Section 16.5. Single-Sample Confidence Interval for $\sigma$

**Assumptions:** $Y_1, Y_2, \ldots, Y_n \sim_{iid} N(\mu, \sigma^2)$

**R function:** R does not have a built-in function for this, but it is easy to create one:

```r
sd.interval = function(data, conf.level = 0.95) {
  alpha = 1 - conf.level
  df = length(data) - 1
  c.U = sqrt( qchisq(1 - alpha/2, df) / df)
  c.L = sqrt( qchisq( alpha/2, df) / df)
  sigma.hat = sd(data)
  c(sigma.hat/c.U, sigma.hat/c.L)
}
```

**Example in the book:**

```r
g failure.times = c(3.2, 3.4)
sd.interval(failure.times, .95)
```

**Result:** 0.06309502 4.51277801. Interpretation: Assuming the data were produced as $Y_1, Y_2 \sim_{iid} N(\mu, \sigma^2)$, we are 95% confident that $\sigma$ lies between 0.063 and 4.513. In other words, in 95% of repeated samples $Y_1, Y_2 \sim_{iid} N(\mu, \sigma^2)$, the true, unknown value of $\sigma$ will lie between similarly constructed endpoints.

**Understanding the result through simulation, where you know the true parameters.**

```r
n = 2
data = rnorm(n, 4, 1.5)  ## In the simulation, $\mu = 4$ and $\sigma = 1.5$.
sd.interval(data, .95)
```

**Result:** (Yours will vary). 1.38 98.8

Interpretation: In 95% of repeated samples $Y_1, Y_2 \sim_{iid} N(4, 1.5^2)$, similarly constructed endpoints will contain the value $\sigma = 1.5$. 
Section 16.6. Single-Sample Confidence Interval for $\mu$

**Assumptions:** $Y_1, Y_2, \ldots, Y_n \sim_{iid} \mathcal{N}(\mu, \sigma^2)$  (same as for the single-sample confidence interval for $\sigma$).

**R function:** t.test

**Example in the book:**

```r
failure.times = c(3.2, 3.4)
t.test(failure.times)
```

**Result:**

```
One Sample t-test

data:  failure.times
t = 33, df = 1, p-value = 0.01929
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 2.02938 4.57062
sample estimates:
mean of x
3.3
```

**Interpretation:** Assuming the data were produced as $Y_1, Y_2 \sim_{iid} \mathcal{N}(\mu, \sigma^2)$, we are 95% confident that $\mu$ lies between 2.02938 and 4.57062. In other words, in 95% of repeated samples $Y_1, Y_2 \sim_{iid} \mathcal{N}(\mu, \sigma^2)$, the true, unknown value of $\mu$ will lie between similarly constructed endpoints.

**Understanding the result through simulation, where you know the true parameters:**

```r
n = 2
data = rnorm(n, 4, 1.5)
t.test(data)
```

**Result:** (Yours will vary).

```
95 percent confidence interval:
-18.72069  25.95036
```

**Interpretation:** In 95% of repeated samples $Y_1, Y_2 \sim_{iid} \mathcal{N}(4, 1.5^2)$, similarly constructed endpoints will contain the value $\mu = 4.0$. 
Section 16.7: Two-Sample (independent samples) Confidence Interval for $\mu_1 - \mu_2$

**Assumptions:** $Y_{ij} \sim \text{ind } N(\mu_i, \sigma^2)$, for $i = 1,2$ and $j = 1,\ldots,n_i$.

**R function:** `t.test` (again)

**Example in the book:** Ages of people sitting in front versus back. There are two types of data input: (i) use of separate data vectors for each group, and (ii) use of a single combined vector with all data, and with an additional vector indicating group membership. The latter form is more common to see in practice, because that is the way information is kept in databases.

(i)  
Front.ages = c(36, 23, 22, 27, 26, 24, 28, 23)  
Back.ages = c(30, 25, 22, 26, 22, 35, 24, 36)  
`t.test(Back.ages, Front.ages, var.equal=T)`

(ii) Typically, you will read the data set from an external source and it will have the data frame format given after the following code is run.

```r
Ages = c(Front.ages, Back.ages)  
Where = c(rep("Front",8), rep("Back",8))  
Age.seat = data.frame(Ages, Where)  
## When you read data from an external source, it will look like this:  
Age.seat
```

`t.test(Ages ~ Where, data=Age.seat, var.equal=T)`

**Result:** Either way, you get the following output:

```
Two Sample t-test

data:  Ages by Where
 t = 0.54316, df = 14, p-value = 0.5956
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:  
-4.054523  6.804523
sample estimates:  
mean in group Back mean in group Front
 27.500         26.125
```
**Interpretation:** We are 95% confident that $\mu_1 - \mu_2$ lies in the range $-4.054523$ to $6.804523$. The reason is that in 95% of repeated samples $Y_{ij} \sim \text{ind } N(\mu_i, \sigma^2)$, with 8 observations per group, similarly constructed endpoints will contain the value $\mu_1 - \mu_2$.

**Understanding the result through simulation, where you know the true parameters:**

n1 = 8  
n2 = 8  
Back.r = rnorm(n1, 26, 4)  
Front.r = rnorm(n2, 32, 4)  
t.test(Back.r, Front.r, var.equal=T)

**Result:** (Yours will vary).

95 percent confidence interval:  
-11.022256  -4.630458

**Interpretation:** In 95% of repeated samples $Y_{ij} \sim \text{ind } N(\mu_i, \sigma^2)$, with $i=1,2; j=1,...,8$, $\mu_1 = 26$ and $\mu_2 = 32$, similarly constructed endpoints will contain the value $\mu_1 - \mu_2 = 26-32 = -6$.

**Section 16.8: Two-Sample (independent samples) t-test for testing $H_0: \mu_1 = \mu_2$**

**Assumptions, null model:** $Y_{ij} \sim \text{iid } N(\mu, \sigma^2)$, for $i = 1,2$ and $j = 1,...,n_i$. (again)

**R function:** t.test (again)

The R code and data set issues are identical to the interval analysis shown above. Let’s look at the output as it relates to the t test (see boldface text)

**Two Sample t-test**

data:  Ages by Where  
t = 0.54316, df = 14, p-value = 0.5956  
alternative hypothesis: true difference in means is not equal to 0  
95 percent confidence interval:  
-4.054523  6.804523  
sample estimates:  
mean in group Back mean in group Front  
27.500 26.125
Interpretation: In 59.56% of repeated samples $Y_{ij} \sim_{ind} N(\mu_i, \sigma^2)$, with 8 observations per group and where $\mu_1 = \mu_2$, the absolute difference between sample averages will be more than 0.543 standard errors. Thus, the observed difference between sample averages is explainable by chance alone. In other words, the observed difference between sample averages is within the realm of differences that are seen when, in reality, $\mu_1 = \mu_2$.

**Understanding the result through simulation, where you know the true parameters:**

Run the following code several times and keep track of the t statistics. Notice that the null model is true in this simulation because $\mu_1 = \mu_2 = 27$.

```r
n1 = 8
n2 = 8
Front.r = rnorm(n1, 27, 4)
Back.r = rnorm(n2, 27, 4)
t.test(Back.r, Front.r, var.equal=T)
```

**Result:**
I get (yours will vary) the following t-statistics from 13 samples. Samples giving more extreme results than in the original data are shown in bold.

```
-.455, -2.211, 0.0102, -0.276, 0.755, -0.107, 0.522, 1.203, 1.866, 1.723, 0.706, -0.295, -0.369
```

There are 6/13 = 0.461 cases of a more extreme difference. The true p-value 0.5956 is the result of infinitely many such simulations.

**Section 16.9: Multi-Sample (independent samples) F-test**
(analysis of variance test) for testing $H_0: \mu_1 = \mu_2 = ... = \mu_g$

**Assumptions, null model:** $Y_{ij} \sim_{iid} N(\mu, \sigma^2)$, for $i = 1,2, ..., g$ and $j = 1,...,n_i$. (a generalization of the two-sample model to $g$ samples).

**R functions:** aov, summary

**Example in the book:** Comparisons of Alzheimer’s treatments. I have created a data set having the same means and standard deviations as shown in Table 16.1 and you can read it as

```r
Alz.dat = read.table("http://westfall.ba.ttu.edu/isqs5347/Table16_1.txt")
Alz.dat
```
You can see that the within-group means and standard deviations are as shown in Table 16.1 by using the “aggregate” function of R:

```r
aggregate( Alz ~Trt, Alz.dat , mean)
aggregate( Alz ~Trt, Alz.dat , sd)
```

The ANOVA F test is calculated as

```r
summary(aov(Alz ~ Trt, data=Alz.dat))
```

with the following results:

<table>
<thead>
<tr>
<th></th>
<th>Df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Trt</td>
<td>4</td>
<td>11670</td>
<td>2918</td>
<td>32.79</td>
<td>1.19e-13</td>
</tr>
<tr>
<td>Residuals</td>
<td>52</td>
<td>4627</td>
<td>89</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

**Interpretation:** In about 1 out of every $10^{13}$ samples produced by $Y_i \sim_{iid} N(\mu, \sigma^2)$, with sample sizes as given, the overall difference between sample averages, as measured by the F statistic, will be more than 32.79. Thus, the observed differences between sample averages are not easily explained by chance alone. In other words, the observed differences between sample averages are not within the typical realm of differences that are seen when, in reality, $\mu_1 = \mu_2 = \ldots = \mu_5$. Thus it is very unlikely that the means $\mu_1, \mu_2, \ldots, \mu_5$ are all equal.

**Understanding the result through simulation, where you know the true parameters:**

Run the following code several times and keep track of the F statistics. Notice that the null model is true in this simulation, as $\mu_1 = \mu_2 = \ldots = \mu_5 = 50$.

```r
n.tot = nrow(Alz.dat)
Alz.r = rnorm(n.tot, 50, 10)
Alz.r.dat = data.frame(Alz.r, Trt)
summary(aov(Alz.r ~ Trt, data=Alz.r.dat))
```

I get (yours will vary) the following F-statistics from 5 such samples.

2.52, 1.021, 0.449, 1.484, 1.144
There are no cases where a simulated F is more extreme than the observed 32.79, given an estimated p-value of 0/5 = 0.0. The true p-value $1.19e^{-13}$ is the result of infinitely many such simulations.

Section 16.10: Two-sample (independent samples) interval for $\sigma_1/\sigma_2$ and test for $H_0: \sigma_1/\sigma_2 = 1$.

Assumptions: $Y_{ij} \sim \text{ind} N(\mu_i, \sigma_i^2)$, for $i = 1,2$ and $j = 1,\ldots,n_i$ (a generalization of the two-sample models above to allow for different variances.)

R function: var.test

Example in the book: The first two groups in the Alzheimer data set. The symbol “|” in the subset function means “or”.

```r
Alz.12 = subset(Alz.dat, Trt == "Trt1" | Trt == "Trt2")
Alz.12

var.test(Alz ~ Trt, data = Alz.12)
```

Result:

```
F test to compare two variances
data:  Alz by Trt
F = 0.86049, num df = 12, denom df = 11, p-value = 0.7965
alternative hypothesis: true ratio of variances is not equal to 1

95 percent confidence interval:
 0.2508988 2.8580869

sample estimates:
  ratio of variances
   0.8604856
```

Notice that the software gives a confidence interval for the ratio of variances. To see the interval for the ratio of standard deviations as given in the book, just take the square root:

```r
sqrt(var.test(Alz ~ Trt, data = Alz.12)$conf.int)
```
This gives

[1] 0.5008979 1.6905877

as in the book, p. 443.

**Interpretation:** Assuming the data were produced as $Y_{ij} \sim_{\text{ind}} N(\mu_i, \sigma_i^2)$, with sample sizes as given, we are 95% confident that $\sigma_1/\sigma_2$ lies between 0.5008979 and 1.6905877. In other words, in 95% of repeated samples $Y_{ij} \sim_{\text{ind}} N(\mu_i, \sigma_i^2)$, with sample sizes as given, the true, unknown value of $\sigma_1/\sigma_2$ will lie between similarly constructed endpoints.

**Understanding the result through simulation, where you know the true parameters:**

In my simulation code the true ratio is $\sigma_1/\sigma_2 = 8/5 = 1.6$.

```r
mu1 = 50
mu2 = 55
sig1 = 8
sig2 = 5

Alz1 = rnorm(13, mu1, sig1)
Alz2 = rnorm(12, mu2, sig2)
Alz.r.12 = c(Alz1, Alz2)
Trt.12 = Alz.r.12[,2]
sqrt(var.test(Alz.r.12 ~ Trt.12)$conf.int)

Results:
I get 0.7028909 2.3723370, but your results will vary.

**Interpretation:** In 95% of repeated simulated samples, similarly constructed endpoints will contain the value $\sigma_1/\sigma_2 = 8/5 = 1.6$. 