

# Length of stay in the ICU

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(Note: Updated and modified from the hst953-edx version authored by Tom Pollard.)

## Source MIMIC-III data

In the original version (on the hst953-edx github site), they used the MIMIC-III demo version directly loaded. Now, I have in *mimic\_base\_dir*/database/mimic3.db the SQLite version of the full MIMIC-III v1.4 database loaded. I'll use that in the processing below - with some pre-coded inclusion criteria to extract just the demo data. The following code chunk attaches the database and loads auxiliary functions (available in *mimic\_base\_dir*/mimic\_concepts) for extracting database data (*db\_functions.R*) and for doing some MIMIC data interpretation and pre-processing (*mimic3\_meta\_data.R*).

```
base_dir <- here::here("")
mimic_base_dir <- fs::path(base_dir, "../MIMIC-research")
db_file <- fs::path(mimic_base_dir, "database/mimic3.db")
if(dbCanConnect(RSQLite::SQLite(), db_file)) {
  mimic3 <- dbConnect(RSQLite::SQLite(), db_file)
} else {
  stop(str_c("Database file: ", db_file, " not found.", sep=""))
}
source(fs::path(mimic_base_dir, "mimic_concepts/db_functions.R"))
source(fs::path(mimic_base_dir, "mimic_concepts/mimic3_meta_data.R"))
```

## Extract ICU stay data

```
data <- db_get_icustays(mimic3) %>% select(SUBJECT_ID, HADM_ID, LOS)

str(data)
#> tibble [61,532 x 3] (S3: tbl_df/tbl/data.frame)
#> $ SUBJECT_ID: int [1:61532] 268 269 270 271 272 273 274 275 276 277 ...
#> $ HADM_ID   : int [1:61532] 110404 106296 188028 173727 164716 158689 130546 129886 135156 171601 .
#> $ LOS       : num [1:61532] 3.25 3.28 2.89 2.06 1.62 ...
```

## Calculate median stay length

This document shows how RMarkdown can be used to create a reproducible analysis using MIMIC-III (version 1.4). Let's calculate the median length of stay in the ICU and then include this value in our document.

So the median length of stay in the ICU is 2.09225 days. Rounded to two decimal places, this is 2.09 days.

## Plot the data

We can plot the distribution of length of stay using `ggplot` and `geom_histogram`:

