

Supplement 1

Co-oximetry

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1 Research question

1. Descriptive statistics on co-oximetry results, namely, total haemoglobin concentration (Hb, g/dl) functional oxyhaemoglobin saturation (SaO₂, %Hb), fractional oxyhaemoglobin saturation (FO₂Hb, %Hb), carboxyhaemoglobin (COHb, %Hb), and methaemoglobin (MetHb, %Hb).
-

2 Load data

```
data <- read_rds('data-cleaned/clean-data.rds')
```

3 Quick look at the data

```
dim(data)
```

```
## [1] 163 22
```

```
names(data)
```

```
## [1] "Animal_ID"      "Trial"           "Dpat"
## [4] "Time_min"        "l_star"          "a_star"
## [7] "b_star"          "PaO2"            "cal_SaO2"
## [10] "PaCO2"           "Cl"              "HCO3"
## [13] "Temp"            "pH"              "Cartridge_expired"
## [16] "Coox_SaO2"       "Hct"             "total_Hb"
## [19] "O2Hb"            "COHb"            "MetHb"
## [22] "O2_suppl"
```

```
glimpse(data)
```

```
## Rows: 163
## Columns: 22
## $ Animal_ID      <chr> "I1", "I1", "I1", "I1", "I1", "I1", "I1", "I1", "...
## $ Trial           <dbl> 1, 1, 1, 1, 1, 4, 4, 4, 4, 4, 5, 5, 5, 5, 5, 5, 5...
## $ Dpat           <dbl> 0, 0, 0, 0, 0, 5, 5, 5, 5, 5, 0, 0, 0, 0, 0, 0, 0...
## $ Time_min       <dbl> 5, 10, 15, 20, 30, 5, 10, 15, 20, 30, 5, 10, 15, ...
## $ l_star         <dbl> 11.3, 12.9, 13.5, 14.6, 15.6, 12.6, 13.6, 13.8, 1...
## $ a_star         <dbl> 24.5, 31.5, 31.4, 34.1, 34.8, 30.7, 33.0, 31.4, 3...
## $ b_star         <dbl> 11.5, 17.5, 14.7, 19.9, 20.1, 16.5, 18.1, 18.2, 2...
## $ PaO2           <dbl> 27.9, 40.4, 35.3, 41.7, 40.3, 33.9, 34.9, 36.5, 4...
## $ cal_SaO2       <dbl> 45.6, 71.0, 62.3, 73.4, 71.9, 56.7, 60.1, 61.5, 7...
## $ PaCO2          <dbl> 54.9, 55.6, 58.5, 56.3, 57.6, 63.4, 62.4, 63.8, 6...
## $ Cl             <dbl> 113, 113, 111, 111, 109, 107, 106, 106, 105, 105,...
## $ HCO3           <dbl> 27.9, 29.9, 31.3, 31.3, 33.0, 31.0, 32.0, 31.0, 3...
## $ Temp           <dbl> 39.2, 39.7, 39.7, 39.7, 39.6, 39.2, 39.6, 39.6, 3...
## $ pH             <dbl> 7.31, 7.34, 7.34, 7.35, 7.37, 7.30, 7.32, 7.29, 7...
## $ Cartridge_expired <chr> "No", "No", "No", "No", "No", "No", "No", "No", "...
## $ Coox_SaO2      <dbl> 53.0, 67.8, 63.3, 74.1, 73.1, 53.8, 64.2, 56.2, 7...
## $ Hct            <dbl> 23, 24, 21, 20, 18, 27, 23, 26, 20, 19, 21, 20, 1...
## $ total_Hb       <dbl> 8.7, 7.8, 7.6, 7.2, 6.7, 9.6, 8.9, 9.8, 7.7, 7.3,...
## $ O2Hb           <dbl> 51.0, 65.4, 60.0, 71.0, 69.4, 51.9, 61.7, 54.2, 6...
## $ COHb           <dbl> 0.0, 1.2, 2.4, 1.0, 1.7, 0.0, 0.8, 0.0, 1.5, 1.4,...
## $ MetHb          <dbl> 3.7, 2.3, 2.8, 3.2, 3.3, 3.4, 3.1, 3.4, 2.4, 2.9,...
## $ O2_suppl       <chr> "No", "No", "No", "No", "No", "No", "No", "No", "...

```

4 Prepare data

```
# Select columns
data_cols <- data %>%
  select(Animal_ID, Trial, Time_min, total_Hb,
         Coox_SaO2, O2Hb, COHb, MetHb) %>%
  # Rename columns
  rename(Time_minutes = Time_min,
         `Hb (g/dl)` = total_Hb,
         `SaO2 (%)` = Coox_SaO2,
         `FO2Hb (%)` = O2Hb,
         `COHb (%)` = COHb,
         `MetHb (%)` = MetHb) %>%
  # Limit time to first 30 minutes
  filter(Time_minutes <= 30)
# Data points per animal
data_n <-

# Average over trials for each animal
data_compact <- data_cols %>%

```

```

# Calculate average response over trials for each animal
group_by(Animal_ID, Time_minutes) %>%
summarise(`Hb (g/dl)` = mean(`Hb (g/dl)` , na.rm = TRUE),
          `SaO2 (%)` = mean(`SaO2 (%)` , na.rm = TRUE),
          `FO2Hb (%)` = mean(`FO2Hb (%)` , na.rm = TRUE),
          `COHb (%)` = mean(`COHb (%)` , na.rm = TRUE),
          `MetHb (%)` = mean(`MetHb (%)` , na.rm = TRUE)) %>%
ungroup() %>%
select(-Animal_ID) %>%
complete(Time_minutes)

```

5 Tabulate

Trials: number of separate immobilization events.

5.1 Number of immobilization trials and data points per animal

```

# Trials
trials <- data_cols %>%
  select(Animal_ID, Trial) %>%
  distinct() %>%
  group_by(Animal_ID) %>%
  summarise(`Number of trials` = n()) %>%
  ungroup() %>%
  rename(Animal = Animal_ID) %>%
  mutate(Animal = str_remove(Animal,
                             pattern = 'I'),
         Animal = as.numeric(Animal)) %>%
  arrange(Animal)

# Data points
data_points <- data_cols %>%
  select(Animal_ID) %>%
  group_by(Animal_ID) %>%
  summarise(`Number of data points` = n()) %>%
  ungroup() %>%
  rename(Animal = Animal_ID) %>%
  mutate(Animal = str_remove(Animal,
                             pattern = 'I'),
         Animal = as.numeric(Animal)) %>%
  arrange(Animal)

# Table
trials %>%
  left_join(data_points) %>%
  kable(caption = 'Number of trails and measurements')

```

Table 1: Number of trails and measurements

Animal	Number of trials	Number of data points
1	3	15
2	1	5
3	1	5

Animal	Number of trials	Number of data points
4	3	15
5	5	25
6	2	10
8	3	15
9	4	19
10	1	4
11	3	14

5.2 Summary statistics fro co-oximetry measurements

Where animals were involved in more than one trial, data points occurring at the same time-point across trials were averaged.

```
# Average over trials for each animal
data_cols %>%
  # Calculate average response over trials for each animal
  group_by(Animal_ID, Time_minutes) %>%
  summarise(`Hb (g/dl)` = mean(`Hb (g/dl)`, na.rm = TRUE),
            `SaO2 (%)` = mean(`SaO2 (%)`, na.rm = TRUE),
            `FO2Hb (%)` = mean(`FO2Hb (%)`, na.rm = TRUE),
            `COHb (%)` = mean(`COHb (%)`, na.rm = TRUE),
            `MetHb (%)` = mean(`MetHb (%)`, na.rm = TRUE)) %>%
  ungroup() %>%
  group_by(Time_minutes) %>%
  select(-Animal_ID) %>%
  my_skim()
```

Table 2: Data summary

Name	Piped data
Number of rows	49
Number of columns	6
Column type frequency: numeric	5
Group variables	Time_minutes

Variable type: numeric

skim_variable	Time_minutes	n_missing	complete_rate	mean	sd
Hb (g/dl)	5	0	1	10.41	1.17
Hb (g/dl)	10	0	1	9.37	1.34
Hb (g/dl)	15	0	1	8.82	1.25
Hb (g/dl)	20	0	1	8.55	1.33
Hb (g/dl)	30	0	1	7.88	0.77
SaO2 (%)	5	0	1	63.25	19.03
SaO2 (%)	10	0	1	75.73	13.40
SaO2 (%)	15	0	1	81.59	7.69
SaO2 (%)	20	0	1	83.35	6.04
SaO2 (%)	30	0	1	88.03	4.67
FO2Hb (%)	5	0	1	61.16	18.39
FO2Hb (%)	10	0	1	73.02	12.90
FO2Hb (%)	15	0	1	78.53	7.34

skim_variable	Time_minutes	n_missing	complete_rate	mean	sd
FO2Hb (%)	20	0	1	80.43	5.75
FO2Hb (%)	30	0	1	84.54	4.61
COHb (%)	5	0	1	0.66	0.47
COHb (%)	10	0	1	1.35	0.62
COHb (%)	15	0	1	1.65	0.70
COHb (%)	20	0	1	1.50	0.78
COHb (%)	30	0	1	2.14	0.41
MetHb (%)	5	0	1	2.60	0.41
MetHb (%)	10	0	1	2.22	0.38
MetHb (%)	15	0	1	2.05	0.24
MetHb (%)	20	0	1	1.98	0.36
MetHb (%)	30	0	1	1.82	0.35

6 Session Information

```
sessionInfo()
```

```
## R version 3.6.3 (2020-02-29)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Catalina 10.15.4
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] knitr_1.28      skimr_2.1      magrittr_1.5   forcats_0.5.0
## [5] stringr_1.4.0   dplyr_0.8.5    purrr_0.3.3    readr_1.3.1
## [9] tidyr_1.0.2     tibble_3.0.0   ggplot2_3.3.0.9000 tidyverse_1.3.0
##
## loaded via a namespace (and not attached):
## [1] tidyselect_1.0.0 xfun_0.12      repr_1.1.0     haven_2.2.0
## [5] lattice_0.20-38  colorspace_1.4-1 vctrs_0.2.4    generics_0.0.2
## [9] htmltools_0.4.0 base64enc_0.1-3 yaml_2.2.1     utf8_1.1.4
## [13] rlang_0.4.5      pillar_1.4.3   withr_2.1.2    glue_1.3.2
## [17] DBI_1.1.0         dbplyr_1.4.2   modelr_0.1.6    readxl_1.3.1
## [21] lifecycle_0.2.0  munsell_0.5.0  gtable_0.3.0    cellranger_1.1.0
## [25] rvest_0.3.5       evaluate_0.14   fansi_0.4.1     highr_0.8
## [29] broom_0.5.5      Rcpp_1.0.4     backports_1.1.5 scales_1.1.0
## [33] jsonlite_1.6.1    fs_1.3.1        hms_0.5.3       digest_0.6.25
## [37] stringi_1.4.6     grid_3.6.3      cli_2.0.2        tools_3.6.3
## [41] crayon_1.3.4      pkgconfig_2.0.3 ellipsis_0.3.0   xml2_1.3.0
## [45] reprex_0.3.0      lubridate_1.7.4 assertthat_0.2.1 rmarkdown_2.1
## [49] httr_1.4.1        rstudioapi_0.11 R6_2.4.1         nlme_3.1-145
## [53] compiler_3.6.3
```