

Instructions: Lab 1 Group Data Analysis

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Download *Lab 1 Group Data Files*

1. Move all the files in the `*Move_Files_Folder` in your `"my_lab_1.0_additional_files"` folder that is inside your lab report folder from last week.
2. Move the `my_lab_1.5b_Group_Results_broken.Rmd` into your lab report folder
3. Delete the `my_lab_1.5b_Group_Results.Rmd` file inside your lab report folder

Fix the `my_lab_1.5b_Group_Results_broken.Rmd` file

1. Open the Lab 1 project in RStudio
2. Open the `my_lab_1.5b_Group_Results_broken.Rmd` file so you can edit it in RStudio

There are nine code chunks that are broken. One at a time fix each chunk using the code below. When you fix a chunk, choose "Run All" from the "Run" tab to make sure that everything works up to the point that you have fixed. The correct code is given here.

brokenGp1

This code chunk reads in the group data file. The file contains the essential results from each person in the class from last week's experiment on face recognition.

```
# group data file name: lab1_group_data_wide_2018_Fall.csv

# Read in group data in wide format from text file:
file_name <- "lab1_group_data_wide_2018_Fall.csv"
df_wide <- read.csv(file.path(path_to_additional_files, file_name))
```

brokenGp2

This code chunk computes the effect sizes of eyes and of model for each subject to be used the bootstrap evaluation.

```
# add within-subject eyes effect size on d-sub-a to data frame
df_wide$eyes_effect <- (df_wide$da_with_eyes - df_wide$da_no_eyes)

# add within subject model effect size on AIC to data frame
df_wide$model_effect <- df_wide$htm_AIC - df_wide$sdt_AIC

kable(head(df_wide, 10), digits = 2, caption = "The wide format data of the first 10 subjects.",
      col.names = c("subj", "sect",
                    "d~a~ no eyes", "d~a~ eyes", "sdt AIC",
                    "htm no eyes", "htm eyes", "htm AIC",
                    "eyes ES", "model ES"))
```

brokenGp3

This code chunk shows how to compute means and standard deviations of the aic measure and print a nice table of the results.

```
aic_summarystats <- with(df, cbind(mean = tapply(aic, mod, mean),
                                     std.dev = tapply(aic, mod, sd),
                                     n = tapply(aic, mod, length)))
kable(aic_summarystats, digits = 1,
      caption = "AIC for sdt and HTM Models")
```

brokenGp4

This code chunk shows how to compute means and standard deviations of the signal detection sensitivity measure, d_a , and print a nice table of the results.

```
da.summarystats <- with(df, cbind(mean = tapply(da, eyes, mean),
                                     std.dev = tapply(da, eyes, sd),
                                     n = tapply(da, eyes, length)))
kable(da.summarystats, digits = 2,
      col.names = c("Mean SDT d-sub-a", "Standard Deviation", "N"),
      caption = "SDT sensitivity (d~a~) for eyes and no-eyes")
```

brokenGp5

This code chunk shows how to compute means and standard deviations of the high threshold model sensitivity measure, p (the probability that a signal is above threshold), and print a nice table of the results.

```
p.summarystats <- with(df, cbind(mean = tapply(htm_p, eyes, mean),
                                     std.dev = tapply(htm_p, eyes, sd),
                                     n = tapply(htm_p, eyes, length)))
kable(p.summarystats, digits = 2,
      col.names = c("Mean HTM p", "Standard Deviation", "N"),
      caption = "HTM sensitivity (p) for eyes and no-eyes")
```

brokenGp6

This code chunk computes the bootstrap analysis of the effect size for eyes (no eyes vs eyes) and the effect size of model (SDT vs HTM). After you get this chunk working, you could change the `plot` argument from `plot = FALSE` to `plot = TRUE` to show a histogram of the bootstrap results. Change it back to `FALSE` so it does not appear in your final report, unless of course you want to keep it.

```
# compute effect size and confidence interval with bootstrap
n.boot = 5000
# eyes effect on da
bs.da.u <- bootES(data = df_wide,
                  R = n.boot,
                  data.col = "eyes_effect",
                  effect.type = "unstandardized",
                  plot = FALSE)

bs.da.d <- bootES(data = df_wide,
                  R = n.boot,
                  data.col = "eyes_effect",
                  effect.type = "cohens.d",
                  plot = FALSE)

# model effect on AIC
bs.aic.u <- bootES(data = df_wide,
                  R = n.boot,
                  data.col = "model_effect",
                  effect.type = "unstandardized",
                  plot = FALSE)

bs.aic.d <- bootES(data = df_wide,
                  R = n.boot,
                  data.col = "model_effect",
                  effect.type = "cohens.d",
                  plot = FALSE)
```

brokenGp7

This code chunk computes a linear, mixed-effects model of the effects of detection model type and lab section on the goodness of fit of the model to the data.

```
lmer.mod.aic <- lmer(aic ~ mod * section + (1 | subj), data = df)

analysis_aic <- anova(lmer.mod.aic)
kable(analysis_aic, digits = c(2, 2, 1, 1, 2, 5),
      caption = "Linear mixed-effects model of AIC")
```

brokenGp8

This code chunk plots the probability and z-score ROC curves for the signal detection model based on the aggregated data of all subjects. It uses plot functions that are written by us for this lab. The code that defines these plot functions is in the additional files folder and is read into your R environment in the top of the script in the first code chunk.

```
# read in the grf RScorePlus file ("lab1_all_gauss_grf.txt")
file_name <- "lab1_all_gauss_grf.txt"

df_grf_all <- read.delim(file.path(path_to_additional_files, file_name), header = TRUE) # reads tab

par(mfcol = c(1, 2))
plot_proc(df_grf_all, main = "Aggregated pROC")
plot_zroc(df_grf_all, main = "Aggregated zROC")
par(mfcol = c(1, 1))
```

brokenGp9

In this code chunk the linear, mixed-effects regression model is computed to test the effect of eyes and of lab section on the SDT sensitivity measure, d_a . It also illustrates how you print a nice ANOVA table of the results.

```
lmer.mod.da <- lmer(da ~ eyes * section + (1 | subj), data = df)
analysis_da <- anova(lmer.mod.da)
pFda <- analysis_da$Pr[1]
kable(analysis_da, digits = 2,
      caption = "Linear mixed-effects model of  $d_a$ ~.")
```

Final Report

Once all is working correctly, change the name of of the file to remove the `_broken`. Use the **Save As** command under the **File** menu of RStudio. Now when you knit your whole report, this group analysis section will be included.