C91AR | Advanced Statistics using R

Lecture 5: Screening Data & Tests of Normality

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Contents

1 Packages for today

```
# load packages
pacman::p_load(tidyverse,
               snakecase,
               psych,
               summarytools,
               messy,
               tidyplots)
```

2 Reading for Today

Chapter 12: Screening data

3 Aims for this module

- I'll show you how to deliberately untidy data using the **messy** package
- We'll do some more label tidying
- Examined the case of listwise deletion (the reading covers other approaches)
- Test distribution normality
- Show you **tidyplots** as an alternative to **ggplot2**

4 Read in tidy data

```
# read in dataset
df <-
  read_csv("data_tidy/c91ar_maze_data.csv",
           col_types = "cccdccd")
```

5 Maze study metadata

- `id` = anon participant code
- `condition` = ToM manipulation with three levels (Baseline, No-ToM, and ToM)
- `trial` = experiment trial
- `rt` = response time
- `follow robot` = whether participants followed the robot's suggestion
- `accuracy` = whether or not their maze route selection was correct
- `conf` = participants self reported confidence for each route decision.

6 Untidy the dataset

```
# make script reproducible
set.seed(1234)

# untidy our maze data
df_messy <-
  df |>
  make_missing(cols = "follow_robot",
               missing = NA,
               messiness = 0.05) |> # add missing values to follow_robot
```

```
  make_missing(cols = "rt",
               missing = NA,
               messiness = 0.3) |> # add missing and erroneous values to rt
  add_special_chars(cols = "condition") # add special chars to condition levels
```

7 Examine the data

```
df_messy |>
  dfSummary()
```

- What do you notice from the output of `dfSummary`?
- What have we done??

8 Recode our condition levels

- Check variable levels

```
unique(df_messy$condition) # what a mess!
```

- What a mess! This was created using the `messy::add_special_chars` function
- Tidying up the mess

```
# using a combination of case_when and str_detect
df_messy_levels <-
  df_messy |>
  mutate(
    condition = str_replace_all(condition,
                                "[^[:alnum:][:space:]]", "")
  )

unique(df_messy_levels$condition)
```

9 Still not happy with the level labels?

```
# Probably we do a little more tidying
df_messy_levels <-
  df_messy_levels |>
  mutate(condition = case_match(condition,
                                "NoToM" ~ "No_ToM",
                                "baseline" ~ "Baseline",
                                .default = condition))

unique(df_messy_levels$condition)
```

10 Tidy up our object list

- You can see how our list of objects is growing in the global environment.
- You may decide at a certain point to drop some of the objects to keep the list short
- Let's update `df_messy` and remove `df_messy_levels`

```
# Update df_messy with df_messy_levels values
df_messy <-
  df_messy_levels

# remove df_messy levels - as this is now contained in df_messy
rm(df_messy_levels)

# check data
unique(df_messy$condition)
```

11 Listwise deletion

- The `drop_na` function from **`tidyr`** removes any row of data that contains an NA (i.e., missing) value
- But this may not be ideal as we might end up removing a lot of useful observations from the dataset
- It may only pertain to a variable that is not integral to our research question, so could be ignored

12 Using `drop_na`

```
df_messy_na <-
  df_messy |>
  drop_na()
```

- What percentage of the observations is missing?

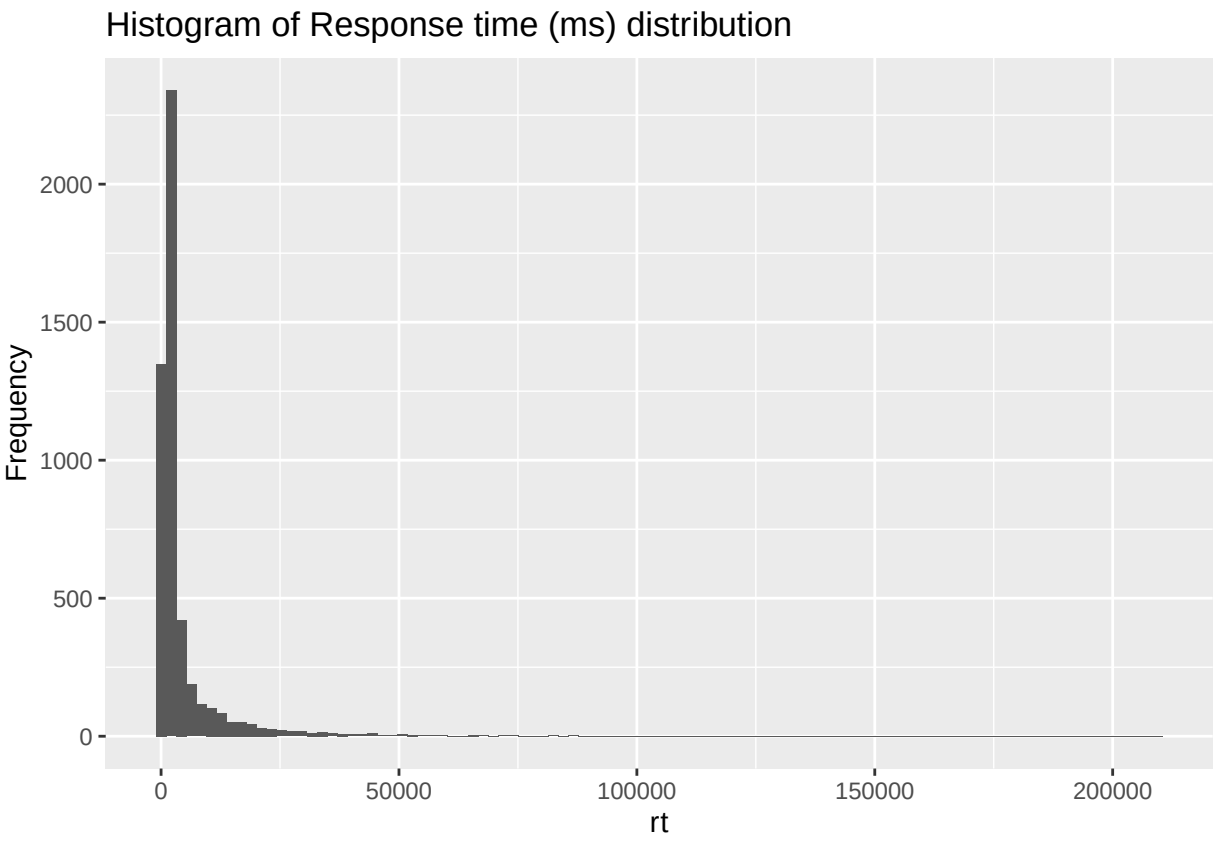
13 Remove `df_messy_na`

```
rm(df_messy_na)
```

14 Replacing missing values with the mean

- Say we have a continuous variable that **is integral** to our analysis
- An option is to replace missing values in a normal distribution with the mean

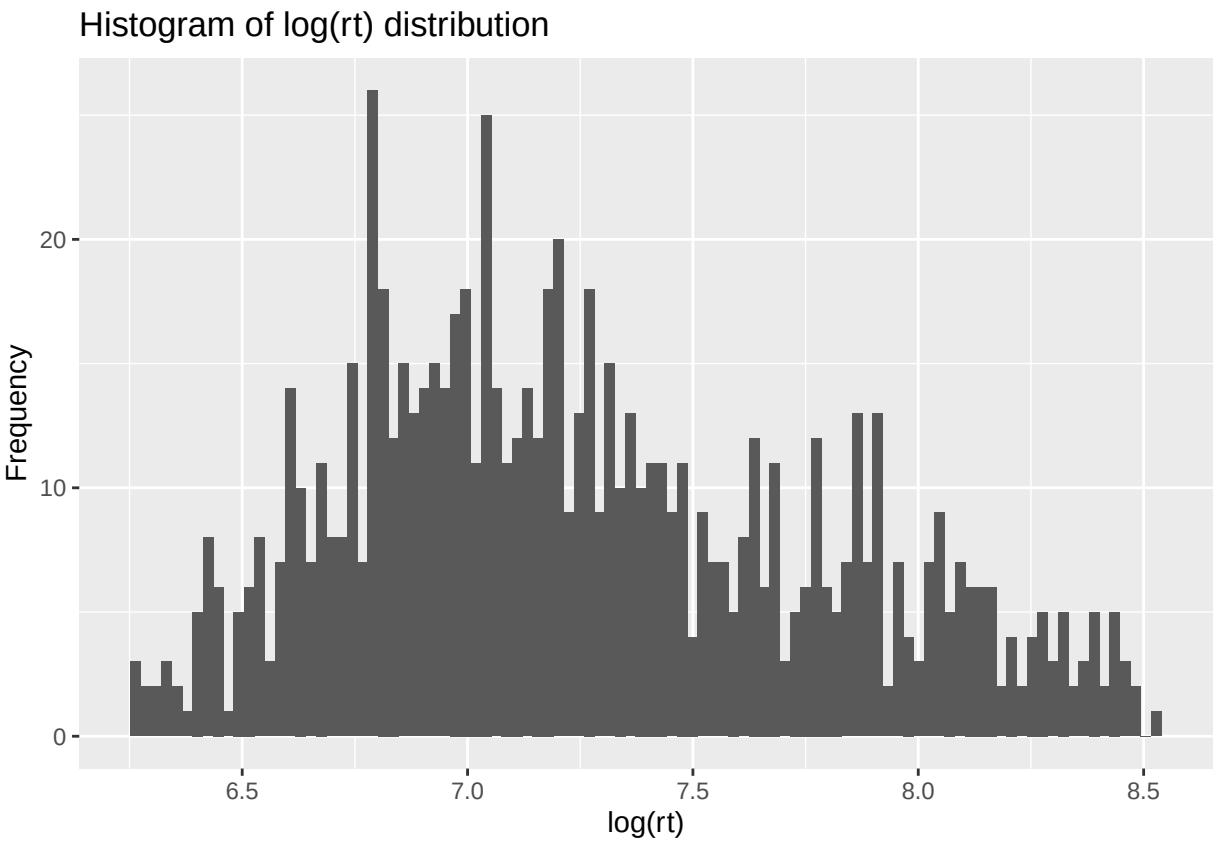
```
# examine the histogram
df_messy |>
  ggplot(mapping = aes(rt)) +
  geom_histogram(bins = 100) +
  labs(y = "Frequency",
       title = "Histogram of Response time (ms) distribution")
```



15 Cleaning

- Let's set the bounds that we had previously, between 500:5000 ms and take the log

```
df_messy |>
  filter(rt %in% c(500:5000)) |>
  ggplot(mapping = aes(log(rt))) +
  geom_histogram(bins = 100) +
  labs(y = "Frequency",
       title = "Histogram of log(rt) distribution")
```



16 Calculate the mean for log(rt)

```
df_messy |>
  filter(rt %in% c(500:5000)) |>
  summarise(avg_rt = mean(rt))
```

17 Replace missing values with avg_rt

```
# Create mean variable
avg_rt <- 1646.523

# create new object that replaces missing rt values with the mean
df_messy1 <-
  df_messy |>
  filter(rt %in% c(500:5000)) |>              # remember to set the new bounds!
  mutate(rt = if_else(is.na(rt),
                      avg_rt, # if the cell is empty, enter the mean of the vector
                      rt))                     # otherwise, put what was there already
```

18 Examine the vector

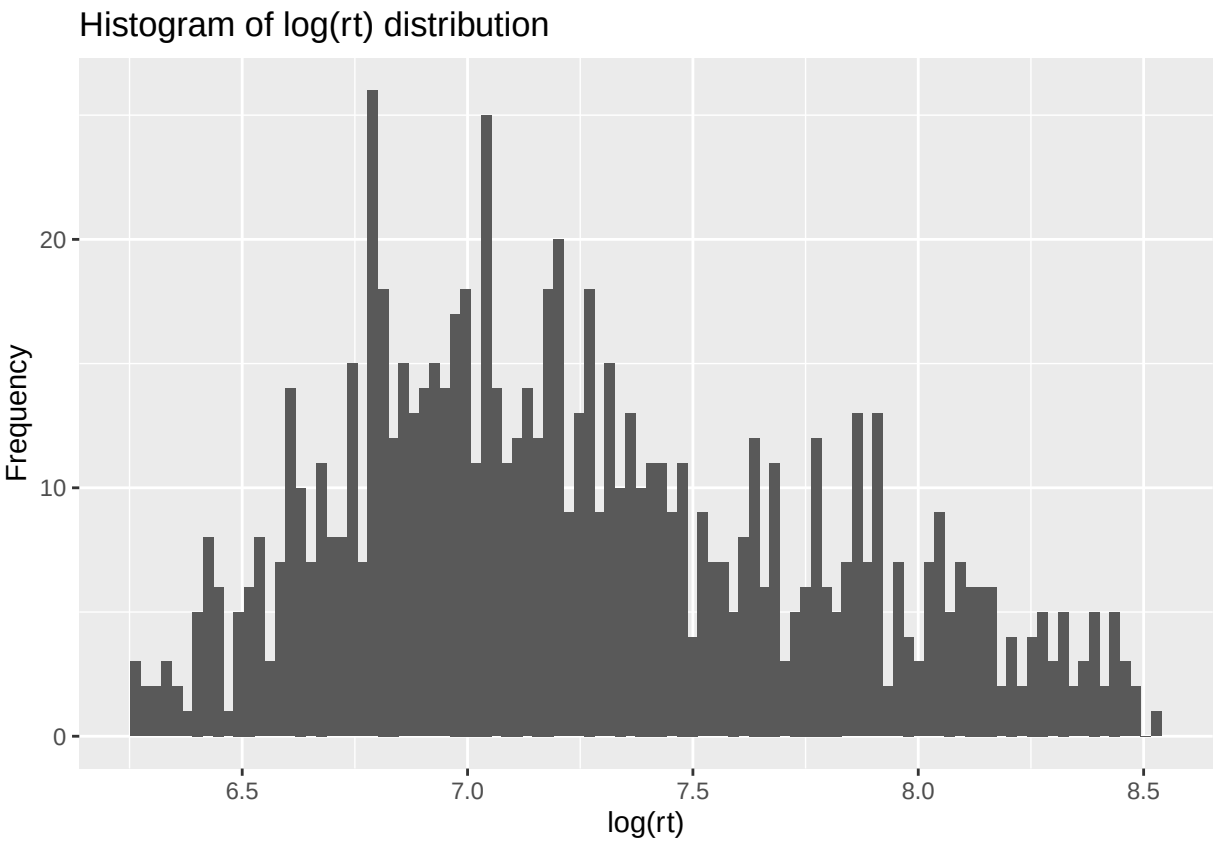
```
# Check for old
df_messy |>
  summarise(count_nas = is.na(rt) |>
              sum()) |>
  pluck("count_nas")

# Check for new
df_messy1 |>
  summarise(count_nas = is.na(rt) |>
              sum()) |>
  pluck("count_nas")
```

19 How big are the group sizes after removing missing cases?

```
# What would I write here to check the group sizes?
```

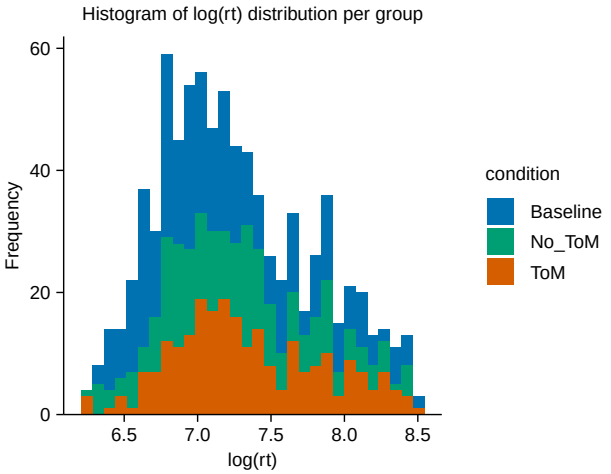
20 Plot the data

```
df_messy1 |>
  ggplot(mapping = aes(log(rt))) +
  geom_histogram(bins = 100) +
  labs(y = "Frequency",
       title = "Histogram of log(rt) distribution")
```



21 Tidyplots equivalent

```
# using tidyplots
df_messy1 <-
  df_messy1 |>
  mutate(log_rt = log(rt)) # tidyplots needs to be passed existing vectors

df_messy1 |>
  tidyplot(x = log_rt, color = condition) |>
  add_histogram(bins = 30) |>
  add_title("Histogram of log(rt) distribution per group") |>
  adjust_x_axis_title("log(rt)") |>
  adjust_y_axis_title("Frequency")
```



22 Checking the normality of the data using psych

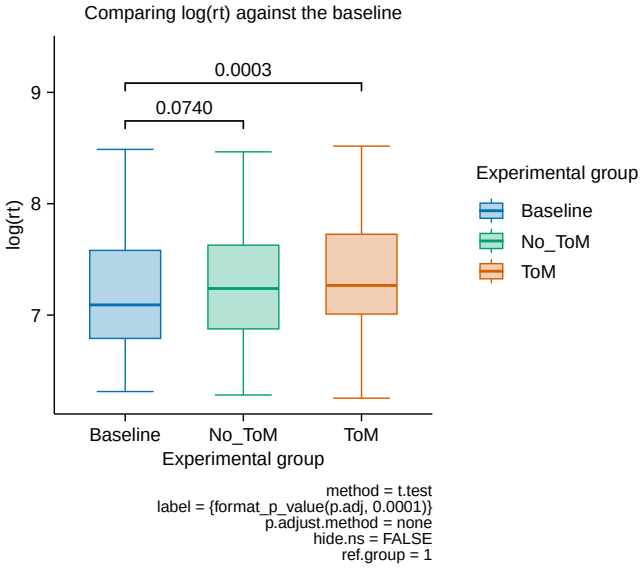
```
# Overall
describe(df_messy1$log_rt) |>
  select(11,12)

# By group
describeBy(log_rt ~ condition,
           mat = TRUE,
           data = df_messy1) |>
  select(2, 13:14)
```

- What is `select` doing here?
- What are the rules for violations to Skew and Kurtosis?

23 Boxplot with comparison analysis from tidyplots

```
df_messy1 |>
  tidyplot(x = condition,
           y = log_rt,
           color = condition) |>
  add_boxplot() |>
  add_test_pvalue(ref.group = 1) |>
  add_title("Comparing log(rt) against the baseline") |>
  adjust_x_axis_title("Experimental group") |>
```

```
  adjust_y_axis_title("log(rt)") |>
  adjust_legend_title("Experimental group")
```



24 Roundup

- I showed you how to deliberately untidy data using the **messy** package
- We did some label tidying
- We examined the case of listwise deletion, with your reading covering other approaches to missing data
- We examined test statistics for distribution normality
- Gave you a fist look at **tidyplots** as an alternative to **ggplot2**

25 Cleanup

```
# Clear data
rm(list = ls())  # Removes all objects from environment

# Clear packages
p_unload(all)  # Remove all contributed packages

# Clear plots
graphics.off()  # Clears plots, closes all graphics devices
```

```r
# Clear console
cat("\014")  # Mimics ctrl+L
```

26 References