

Teste_t_notebook

June 18, 2021

```
[21]: library(tidyverse)
library(patchwork)
options(repr.plot.width=5, repr.plot.height=5)
```

1 Distribuição t de Student: Biometrika. 1908, vol. 6, 1-15

1.1 Teste t de *Student* para uma média

```
[2]: X = c(2.92, 2.69, 2.99, 3.6, 2.83, 2.64, 2.53, 2.99, 2.67, 2.55)
X
```

1. 2.92 2. 2.69 3. 2.99 4. 3.6 5. 2.83 6. 2.64 7. 2.53 8. 2.99 9. 2.67 10. 2.55

```
[3]: (mu = 2.65) # média populacional segundo H0
(xb = mean(X)) # Média amostral
(n = length(X)) # Tamanho da amostra
(gl = n - 1) # Graus de liberdade
(s = sd(X)) # desvio padrão
(sxb = s/sqrt(n)) #erro padrão da média
```

2.65

2.841

10

9

0.316348963435423

0.100038325988926

```
[4]: (tc = (xb - 2.65) / sxb) # t calculado
```

1.90926825406038

Teste bicaudal

```
[5]: pt(-tc, df = gl, lower.tail = TRUE) * 2
```

0.0885652565561912

Usando a função do R

```
[6]: t.test(X, mu = 2.65, alternative = "two.sided")
```

One Sample t-test

```
data: X
t = 1.9093, df = 9, p-value = 0.08857
alternative hypothesis: true mean is not equal to 2.65
95 percent confidence interval:
 2.614698 3.067302
sample estimates:
mean of x
 2.841
```

Teste uniaucal

```
[7]: pt(-tc, df = gl, lower.tail = TRUE)
```

0.0442826282780956

Usando a função do R

```
[8]: t.test(X, mu = 2.65, alternative = "greater")
```

One Sample t-test

```
data: X
t = 1.9093, df = 9, p-value = 0.04428
alternative hypothesis: true mean is greater than 2.65
95 percent confidence interval:
 2.657618      Inf
sample estimates:
mean of x
 2.841
```

```
[9]: help(t.test)
```

1.2 Teste t de *Student* para duas amostras: Chacais dourados

1.2.1 Teste t de Welch - variâncias heterogêneas

Existe evidência de que o tamanho das mandíbulas de Chacais dourados seja diferente em machos e fêmeas?

```
[10]: jackal <- read.csv('datasets/jackal.csv', sep = ';', header = TRUE)
jackal
```

Comprimento	Sexo
120	Macho
107	Macho
110	Macho
116	Macho
114	Macho
111	Macho
113	Macho
117	Macho
114	Macho
112	Macho
110	Femea
111	Femea
107	Femea
108	Femea
110	Femea
105	Femea
107	Femea
106	Femea
111	Femea
111	Femea

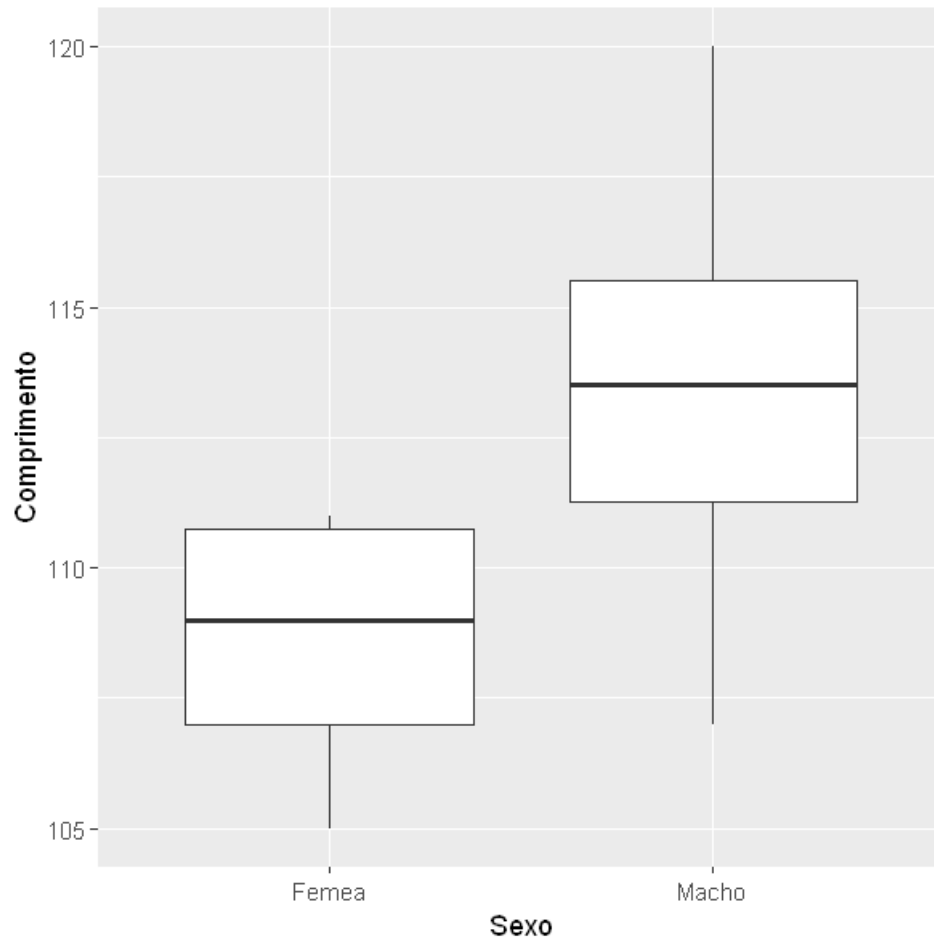
```
[11]: jackal %>% group_by(Sexo) %>%
      summarize(Medias = mean(Comprimento))
```

Sexo	Medias
Femea	108.6
Macho	113.4

```
[12]: jackal %>% group_by(Sexo) %>%
      summarize(Desvio = sd(Comprimento))
```

Sexo	Desvio
Femea	2.270585
Macho	3.717825

```
[13]: ggplot(jackal, aes(x = Sexo, y = Comprimento)) +
      geom_boxplot()
```



```
[14]: t.test(Comprimento ~ Sexo, data = jackal, alternative = 'two.sided', var.equal =
      FALSE) # Variâncias heterogêneas
```

Welch Two Sample t-test

data: Comprimento by Sexo

t = -3.4843, df = 14.894, p-value = 0.00336

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

-7.738105 -1.861895

sample estimates:

mean in group Femea	mean in group Macho
108.6	113.4

1.2.2 Teste pareado: Hoffman et. al. (2003)

Dados retirados de:

Hoffmann, William A., Birgit Orthen, and Paula Kielse Vargas do Nascimento. Comparative fire ecology of tropical savanna and forest trees. *Functional Ecology* 17.6 (2003): 720-726.

```
[15]: hof = read.csv("datasets/Hoffman_et_al_2003.csv", header = TRUE, sep = ";", dec_
      ↪= ',')
      hof
```

Gênero	Cerrado	Floresta
Aspidosperma	0.82	1.28
Byrsonima	0.52	1.10
Didymopanax	0.43	1.36
Guapira	0.74	0.65
Hymenaea	1.38	1.30
Miconia	0.49	1.09
Myrsine	0.69	1.97
Ouratea	1.66	1.62
Salacia	0.77	0.47
Vochysia	1.09	1.92

```
[16]: n = nrow(hof)

hof_errbar = hof %>% summarise_at(
  vars(Cerrado, Floresta), list(media = mean, desvio = sd)
) %>%
gather(indicador,value,Cerrado_media:Floresta_desvio) %>%
separate(indicador, into = c("Vegetacao", "indicador")) %>%
spread(indicador, value)

hof_diff = hof %>%
  mutate(Dif = Cerrado - Floresta)

df = data.frame(x = 1, xend = 2,
  y = hof_errbar[1,3],
  yend = hof_errbar[2,3])

gerrbar = ggplot(data = hof_errbar,
  aes(x = Vegetacao, y = media)) +
  geom_errorbar(aes(ymin = media - (desvio/sqrt(n))*1.96,
    ymax = media + (desvio/sqrt(n))*1.96), width=.1) +
  geom_point(size = 3) +
  theme_classic(base_size = 20) +
  theme(axis.title.y = element_text(size = 17)) +
  xlab('') + ylab('Espessura relativa da casca') +
  geom_segment(aes(x = x, y = y, xend = xend, yend = yend),
    colour = "red", linetype = 2, data = df)
```

```

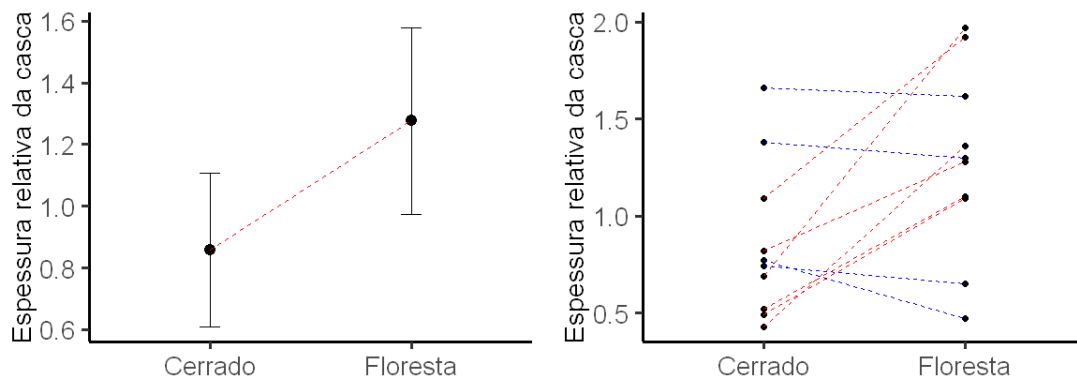
gpaired = ggplot(data = hof) +
  geom_point(aes(x = rep(1, nrow(hof)), y = Cerrado)) +
  geom_point(aes(x = rep(2, nrow(hof)), y = Floresta)) +
  scale_x_continuous(name = '', breaks = c(1,2),
                     labels = colnames(hof)[-1],
                     limits = c(0.5, 2.5)) +
  ylab("Espessura relativa da casca") +
  theme_classic(base_size = 20) +
  theme(axis.title.y = element_text(size = 17)) +
  geom_segment(aes(x = rep(1, nrow(hof)), y = Cerrado,
                  xend = rep(2, nrow(hof)), yend = Floresta),
              colour = ifelse(test = hof_diff$Dif <= 0, yes = "red", no = "blue"), linetype = 2)

```

```

[17]: options(repr.plot.width=10, repr.plot.height=4)
gerrbar + gpaired

```



O teste t

```

[18]: ttest_casca = t.test(hof$Cerrado, hof$Floresta,
                          alternative = 'two.sided',
                          paired = TRUE)

ttest_casca

```

Paired t-test

```

data: hof$Cerrado and hof$Floresta
t = -2.5185, df = 9, p-value = 0.03285
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
-0.79156068 -0.04243932

```

```
sample estimates:
mean of the differences
      -0.417
```

O teste t pareado é **equivalente** ao teste t para uma amostra se este for conduzido sobre a diferença entre os pares de observações.

```
[19]: hof_diff
```

Gênero	Cerrado	Floresta	Dif
Aspidosperma	0.82	1.28	-0.46
Byrsonima	0.52	1.10	-0.58
Didymopanax	0.43	1.36	-0.93
Guapira	0.74	0.65	0.09
Hymenaea	1.38	1.30	0.08
Miconia	0.49	1.09	-0.60
Myrsine	0.69	1.97	-1.28
Ouratea	1.66	1.62	0.04
Salacia	0.77	0.47	0.30
Vochysia	1.09	1.92	-0.83

```
[20]: t.test(hof_diff$Dif, mu = 0, alternative = 'two.sided')
```

One Sample t-test

```
data: hof_diff$Dif
t = -2.5185, df = 9, p-value = 0.03285
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.79156068 -0.04243932
sample estimates:
mean of x
      -0.417
```