Sample analysis: Streptomycin on TB

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Table of contents

Set Up

```r
library(medicaldata)

library(dplyr)
library(tidyr)
library(janitor)

library(knitr)
library(gt)
library(gtsummary)

strep_tb <- medicaldata::strep_tb |> as_tibble()
```

Baseline vs outcome

In reviewing this study, notice that outcomes are both improvements, but different effect sizes.

1

```
strep_base <-
  strep_tb |>
  select(arm, baseline_condition, gender, rad_num) |>
  separate(baseline_condition, into = c("baseline_num", "baseline_cond")) |>
  mutate(baseline_num = as.numeric(baseline_num))

strep_base_sum <-
  strep_base |>
  group_by(arm) |>
  summarise(
    n_pt = n(),
    mean_baseline = mean(baseline_num),
    mean_outcome = mean(rad_num)
  )

strep_base_sum |>
  kable(digits = 3)
```

arm	n_pt	mean_baseline	mean_outcome
Streptomycin	55	2.400	4.673
Control	52	2.308	3.135

Treatment vs outcome

The point above is important for interpreting the tables below.

```
strep_tb |>
  count(radiologic_6m, improved)
```

```
# A tibble: 6 x 3
  radiologic_6m                improved      n
  <fct>                        <lgl>     <int>
1 6_Considerable_improvement   TRUE         32
2 5_Moderate_improvement       TRUE         23
3 4_No_change                  FALSE         5
4 3_Moderate_deterioration     FALSE        17
5 2_Considerable_deterioration FALSE        12
6 1_Death                      FALSE        18
```

```
strep_tb |>
  tabyl(arm, improved) |>
  kable(caption = "Improved F/T")
```

Table 2: Improved F/T

arm	FALSE	TRUE
Streptomycin	17	38
Control	35	17

That is, strictly speaking, on average both treatment groups "improved", but for the category "improved" defined on a likert scale, more of the treated vs control were "improved".