d-prime_analyse1

```r
library(tidyverse)
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.4     v readr     2.1.5
v forcats   1.0.1     v stringr   1.5.2
v ggplot2   4.0.0     v tibble    3.3.0
v lubridate 1.9.4     v tidyr     1.3.1
v purrr     1.1.0
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becon
```

```r
path <- "~/Desktop/Python/EM2-audio/experiment/control_experiment/data_detection/gammel_data'


all_files <- fs::dir_ls(path, glob = "*.csv")
raw_data <- map_dfr(all_files, read_csv, .id = "source_file")
```

```
New names:
Rows: 224 Columns: 25
-- Column specification
-------------------------------------------------------- Delimiter: "," chr
(11): signal_type, prime_file, correct_word, babbling_file, mask1_file, ... dbl
(11): compression_level, practice.thisRepN, practice.thisTrialN, practic... lgl
(3): thisRow.t, notes, ...25
i Use `spec()` to retrieve the full column specification for this data. i
Specify the column types or set `show_col_types = FALSE` to quiet this message.
New names:
Rows: 224 Columns: 25
-- Column specification
```

```
-------------------------------------------------------- Delimiter: "," chr
(11): signal_type, prime_file, correct_word, babbling_file, mask1_file, ... dbl
(11): compression_level, practice.thisRepN, practice.thisTrialN, practic... lgl
(3): thisRow.t, notes, ...25
i Use `spec()` to retrieve the full column specification for this data. i
Specify the column types or set `show_col_types = FALSE` to quiet this message.
* `` -> `...25`
```

```r
tidy_data <- raw_data %>%

  # --- Remove Practice Trials ---
  # This logic is still correct. We keep rows where the 'main'
  # loop was running (i.e., 'main.thisN' is not NA).
  filter(!is.na(main.thisN)) %>%

  # --- Select Only the Useful Columns ---
  # We use the REAL column names from your glimpse() output.
  # Use backticks `` for names with spaces like `Participant ID`.
  select(
    # Participant info
    participant = `Participant ID`, # Rename `Participant ID` to `participant`
    session = Session,          # Rename `Session` to `session`

    # Trial info
    trial_num = main.thisN,     # This is the trial number

    # Experiment condition columns (from your data)
    signal_type,
    compression_level,
    prime_file,
    correct_word,
    babbling_file,
    mask1_file,
    mask2_file,

    # Dependent Variables (the participant's response)
    key_pressed = response_key, # Rename `response_key` to `key_pressed`
    rt,
    trial_outcome
  ) %>%

  # --- Fix Data Types ---
  # Convert columns to the correct type for analysis
  mutate(
    # Convert RT to numeric
    rt = as.numeric(rt),

    # Convert key identifiers to factors (categorical variables)
    participant = as.factor(participant),
    session = as.factor(session),
    key_pressed = as.factor(key_pressed),

    # Convert valences to factors
    signal_type = as.factor(signal_type),
    trial_outcome = as.factor(trial_outcome)
  )

# 4. SHOW THE RESULT
#-------------------------------------------------------------------
# Print the first few rows of your new, clean data frame
print(tidy_data)
```

```
# A tibble: 448 x 13
   participant session trial_num signal_type compression_level prime_file
   <fct>       <fct>       <dbl> <fct>                   <dbl> <chr>
 1 johanv1     001            -1 absent                    0.1 SILENCE
 2 johanv1     001            -1 absent                    0.5 SILENCE
 3 johanv1     001            -1 present                   0.5 sæde_compressed.~
 4 johanv1     001            -1 absent                    0.7 SILENCE
 5 johanv1     001            -1 absent                    0.4 SILENCE
 6 johanv1     001            -1 absent                    0.3 SILENCE
 7 johanv1     001            -1 present                   0.2 talent_compresse~
 8 johanv1     001            -1 present                   0.6 venlig_compresse~
 9 johanv1     001            -1 absent                    0.2 SILENCE
10 johanv1     001            -1 absent                    0.6 SILENCE
# i 438 more rows
# i 7 more variables: correct_word <chr>, babbling_file <chr>,
#   mask1_file <chr>, mask2_file <chr>, key_pressed <fct>, rt <dbl>,
#   trial_outcome <fct>
```

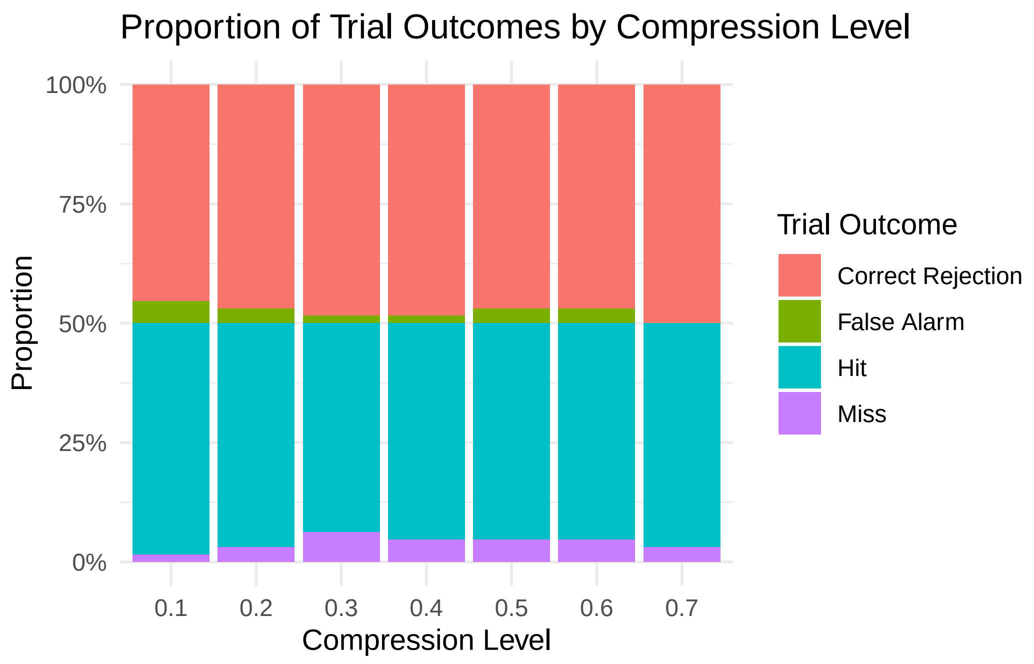
```r
# Show a summary of the data frame structure
glimpse(tidy_data)
```

```
Rows: 448
```

```
Columns: 13
$ participant       <fct> johanv1, johanv1, johanv1, johanv1, johanv1, johanv1~
$ session           <fct> 001, 001, 001, 001, 001, 001, 001, 001, 001, 001, 00~
$ trial_num         <dbl> -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, ~
$ signal_type       <fct> absent, absent, present, absent, absent, absent, pre~
$ compression_level <dbl> 0.1, 0.5, 0.5, 0.7, 0.4, 0.3, 0.2, 0.6, 0.2, 0.6, 0.~
$ prime_file        <chr> "SILENCE", "SILENCE", "sæde_compressed.wav", "SILENC~
$ correct_word      <chr> NA, NA, "sæde", NA, NA, NA, "talent", "venlig", NA, ~
$ babbling_file     <chr> "bab5.wav", "bab9.wav", "bab21.wav", "bab4.wav", "ba~
$ mask1_file        <chr> "rotte_reversed.wav", "avis_reversed.wav", "patent_r~
$ mask2_file        <chr> "humor_reversed.wav", "kande_reversed.wav", "talent_~
$ key_pressed       <fct> z, z, z, z, z, z, m, z, z, z, m, m, m, m, m, m, z, m~
$ rt                <dbl> 1.4244805, 1.0472129, 0.9887177, 0.9378766, 4.605587~
$ trial_outcome     <fct> Correct Rejection, Correct Rejection, Miss, Correct ~
```

```r
# Load the ggplot2 library (part of tidyverse)
library(ggplot2)

# Create the 100% stacked bar chart
# We use the 'tidy_data' data frame from the previous step

compression_plot <- ggplot(tidy_data, aes(x = factor(compression_level), fill = trial_outcome

  # geom_bar(position = "fill") creates a 100% stacked bar chart,
  # which is perfect for comparing proportions across groups.
  geom_bar(position = "fill") +

  # Add clear labels
  labs(
    title = "Proportion of Trial Outcomes by Compression Level",
    x = "Compression Level",
    y = "Proportion",
    fill = "Trial Outcome"
  ) +

  # Format the y-axis to show percentages (e.g., 25%, 50%)
  scale_y_continuous(labels = scales::percent_format()) +

  # Apply a clean theme
  theme_minimal()

# Save the plot to a file
```

```r
ggsave("compression_outcomes_plot.png", plot = compression_plot, width = 10, height = 6)

# Print the plot object so it displays
print(compression_plot)
```


Proportion of Trial Outcomes by Compression Level
Proportion
Compression Level
Trial Outcome
Correct Rejection
False Alarm
Hit
Miss