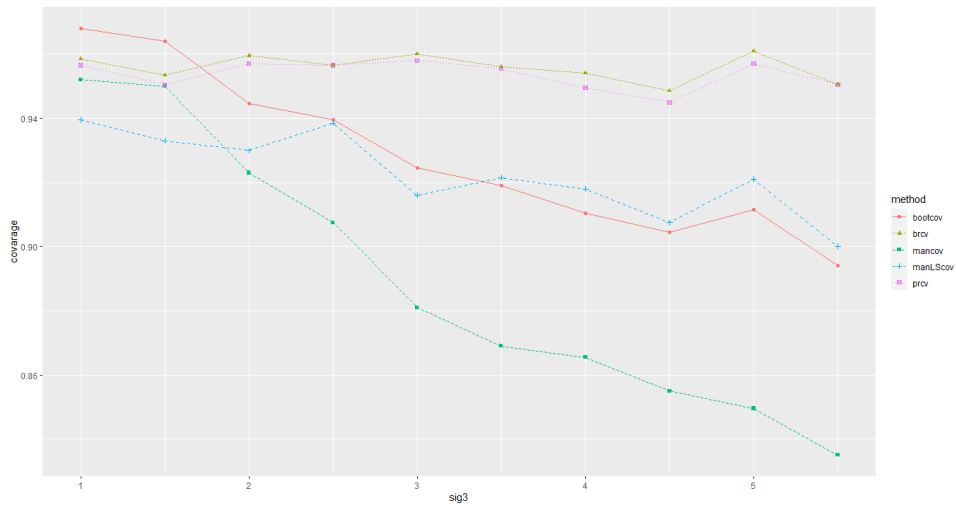


Figure 10.2. MANOVA Coverage graph for lognormal data with $n1=200, n2=200, n3=200, m=5, B=400$ and $\sigma_1 = 1, \sigma_2 = 1$ and different σ_3 levels.

CHAPTER 11

HIGH DIMENSIONAL ONE WAY MANOVA TYPE TEST

11.1 SIMULATION HIGH DIMENSIONAL ONE WAY MANOVA TYPE TEST

Use $C_n = I$. Use the data as well as the scaled data where each predictor in each group is divided by its sample standard deviation.

```
args(hdmansim)
function (n1 = 100, n2 = 100, n3 = 100, m = 2, B = 100, nruns = 100,
ytype = 1, sig2 = 1, sig3 = 1, eps = 0.4, dd = 4, delta1 = 0,
delta2 = 0, delta3 = 0, cov3I = F, alpha = 0.1)
```

Tables 11.1 to 11.8 show that standardizing the data is unreliable. When $\alpha = 0.1$, usually PR and BR had type I error near or less than 0.1.

Table 11.1. HD One Way MANOVA Type Test, Type I Error for MVN data with $\Sigma_3 \neq c\mathbf{I}$ with m=100

n1,n2,n3	B	σ_2, σ_3	prcv	brcv	sprcv	sbrcv
20,20,20	100	1,1	0.0755	0.0525	0.2925	0.236
	200	1,1	0.0595	0.05	0.2305	0.208
	100	2,3	0.051	0.0405	0.2795	0.2255
	200	2,3	0.0395	0.0335	0.234	0.21
20,40,60	100	1,1	0.073	0.0525	0.207	0.161
	200	1,1	0.0595	0.045	0.176	0.15
	100	2,3	0.103	0.078	0.217	0.1735
	200	2,3	0.071	0.0605	0.17	0.1525
50,50,50	100	1,1	0.093	0.0715	0.1555	0.1185
	200	1,1	0.075	0.066	0.135	0.117
	100	2,3	0.0635	0.0505	0.15	0.109
	200	2,3	0.0575	0.0515	0.1295	0.1155
100,100,100	100	1,1	0.117	0.088	0.151	0.113
	200	1,1	0.0865	0.0765	0.1095	0.094
	100	2,3	0.0955	0.069	0.138	0.1015
	200	2,3	0.073	0.064	0.1205	0.108

Table 11.2. HD One Way MANOVA Type Test, Type I Error for lognormal data with $\Sigma_3 \neq c\mathbf{I}$ with m=100

n1,n2,n3	B	σ_2, σ_3	prcv	brcv	sprcv	sbrcv
20,20,20	100	1,1	0.044	0.0285	0.9995	0.9995
	200	1,1	0.029	0.026	0.9995	0.9995
	100	2,3	0.0365	0.0275	1	1
	200	2,3	0.0255	0.021	1	1
20,40,60	100	1,1	0.0415	0.0285	0.998	0.997
	200	1,1	0.0315	0.0275	0.996	0.9955
	100	2,3	0.0565	0.042	0.9985	0.997
	200	2,3	0.051	0.042	0.998	0.998
50,50,50	100	1,1	0.0545	0.043	0.961	0.948
	200	1,1	0.046	0.0405	0.968	0.965
	100	2,3	0.0425	0.031	0.968	0.959
	200	2,3	0.0365	0.0285	0.971	0.966
100,100,100	100	1,1	0.0685	0.0565	0.8265	0.7945
	200	1,1	0.0585	0.05	0.82	0.8005
	100	2,3	0.061	0.048	0.822	0.776
	200	2,3	0.0505	0.042	0.8005	0.779

Table 11.3. HD One Way MANOVA Type Test, Type I Error for Mixture Normal data with $\Sigma_3 \neq c\mathbf{I}$ with m=100

n1,n2,n3	B	σ_2, σ_3	prcv	brcv	sprcv	sbrcv
20,20,20	100	1,1	0.015	0.016	0.068	0.053
	200	1,1	0.0105	0.0095	0.0355	0.026
	100	2,3	0.013	0.012	0.072	0.0555
	200	2,3	0.006	0.0065	0.0365	0.0295
20,40,60	100	1,1	0.0185	0.013	0.0435	0.036
	200	1,1	0.013	0.012	0.039	0.0265
	100	2,3	0.0405	0.025	0.051	0.035
	200	2,3	0.0225	0.02	0.0345	0.0275
50,50,50	100	1,1	0.0415	0.0295	0.0515	0.0345
	200	1,1	0.0245	0.021	0.0365	0.03
	100	2,3	0.024	0.021	0.054	0.0405
	200	2,3	0.018	0.014	0.033	0.029
100,100,100	100	1,1	0.0525	0.037	0.0675	0.0465
	200	1,1	0.0495	0.04	0.05	0.0415
	100	2,3	0.058	0.041	0.0795	0.057
	200	2,3	0.0405	0.031	0.057	0.05

Table 11.4. HD One Way MANOVA Type Test, Type I Error for Multivariate t data with $\Sigma_3 \neq c\mathbf{I}$ with m=100

n1,n2,n3	B	σ_2, σ_3	prcv	brcv	sprcv	sbrcv
20,20,20	100	1,1	0.024	0.023	0.1345	0.0995
	200	1,1	0.0175	0.015	0.105	0.0975
	100	2,3	0.028	0.024	0.1505	0.115
	200	2,3	0.016	0.013	0.1005	0.085
20,40,60	100	1,1	0.0315	0.0225	0.083	0.0665
	200	1,1	0.026	0.0205	0.0755	0.0625
	100	2,3	0.0515	0.0355	0.093	0.0715
	200	2,3	0.03	0.028	0.069	0.0595
50,50,50	100	1,1	0.038	0.026	0.072	0.054
	200	1,1	0.032	0.0265	0.0535	0.043
	100	2,3	0.036	0.022	0.08	0.0625
	200	2,3	0.0225	0.0205	0.054	0.047
100,100,100	100	1,1	0.058	0.0475	0.079	0.058
	200	1,1	0.046	0.038	0.058	0.0515
	100	2,3	0.044	0.035	0.0635	0.042
	200	2,3	0.0385	0.0355	0.0565	0.047

Table 11.5. HD One Way MANOVA Type Test, Type I Error for MVN data with $\Sigma_3 = c\mathbf{I}$ with m=100

n1,n2,n3	B	σ_2, σ_3	prcv	brcv	sprcv	sbrcv
20,20,20	100	1,1	0.0395	0.0265	0.2645	0.2175
	200	1,1	0.0275	0.0225	0.2345	0.2185
	100	2,3	0.0415	0.0285	0.265	0.219
	200	2,3	0.0315	0.027	0.243	0.2245
20,40,60	100	1,1	0.045	0.029	0.211	0.1635
	200	1,1	0.033	0.026	0.179	0.154
	100	2,3	0.048	0.0335	0.1935	0.1565
	200	2,3	0.037	0.0305	0.1675	0.1415
50,50,50	100	1,1	0.0785	0.054	0.15	0.107
	200	1,1	0.053	0.0395	0.131	0.1105
	100	2,3	0.069	0.05	0.159	0.115
	200	2,3	0.057	0.048	0.1355	0.116
100,100,100	100	1,1	0.0915	0.0645	0.1435	0.112
	200	1,1	0.078	0.0675	0.109	0.096
	100	2,3	0.0935	0.0715	0.1445	0.108
	200	2,3	0.0775	0.061	0.124	0.106

Table 11.6. HD One Way MANOVA Type Test, Type I Error for lognormal data with $\Sigma_3 = c\mathbf{I}$ with m=100

n1,n2,n3	B	σ_2, σ_3	prcv	brcv	sprcv	sbrcv
20,20,20	100	1,1	0.02	0.0155	0.9995	1
	200	1,1	0.013	0.012	1	1
	100	2,3	0.0285	0.023	0.9995	0.999
	200	2,3	0.0155	0.014	0.999	0.999
20,40,60	100	1,1	0.028	0.0205	0.9985	0.9975
	200	1,1	0.013	0.011	0.998	0.9985
	100	2,3	0.026	0.021	0.997	0.9965
	200	2,3	0.0245	0.0195	0.996	0.995
50,50,50	100	1,1	0.0325	0.0225	0.972	0.9615
	200	1,1	0.023	0.0195	0.967	0.961
	100	2,3	0.0445	0.0365	0.976	0.969
	200	2,3	0.0295	0.022	0.9735	0.969
100,100,100	100	1,1	0.063	0.0475	0.835	0.798
	200	1,1	0.041	0.0335	0.7995	0.783
	100	2,3	0.0635	0.0495	0.82	0.779
	200	2,3	0.044	0.0415	0.8115	0.7835

Table 11.7. HD One Way MANOVA Type Test, Type I Error for Mixture of Normal data with $\Sigma_3 = c\mathbf{I}$ with m=100

n1,n2,n3	B	σ_2, σ_3	prcv	brcv	sprcv	sbrcv
20,20,20	100	1,1	0.007	0.008	0.06	0.046
	200	1,1	0.003	0.0015	0.0345	0.03
	100	2,3	0.006	0.002	0.0515	0.0385
	200	2,3	0.003	0.004	0.039	0.0335
20,40,60	100	1,1	0.008	0.0055	0.0405	0.032
	200	1,1	0.003	0.002	0.0315	0.0225
	100	2,3	0.012	0.009	0.0465	0.034
	200	2,3	0.006	0.006	0.0355	0.034
50,50,50	100	1,1	0.017	0.0105	0.0515	0.04
	200	1,1	0.012	0.008	0.0375	0.0335
	100	2,3	0.0165	0.0125	0.043	0.032
	200	2,3	0.013	0.011	0.037	0.03
100,100,100	100	1,1	0.0355	0.0275	0.0725	0.0575
	200	1,1	0.026	0.018	0.0495	0.038
	100	2,3	0.037	0.0265	0.0675	0.0475
	200	2,3	0.0245	0.0195	0.0605	0.0565

Table 11.8. HD One Way MANOVA Type Test, Type I Error for Multivariate t data with $\Sigma_3 = c\mathbf{I}$ with m=100

n1,n2,n3	B	σ_2, σ_3	prcv	brcv	sprcv	sbrcv
20,20,20	100	1,1	0.0125	0.006	0.1495	0.1205
	200	1,1	0.0075	0.0055	0.101	0.091
	100	2,3	0.0175	0.0115	0.143	0.1135
	200	2,3	0.011	0.012	0.126	0.1
20,40,60	100	1,1	0.016	0.014	0.0895	0.0725
	200	1,1	0.012	0.0095	0.07	0.0555
	100	2,3	0.0205	0.015	0.097	0.0685
	200	2,3	0.013	0.012	0.0665	0.059
50,50,50	100	1,1	0.024	0.014	0.077	0.062
	200	1,1	0.02	0.0175	0.055	0.049
	100	2,3	0.028	0.0165	0.0745	0.052
	200	2,3	0.023	0.019	0.058	0.0485
100,100,100	100	1,1	0.035	0.026	0.069	0.05
	200	1,1	0.03	0.0225	0.0625	0.0525
	100	2,3	0.038	0.0255	0.078	0.048
	200	2,3	0.031	0.026	0.053	0.046

CHAPTER 12
WEIGHTED LEAST SQUARES

The weighted least squares (WLS) model is $Y_i = \beta_1 + x_{i,2}\beta_2 + \cdots + x_{i,p}\beta_p + e_i$ for $i = 1, \dots, n$ where the e_i are independent with $E(e_i) = 0$ and $V(e_i) = \sigma_i^2$. In matrix form, this model is

$$\mathbf{Y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{e},$$

where \mathbf{Y} is an $n \times 1$ vector of dependent variables, \mathbf{X} is an $n \times p$ matrix of predictors, $\boldsymbol{\beta}$ is a $p \times 1$ vector of unknown coefficients, and \mathbf{e} is an $n \times 1$ vector of unknown errors. Also $E(\mathbf{e}) = \mathbf{0}$ and $\text{Cov}(\mathbf{e}) = \boldsymbol{\Sigma}_e = \text{diag}(\sigma_i^2) = \text{diag}(\sigma_1^2, \dots, \sigma_n^2)$ is an $n \times n$ positive definite matrix.

The least squares estimator $\hat{\boldsymbol{\beta}} = \hat{\boldsymbol{\beta}}_{OLS} = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \mathbf{Y}$ can be shown to be a consistent estimator of $\boldsymbol{\beta}$ with $E(\hat{\boldsymbol{\beta}}) = \boldsymbol{\beta}$ and $\text{Cov}(\hat{\boldsymbol{\beta}}) = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \boldsymbol{\Sigma}_e \mathbf{X} (\mathbf{X}^T \mathbf{X})^{-1}$. Assume $n\text{Cov}(\hat{\boldsymbol{\beta}}) \xrightarrow{P} \mathbf{V}$ as $n \rightarrow \infty$. If $\mathbf{X}^T \mathbf{X}/n \rightarrow \mathbf{W}^{-1}$ and $\mathbf{X}^T \boldsymbol{\Sigma}_e \mathbf{X}/n \xrightarrow{P} \mathbf{U}$, then $\mathbf{V} = \mathbf{W} \mathbf{U} \mathbf{W}$. We assume that a constant x_1 is in the model so that the OLS residuals sum to 0.

A sandwich estimator is $\widehat{\text{Cov}}(\hat{\boldsymbol{\beta}}_{OLS}) = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \hat{\mathbf{D}} \mathbf{X} (\mathbf{X}^T \mathbf{X})^{-1}$. Often $\hat{\mathbf{D}}$ is not a consistent estimator of $\boldsymbol{\Sigma}_e$, but often $\mathbf{X}^T \hat{\mathbf{D}} \mathbf{X}/n \xrightarrow{P} \mathbf{U}$ under regularity conditions. For the wild bootstrap, we will use $\hat{\mathbf{D}}_W = n \text{diag}(r_1^2, \dots, r_n^2)/(n-p)$ where the r_i are the OLS residuals. Often $\hat{\mathbf{D}} = \text{diag}(d_i^2 r_i^2)$, where $\hat{\mathbf{D}}_W$ uses $d_i^2 = n/(n-p)$. See Buja et al. (2019), Eicker (1963, 1967), Hinkley (1977), MacKinnon and White (1985), Pötscher and Preinerstorfer (2020), and White (1980).

The *nonparametric bootstrap = pairs bootstrap* samples the cases (Y_i, \mathbf{x}_i) with replacement, and uses

$$\mathbf{Y}^* = \mathbf{X}^* \hat{\boldsymbol{\beta}} + \mathbf{e}^*$$

with $\mathbf{e}^* = \mathbf{r}^*$ where (Y_i, \mathbf{x}_i, r_i) are selected with replacement to form $\mathbf{Y}^*, \mathbf{X}^*$ and \mathbf{r}^* . Then $\hat{\boldsymbol{\beta}}^* = (\mathbf{X}^{*T} \mathbf{X}^*)^{-1} \mathbf{X}^{*T} \mathbf{Y}^* = \hat{\boldsymbol{\beta}} + (\mathbf{X}^{*T} \mathbf{X}^*)^{-1} \mathbf{X}^{*T} \mathbf{r}^* = \hat{\boldsymbol{\beta}} + \mathbf{b}^*$ is obtained from

the OLS regression of \mathbf{Y}^* on \mathbf{X}^* . Thus $E(\hat{\boldsymbol{\beta}}^*) = \hat{\boldsymbol{\beta}} + E[(\mathbf{X}^{*T} \mathbf{X}^*)^{-1} \mathbf{X}^{*T} \mathbf{r}^*] = \hat{\boldsymbol{\beta}} + \mathbf{b}$ where the bias vector $\mathbf{b} = E(\mathbf{b}^*)$. Freedman (1981) showed that the nonparametric bootstrap can be useful for the WLS model with the e_i independent, suggesting that $\mathbf{b}^* = o_p(n^{-1/2})$ or $\mathbf{b}^* = O_p(n^{-1/2})$. With respect to the bootstrap distribution, $\text{Cov}(\hat{\boldsymbol{\beta}}^*) = \text{Cov}[(\mathbf{X}^{*T} \mathbf{X}^*)^{-1} \mathbf{X}^{*T} \mathbf{r}^*] = E[(\mathbf{X}^{*T} \mathbf{X}^*)^{-1} \mathbf{X}^{*T} \mathbf{r}^* \mathbf{r}^{*T} \mathbf{X}^* (\mathbf{X}^{*T} \mathbf{X}^*)^{-1}] - \mathbf{b} \mathbf{b}^T$. This result suggests that $\text{Cov}(\hat{\boldsymbol{\beta}}^*)$ is estimating the sandwich estimator

$$(\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \mathbf{r} \mathbf{r}^T \mathbf{X} (\mathbf{X}^T \mathbf{X})^{-1},$$

which replaces $\text{diag}(r_i^2)$ by $\mathbf{r} \mathbf{r}^T$.

A version of the *wild bootstrap* uses

$$\mathbf{Y}^* = \mathbf{X} \hat{\boldsymbol{\beta}} + \mathbf{e}^*$$

with $e_i^* = W_i c_n r_i$ where $P(W_i = \pm 1) = 0.5$, $E(W_i) = 0$, $V(W_i) = 1$ and $c_n = \sqrt{n/(n-p)}$. Note that $W_i = 2Z_i - 1$ where $Z_i \sim \text{binomial}(m = 1, p = 0.5) \sim \text{Bernoulli}(p = 0.5)$. See Flachaire (2005). With respect to the bootstrap distribution, the $c_n r_i$ are constants, and the e_i^* are independent with $E(e_i^*) = E(W_i) c_n r_i = 0$, and $V(e_i^*) = E(e_i^{*2}) = E(W_i^2) c_n^2 r_i^2 = c_n^2 r_i^2$. Thus $E(\mathbf{e}^*) = \mathbf{0}$ and $\text{Cov}(\mathbf{e}^*) = \hat{\mathbf{D}}_W$. Then $\hat{\boldsymbol{\beta}}^* = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \mathbf{Y}^*$ with $E(\hat{\boldsymbol{\beta}}^*) = \hat{\boldsymbol{\beta}}$ and $\text{Cov}(\hat{\boldsymbol{\beta}}^*) = \widehat{\text{Cov}}(\hat{\boldsymbol{\beta}}_{OLS}) = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \hat{\mathbf{D}}_W \mathbf{X} (\mathbf{X}^T \mathbf{X})^{-1}$, a sandwich estimator. Note that $\text{Cov}(\hat{\boldsymbol{\beta}}^*) = \text{Cov}(\hat{\boldsymbol{\beta}}) + (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T [\hat{\mathbf{D}}_W - \boldsymbol{\Sigma}_e] \mathbf{X} (\mathbf{X}^T \mathbf{X})^{-1}$.

The following method is new. For the OLS model, $V(e_i) = V(Y_i | \mathbf{x}_i) = V(Y_i | \mathbf{x}_i^T \boldsymbol{\beta}) = \sigma^2$. Hence $Y_i = Y_i | \mathbf{x}_i = Y_i | \mathbf{x}_i^T \boldsymbol{\beta} = \mathbf{x}_i^T \boldsymbol{\beta} + e_i$ with $V(e_i) = \sigma^2$. For the WLS model, $Y_i = Y_i | \mathbf{x}_i = \mathbf{x}_i^T \boldsymbol{\beta} + e_i$ with $V(e_i) = \sigma_i^2$, while $Y_i = Y_i | \mathbf{x}_i^T \boldsymbol{\beta}_i = \mathbf{x}_i^T \boldsymbol{\beta} + \epsilon_i$ with $V(\epsilon_i) = \tau_i^2$. The τ_i^2 can be estimated as follows. Make the residual plot of $\hat{Y}_i = \mathbf{x}_i^T \hat{\boldsymbol{\beta}}$ versus r_i on the vertical axis. Divide the $\mathbf{x}_i^T \hat{\boldsymbol{\beta}}$ into m_s slices each containing approximately n/m_s cases, and find the variance of the residuals v_j^2 in the j th slice for $j = 1, \dots, m_s$. Then $\hat{\tau}_i^2 = n v_j^2 / (n - p)$ if case i is in the j th slice. If the \mathbf{x}_i are bounded, the maximum slice width $\rightarrow 0$, and the number of cases in each slice $\rightarrow \infty$ as $n \rightarrow \infty$, then $\hat{\tau}_i^2$ is a consistent

estimator of τ_i^2 . This method acts as if the variance τ_j^2 is constant within each slice j , and replaces $\hat{\mathbf{D}}_W = n \text{diag}(r_1^2, \dots, r_n^2)/(n-p)$ by $\text{diag}(\hat{\tau}_1^2, \dots, \hat{\tau}_n^2)$, a smoothed version of $\hat{\mathbf{D}}_W$. Another option would use a scatterplot smoother in a plot of \hat{Y}_i vs. r_i^2 .

The *parametric bootstrap* **does not assume** that the e_i are normal, but uses

$$\mathbf{Y}^* = \mathbf{X}\hat{\boldsymbol{\beta}} + \mathbf{e}^*$$

where the $e_i^* \sim N(0, \hat{\tau}_i^2)$ are independent. Hence $\hat{\boldsymbol{\beta}}^* = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \mathbf{Y}^* \sim$

$$N_p[\hat{\boldsymbol{\beta}}, (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \text{diag}(\hat{\tau}_1^2, \dots, \hat{\tau}_n^2) \mathbf{X} (\mathbf{X}^T \mathbf{X})^{-1}].$$

12.1 SIMULATION FOR WEIGHTED LEAST SQUARES

A simulation study was done using $B = \max(200, 50p)$ and 5000 runs. The simulation is similar to that for the full OLS model done by Pelawa Watagoda and Olive (2021). The simulation used $p = 4, 8$, and 10 ; $n = 25p$ and $50p$; $\psi = 0, 1/\sqrt{p}, 0.5$, and 0.9 ; and $k = 1$ and $p - 2$ where k and ψ are defined in the following paragraph.

Let $\mathbf{x} = (1 \ \mathbf{u}^T)^T$ where \mathbf{u} is the $(p-1) \times 1$ vector of nontrivial predictors. In the simulations, for $i = 1, \dots, n$, we generated $\mathbf{w}_i \sim N_{p-1}(\mathbf{0}, \mathbf{I})$ where the $m = p-1$ elements of the vector \mathbf{w}_i are iid $N(0,1)$. Let the $m \times m$ matrix $\mathbf{A} = (a_{ij})$ with $a_{ii} = 1$ and $a_{ij} = \psi$ where $0 \leq \psi < 1$ for $i \neq j$. Then the vector $\mathbf{u}_i = \mathbf{A}\mathbf{w}_i$ so that $\text{Cov}(\mathbf{u}_i) = \boldsymbol{\Sigma}\mathbf{u} = \mathbf{A}\mathbf{A}^T = (\sigma_{ij})$ where the diagonal entries $\sigma_{ii} = [1 + (m-1)\psi^2]$ and the off diagonal entries $\sigma_{ij} = [2\psi + (m-2)\psi^2]$. Hence the correlations are $\text{cor}(x_i, x_j) = \rho = (2\psi + (m-2)\psi^2)/(1 + (m-1)\psi^2)$ for $i \neq j$ where x_i and x_j are nontrivial predictors. If $\psi = 1/\sqrt{cp}$, then $\rho \rightarrow 1/(c+1)$ as $p \rightarrow \infty$ where $c > 0$. As ψ gets close to 1, the predictor vectors cluster about the line in the direction of $(1, \dots, 1)^T$. Let $Y_i = 1 + 1x_{i,2} + \dots + 1x_{i,k+1} + e_i$ for $i = 1, \dots, n$. Hence $\boldsymbol{\beta} = (1, \dots, 1, 0, \dots, 0)^T$ with $k+1$ ones and $p-k-1$ zeros.

The zero mean iid errors ϵ_i were iid from five distributions: i) $N(0,1)$, ii) t_3 , iii) $\text{EXP}(1) - 1$, iv) $\text{uniform}(-1, 1)$, and v) $0.9 N(0,1) + 0.1 N(0,100)$. Only distribution iii) is not symmetric. Then $\text{wtype} = 1$ if $e_i = \epsilon_i$ (the WLS model is the OLS model), 2 if

$e_i = |\mathbf{x}_i^T \boldsymbol{\beta} - 5| \epsilon_i$, 3 if $e_i = \sqrt{(1 + 0.5x_{i2}^2)} \epsilon_i$, 4 if $e_i = \exp[1 + \log(|x_{i2}|) + \dots + \log(|x_{ip}|)] \epsilon_i$, 5 if $e_i = [1 + \log(|x_{i2}|) + \dots + \log(|x_{ip}|)] \epsilon_i$, 6 if $e_i = [\exp([\log(|x_{i2}|) + \dots + \log(|x_{ip}|)] / (p - 1))] \epsilon_i$, 7 if $e_i = [[\log(|x_{i2}|) + \dots + \log(|x_{ip}|)] / (p - 1)] \epsilon_i$. The last four types were special cases of types suggested by Romano and Wolf (2017). For type 6, the weighting function is the geometric mean of $|x_{i2}|, \dots, |x_{ip}|$.

`args(wlsbootsim)`

`function (n = 100, p = 4, k = 1, nruns = 100, nslices = 7, eps = 0.1,
shift = 9, etype = 1, wtype = 1, psi = 0, BB = 200, alph = 0.05)`

When $\psi = 0$ and $wtype = 1$, the full model least squares confidence intervals for β_i should have length near $2t_{96,0.975}\sigma/\sqrt{n} \approx 2(1.96)\sigma/10 = 0.392\sigma$ when $n = 100$ and the iid zero mean errors have variance σ^2 . The simulation computed the Frey shorth(c) interval for each β_i and used bootstrap confidence regions to test $H_0 : \boldsymbol{\beta}_S = \mathbf{1}$ (whether first $k + 1$ $\beta_i = 1$) and $H_0 : \boldsymbol{\beta}_E = \mathbf{0}$ (whether the last $p - k - 1$ $\beta_i = 0$). The nominal coverage was 0.95 with $\delta = 0.05$. Observed coverage between 0.94 and 0.96 suggests coverage is close to the nominal value.

The tables show two rows for each model giving the observed confidence interval coverages of the confidence intervals. The term “npar” is for the non-parametric method, the term “wild” is for wild bootstrap method, and the term “par” is for the parametric method. The last six columns give results for the tests. The terms pr, hyb, and br are for the prediction region method (2.9), hybrid region, and Bickel and Ren region (2.8). The 0 indicates the test was $H_0 : \boldsymbol{\beta}_E = \mathbf{0}$, while the 1 indicates that the test was $H_0 : \boldsymbol{\beta}_S = \mathbf{1}$. The length and coverage = $P(\text{fail to reject } H_0)$ for the interval $[0, D_{(U_B)}]$ or $[0, D_{(U_{B,T})}]$ where $D_{(U_B)}$ or $D_{(U_{B,T})}$ is the cutoff for the confidence region. The cutoff will often be near $\sqrt{\chi_{g,0.95}^2}$ if the statistic T is asymptotically normal. Note that $\sqrt{\chi_{2,0.95}^2} = 2.448$. We want $B \geq 25p$ and $n \geq 10p$.

For normal error type with $wtype=2$, (Table 12.1 - Table 12.4), it can be seen that either non-parametric or parametric method work well when $\psi = 0$. For example in

Table 12.3, the parametric method gives coverage near the nominal for β_i 's, $H_0 : \beta_E = \mathbf{0}$, and $H_0 : \beta_S = \mathbf{1}$. For other wtypes for the normal error type, $\psi = 0$ gives either over coverage or under coverage. But when ψ increases to 1, the parametric method and non-parametric method tend to give good results. The t distribution gives the similar results in the Tables 12.19-12.36. For skewed errors types like EXP(1) - 1, often all three methods struggle to get the coverage near nominal for $H_0 : \beta_E = \mathbf{0}$, and $H_0 : \beta_S = \mathbf{1}$ even if ψ is close to 1. The uniform error type has under coverage for the situations with ψ lower. But when ψ is closer to 1 non-parametric method and parametric method gives the best coverage. When its comes to the mixture distribution error type, the wild bootstrap method gives the coverage near the nominal coverage for any ψ value. The parametric method and non-parametric method give over coverage or under coverage.

Table 12.1. Bootstrapping WLS, n=100, BB=200, wtype = 2,p=4,
k=1, etype= $N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.947	0.932	0.949	0.950	0.938	0.942	0.944	0.940	0.942	0.943
len	1.697	1.777	1.712	1.704	2.477	2.477	2.485	2.469	2.469	2.478
wild,0	0.953	0.918	0.944	0.942	0.933	0.930	0.931	0.928	0.928	0.929
len	1.691	1.733	1.660	1.665	2.419	2.419	2.426	2.425	2.425	2.432
par,0	0.957	0.931	0.949	0.954	0.943	0.942	0.943	0.940	0.941	0.941
len	1.720	1.764	1.722	1.732	2.458	2.458	2.464	2.461	2.461	2.469
npar,0.5	0.956	0.941	0.942	0.952	0.931	0.932	0.933	0.934	0.936	0.937
len	1.720	2.911	2.879	2.855	2.476	2.476	2.486	2.470	2.470	2.479
wild,0.5	0.953	0.937	0.940	0.947	0.918	0.917	0.919	0.923	0.922	0.926
len	1.713	2.829	2.802	2.797	2.416	2.416	2.421	2.426	2.426	2.433
par,0.5	0.954	0.940	0.949	0.956	0.949	0.945	0.946	0.937	0.935	0.937
len	1.741	2.927	2.909	2.907	2.460	2.460	2.467	2.461	2.461	2.467
npar,0.9	0.949	0.947	0.948	0.945	0.936	0.939	0.939	0.929	0.930	0.929
len	1.775	14.612	14.643	14.591	2.479	2.479	2.489	2.470	2.470	2.479
wild,0.9	0.948	0.939	0.945	0.938	0.923	0.924	0.925	0.916	0.916	0.918
len	1.766	14.181	14.252	14.188	2.415	2.415	2.419	2.417	2.417	2.423
par,0.9	0.953	0.949	0.957	0.947	0.944	0.943	0.945	0.929	0.927	0.930
len	1.797	14.823	14.846	14.846	2.458	2.458	2.465	2.461	2.461	2.466

Table 12.2. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=4,
k=p-2, etype= $N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.951	0.946	0.944	0.937	0.929	0.928	0.930	0.938	0.937	0.940
len	1.754	1.838	1.823	1.771	1.964	1.964	1.970	2.853	2.853	2.862
wild,0	0.951	0.946	0.941	0.933	0.925	0.925	0.927	0.928	0.927	0.926
len	1.749	1.783	1.772	1.726	1.939	1.939	1.945	2.762	2.762	2.767
par,0	0.947	0.950	0.940	0.947	0.934	0.935	0.936	0.927	0.931	0.932
len	1.776	1.824	1.823	1.791	1.958	1.958	1.963	2.823	2.823	2.831
npar,0.5	0.944	0.950	0.945	0.949	0.942	0.946	0.947	0.931	0.930	0.933
len	1.893	3.217	3.204	3.182	1.961	1.961	1.967	2.850	2.850	2.861
wild,0.5	0.943	0.942	0.944	0.943	0.937	0.935	0.936	0.911	0.915	0.916
len	1.889	3.109	3.124	3.084	1.935	1.935	1.941	2.751	2.751	2.755
par,0.5	0.947	0.955	0.957	0.952	0.947	0.946	0.946	0.932	0.933	0.932
len	1.927	3.253	3.253	3.233	1.958	1.958	1.963	2.822	2.822	2.829
npar,0.9	0.941	0.953	0.948	0.940	0.937	0.935	0.934	0.934	0.931	0.933
len	2.092	17.291	17.263	17.265	1.962	1.962	1.969	2.855	2.855	2.864
wild,0.9	0.947	0.953	0.947	0.934	0.927	0.925	0.924	0.907	0.909	0.911
len	2.083	16.817	16.750	16.687	1.933	1.933	1.937	2.742	2.742	2.748
par,0.9	0.946	0.961	0.956	0.947	0.941	0.943	0.945	0.930	0.932	0.929
len	2.125	17.633	17.606	17.646	1.955	1.955	1.960	2.822	2.822	2.830

Table 12.3. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=8, k=1, etype= $N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.947	0.946	0.952	0.948	0.926	0.925	0.928	0.947	0.947	0.948
len	1.753	1.822	1.765	1.763	3.714	3.714	3.731	2.477	2.477	2.486
wild,0	0.949	0.94	0.946	0.938	0.873	0.875	0.875	0.935	0.935	0.935
len	1.734	1.759	1.704	1.7	3.505	3.505	3.515	2.427	2.427	2.433
par,0	0.953	0.942	0.958	0.952	0.944	0.942	0.942	0.939	0.941	0.943
len	1.763	1.782	1.769	1.768	3.625	3.625	3.632	2.46	2.46	2.467
npar,0.5	0.951	0.956	0.949	0.953	0.934	0.932	0.936	0.951	0.951	0.949
len	1.816	3.448	3.411	3.414	3.722	3.722	3.738	2.475	2.475	2.483
wild,0.5	0.948	0.951	0.948	0.948	0.875	0.878	0.878	0.934	0.938	0.938
len	1.792	3.324	3.283	3.29	3.497	3.497	3.505	2.421	2.421	2.426
par,0.5	0.954	0.956	0.952	0.965	0.939	0.941	0.94	0.949	0.949	0.949
len	1.825	3.421	3.399	3.407	3.626	3.626	3.636	2.456	2.456	2.463
npar,0.9	0.953	0.95	0.949	0.952	0.946	0.947	0.95	0.936	0.937	0.938
len	1.974	18.394	18.472	18.44	3.732	3.732	3.747	2.472	2.472	2.481
wild,0.9	0.948	0.946	0.937	0.955	0.89	0.893	0.893	0.921	0.919	0.92
len	1.952	17.638	17.746	17.701	3.482	3.482	3.488	2.416	2.416	2.42
par,0.9	0.949	0.95	0.949	0.958	0.943	0.943	0.943	0.932	0.935	0.935
len	1.98	18.418	18.456	18.515	3.623	3.623	3.634	2.454	2.454	2.461

Table 12.4. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=8,
k=p-2, etype= $N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.951	0.953	0.948	0.949	0.944	0.946	0.945	0.938	0.938	0.940
len	1.974	2.054	2.042	1.985	1.962	1.962	1.969	3.983	3.983	4.001
wild,0	0.951	0.944	0.937	0.940	0.934	0.936	0.937	0.864	0.866	0.869
len	1.950	1.977	1.968	1.906	1.937	1.937	1.942	3.688	3.688	3.696
par,0	0.955	0.943	0.941	0.951	0.942	0.946	0.947	0.890	0.892	0.894
len	1.983	2.029	2.022	1.990	1.958	1.958	1.963	3.844	3.844	3.856
npar,0.5	0.949	0.956	0.955	0.949	0.946	0.945	0.947	0.953	0.954	0.956
len	4.107	7.697	7.660	7.702	1.961	1.961	1.968	3.992	3.992	4.005
wild,0.5	0.945	0.945	0.943	0.943	0.937	0.939	0.938	0.885	0.888	0.888
len	4.049	7.352	7.313	7.395	1.933	1.933	1.938	3.657	3.657	3.664
par,0.5	0.946	0.956	0.958	0.954	0.945	0.946	0.946	0.934	0.937	0.937
len	4.144	7.777	7.772	7.791	1.957	1.957	1.962	3.848	3.848	3.859
npar,0.9	0.947	0.949	0.948	0.957	0.953	0.949	0.951	0.962	0.959	0.962
len	6.235	58.283	58.322	58.226	1.965	1.965	1.969	3.997	3.997	4.010
wild,0.9	0.949	0.944	0.941	0.951	0.940	0.942	0.942	0.887	0.892	0.891
len	6.136	55.826	55.922	55.603	1.926	1.926	1.928	3.659	3.659	3.668
par,0.9	0.951	0.961	0.949	0.962	0.956	0.957	0.960	0.947	0.948	0.948
len	6.274	59.046	58.930	58.975	1.957	1.957	1.963	3.850	3.850	3.860

Table 12.5. Bootstrapping WLS, n=100, BB=200, wtype = 3,p=4,
k=1, etype= $N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.951	0.932	0.947	0.951	0.942	0.943	0.945	0.924	0.921	0.922
len	0.576	0.783	0.580	0.581	2.481	2.481	2.489	2.463	2.463	2.471
wild,0	0.951	0.927	0.949	0.942	0.929	0.930	0.929	0.906	0.909	0.911
len	0.576	0.771	0.565	0.567	2.419	2.419	2.422	2.410	2.410	2.416
par,0	0.954	0.904	0.952	0.956	0.955	0.959	0.959	0.903	0.903	0.904
len	0.585	0.722	0.592	0.594	2.459	2.459	2.465	2.457	2.457	2.463
npar,0.5	0.946	0.941	0.954	0.942	0.942	0.939	0.940	0.927	0.927	0.926
len	0.639	1.189	1.071	1.076	2.479	2.479	2.486	2.464	2.464	2.473
wild,0.5	0.946	0.933	0.951	0.931	0.926	0.926	0.928	0.914	0.915	0.915
len	0.639	1.162	1.043	1.046	2.413	2.413	2.418	2.411	2.411	2.415
par,0.5	0.947	0.930	0.962	0.957	0.953	0.956	0.957	0.916	0.920	0.925
len	0.652	1.173	1.095	1.103	2.459	2.459	2.465	2.459	2.459	2.465
npar,0.9	0.955	0.938	0.953	0.950	0.940	0.940	0.940	0.941	0.940	0.938
len	0.769	6.369	6.332	6.376	2.479	2.479	2.486	2.473	2.473	2.481
wild,0.9	0.952	0.931	0.949	0.945	0.930	0.931	0.933	0.926	0.927	0.927
len	0.765	6.184	6.155	6.198	2.406	2.406	2.413	2.418	2.418	2.423
par,0.9	0.953	0.954	0.963	0.956	0.960	0.959	0.960	0.941	0.941	0.942
len	0.781	6.515	6.500	6.494	2.461	2.461	2.467	2.459	2.459	2.467

Table 12.6. Bootstrapping WLS, $n=100$, $BB=200$, $wtype = 3$, $p=4$,
 $k=p-2$, $etype= N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.945	0.940	0.955	0.944	0.943	0.939	0.940	0.931	0.927	0.929
len	0.575	0.774	0.582	0.584	1.960	1.960	1.969	2.836	2.836	2.846
wild,0	0.951	0.940	0.943	0.938	0.930	0.929	0.932	0.913	0.911	0.913
len	0.576	0.762	0.566	0.569	1.940	1.940	1.946	2.750	2.750	2.756
par,0	0.951	0.894	0.964	0.943	0.941	0.940	0.942	0.905	0.909	0.909
len	0.585	0.634	0.624	0.593	1.959	1.959	1.963	2.824	2.824	2.831
npar,0.5	0.949	0.943	0.943	0.949	0.942	0.934	0.935	0.928	0.920	0.923
len	0.638	1.181	1.070	1.061	1.960	1.960	1.966	2.839	2.839	2.849
wild,0.5	0.948	0.938	0.935	0.943	0.933	0.933	0.933	0.902	0.904	0.904
len	0.640	1.154	1.042	1.034	1.939	1.939	1.943	2.753	2.753	2.759
par,0.5	0.947	0.930	0.952	0.957	0.948	0.948	0.948	0.925	0.926	0.924
len	0.652	1.111	1.107	1.089	1.957	1.957	1.961	2.822	2.822	2.829
npar,0.9	0.949	0.955	0.954	0.945	0.939	0.938	0.939	0.939	0.933	0.935
len	0.769	6.347	6.313	6.321	1.960	1.960	1.967	2.852	2.852	2.861
wild,0.9	0.946	0.948	0.950	0.936	0.934	0.933	0.931	0.915	0.917	0.919
len	0.767	6.179	6.144	6.166	1.939	1.939	1.943	2.751	2.751	2.758
par,0.9	0.945	0.960	0.960	0.945	0.941	0.941	0.942	0.950	0.949	0.951
len	0.782	6.481	6.461	6.446	1.959	1.959	1.964	2.828	2.828	2.835

Table 12.7. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=8, k=1, etype= $N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.954	0.938	0.951	0.953	0.938	0.938	0.941	0.929	0.932	0.932
len	0.596	0.780	0.601	0.603	3.723	3.723	3.740	2.464	2.464	2.475
wild,0	0.951	0.929	0.939	0.950	0.873	0.878	0.881	0.920	0.921	0.923
len	0.588	0.769	0.578	0.580	3.505	3.505	3.513	2.410	2.410	2.415
par,0	0.950	0.912	0.953	0.959	0.950	0.953	0.954	0.911	0.912	0.910
len	0.599	0.713	0.604	0.608	3.626	3.626	3.636	2.460	2.460	2.466
npar,0.5	0.950	0.953	0.954	0.952	0.944	0.941	0.945	0.937	0.935	0.937
len	0.781	1.541	1.466	1.458	3.732	3.732	3.746	2.473	2.473	2.480
wild,0.5	0.949	0.934	0.947	0.942	0.879	0.884	0.885	0.923	0.926	0.925
len	0.771	1.487	1.411	1.406	3.488	3.488	3.498	2.412	2.412	2.419
par,0.5	0.949	0.944	0.957	0.951	0.952	0.953	0.952	0.936	0.935	0.938
len	0.788	1.533	1.474	1.481	3.623	3.623	3.633	2.457	2.457	2.463
npar,0.9	0.958	0.953	0.955	0.942	0.948	0.951	0.951	0.953	0.949	0.951
len	1.082	10.150	10.159	10.152	3.741	3.741	3.757	2.474	2.474	2.484
wild,0.9	0.955	0.942	0.950	0.930	0.881	0.883	0.885	0.944	0.943	0.943
len	1.071	9.756	9.791	9.724	3.479	3.479	3.484	2.413	2.413	2.418
par,0.9	0.955	0.955	0.959	0.947	0.949	0.946	0.948	0.946	0.948	0.949
len	1.092	10.257	10.272	10.240	3.624	3.624	3.633	2.458	2.458	2.465

Table 12.8. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=8,
k=p-2, etype= $N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.951	0.935	0.952	0.957	0.948	0.949	0.950	0.912	0.913	0.915
len	0.592	0.783	0.603	0.602	1.965	1.965	1.972	3.951	3.951	3.970
wild,0	0.946	0.922	0.943	0.945	0.938	0.936	0.940	0.838	0.847	0.848
len	0.587	0.767	0.582	0.578	1.940	1.940	1.946	3.705	3.705	3.712
par,0	0.946	0.854	0.950	0.956	0.952	0.953	0.952	0.899	0.898	0.901
len	0.598	0.620	0.607	0.604	1.958	1.958	1.963	3.847	3.847	3.859
npar,0.5	0.960	0.952	0.956	0.955	0.947	0.947	0.946	0.940	0.938	0.939
len	0.780	1.548	1.469	1.460	1.962	1.962	1.968	3.966	3.966	3.981
wild,0.5	0.958	0.944	0.938	0.945	0.934	0.934	0.935	0.861	0.861	0.865
len	0.770	1.498	1.413	1.408	1.936	1.936	1.941	3.694	3.694	3.704
par,0.5	0.956	0.945	0.949	0.951	0.948	0.949	0.948	0.927	0.928	0.929
len	0.788	1.484	1.479	1.477	1.960	1.960	1.965	3.845	3.845	3.856
npar,0.9	0.942	0.953	0.952	0.953	0.953	0.950	0.950	0.951	0.951	0.951
len	1.090	10.228	10.192	10.201	1.961	1.961	1.967	3.985	3.985	4.000
wild,0.9	0.934	0.947	0.946	0.950	0.942	0.941	0.943	0.877	0.884	0.880
len	1.076	9.810	9.788	9.821	1.935	1.935	1.939	3.684	3.684	3.690
par,0.9	0.943	0.956	0.956	0.955	0.949	0.950	0.951	0.947	0.949	0.952
len	1.099	10.350	10.288	10.325	1.961	1.961	1.965	3.840	3.840	3.851

Table 12.9. Bootstrapping WLS, n=100, BB=200, wtype = 4,p=4,
k=1, etype= $N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.951	0.924	0.937	0.941	0.944	0.938	0.937	0.948	0.936	0.936
len	0.990	1.522	1.512	1.519	2.449	2.449	2.449	2.467	2.467	2.467
wild,0	0.943	0.920	0.929	0.932	0.918	0.919	0.921	0.914	0.917	0.918
len	0.969	1.459	1.450	1.457	2.285	2.285	2.287	2.308	2.308	2.311
par,0	0.960	0.870	0.821	0.829	0.756	0.756	0.756	0.873	0.875	0.878
len	1.046	1.331	1.141	1.143	2.459	2.459	2.467	2.460	2.460	2.468
npar,0.5	0.946	0.957	0.954	0.956	0.974	0.967	0.968	0.977	0.971	0.972
len	5.398	9.118	9.122	9.127	2.507	2.507	2.505	2.504	2.504	2.500
wild,0.5	0.953	0.951	0.949	0.949	0.939	0.937	0.939	0.949	0.952	0.952
len	5.206	8.379	8.370	8.404	2.276	2.276	2.278	2.295	2.295	2.299
par,0.5	0.958	0.969	0.963	0.973	0.962	0.964	0.965	0.968	0.969	0.970
len	5.666	10.337	10.225	10.310	2.462	2.462	2.468	2.460	2.460	2.466
npar,0.9	0.952	0.956	0.956	0.952	0.984	0.978	0.975	0.978	0.970	0.969
len	15.56	124.40	125.52	124.89	2.515	2.515	2.512	2.506	2.506	2.503
wild,0.9	0.949	0.955	0.955	0.953	0.953	0.954	0.954	0.945	0.946	0.947
len	15.07	114.69	115.85	115.23	2.295	2.295	2.298	2.301	2.301	2.305
par,0.9	0.957	0.974	0.972	0.974	0.979	0.979	0.980	0.973	0.971	0.973
len	16.30	144.07	145.21	143.50	2.459	2.459	2.467	2.458	2.458	2.465

Table 12.10. Bootstrapping WLS, n=100, BB=200, wtype = 4,p=4,
k=p-2, etype= $N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.947	0.929	0.943	0.933	0.933	0.924	0.925	0.961	0.951	0.949
len	0.985	1.509	1.500	1.503	1.935	1.935	1.940	2.867	2.867	2.866
wild,0	0.943	0.924	0.937	0.924	0.916	0.921	0.920	0.897	0.902	0.904
len	0.965	1.440	1.437	1.444	1.858	1.858	1.863	2.618	2.618	2.622
par,0	0.953	0.841	0.854	0.813	0.791	0.791	0.792	0.798	0.798	0.801
len	1.041	1.216	1.224	1.125	1.958	1.958	1.964	2.823	2.823	2.830
npar,0.5	0.946	0.958	0.956	0.950	0.963	0.956	0.956	0.985	0.981	0.981
len	5.379	8.954	9.140	9.051	1.948	1.948	1.949	2.932	2.932	2.929
wild,0.5	0.944	0.950	0.941	0.950	0.943	0.940	0.942	0.941	0.946	0.947
len	5.209	8.239	8.372	8.297	1.851	1.851	1.854	2.603	2.603	2.607
par,0.5	0.956	0.975	0.968	0.966	0.962	0.962	0.963	0.966	0.970	0.969
len	5.674	10.216	10.257	10.131	1.957	1.957	1.962	2.825	2.825	2.832
npar,0.9	0.946	0.961	0.956	0.953	0.967	0.957	0.956	0.988	0.982	0.982
len	15.26	124.46	123.31	122.10	1.955	1.955	1.957	2.937	2.937	2.934
wild,0.9	0.950	0.954	0.952	0.951	0.946	0.946	0.944	0.944	0.945	0.946
len	14.72	114.40	113.74	112.48	1.862	1.862	1.866	2.614	2.614	2.620
par,0.9	0.953	0.973	0.973	0.973	0.968	0.968	0.968	0.973	0.974	0.975
len	15.90	141.32	141.61	140.64	1.960	1.960	1.963	2.825	2.825	2.832

Table 12.11. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=4, k=1, etype= $N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.946	0.953	0.944	0.945	0.945	0.948	0.948	0.946	0.948	0.949
len	0.886	0.681	0.680	0.684	2.488	2.488	2.499	2.485	2.485	2.494
wild,0	0.946	0.947	0.949	0.944	0.925	0.925	0.925	0.936	0.933	0.933
len	0.867	0.650	0.648	0.652	2.388	2.388	2.393	2.397	2.397	2.403
par,0	0.950	0.951	0.983	0.983	0.983	0.983	0.984	0.943	0.943	0.944
len	0.884	0.696	0.874	0.873	2.458	2.458	2.463	2.459	2.459	2.466
npar,0.5	0.950	0.951	0.951	0.945	0.949	0.948	0.949	0.953	0.957	0.957
len	1.065	1.579	1.584	1.567	2.489	2.489	2.500	2.482	2.482	2.490
wild,0.5	0.954	0.949	0.952	0.946	0.935	0.930	0.934	0.939	0.941	0.942
len	1.053	1.516	1.523	1.496	2.401	2.401	2.407	2.401	2.401	2.409
par,0.5	0.956	0.969	0.968	0.969	0.971	0.970	0.970	0.963	0.960	0.963
len	1.072	1.765	1.786	1.774	2.462	2.462	2.469	2.461	2.461	2.467
npar,0.9	0.946	0.949	0.956	0.958	0.950	0.948	0.948	0.938	0.936	0.938
len	1.326	10.751	10.743	10.755	2.481	2.481	2.489	2.477	2.477	2.486
wild,0.9	0.946	0.941	0.950	0.950	0.933	0.933	0.933	0.927	0.926	0.928
len	1.317	10.348	10.329	10.335	2.392	2.392	2.396	2.399	2.399	2.406
par,0.9	0.954	0.950	0.959	0.956	0.950	0.949	0.951	0.939	0.939	0.940
len	1.345	11.066	11.031	11.077	2.460	2.460	2.465	2.463	2.463	2.469

Table 12.12. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=4,
k=p-2, etype= $N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.945	0.946	0.957	0.954	0.954	0.952	0.954	0.958	0.958	0.961
len	0.895	0.687	0.692	0.690	1.964	1.964	1.969	2.876	2.876	2.889
wild,0	0.948	0.946	0.956	0.952	0.942	0.944	0.945	0.932	0.930	0.930
len	0.875	0.655	0.659	0.658	1.927	1.927	1.931	2.723	2.723	2.728
par,0	0.956	0.969	0.975	0.985	0.981	0.982	0.982	0.966	0.966	0.968
len	0.896	0.797	0.799	0.888	1.957	1.957	1.962	2.824	2.824	2.832
npar,0.5	0.949	0.947	0.951	0.947	0.942	0.941	0.943	0.948	0.947	0.948
len	1.064	1.578	1.579	1.584	1.966	1.966	1.971	2.868	2.868	2.877
wild,0.5	0.954	0.951	0.949	0.946	0.935	0.935	0.937	0.930	0.936	0.937
len	1.050	1.511	1.513	1.520	1.932	1.932	1.936	2.739	2.739	2.746
par,0.5	0.956	0.974	0.968	0.970	0.968	0.968	0.968	0.962	0.962	0.962
len	1.068	1.777	1.772	1.777	1.957	1.957	1.962	2.824	2.824	2.832
npar,0.9	0.947	0.948	0.937	0.945	0.943	0.945	0.946	0.943	0.944	0.946
len	1.327	10.713	10.732	10.693	1.962	1.962	1.970	2.862	2.862	2.873
wild,0.9	0.947	0.950	0.945	0.945	0.935	0.937	0.940	0.918	0.919	0.919
len	1.314	10.345	10.381	10.288	1.929	1.929	1.934	2.730	2.730	2.734
par,0.9	0.951	0.953	0.951	0.947	0.944	0.945	0.944	0.939	0.939	0.942
len	1.339	11.001	11.007	10.984	1.958	1.958	1.963	2.823	2.823	2.830

Table 12.13. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=8,
k=1, etype= $N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.954	0.952	0.957	0.957	0.979	0.984	0.987	0.955	0.964	0.967
len	1.972	1.686	1.694	1.678	3.802	3.802	3.827	2.485	2.485	2.498
wild,0	0.959	0.953	0.955	0.952	0.933	0.934	0.935	0.951	0.953	0.952
len	1.926	1.576	1.584	1.571	3.484	3.484	3.491	2.408	2.408	2.414
par,0	0.962	0.976	0.980	0.978	0.983	0.983	0.983	0.968	0.968	0.969
len	1.947	1.839	1.933	1.932	3.627	3.627	3.637	2.460	2.460	2.466
npar,0.5	0.953	0.953	0.962	0.954	0.956	0.958	0.960	0.961	0.961	0.961
len	2.522	4.541	4.517	4.525	3.746	3.746	3.767	2.481	2.481	2.490
wild,0.5	0.949	0.947	0.954	0.949	0.895	0.896	0.899	0.943	0.943	0.943
len	2.471	4.342	4.317	4.326	3.481	3.481	3.490	2.414	2.414	2.421
par,0.5	0.954	0.966	0.968	0.966	0.967	0.969	0.968	0.957	0.957	0.960
len	2.520	4.705	4.700	4.691	3.631	3.631	3.639	2.461	2.461	2.468
npar,0.9	0.955	0.957	0.956	0.945	0.951	0.953	0.957	0.951	0.951	0.951
len	3.356	31.325	31.163	31.306	3.751	3.751	3.767	2.479	2.479	2.488
wild,0.9	0.951	0.949	0.951	0.938	0.898	0.897	0.900	0.941	0.941	0.941
len	3.310	30.005	29.916	29.959	3.469	3.469	3.476	2.406	2.406	2.412
par,0.9	0.960	0.960	0.962	0.955	0.965	0.967	0.968	0.956	0.954	0.956
len	3.386	31.856	31.823	31.822	3.627	3.627	3.637	2.462	2.462	2.470

Table 12.14. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=8,
k=p-2, etype= $N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.962	0.952	0.962	0.964	0.964	0.970	0.969	0.972	0.978	0.980
len	1.968	1.677	1.699	1.690	1.964	1.964	1.973	4.039	4.039	4.066
wild,0	0.962	0.955	0.956	0.958	0.954	0.955	0.954	0.926	0.927	0.924
len	1.924	1.565	1.586	1.581	1.928	1.928	1.933	3.683	3.683	3.692
par,0	0.961	0.974	0.981	0.982	0.980	0.978	0.978	0.981	0.980	0.980
len	1.945	1.902	1.914	1.935	1.956	1.956	1.960	3.845	3.845	3.855
npar,0.5	0.947	0.957	0.951	0.955	0.951	0.952	0.954	0.960	0.959	0.960
len	2.492	4.483	4.468	4.470	1.962	1.962	1.971	3.989	3.989	4.010
wild,0.5	0.947	0.949	0.947	0.952	0.951	0.951	0.953	0.895	0.896	0.898
len	2.453	4.276	4.285	4.294	1.939	1.939	1.944	3.686	3.686	3.695
par,0.5	0.948	0.965	0.960	0.966	0.959	0.959	0.960	0.948	0.951	0.950
len	2.491	4.647	4.629	4.636	1.955	1.955	1.962	3.850	3.850	3.859
npar,0.9	0.946	0.955	0.949	0.948	0.944	0.942	0.943	0.954	0.955	0.956
len	3.364	31.161	31.357	31.350	1.960	1.960	1.969	3.989	3.989	4.007
wild,0.9	0.942	0.948	0.946	0.942	0.935	0.933	0.935	0.878	0.886	0.888
len	3.306	29.739	29.955	30.009	1.933	1.933	1.938	3.673	3.673	3.681
par,0.9	0.946	0.958	0.951	0.949	0.942	0.943	0.945	0.931	0.932	0.934
len	3.374	31.315	31.431	31.486	1.959	1.959	1.963	3.847	3.847	3.859

Table 12.15. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=4, k=1, etype= $N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.946	0.949	0.940	0.928	0.927	0.921	0.916	0.938	0.932	0.932
len	0.286	0.360	0.358	0.357	2.467	2.467	2.475	2.467	2.467	2.473
wild,0	0.947	0.940	0.932	0.925	0.897	0.896	0.896	0.912	0.917	0.917
len	0.286	0.355	0.353	0.351	2.390	2.390	2.395	2.405	2.405	2.411
par,0	0.942	0.945	0.889	0.879	0.833	0.835	0.836	0.931	0.929	0.933
len	0.294	0.358	0.301	0.302	2.461	2.461	2.468	2.459	2.459	2.466
npar,0.5	0.949	0.940	0.951	0.940	0.933	0.929	0.929	0.947	0.940	0.941
len	0.444	0.748	0.749	0.747	2.478	2.478	2.485	2.476	2.476	2.484
wild,0.5	0.952	0.938	0.950	0.933	0.919	0.919	0.918	0.926	0.926	0.927
len	0.442	0.724	0.725	0.722	2.386	2.386	2.392	2.397	2.397	2.404
par,0.5	0.952	0.968	0.962	0.949	0.938	0.936	0.938	0.953	0.952	0.952
len	0.454	0.844	0.763	0.764	2.458	2.458	2.464	2.458	2.458	2.464
npar,0.9	0.948	0.949	0.950	0.945	0.951	0.947	0.947	0.946	0.942	0.944
len	0.646	5.290	5.329	5.321	2.479	2.479	2.488	2.478	2.478	2.485
wild,0.9	0.947	0.949	0.950	0.941	0.935	0.935	0.936	0.933	0.935	0.939
len	0.647	5.107	5.159	5.132	2.388	2.388	2.393	2.403	2.403	2.408
par,0.9	0.948	0.955	0.955	0.959	0.948	0.952	0.953	0.948	0.949	0.951
len	0.660	5.481	5.459	5.482	2.459	2.459	2.464	2.458	2.458	2.465

Table 12.16. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=4, k=p-2, etype= $N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.953	0.943	0.937	0.935	0.929	0.928	0.926	0.924	0.918	0.922
len	0.287	0.361	0.363	0.362	1.959	1.959	1.965	2.835	2.835	2.844
wild,0	0.950	0.936	0.931	0.927	0.918	0.925	0.925	0.908	0.907	0.909
len	0.288	0.356	0.356	0.355	1.930	1.930	1.936	2.732	2.732	2.737
par,0	0.954	0.906	0.906	0.880	0.872	0.874	0.875	0.885	0.884	0.883
len	0.295	0.324	0.325	0.303	1.959	1.959	1.965	2.826	2.826	2.834
npar,0.5	0.950	0.951	0.949	0.955	0.951	0.951	0.951	0.941	0.933	0.935
len	0.444	0.752	0.750	0.750	1.963	1.963	1.969	2.854	2.854	2.863
wild,0.5	0.949	0.943	0.943	0.940	0.932	0.932	0.933	0.907	0.910	0.910
len	0.443	0.728	0.726	0.723	1.925	1.925	1.930	2.726	2.726	2.731
par,0.5	0.948	0.954	0.965	0.950	0.945	0.947	0.946	0.941	0.941	0.942
len	0.454	0.786	0.785	0.761	1.959	1.959	1.964	2.826	2.826	2.832
npar,0.9	0.958	0.951	0.947	0.943	0.941	0.937	0.938	0.950	0.947	0.948
len	0.644	5.292	5.327	5.293	1.965	1.965	1.970	2.855	2.855	2.865
wild,0.9	0.951	0.944	0.946	0.938	0.931	0.932	0.935	0.924	0.926	0.924
len	0.643	5.132	5.143	5.119	1.926	1.926	1.932	2.729	2.729	2.735
par,0.9	0.956	0.955	0.955	0.957	0.950	0.949	0.950	0.938	0.941	0.943
len	0.658	5.447	5.477	5.436	1.957	1.957	1.963	2.823	2.823	2.831

Table 12.17. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=8, k=1, etype= $N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.948	0.952	0.950	0.950	0.912	0.908	0.910	0.934	0.931	0.931
len	0.255	0.283	0.283	0.284	3.698	3.698	3.714	2.468	2.468	2.475
wild,0	0.942	0.935	0.943	0.941	0.849	0.848	0.850	0.916	0.919	0.920
len	0.253	0.275	0.276	0.276	3.479	3.479	3.487	2.418	2.418	2.424
par,0	0.954	0.944	0.932	0.935	0.870	0.872	0.871	0.939	0.938	0.938
len	0.260	0.284	0.263	0.264	3.631	3.631	3.638	2.462	2.462	2.468
npar,0.5	0.956	0.951	0.952	0.952	0.962	0.959	0.958	0.957	0.951	0.952
len	0.603	1.126	1.124	1.134	3.758	3.758	3.770	2.479	2.479	2.486
wild,0.5	0.949	0.942	0.944	0.940	0.891	0.891	0.892	0.933	0.934	0.934
len	0.594	1.076	1.073	1.082	3.455	3.455	3.462	2.400	2.400	2.406
par,0.5	0.950	0.960	0.959	0.949	0.951	0.951	0.952	0.953	0.952	0.951
len	0.610	1.199	1.146	1.152	3.628	3.628	3.637	2.459	2.459	2.466
npar,0.9	0.946	0.956	0.954	0.948	0.969	0.966	0.968	0.948	0.944	0.946
len	0.996	9.313	9.299	9.199	3.751	3.751	3.765	2.471	2.471	2.480
wild,0.9	0.943	0.947	0.939	0.940	0.900	0.901	0.903	0.933	0.931	0.933
len	0.986	8.939	8.913	8.820	3.457	3.457	3.464	2.401	2.401	2.407
par,0.9	0.945	0.960	0.951	0.952	0.957	0.958	0.960	0.944	0.946	0.947
len	1.006	9.507	9.417	9.422	3.626	3.626	3.637	2.461	2.461	2.467

Table 12.18. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=8, k=p-2, etype= $N(0, 1)$

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.949	0.945	0.945	0.950	0.938	0.938	0.936	0.902	0.897	0.901
len	0.254	0.284	0.283	0.283	1.960	1.960	1.966	3.936	3.936	3.953
wild,0	0.948	0.944	0.938	0.944	0.935	0.933	0.934	0.829	0.833	0.837
len	0.252	0.276	0.275	0.277	1.938	1.938	1.943	3.688	3.688	3.696
par,0	0.949	0.931	0.931	0.928	0.920	0.921	0.921	0.878	0.879	0.881
len	0.259	0.265	0.266	0.262	1.956	1.956	1.960	3.850	3.850	3.860
npar,0.5	0.941	0.962	0.951	0.947	0.946	0.941	0.944	0.966	0.964	0.965
len	0.605	1.128	1.125	1.134	1.961	1.961	1.967	4.004	4.004	4.018
wild,0.5	0.943	0.951	0.947	0.937	0.933	0.933	0.933	0.877	0.877	0.879
len	0.596	1.077	1.075	1.084	1.928	1.928	1.933	3.658	3.658	3.665
par,0.5	0.945	0.964	0.958	0.955	0.945	0.944	0.944	0.948	0.952	0.951
len	0.610	1.147	1.151	1.152	1.960	1.960	1.965	3.846	3.846	3.858
npar,0.9	0.943	0.949	0.951	0.949	0.946	0.943	0.945	0.964	0.960	0.963
len	0.996	9.329	9.282	9.355	1.960	1.960	1.968	4.000	4.000	4.013
wild,0.9	0.941	0.942	0.942	0.940	0.937	0.934	0.936	0.890	0.891	0.892
len	0.981	8.926	8.888	8.959	1.930	1.930	1.937	3.665	3.665	3.673
par,0.9	0.946	0.947	0.953	0.947	0.938	0.942	0.944	0.942	0.942	0.943
len	1.008	9.408	9.403	9.410	1.961	1.961	1.966	3.847	3.847	3.856

Table 12.19. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=4, k=1, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.936	0.952	0.957	0.950	0.948	0.947	0.948	0.943	0.942	0.943
len	2.816	2.911	2.809	2.778	2.487	2.487	2.494	2.479	2.479	2.489
wild,0	0.948	0.944	0.950	0.948	0.933	0.932	0.932	0.933	0.932	0.934
len	2.754	2.758	2.676	2.648	2.383	2.383	2.389	2.389	2.389	2.395
par,0	0.949	0.950	0.960	0.963	0.954	0.956	0.957	0.944	0.945	0.945
len	2.868	2.938	2.927	2.925	2.464	2.464	2.470	2.462	2.462	2.470
npar,0.5	0.951	0.952	0.944	0.951	0.950	0.949	0.952	0.955	0.952	0.955
len	2.874	4.831	4.723	4.757	2.486	2.486	2.496	2.480	2.480	2.489
wild,0.5	0.954	0.949	0.946	0.949	0.932	0.932	0.931	0.939	0.941	0.942
len	2.810	4.562	4.479	4.519	2.376	2.376	2.380	2.383	2.383	2.387
par,0.5	0.956	0.957	0.959	0.958	0.954	0.955	0.956	0.964	0.959	0.960
len	2.931	4.942	4.925	4.922	2.459	2.459	2.466	2.463	2.463	2.468
npar,0.9	0.942	0.947	0.951	0.953	0.953	0.954	0.955	0.941	0.940	0.942
len	2.908	23.512	23.206	23.538	2.489	2.489	2.498	2.478	2.478	2.486
wild,0.9	0.950	0.944	0.946	0.947	0.935	0.935	0.935	0.929	0.930	0.931
len	2.849	22.339	22.044	22.359	2.378	2.378	2.382	2.379	2.379	2.384
par,0.9	0.954	0.952	0.964	0.956	0.946	0.945	0.946	0.942	0.942	0.940
len	2.968	24.554	24.356	24.514	2.456	2.456	2.464	2.461	2.461	2.468

Table 12.20. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=4, k=p-2, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.949	0.940	0.941	0.947	0.947	0.950	0.950	0.952	0.953	0.954
len	2.852	2.938	2.910	2.847	1.960	1.960	1.966	2.871	2.871	2.881
wild,0	0.947	0.942	0.937	0.945	0.936	0.942	0.941	0.925	0.925	0.926
len	2.794	2.790	2.758	2.715	1.912	1.912	1.916	2.718	2.718	2.723
par,0	0.955	0.948	0.953	0.956	0.951	0.952	0.951	0.937	0.937	0.940
len	2.908	3.012	2.980	2.951	1.959	1.959	1.964	2.822	2.822	2.827
npar,0.5	0.950	0.956	0.947	0.946	0.950	0.954	0.952	0.954	0.954	0.956
len	3.084	5.124	5.097	5.037	1.959	1.959	1.964	2.875	2.875	2.885
wild,0.5	0.941	0.944	0.943	0.949	0.941	0.942	0.941	0.931	0.930	0.933
len	3.019	4.856	4.848	4.789	1.906	1.906	1.911	2.708	2.708	2.713
par,0.5	0.952	0.955	0.954	0.959	0.953	0.956	0.956	0.933	0.936	0.939
len	3.133	5.264	5.253	5.251	1.957	1.957	1.962	2.826	2.826	2.833
npar,0.9	0.948	0.953	0.957	0.952	0.954	0.957	0.958	0.952	0.951	0.953
len	3.378	26.887	27.203	27.397	1.961	1.961	1.968	2.874	2.874	2.885
wild,0.9	0.948	0.948	0.957	0.953	0.943	0.944	0.945	0.924	0.926	0.928
len	3.294	25.497	25.735	25.773	1.906	1.906	1.910	2.703	2.703	2.709
par,0.9	0.953	0.964	0.964	0.958	0.954	0.953	0.953	0.938	0.937	0.937
len	3.438	28.393	28.657	28.484	1.958	1.958	1.964	2.824	2.824	2.832

Table 12.21. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=8, k=1, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.951	0.943	0.957	0.958	0.958	0.957	0.959	0.952	0.951	0.953
len	2.864	2.910	2.856	2.844	3.778	3.778	3.795	2.481	2.481	2.491
wild,0	0.950	0.941	0.951	0.952	0.901	0.905	0.906	0.933	0.929	0.932
len	2.780	2.751	2.707	2.686	3.468	3.468	3.474	2.391	2.391	2.395
par,0	0.960	0.949	0.965	0.966	0.968	0.964	0.965	0.951	0.951	0.954
len	2.879	2.959	2.930	2.922	3.626	3.626	3.635	2.461	2.461	2.466
npar,0.5	0.955	0.956	0.953	0.948	0.963	0.965	0.966	0.959	0.960	0.961
len	2.997	5.534	5.566	5.541	3.787	3.787	3.803	2.476	2.476	2.487
wild,0.5	0.954	0.951	0.952	0.951	0.904	0.908	0.907	0.945	0.945	0.948
len	2.915	5.229	5.237	5.221	3.456	3.456	3.465	2.385	2.385	2.391
par,0.5	0.957	0.953	0.962	0.954	0.959	0.961	0.963	0.953	0.956	0.957
len	3.036	5.715	5.692	5.662	3.628	3.628	3.639	2.460	2.460	2.467
npar,0.9	0.948	0.955	0.951	0.945	0.972	0.971	0.974	0.957	0.955	0.959
len	3.238	29.797	30.240	30.068	3.797	3.797	3.813	2.480	2.480	2.489
wild,0.9	0.951	0.944	0.944	0.939	0.914	0.919	0.920	0.935	0.935	0.936
len	3.138	28.062	28.360	28.224	3.448	3.448	3.455	2.377	2.377	2.382
par,0.9	0.957	0.951	0.958	0.952	0.955	0.958	0.957	0.946	0.947	0.948
len	3.270	30.554	30.750	30.560	3.628	3.628	3.636	2.461	2.461	2.467

Table 12.22. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=8, k=p-2, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.945	0.956	0.954	0.947	0.946	0.948	0.950	0.970	0.969	0.970
len	3.248	3.301	3.289	3.238	1.957	1.957	1.964	4.068	4.068	4.086
wild,0	0.944	0.953	0.953	0.942	0.935	0.940	0.939	0.904	0.908	0.909
len	3.135	3.105	3.089	3.030	1.912	1.912	1.916	3.654	3.654	3.660
par,0	0.949	0.955	0.954	0.952	0.944	0.946	0.946	0.931	0.935	0.935
len	3.273	3.351	3.334	3.316	1.959	1.959	1.964	3.849	3.849	3.859
npar,0.5	0.949	0.957	0.955	0.954	0.955	0.953	0.954	0.980	0.978	0.980
len	6.615	12.176	12.114	12.277	1.961	1.961	1.968	4.085	4.085	4.100
wild,0.5	0.950	0.951	0.945	0.947	0.938	0.940	0.939	0.909	0.912	0.914
len	6.384	11.377	11.307	11.449	1.903	1.903	1.908	3.634	3.634	3.641
par,0.5	0.958	0.953	0.958	0.958	0.945	0.946	0.947	0.940	0.940	0.942
len	6.734	12.649	12.623	12.605	1.958	1.958	1.961	3.849	3.849	3.859
npar,0.9	0.951	0.955	0.950	0.961	0.957	0.954	0.956	0.979	0.976	0.976
len	10.106	93.885	93.872	92.715	1.957	1.957	1.963	4.092	4.092	4.104
wild,0.9	0.948	0.944	0.945	0.953	0.949	0.949	0.949	0.914	0.914	0.917
len	9.782	88.039	87.720	86.695	1.905	1.905	1.909	3.637	3.637	3.644
par,0.9	0.959	0.955	0.955	0.952	0.948	0.950	0.950	0.953	0.952	0.954
len	10.311	97.010	97.078	96.304	1.955	1.955	1.959	3.844	3.844	3.855

Table 12.23. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=4, k=1, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.948	0.945	0.950	0.940	0.950	0.950	0.945	0.945	0.940	0.940
len	0.944	1.241	0.939	0.945	2.486	2.486	2.494	2.464	2.464	2.472
wild,0	0.949	0.936	0.947	0.943	0.929	0.933	0.932	0.919	0.919	0.923
len	0.929	1.186	0.894	0.901	2.380	2.380	2.385	2.370	2.370	2.375
par,0	0.956	0.910	0.954	0.958	0.956	0.956	0.955	0.908	0.908	0.911
len	0.961	1.137	0.985	0.989	2.459	2.459	2.466	2.457	2.457	2.461
npar,0.5	0.940	0.947	0.952	0.951	0.947	0.947	0.947	0.938	0.936	0.936
len	1.047	1.903	1.746	1.730	2.488	2.488	2.495	2.472	2.472	2.479
wild,0.5	0.948	0.943	0.948	0.946	0.927	0.931	0.929	0.926	0.924	0.924
len	1.029	1.816	1.662	1.649	2.375	2.375	2.382	2.377	2.377	2.382
par,0.5	0.957	0.943	0.955	0.959	0.951	0.952	0.953	0.934	0.932	0.933
len	1.069	1.913	1.820	1.816	2.462	2.462	2.468	2.460	2.460	2.466
npar,0.9	0.944	0.947	0.949	0.950	0.955	0.952	0.952	0.946	0.944	0.944
len	1.259	10.278	10.317	10.209	2.486	2.486	2.494	2.482	2.482	2.489
wild,0.9	0.950	0.939	0.941	0.949	0.929	0.928	0.929	0.928	0.929	0.929
len	1.233	9.735	9.786	9.725	2.372	2.372	2.377	2.380	2.380	2.387
par,0.9	0.955	0.952	0.954	0.956	0.953	0.954	0.955	0.946	0.946	0.947
len	1.287	10.804	10.798	10.795	2.461	2.461	2.466	2.462	2.462	2.467

Table 12.24. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=4, k=p-2, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.950	0.939	0.941	0.951	0.950	0.948	0.950	0.945	0.945	0.944
len	0.964	1.254	0.955	0.958	1.960	1.960	1.967	2.864	2.864	2.872
wild,0	0.949	0.935	0.943	0.946	0.940	0.939	0.941	0.911	0.912	0.914
len	0.945	1.198	0.909	0.911	1.911	1.911	1.915	2.707	2.707	2.712
par,0	0.961	0.897	0.959	0.952	0.949	0.949	0.950	0.915	0.917	0.918
len	0.985	1.071	1.032	0.994	1.958	1.958	1.962	2.824	2.824	2.832
npar,0.5	0.944	0.948	0.945	0.963	0.958	0.961	0.959	0.952	0.951	0.952
len	1.060	1.931	1.730	1.755	1.956	1.956	1.963	2.863	2.863	2.872
wild,0.5	0.948	0.938	0.946	0.957	0.952	0.957	0.955	0.923	0.926	0.928
len	1.037	1.842	1.655	1.676	1.911	1.911	1.914	2.713	2.713	2.717
par,0.5	0.951	0.936	0.954	0.970	0.965	0.966	0.966	0.933	0.939	0.940
len	1.081	1.864	1.843	1.830	1.958	1.958	1.963	2.826	2.826	2.833
npar,0.9	0.948	0.938	0.941	0.953	0.948	0.946	0.948	0.946	0.943	0.944
len	1.263	10.263	10.287	10.277	1.959	1.959	1.965	2.873	2.873	2.881
wild,0.9	0.950	0.939	0.936	0.946	0.941	0.942	0.941	0.916	0.915	0.915
len	1.240	9.730	9.800	9.740	1.909	1.909	1.913	2.711	2.711	2.717
par,0.9	0.950	0.950	0.952	0.950	0.945	0.945	0.944	0.941	0.941	0.942
len	1.290	10.687	10.734	10.680	1.958	1.958	1.962	2.823	2.823	2.830

Table 12.25. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=8, k=1, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.954	0.942	0.951	0.956	0.961	0.961	0.962	0.943	0.941	0.942
len	0.978	1.253	0.961	0.971	3.780	3.780	3.796	2.467	2.467	2.475
wild,0	0.959	0.935	0.944	0.945	0.892	0.896	0.894	0.928	0.929	0.929
len	0.951	1.200	0.910	0.913	3.466	3.466	3.475	2.375	2.375	2.381
par,0	0.959	0.906	0.959	0.960	0.961	0.962	0.961	0.910	0.914	0.914
len	0.988	1.136	0.999	1.001	3.626	3.626	3.635	2.460	2.460	2.466
npar,0.5	0.946	0.949	0.944	0.950	0.966	0.965	0.963	0.950	0.949	0.951
len	1.258	2.439	2.324	2.325	3.793	3.793	3.806	2.477	2.477	2.485
wild,0.5	0.951	0.940	0.940	0.938	0.892	0.892	0.893	0.932	0.933	0.934
len	1.224	2.305	2.196	2.191	3.458	3.458	3.464	2.382	2.382	2.385
par,0.5	0.950	0.949	0.955	0.961	0.958	0.962	0.963	0.939	0.940	0.941
len	1.276	2.468	2.400	2.390	3.624	3.624	3.633	2.460	2.460	2.466
npar,0.9	0.957	0.953	0.958	0.963	0.965	0.966	0.968	0.957	0.956	0.957
len	1.775	16.674	16.467	16.475	3.815	3.815	3.830	2.482	2.482	2.491
wild,0.9	0.952	0.949	0.959	0.950	0.902	0.898	0.901	0.940	0.939	0.940
len	1.722	15.631	15.456	15.522	3.445	3.445	3.452	2.376	2.376	2.381
par,0.9	0.962	0.961	0.957	0.959	0.962	0.966	0.963	0.955	0.957	0.956
len	1.810	17.122	17.062	17.094	3.624	3.624	3.633	2.460	2.460	2.466

Table 12.26. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=8, k=p-2, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.950	0.933	0.957	0.958	0.959	0.959	0.958	0.955	0.952	0.956
len	0.971	1.237	0.974	0.978	1.958	1.958	1.964	4.020	4.020	4.035
wild,0	0.942	0.930	0.951	0.952	0.945	0.944	0.947	0.874	0.878	0.881
len	0.948	1.185	0.923	0.926	1.916	1.916	1.920	3.657	3.657	3.665
par,0	0.952	0.884	0.961	0.962	0.952	0.952	0.954	0.915	0.914	0.918
len	0.985	1.016	0.998	0.997	1.954	1.954	1.960	3.847	3.847	3.857
npar,0.5	0.956	0.951	0.955	0.957	0.958	0.955	0.957	0.967	0.964	0.966
len	1.274	2.494	2.369	2.374	1.962	1.962	1.969	4.047	4.047	4.062
wild,0.5	0.961	0.942	0.944	0.947	0.944	0.945	0.946	0.881	0.883	0.885
len	1.242	2.350	2.242	2.243	1.915	1.915	1.920	3.654	3.654	3.663
par,0.5	0.959	0.943	0.960	0.959	0.948	0.948	0.947	0.945	0.951	0.950
len	1.299	2.430	2.434	2.444	1.957	1.957	1.961	3.848	3.848	3.858
npar,0.9	0.948	0.952	0.959	0.953	0.953	0.951	0.951	0.973	0.971	0.972
len	1.782	16.500	16.418	16.378	1.959	1.959	1.966	4.067	4.067	4.081
wild,0.9	0.948	0.949	0.953	0.949	0.940	0.938	0.937	0.907	0.905	0.908
len	1.734	15.551	15.453	15.370	1.910	1.910	1.915	3.651	3.651	3.659
par,0.9	0.948	0.954	0.955	0.953	0.940	0.939	0.939	0.940	0.939	0.941
len	1.815	17.021	16.976	16.956	1.961	1.961	1.967	3.849	3.849	3.859

Table 12.27. Bootstrapping WLS, n=100, BB=200, wtype = 4, p=4, k=1, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.949	0.946	0.944	0.936	0.950	0.942	0.946	0.962	0.957	0.958
len	1.522	2.294	2.273	2.314	2.465	2.465	2.466	2.480	2.480	2.480
wild,0	0.948	0.934	0.941	0.926	0.913	0.913	0.915	0.931	0.932	0.931
len	1.467	2.161	2.142	2.174	2.264	2.264	2.267	2.291	2.291	2.294
par,0	0.959	0.882	0.867	0.860	0.835	0.839	0.840	0.896	0.898	0.897
len	1.629	2.012	1.814	1.839	2.461	2.461	2.467	2.459	2.459	2.466
npar,0.5	0.947	0.956	0.964	0.953	0.983	0.979	0.981	0.976	0.972	0.971
len	7.932	13.239	13.077	13.232	2.516	2.516	2.514	2.517	2.517	2.513
wild,0.5	0.950	0.954	0.964	0.952	0.958	0.958	0.958	0.945	0.946	0.942
len	7.537	11.970	11.838	12.033	2.262	2.262	2.267	2.275	2.275	2.279
par,0.5	0.963	0.967	0.974	0.970	0.976	0.976	0.976	0.965	0.966	0.967
len	8.374	15.279	15.035	15.221	2.460	2.460	2.468	2.460	2.460	2.465
npar,0.9	0.954	0.957	0.945	0.955	0.984	0.981	0.981	0.979	0.977	0.976
len	23.95	188.77	188.05	191.56	2.530	2.530	2.529	2.522	2.522	2.516
wild,0.9	0.956	0.952	0.947	0.949	0.947	0.947	0.948	0.947	0.948	0.948
len	22.72	172.11	170.55	174.25	2.279	2.279	2.283	2.276	2.276	2.281
par,0.9	0.964	0.975	0.972	0.972	0.978	0.977	0.978	0.976	0.978	0.978
len	25.44	222.79	223.18	224.63	2.461	2.461	2.466	2.463	2.463	2.469

Table 12.28. Bootstrapping WLS, n=100, BB=200, wtype = 4, p=4, k=p-2, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.945	0.943	0.935	0.938	0.942	0.933	0.936	0.966	0.957	0.958
len	1.512	2.279	2.319	2.251	1.935	1.935	1.937	2.885	2.885	2.883
wild,0	0.945	0.932	0.922	0.924	0.919	0.918	0.917	0.920	0.923	0.922
len	1.454	2.138	2.175	2.110	1.840	1.840	1.843	2.608	2.608	2.612
par,0	0.955	0.860	0.851	0.825	0.807	0.810	0.813	0.831	0.834	0.836
len	1.610	1.908	1.920	1.791	1.959	1.959	1.965	2.827	2.827	2.833
npar,0.5	0.955	0.953	0.950	0.953	0.965	0.959	0.957	0.983	0.981	0.982
len	8.177	13.678	13.692	13.492	1.945	1.945	1.944	2.962	2.962	2.958
wild,0.5	0.953	0.951	0.951	0.952	0.943	0.948	0.949	0.948	0.950	0.949
len	7.753	12.364	12.357	12.219	1.831	1.831	1.834	2.592	2.592	2.597
par,0.5	0.968	0.967	0.968	0.972	0.968	0.971	0.972	0.962	0.963	0.965
len	8.658	15.775	15.784	15.614	1.959	1.959	1.965	2.825	2.825	2.833
npar,0.9	0.942	0.954	0.957	0.953	0.966	0.959	0.962	0.990	0.987	0.984
len	23.82	188.59	189.37	190.09	1.950	1.950	1.950	2.970	2.970	2.965
wild,0.9	0.951	0.954	0.958	0.953	0.949	0.954	0.952	0.951	0.954	0.955
len	22.63	171.49	171.85	172.90	1.846	1.846	1.849	2.605	2.605	2.609
par,0.9	0.961	0.973	0.973	0.973	0.970	0.970	0.970	0.978	0.979	0.980
len	25.20	221.44	222.57	222.92	1.958	1.958	1.962	2.823	2.823	2.830

Table 12.29. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=4, k=1, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.947	0.949	0.951	0.951	0.954	0.956	0.957	0.960	0.959	0.961
len	1.405	1.074	1.074	1.085	2.495	2.495	2.505	2.490	2.490	2.502
wild,0	0.951	0.949	0.946	0.943	0.934	0.935	0.935	0.943	0.946	0.943
len	1.342	1.000	1.001	1.011	2.354	2.354	2.360	2.363	2.363	2.369
par,0	0.955	0.966	0.975	0.976	0.972	0.972	0.973	0.963	0.963	0.962
len	1.413	1.157	1.397	1.388	2.460	2.460	2.468	2.463	2.463	2.469
npar,0.5	0.942	0.945	0.944	0.947	0.959	0.962	0.962	0.953	0.953	0.954
len	1.711	2.526	2.521	2.510	2.498	2.498	2.507	2.486	2.486	2.496
wild,0.5	0.944	0.946	0.947	0.951	0.930	0.933	0.933	0.934	0.936	0.936
len	1.655	2.365	2.366	2.357	2.366	2.366	2.373	2.369	2.369	2.373
par,0.5	0.959	0.968	0.970	0.975	0.963	0.962	0.963	0.957	0.955	0.959
len	1.735	2.844	2.860	2.861	2.459	2.459	2.465	2.464	2.464	2.469
npar,0.9	0.944	0.955	0.951	0.947	0.955	0.953	0.956	0.953	0.952	0.953
len	2.169	17.479	17.295	17.392	2.493	2.493	2.502	2.485	2.485	2.494
wild,0.9	0.944	0.949	0.951	0.946	0.939	0.942	0.939	0.929	0.931	0.929
len	2.098	16.363	16.304	16.379	2.354	2.354	2.358	2.357	2.357	2.362
par,0.9	0.959	0.963	0.960	0.950	0.951	0.955	0.957	0.955	0.956	0.957
len	2.212	18.446	18.372	18.493	2.457	2.457	2.465	2.458	2.458	2.464

Table 12.30. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=4, k=p-2, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.950	0.954	0.958	0.947	0.952	0.950	0.950	0.962	0.966	0.968
len	1.424	1.089	1.088	1.083	1.956	1.956	1.964	2.895	2.895	2.907
wild,0	0.952	0.951	0.950	0.939	0.934	0.936	0.937	0.934	0.934	0.938
len	1.356	1.009	1.012	1.010	1.894	1.894	1.899	2.686	2.686	2.692
par,0	0.957	0.979	0.980	0.976	0.970	0.972	0.972	0.963	0.969	0.969
len	1.434	1.296	1.286	1.420	1.958	1.958	1.962	2.823	2.823	2.832
npar,0.5	0.946	0.950	0.951	0.952	0.954	0.961	0.962	0.962	0.959	0.960
len	1.730	2.521	2.515	2.489	1.956	1.956	1.963	2.885	2.885	2.896
wild,0.5	0.955	0.948	0.954	0.948	0.944	0.945	0.946	0.933	0.937	0.938
len	1.674	2.360	2.362	2.344	1.904	1.904	1.909	2.700	2.700	2.705
par,0.5	0.958	0.968	0.971	0.975	0.967	0.967	0.969	0.967	0.967	0.968
len	1.748	2.898	2.888	2.890	1.957	1.957	1.962	2.828	2.828	2.834
npar,0.9	0.944	0.957	0.941	0.949	0.955	0.958	0.957	0.960	0.960	0.960
len	2.171	17.105	17.243	17.079	1.959	1.959	1.966	2.883	2.883	2.894
wild,0.9	0.950	0.953	0.938	0.953	0.944	0.944	0.945	0.925	0.926	0.930
len	2.105	16.103	16.194	16.091	1.902	1.902	1.906	2.691	2.691	2.697
par,0.9	0.957	0.966	0.957	0.959	0.953	0.952	0.951	0.946	0.946	0.947
len	2.216	18.113	18.229	18.185	1.957	1.957	1.962	2.825	2.825	2.832

Table 12.31. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=8, k=1, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.950	0.951	0.954	0.959	0.986	0.990	0.990	0.963	0.965	0.966
len	3.168	2.650	2.709	2.719	3.863	3.863	3.889	2.495	2.495	2.508
wild,0	0.954	0.955	0.948	0.962	0.954	0.954	0.955	0.937	0.944	0.944
len	3.036	2.429	2.479	2.495	3.449	3.449	3.454	2.369	2.369	2.375
par,0	0.956	0.978	0.979	0.982	0.990	0.991	0.992	0.966	0.965	0.968
len	3.152	3.120	3.164	3.147	3.625	3.625	3.635	2.460	2.460	2.466
npar,0.5	0.943	0.946	0.953	0.951	0.973	0.975	0.978	0.951	0.953	0.952
len	4.105	7.285	7.302	7.282	3.812	3.812	3.831	2.486	2.486	2.495
wild,0.5	0.949	0.948	0.952	0.948	0.915	0.917	0.915	0.934	0.937	0.938
len	3.959	6.815	6.823	6.799	3.445	3.445	3.451	2.373	2.373	2.380
par,0.5	0.952	0.960	0.963	0.967	0.976	0.976	0.975	0.961	0.960	0.962
len	4.134	7.808	7.798	7.815	3.626	3.626	3.636	2.456	2.456	2.463
npar,0.9	0.958	0.951	0.952	0.955	0.972	0.970	0.971	0.954	0.952	0.955
len	5.441	50.272	50.007	50.237	3.810	3.810	3.826	2.485	2.485	2.496
wild,0.9	0.960	0.944	0.946	0.948	0.914	0.915	0.917	0.935	0.938	0.937
len	5.267	47.062	46.810	47.016	3.442	3.442	3.449	2.375	2.375	2.379
par,0.9	0.962	0.963	0.962	0.962	0.970	0.971	0.971	0.959	0.961	0.961
len	5.510	52.497	52.060	52.484	3.628	3.628	3.638	2.458	2.458	2.463

Table 12.32. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=8, k=p-2, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.949	0.948	0.954	0.953	0.958	0.963	0.966	0.988	0.991	0.991
len	3.234	2.733	2.722	2.751	1.963	1.963	1.974	4.126	4.126	4.154
wild,0	0.954	0.951	0.954	0.953	0.945	0.949	0.950	0.943	0.943	0.944
len	3.079	2.494	2.482	2.516	1.907	1.907	1.910	3.649	3.649	3.657
par,0	0.961	0.978	0.980	0.978	0.974	0.974	0.973	0.986	0.988	0.989
len	3.214	3.182	3.179	3.222	1.955	1.955	1.960	3.848	3.848	3.858
npar,0.5	0.954	0.961	0.957	0.960	0.957	0.960	0.959	0.980	0.981	0.981
len	4.120	7.329	7.320	7.316	1.961	1.961	1.970	4.072	4.072	4.092
wild,0.5	0.948	0.950	0.952	0.952	0.947	0.951	0.951	0.910	0.916	0.916
len	3.956	6.832	6.840	6.825	1.911	1.911	1.915	3.650	3.650	3.659
par,0.5	0.953	0.959	0.963	0.965	0.956	0.958	0.957	0.966	0.965	0.965
len	4.143	7.695	7.695	7.693	1.958	1.958	1.964	3.844	3.844	3.854
npar,0.9	0.951	0.953	0.956	0.949	0.945	0.947	0.949	0.979	0.978	0.978
len	5.455	50.266	50.818	49.844	1.959	1.959	1.966	4.071	4.071	4.087
wild,0.9	0.950	0.949	0.945	0.940	0.936	0.935	0.936	0.920	0.923	0.924
len	5.286	46.993	47.408	46.463	1.910	1.910	1.916	3.644	3.644	3.653
par,0.9	0.958	0.954	0.950	0.955	0.947	0.947	0.947	0.950	0.950	0.952
len	5.568	51.767	51.978	51.713	1.957	1.957	1.962	3.847	3.847	3.857

Table 12.33. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=4, k=1, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.950	0.948	0.941	0.937	0.930	0.930	0.929	0.950	0.945	0.943
len	0.474	0.579	0.577	0.581	2.471	2.471	2.478	2.473	2.473	2.479
wild,0	0.947	0.937	0.931	0.931	0.910	0.907	0.907	0.925	0.925	0.926
len	0.465	0.556	0.552	0.557	2.354	2.354	2.360	2.364	2.364	2.367
par,0	0.960	0.939	0.892	0.892	0.846	0.850	0.853	0.940	0.940	0.941
len	0.489	0.572	0.500	0.502	2.464	2.464	2.470	2.459	2.459	2.466
npar,0.5	0.950	0.952	0.945	0.939	0.943	0.941	0.942	0.948	0.946	0.944
len	0.725	1.211	1.203	1.211	2.490	2.490	2.496	2.483	2.483	2.489
wild,0.5	0.953	0.945	0.935	0.931	0.914	0.915	0.914	0.930	0.929	0.930
len	0.705	1.135	1.135	1.141	2.351	2.351	2.358	2.364	2.364	2.369
par,0.5	0.954	0.964	0.946	0.952	0.937	0.941	0.942	0.950	0.949	0.950
len	0.744	1.361	1.267	1.261	2.459	2.459	2.466	2.462	2.462	2.468
npar,0.9	0.944	0.943	0.947	0.955	0.955	0.950	0.949	0.952	0.946	0.948
len	1.051	8.414	8.462	8.390	2.492	2.492	2.498	2.485	2.485	2.492
wild,0.9	0.949	0.942	0.943	0.952	0.933	0.930	0.931	0.932	0.934	0.934
len	1.025	7.972	7.979	7.937	2.356	2.356	2.360	2.363	2.363	2.367
par,0.9	0.953	0.955	0.965	0.961	0.954	0.953	0.953	0.947	0.948	0.950
len	1.085	9.038	9.069	9.025	2.461	2.461	2.468	2.462	2.462	2.470

Table 12.34. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=4, k=p-2, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.951	0.940	0.929	0.949	0.950	0.945	0.945	0.941	0.937	0.934
len	0.472	0.578	0.587	0.583	1.953	1.953	1.959	2.857	2.857	2.865
wild,0	0.958	0.941	0.929	0.943	0.935	0.937	0.937	0.909	0.908	0.908
len	0.463	0.554	0.562	0.557	1.900	1.900	1.902	2.690	2.690	2.695
par,0	0.965	0.916	0.907	0.907	0.890	0.890	0.890	0.897	0.899	0.901
len	0.488	0.530	0.536	0.500	1.958	1.958	1.962	2.822	2.822	2.828
npar,0.5	0.942	0.943	0.947	0.947	0.948	0.947	0.945	0.946	0.946	0.947
len	0.721	1.199	1.201	1.201	1.962	1.962	1.968	2.880	2.880	2.888
wild,0.5	0.946	0.945	0.954	0.944	0.936	0.934	0.935	0.923	0.925	0.927
len	0.703	1.130	1.134	1.130	1.898	1.898	1.903	2.689	2.689	2.694
par,0.5	0.951	0.953	0.960	0.954	0.947	0.946	0.947	0.941	0.942	0.942
len	0.740	1.294	1.283	1.254	1.957	1.957	1.962	2.822	2.822	2.830
npar,0.9	0.951	0.954	0.952	0.953	0.954	0.953	0.952	0.961	0.959	0.959
len	1.056	8.537	8.453	8.520	1.956	1.956	1.960	2.883	2.883	2.888
wild,0.9	0.951	0.949	0.942	0.949	0.944	0.945	0.947	0.927	0.928	0.929
len	1.031	8.066	7.987	8.021	1.898	1.898	1.902	2.691	2.691	2.697
par,0.9	0.958	0.960	0.951	0.953	0.946	0.946	0.946	0.953	0.955	0.954
len	1.089	9.062	9.010	9.040	1.961	1.961	1.966	2.826	2.826	2.833

Table 12.35. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=8, k=1, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.946	0.961	0.955	0.940	0.939	0.934	0.935	0.930	0.928	0.928
len	0.253	0.282	0.279	0.279	3.740	3.740	3.754	2.466	2.466	2.475
wild,0	0.934	0.954	0.945	0.939	0.868	0.871	0.873	0.913	0.911	0.910
len	0.250	0.270	0.269	0.269	3.459	3.459	3.468	2.389	2.389	2.394
par,0	0.941	0.954	0.935	0.919	0.875	0.879	0.878	0.919	0.922	0.922
len	0.259	0.283	0.264	0.262	3.627	3.627	3.635	2.457	2.457	2.464
npar,0.5	0.944	0.961	0.944	0.948	0.976	0.974	0.975	0.937	0.935	0.936
len	0.588	1.099	1.094	1.103	3.807	3.807	3.820	2.479	2.479	2.485
wild,0.5	0.935	0.951	0.937	0.946	0.908	0.911	0.908	0.914	0.916	0.918
len	0.576	1.030	1.031	1.036	3.443	3.443	3.450	2.379	2.379	2.383
par,0.5	0.940	0.965	0.948	0.955	0.946	0.946	0.948	0.940	0.940	0.941
len	0.600	1.184	1.129	1.130	3.623	3.623	3.632	2.461	2.461	2.467
npar,0.9	0.933	0.959	0.951	0.954	0.978	0.975	0.976	0.934	0.929	0.931
len	0.985	9.110	9.143	9.152	3.810	3.810	3.823	2.478	2.478	2.487
wild,0.9	0.929	0.949	0.937	0.947	0.919	0.921	0.920	0.913	0.915	0.915
len	0.963	8.600	8.614	8.621	3.448	3.448	3.455	2.378	2.378	2.384
par,0.9	0.932	0.955	0.953	0.957	0.955	0.955	0.957	0.929	0.928	0.931
len	0.999	9.339	9.360	9.383	3.629	3.629	3.639	2.456	2.456	2.464

Table 12.36. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=8, k=p-2, etype= t_3

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.941	0.939	0.957	0.945	0.941	0.941	0.943	0.852	0.848	0.849
len	0.251	0.278	0.278	0.279	1.959	1.959	1.967	3.991	3.991	4.009
wild,0	0.935	0.937	0.945	0.940	0.936	0.932	0.932	0.736	0.736	0.737
len	0.248	0.267	0.267	0.268	1.924	1.924	1.929	3.666	3.666	3.674
par,0	0.944	0.927	0.938	0.929	0.923	0.923	0.925	0.860	0.860	0.863
len	0.256	0.262	0.262	0.261	1.959	1.959	1.965	3.849	3.849	3.859
npar,0.5	0.940	0.953	0.946	0.946	0.943	0.943	0.941	0.919	0.913	0.915
len	0.586	1.097	1.095	1.096	1.959	1.959	1.965	4.062	4.062	4.078
wild,0.5	0.932	0.942	0.936	0.939	0.932	0.932	0.937	0.799	0.800	0.803
len	0.575	1.035	1.033	1.031	1.913	1.913	1.918	3.647	3.647	3.655
par,0.5	0.935	0.941	0.945	0.954	0.945	0.945	0.946	0.938	0.941	0.943
len	0.598	1.122	1.119	1.124	1.959	1.959	1.964	3.850	3.850	3.862
npar,0.9	0.945	0.955	0.949	0.959	0.962	0.958	0.960	0.933	0.930	0.930
len	0.975	9.136	9.096	9.129	1.958	1.958	1.965	4.063	4.063	4.076
wild,0.9	0.929	0.952	0.941	0.949	0.942	0.944	0.944	0.817	0.816	0.818
len	0.954	8.635	8.567	8.596	1.911	1.911	1.915	3.653	3.653	3.660
par,0.9	0.938	0.955	0.945	0.957	0.954	0.954	0.954	0.939	0.940	0.942
len	0.997	9.343	9.355	9.303	1.958	1.958	1.962	3.844	3.844	3.854

Table 12.37. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=4, k=1, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.937	0.930	0.942	0.949	0.950	0.954	0.954	0.914	0.914	0.914
len	1.677	1.745	1.683	1.690	2.481	2.481	2.492	2.472	2.472	2.479
wild,0	0.932	0.925	0.940	0.943	0.937	0.932	0.933	0.899	0.901	0.903
len	1.664	1.670	1.617	1.626	2.393	2.393	2.400	2.397	2.397	2.403
par,0	0.938	0.927	0.949	0.944	0.939	0.941	0.941	0.913	0.914	0.914
len	1.705	1.690	1.712	1.710	2.460	2.460	2.467	2.461	2.461	2.465
npar,0.5	0.943	0.946	0.949	0.960	0.953	0.952	0.954	0.918	0.918	0.917
len	1.697	2.860	2.817	2.816	2.483	2.483	2.492	2.468	2.468	2.477
wild,0.5	0.948	0.936	0.945	0.953	0.935	0.938	0.938	0.900	0.904	0.905
len	1.684	2.744	2.715	2.702	2.390	2.390	2.394	2.398	2.398	2.403
par,0.5	0.946	0.939	0.962	0.958	0.948	0.946	0.948	0.935	0.934	0.935
len	1.730	2.871	2.870	2.865	2.456	2.456	2.461	2.462	2.462	2.468
npar,0.9	0.948	0.950	0.946	0.942	0.953	0.952	0.950	0.920	0.924	0.925
len	1.758	14.415	14.363	14.389	2.483	2.483	2.493	2.472	2.472	2.479
wild,0.9	0.945	0.951	0.939	0.951	0.933	0.930	0.930	0.915	0.910	0.913
len	1.742	13.801	13.763	13.839	2.384	2.384	2.389	2.392	2.392	2.398
par,0.9	0.952	0.948	0.949	0.951	0.943	0.943	0.946	0.940	0.939	0.941
len	1.794	14.697	14.694	14.694	2.459	2.459	2.465	2.459	2.459	2.464

Table 12.38. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=4,
k=p-2, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.945	0.948	0.938	0.943	0.945	0.943	0.945	0.913	0.914	0.914
len	1.736	1.802	1.784	1.733	1.962	1.962	1.969	2.868	2.868	2.878
wild,0	0.944	0.943	0.927	0.943	0.939	0.941	0.940	0.886	0.885	0.884
len	1.724	1.721	1.710	1.666	1.920	1.920	1.925	2.730	2.730	2.737
par,0	0.946	0.946	0.929	0.943	0.937	0.935	0.938	0.920	0.919	0.921
len	1.761	1.766	1.758	1.767	1.957	1.957	1.961	2.825	2.825	2.831
npar,0.5	0.943	0.946	0.943	0.942	0.945	0.945	0.947	0.895	0.896	0.898
len	1.869	3.158	3.160	3.128	1.959	1.959	1.966	2.864	2.864	2.873
wild,0.5	0.935	0.945	0.938	0.943	0.932	0.933	0.934	0.861	0.867	0.867
len	1.855	3.012	3.020	2.988	1.917	1.917	1.921	2.715	2.715	2.721
par,0.5	0.940	0.955	0.948	0.953	0.943	0.942	0.943	0.922	0.925	0.926
len	1.908	3.210	3.204	3.198	1.959	1.959	1.964	2.823	2.823	2.831
npar,0.9	0.933	0.944	0.938	0.946	0.948	0.946	0.949	0.886	0.884	0.885
len	2.036	16.696	16.647	16.578	1.961	1.961	1.967	2.867	2.867	2.877
wild,0.9	0.924	0.937	0.937	0.946	0.934	0.935	0.936	0.847	0.848	0.846
len	2.011	15.922	15.857	15.836	1.913	1.913	1.917	2.708	2.708	2.716
par,0.9	0.936	0.948	0.943	0.954	0.952	0.952	0.954	0.911	0.911	0.912
len	2.082	17.159	17.099	17.205	1.957	1.957	1.961	2.823	2.823	2.830

Table 12.39. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=8,
k=1, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.565	0.956	0.964	0.968	0.987	0.992	0.994	0.536	0.542	0.542
len	2.271	1.970	1.982	1.978	3.830	3.830	3.856	2.481	2.481	2.491
wild,0	0.532	0.957	0.964	0.964	0.954	0.956	0.955	0.496	0.498	0.503
len	2.211	1.823	1.833	1.826	3.473	3.473	3.483	2.384	2.384	2.391
par,0	0.551	0.977	0.982	0.981	0.987	0.987	0.988	0.565	0.569	0.570
len	2.272	2.229	2.252	2.256	3.625	3.625	3.635	2.462	2.462	2.467
npar,0.5	0.605	0.951	0.960	0.947	0.966	0.967	0.966	0.605	0.614	0.614
len	2.539	4.534	4.528	4.513	3.788	3.788	3.810	2.478	2.478	2.487
wild,0.5	0.590	0.946	0.953	0.935	0.913	0.913	0.915	0.574	0.568	0.572
len	2.456	4.264	4.277	4.246	3.461	3.461	3.469	2.386	2.386	2.390
par,0.5	0.608	0.960	0.964	0.955	0.964	0.966	0.965	0.648	0.653	0.653
len	2.540	4.738	4.744	4.727	3.624	3.624	3.633	2.460	2.460	2.467
npar,0.9	0.730	0.956	0.952	0.952	0.973	0.974	0.975	0.780	0.783	0.787
len	3.175	29.477	29.328	29.124	3.789	3.789	3.806	2.482	2.482	2.493
wild,0.9	0.725	0.949	0.943	0.944	0.900	0.901	0.902	0.740	0.740	0.744
len	3.084	27.829	27.618	27.454	3.455	3.455	3.463	2.382	2.382	2.388
par,0.9	0.748	0.958	0.956	0.961	0.965	0.967	0.967	0.789	0.788	0.791
len	3.211	29.997	30.096	30.117	3.630	3.630	3.639	2.456	2.456	2.465

Table 12.40. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=8,
k=p-2, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.942	0.942	0.944	0.949	0.950	0.950	0.949	0.889	0.889	0.890
len	1.948	2.028	2.019	1.983	1.960	1.960	1.968	4.056	4.056	4.075
wild,0	0.936	0.941	0.933	0.945	0.937	0.938	0.939	0.785	0.786	0.790
len	1.902	1.927	1.921	1.876	1.920	1.920	1.924	3.668	3.668	3.676
par,0	0.946	0.947	0.936	0.947	0.940	0.946	0.946	0.887	0.885	0.886
len	1.984	1.986	1.992	1.994	1.960	1.960	1.964	3.849	3.849	3.860
npar,0.5	0.937	0.959	0.954	0.960	0.955	0.951	0.953	0.912	0.911	0.910
len	4.063	7.553	7.574	7.530	1.959	1.959	1.966	4.058	4.058	4.075
wild,0.5	0.940	0.945	0.946	0.950	0.944	0.944	0.946	0.787	0.787	0.791
len	3.973	7.136	7.134	7.108	1.913	1.913	1.917	3.648	3.648	3.656
par,0.5	0.937	0.948	0.953	0.954	0.945	0.944	0.947	0.915	0.916	0.917
len	4.101	7.689	7.684	7.734	1.957	1.957	1.962	3.849	3.849	3.860
npar,0.9	0.935	0.960	0.950	0.952	0.954	0.949	0.948	0.916	0.909	0.911
len	6.064	56.446	56.487	56.026	1.958	1.958	1.964	4.061	4.061	4.075
wild,0.9	0.929	0.955	0.938	0.942	0.938	0.939	0.938	0.790	0.793	0.794
len	5.929	53.352	53.186	52.960	1.914	1.914	1.918	3.651	3.651	3.659
par,0.9	0.933	0.957	0.952	0.958	0.951	0.953	0.952	0.920	0.921	0.925
len	6.163	57.696	57.804	57.907	1.959	1.959	1.964	3.849	3.849	3.858

Table 12.41. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=4, k=1, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.943	0.932	0.948	0.957	0.950	0.946	0.947	0.889	0.888	0.888
len	0.568	0.754	0.569	0.573	2.479	2.479	2.487	2.458	2.458	2.469
wild,0	0.943	0.931	0.948	0.959	0.932	0.936	0.937	0.874	0.874	0.876
len	0.565	0.732	0.549	0.551	2.387	2.387	2.394	2.381	2.381	2.385
par,0	0.943	0.907	0.954	0.961	0.961	0.960	0.962	0.877	0.876	0.875
len	0.580	0.705	0.588	0.587	2.460	2.460	2.466	2.460	2.460	2.466
npar,0.5	0.932	0.940	0.953	0.950	0.958	0.958	0.959	0.900	0.896	0.897
len	0.632	1.162	1.045	1.049	2.484	2.484	2.491	2.468	2.468	2.475
wild,0.5	0.936	0.926	0.947	0.949	0.931	0.937	0.938	0.889	0.888	0.887
len	0.627	1.119	1.002	1.009	2.390	2.390	2.395	2.390	2.390	2.394
par,0.5	0.940	0.927	0.960	0.956	0.953	0.956	0.957	0.907	0.907	0.906
len	0.644	1.156	1.081	1.082	2.462	2.462	2.468	2.461	2.461	2.466
npar,0.9	0.950	0.947	0.955	0.950	0.950	0.952	0.952	0.919	0.917	0.916
len	0.757	6.215	6.201	6.209	2.486	2.486	2.494	2.475	2.475	2.481
wild,0.9	0.945	0.943	0.952	0.945	0.927	0.931	0.933	0.905	0.909	0.910
len	0.750	5.946	5.934	5.963	2.381	2.381	2.387	2.392	2.392	2.396
par,0.9	0.945	0.957	0.956	0.953	0.954	0.956	0.956	0.936	0.934	0.936
len	0.772	6.397	6.393	6.400	2.457	2.457	2.465	2.460	2.460	2.466

Table 12.42. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=4, k=p-2, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.948	0.945	0.944	0.944	0.940	0.940	0.938	0.895	0.891	0.894
len	0.572	0.761	0.567	0.573	1.961	1.961	1.968	2.850	2.850	2.858
wild,0	0.941	0.938	0.944	0.938	0.935	0.933	0.933	0.856	0.857	0.859
len	0.567	0.736	0.546	0.551	1.924	1.924	1.928	2.719	2.719	2.725
par,0	0.946	0.882	0.962	0.954	0.946	0.947	0.946	0.879	0.881	0.883
len	0.585	0.631	0.615	0.588	1.955	1.955	1.960	2.825	2.825	2.831
npar,0.5	0.948	0.945	0.953	0.951	0.948	0.950	0.949	0.905	0.903	0.905
len	0.634	1.158	1.057	1.055	1.962	1.962	1.967	2.855	2.855	2.865
wild,0.5	0.946	0.938	0.947	0.948	0.939	0.939	0.943	0.887	0.883	0.882
len	0.628	1.115	1.015	1.011	1.922	1.922	1.926	2.719	2.719	2.724
par,0.5	0.944	0.936	0.961	0.955	0.952	0.953	0.953	0.931	0.931	0.932
len	0.649	1.104	1.103	1.083	1.960	1.960	1.964	2.825	2.825	2.830
npar,0.9	0.941	0.951	0.952	0.950	0.948	0.948	0.949	0.906	0.904	0.906
len	0.758	6.198	6.177	6.197	1.960	1.960	1.967	2.862	2.862	2.871
wild,0.9	0.942	0.951	0.946	0.949	0.944	0.945	0.946	0.871	0.874	0.875
len	0.751	5.949	5.930	5.946	1.923	1.923	1.927	2.720	2.720	2.727
par,0.9	0.945	0.960	0.956	0.953	0.944	0.947	0.947	0.934	0.936	0.935
len	0.772	6.409	6.370	6.391	1.958	1.958	1.964	2.825	2.825	2.832

Table 12.43. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=8,
k=1, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.941	0.935	0.954	0.954	0.958	0.959	0.957	0.907	0.906	0.906
len	0.582	0.760	0.586	0.591	3.761	3.761	3.778	2.463	2.463	2.471
wild,0	0.936	0.930	0.950	0.947	0.890	0.894	0.894	0.891	0.890	0.891
len	0.572	0.734	0.561	0.562	3.478	3.478	3.486	2.387	2.387	2.391
par,0	0.942	0.910	0.956	0.956	0.952	0.953	0.955	0.881	0.884	0.884
len	0.592	0.695	0.596	0.599	3.626	3.626	3.635	2.460	2.460	2.467
npar,0.5	0.941	0.949	0.954	0.949	0.959	0.960	0.959	0.921	0.919	0.920
len	0.762	1.499	1.426	1.422	3.772	3.772	3.788	2.471	2.471	2.478
wild,0.5	0.936	0.940	0.949	0.942	0.901	0.900	0.907	0.894	0.897	0.899
len	0.748	1.432	1.357	1.353	3.470	3.470	3.477	2.390	2.390	2.397
par,0.5	0.944	0.939	0.952	0.950	0.951	0.955	0.955	0.923	0.924	0.924
len	0.771	1.495	1.456	1.451	3.625	3.625	3.635	2.459	2.459	2.467
npar,0.9	0.936	0.954	0.944	0.951	0.960	0.959	0.962	0.927	0.923	0.926
len	1.062	9.982	9.989	9.896	3.787	3.787	3.802	2.477	2.477	2.486
wild,0.9	0.935	0.945	0.940	0.952	0.888	0.891	0.893	0.904	0.902	0.906
len	1.044	9.460	9.464	9.385	3.462	3.462	3.469	2.389	2.389	2.394
par,0.9	0.934	0.947	0.951	0.954	0.936	0.937	0.940	0.927	0.927	0.928
len	1.080	10.123	10.129	10.093	3.625	3.625	3.635	2.463	2.463	2.468

Table 12.44. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=8,
k=p-2, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.947	0.944	0.956	0.944	0.942	0.942	0.944	0.867	0.866	0.866
len	0.584	0.761	0.590	0.591	1.962	1.962	1.970	4.007	4.007	4.022
wild,0	0.943	0.932	0.953	0.939	0.927	0.930	0.931	0.756	0.757	0.759
len	0.577	0.736	0.563	0.562	1.924	1.924	1.928	3.675	3.675	3.684
par,0	0.950	0.861	0.963	0.948	0.941	0.942	0.944	0.885	0.886	0.888
len	0.594	0.612	0.600	0.598	1.960	1.960	1.965	3.844	3.844	3.854
npar,0.5	0.934	0.948	0.951	0.956	0.951	0.953	0.953	0.903	0.896	0.896
len	0.770	1.503	1.437	1.447	1.963	1.963	1.970	4.017	4.017	4.032
wild,0.5	0.931	0.939	0.946	0.946	0.938	0.937	0.941	0.786	0.785	0.789
len	0.758	1.435	1.370	1.374	1.922	1.922	1.926	3.672	3.672	3.680
par,0.5	0.938	0.936	0.956	0.952	0.944	0.947	0.946	0.935	0.935	0.935
len	0.780	1.463	1.459	1.467	1.958	1.958	1.963	3.850	3.850	3.860
npar,0.9	0.938	0.946	0.959	0.950	0.948	0.947	0.948	0.915	0.911	0.912
len	1.062	9.974	9.893	9.817	1.961	1.961	1.969	4.045	4.045	4.060
wild,0.9	0.934	0.942	0.945	0.944	0.939	0.939	0.940	0.812	0.818	0.816
len	1.044	9.438	9.386	9.310	1.922	1.922	1.927	3.663	3.663	3.672
par,0.9	0.937	0.944	0.954	0.960	0.956	0.955	0.956	0.940	0.941	0.943
len	1.080	10.118	10.120	10.105	1.959	1.959	1.964	3.847	3.847	3.858

Table 12.45. Bootstrapping WLS, n=100, BB=200, wtype = 4, p=4, k=1, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.937	0.933	0.941	0.935	0.945	0.936	0.936	0.929	0.917	0.914
len	0.945	1.437	1.456	1.442	2.462	2.462	2.460	2.474	2.474	2.474
wild,0	0.930	0.929	0.933	0.926	0.908	0.906	0.904	0.880	0.887	0.889
len	0.923	1.365	1.383	1.365	2.279	2.279	2.283	2.301	2.301	2.307
par,0	0.945	0.885	0.838	0.826	0.751	0.754	0.755	0.863	0.863	0.866
len	1.009	1.262	1.106	1.098	2.460	2.460	2.468	2.460	2.460	2.466
npar,0.5	0.922	0.960	0.952	0.960	0.973	0.968	0.967	0.951	0.943	0.941
len	5.194	8.717	8.612	8.726	2.512	2.512	2.511	2.506	2.506	2.504
wild,0.5	0.916	0.951	0.951	0.954	0.940	0.941	0.941	0.906	0.905	0.906
len	4.988	7.936	7.866	7.944	2.268	2.268	2.270	2.284	2.284	2.289
par,0.5	0.930	0.969	0.976	0.970	0.968	0.967	0.966	0.934	0.933	0.933
len	5.497	9.931	9.847	9.834	2.460	2.460	2.468	2.458	2.458	2.464
npar,0.9	0.925	0.952	0.953	0.969	0.980	0.976	0.975	0.946	0.938	0.935
len	14.777	119.53	119.78	120.08	2.523	2.523	2.522	2.513	2.513	2.509
wild,0.9	0.928	0.949	0.958	0.962	0.952	0.954	0.955	0.903	0.904	0.906
len	14.136	109.38	109.73	110.08	2.286	2.286	2.291	2.291	2.291	2.296
par,0.9	0.932	0.968	0.973	0.972	0.971	0.973	0.974	0.944	0.942	0.941
len	15.631	138.93	138.50	138.65	2.458	2.458	2.463	2.461	2.461	2.466

Table 12.46. Bootstrapping WLS, n=100, BB=200, wtype = 4, p=4,
k=p-2, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.927	0.932	0.954	0.931	0.929	0.923	0.924	0.918	0.909	0.909
len	0.925	1.395	1.402	1.405	1.939	1.939	1.943	2.871	2.871	2.870
wild,0	0.921	0.929	0.938	0.922	0.905	0.909	0.911	0.854	0.856	0.855
len	0.901	1.329	1.332	1.336	1.856	1.856	1.859	2.615	2.615	2.619
par,0	0.931	0.852	0.870	0.811	0.789	0.785	0.786	0.781	0.782	0.786
len	0.984	1.150	1.150	1.064	1.960	1.960	1.966	2.820	2.820	2.828
npar,0.5	0.921	0.957	0.955	0.951	0.958	0.951	0.951	0.958	0.951	0.952
len	5.097	8.635	8.456	8.591	1.948	1.948	1.949	2.942	2.942	2.938
wild,0.5	0.916	0.953	0.953	0.934	0.924	0.927	0.930	0.888	0.893	0.893
len	4.891	7.870	7.718	7.809	1.840	1.840	1.843	2.600	2.600	2.605
par,0.5	0.930	0.972	0.965	0.964	0.960	0.960	0.961	0.932	0.934	0.934
len	5.396	9.671	9.710	9.664	1.958	1.958	1.964	2.824	2.824	2.830
npar,0.9	0.919	0.962	0.958	0.966	0.972	0.965	0.966	0.967	0.962	0.963
len	14.518	118.52	116.47	119.21	1.946	1.946	1.947	2.951	2.951	2.947
wild,0.9	0.921	0.952	0.959	0.955	0.951	0.951	0.952	0.914	0.917	0.917
len	14.000	108.43	106.21	109.79	1.850	1.850	1.854	2.613	2.613	2.617
par,0.9	0.921	0.972	0.979	0.976	0.974	0.972	0.973	0.956	0.957	0.957
len	15.262	134.75	134.37	135.79	1.957	1.957	1.961	2.823	2.823	2.830

Table 12.47. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=4, k=1, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.942	0.944	0.955	0.955	0.956	0.955	0.956	0.936	0.941	0.939
len	0.864	0.670	0.664	0.671	2.494	2.494	2.505	2.489	2.489	2.498
wild,0	0.939	0.940	0.947	0.948	0.935	0.939	0.938	0.923	0.922	0.923
len	0.835	0.627	0.623	0.630	2.369	2.369	2.373	2.370	2.370	2.374
par,0	0.944	0.956	0.978	0.981	0.979	0.979	0.980	0.934	0.935	0.937
len	0.866	0.694	0.859	0.857	2.462	2.462	2.468	2.459	2.459	2.467
npar,0.5	0.940	0.947	0.948	0.952	0.955	0.956	0.958	0.950	0.950	0.951
len	1.038	1.523	1.516	1.532	2.493	2.493	2.503	2.485	2.485	2.493
wild,0.5	0.946	0.946	0.950	0.947	0.935	0.934	0.935	0.937	0.939	0.938
len	1.009	1.441	1.437	1.449	2.380	2.380	2.384	2.379	2.379	2.385
par,0.5	0.948	0.970	0.968	0.970	0.971	0.972	0.973	0.958	0.958	0.958
len	1.044	1.715	1.731	1.740	2.465	2.465	2.471	2.462	2.462	2.469
npar,0.9	0.942	0.945	0.940	0.951	0.950	0.950	0.951	0.945	0.946	0.946
len	1.309	10.497	10.474	10.387	2.487	2.487	2.496	2.482	2.482	2.491
wild,0.9	0.940	0.948	0.943	0.943	0.929	0.928	0.931	0.925	0.929	0.931
len	1.280	9.940	9.949	9.867	2.367	2.367	2.374	2.378	2.378	2.383
par,0.9	0.950	0.948	0.951	0.954	0.947	0.946	0.948	0.943	0.946	0.946
len	1.325	10.864	10.913	10.904	2.461	2.461	2.466	2.461	2.461	2.468

Table 12.48. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=4,
k=p-2, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.940	0.943	0.956	0.952	0.948	0.948	0.949	0.946	0.951	0.953
len	0.859	0.667	0.664	0.671	1.963	1.963	1.970	2.885	2.885	2.896
wild,0	0.943	0.938	0.954	0.946	0.934	0.937	0.936	0.918	0.917	0.917
len	0.834	0.626	0.624	0.629	1.903	1.903	1.908	2.703	2.703	2.708
par,0	0.942	0.975	0.976	0.976	0.975	0.975	0.973	0.950	0.946	0.947
len	0.865	0.777	0.773	0.855	1.956	1.956	1.961	2.823	2.823	2.830
npar,0.5	0.950	0.944	0.951	0.942	0.943	0.941	0.941	0.952	0.951	0.954
len	1.050	1.554	1.553	1.561	1.960	1.960	1.967	2.878	2.878	2.890
wild,0.5	0.950	0.944	0.944	0.943	0.933	0.931	0.932	0.922	0.920	0.923
len	1.027	1.475	1.469	1.475	1.914	1.914	1.919	2.713	2.713	2.718
par,0.5	0.954	0.968	0.967	0.967	0.962	0.964	0.965	0.960	0.959	0.960
len	1.060	1.757	1.754	1.761	1.957	1.957	1.961	2.826	2.826	2.832
npar,0.9	0.947	0.950	0.941	0.945	0.943	0.944	0.946	0.949	0.946	0.947
len	1.297	10.571	10.343	10.422	1.958	1.958	1.964	2.871	2.871	2.882
wild,0.9	0.949	0.956	0.941	0.939	0.934	0.932	0.932	0.923	0.925	0.927
len	1.270	9.997	9.849	9.917	1.914	1.914	1.918	2.709	2.709	2.714
par,0.9	0.958	0.952	0.951	0.954	0.948	0.947	0.948	0.944	0.944	0.943
len	1.314	10.796	10.811	10.777	1.957	1.957	1.961	2.824	2.824	2.831

Table 12.49. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=8,
k=1, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.940	0.956	0.953	0.956	0.988	0.992	0.991	0.933	0.940	0.939
len	1.922	1.647	1.642	1.644	3.844	3.844	3.868	2.484	2.484	2.495
wild,0	0.940	0.952	0.961	0.956	0.944	0.947	0.948	0.913	0.909	0.911
len	1.867	1.522	1.513	1.517	3.466	3.466	3.474	2.381	2.381	2.386
par,0	0.950	0.974	0.982	0.981	0.989	0.991	0.990	0.948	0.946	0.948
len	1.919	1.854	1.904	1.908	3.626	3.626	3.636	2.459	2.459	2.467
npar,0.5	0.951	0.952	0.953	0.963	0.971	0.971	0.973	0.957	0.959	0.957
len	2.471	4.432	4.420	4.457	3.787	3.787	3.807	2.481	2.481	2.493
wild,0.5	0.946	0.957	0.947	0.954	0.917	0.918	0.917	0.936	0.940	0.939
len	2.395	4.178	4.169	4.203	3.462	3.462	3.468	2.384	2.384	2.389
par,0.5	0.961	0.968	0.961	0.967	0.970	0.971	0.971	0.963	0.961	0.962
len	2.475	4.634	4.633	4.650	3.627	3.627	3.636	2.462	2.462	2.469
npar,0.9	0.948	0.961	0.952	0.954	0.973	0.971	0.971	0.955	0.950	0.951
len	3.318	30.920	30.702	30.879	3.783	3.783	3.799	2.483	2.483	2.491
wild,0.9	0.947	0.952	0.951	0.953	0.913	0.910	0.916	0.932	0.931	0.935
len	3.235	29.148	28.893	29.129	3.453	3.453	3.460	2.382	2.382	2.389
par,0.9	0.949	0.963	0.955	0.965	0.967	0.969	0.969	0.954	0.957	0.958
len	3.348	31.534	31.449	31.555	3.624	3.624	3.634	2.458	2.458	2.465

Table 12.50. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=8,
k=p-2, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.940	0.950	0.951	0.957	0.962	0.965	0.966	0.938	0.951	0.955
len	1.925	1.641	1.633	1.644	1.962	1.962	1.971	4.102	4.102	4.126
wild,0	0.938	0.949	0.953	0.955	0.949	0.952	0.952	0.845	0.849	0.851
len	1.855	1.515	1.503	1.513	1.916	1.916	1.920	3.669	3.669	3.678
par,0	0.942	0.972	0.975	0.978	0.975	0.976	0.977	0.971	0.971	0.971
len	1.913	1.886	1.877	1.907	1.959	1.959	1.965	3.845	3.845	3.854
npar,0.5	0.943	0.953	0.949	0.958	0.954	0.956	0.956	0.966	0.967	0.968
len	2.445	4.366	4.422	4.412	1.962	1.962	1.970	4.032	4.032	4.050
wild,0.5	0.948	0.948	0.945	0.947	0.942	0.941	0.941	0.898	0.898	0.901
len	2.375	4.129	4.157	4.157	1.921	1.921	1.926	3.668	3.668	3.674
par,0.5	0.952	0.960	0.961	0.959	0.951	0.953	0.953	0.941	0.944	0.947
len	2.462	4.570	4.588	4.579	1.958	1.958	1.963	3.846	3.846	3.858
npar,0.9	0.956	0.950	0.956	0.959	0.955	0.958	0.959	0.963	0.963	0.964
len	3.292	30.458	30.387	30.451	1.958	1.958	1.968	4.035	4.035	4.053
wild,0.9	0.958	0.945	0.941	0.950	0.942	0.946	0.944	0.890	0.890	0.892
len	3.209	28.864	28.668	28.822	1.918	1.918	1.921	3.657	3.657	3.666
par,0.9	0.960	0.949	0.952	0.955	0.950	0.947	0.951	0.946	0.946	0.948
len	3.309	30.920	30.778	30.823	1.954	1.954	1.960	3.848	3.848	3.858

Table 12.51. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=4, k=1, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.946	0.941	0.936	0.943	0.935	0.933	0.933	0.907	0.906	0.904
len	0.283	0.351	0.353	0.355	2.468	2.468	2.477	2.463	2.463	2.473
wild,0	0.941	0.938	0.937	0.935	0.911	0.912	0.914	0.888	0.887	0.887
len	0.282	0.341	0.342	0.344	2.365	2.365	2.371	2.376	2.376	2.382
par,0	0.944	0.943	0.878	0.896	0.839	0.843	0.846	0.897	0.896	0.899
len	0.292	0.352	0.301	0.301	2.460	2.460	2.466	2.463	2.463	2.470
npar,0.5	0.938	0.953	0.936	0.944	0.939	0.934	0.936	0.924	0.920	0.920
len	0.434	0.729	0.727	0.727	2.484	2.484	2.492	2.477	2.477	2.484
wild,0.5	0.930	0.950	0.933	0.931	0.909	0.913	0.914	0.899	0.899	0.898
len	0.429	0.694	0.696	0.693	2.363	2.363	2.369	2.372	2.372	2.378
par,0.5	0.938	0.968	0.939	0.945	0.926	0.929	0.929	0.937	0.935	0.937
len	0.447	0.826	0.755	0.752	2.458	2.458	2.464	2.460	2.460	2.468
npar,0.9	0.946	0.948	0.952	0.937	0.958	0.956	0.955	0.916	0.914	0.913
len	0.624	5.111	5.090	5.136	2.488	2.488	2.496	2.471	2.471	2.478
wild,0.9	0.938	0.948	0.944	0.933	0.929	0.930	0.932	0.896	0.897	0.898
len	0.618	4.864	4.853	4.899	2.368	2.368	2.373	2.374	2.374	2.379
par,0.9	0.939	0.957	0.953	0.946	0.941	0.942	0.945	0.931	0.931	0.933
len	0.642	5.341	5.305	5.331	2.459	2.459	2.466	2.460	2.460	2.467

Table 12.52. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=4, k=p-2, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.936	0.953	0.941	0.937	0.932	0.923	0.923	0.888	0.885	0.888
len	0.285	0.356	0.356	0.354	1.953	1.953	1.960	2.850	2.850	2.859
wild,0	0.929	0.942	0.938	0.934	0.920	0.916	0.918	0.862	0.864	0.866
len	0.284	0.344	0.344	0.342	1.908	1.908	1.913	2.704	2.704	2.710
par,0	0.935	0.916	0.907	0.883	0.867	0.868	0.868	0.871	0.867	0.871
len	0.293	0.322	0.319	0.301	1.960	1.960	1.966	2.827	2.827	2.834
npar,0.5	0.936	0.953	0.945	0.944	0.944	0.941	0.942	0.905	0.901	0.903
len	0.435	0.731	0.726	0.724	1.955	1.955	1.960	2.868	2.868	2.877
wild,0.5	0.933	0.947	0.941	0.936	0.931	0.933	0.934	0.865	0.866	0.866
len	0.430	0.697	0.689	0.690	1.908	1.908	1.912	2.701	2.701	2.708
par,0.5	0.937	0.949	0.954	0.949	0.943	0.941	0.942	0.924	0.923	0.923
len	0.446	0.769	0.768	0.746	1.957	1.957	1.963	2.822	2.822	2.829
npar,0.9	0.931	0.959	0.955	0.957	0.953	0.953	0.952	0.914	0.910	0.911
len	0.629	5.170	5.125	5.192	1.958	1.958	1.964	2.873	2.873	2.880
wild,0.9	0.929	0.949	0.955	0.947	0.940	0.943	0.943	0.885	0.883	0.885
len	0.623	4.912	4.889	4.945	1.908	1.908	1.912	2.705	2.705	2.711
par,0.9	0.933	0.957	0.964	0.956	0.950	0.955	0.955	0.939	0.940	0.941
len	0.646	5.357	5.355	5.363	1.956	1.956	1.961	2.822	2.822	2.829

Table 12.53. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=8, k=1, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.946	0.961	0.955	0.940	0.939	0.934	0.935	0.930	0.928	0.928
len	0.253	0.282	0.279	0.279	3.740	3.740	3.754	2.466	2.466	2.475
wild,0	0.934	0.954	0.945	0.939	0.868	0.871	0.873	0.913	0.911	0.910
len	0.250	0.270	0.269	0.269	3.459	3.459	3.468	2.389	2.389	2.394
par,0	0.941	0.954	0.935	0.919	0.875	0.879	0.878	0.919	0.922	0.922
len	0.259	0.283	0.264	0.262	3.627	3.627	3.635	2.457	2.457	2.464
npar,0.5	0.944	0.961	0.944	0.948	0.976	0.974	0.975	0.937	0.935	0.936
len	0.588	1.099	1.094	1.103	3.807	3.807	3.820	2.479	2.479	2.485
wild,0.5	0.935	0.951	0.937	0.946	0.908	0.911	0.908	0.914	0.916	0.918
len	0.576	1.030	1.031	1.036	3.443	3.443	3.450	2.379	2.379	2.383
par,0.5	0.940	0.965	0.948	0.955	0.946	0.946	0.948	0.940	0.940	0.941
len	0.600	1.184	1.129	1.130	3.623	3.623	3.632	2.461	2.461	2.467
npar,0.9	0.933	0.959	0.951	0.954	0.978	0.975	0.976	0.934	0.929	0.931
len	0.985	9.110	9.143	9.152	3.810	3.810	3.823	2.478	2.478	2.487
wild,0.9	0.929	0.949	0.937	0.947	0.919	0.921	0.920	0.913	0.915	0.915
len	0.963	8.600	8.614	8.621	3.448	3.448	3.455	2.378	2.378	2.384
par,0.9	0.932	0.955	0.953	0.957	0.955	0.955	0.957	0.929	0.928	0.931
len	0.999	9.339	9.360	9.383	3.629	3.629	3.639	2.456	2.456	2.464

Table 12.54. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=8,
k=p-2, etype= EXP(1) - 1

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.941	0.939	0.957	0.945	0.941	0.941	0.943	0.852	0.848	0.849
len	0.251	0.278	0.278	0.279	1.959	1.959	1.967	3.991	3.991	4.009
wild,0	0.935	0.937	0.945	0.940	0.936	0.932	0.932	0.736	0.736	0.737
len	0.248	0.267	0.267	0.268	1.924	1.924	1.929	3.666	3.666	3.674
par,0	0.944	0.927	0.938	0.929	0.923	0.923	0.925	0.860	0.860	0.863
len	0.256	0.262	0.262	0.261	1.959	1.959	1.965	3.849	3.849	3.859
npar,0.5	0.940	0.953	0.946	0.946	0.943	0.943	0.941	0.919	0.913	0.915
len	0.586	1.097	1.095	1.096	1.959	1.959	1.965	4.062	4.062	4.078
wild,0.5	0.932	0.942	0.936	0.939	0.932	0.932	0.937	0.799	0.800	0.803
len	0.575	1.035	1.033	1.031	1.913	1.913	1.918	3.647	3.647	3.655
par,0.5	0.935	0.941	0.945	0.954	0.945	0.945	0.946	0.938	0.941	0.943
len	0.598	1.122	1.119	1.124	1.959	1.959	1.964	3.850	3.850	3.862
npar,0.9	0.945	0.955	0.949	0.959	0.962	0.958	0.960	0.933	0.930	0.930
len	0.975	9.136	9.096	9.129	1.958	1.958	1.965	4.063	4.063	4.076
wild,0.9	0.929	0.952	0.941	0.949	0.942	0.944	0.944	0.817	0.816	0.818
len	0.954	8.635	8.567	8.596	1.911	1.911	1.915	3.653	3.653	3.660
par,0.9	0.938	0.955	0.945	0.957	0.954	0.954	0.954	0.939	0.940	0.942
len	0.997	9.343	9.355	9.303	1.958	1.958	1.962	3.844	3.844	3.854

Table 12.55. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=4, k=1, etype= uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.948	0.937	0.945	0.953	0.930	0.929	0.933	0.933	0.933	0.934
len	0.980	1.030	0.995	0.990	2.473	2.473	2.483	2.471	2.471	2.480
wild,0	0.944	0.932	0.943	0.943	0.923	0.924	0.925	0.927	0.927	0.927
len	0.982	1.007	0.975	0.970	2.432	2.432	2.437	2.437	2.437	2.443
par,0	0.957	0.933	0.950	0.951	0.941	0.945	0.945	0.934	0.935	0.936
len	0.996	1.022	1.003	1.002	2.461	2.461	2.466	2.462	2.462	2.469
npar,0.5	0.947	0.938	0.950	0.946	0.922	0.923	0.924	0.934	0.931	0.932
len	0.996	1.699	1.671	1.672	2.474	2.474	2.484	2.467	2.467	2.476
wild,0.5	0.950	0.930	0.943	0.932	0.909	0.911	0.915	0.923	0.925	0.923
len	0.994	1.662	1.633	1.636	2.431	2.431	2.437	2.435	2.435	2.440
par,0.5	0.953	0.948	0.953	0.949	0.935	0.936	0.939	0.938	0.938	0.938
len	1.012	1.705	1.684	1.688	2.460	2.460	2.466	2.461	2.461	2.467
npar,0.9	0.939	0.955	0.937	0.948	0.936	0.937	0.938	0.932	0.932	0.934
len	1.027	8.507	8.509	8.487	2.477	2.477	2.486	2.467	2.467	2.475
wild,0.9	0.941	0.950	0.939	0.948	0.919	0.923	0.924	0.921	0.923	0.923
len	1.026	8.328	8.316	8.297	2.429	2.429	2.435	2.429	2.429	2.434
par,0.9	0.946	0.961	0.949	0.946	0.943	0.943	0.944	0.943	0.941	0.942
len	1.042	8.604	8.622	8.551	2.463	2.463	2.468	2.462	2.462	2.468

Table 12.56. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=4,
k=p-2, etype= uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.946	0.949	0.940	0.939	0.931	0.931	0.930	0.932	0.936	0.936
len	1.008	1.053	1.059	1.017	1.961	1.961	1.968	2.848	2.848	2.859
wild,0	0.948	0.945	0.931	0.932	0.925	0.924	0.926	0.914	0.919	0.919
len	1.007	1.030	1.033	0.993	1.944	1.944	1.948	2.778	2.778	2.784
par,0	0.954	0.946	0.937	0.944	0.936	0.936	0.937	0.936	0.937	0.940
len	1.021	1.053	1.054	1.027	1.956	1.956	1.962	2.823	2.823	2.831
npar,0.5	0.952	0.947	0.957	0.946	0.935	0.937	0.937	0.921	0.921	0.920
len	1.099	1.861	1.864	1.840	1.964	1.964	1.970	2.844	2.844	2.855
wild,0.5	0.948	0.941	0.951	0.939	0.932	0.936	0.935	0.908	0.907	0.908
len	1.098	1.816	1.823	1.801	1.944	1.944	1.948	2.766	2.766	2.773
par,0.5	0.951	0.950	0.959	0.945	0.941	0.940	0.943	0.926	0.926	0.928
len	1.112	1.868	1.879	1.858	1.958	1.958	1.965	2.824	2.824	2.831
npar,0.9	0.954	0.948	0.956	0.955	0.947	0.943	0.944	0.943	0.937	0.941
len	1.212	10.030	10.003	10.020	1.964	1.964	1.969	2.844	2.844	2.854
wild,0.9	0.956	0.945	0.949	0.942	0.935	0.939	0.940	0.922	0.921	0.925
len	1.212	9.768	9.750	9.740	1.939	1.939	1.944	2.758	2.758	2.767
par,0.9	0.956	0.958	0.956	0.954	0.946	0.948	0.949	0.945	0.945	0.947
len	1.231	10.140	10.113	10.139	1.954	1.954	1.959	2.826	2.826	2.834

Table 12.57. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=8,
k=1, etype = uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.947	0.953	0.949	0.959	0.916	0.916	0.919	0.940	0.944	0.944
len	1.014	1.069	1.026	1.024	3.699	3.699	3.717	2.474	2.474	2.483
wild,0	0.943	0.945	0.945	0.951	0.869	0.868	0.867	0.928	0.932	0.934
len	1.006	1.035	0.996	0.996	3.534	3.534	3.543	2.436	2.436	2.440
par,0	0.947	0.944	0.957	0.955	0.940	0.942	0.943	0.943	0.943	0.945
len	1.017	1.038	1.023	1.027	3.624	3.624	3.634	2.465	2.465	2.470
npar,0.5	0.949	0.945	0.954	0.949	0.918	0.918	0.921	0.933	0.935	0.937
len	1.052	1.998	1.982	1.982	3.710	3.710	3.728	2.470	2.470	2.480
wild,0.5	0.948	0.939	0.945	0.942	0.867	0.866	0.867	0.924	0.921	0.922
len	1.045	1.933	1.909	1.916	3.520	3.520	3.529	2.429	2.429	2.436
par,0.5	0.954	0.940	0.951	0.953	0.941	0.940	0.944	0.934	0.931	0.935
len	1.054	1.982	1.971	1.976	3.625	3.625	3.635	2.462	2.462	2.468
npar,0.9	0.948	0.946	0.944	0.958	0.930	0.929	0.934	0.926	0.928	0.926
len	1.139	10.662	10.703	10.621	3.715	3.715	3.731	2.472	2.472	2.482
wild,0.9	0.933	0.943	0.939	0.943	0.877	0.878	0.880	0.914	0.916	0.917
len	1.131	10.294	10.311	10.250	3.502	3.502	3.511	2.427	2.427	2.434
par,0.9	0.941	0.950	0.951	0.954	0.941	0.941	0.942	0.936	0.938	0.937
len	1.142	10.643	10.716	10.631	3.625	3.625	3.634	2.459	2.459	2.464

Table 12.58. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=8,
k=p-2, etype= uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.948	0.945	0.946	0.946	0.941	0.942	0.942	0.910	0.911	0.916
len	1.146	1.189	1.191	1.159	1.962	1.962	1.969	3.966	3.966	3.985
wild,0	0.948	0.940	0.933	0.941	0.932	0.930	0.933	0.849	0.845	0.850
len	1.135	1.148	1.148	1.122	1.943	1.943	1.947	3.710	3.710	3.718
par,0	0.946	0.945	0.941	0.944	0.943	0.943	0.946	0.906	0.907	0.908
len	1.146	1.178	1.177	1.152	1.956	1.956	1.962	3.848	3.848	3.857
npar,0.5	0.954	0.956	0.947	0.954	0.953	0.949	0.948	0.941	0.938	0.939
len	2.380	4.499	4.477	4.496	1.966	1.966	1.972	3.966	3.966	3.982
wild,0.5	0.953	0.947	0.936	0.940	0.938	0.939	0.938	0.869	0.872	0.873
len	2.361	4.328	4.311	4.308	1.936	1.936	1.941	3.680	3.680	3.689
par,0.5	0.952	0.960	0.949	0.959	0.954	0.954	0.955	0.938	0.943	0.944
len	2.417	4.523	4.503	4.508	1.958	1.958	1.963	3.847	3.847	3.857
npar,0.9	0.945	0.949	0.953	0.956	0.948	0.947	0.949	0.947	0.943	0.942
len	3.596	33.528	33.895	33.583	1.963	1.963	1.969	3.974	3.974	3.988
wild,0.9	0.943	0.933	0.945	0.945	0.941	0.939	0.939	0.862	0.864	0.867
len	3.568	32.316	32.607	32.343	1.937	1.937	1.942	3.684	3.684	3.692
par,0.9	0.942	0.950	0.953	0.955	0.954	0.955	0.953	0.945	0.948	0.949
len	3.631	34.122	34.097	34.110	1.959	1.959	1.964	3.851	3.851	3.863

Table 12.59. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=4, k=1, etype= uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.952	0.929	0.949	0.954	0.941	0.939	0.940	0.923	0.921	0.923
len	0.332	0.452	0.339	0.336	2.474	2.474	2.482	2.458	2.458	2.466
wild,0	0.944	0.925	0.942	0.948	0.926	0.927	0.928	0.913	0.915	0.913
len	0.333	0.448	0.332	0.330	2.430	2.430	2.435	2.423	2.423	2.429
par,0	0.950	0.913	0.948	0.961	0.954	0.956	0.955	0.903	0.903	0.904
len	0.339	0.422	0.343	0.342	2.462	2.462	2.468	2.459	2.459	2.467
npar,0.5	0.947	0.945	0.948	0.952	0.930	0.929	0.929	0.928	0.930	0.932
len	0.371	0.691	0.620	0.623	2.474	2.474	2.483	2.463	2.463	2.473
wild,0.5	0.951	0.937	0.934	0.948	0.916	0.915	0.914	0.919	0.924	0.923
len	0.373	0.678	0.608	0.610	2.424	2.424	2.429	2.425	2.425	2.429
par,0.5	0.949	0.942	0.954	0.952	0.940	0.941	0.942	0.930	0.930	0.933
len	0.378	0.681	0.632	0.636	2.458	2.458	2.465	2.462	2.462	2.468
npar,0.9	0.958	0.946	0.954	0.956	0.943	0.941	0.943	0.946	0.943	0.945
len	0.445	3.687	3.668	3.681	2.480	2.480	2.488	2.469	2.469	2.477
wild,0.9	0.958	0.938	0.948	0.951	0.928	0.928	0.929	0.931	0.929	0.931
len	0.447	3.602	3.589	3.591	2.421	2.421	2.426	2.431	2.431	2.436
par,0.9	0.954	0.954	0.964	0.962	0.955	0.955	0.955	0.952	0.953	0.953
len	0.454	3.742	3.746	3.745	2.459	2.459	2.465	2.456	2.456	2.463

Table 12.60. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=4, k=p-2, etype= uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.947	0.942	0.955	0.950	0.942	0.940	0.943	0.917	0.915	0.917
len	0.333	0.451	0.336	0.335	1.963	1.963	1.969	2.830	2.830	2.839
wild,0	0.940	0.942	0.953	0.937	0.932	0.932	0.934	0.905	0.902	0.905
len	0.333	0.448	0.328	0.329	1.945	1.945	1.949	2.767	2.767	2.773
par,0	0.950	0.886	0.966	0.951	0.945	0.946	0.947	0.897	0.901	0.900
len	0.340	0.369	0.363	0.342	1.958	1.958	1.963	2.825	2.825	2.834
npar,0.5	0.954	0.937	0.948	0.954	0.945	0.947	0.946	0.913	0.911	0.913
len	0.372	0.690	0.621	0.625	1.962	1.962	1.968	2.839	2.839	2.850
wild,0.5	0.946	0.925	0.939	0.940	0.935	0.937	0.937	0.894	0.897	0.897
len	0.372	0.679	0.611	0.613	1.944	1.944	1.950	2.767	2.767	2.772
par,0.5	0.953	0.918	0.958	0.950	0.945	0.945	0.946	0.920	0.922	0.923
len	0.378	0.650	0.645	0.635	1.958	1.958	1.963	2.824	2.824	2.830
npar,0.9	0.951	0.949	0.950	0.948	0.941	0.939	0.939	0.939	0.933	0.937
len	0.445	3.698	3.672	3.678	1.961	1.961	1.967	2.843	2.843	2.853
wild,0.9	0.956	0.940	0.952	0.934	0.928	0.929	0.930	0.925	0.928	0.928
len	0.447	3.609	3.580	3.592	1.943	1.943	1.947	2.768	2.768	2.776
par,0.9	0.951	0.948	0.961	0.950	0.947	0.948	0.947	0.948	0.947	0.947
len	0.453	3.733	3.742	3.730	1.958	1.958	1.962	2.823	2.823	2.830

Table 12.61. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=8, k=1, etype= uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.951	0.946	0.947	0.952	0.907	0.905	0.906	0.931	0.928	0.930
len	0.342	0.453	0.345	0.347	3.710	3.710	3.727	2.462	2.462	2.470
wild,0	0.947	0.940	0.942	0.945	0.855	0.856	0.857	0.917	0.919	0.922
len	0.339	0.448	0.335	0.337	3.527	3.527	3.535	2.420	2.420	2.427
par,0	0.949	0.928	0.953	0.957	0.940	0.942	0.941	0.913	0.913	0.915
len	0.346	0.421	0.348	0.348	3.630	3.630	3.640	2.462	2.462	2.468
npar,0.5	0.951	0.950	0.948	0.947	0.908	0.907	0.914	0.935	0.931	0.932
len	0.450	0.896	0.843	0.847	3.716	3.716	3.732	2.467	2.467	2.477
wild,0.5	0.945	0.941	0.936	0.939	0.843	0.846	0.846	0.918	0.920	0.922
len	0.446	0.871	0.816	0.821	3.511	3.511	3.519	2.421	2.421	2.429
par,0.5	0.945	0.946	0.948	0.953	0.940	0.944	0.944	0.934	0.938	0.939
len	0.454	0.885	0.854	0.854	3.627	3.627	3.637	2.465	2.465	2.472
npar,0.9	0.957	0.945	0.954	0.952	0.934	0.933	0.934	0.938	0.933	0.935
len	0.628	5.924	5.917	5.897	3.724	3.724	3.740	2.477	2.477	2.486
wild,0.9	0.953	0.942	0.940	0.941	0.858	0.859	0.859	0.927	0.927	0.927
len	0.622	5.711	5.693	5.667	3.499	3.499	3.505	2.423	2.423	2.430
par,0.9	0.953	0.951	0.957	0.959	0.941	0.942	0.940	0.940	0.940	0.942
len	0.635	5.938	5.947	5.945	3.629	3.629	3.637	2.461	2.461	2.466

Table 12.62. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=8,
k=p-2, etype= uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.955	0.935	0.948	0.954	0.944	0.947	0.947	0.891	0.888	0.890
len	0.342	0.454	0.348	0.349	1.962	1.962	1.970	3.929	3.929	3.950
wild,0	0.948	0.929	0.942	0.948	0.938	0.937	0.941	0.819	0.823	0.826
len	0.341	0.449	0.338	0.338	1.945	1.945	1.951	3.725	3.725	3.733
par,0	0.954	0.858	0.949	0.950	0.949	0.948	0.949	0.884	0.888	0.889
len	0.347	0.358	0.352	0.351	1.958	1.958	1.964	3.846	3.846	3.855
npar,0.5	0.952	0.946	0.954	0.943	0.935	0.933	0.931	0.913	0.909	0.915
len	0.452	0.891	0.854	0.848	1.962	1.962	1.969	3.948	3.948	3.963
wild,0.5	0.947	0.930	0.941	0.935	0.923	0.924	0.925	0.827	0.829	0.832
len	0.446	0.866	0.824	0.819	1.942	1.942	1.946	3.716	3.716	3.724
par,0.5	0.953	0.931	0.951	0.946	0.938	0.938	0.938	0.928	0.930	0.930
len	0.456	0.854	0.856	0.854	1.961	1.961	1.966	3.845	3.845	3.855
npar,0.9	0.951	0.951	0.950	0.947	0.940	0.939	0.937	0.929	0.927	0.928
len	0.625	5.884	5.898	5.916	1.962	1.962	1.970	3.967	3.967	3.982
wild,0.9	0.944	0.945	0.944	0.944	0.935	0.932	0.934	0.848	0.850	0.853
len	0.621	5.658	5.675	5.714	1.940	1.940	1.945	3.706	3.706	3.713
par,0.9	0.945	0.947	0.956	0.952	0.947	0.947	0.948	0.938	0.941	0.942
len	0.632	5.926	5.958	5.943	1.956	1.956	1.961	3.847	3.847	3.857

Table 12.63. Bootstrapping WLS, n=100, BB=200, wtype = 4, p=4, k=1, etype= uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.957	0.935	0.926	0.924	0.928	0.916	0.917	0.944	0.931	0.932
len	0.571	0.883	0.874	0.886	2.453	2.453	2.454	2.467	2.467	2.468
wild,0	0.945	0.933	0.922	0.924	0.897	0.897	0.899	0.917	0.921	0.919
len	0.564	0.856	0.848	0.857	2.297	2.297	2.302	2.323	2.323	2.327
par,0	0.957	0.891	0.793	0.810	0.713	0.716	0.720	0.899	0.899	0.900
len	0.602	0.799	0.637	0.642	2.459	2.459	2.466	2.461	2.461	2.467
npar,0.5	0.956	0.953	0.957	0.963	0.972	0.966	0.966	0.980	0.976	0.974
len	3.258	5.498	5.550	5.479	2.495	2.495	2.494	2.502	2.502	2.498
wild,0.5	0.960	0.946	0.951	0.954	0.940	0.940	0.942	0.952	0.954	0.955
len	3.160	5.064	5.133	5.073	2.280	2.280	2.282	2.298	2.298	2.302
par,0.5	0.961	0.968	0.970	0.970	0.964	0.963	0.963	0.969	0.969	0.969
len	3.398	6.158	6.108	6.064	2.463	2.463	2.468	2.463	2.463	2.468
npar,0.9	0.946	0.954	0.955	0.960	0.984	0.981	0.980	0.974	0.967	0.967
len	9.173	74.825	75.506	74.788	2.508	2.508	2.506	2.500	2.500	2.497
wild,0.9	0.947	0.954	0.953	0.948	0.951	0.950	0.952	0.946	0.945	0.946
len	8.924	69.570	70.168	69.540	2.302	2.302	2.305	2.316	2.316	2.319
par,0.9	0.954	0.974	0.974	0.971	0.973	0.975	0.977	0.966	0.969	0.969
len	9.558	84.944	84.915	84.739	2.461	2.461	2.467	2.457	2.457	2.463

Table 12.64. Bootstrapping WLS, n=100, BB=200, wtype = 4, p=4,
k=p-2, etype= uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.945	0.931	0.928	0.941	0.943	0.931	0.933	0.949	0.941	0.941
len	0.578	0.891	0.892	0.897	1.942	1.942	1.946	2.847	2.847	2.847
wild,0	0.941	0.921	0.924	0.934	0.923	0.928	0.928	0.897	0.899	0.900
len	0.569	0.862	0.865	0.866	1.872	1.872	1.876	2.632	2.632	2.636
par,0	0.954	0.844	0.849	0.808	0.793	0.793	0.794	0.803	0.801	0.800
len	0.608	0.713	0.718	0.649	1.961	1.961	1.966	2.819	2.819	2.827
npar,0.5	0.950	0.956	0.951	0.958	0.964	0.956	0.956	0.981	0.975	0.977
len	3.164	5.373	5.429	5.339	1.950	1.950	1.951	2.914	2.914	2.911
wild,0.5	0.951	0.950	0.939	0.951	0.935	0.936	0.938	0.939	0.938	0.938
len	3.090	4.957	5.016	4.946	1.859	1.859	1.862	2.608	2.608	2.613
par,0.5	0.954	0.966	0.962	0.962	0.954	0.956	0.956	0.953	0.954	0.954
len	3.335	5.973	6.003	5.870	1.958	1.958	1.963	2.829	2.829	2.836
npar,0.9	0.948	0.959	0.957	0.960	0.970	0.960	0.960	0.983	0.979	0.978
len	9.151	74.453	73.355	74.793	1.952	1.952	1.952	2.931	2.931	2.928
wild,0.9	0.948	0.955	0.949	0.959	0.953	0.947	0.949	0.946	0.948	0.950
len	8.906	69.261	68.254	69.367	1.867	1.867	1.870	2.627	2.627	2.632
par,0.9	0.961	0.975	0.974	0.972	0.966	0.967	0.966	0.968	0.970	0.971
len	9.563	84.089	83.713	83.929	1.957	1.957	1.962	2.823	2.823	2.830

Table 12.65. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=4, k=1, etype= uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.948	0.949	0.949	0.954	0.946	0.947	0.947	0.950	0.952	0.952
len	0.512	0.398	0.399	0.399	2.485	2.485	2.495	2.478	2.478	2.488
wild,0	0.957	0.942	0.945	0.948	0.926	0.929	0.931	0.935	0.937	0.937
len	0.505	0.382	0.382	0.383	2.408	2.408	2.412	2.409	2.409	2.415
par,0	0.954	0.954	0.982	0.982	0.987	0.987	0.987	0.946	0.949	0.948
len	0.511	0.401	0.509	0.506	2.462	2.462	2.469	2.461	2.461	2.466
npar,0.5	0.954	0.954	0.953	0.954	0.951	0.953	0.953	0.955	0.954	0.956
len	0.618	0.914	0.911	0.914	2.489	2.489	2.499	2.474	2.474	2.484
wild,0.5	0.950	0.948	0.958	0.950	0.942	0.943	0.945	0.945	0.944	0.947
len	0.612	0.882	0.880	0.885	2.414	2.414	2.421	2.421	2.421	2.428
par,0.5	0.946	0.973	0.978	0.976	0.973	0.976	0.974	0.962	0.964	0.964
len	0.623	1.022	1.033	1.035	2.462	2.462	2.469	2.456	2.456	2.464
npar,0.9	0.947	0.946	0.940	0.955	0.937	0.937	0.939	0.936	0.937	0.938
len	0.771	6.223	6.225	6.234	2.479	2.479	2.488	2.477	2.477	2.485
wild,0.9	0.955	0.938	0.935	0.943	0.918	0.920	0.920	0.926	0.927	0.926
len	0.766	6.031	6.049	6.050	2.405	2.405	2.409	2.414	2.414	2.419
par,0.9	0.951	0.956	0.946	0.952	0.942	0.943	0.944	0.933	0.935	0.935
len	0.776	6.394	6.377	6.383	2.460	2.460	2.465	2.459	2.459	2.465

Table 12.66. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=4, k=p-2, etype= uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.949	0.953	0.957	0.950	0.945	0.945	0.946	0.950	0.954	0.956
len	0.515	0.401	0.398	0.400	1.961	1.961	1.968	2.863	2.863	2.874
wild,0	0.951	0.943	0.949	0.949	0.935	0.937	0.938	0.933	0.933	0.933
len	0.506	0.384	0.383	0.384	1.933	1.933	1.938	2.748	2.748	2.754
par,0	0.947	0.975	0.978	0.984	0.983	0.985	0.986	0.958	0.959	0.959
len	0.512	0.457	0.458	0.509	1.961	1.961	1.966	2.822	2.822	2.830
npar,0.5	0.941	0.942	0.942	0.944	0.940	0.947	0.947	0.931	0.932	0.933
len	0.621	0.916	0.921	0.914	1.962	1.962	1.970	2.860	2.860	2.872
wild,0.5	0.949	0.933	0.938	0.944	0.938	0.935	0.938	0.914	0.912	0.910
len	0.616	0.884	0.888	0.884	1.941	1.941	1.946	2.757	2.757	2.763
par,0.5	0.943	0.969	0.969	0.964	0.963	0.964	0.965	0.959	0.959	0.960
len	0.623	1.033	1.034	1.037	1.956	1.956	1.961	2.827	2.827	2.833
npar,0.9	0.945	0.953	0.946	0.946	0.943	0.946	0.945	0.936	0.935	0.939
len	0.772	6.250	6.247	6.222	1.963	1.963	1.969	2.857	2.857	2.869
wild,0.9	0.948	0.950	0.947	0.946	0.936	0.940	0.940	0.919	0.918	0.920
len	0.766	6.049	6.068	6.018	1.935	1.935	1.940	2.745	2.745	2.753
par,0.9	0.948	0.957	0.952	0.949	0.942	0.948	0.947	0.939	0.939	0.942
len	0.779	6.394	6.376	6.387	1.960	1.960	1.963	2.820	2.820	2.829

Table 12.67. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=8,
k=1, etype= uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.950	0.957	0.952	0.955	0.967	0.977	0.978	0.949	0.960	0.962
len	1.145	0.988	0.980	0.982	3.774	3.774	3.797	2.479	2.479	2.489
wild,0	0.953	0.960	0.948	0.950	0.921	0.920	0.922	0.944	0.945	0.949
len	1.119	0.929	0.924	0.927	3.505	3.505	3.513	2.416	2.416	2.423
par,0	0.956	0.974	0.977	0.980	0.985	0.987	0.988	0.960	0.962	0.963
len	1.124	1.024	1.118	1.124	3.631	3.631	3.640	2.461	2.461	2.468
npar,0.5	0.962	0.951	0.951	0.954	0.938	0.942	0.944	0.951	0.952	0.952
len	1.452	2.625	2.619	2.619	3.730	3.730	3.751	2.477	2.477	2.485
wild,0.5	0.959	0.937	0.940	0.947	0.880	0.878	0.880	0.934	0.938	0.939
len	1.441	2.514	2.515	2.509	3.508	3.508	3.516	2.427	2.427	2.432
par,0.5	0.959	0.962	0.956	0.961	0.958	0.960	0.962	0.954	0.955	0.957
len	1.459	2.728	2.709	2.715	3.631	3.631	3.642	2.462	2.462	2.468
npar,0.9	0.950	0.949	0.951	0.953	0.942	0.942	0.944	0.943	0.941	0.943
len	1.941	18.092	18.295	18.120	3.724	3.724	3.742	2.472	2.472	2.481
wild,0.9	0.948	0.945	0.946	0.944	0.875	0.874	0.874	0.931	0.933	0.935
len	1.925	17.372	17.615	17.469	3.491	3.491	3.498	2.422	2.422	2.429
par,0.9	0.953	0.952	0.961	0.957	0.961	0.960	0.962	0.950	0.951	0.951
len	1.961	18.283	18.377	18.353	3.627	3.627	3.638	2.463	2.463	2.470

Table 12.68. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=8,
k=p-2, etype= uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.953	0.961	0.959	0.964	0.962	0.964	0.965	0.965	0.971	0.974
len	1.145	0.985	0.982	0.981	1.965	1.965	1.975	4.019	4.019	4.044
wild,0	0.956	0.952	0.956	0.956	0.956	0.956	0.954	0.913	0.912	0.916
len	1.122	0.924	0.926	0.927	1.938	1.938	1.943	3.706	3.706	3.715
par,0	0.959	0.982	0.987	0.983	0.982	0.982	0.983	0.983	0.984	0.984
len	1.127	1.107	1.104	1.123	1.957	1.957	1.961	3.849	3.849	3.860
npar,0.5	0.943	0.954	0.955	0.953	0.947	0.947	0.947	0.930	0.935	0.937
len	1.455	2.634	2.617	2.605	1.966	1.966	1.973	3.963	3.963	3.983
wild,0.5	0.946	0.950	0.942	0.946	0.937	0.938	0.938	0.869	0.870	0.871
len	1.439	2.534	2.511	2.504	1.938	1.938	1.944	3.707	3.707	3.715
par,0.5	0.943	0.962	0.958	0.961	0.953	0.957	0.958	0.949	0.951	0.954
len	1.450	2.712	2.714	2.712	1.961	1.961	1.965	3.852	3.852	3.862
npar,0.9	0.958	0.951	0.952	0.953	0.949	0.948	0.949	0.937	0.939	0.940
len	1.949	18.170	18.210	18.117	1.961	1.961	1.969	3.966	3.966	3.983
wild,0.9	0.955	0.944	0.945	0.950	0.943	0.944	0.946	0.865	0.869	0.870
len	1.923	17.468	17.465	17.458	1.940	1.940	1.943	3.702	3.702	3.709
par,0.9	0.956	0.957	0.951	0.955	0.950	0.951	0.952	0.941	0.941	0.943
len	1.960	18.251	18.182	18.242	1.958	1.958	1.963	3.846	3.846	3.858

Table 12.69. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=4, k=1, etype= uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.945	0.948	0.937	0.935	0.909	0.906	0.907	0.924	0.924	0.923
len	0.167	0.209	0.210	0.211	2.461	2.461	2.471	2.462	2.462	2.471
wild,0	0.939	0.939	0.928	0.922	0.896	0.893	0.894	0.918	0.919	0.919
len	0.168	0.207	0.208	0.209	2.406	2.406	2.412	2.418	2.418	2.423
par,0	0.947	0.938	0.880	0.875	0.819	0.824	0.825	0.924	0.922	0.923
len	0.172	0.208	0.176	0.176	2.458	2.458	2.464	2.462	2.462	2.468
npar,0.5	0.955	0.956	0.955	0.945	0.942	0.941	0.940	0.950	0.947	0.947
len	0.259	0.437	0.438	0.435	2.474	2.474	2.483	2.472	2.472	2.480
wild,0.5	0.946	0.951	0.949	0.943	0.918	0.920	0.923	0.936	0.937	0.937
len	0.259	0.425	0.426	0.423	2.400	2.400	2.406	2.412	2.412	2.416
par,0.5	0.954	0.974	0.961	0.951	0.943	0.948	0.946	0.960	0.961	0.959
len	0.265	0.491	0.445	0.442	2.462	2.462	2.467	2.461	2.461	2.467
npar,0.9	0.954	0.943	0.945	0.945	0.933	0.926	0.932	0.949	0.942	0.944
len	0.374	3.093	3.081	3.076	2.478	2.478	2.488	2.475	2.475	2.482
wild,0.9	0.962	0.938	0.928	0.939	0.913	0.912	0.912	0.929	0.928	0.928
len	0.376	3.005	3.000	2.997	2.404	2.404	2.408	2.416	2.416	2.421
par,0.9	0.952	0.950	0.949	0.956	0.941	0.942	0.942	0.950	0.951	0.952
len	0.382	3.181	3.156	3.155	2.461	2.461	2.469	2.461	2.461	2.466

Table 12.70. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=4, k=p-2, etype= uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.941	0.942	0.949	0.933	0.928	0.926	0.926	0.920	0.915	0.916
len	0.167	0.211	0.210	0.210	1.958	1.958	1.964	2.829	2.829	2.839
wild,0	0.941	0.930	0.939	0.926	0.922	0.920	0.920	0.893	0.894	0.895
len	0.168	0.208	0.208	0.208	1.938	1.938	1.942	2.749	2.749	2.753
par,0	0.949	0.900	0.919	0.884	0.861	0.865	0.864	0.871	0.872	0.874
len	0.171	0.187	0.187	0.175	1.958	1.958	1.964	2.821	2.821	2.827
npar,0.5	0.957	0.947	0.951	0.944	0.934	0.932	0.935	0.936	0.932	0.933
len	0.257	0.436	0.439	0.435	1.962	1.962	1.969	2.849	2.849	2.857
wild,0.5	0.948	0.935	0.944	0.935	0.931	0.928	0.930	0.907	0.909	0.907
len	0.257	0.425	0.426	0.423	1.933	1.933	1.938	2.743	2.743	2.749
par,0.5	0.956	0.958	0.956	0.950	0.940	0.940	0.940	0.943	0.942	0.943
len	0.263	0.458	0.458	0.442	1.960	1.960	1.965	2.823	2.823	2.829
npar,0.9	0.954	0.943	0.954	0.950	0.944	0.938	0.944	0.935	0.932	0.935
len	0.374	3.069	3.066	3.056	1.961	1.961	1.968	2.855	2.855	2.863
wild,0.9	0.959	0.938	0.941	0.942	0.937	0.936	0.936	0.914	0.917	0.919
len	0.373	2.997	2.984	2.975	1.939	1.939	1.943	2.747	2.747	2.754
par,0.9	0.951	0.950	0.957	0.951	0.945	0.948	0.948	0.941	0.940	0.943
len	0.380	3.135	3.148	3.130	1.956	1.956	1.961	2.821	2.821	2.830

Table 12.71. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=8, k=1, etype= uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.954	0.943	0.944	0.946	0.881	0.875	0.880	0.930	0.926	0.928
len	0.148	0.164	0.165	0.164	3.684	3.684	3.700	2.470	2.470	2.479
wild,0	0.952	0.937	0.937	0.937	0.821	0.825	0.828	0.916	0.915	0.917
len	0.147	0.160	0.162	0.161	3.501	3.501	3.511	2.429	2.429	2.435
par,0	0.955	0.942	0.920	0.926	0.861	0.860	0.863	0.931	0.929	0.931
len	0.150	0.165	0.152	0.152	3.622	3.622	3.632	2.463	2.463	2.469
npar,0.5	0.948	0.955	0.942	0.955	0.953	0.949	0.950	0.951	0.948	0.950
len	0.348	0.650	0.653	0.650	3.732	3.732	3.747	2.473	2.473	2.483
wild,0.5	0.950	0.950	0.933	0.942	0.885	0.888	0.891	0.931	0.934	0.935
len	0.344	0.624	0.627	0.624	3.475	3.475	3.482	2.414	2.414	2.420
par,0.5	0.949	0.961	0.951	0.952	0.941	0.942	0.945	0.952	0.952	0.952
len	0.352	0.695	0.661	0.660	3.627	3.627	3.636	2.460	2.460	2.467
npar,0.9	0.949	0.951	0.956	0.950	0.941	0.939	0.939	0.941	0.937	0.940
len	0.576	5.431	5.386	5.395	3.734	3.734	3.748	2.475	2.475	2.483
wild,0.9	0.947	0.939	0.939	0.941	0.869	0.869	0.871	0.930	0.931	0.933
len	0.573	5.223	5.192	5.197	3.486	3.486	3.492	2.420	2.420	2.424
par,0.9	0.951	0.953	0.953	0.954	0.948	0.948	0.948	0.936	0.938	0.939
len	0.584	5.490	5.466	5.462	3.620	3.620	3.631	2.460	2.460	2.467

Table 12.72. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=8,
k=p-2, etype= uniform(-1, 1)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.951	0.954	0.948	0.939	0.932	0.930	0.930	0.881	0.869	0.875
len	0.147	0.164	0.165	0.164	1.957	1.957	1.965	3.917	3.917	3.935
wild,0	0.938	0.937	0.934	0.931	0.926	0.929	0.928	0.812	0.814	0.817
len	0.147	0.160	0.161	0.161	1.945	1.945	1.950	3.714	3.714	3.723
par,0	0.949	0.939	0.930	0.921	0.913	0.912	0.913	0.869	0.869	0.870
len	0.150	0.154	0.154	0.152	1.955	1.955	1.960	3.846	3.846	3.856
npar,0.5	0.945	0.958	0.959	0.961	0.955	0.950	0.949	0.948	0.943	0.945
len	0.348	0.655	0.659	0.653	1.966	1.966	1.972	3.974	3.974	3.991
wild,0.5	0.943	0.953	0.951	0.950	0.945	0.944	0.946	0.860	0.865	0.869
len	0.346	0.632	0.632	0.625	1.932	1.932	1.937	3.677	3.677	3.684
par,0.5	0.945	0.963	0.960	0.958	0.956	0.959	0.958	0.944	0.949	0.950
len	0.353	0.666	0.664	0.659	1.957	1.957	1.962	3.848	3.848	3.859
npar,0.9	0.952	0.959	0.951	0.950	0.949	0.946	0.947	0.949	0.947	0.949
len	0.579	5.425	5.446	5.449	1.963	1.963	1.969	3.981	3.981	3.995
wild,0.9	0.942	0.952	0.946	0.945	0.942	0.939	0.941	0.886	0.884	0.890
len	0.573	5.247	5.234	5.248	1.938	1.938	1.944	3.688	3.688	3.695
par,0.9	0.944	0.961	0.957	0.954	0.948	0.949	0.949	0.951	0.951	0.953
len	0.584	5.495	5.484	5.516	1.959	1.959	1.964	3.846	3.846	3.856

Table 12.73. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=4, k=1, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.941	0.947	0.942	0.946	0.976	0.976	0.978	0.967	0.966	0.968
len	5.476	5.500	5.376	5.370	2.507	2.507	2.517	2.498	2.498	2.504
wild,0	0.946	0.951	0.949	0.959	0.943	0.943	0.942	0.942	0.946	0.944
len	5.259	5.035	4.952	4.930	2.281	2.281	2.286	2.300	2.300	2.303
par,0	0.959	0.970	0.968	0.970	0.972	0.974	0.975	0.973	0.972	0.974
len	5.564	5.827	5.734	5.734	2.462	2.462	2.468	2.461	2.461	2.468
npar,0.5	0.942	0.948	0.945	0.948	0.976	0.975	0.976	0.969	0.969	0.970
len	5.404	8.743	8.776	8.736	2.502	2.502	2.510	2.495	2.495	2.505
wild,0.5	0.948	0.952	0.945	0.956	0.943	0.944	0.946	0.941	0.945	0.945
len	5.199	8.023	8.057	8.050	2.286	2.286	2.289	2.301	2.301	2.305
par,0.5	0.956	0.971	0.967	0.971	0.973	0.973	0.975	0.971	0.974	0.973
len	5.504	9.376	9.382	9.351	2.457	2.457	2.464	2.462	2.462	2.467
npar,0.9	0.937	0.949	0.955	0.950	0.972	0.973	0.973	0.963	0.963	0.964
len	5.624	44.664	44.407	44.591	2.507	2.507	2.517	2.495	2.495	2.502
wild,0.9	0.949	0.949	0.956	0.951	0.941	0.944	0.945	0.935	0.938	0.935
len	5.384	41.027	40.664	40.805	2.283	2.283	2.287	2.293	2.293	2.297
par,0.9	0.957	0.965	0.969	0.965	0.969	0.969	0.971	0.965	0.968	0.968
len	5.723	48.080	47.958	48.031	2.459	2.459	2.465	2.460	2.460	2.467

Table 12.74. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=4,
k=p-2, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.940	0.948	0.945	0.951	0.955	0.955	0.956	0.983	0.984	0.984
len	5.522	5.479	5.469	5.397	1.950	1.950	1.956	2.925	2.925	2.936
wild,0	0.955	0.953	0.958	0.944	0.939	0.942	0.943	0.950	0.950	0.951
len	5.299	4.993	4.988	4.945	1.859	1.859	1.863	2.617	2.617	2.620
par,0	0.959	0.968	0.969	0.967	0.959	0.964	0.963	0.973	0.975	0.976
len	5.610	5.822	5.828	5.783	1.956	1.956	1.962	2.825	2.825	2.833
npar,0.5	0.942	0.949	0.955	0.944	0.959	0.963	0.961	0.982	0.982	0.983
len	5.877	9.462	9.473	9.319	1.950	1.950	1.956	2.928	2.928	2.938
wild,0.5	0.949	0.955	0.954	0.955	0.939	0.944	0.945	0.947	0.948	0.949
len	5.599	8.596	8.582	8.477	1.846	1.846	1.851	2.605	2.605	2.608
par,0.5	0.961	0.956	0.967	0.966	0.961	0.959	0.958	0.967	0.968	0.970
len	6.002	10.202	10.160	10.120	1.962	1.962	1.966	2.822	2.822	2.830
npar,0.9	0.941	0.960	0.951	0.964	0.969	0.968	0.971	0.981	0.980	0.979
len	6.494	51.636	51.262	51.534	1.945	1.945	1.951	2.934	2.934	2.942
wild,0.9	0.949	0.960	0.961	0.963	0.959	0.958	0.959	0.942	0.942	0.948
len	6.165	46.887	46.627	46.916	1.841	1.841	1.844	2.602	2.602	2.606
par,0.9	0.960	0.967	0.968	0.968	0.959	0.957	0.959	0.967	0.967	0.967
len	6.672	55.980	56.002	55.708	1.959	1.959	1.963	2.829	2.829	2.836

Table 12.75. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=8,
k=1, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.947	0.952	0.955	0.958	0.997	0.997	0.997	0.973	0.973	0.973
len	5.576	5.560	5.483	5.492	3.934	3.934	3.950	2.495	2.495	2.505
wild,0	0.953	0.950	0.954	0.950	0.956	0.955	0.959	0.947	0.947	0.948
len	5.328	5.087	5.002	5.027	3.374	3.374	3.379	2.318	2.318	2.323
par,0	0.965	0.968	0.977	0.969	0.992	0.993	0.992	0.974	0.973	0.975
len	5.637	5.921	5.808	5.840	3.626	3.626	3.636	2.456	2.456	2.465
npar,0.5	0.947	0.953	0.949	0.956	0.995	0.995	0.995	0.971	0.976	0.976
len	5.681	10.339	10.297	10.384	3.946	3.946	3.966	2.497	2.497	2.506
wild,0.5	0.949	0.953	0.948	0.953	0.954	0.952	0.954	0.948	0.951	0.953
len	5.398	9.409	9.407	9.503	3.378	3.378	3.384	2.306	2.306	2.309
par,0.5	0.958	0.969	0.968	0.965	0.989	0.991	0.991	0.978	0.978	0.979
len	5.746	11.021	10.977	10.968	3.624	3.624	3.635	2.459	2.459	2.465
npar,0.9	0.950	0.964	0.951	0.959	0.997	0.997	0.997	0.977	0.977	0.978
len	6.176	56.355	55.421	55.902	3.974	3.974	3.991	2.500	2.500	2.507
wild,0.9	0.952	0.958	0.956	0.955	0.962	0.963	0.965	0.955	0.957	0.957
len	5.850	51.179	50.346	50.669	3.375	3.375	3.382	2.297	2.297	2.300
par,0.9	0.965	0.972	0.966	0.965	0.988	0.990	0.990	0.978	0.980	0.981
len	6.306	59.870	59.872	59.891	3.627	3.627	3.634	2.462	2.462	2.468

Table 12.76. Bootstrapping WLS, n=100, BB=200, wtype = 2, p=8,
k=p-2, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.955	0.957	0.956	0.960	0.970	0.969	0.973	0.996	0.996	0.998
len	6.114	6.129	6.066	5.942	1.948	1.948	1.954	4.277	4.277	4.294
wild,0	0.958	0.954	0.959	0.954	0.948	0.951	0.953	0.963	0.963	0.963
len	5.781	5.544	5.495	5.395	1.856	1.856	1.859	3.590	3.590	3.596
par,0	0.967	0.965	0.968	0.968	0.965	0.966	0.967	0.983	0.983	0.984
len	6.249	6.493	6.495	6.396	1.955	1.955	1.960	3.844	3.844	3.853
npar,0.5	0.947	0.963	0.958	0.957	0.962	0.964	0.965	0.995	0.994	0.995
len	12.333	22.448	22.728	22.221	1.949	1.949	1.956	4.310	4.310	4.320
wild,0.5	0.951	0.964	0.957	0.955	0.949	0.951	0.951	0.968	0.963	0.965
len	11.641	20.300	20.510	20.038	1.853	1.853	1.856	3.591	3.591	3.598
par,0.5	0.968	0.972	0.961	0.961	0.955	0.953	0.956	0.970	0.970	0.970
len	12.697	24.042	24.156	23.970	1.957	1.957	1.963	3.848	3.848	3.857
npar,0.9	0.949	0.961	0.949	0.959	0.967	0.968	0.968	0.994	0.995	0.994
len	18.889	170.52	172.19	172.24	1.948	1.948	1.954	4.326	4.326	4.341
wild,0.9	0.956	0.960	0.948	0.958	0.952	0.953	0.953	0.962	0.961	0.963
len	17.811	154.10	155.41	155.12	1.847	1.847	1.851	3.589	3.589	3.595
par,0.9	0.967	0.965	0.959	0.959	0.957	0.958	0.959	0.979	0.979	0.980
len	19.419	184.63	185.13	184.76	1.957	1.957	1.962	3.848	3.848	3.859

Table 12.77. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=4,
k=1, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.946	0.951	0.951	0.949	0.971	0.971	0.973	0.966	0.964	0.966
len	1.855	2.334	1.810	1.790	2.503	2.503	2.514	2.487	2.487	2.495
wild,0	0.945	0.954	0.950	0.956	0.941	0.945	0.944	0.943	0.947	0.947
len	1.786	2.142	1.665	1.649	2.293	2.293	2.296	2.286	2.286	2.290
par,0	0.965	0.930	0.961	0.964	0.964	0.964	0.964	0.938	0.940	0.941
len	1.888	2.128	1.928	1.943	2.460	2.460	2.463	2.460	2.460	2.466
npar,0.5	0.947	0.951	0.953	0.953	0.974	0.976	0.975	0.971	0.970	0.973
len	2.012	3.561	3.267	3.258	2.508	2.508	2.515	2.491	2.491	2.498
wild,0.5	0.952	0.949	0.957	0.949	0.945	0.948	0.947	0.944	0.947	0.950
len	1.934	3.256	2.991	2.997	2.290	2.290	2.294	2.295	2.295	2.299
par,0.5	0.971	0.951	0.961	0.959	0.958	0.960	0.958	0.964	0.964	0.964
len	2.060	3.631	3.482	3.516	2.460	2.460	2.467	2.461	2.461	2.468
npar,0.9	0.942	0.942	0.953	0.956	0.975	0.976	0.977	0.969	0.968	0.971
len	2.406	19.030	18.958	18.876	2.510	2.510	2.518	2.497	2.497	2.503
wild,0.9	0.948	0.945	0.957	0.960	0.945	0.950	0.951	0.946	0.949	0.951
len	2.311	17.495	17.405	17.329	2.290	2.290	2.295	2.296	2.296	2.300
par,0.9	0.960	0.954	0.961	0.961	0.956	0.958	0.959	0.956	0.960	0.959
len	2.463	20.595	20.548	20.548	2.459	2.459	2.464	2.456	2.456	2.463

Table 12.78. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=4,
k=p-2, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.941	0.953	0.949	0.950	0.961	0.959	0.959	0.976	0.974	0.974
len	1.829	2.268	1.793	1.800	1.951	1.951	1.957	2.904	2.904	2.912
wild,0	0.949	0.952	0.957	0.954	0.950	0.950	0.953	0.937	0.939	0.941
len	1.764	2.083	1.649	1.661	1.860	1.860	1.863	2.613	2.613	2.616
par,0	0.957	0.925	0.967	0.960	0.949	0.948	0.950	0.944	0.945	0.945
len	1.865	2.017	1.943	1.904	1.960	1.960	1.966	2.824	2.824	2.830
npar,0.5	0.939	0.953	0.949	0.949	0.960	0.961	0.961	0.976	0.975	0.977
len	2.048	3.555	3.294	3.306	1.954	1.954	1.960	2.916	2.916	2.923
wild,0.5	0.948	0.953	0.953	0.957	0.951	0.951	0.952	0.944	0.942	0.943
len	1.973	3.258	3.036	3.046	1.863	1.863	1.865	2.613	2.613	2.617
par,0.5	0.958	0.949	0.951	0.953	0.949	0.949	0.950	0.943	0.944	0.944
len	2.091	3.562	3.531	3.519	1.960	1.960	1.964	2.826	2.826	2.833
npar,0.9	0.946	0.953	0.941	0.948	0.957	0.959	0.960	0.982	0.981	0.981
len	2.398	19.374	19.118	19.101	1.948	1.948	1.955	2.923	2.923	2.931
wild,0.9	0.948	0.948	0.953	0.949	0.946	0.944	0.946	0.942	0.944	0.947
len	2.313	17.734	17.580	17.581	1.860	1.860	1.863	2.614	2.614	2.618
par,0.9	0.963	0.953	0.956	0.952	0.947	0.949	0.950	0.953	0.956	0.955
len	2.463	20.485	20.476	20.512	1.961	1.961	1.965	2.825	2.825	2.834

Table 12.79. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=8,
k=1, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.951	0.949	0.961	0.963	0.998	0.998	0.998	0.969	0.966	0.967
len	1.869	2.254	1.856	1.850	3.939	3.939	3.952	2.485	2.485	2.493
wild,0	0.948	0.941	0.958	0.956	0.960	0.960	0.963	0.944	0.946	0.945
len	1.782	2.082	1.701	1.692	3.376	3.376	3.382	2.303	2.303	2.307
par,0	0.965	0.927	0.966	0.961	0.982	0.984	0.985	0.933	0.931	0.934
len	1.897	2.078	1.938	1.927	3.626	3.626	3.635	2.459	2.459	2.466
npar,0.5	0.954	0.949	0.947	0.956	0.997	0.996	0.997	0.974	0.975	0.976
len	2.459	4.657	4.506	4.526	3.960	3.960	3.974	2.498	2.498	2.504
wild,0.5	0.955	0.952	0.946	0.950	0.961	0.962	0.963	0.951	0.952	0.951
len	2.336	4.270	4.122	4.112	3.383	3.383	3.389	2.306	2.306	2.311
par,0.5	0.968	0.961	0.956	0.957	0.977	0.977	0.978	0.962	0.965	0.965
len	2.520	4.824	4.744	4.778	3.625	3.625	3.635	2.457	2.457	2.464
npar,0.9	0.952	0.959	0.952	0.954	0.997	0.998	0.998	0.977	0.976	0.976
len	3.308	30.444	30.303	30.226	3.974	3.974	3.988	2.504	2.504	2.510
wild,0.9	0.948	0.960	0.953	0.953	0.965	0.966	0.966	0.951	0.956	0.956
len	3.146	27.752	27.498	27.538	3.387	3.387	3.394	2.306	2.306	2.309
par,0.9	0.963	0.955	0.960	0.963	0.974	0.977	0.978	0.964	0.966	0.967
len	3.399	32.284	32.202	32.221	3.628	3.628	3.638	2.463	2.463	2.470

Table 12.80. Bootstrapping WLS, n=100, BB=200, wtype = 3, p=8,
k=p-2, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.951	0.941	0.954	0.957	0.967	0.962	0.962	0.996	0.996	0.996
len	1.893	2.329	1.868	1.879	1.952	1.952	1.960	4.213	4.213	4.229
wild,0	0.953	0.943	0.953	0.951	0.947	0.951	0.950	0.953	0.954	0.955
len	1.805	2.144	1.711	1.723	1.872	1.872	1.875	3.581	3.581	3.589
par,0	0.959	0.895	0.959	0.958	0.952	0.954	0.954	0.946	0.948	0.948
len	1.923	1.999	1.951	1.937	1.955	1.955	1.961	3.851	3.851	3.861
npar,0.5	0.950	0.955	0.952	0.956	0.963	0.966	0.965	0.996	0.997	0.997
len	2.436	4.643	4.404	4.462	1.949	1.949	1.956	4.247	4.247	4.262
wild,0.5	0.957	0.950	0.951	0.960	0.950	0.953	0.953	0.958	0.956	0.959
len	2.318	4.244	4.020	4.076	1.866	1.866	1.870	3.585	3.585	3.591
par,0.5	0.961	0.949	0.951	0.954	0.946	0.949	0.949	0.950	0.952	0.954
len	2.478	4.665	4.631	4.647	1.959	1.959	1.963	3.848	3.848	3.859
npar,0.9	0.952	0.955	0.952	0.951	0.963	0.960	0.962	0.997	0.997	0.998
len	3.318	30.850	30.527	30.611	1.950	1.950	1.957	4.275	4.275	4.288
wild,0.9	0.956	0.955	0.951	0.953	0.942	0.943	0.946	0.969	0.971	0.970
len	3.145	28.096	27.639	27.833	1.861	1.861	1.865	3.588	3.588	3.595
par,0.9	0.968	0.956	0.952	0.953	0.946	0.947	0.946	0.948	0.948	0.949
len	3.410	32.000	31.949	31.934	1.954	1.954	1.959	3.847	3.847	3.857

Table 12.81. Bootstrapping WLS, n=100, BB=200, wtype = 4, p=4,
k=1, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.956	0.950	0.940	0.943	0.967	0.956	0.955	0.975	0.972	0.972
len	2.597	3.764	3.740	3.785	2.496	2.496	2.496	2.512	2.512	2.510
wild,0	0.961	0.943	0.937	0.940	0.927	0.927	0.928	0.942	0.944	0.946
len	2.424	3.409	3.401	3.420	2.228	2.228	2.230	2.249	2.249	2.254
par,0	0.969	0.910	0.899	0.905	0.894	0.894	0.896	0.939	0.937	0.936
len	2.798	3.412	3.280	3.300	2.462	2.462	2.468	2.459	2.459	2.466
npar,0.5	0.950	0.962	0.963	0.960	0.985	0.982	0.983	0.992	0.991	0.990
len	14.300	23.418	23.201	23.295	2.557	2.557	2.554	2.551	2.551	2.546
wild,0.5	0.961	0.964	0.966	0.960	0.951	0.953	0.955	0.966	0.966	0.967
len	13.250	20.649	20.414	20.494	2.237	2.237	2.240	2.237	2.237	2.240
par,0.5	0.974	0.977	0.980	0.976	0.980	0.980	0.980	0.983	0.985	0.985
len	15.739	28.848	28.612	28.678	2.461	2.461	2.468	2.460	2.460	2.467
npar,0.9	0.949	0.966	0.961	0.956	0.988	0.986	0.986	0.982	0.978	0.977
len	39.680	312.85	312.53	309.39	2.570	2.570	2.566	2.547	2.547	2.542
wild,0.9	0.962	0.960	0.959	0.964	0.961	0.963	0.963	0.960	0.960	0.962
len	36.626	275.45	274.22	273.01	2.250	2.250	2.253	2.245	2.245	2.248
par,0.9	0.972	0.979	0.981	0.979	0.987	0.986	0.988	0.977	0.979	0.979
len	43.112	383.41	387.37	383.82	2.458	2.458	2.466	2.463	2.463	2.468

Table 12.82. Bootstrapping WLS, n=100, BB=200, wtype = 4, p=4,
k=p-2, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.949	0.940	0.937	0.941	0.954	0.950	0.949	0.980	0.975	0.975
len	2.657	3.855	3.813	3.870	1.923	1.923	1.925	2.954	2.954	2.952
wild,0	0.951	0.939	0.934	0.934	0.922	0.923	0.924	0.935	0.936	0.934
len	2.479	3.488	3.458	3.507	1.786	1.786	1.789	2.575	2.575	2.579
par,0	0.967	0.905	0.884	0.882	0.861	0.861	0.864	0.893	0.901	0.901
len	2.871	3.409	3.362	3.308	1.957	1.957	1.962	2.825	2.825	2.833
npar,0.5	0.948	0.960	0.959	0.955	0.971	0.968	0.968	0.995	0.994	0.992
len	14.131	23.028	22.837	23.194	1.939	1.939	1.938	3.026	3.026	3.023
wild,0.5	0.954	0.958	0.958	0.951	0.946	0.950	0.947	0.970	0.967	0.967
len	13.038	20.355	20.171	20.499	1.792	1.792	1.794	2.578	2.578	2.581
par,0.5	0.969	0.971	0.972	0.970	0.968	0.971	0.970	0.979	0.982	0.983
len	15.390	28.190	27.971	28.145	1.958	1.958	1.964	2.823	2.823	2.828
npar,0.9	0.956	0.959	0.964	0.969	0.977	0.971	0.971	0.993	0.992	0.991
len	40.135	314.23	315.25	314.18	1.942	1.942	1.941	3.036	3.036	3.031
wild,0.9	0.960	0.960	0.961	0.961	0.958	0.959	0.961	0.970	0.974	0.975
len	37.002	277.36	277.11	276.91	1.799	1.799	1.803	2.587	2.587	2.590
par,0.9	0.973	0.976	0.978	0.973	0.970	0.970	0.970	0.984	0.985	0.985
len	43.575	387.36	387.12	385.93	1.958	1.958	1.963	2.823	2.823	2.831

Table 12.83. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=4, k=1, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.953	0.954	0.956	0.952	0.985	0.985	0.986	0.971	0.973	0.975
len	2.617	1.974	1.997	1.983	2.526	2.526	2.535	2.514	2.514	2.523
wild,0	0.958	0.955	0.960	0.961	0.955	0.952	0.956	0.947	0.949	0.950
len	2.400	1.756	1.778	1.768	2.276	2.276	2.281	2.271	2.271	2.273
par,0	0.967	0.977	0.975	0.975	0.981	0.982	0.981	0.964	0.964	0.965
len	2.667	2.379	2.607	2.585	2.464	2.464	2.470	2.464	2.464	2.470
npar,0.5	0.951	0.949	0.960	0.953	0.985	0.982	0.983	0.977	0.977	0.977
len	3.231	4.756	4.740	4.703	2.524	2.524	2.535	2.506	2.506	2.515
wild,0.5	0.950	0.953	0.958	0.955	0.956	0.955	0.955	0.956	0.956	0.959
len	3.024	4.296	4.281	4.251	2.277	2.277	2.280	2.276	2.276	2.279
par,0.5	0.971	0.970	0.978	0.976	0.979	0.979	0.981	0.979	0.978	0.979
len	3.305	5.498	5.534	5.507	2.459	2.459	2.465	2.462	2.462	2.468
npar,0.9	0.951	0.959	0.957	0.957	0.986	0.987	0.987	0.981	0.982	0.983
len	4.010	31.637	31.346	31.361	2.518	2.518	2.529	2.507	2.507	2.517
wild,0.9	0.954	0.959	0.961	0.965	0.954	0.960	0.958	0.954	0.956	0.959
len	3.760	28.462	28.280	28.262	2.272	2.272	2.276	2.273	2.273	2.277
par,0.9	0.964	0.974	0.965	0.966	0.973	0.975	0.976	0.970	0.971	0.971
len	4.120	34.838	34.752	34.551	2.459	2.459	2.465	2.461	2.461	2.465

Table 12.84. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=4,
k=p-2, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.937	0.955	0.957	0.964	0.971	0.975	0.974	0.985	0.985	0.985
len	2.604	1.988	1.974	1.967	1.950	1.950	1.958	2.951	2.951	2.962
wild,0	0.948	0.950	0.955	0.964	0.961	0.961	0.961	0.946	0.946	0.946
len	2.392	1.775	1.759	1.754	1.838	1.838	1.840	2.600	2.600	2.604
par,0	0.961	0.975	0.975	0.983	0.981	0.980	0.981	0.972	0.972	0.971
len	2.652	2.440	2.446	2.604	1.953	1.953	1.957	2.822	2.822	2.830
npar,0.5	0.955	0.957	0.956	0.959	0.970	0.975	0.974	0.985	0.987	0.986
len	3.241	4.666	4.692	4.687	1.949	1.949	1.957	2.937	2.937	2.951
wild,0.5	0.956	0.963	0.959	0.962	0.956	0.958	0.959	0.958	0.959	0.959
len	3.030	4.202	4.237	4.224	1.847	1.847	1.849	2.604	2.604	2.607
par,0.5	0.972	0.977	0.970	0.972	0.967	0.970	0.970	0.975	0.977	0.976
len	3.310	5.455	5.445	5.463	1.957	1.957	1.962	2.824	2.824	2.830
npar,0.9	0.944	0.955	0.953	0.948	0.960	0.961	0.962	0.985	0.985	0.985
len	4.033	31.774	31.509	31.577	1.951	1.951	1.959	2.935	2.935	2.943
wild,0.9	0.951	0.960	0.963	0.956	0.946	0.950	0.949	0.955	0.953	0.954
len	3.801	28.582	28.474	28.479	1.840	1.840	1.842	2.604	2.604	2.608
par,0.9	0.964	0.964	0.960	0.962	0.953	0.955	0.954	0.962	0.964	0.965
len	4.159	34.584	34.536	34.294	1.956	1.956	1.960	2.824	2.824	2.831

Table 12.85. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=8,
k=1, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.945	0.967	0.961	0.962	0.998	0.998	0.998	0.979	0.981	0.981
len	5.980	4.980	4.985	5.014	4.050	4.050	4.075	2.515	2.515	2.531
wild,0	0.952	0.972	0.967	0.963	0.981	0.981	0.981	0.961	0.964	0.964
len	5.516	4.418	4.393	4.411	3.383	3.383	3.389	2.291	2.291	2.293
par,0	0.972	0.987	0.990	0.988	0.999	0.999	0.999	0.984	0.985	0.987
len	6.084	6.261	6.160	6.162	3.628	3.628	3.637	2.462	2.462	2.467
npar,0.5	0.944	0.951	0.953	0.955	0.995	0.995	0.994	0.978	0.978	0.977
len	7.754	13.577	13.664	13.624	3.989	3.989	4.008	2.501	2.501	2.512
wild,0.5	0.953	0.956	0.955	0.959	0.965	0.965	0.966	0.953	0.955	0.956
len	7.300	12.291	12.331	12.271	3.380	3.380	3.386	2.293	2.293	2.297
par,0.5	0.969	0.977	0.982	0.974	0.992	0.992	0.993	0.980	0.979	0.980
len	7.944	15.105	15.129	15.100	3.627	3.627	3.635	2.459	2.459	2.465
npar,0.9	0.951	0.954	0.955	0.946	0.996	0.996	0.996	0.978	0.978	0.978
len	10.291	94.150	93.717	93.896	4.001	4.001	4.017	2.505	2.505	2.513
wild,0.9	0.955	0.954	0.959	0.942	0.959	0.962	0.962	0.953	0.955	0.953
len	9.690	84.658	84.411	84.576	3.378	3.378	3.386	2.291	2.291	2.295
par,0.9	0.969	0.970	0.970	0.965	0.987	0.990	0.990	0.977	0.975	0.976
len	10.562	101.55	101.69	101.33	3.625	3.625	3.636	2.458	2.458	2.465

Table 12.86. Bootstrapping WLS, n=100, BB=200, wtype = 5, p=8,
k=p-2, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.941	0.957	0.963	0.967	0.977	0.981	0.981	0.997	0.998	0.998
len	6.114	5.028	5.056	5.015	1.954	1.954	1.966	4.342	4.342	4.370
wild,0	0.955	0.960	0.967	0.969	0.963	0.965	0.965	0.975	0.978	0.979
len	5.658	4.421	4.439	4.426	1.856	1.856	1.858	3.598	3.598	3.605
par,0	0.970	0.978	0.983	0.983	0.981	0.981	0.982	0.993	0.993	0.994
len	6.154	6.212	6.196	6.169	1.959	1.959	1.965	3.849	3.849	3.860
npar,0.5	0.947	0.956	0.960	0.956	0.966	0.968	0.969	0.998	0.999	0.999
len	7.722	13.549	13.562	13.608	1.948	1.948	1.957	4.292	4.292	4.309
wild,0.5	0.951	0.952	0.961	0.960	0.950	0.953	0.953	0.967	0.968	0.969
len	7.255	12.193	12.247	12.264	1.853	1.853	1.856	3.593	3.593	3.599
par,0.5	0.968	0.958	0.961	0.961	0.955	0.955	0.955	0.972	0.969	0.972
len	7.847	14.584	14.621	14.603	1.957	1.957	1.963	3.849	3.849	3.861
npar,0.9	0.940	0.961	0.954	0.956	0.965	0.965	0.968	0.999	0.998	0.999
len	10.323	92.347	94.428	93.273	1.945	1.945	1.954	4.294	4.294	4.311
wild,0.9	0.952	0.962	0.961	0.956	0.950	0.948	0.949	0.966	0.966	0.967
len	9.757	83.617	85.481	84.363	1.851	1.851	1.854	3.592	3.592	3.600
par,0.9	0.960	0.959	0.958	0.957	0.942	0.942	0.945	0.964	0.967	0.965
len	10.566	98.948	98.772	98.756	1.958	1.958	1.963	3.848	3.848	3.858

Table 12.87. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=4, k=1, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.939	0.950	0.950	0.944	0.970	0.969	0.972	0.970	0.968	0.969
len	0.886	1.050	1.067	1.055	2.494	2.494	2.500	2.493	2.493	2.498
wild,0	0.949	0.947	0.944	0.943	0.940	0.943	0.945	0.940	0.936	0.935
len	0.848	0.965	0.984	0.973	2.267	2.267	2.270	2.278	2.278	2.283
par,0	0.954	0.936	0.911	0.921	0.890	0.891	0.892	0.938	0.938	0.937
len	0.919	1.043	0.952	0.954	2.457	2.457	2.463	2.459	2.459	2.465
npar,0.5	0.950	0.954	0.952	0.954	0.977	0.978	0.977	0.980	0.979	0.979
len	1.353	2.197	2.196	2.203	2.519	2.519	2.525	2.505	2.505	2.512
wild,0.5	0.962	0.957	0.960	0.959	0.947	0.950	0.951	0.955	0.955	0.958
len	1.279	1.987	1.986	1.996	2.276	2.276	2.280	2.280	2.280	2.285
par,0.5	0.971	0.962	0.959	0.956	0.949	0.952	0.955	0.963	0.964	0.967
len	1.402	2.475	2.381	2.397	2.461	2.461	2.469	2.459	2.459	2.463
npar,0.9	0.949	0.951	0.951	0.957	0.983	0.982	0.982	0.976	0.974	0.974
len	1.959	15.439	15.372	15.389	2.518	2.518	2.524	2.510	2.510	2.513
wild,0.9	0.952	0.953	0.954	0.967	0.954	0.956	0.957	0.946	0.950	0.950
len	1.857	14.016	13.963	13.936	2.273	2.273	2.277	2.277	2.277	2.282
par,0.9	0.964	0.964	0.965	0.963	0.965	0.968	0.968	0.963	0.963	0.964
len	2.027	17.145	17.196	17.148	2.458	2.458	2.464	2.464	2.464	2.468

Table 12.88. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=4,
k=p-2, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.941	0.941	0.947	0.947	0.957	0.959	0.960	0.982	0.979	0.979
len	0.907	1.077	1.075	1.075	1.942	1.942	1.948	2.912	2.912	2.918
wild,0	0.950	0.944	0.947	0.950	0.941	0.942	0.942	0.938	0.937	0.937
len	0.866	0.988	0.988	0.986	1.833	1.833	1.835	2.602	2.602	2.606
par,0	0.962	0.934	0.922	0.918	0.902	0.900	0.903	0.924	0.924	0.925
len	0.933	1.023	1.019	0.961	1.959	1.959	1.963	2.822	2.822	2.829
npar,0.5	0.940	0.949	0.958	0.944	0.957	0.955	0.953	0.985	0.983	0.984
len	1.352	2.195	2.182	2.200	1.944	1.944	1.948	2.940	2.940	2.944
wild,0.5	0.946	0.950	0.961	0.941	0.937	0.939	0.937	0.957	0.954	0.955
len	1.284	1.988	1.976	1.992	1.838	1.838	1.840	2.604	2.604	2.609
par,0.5	0.956	0.951	0.957	0.947	0.941	0.940	0.941	0.949	0.951	0.951
len	1.398	2.403	2.413	2.344	1.957	1.957	1.963	2.823	2.823	2.831
npar,0.9	0.936	0.958	0.955	0.958	0.969	0.965	0.966	0.980	0.982	0.982
len	1.990	15.725	15.584	15.621	1.945	1.945	1.949	2.944	2.944	2.950
wild,0.9	0.940	0.959	0.951	0.958	0.952	0.954	0.955	0.945	0.945	0.946
len	1.877	14.240	14.157	14.157	1.839	1.839	1.842	2.603	2.603	2.607
par,0.9	0.961	0.958	0.956	0.962	0.957	0.957	0.958	0.953	0.956	0.957
len	2.053	17.106	17.047	17.146	1.963	1.963	1.967	2.825	2.825	2.833

Table 12.89. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=8,
k=1, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.953	0.949	0.955	0.952	0.995	0.996	0.996	0.977	0.975	0.975
len	0.804	0.865	0.861	0.871	3.925	3.925	3.939	2.494	2.494	2.500
wild,0	0.960	0.949	0.959	0.951	0.948	0.952	0.952	0.952	0.953	0.954
len	0.770	0.799	0.795	0.801	3.372	3.372	3.379	2.307	2.307	2.311
par,0	0.969	0.954	0.946	0.934	0.934	0.934	0.936	0.946	0.945	0.947
len	0.829	0.909	0.838	0.843	3.629	3.629	3.639	2.460	2.460	2.465
npar,0.5	0.949	0.959	0.957	0.961	0.997	0.996	0.997	0.980	0.979	0.979
len	1.850	3.324	3.351	3.325	4.031	4.031	4.042	2.516	2.516	2.522
wild,0.5	0.954	0.958	0.963	0.959	0.963	0.967	0.968	0.956	0.956	0.959
len	1.740	2.990	3.016	3.003	3.386	3.386	3.392	2.294	2.294	2.298
par,0.5	0.960	0.967	0.954	0.971	0.969	0.971	0.972	0.963	0.963	0.965
len	1.901	3.662	3.609	3.604	3.623	3.623	3.635	2.461	2.461	2.470
npar,0.9	0.946	0.962	0.966	0.949	0.994	0.995	0.995	0.979	0.975	0.977
len	2.968	27.281	27.184	26.939	4.021	4.021	4.031	2.511	2.511	2.514
wild,0.9	0.956	0.965	0.962	0.952	0.962	0.967	0.969	0.955	0.957	0.958
len	2.804	24.676	24.457	24.430	3.383	3.383	3.389	2.293	2.293	2.297
par,0.9	0.963	0.960	0.970	0.959	0.980	0.980	0.980	0.966	0.965	0.966
len	3.067	29.144	29.152	29.039	3.630	3.630	3.639	2.463	2.463	2.470

Table 12.90. Bootstrapping WLS, n=100, BB=200, wtype = 6, p=8,
k=p-2, etype= 0.9 N(0,1) + 0.1 N(0,100)

ψ	β_1	β_2	β_{p-1}	β_p	pr0	hyb0	br0	pr1	hyb1	br1
npar,0	0.951	0.948	0.944	0.955	0.962	0.962	0.964	0.994	0.993	0.994
len	0.804	0.867	0.864	0.864	1.949	1.949	1.955	4.217	4.217	4.230
wild,0	0.951	0.946	0.943	0.954	0.947	0.945	0.945	0.946	0.944	0.945
len	0.769	0.800	0.798	0.795	1.863	1.863	1.866	3.588	3.588	3.593
par,0	0.961	0.938	0.926	0.943	0.931	0.931	0.932	0.910	0.915	0.915
len	0.829	0.846	0.845	0.831	1.956	1.956	1.961	3.846	3.846	3.857
npar,0.5	0.950	0.955	0.952	0.960	0.968	0.969	0.969	0.997	0.997	0.997
len	1.869	3.357	3.383	3.397	1.947	1.947	1.954	4.322	4.322	4.334
wild,0.5	0.956	0.955	0.957	0.962	0.953	0.956	0.953	0.960	0.962	0.964
len	1.757	3.043	3.063	3.070	1.850	1.850	1.852	3.590	3.590	3.595
par,0.5	0.962	0.957	0.953	0.959	0.948	0.948	0.949	0.949	0.949	0.951
len	1.922	3.579	3.618	3.590	1.955	1.955	1.961	3.846	3.846	3.857
npar,0.9	0.947	0.955	0.952	0.956	0.966	0.963	0.964	0.998	0.998	0.997
len	3.067	27.680	27.938	27.457	1.949	1.949	1.953	4.326	4.326	4.336
wild,0.9	0.957	0.954	0.949	0.956	0.945	0.951	0.953	0.970	0.971	0.972
len	2.896	24.981	25.231	24.784	1.854	1.854	1.857	3.590	3.590	3.596
par,0.9	0.964	0.957	0.945	0.949	0.946	0.946	0.946	0.950	0.951	0.952
len	3.150	29.591	29.482	29.436	1.957	1.957	1.962	3.842	3.842	3.852

CHAPTER 13

CONCLUSIONS

The theory showing that the bootstrap BR and PR confidence regions give large sample tests is very simple. We need $\sqrt{n}(T_n - \boldsymbol{\mu}) \xrightarrow{D} \mathbf{u}$, $\sqrt{n}(T_n^* - T_n) \xrightarrow{D} \mathbf{u}$, and $\mathbf{C}_n^{-1} \xrightarrow{P} \mathbf{C}^{-1}$. The results also hold if \mathbf{G}_n replaces \mathbf{C}_n^{-1} and \mathbf{G} replaces \mathbf{C}^{-1} where \mathbf{G}_n and \mathbf{G} are not necessarily nonsingular. An interesting result is that the BR and PR confidence intervals do not depend on whether the wrong or right dispersion matrix was used.

Tests with the wrong dispersion matrix tend to be inferior to tests that use a consistent estimator of the correct covariance matrix if the sample sizes are large enough. Hence tests based on (3.3) and (3.6) are better than tests that make the common covariance matrix assumption if the $n_i \geq 20m$ are large enough. A useful diagnostic for tests that make the common covariance matrix assumption is to check whether the test cutoff is close to the bootstrap PR or BR cutoff. If the n_i are not large or if a test that uses a consistent estimator of the correct covariance matrix is not available, then the PR and BR tests can be useful.

Tests using the wrong dispersion matrix \mathbf{I} are useful to illustrate the previous paragraph. If $\sqrt{n}(T_n - \boldsymbol{\theta}) \xrightarrow{D} N_g(\mathbf{0}, \boldsymbol{\Sigma})$, then $\{\mathbf{w} : (\mathbf{w} - T_n)^T \hat{\boldsymbol{\Sigma}}(\mathbf{w} - T_n) \leq D^2\}$ is a hyperellipsoid. A hypersphere could be used to approximately cover the hyperellipsoid, but the power from the hypersphere test will be lower than that from the hyperellipsoid test if the sample sizes n_i are large. For large sample level α tests, the hypersphere volume tends to be much larger than the hyperellipsoid volume unless $\boldsymbol{\Sigma} \approx k\mathbf{I}$ for some real $k > 0$.

The Rupasinghe Arachchige Don and Olive (2019) bootstrap one way MANOVA type tests needed $B \geq 50m(p-1)$, $n \geq (m+p)^2$, and $n_i \geq 40m$. Large B was needed so \mathbf{S}_T^* would be a good estimator when the test statistic \mathbf{T} is an $m(p-1) \times 1$ vector. The new tests can use much smaller B if \mathbf{C}_n^{-1} does not depend on the bootstrap sample.

For high dimensional tests, choices of \mathbf{C}_n other than $\mathbf{C}_n = \mathbf{I}$ can be used as long as the computational complexity of \mathbf{C}_n^{-1} is not too high.

Some high dimensional one sample tests include Chen et al. (2011), Hyodo and Nishiyama (2017), Srivastava and Du (2008), and Wang, Peng, and Li (2015).

The *R* software was used in the simulations. See R Core Team (2016). Programs are in the Olive (2017b) collection of *R* functions *mpack.txt* available from (<http://parker.ad.siu.edu/Olive/mpack.txt>).

pooled *t* test: The function `pcsim2` was used in the simulations.

one way ANOVA: The function `anovasim2` was used in the simulations.

one sample Hotelling's T^2 test: The function `hdhot1wsim` was used for high dimensional data.

two sample Hotelling's T^2 test: The function `hot2sampsim` was used to simulate the tests of hypotheses in Section 8. The function `hdhot2wsim` was used for high dimensional data used in the tests of Section 9.

one way MANOVA: The function `manovasim` was used to simulate the tests of hypotheses. The function `hdmansim` was used to simulate the high dimensional test.

OLS for Weighted Least Squares: The function `wildboot` was used to bootstrap the nonparametric, wild, and parametric bootstrap. The function `wlsbootsim` was used for the simulation.

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Dissertation Paper Title:

Wald Type Tests With the Wrong Dispersion Matrix

Major professor: Dr. David Olive