Supplement 1
Co-oximetry

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Contents

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1 Research question

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

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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

```r
# 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) %>%
    # Compact 40+ minutes into one group
    mutate(Time_minutes = ifelse(Time_minutes > 30,
                          yes = 40,
                          no = Time_minutes)) #%>%
```

```
    # Limit time to first 30 minutes
    #filter(Time_minutes <= 30)

# 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 immobilzation 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	4	20
2	2	9
3	1	5
4	4	21
5	5	30
6	2	11
8	4	21
9	5	24
10	2	8
11	3	14

5.2 Summary statistics for co-oximetry measurements

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

5.2.1 Number of animals per time point

```
data_cols %>%
    group_by(Animal_ID) %>%
    distinct_at(.vars = vars(Time_minutes)) %>%
    group_by(Time_minutes) %>%
    summarise(Count = n()) %>%
    kable(caption = 'Number of animals per time point',
          col.names = c('Time (minutes)', 'Number of animals'))
```

Table 2: Number of animals per time point

Time (minutes)	Number of animals
5	10
10	10
15	10
20	10
30	9
40	8

5.2.2 Tabulated data

```
# 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 3: Data summary

Name	Piped data
Number of rows	57
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
Hb (g/dl)	40	0	1	8.94	1.36
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
SaO2 (%)	40	0	1	95.53	2.32
FO2Hb (%)	5	0	1	61.16	18.39
FO2Hb (%)	10	0	1	73.02	12.90
FO2Hb (%)	15	0	1	78.53	7.34
FO2Hb (%)	20	0	1	80.43	5.75
FO2Hb (%)	30	0	1	84.54	4.61
FO2Hb (%)	40	0	1	91.85	1.58
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
COHb (%)	40	0	1	2.80	0.87
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
MetHb (%)	40	0	1	1.23	0.30

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
```