Exercice n°5

Sampling Intervals for Models

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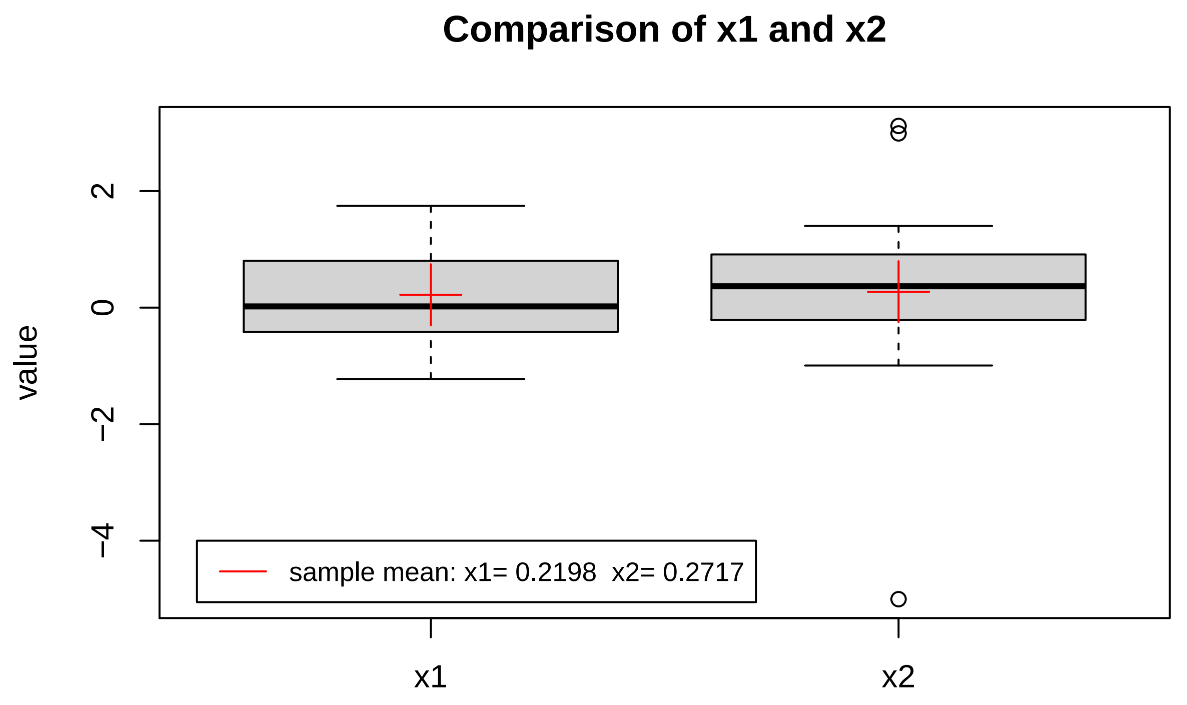
Task n°1

Consider a two sample problem and the hypothesis $H_0 : \mu 1 = \mu 2 vs H_1 : \mu 1 \neq \mu 2$, where $\mu 1$ and $\mu 2$ are the corresponding sample locations. The two samples are:

```
matricul.number <- 12202211
x1 <- c(-0.673, -0.584, 0.572, -0.341, -0.218, 0.603, -0.415, -0.013, 0.763, 0.804, 0.054, 1.746, -0.47
x2 <- c(0.913, -0.639, 2.99, -5.004, 3.118, 0.1, 1.128, 0.579, 0.32, -0.488, -0.994, -0.212, 0.413, 1.4
#x2 <- c(1000,1005,1007,1006,1009,1005,908,807)
set.seed(matricul.number)
```

I.1 Plot the data in a way which visualises the comparison of means appropriately.

```
library(ggplot2)
par(mfrow=c(1,1))
boxplot(x1,x2, main = "Comparison of x1 and x2", ylab = "value", names = c("x1", "x2"))
points(x=1, y = mean(x1), col='red', pch=3, cex = 3)
points(x=2, y = mean(x2), col='red', pch=3, cex = 3)
legend(.5,-4 , legend=c(paste("sample mean: x1=",round(mean(x1),digits=4), " x2=",round(mean(x2),digits
       col=c("red"), lty=1:2, cex=0.8)
```



## I.2 Consider different sampling schemes - Sampling with replacement from each group - Centering both samples and then resample from the combined samples x1 and x2 for n1 and n2 times.

```
#Sampling with replacement from each group
sampling_1 <- function(data,n, size=length(data)){
  samples = numeric(n)
  return(replicate(n, sample(data, size=size, replace=TRUE)))
}

#Centering both samples and then resample from the combined samples x1 and x2 for n1 and n2 times.
sampling_2 <- function(data1,data2,n1,n2, size1=length(data1),size2=length(data2)){
  #centreing
  data1 <- data1-mean(data1)
  data2 <- data2-mean(data2)
  combined <- c(data1,data2)
  sampl_x1 <- replicate(10000, sample(combined, size=size1, replace=TRUE))
  sampl_x2 <- replicate(10000, sample(combined, size=size2, replace=TRUE))
  return(list("sampl_x1" = sampl_x1, "sampl_x2" = sampl_x2))
}
```

Argue for choice what is more natural and which advantages or disadvantages may apply.
Our goal is to determine the whether the sample locations are the same. In the first case, we have the most common and the most natural way to do it using bootstrapping. We can estimate the parameter of x1 and x2 with their bootstrap and use test statistic and compare their value to a test statistic computed with the original samples. With those comparison, we can obtain a p-value and conclude on our hypothesis. The second method is less common, we will use the exact same process as with method one but the main difference is that our test statistic values will contain less information on the mean since the bootsrap come from the

same combined values. But the comparison with the original test statistic value will enable us to obtain a similar result as befor. The second method may give better results if the samples size are significantly different but the first one is easier to understand.

I.3 Bootstrap using both strategies mentioned above using the t-test statistic. Calculate the bootstrap p-value based on 10'000 bootstrap samples and 0.95 as well as 0.99 confidence intervals. Make your decision at the significance level 0.05 or 0.01, respectively.

```
test_stat <- function(x1,x2){
  return((mean(x1) - mean(x2))/sd(x1))
}
```

```
#Generating bootstraps
n=10000
mean_x1 = mean(x1)
mean_x2 = mean(x2)
boot1_x1<- sampling_1(x1, n=n)
boot1_x2 <- sampling_1(x2, n=n)

boot2 <- sampling_2(x1,x2,n,n)
boot2_x1 <- boot2[[1]]
boot2_x2 <- boot2[[2]]

tests_x1 <- test_stat(x1,x2) #H0: x1 = x2
tests_x2 <- test_stat(x2,x1) #H0: x2 = x1
```

```
#Methode 1
#test statistique
bootstap_tests_x1 <- numeric(n)
bootstap_tests_x2 <- numeric(n)
p_value_x1 <- 1
p_value_x2 <- 1

for(i in 1:n){
  bootstap_tests_x1[i] <- test_stat(boot1_x2[,i],x2)
  bootstap_tests_x2[i] <- test_stat(boot1_x1[,i],x1)
  if(abs(bootstap_tests_x1[i]) > abs(tests_x1)){
    p_value_x1 <- p_value_x1 + 1}
  if(abs(bootstap_tests_x2[i]) > abs(tests_x2)){
    p_value_x2 <- p_value_x2 + 1}
}
p_value_x1 <- p_value_x1/(n+1)
p_value_x2 <- p_value_x2/(n+1)

# CI
a = .025
b = 1-a

ci_1_x1 <-  quantile(bootstap_tests_x1,c(a,b))
ci_1_x2 <-  quantile(bootstap_tests_x2, c(a,b))
```

```r
a = .005
b = 1-a

ci_1_x1_99 <-  quantile(bootstap_tests_x1,c(a,b))
ci_1_x2_99 <-  quantile(bootstap_tests_x2, c(a,b))
```

Method n°1 hypothese | H0:x1=x2 | | ‘H0:x1=x2’| | ———-|———-|-|————|-| p_value | 0.8060194 | | 0.889611 | | CI 95% | 2.5% | 97.5% | 2.5% | 97.5% | -0.4009562 | 0.5834701 | -0.4563763 | 0.6397644 CI 99% | .5% | 99.5% | .5% | 99.5% | -0.5095706 | 0.7340501 | -0.637585 | 0.6397644

```r
#Method 2
# h0: x1=x2
p_value2_x1 <- 1
t_values1 = numeric(n)
# h0: x2=x1
p_value2_x2 <- 1
t_values2 = numeric(n)

for(i in 1:n){
    t_values1[i] <- test_stat(boot2_x1[,i],boot2_x2[,i])  # bootstrap test statistic
    if( (abs(t_values1[i]) > abs(tests_x1)) ){
      p_value2_x1 <- p_value2_x1 + 1}
     t_values2[i] <- test_stat(boot2_x2[,i],boot2_x1[,i])  # bootstrap test statistic
    if( (abs(t_values2[i]) > abs(tests_x2)) ){
      p_value2_x2 <- p_value2_x2 + 1}
}

p_value2_x1 <- p_value2_x1/(n+1)
p_value2_x2 <- p_value2_x2/(n+1)


# CI
a = .025
b = 1-a

ci_2_x1 <-  quantile(t_values1,c(a,b))
ci_2_x2 <-  quantile(t_values2, c(a,b))

a = .005
b = 1-a

ci_2_x1_99 <-  quantile(t_values1,c(a,b))
ci_2_x2_99 <-  quantile(t_values2, c(a,b))
```

Method n°2 hypothese | H0:x1=x2 | | ‘H0:x1=x2’| | ———-|———-|-|————|-| p_value | 0.8453155 | | 0.929607 | | CI 95% | 2.5% | 97.5% | 2.5% | 97.5% | -0.6176585 | 0.812572 | -0.6502974 | 0.8016758 CI 99% | .5% | 99.5% | .5% | 99.5% | -0.8629164 | 1.0921075 | -0.9353396 | 1.0875825

BLABLA BLA

I.4 What would be a permutation version of the test? Implement the corresponding permutation test and obtain p-value and confidence intervals as in 3. to get a corresponding test decision at the same significance levels.

A permutation version of the test would be a permutation of the values between x1 and x2.

```r
indices <- seq(from = 1, to = length(x1) + length(x2), by = 1)
combined <- c(x1, x2)

t_stat_x1 <- c()
t_stat_x2 <- c()

for (i in 1:n) {
  x1_indices <- sample(indices, size = length(x1), replace = FALSE)

  boot_x1 <- combined[x1_indices]
  boot_x2 <- setdiff(combined, boot_x1)

  t_stat_x1 <- c(t_stat_x1, test_stat(boot_x1,x2))
  t_stat_x2 <- c(t_stat_x2, test_stat(boot_x2,x1))
}

p_value_x1 <- 1
p_value_x2 <- 1

for(i in 1:n){
  if(abs(t_stat_x1[i]) > abs(tests_x1)){
    p_value_x1 <- p_value_x1 + 1}
  if(abs(t_stat_x2[i]) > abs(tests_x2)){
    p_value_x2 <- p_value_x2 + 1}
}
p_value3_x1 <- p_value_x1/(n+1)
p_value3_x2 <- p_value_x2/(n+1)

# CI
a = .025
b = 1-a

ci_3_x1 <-  quantile(t_stat_x1,c(a,b))
ci_3_x2 <-  quantile(t_stat_x2, c(a,b))

a = .005
b = 1-a

ci_3_x1_99 <-  quantile(t_values1,c(a,b))
ci_3_x2_99 <-  quantile(t_values2, c(a,b))
```

Permutation

hypothese	H0:x1=x2		'H0:x1=x2'	
p_value	0.6977302		0.8835116	
CI 95%	2.5%	97.5%	2.5%	97.5%

hypothese	H0:x1=x2		‘H0:x1=x2’	
-0.2964934	0.3178029	-0.3021192	0.4383368	
CI 99%	.5%	99.5%	.5%	99.5%
-0.8629164	1.0921075	-0.9353396	1.0875825	

I.5 The Wilxocon rank sum test statistic is the sum of ranks of the observations of sample 1 computed in the combined sample. Use bootstrapping with both strategies mentioned above and obtain p-value and confidence intervals as in 3. to get a corresponding test decision at the same significance levels.

```r
# First method
Wilcox_boot_x1 <- c()
for(i in 1:n){
  Wilcox_boot_x1 <- c(Wilcox_boot_x1, wilcox.test(boot1_x1[,i], x2, paired = FALSE)$statistic)
}

will_original <- wilcox.test(x1, x2, paired = FALSE)$statistic
print(paste('will_original H0=x1=x2',will_original))
```

```
## [1] "will_original H0=x1=x2 181"
```

```r
p_value_x1 <- 1
for(i in 1:n){
  if(abs(Wilcox_boot_x1[i]) > abs(will_original)){
    p_value_x1 <- p_value_x1 + 1}
}
p_value_x1 <- p_value_x1/(n+1)
print(p_value_x1)
```

```
## [1] 0.4966503
```

```r
Wilcox_boot_x2 <- c()
for(i in 1:n){
  Wilcox_boot_x2 <- c(Wilcox_boot_x2, wilcox.test(boot1_x2[,i], x1, paired = FALSE)$statistic)
}
will_original2 <- wilcox.test(x2, x1, paired = FALSE)$statistic
print(paste('will_original H0=x1=x2',will_original2))
```

```
## [1] "will_original H0=x1=x2 215"
```

```r
p_value_x2 <- 1
for(i in 1:n){
  if(abs(Wilcox_boot_x2[i]) > abs(will_original2)){
    p_value_x2 <- p_value_x2 + 1}
}
p_value_x2 <- p_value_x2/(n+1)
print(p_value_x2)
```

```
## [1] 0.4971503
```

```
# Saecond method
## x1
Wilcox_boot_x1_2 <- c()
for(i in 1:n){
  Wilcox_boot_x1_2 <- c(Wilcox_boot_x1_2, wilcox.test(boot2_x1[,i], x2, paired = FALSE)$statistic)
}
p_value_x1_2 <- 1
for(i in 1:n){
  if(abs(Wilcox_boot_x1_2[i]) > abs(will_original)){
    p_value_x1_2 <- p_value_x1_2 + 1}
}
p_value_x1_2 <- p_value_x1_2/(n+1)
print(paste('p_value_x1_2',p_value_x1_2))
```

```
## [1] "p_value_x1_2 0.179482051794821"
```

```
## x2
Wilcox_boot_x2_2 <- c()
for(i in 1:n){
  Wilcox_boot_x2_2 <- c(Wilcox_boot_x2_2, wilcox.test(boot2_x2[,i], x1, paired = FALSE)$statistic)
}
p_value_x2_2 <- 1
for(i in 1:n){
  if(abs(Wilcox_boot_x2_2[i]) > abs(will_original2)){
    p_value_x2_2 <- p_value_x2_2 + 1}
}
p_value_x2_2 <- p_value_x2_2/(n+1)
print(paste('p_value_x2_2',p_value_x2_2))
```

```
## [1] "p_value_x2_2 0.048995100489951"
```

```
# CI
a = .025
b = 1-a

ci_Wilcox_boot_x1 <-  quantile(Wilcox_boot_x1,c(a,b))
ci_Wilcox_boot_x2 <-  quantile(Wilcox_boot_x2, c(a,b))
Wilcox_boot_x1_2 <-  quantile(Wilcox_boot_x1_2,c(a,b))
Wilcox_boot_x2_2 <-  quantile(Wilcox_boot_x2_2, c(a,b))

a = .005
b = 1-a

ci_Wilcox_boot_x1_99 <-  quantile(Wilcox_boot_x1,c(a,b))
ci_Wilcox_boot_x2_99 <-  quantile(Wilcox_boot_x2, c(a,b))
Wilcox_boot_x1_2_99 <-  quantile(Wilcox_boot_x1_2,c(a,b))
Wilcox_boot_x2_2_99 <-  quantile(Wilcox_boot_x2_2, c(a,b))

print('-----')
```

```
## [1] "-----"
```

```r
p_value_x1
```

```
## [1] 0.4966503
```

```r
ci_Wilcox_boot_x1
```

```
##  2.5% 97.5%
##   136   228
```

```r
ci_Wilcox_boot_x1_99
```

```
##  0.5% 99.5%
##   122   244
```

```r
p_value_x2
```

```
## [1] 0.4971503
```

```r
ci_Wilcox_boot_x2
```

```
##  2.5% 97.5%
##   159   270
```

```r
ci_Wilcox_boot_x2_99
```

```
##  0.5% 99.5%
##   141   286
```

```r
p_value_x1_2
```

```
## [1] 0.1794821
```

```r
Wilcox_boot_x1_2
```

```
##  2.5% 97.5%
##   115   207
```

```r
Wilcox_boot_x1_2_99
```

```
##   0.5%  99.5%
## 115.46 206.54
```

```r
p_value_x2_2
```

```
## [1] 0.0489951
```

```
Wilcox_boot_x2_2
```

```
##  2.5% 97.5%
##   114   225
```

```
Wilcox_boot_x2_2_99
```

```
##    0.5%   99.5%
## 114.555 224.445
```

I.6 Compare your results to the results using t.test and wilcox.test.

```
wilcox <- wilcox.test(x1, x2, paired = FALSE)
wilcox
```

```
##
##  Wilcoxon rank sum exact test
##
## data:  x1 and x2
## W = 181, p-value = 0.6572
## alternative hypothesis: true location shift is not equal to 0
```

```
wilcox <- wilcox.test(x2, x1, paired = FALSE)
wilcox
```

```
##
##  Wilcoxon rank sum exact test
##
## data:  x2 and x1
## W = 215, p-value = 0.6572
## alternative hypothesis: true location shift is not equal to 0
```

```
ttest <- t.test(x1,x2, paired = FALSE)
ttest
```

```
##
##  Welch Two Sample t-test
##
## data:  x1 and x2
## t = -0.11881, df = 23.027, p-value = 0.9065
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.9556081  0.8518000
## sample estimates:
## mean of x mean of y
## 0.2198182 0.2717222
```

```r
ttest <- t.test(x2,x1, paired = FALSE)
ttest
```

```
##
##  Welch Two Sample t-test
##
## data:  x2 and x1
## t = 0.11881, df = 23.027, p-value = 0.9065
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.8518000  0.9556081
## sample estimates:
## mean of x mean of y
## 0.2717222 0.2198182
```

Task n°2

Consider the model $y = 3 + 2 * x1 + x2 + e$ where x1 comes from a normal distribution with mean 2 and variance 3, x2 comes from a uniform distribution between 2 and 4 and e from a student's t distribution with 5 degrees of freedom . In addition, there is a predictor x3 coming from a uniform distribution between -2 and 2.

```r
model <- function(n){
  x1 <-  rnorm(n, mean = 2, sd = 3)
  x2 <- runif(n, min = 2, max = 4)
  eps <- rt(n, df = 5)
  x3 <- runif(n, min = -2, max = 2)
  y <- 3+ 2*x1 + x2 + eps
  df <- data.frame(y,x1,x2,x3)
  return(df)
}

x3  <- function(){
  return(runif(1,-2,2))
}
```

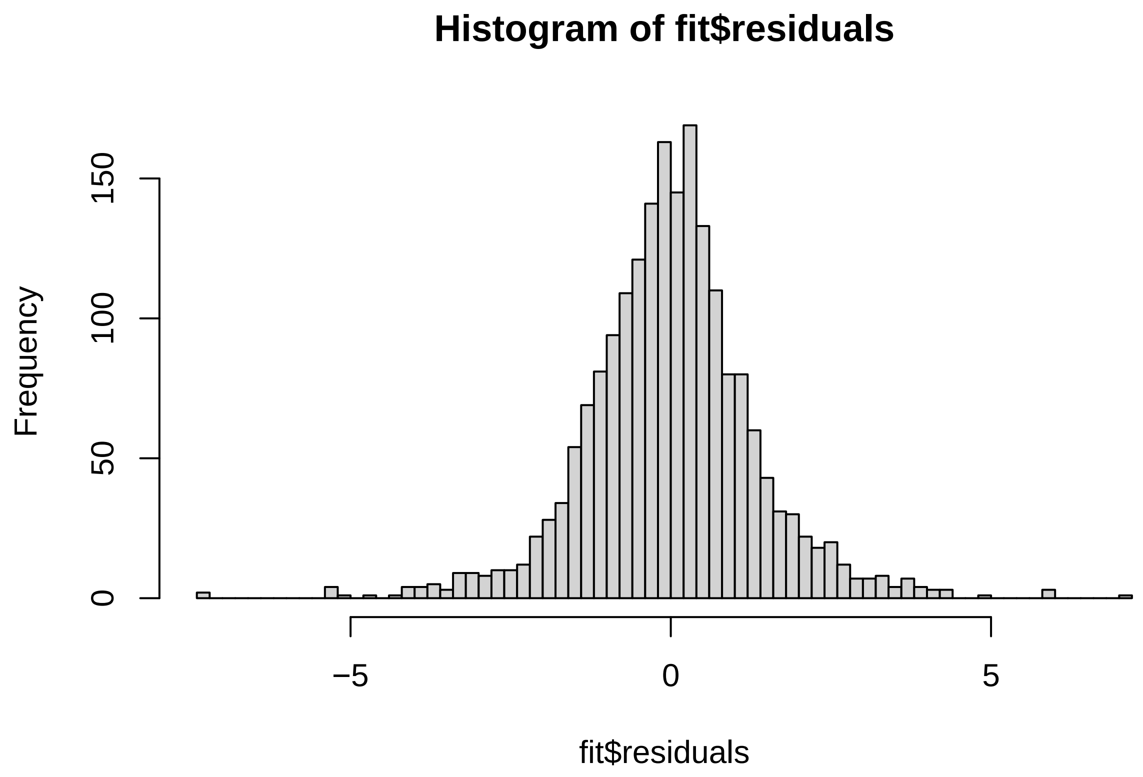
II.1 Create a sample of size 200 from the model above and for the independent predictor x3.

```r
n <- 2000
data <- model(n)
```

II.2 Do residual bootstrap for linear regression and fit the model y follow x1+x2+x3 . Get the percentile CI for the coefficients. Can you exclude x3 ?

```r
library(boot)
```

```r
fit <- lm(y~., data=data)
hist(fit$residuals, breaks = 100)
```



The residual distribution seems to follow a normal distribution, we will use a parametric bootsrap.

```r
reg.fun <- function(x){
  return(coef(lm(y ~ x1+x2+x3, data = x)))
}
reg.sim <- function(x, resi){
  x$y <- (resi$yhat + sample(resi$res, replace = TRUE))
  return(x)
}

res <- resid(fit)
yhat <- fitted(fit)
reg2 <- data.frame(yhat, res)

fit.boot <- boot(data, reg.fun, R=1000, sim="parametric", ran.gen=reg.sim, mle = reg2)
x1_coef_ci <- quantile(fit.boot$t[,2], c(0.01,0.05,0.95, 0.99))
x2_coef_ci <- quantile(fit.boot$t[,3], c(0.01,0.05,0.95, 0.99))
x3_coef_ci <- quantile(fit.boot$t[,4],  c(0.01,0.05,0.95, 0.99))
print(" precentile CI for the x1 coefficients in case of residual bootstraps")
```

```
## [1] " precentile CI for the x1 coefficients in case of residual bootstraps"
```

```r
x1_coef_ci
```

```
##       1%       5%      95%      99% 
## 1.979805 1.986839 2.018347 2.025316
```

```r
print(" precentile CI for the x2 coefficients in case of residual bootstraps")
```

```
## [1] " precentile CI for the x2 coefficients in case of residual bootstraps"
```

```r
x2_coef_ci
```

```
##        1%        5%       95%       99% 
## 0.8279433 0.8606504 1.0333896 1.0688063
```

```r
print(" precentile CI for the x3 coefficients in case of residual bootstraps")
```

```
## [1] " precentile CI for the x3 coefficients in case of residual bootstraps"
```

```r
x3_coef_ci
```

```
##          1%          5%         95%         99% 
## -0.05637036 -0.04168192  0.04414596  0.05739864
```

Do residual bootstrap for linear regression and fit the model yziguigui x1+x2+x3 . Get the percentile CI for the coefficients. Can you exclude x3 ? Do pairs bootstrap for linear regression and fit the model yfollowx1+x2+x3 . Get the percentile CI for the coefficients. Can you exclude x3 ? Compare the two approaches in 2. and 3. and explain the differences in the sampling approach and how this (might) affect(s) the results.

asymptotically they are equivalent when the model is correctly specified. I they perform quite differently for small samples and for the correct model the residual version is more efficient. I the pairs strategy is often considered more robust when the model is misspecified.

Task 3 Summarise the bootstrapping methodology, its advantages and disadvantages based on your exercises for constructing parametric and non-paramteric confidence bounds for estimators, test statistics or model estimates.