

Bootstrap medians (stratified)

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Week 10 In-class Assignment

Differences in median (with the BCa bootstrap 95% confidence intervals)

- * maternal
- * infant
- * neonatal
- * under-5

mortality between the countries exposed to versus not exposed to armed conflict for the year 2017

```
library(tidyverse)
```

```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
v dplyr      1.1.3      v readr      2.1.4
v forcats    1.0.0      v stringr    1.5.0
v ggplot2    3.4.4      v tibble     3.2.1
v lubridate  1.9.3      v tidyr      1.3.0
v purrr      1.0.2
```

```
-- 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 become
```

```
library(here)
```

here() starts at /Users/aat/Documents/UofT/Stat Programming/armed_conflict

```

library(boot)
# filter() and lag() are functions that exist in both R packages dplyr and stats
# make default choice the functions from the dplyr package
#filter <- dplyr::filter
#lag <- dplyr::lag

# rfa = ready for analysis
rfa <- read.csv(paste0(here(), "/data/final_dat_300923.csv"), stringsAsFactors = FALSE) |>
  dplyr::filter(year == 2017) |>
  select(confl.IND, mat.mort, inf.mort, neonat.mort, und5.mort)

set.seed(231)

res <- matrix(NA, 4, 4)

# getting rid of NAs
rfa.mat <- rfa[!is.na(rfa[, "mat.mort"]), ]
rfa.inf <- rfa[!is.na(rfa[, "inf.mort"]), ]
rfa.neonat <- rfa[!is.na(rfa[, "neonat.mort"]), ]
rfa.und5 <- rfa[!is.na(rfa[, "und5.mort"]), ]

# maternal
getmeddiff.mat <- function(data, indices) {
  sample_data <- data[indices, ]
  group_meds <- tapply(sample_data$mat.mort, sample_data$confl.IND, FUN = median)
  meddiff <- group_meds[2] - group_meds[1]
  return(meddiff)
}
bootout.mat <- boot(rfa.mat, statistic = getmeddiff.mat, strata = rfa.mat$confl.IND, R = 1000)
ci.mat <- boot.ci(boot.out = bootout.mat, conf = 0.95, type = "bca")
res[1,] <- c(nrow(rfa.mat), ci.mat$t0, ci.mat$bca[c(4,5)])

# infant
getmeddiff.inf <- function(data, indices) {
  sample_data <- data[indices, ]
  group_meds <- tapply(sample_data$inf.mort, sample_data$confl.IND, FUN = median)
  meddiff <- group_meds[2] - group_meds[1]
  return(meddiff)
}
bootout.inf <- boot(rfa.inf, statistic = getmeddiff.inf, strata = rfa.inf$confl.IND, R = 1000)

```

```

ci.inf <- boot.ci(boot.out = bootout.inf, conf = 0.95, type = "bca")
res[2, ] <- c(nrow(rfa.inf), ci.inf$t0, ci.inf$bca[c(4,5)])

# neonatal
getmeddiff.neonat <- function(data, indices) {
  sample_data <- data[indices, ]
  group_meds <- tapply(sample_data$neonat.mort, sample_data$confl.IND, FUN = median)
  meddiff <- group_meds[2] - group_meds[1]
  return(meddiff)
}
bootout.neonat <- boot(rfa.neonat, statistic = getmeddiff.neonat, strata = rfa.neonat$confl.IND, R = 1000)
ci.neonat <- boot.ci(boot.out = bootout.neonat, conf = 0.95, type = "bca")
res[3, ] <- c(nrow(rfa.neonat), ci.neonat$t0, ci.neonat$bca[c(4,5)])

# under 5
getmeddiff.und5 <- function(data, indices) {
  sample_data <- data[indices, ]
  group_meds <- tapply(sample_data$und5.mort, sample_data$confl.IND, FUN = median)
  meddiff <- group_meds[2] - group_meds[1]
  return(meddiff)
}
bootout.und5 <- boot(rfa.und5, statistic = getmeddiff.und5, strata = rfa.und5$confl.IND, R = 1000)
ci.und5 <- boot.ci(boot.out = bootout.und5, conf = 0.95, type = "bca")
res[4, ] <- c(nrow(rfa.und5), ci.und5$t0, ci.und5$bca[c(4,5)])

mort.names <- c("Maternal", "Infant", "Neonatal", "Under 5")
res.fin <- data.frame(mort.names, res)

# res

library(knitr)
kable(res.fin, digits = c(0, 1, 2, 2),
      col.names = c("Type of mortality", "N observations", "Difference", "95% CI lower", "95% CI upper"),
      caption = "Median mortality difference between countries with vs without armed conflict in 2017")

```

Table 1: Median mortality difference between countries with vs without armed conflict in 2017

Type of mortality	N observations	Difference	95% CI lower	95% CI upper
Maternal	183	126.50	40.42	277
Infant	185	19.80	7.44	29

Type of mortality	N observations	Difference	95% CI lower	95% CI upper
Neonatal	185	11.85	3.35	17
Under 5	185	28.90	8.85	46