solutions_R

May 19, 2022

1 ASRR Messy Data Challenge

1.1 Example analysis (R version)

[ ]:

```
# Load library
packages <- c("tidyverse", "data.table", "haven", "skimr", "janitor")
for (p in packages) {
    if (!require(p, character.only = TRUE)) install.packages(p)
    suppressPackageStartupMessages(library(p, character.only = TRUE))
}
```

1.2 Data exploration

1.2.1 Read in data

[2]:

```
df <- read_dta("../data/icu_data.dta")
head(df)
```

A tibble: 6 × 13

age	gender	iculos	hr	temp	sbp	dbp	resp	o2sat	map	sep
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<d
65.36	0	28	71.0	38.11	168.00	56.0	17	94.0	91.0	0
55.00	0	7	76.0	37.50	133.00	74.0	24	96.0	99.0	0
38.00	0	15	77.0	NA	146.00	83.0	17	NA	108.0	0
72.17	1	34	53.5	NA	157.00	60.5	15	95.5	92.5	0
61.26	1	2	72.5	NA	93.25	68.5	18	100.0	79.0	0
21.00	1	19	74.0	NA	118.00	104.0	20	91.0	112.0	0

1.2.2 What's in the dataset

[3]:

```
summary(df)
```

```
      age             gender           iculos             hr
 Min.   : 14.00   Min.   :0.0000   Min.   :  1.00   Min.   : 20.00
 1st Qu.: 51.00   1st Qu.:0.0000   1st Qu.: 10.00   1st Qu.: 72.00
 Median : 63.44   Median :1.0000   Median : 21.00   Median : 83.00
 Mean   : 61.74   Mean   :0.5485   Mean   : 26.18   Mean   : 84.23
 3rd Qu.: 74.00   3rd Qu.:1.0000   3rd Qu.: 34.00   3rd Qu.: 95.50
 Max.   :100.00   Max.   :1.0000   Max.   :336.00   Max.   :223.00
                                                    NA's   :131167
      temp             sbp              dbp              resp
 Min.   :20.9     Min.   : 20.0    Min.   : 20      Min.   :  1.00
 1st Qu.:36.5     1st Qu.:107.0    1st Qu.: 55      1st Qu.: 16.00
 Median :36.9     Median :122.0    Median : 63      Median : 18.00
 Mean   :36.9     Mean   :124.7    Mean   : 65      Mean   : 18.73
 3rd Qu.:37.4     3rd Qu.:140.0    3rd Qu.: 73      3rd Qu.: 21.00
 Max.   :50.0     Max.   :298.0    Max.   :300      Max.   :100.00
 NA's   :822321   NA's   :176747   NA's   :373178   NA's   :205042
     o2sat             map          sepsislabel          hospid
 Min.   : 20.00   Min.   : 20.00   Min.   :0.000000   Length:1201974
 1st Qu.: 96.00   1st Qu.: 72.00   1st Qu.:0.000000   Class :character
 Median : 98.00   Median : 82.00   Median :0.000000   Mode  :character
 Mean   : 97.15   Mean   : 83.55   Mean   :0.001379
 3rd Qu.: 99.00   3rd Qu.: 93.00   3rd Qu.:0.000000
 Max.   :100.00   Max.   :300.00   Max.   :1.000000
 NA's   :170544   NA's   :163352
     patid
 Min.   :    1
 1st Qu.:12317
 Median :23294
 Mean   :22012
 3rd Qu.:31822
 Max.   :40336
```

1.2.3 Distributions of each of the variables

[4]:

```
options(width = 110)
skim(df)
```

```
  Data Summary
                           Values
Name                       df
Number of rows             1201974
Number of columns          13
_______________________
Column type frequency:
  character                1
  numeric                  12
________________________
Group variables            None

  Variable type: character

  skim_variable n_missing complete_rate   min   max empty n_unique whitespace
1 hospid                0             1     1     1     0        2          0
```

```
  Variable type: numeric

   skim_variable n_missing complete_rate        mean         sd    p0      p25
p50     p75  p100 hist
 1 age                     0          1        61.7        16.5     14      51
63.4    74      100
 2 gender                  0          1         0.549       0.498    0       0
1       1       1
 3 iculos                  0          1        26.2        27.9       1      10
21      34      336
 4 hr                 131167          0.891    84.2        17.6     20      72
83      95.5    223
 5 temp               822321          0.316    36.9         0.759   20.9    36.5
36.9    37.4    50
 6 sbp                176747          0.853   125.         23.6     20     107
122     140     298
 7 dbp                373178          0.690    65.0        14.2     20      55
63      73      300
 8 resp               205042          0.829    18.7         5.02      1      16
18      21      100
 9 o2sat              170544          0.858    97.1         2.98    20      96
98      99      100
10 map                163352          0.864    83.5        16.6     20      72
82      93      300
11 sepsislabel             0          1         0.00138     0.0371   0       0
0       0       1
12 patid                   0          1     22012.      11502.        1  12317
23294   31822   40336
```

1.2.4 Complete case indicator

[5]:

```
cols <- c("o2sat", "hr", "temp", "sbp", "map", "resp")
df <- df %>%
    mutate(nvar_miss = rowSums(across(all_of(cols), is.na)),
           cc_fl = ifelse(nvar_miss == 0, TRUE, FALSE))
```

[6]:

```
tabyl(df, cc_fl)
```

A tabyl: 2 × 3

cc_fl	n	percent
<lgl>	<int>	<dbl>
FALSE	865835	0.7203442
TRUE	336139	0.2796558

Only 28% of records have no missing vital signs

1.3 Outcome exploration

1.3.1 How many people were diagnosed with sepsis?

[7]:

```
df %>%
    group_by(patid) %>%
    summarise(any_sepsis = max(sepsislabel)) %>%
    tabyl(any_sepsis)
```

A tabyl: 2 × 3

any_sepsis <dbl>	n <int>	percent <dbl>
0	29268	0.94641876
1	1657	0.05358124

1.3.2 When do people get sepsis in ICU?

[8]:

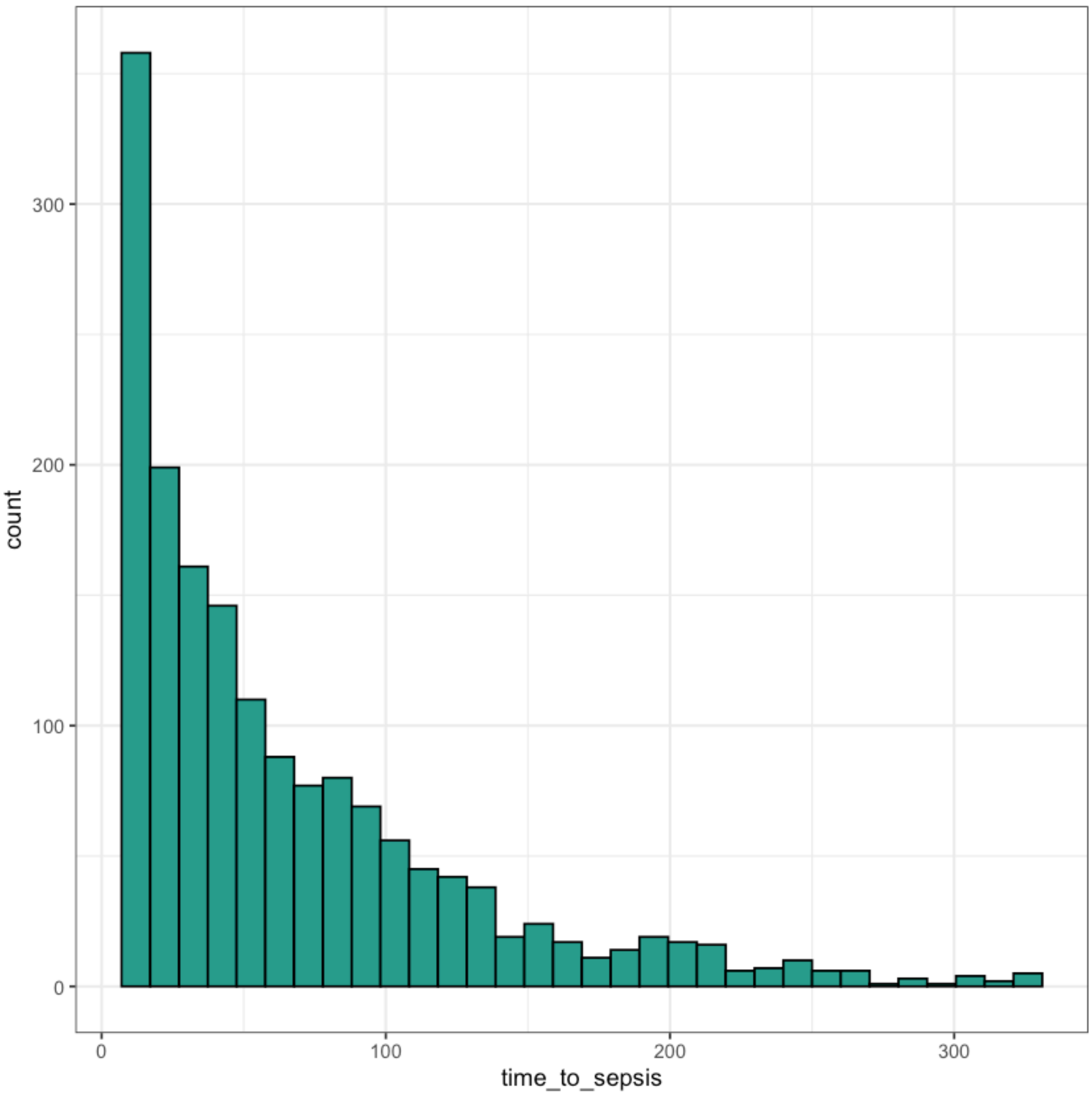
```
df_sepsis <- df %>%
    filter(sepsislabel == 1) %>%
    group_by(patid) %>%
    summarise(time_to_sepsis = min(iculos))
skim(df_sepsis, time_to_sepsis)
```

```
  Data Summary
                           Values
Name                       df_sepsis
Number of rows             1657
Number of columns          2

_______________________
Column type frequency:
  numeric                  1

________________________
Group variables            None

  Variable type: numeric

  skim_variable  n_missing complete_rate  mean    sd    p0   p25   p50   p75
p100 hist
1 time_to_sepsis         0             1  65.7  60.9     7    20    45    91
331
```

- min: 7 hours
- max: 331 hours (13.8 days)
- median: 45 hours

[9]:

```
ggplot(df_sepsis, aes(x = time_to_sepsis)) +
    theme_bw() +
    # these settings are used to match stata output
    geom_histogram(fill = "#2a9d8f", colour = "black", bins = 32,
                   binwidth = 10.125, boundary = 7)
```



1.3.3 Create indicator for patient who get sepsis:

[10]:
```
df <- df %>%
    group_by(patid) %>%
    mutate(any_sepsis = max(sepsislabel, na.rm = TRUE))
```

1.4 Imputing explanatory measures

1.4.1 Mean Imputation

[11]:

```
impute_mean <- function(x) replace_na(x, mean(x, na.rm=T))
# Use only ICULOS <= 5
df_imp <- df %>%
    filter(iculos <= 5) %>%
    group_by(patid) %>%
    arrange(patid, iculos) %>%
    mutate(across(all_of(cols), impute_mean, .names = "{.col}_imp1"))
```

1.4.2 First observation carried backwards

[12]:

```
df_imp <- df_imp %>%
    mutate(across(all_of(cols), ~.x, .names = "{.col}_imp2")) %>%
    fill(ends_with("_imp2"), .direction = "up")

head(df_imp)
```

A grouped_df: 6 × 28

age <dbl>	gender <dbl>	iculos <dbl>	hr <dbl>	temp <dbl>	sbp <dbl>	dbp <dbl>	resp <dbl>	o2sat <dbl>	map <dbl>
83.14	0	1	NA	NA	NA	NA	NA	NA	NA
83.14	0	2	97	NA	98	NA	19.0	95.0	75.33
83.14	0	3	89	NA	122	NA	22.0	99.0	86.00
83.14	0	4	90	NA	NA	NA	30.0	95.0	NA
83.14	0	5	103	NA	122	NA	24.5	88.5	91.33
75.91	0	1	NA	NA	NA	NA	NA	NA	NA

1.4.3 Inspect missingness again among imputed variables

[13]:

```
df_imp <- df_imp %>%
    ungroup() %>%
    mutate(nvar_miss_imp1 = rowSums(across(ends_with("_imp1"), is.na)),
           nvar_miss_imp2 = rowSums(across(ends_with("_imp2"), is.na)),
           cc_fl_imp1 = ifelse(nvar_miss_imp1 == 0, TRUE, FALSE),
           cc_fl_imp2 = ifelse(nvar_miss_imp2 == 0, TRUE, FALSE))
```

[14]:

```
df_imp %>%
    filter(iculos == 1) %>%
    tabyl(cc_fl_imp1)
```

A tabyl: 2 × 3

cc_fl_imp1 <lgl>	n <int>	percent <dbl>
FALSE	6897	0.2230234
TRUE	24028	0.7769766

[15]:

```
df_imp %>%
    filter(iculos == 1) %>%
    tabyl(cc_fl_imp2)
```

A tabyl: 2 × 3

cc_fl_imp2	n	percent
<lgl>	<int>	<dbl>
FALSE	6897	0.2230234
TRUE	24028	0.7769766

78% of rows non-missing for each imputation method

1.5 Modelling

1.5.1 Dummy indicators for hospital:

In R, dummy indicators for a binary / categorical (a.k.a factor) variable will be created automatically when creating a formula object to be used in generalised-linear model with `glm()`.

However, a no-intercept model is needed when fitting the regression to avoid multicollinearity issue due to singular matrix. For more discussion, see: https://stats.stackexchange.com/a/94021

1.5.2 Mean imputation

[16]:

```
model_imp1 <- glm(
    # the -1 term will suppress intercept, which is needed to avoid singularity␣
↪matrix issue
    any_sepsis ~ -1 + age + gender + o2sat_imp1 + hr_imp1 + temp_imp1
                 + sbp_imp1 + map_imp1 + resp_imp1 + factor(hospid),
    data = filter(df_imp, iculos == 1),
    family = binomial(link = "logit")
)
```

[17]:

```
summary(model_imp1)
```

```
Call:
glm(formula = any_sepsis ~ -1 + age + gender + o2sat_imp1 + hr_imp1 +
    temp_imp1 + sbp_imp1 + map_imp1 + resp_imp1 + factor(hospid),
    family = binomial(link = "logit"), data = filter(df_imp,
        iculos == 1))

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.0167  -0.3480  -0.2962  -0.2514   2.9621

Coefficients:
                 Estimate Std. Error z value Pr(>|z|)
age              0.001538   0.001873   0.821  0.41162
gender           0.182319   0.060440   3.017  0.00256 **
o2sat_imp1       0.014192   0.011535   1.230  0.21855
```

```
hr_imp1           0.011620   0.001835   6.334 2.39e-10 ***
temp_imp1         0.007815   0.040582   0.193  0.84730
sbp_imp1          0.002920   0.002554   1.143  0.25302
map_imp1         -0.016736   0.003827  -4.373 1.23e-05 ***
resp_imp1         0.050361   0.006298   7.996 1.29e-15 ***
factor(hospid)A -5.496563   1.878954  -2.925  0.00344 **
factor(hospid)B -5.923873   1.876972  -3.156  0.00160 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 33309.9  on 24028  degrees of freedom
Residual deviance:  9321.4  on 24018  degrees of freedom
  (6897 observations deleted due to missingness)
AIC: 9341.4

Number of Fisher Scoring iterations: 6
```

[18]:

```
# Calculate odds ratio & 95% confidence interval
exp(coefficients(model_imp1)) %>%
    enframe(name = "variable", value = "odds ratio") %>%
    add_column(as_tibble(exp(confint(model_imp1))))
```

```
Waiting for profiling to be done…
```

A tibble: 10 × 4

variable <chr>	odds ratio <dbl>	2.5 % <dbl>	97.5 % <dbl>
age	1.00153917	9.978819e-01	1.0052367
gender	1.19999753	1.066285e+00	1.3514246
o2sat_imp1	1.01429313	9.925303e-01	1.0383737
hr_imp1	1.01168795	1.008049e+00	1.0153248
temp_imp1	1.00784512	9.309287e-01	1.0914074
sbp_imp1	1.00292389	9.978885e-01	1.0079298
map_imp1	0.98340323	9.760605e-01	0.9908138
resp_imp1	1.05165073	1.038685e+00	1.0646521
factor(hospid)A	0.00410084	9.841101e-05	0.1554736
factor(hospid)B	0.00267482	6.446135e-05	0.1010534

First observation carried backwards

[19]:

```
model_imp2 <- glm(
    # the -1 term will suppress intercept, which is needed to avoid singularity␣
 ↪matrix issue
    any_sepsis ~ -1 + age + gender + o2sat_imp2 + hr_imp2 + temp_imp2
                + sbp_imp2 + map_imp2 + resp_imp2 + factor(hospid),
    data = filter(df_imp, iculos == 1),
    family = binomial(link = "logit")
)
```

[20]:

```
summary(model_imp2)
```

```
Call:
glm(formula = any_sepsis ~ -1 + age + gender + o2sat_imp2 + hr_imp2 +
    temp_imp2 + sbp_imp2 + map_imp2 + resp_imp2 + factor(hospid),
    family = binomial(link = "logit"), data = filter(df_imp,
        iculos == 1))

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.1188  -0.3487  -0.2969  -0.2530   2.9213

Coefficients:
                 Estimate Std. Error z value Pr(>|z|)
age              0.002011   0.001858   1.083 0.278993
gender           0.179775   0.060351   2.979 0.002894 **
o2sat_imp2      -0.003505   0.008713  -0.402 0.687495
hr_imp2          0.011096   0.001669   6.647 2.98e-11 ***
temp_imp2        0.036431   0.038238   0.953 0.340720
sbp_imp2         0.001067   0.002164   0.493 0.622103
map_imp2        -0.012117   0.003177  -3.814 0.000137 ***
resp_imp2        0.034078   0.005201   6.552 5.69e-11 ***
factor(hospid)A -4.629805   1.652233  -2.802 0.005076 **
factor(hospid)B -5.080070   1.648675  -3.081 0.002061 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 33309.9  on 24028  degrees of freedom
Residual deviance:  9339.9  on 24018  degrees of freedom
  (6897 observations deleted due to missingness)
AIC: 9359.9

Number of Fisher Scoring iterations: 6
```

[21]:

```
# Calculate odds ratio & 95% confidence interval
exp(coefficients(model_imp2)) %>%
    enframe(name = "variable", value = "odds ratio") %>%
    add_column(as_tibble(exp(confint(model_imp2))))
```

```
Waiting for profiling to be done…
```

A tibble: 10 × 4

variable	odds ratio	2.5 %	97.5 %
<chr>	<dbl>	<dbl>	<dbl>
age	1.002013075	0.9983839947	1.0056812
gender	1.196947746	1.0637620110	1.3477559
o2sat_imp2	0.996501380	0.9804169530	1.0145076
hr_imp2	1.011157302	1.0078466742	1.0144630
temp_imp2	1.037102407	0.9623432758	1.1179221
sbp_imp2	1.001067178	0.9968119421	1.0053017
map_imp2	0.987955994	0.9818196556	0.9941161
resp_imp2	1.034665510	1.0240921583	1.0452040
factor(hospid)A	0.009756666	0.0003699473	0.2408788
factor(hospid)B	0.006219472	0.0002375450	0.1525313

1.5.3 Higher respiration rate among those with sepsis?

[22]:

```
df_imp %>%
    group_by(patid) %>%
    filter(iculos == 1) %>%
    ungroup() %>% group_by(any_sepsis) %>%
    skim(resp_imp1)
```

```
  Data Summary
                           Values
Name                       Piped data
Number of rows             30925
Number of columns          32

_______________________
Column type frequency:
  numeric                  1

________________________
Group variables            any_sepsis

  Variable type: numeric

  skim_variable any_sepsis n_missing complete_rate  mean    sd    p0   p25   p50
p75  p100 hist
1 resp_imp1              0       960         0.967  18.2  4.42     1  15.4  17.9
20.4  98
2 resp_imp1              1        68         0.959  19.6  5.54     1  15.9  18.8
22.4  44.5
```

[23]:

```
df_imp %>%
    group_by(patid) %>%
    filter(iculos == 1) %>%
    ungroup() %>% group_by(any_sepsis) %>%
    skim(resp_imp2)
```

```
  Data Summary
                           Values
Name                       Piped data
Number of rows             30925
Number of columns          32
_______________________
Column type frequency:
  numeric                  1
________________________
Group variables            any_sepsis

  Variable type: numeric

  skim_variable any_sepsis n_missing complete_rate  mean    sd    p0   p25   p50
p75  p100 hist
1 resp_imp2              0       960         0.967  18.2  5.20     1  15      18
21      98
2 resp_imp2              1        68         0.959  19.5  6.08     1  15.5    19
22.5    50
```