

# Example t-test

2025-03-04

```
#1. Import libraries and load packages
```

```
library(tidyverse)
library(lessR)
library(readxl)
library(BSDA)
library(RVAideMemoire) # shapiro
library(coin) # effect size
library(rstatix) # effect size
```

```
#2. Import your data
```

```
lizards <- read.csv("chap12e3HornedLizards.csv")
```

```
byf.shapiro(squamosalHornLength ~ Survival, data=lizards)
```

```
##
##  Shapiro-Wilk normality tests
##
## data:  squamosalHornLength by Survival
##
##           W      p-value
## killed 0.9345 0.0648207 .
## living 0.9606 0.0002234 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#var.test
```

```
var.test(squamosalHornLength ~ Survival, data=lizards)
```

```
##
##  F test to compare two variances
##
## data:  squamosalHornLength by Survival
## F = 1.0607, num df = 29, denom df = 153, p-value = 0.7859
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  0.6339331 1.9831398
## sample estimates:
## ratio of variances
##           1.060711
```

```
wilcox.test(squamosalHornLength ~ Survival,
            data = lizards,
            paired = FALSE,
            var.equal = TRUE,
            alternative='two.sided')
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: squamosalHornLength by Survival
## W = 1181.5, p-value = 0.00002366
## alternative hypothesis: true location shift is not equal to 0
```

```
lizards %>%
  wilcox_effsize(squamosalHornLength ~ Survival, paired = F)
```

```
## # A tibble: 1 x 7
##   .y.      group1 group2 effsize    n1    n2 magnitude
## * <chr>      <chr> <chr>   <dbl> <int> <int> <ord>
## 1 squamosalHornLength killed living  0.312   30  154 moderate
```

## References

<https://bookdown.org/ybrandvain/Applied-Biostats/tsample.html#a-two-sample-t-test-in-r>