Acute Stress Reduction Analysis: Music vs. Podcast Intervention

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Contents

Data analysis for an experiment that investigated whether listening to music (experimental group) for 25 minutes versus listening to a podcast (control group) for 25 minutes reduces participants' stress levels

Preparing data

```r
library(readxl)      #read .xlsx files
library(haven)       #treat data
library(ggplot2)     #draw images
```

```
## Warning: pacote 'ggplot2' foi compilado no R versão 4.4.3
```

```r
library(gridExtra)   #treat images
library(nparLD)      #non parametric ANOVA
```

```
## Warning: pacote 'nparLD' foi compilado no R versão 4.4.3
```

```
## Carregando pacotes exigidos: MASS
```

```r
library(dplyr)       #allow code in pipelines
```

```
##
## Anexando pacote: 'dplyr'
```

```
## O seguinte objeto é mascarado por 'package:MASS':
##
##     select
```

```
## O seguinte objeto é mascarado por 'package:gridExtra':
##
##     combine
```

```
## Os seguintes objetos são mascarados por 'package:stats':
##
##     filter, lag


## Os seguintes objetos são mascarados por 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
library(rstatix)    #estimate effect sizes
```

```
##
## Anexando pacote: 'rstatix'


## O seguinte objeto é mascarado por 'package:MASS':
##
##     select


## O seguinte objeto é mascarado por 'package:stats':
##
##     filter
```

```r
dado <- read_excel("~/Isabela/Dados_Agudo.xlsx")
dado$Grupo <- ifelse(dado$Grupo == "Controle", "Control", "Experimental")
dado <- as_factor(dado)
table(dado$Grupo)
```

```
##
##      Control Experimental
##           26           28
```

Preparing salivary cortisol data

The values for salivary cortisol (Cortpre and Cortpos) were multiplied by 27.7 to convert the units from nmol/L to ng/dL. This conversion is necessary because some reference ranges and comparative studies report cortisol levels in ng/dL. The factor 27.7 is derived from the molecular weight of cortisol (approximately 362.5 g/mol), allowing for consistent interpretation and comparison of results across different measurement systems.

The data do not follow a normal distribution.

```r
dado$Cortpre <- dado$Cortpre * 27.7
dado$Cortpos <- dado$Cortpos * 27.7
shapiro.test(dado$Cortpre)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  dado$Cortpre
## W = 0.73659, p-value = 1.677e-08
```

```r
shapiro.test(dado$Cortpos)
```

```
## 
##  Shapiro-Wilk normality test
## 
## data:  dado$Cortpos
## W = 0.51903, p-value = 4.822e-12
```

```r
# Subset data by group
intervention_data <- dado[dado$Grupo == "Experimental", ]
control_data <- dado[dado$Grupo == "Control", ]

# Create a combined boxplot and scatter plot for Cortpre in the Experimental group
combined_plot_intervention_pre <- ggplot(intervention_data, aes(x = Grupo, y = Cortpre)) +
  geom_boxplot(position = position_dodge(width = 0.8), color = "black", fill = "white") +
  geom_jitter(position = position_jitter(width = 0.2), size = 2) +
  labs(title = "Before",
       x = "",
       y = "Cortisol Level (µg/dL)") +
  ylim(0, 45) +
  scale_x_discrete(labels = c("Experimental")) +
  theme(legend.position = "none")

# Create a combined boxplot and scatter plot for Cortpos in the Experimental group
combined_plot_intervention_pos <- ggplot(intervention_data, aes(x = Grupo, y = Cortpos)) +
  geom_boxplot(position = position_dodge(width = 0.8), color = "black", fill = "white") +
  geom_jitter(position = position_jitter(width = 0.2), size = 2) +
  labs(title = "After",
       x = "",
       y = "Cortisol Level (µg/dL)") +
  ylim(0, 45) +
  scale_x_discrete(labels = c("Experimental")) +
  theme(legend.position = "none")

# Create a combined boxplot and scatter plot for Cortpre in the Control group
combined_plot_control_pre <- ggplot(control_data, aes(x = Grupo, y = Cortpre)) +
  geom_boxplot(position = position_dodge(width = 0.8), color = "black", fill = "white") +
  geom_jitter(position = position_jitter(width = 0.2), size = 2) +
  labs(title = "Before",
       x = "",
       y = "Cortisol Level (µg/dL)") +
  ylim(0, 45) +
  scale_x_discrete(labels = c("Control")) +
  theme(legend.position = "none")

# Create a combined boxplot and scatter plot for Cortpos in the Control group
combined_plot_control_pos <- ggplot(control_data, aes(x = Grupo, y = Cortpos)) +
  geom_boxplot(position = position_dodge(width = 0.8), color = "black", fill = "white") +
  geom_jitter(position = position_jitter(width = 0.2), size = 2) +
  labs(title = "After",
       x = "",
       y = "Cortisol Level (µg/dL)") +
  ylim(0, 45) +
```
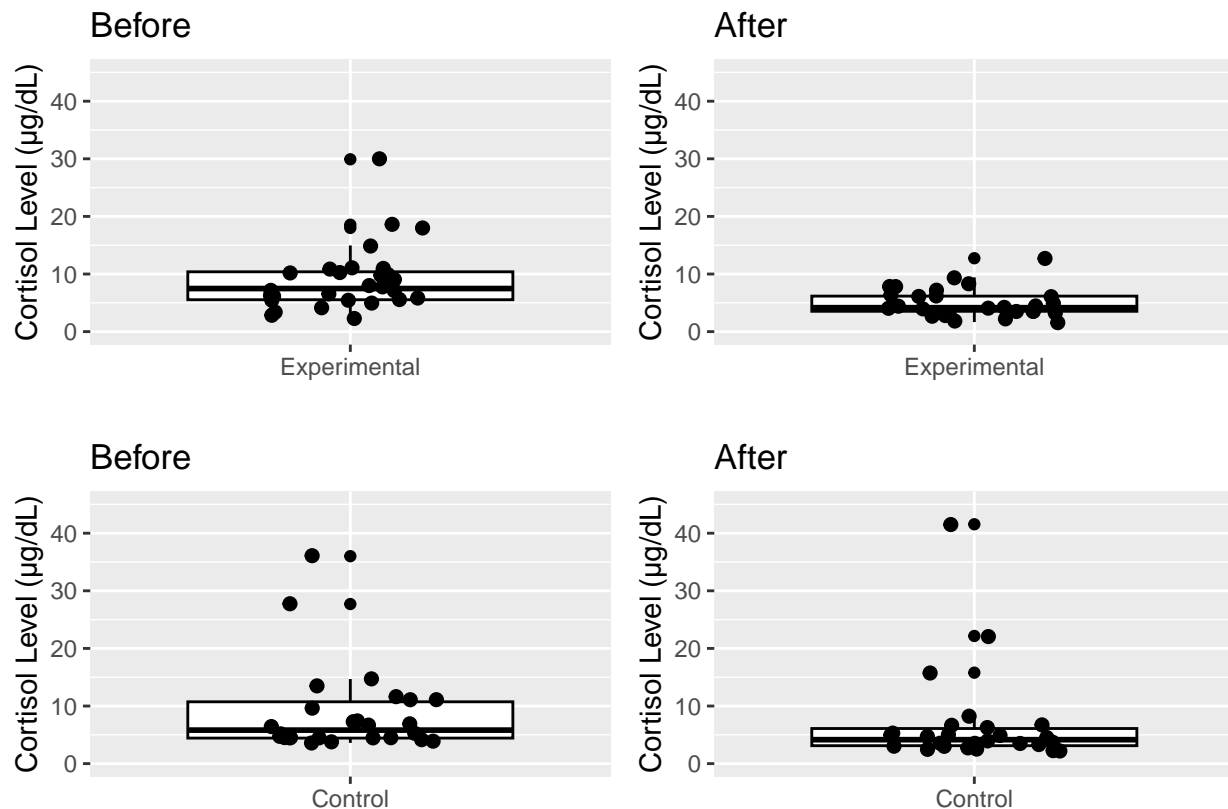
```
    scale_x_discrete(labels = c("Control")) +
    theme(legend.position = "none")

# Display the plots side by side
(grid_arrangement <- grid.arrange(combined_plot_intervention_pre, combined_plot_intervention_pos, combin
```



```
## TableGrob (2 x 2) "arrange": 4 grobs
##   z     cells     name              grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
## 3 3 (2-2,1-1) arrange gtable[layout]
## 4 4 (2-2,2-2) arrange gtable[layout]
```

Transforming data em long style

```
dado_longo <- read_excel("~/Isabela/dado_longo.xlsx")
dado_longo$Cort <- dado_longo$Cort * 27.7



dado_longo <- dado_longo %>%
  mutate(
    Grupo = recode(Grupo,
```

```
                  "Controle" = "Control",
                  "Intervenção" = "Experimental"),
    Tempo = recode(Tempo,
                  "1" = "Before",
                  "2" = "After")
  ) %>%
  rename(
    Group = Grupo,
    Time = Tempo
 )



dado_longo <- dado_longo %>%
  mutate(ID = rep(1:(nrow(dado_longo) / 2), each = 2))


dado_longo$Grupo <- as.factor(dado_longo$Group)
dado_longo$Tempo <- as.factor(dado_longo$Time)
```

Nonparametric Factorial Repeated Measures ANOVA

There are no diferences beetween the to groups.

```
mod_1x1 <- nparLD(formula = Cort ~ Time*Group, # Fórmula como ANOVA
                  data = dado_longo,
                  subject= dado_longo$ID, # Variável do sujeito
                  description = F  # Descrição da análise

)
```

```
##  F1 LD F1 Model
##  -----------------------
##  Check that the order of the time and group levels are correct.
##  Time level:   Before After
##  Group level:   Experimental Control
##  If the order is not correct, specify the correct order in time.order or group.order.
```

```
summary(mod_1x1)
```

```
## Model:
## F1 LD F1 Model
##
## Call:
## Cort ~ Time * Group
##
## Relative Treatment Effect (RTE):
##                               RankMeans Nobs        RTE
## GroupExperimental              56.21429   56 0.5158730
## GroupControl                   52.65385   52 0.4829060
## TimeBefore                     67.13874   54 0.6170253
## TimeAfter                      41.72940   54 0.3817537
## GroupExperimental:TimeBefore   70.64286   28 0.6494709
```

```
## GroupExperimental:TimeAfter   41.78571   28 0.3822751
## GroupControl:TimeBefore       63.63462   26 0.5845798
## GroupControl:TimeAfter        41.67308   26 0.3812322
##
## Wald-Type Statistc (WTS):
##             Statistic df      p-value
## Group       0.2751637  1 5.998888e-01
## Time       40.6433889  1 1.827043e-10
## Group:Time  0.7483208  1 3.870084e-01
##
## ANOVA-Type Statistc (ATS):
##             Statistic df      p-value
## Group       0.2751637  1 5.998888e-01
## Time       40.6433889  1 1.827043e-10
## Group:Time  0.7483208  1 3.870084e-01
##
## Modified ANOVA-Type Statistic for the Whole-Plot Factors:
##       Statistic df1    df2   p-value
## Group 0.2751637   1 51.9827 0.6021187
```

There is no difference beetween groups over time, but there are within-group effects. Besides that, we can investigate the magnitude of this difference internally.

```r
data_wilcox_exp <- data.frame(
  Cortisol_pre = intervention_data$Cortpre,
  Cortisol_pos = intervention_data$Cortpos
)

data_wilcox_exp <- stack(data_wilcox_exp)

# Executar o teste de Wilcoxon
wilcox_result_exp <- wilcox.test(values ~ ind, data = data_wilcox_exp)
```

```
## Warning in wilcox.test.default(x = DATA[[1L]], y = DATA[[2L]], ...): não é
## possível computar o valor de p exato com o de desempate
```

```r
# Imprimir os resultados
print(wilcox_result_exp)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  values by ind
## W = 599.5, p-value = 0.0006853
## alternative hypothesis: true location shift is not equal to 0
```

```r
effect <- wilcox_effsize(values ~ ind, data= data_wilcox_exp, paired = TRUE,
                         ci=TRUE, ci.type= "bca", nboot= 1000)
effect
```

```
## # A tibble: 1 x 9
##   .y.    group1       group2   effsize    n1    n2 conf.low conf.high magnitude
## * <chr>  <chr>        <chr>      <dbl> <int> <int>    <dbl>     <dbl> <ord>
## 1 values Cortisol_pre Cortisol~  0.850    28    28     0.74      0.87 large
```

```r
# Criar um objeto de dados
data_wilcox_C <- data.frame(
  Cortisol_pre = control_data$Cortpre,
  Cortisol_pos = control_data$Cortpos
)

# Criar um objeto de dados no formato longo a partir de dados_wilcox
data_wilcox_C <- stack(data_wilcox_C)

# Executar o teste de Wilcoxon
wilcox_result_C <- wilcox.test(values ~ ind, data = data_wilcox_C)
```

```
## Warning in wilcox.test.default(x = DATA[[1L]], y = DATA[[2L]], ...): não é
## possível computar o valor de p exato com o de desempate
```

```r
# Imprimir os resultados
print(wilcox_result_C)
```

```
##
##   Wilcoxon rank sum test with continuity correction
##
## data:  values by ind
## W = 475, p-value = 0.0123
## alternative hypothesis: true location shift is not equal to 0
```

```r
effectC <- wilcox_effsize(values ~ ind, data= data_wilcox_C,
                          ci=TRUE, ci.type= "bca", nboot= 1000)
effectC
```

```
## # A tibble: 1 x 9
##   .y.    group1       group2   effsize    n1    n2 conf.low conf.high magnitude
## * <chr>  <chr>        <chr>      <dbl> <int> <int>    <dbl>     <dbl> <ord>
## 1 values Cortisol_pre Cortisol~  0.348    26    26     0.08      0.58 moderate
```

The effect is larger in the experimental group.

```r
sessionInfo()
```

```
## R version 4.4.2 (2024-10-31 ucrt)
## Platform: x86_64-w64-mingw32/x64
## Running under: Windows 11 x64 (build 26100)
##
## Matrix products: default
##
##
## locale:
## [1] LC_COLLATE=Portuguese_Brazil.utf8  LC_CTYPE=Portuguese_Brazil.utf8
## [3] LC_MONETARY=Portuguese_Brazil.utf8 LC_NUMERIC=C
## [5] LC_TIME=Portuguese_Brazil.utf8
##
## time zone: America/Sao_Paulo
```

```
## tzcode source: internal
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] rstatix_0.7.2 dplyr_1.1.4   nparLD_2.2    MASS_7.3-61   gridExtra_2.3
## [6] ggplot2_3.5.2 haven_2.5.4   readxl_1.4.3
##
## loaded via a namespace (and not attached):
##  [1] gtable_0.3.6      xfun_0.52         coin_1.4-3        lattice_0.22-6
##  [5] vctrs_0.6.5       tools_4.4.2       generics_0.1.3    stats4_4.4.2
##  [9] parallel_4.4.2    sandwich_3.1-1    tibble_3.2.1      pkgconfig_2.0.3
## [13] Matrix_1.7-1      lifecycle_1.0.4   compiler_4.4.2    farver_2.1.2
## [17] munsell_0.5.1     codetools_0.2-20  carData_3.0-5     htmltools_0.5.8.1
## [21] yaml_2.3.10       Formula_1.2-5     pillar_1.10.2     car_3.1-3
## [25] tidyr_1.3.1       boot_1.3-31       abind_1.4-8       multcomp_1.4-26
## [29] tidyselect_1.2.1  digest_0.6.37     mvtnorm_1.3-3     purrr_1.0.2
## [33] labeling_0.4.3    forcats_1.0.0     splines_4.4.2     fastmap_1.2.0
## [37] grid_4.4.2        colorspace_2.1-1  cli_3.6.4         magrittr_2.0.3
## [41] survival_3.7-0    utf8_1.2.4        broom_1.0.8       TH.data_1.1-3
## [45] libcoin_1.0-10    withr_3.0.2       scales_1.3.0      backports_1.5.0
## [49] rmarkdown_2.29    matrixStats_1.5.0 cellranger_1.1.0  zoo_1.8-14
## [53] modeltools_0.2-23 hms_1.1.3         evaluate_1.0.3    knitr_1.50
## [57] rlang_1.1.5       glue_1.8.0        rstudioapi_0.17.1 R6_2.6.1
```