

HIP: Demographic data for the manuscript

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Basic descriptive statistics of core demographic data at baseline (time = 0 weeks) for males, females, and the whole cohort.

Import data

```
# Get data
demo <- read_rds('./data/demographics.rds') %>%
  # Transfer CD4 data to CD4_recent if missing CD4_recent data (i.e. most updated CD4 count available)
  mutate(CD4_uptodate =
    ifelse(is.na(CD4_recent),
      CD4,
      CD4_recent)) %>%
  # Categorise years of schooling into 7 years or less, 8-12 years, and more than 12 years of education
  mutate(Education_category = case_when(
    Years_education <= 7 ~ "0-7 years",
    Years_education > 7 & Years_education <= 12 ~ "8-12 years",
    Years_education > 12 ~ "More than 12 years")) %>%
  # Select required columns
  select(ID,
    Site,
    Sex,
    Age,
    Years_on_ART,
    CD4_uptodate,
    HIV_mx,
    Education_category,
    SOS_mnemonic)

demo %<>% mutate(HIV_mx = case_when(
  HIV_mx == "first-line" ~ "first-line ART",
  HIV_mx == "second-line" ~ "second-line ART",
  HIV_mx == "monitoring" ~ "no ART"))

demo %<>% mutate(HIV_mx = factor(HIV_mx, levels = c("first-line ART", "second-line ART", "no ART")))

# Read in other outcomes info
bdi <- read_rds('./data/bdi.rds') %>%
  mutate(ID = stringr::str_to_upper(ID)) %>%
  select(ID,
    ends_with("BL")) %>%
  # Make a total score column
  mutate_at(.vars = 2:22, as.numeric) %>%
```

```

mutate(bdi_BL = rowSums(.[2:22], na.rm = TRUE),
      # Treat BDI as a discrete scale
      bdi_BL = as.integer(round(bdi_BL))) %>%
select(ID,
      bdi_BL)

bpi <- read_rds('./data/bpi.rds') %>%
mutate(ID = stringr::str_to_upper(ID)) %>%
select(ID,
      ends_with("BL")) %>%
# Select columns
select(ID,
      3:6,
      9:15) %>%
# Calculate PSS at baseline
mutate(PSS_BL = rowMeans(.[2:5], na.rm = TRUE),
      # Treat PSS as a discrete scale
      PSS_BL = as.integer(round(PSS_BL))) %>%
# Calculate PIS at baseline
mutate(PIS_BL = rowMeans(.[6:12], na.rm = TRUE),
      # Treat PIS as a discrete scale
      PIS_BL = as.integer(round(PIS_BL))) %>%
#remove unwanted columns
select(ID,
      PSS_BL,
      PIS_BL)

# EQ5D

eq5d <- read_rds('./data/eq5d.rds') %>%
mutate(ID = stringr::str_to_upper(ID)) %>%
select(ID,
      contains("BL"))

# Calculate eq5d index score for each time point
# Create basic term = 1 for all cases in new column
eq5d$index_core <- 1

# Sum all rows for total BL index score and allocate to a new column in eq5d data frame
eq5d %<>% mutate(BL_index_sum = rowSums(.[2:6], na.rm = TRUE))

# Create constant term to subtract if any domain scores > 1 (i.e. sum > 5)
eq5d %<>% mutate(EQ5D_constant_BL = ifelse(BL_index_sum > 5,
      yes = 0.081,
      no = 0))

# 1. Create variable for subtraction for each domain and time point:
# Call it (for example) BL_Mobility_index
# Use values from table in an ifelse statement
# THEN
# 2. Compute the index score for each time point using:
# BL_index_score = index_core - constant_index - BL_Mobility_index - (etc - for each domain).

```

```

# Baseline #
#####
eq5d %<>% mutate(BL_Mobility_index = ifelse(Mobility.BL == 2,
                                             yes = 0.069,
                                             no = ifelse(Mobility.BL == 3,
                                                         yes = 0.314,
                                                         no = 0)))

eq5d <- eq5d %>% mutate(BL_Self_care_index = ifelse(Self_care.BL == 2,
                                                    yes = 0.104,
                                                    no = ifelse(Self_care.BL == 3,
                                                                yes = 0.214,
                                                                no = 0)))

eq5d <- eq5d %>% mutate(BL_Usual_act_index = ifelse(Usual_activities.BL == 2,
                                                    yes = 0.036,
                                                    no = ifelse(Usual_activities.BL == 3,
                                                                yes = 0.094,
                                                                no = 0)))

eq5d <- eq5d %>% mutate(BL_EQ_Pain_index = ifelse(Pain.BL == 2,
                                                  yes = 0.123,
                                                  no = ifelse(Pain.BL == 3,
                                                              yes = 0.386,
                                                              no = 0)))

eq5d <- eq5d %>% mutate(BL_Anx_depr_index = ifelse(Anxiety_and_depression.BL == 2,
                                                  yes = 0.071,
                                                  no = ifelse(Anxiety_and_depression.BL == 3,
                                                              yes = 0.236,
                                                              no = 0)))

# Index score
eq5d %<>% mutate(eq5d_index_BL = index_core - EQ5D_constant_BL - BL_Mobility_index - BL_Self_care_index

eq5d %<>% select(ID,
                State_of_health.BL,
                eq5d_index_BL)

se6 <- read_rds('./data/se6.rds') %>%
  mutate(ID = stringr::str_to_upper(ID)) %>%
  select(ID,
         ends_with("BL")) %>%
  # Calculate SE6 at baseline
  mutate(se6_BL = rowMeans(.[2:7], na.rm = TRUE),
         # Treat SE6 as a discrete scale
         se6_BL = as.integer(round(se6_BL))) %>%
  #remove unwanted columns
  select(ID,
         se6_BL)

# Bind all together

```

```
Baseline <- left_join(demo, bdi) %>%
  left_join(bpi) %>%
  left_join(eq5d) %>%
  left_join(se6)
```

Quick look

```
glimpse(Baseline)
```

```
## Observations: 160
## Variables: 15
## $ ID <chr> "J1", "J3", "J4", "J5", "J6", "J7", "J9", "...
## $ Site <chr> "U1", "U1", "U1", "U1", "U1", "U1", "U1", "...
## $ Sex <chr> "female", "female", "female", "female", "fe...
## $ Age <dbl> 37, 36, 36, 58, 33, 32, 37, 46, 31, 36, 43,...
## $ Years_on_ART <dbl> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,...
## $ CD4_uptodate <dbl> 354, 728, 172, 189, NA, 86, 667, 205, 325, ...
## $ HIV_mx <fct> first-line ART, first-line ART, first-line ...
## $ Education_category <chr> "8-12 years", NA, "8-12 years", "0-7 years"...
## $ SOS_mnemonic <chr> NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,...
## $ bdi_BL <int> 46, 38, 8, 32, 28, 20, 23, 13, 38, 8, 22, 0...
## $ PSS_BL <int> 6, 4, 2, 7, 4, 6, 5, 6, 7, 0, 6, NA, 4, 6, ...
## $ PIS_BL <int> 5, 9, 1, 7, 3, 3, 3, 4, 6, 0, 5, NA, 5, 6, ...
## $ State_of_health.BL <int> 60, 0, 80, 60, 80, 80, 20, 60, 30, 90, 80, ...
## $ eq5d_index_BL <dbl> NA, 0.533, 0.727, 0.533, 0.812, 0.497, 0.72...
## $ se6_BL <int> 4, NA, 10, 9, 4, 10, 8, 10, 10, 9, 9, NA, 8...
```

```
Baseline %>%
  skim_to_wide() %>%
  select(variable, missing, complete, n) %>%
  mutate_at(.vars = c(2:4),
    .funs = as.numeric) %>%
  arrange(complete) %>%
  kable(caption = 'Tabular summary of data completeness')
```

Table 1: Tabular summary of data completeness

variable	missing	complete	n
Years_on_ART	78	82	160
SOS_mnemonic	47	113	160
se6_BL	18	142	160
eq5d_index_BL	18	142	160
PIS_BL	17	143	160
PSS_BL	16	144	160
State_of_health.BL	16	144	160
CD4_uptodate	8	152	160
HIV_mx	4	156	160
Education_category	2	158	160
ID	0	160	160
Sex	0	160	160

variable	missing	complete	n
Site	0	160	160
bdi_BL	0	160	160
Age	0	160	160

Sample size

```
# Rename a few columns
library(data.table)

Baseline %<>% select(ID,
                     Age,
                     Sex,
                     Education_category,
                     SOS_mnemonic,
                     Years_on_ART,
                     HIV_mx,
                     CD4_uptodate,
                     PSS_BL,
                     PIS_BL,
                     bdi_BL,
                     se6_BL,
                     State_of_health.BL,
                     eq5d_index_BL)

# Set variable labels for use in the table using labelled:var_label command

library(labelled)

# Load package
library(tableone)

# Create a list of the variables we want in Table 1

listVars <- c("Age", "Site", "Education_category", "SOS_mnemonic", "Years_on_ART", "HIV_mx", "CD4_uptodate", "PSS_BL", "PIS_BL", "bdi_BL", "se6_BL", "State_of_health.BL", "eq5d_index_BL")

#listVars <- c("Age", "Site", "CD4_uptodate", "HIV_mx", "Education_category", "SOS_mnemonic")

# Define categorical variables
catVars <- c("Site", "HIV_mx", "Education_category", "SOS_mnemonic", "Sex")

#catVars <- c("Site", "HIV_mx", "Education_category", "SOS_mnemonic", "Sex")

# Create Table 1
table1 <- CreateTableOne(listVars, Baseline, catVars, strata = c("Sex"))
table1
```

Stratified by Sex		
female	male	p

```

n 97 63
Age (mean (sd)) 34.23 (5.97) 36.76 (4.76) 0.005 Education_category (%) 0.511 0-7 years 26 (27.1) 18 (29.0)
8-12 years 68 (70.8) 44 (71.0)
More than 12 years 2 ( 2.1) 0 ( 0.0)
SOS_mnemonic = lhl (%) 59 (89.4) 19 (40.4) <0.001 Years_on_ART (mean (sd)) 3.46 (3.03) 3.92 (2.05)
0.550 HIV_mx (%) 0.101 first-line ART 65 (69.1) 50 (80.6)
second-line ART 24 (25.5) 12 (19.4)
no ART 5 ( 5.3) 0 ( 0.0)
CD4_uptodate (mean (sd)) 433.73 (273.51) 364.63 (202.50) 0.095 PSS_BL (mean (sd)) 5.05 (1.89) 5.00
(2.56) 0.886 PIS_BL (mean (sd)) 5.32 (2.39) 4.76 (2.88) 0.222 bdi_BL (mean (sd)) 24.26 (12.65) 13.62 (11.44)
<0.001 se6_BL (mean (sd)) 6.90 (2.31) 6.98 (2.16) 0.845 State_of_health.BL (mean (sd)) 58.12 (21.02) 62.08
(21.42) 0.285 eq5d_index_BL (mean (sd)) 0.61 (0.19) 0.64 (0.20) 0.282 Stratified by Sex test n
Age (mean (sd))
Education_category (%)
0-7 years
8-12 years
More than 12 years
SOS_mnemonic = lhl (%)
Years_on_ART (mean (sd))
HIV_mx (%)
first-line ART
second-line ART
no ART
CD4_uptodate (mean (sd))
PSS_BL (mean (sd))
PIS_BL (mean (sd))
bdi_BL (mean (sd))
se6_BL (mean (sd))
State_of_health.BL (mean (sd))
eq5d_index_BL (mean (sd))

```

```
summary(table1)
```

```
### Summary of continuous variables ###
```

```

Sex: female n miss p.miss mean sd median p25 p75 min Age 97 0 0 34.2 6.0 35.0 30.0 37.0 18.00 Years_on_ART
97 33 34 3.5 3.0 3.0 1.0 5.0 0.25 CD4_uptodate 97 5 5 433.7 273.5 410.5 244.8 570.5 3.00 PSS_BL 97 4 4 5.1
1.9 5.0 4.0 6.0 0.00 PIS_BL 97 5 5 5.3 2.4 5.0 4.0 7.0 0.00 bdi_BL 97 0 0 24.3 12.6 25.0 16.0 33.0 0.00 se6_BL
97 5 5 6.9 2.3 8.0 5.0 9.0 1.00 State_of_health.BL 97 4 4 58.1 21.0 60.0 50.0 75.0 0.00 eq5d_index_BL 97 5 5
0.6 0.2 0.7 0.5 0.8 -0.05 max skew kurt Age 58 0.52 2.2 Years_on_ART 13 1.20 1.5 CD4_uptodate 1189 0.68
0.3 PSS_BL 10 0.16 0.3 PIS_BL 10 -0.19 -0.4 bdi_BL 55 -0.02 -0.6 se6_BL 10 -0.60 -0.5 State_of_health.BL
90 -0.95 0.6 eq5d_index_BL 1 -0.94 1.1

```

```

Sex: male n miss p.miss
mean sd median p25 p75 min max Age 63 0 0 36.8 4.8 36.0 33.5 39.0 27.0 50 Years_on_ART 63 45 71 3.9
2.0 4.2 2.3 5.5 0.7 8 CD4_uptodate 63 3 5 364.6 202.5 335.0 210.5 491.8 30.0 1180 PSS_BL 63 12 19 5.0
2.6 5.0 4.0 6.0 0.0 10 PIS_BL 63 12 19 4.8 2.9 5.0 2.0 7.0 0.0 9 bdi_BL 63 0 0 13.6 11.4 13.0 4.0 20.0 0.0
45 se6_BL 63 13 21 7.0 2.2 7.0 6.0 8.8 1.0 10 State_of_health.BL 63 12 19 62.1 21.4 70.0 50.0 80.0 10.0
100 eq5d_index_BL 63 13 21 0.6 0.2 0.7 0.5 0.8 -0.2 1 skew kurt Age 0.74 0.90 Years_on_ART 0.19 -0.39
CD4_uptodate 1.15 3.01 PSS_BL -0.04 -0.23 PIS_BL -0.18 -1.18 bdi_BL 0.71 -0.03 se6_BL -0.69 -0.05
State_of_health.BL -0.73 0.38 eq5d_index_BL -1.86 5.46

```

```

p-values pNormal pNonNormal Age 5.177592e-03 3.368960e-03 Years_on_ART 5.501203e-01 1.510416e-
01 CD4_uptodate 9.526438e-02 1.420473e-01 PSS_BL 8.861168e-01 8.404495e-01 PIS_BL 2.222980e-01
3.354505e-01 bdi_BL 2.474301e-07 3.375732e-07 se6_BL 8.446852e-01 9.707170e-01 State_of_health.BL
2.846165e-01 3.083154e-01 eq5d_index_BL 2.823285e-01 2.778867e-01

```

```
Standardize mean differences 1 vs 2 Age 0.46965854 Years_on_ART 0.17638932 CD4_uptodate 0.28712964
```

PSS_BL 0.02388523 PIS_BL 0.20811628 bdi_BL 0.88210651 se6_BL 0.03481697 State_of_health.BL
0.18662583 eq5d_index_BL 0.18776135

=====

Summary of categorical variables

Sex: female var n miss p.miss level freq percent Education_category 97 1 1.0 0-7 years 26 27.1 8-12 years 68
70.8 More than 12 years 2 2.1

SOS_mnemonic	97	31	32.0		h1	7	10.6
					1h1	59	89.4
HIV_mx	97	3	3.1	first-line ART	65	69.1	
				second-line ART	24	25.5	
				no ART	5	5.3	

cum.percent 27.1 97.9 100.0

10.6
100.0

69.1
94.7
100.0

Sex: male var n miss p.miss level freq percent Education_category 63 1 1.6 0-7 years 18 29.0 8-12 years 44
71.0 More than 12 years 0 0.0

SOS_mnemonic	63	16	25.4		h1	28	59.6
					1h1	19	40.4
HIV_mx	63	1	1.6	first-line ART	50	80.6	
				second-line ART	12	19.4	
				no ART	0	0.0	

cum.percent 29.0 100.0 100.0

59.6
100.0

80.6
100.0
100.0

p-values pApprox pExact Education_category 5.109050e-01 6.930533e-01 SOS_mnemonic 9.174593e-08
3.255336e-08 HIV_mx 1.009954e-01 1.069525e-01

Standardize mean differences 1 vs 2 Education_category 0.2085443 SOS_mnemonic 1.1953390 HIV_mx
0.3823404

```
# Specify CD4 count must be treated as non-normal
biomarker <- "CD4_uptodate"
```

```
var_label(Baseline) <- list(
```

```

Education_category = "Education category",
SOS_mnemonic = "SOS mnemonic",
Years_on_ART = "Years on ART",
HIV_mx = "HIV treatment",
CD4_uptodate = "Most recent CD4 count",
PSS_BL = "Pain severity (PSS)",
PIS_BL = "Pain interference (PIS)",
bdi_BL = "Depression (BDI)",
se6_BL = "Self-efficacy (SE-6)",
State_of_health.BL = "HRQOL (EQ5D VAS)",
eq5d_index_BL = "HRQOL (EQ5D index)"

print(table1, nonnormal = biomarker, varLabels = TRUE)

```

Stratified by Sex
female

```

n 97
Age (mean (sd)) 34.23 (5.97)
Education_category (%)
0-7 years 26 (27.1)
8-12 years 68 (70.8)
More than 12 years 2 ( 2.1)
SOS_mnemonic = lhl (%) 59 (89.4)
Years_on_ART (mean (sd)) 3.46 (3.03)
HIV_mx (%)
first-line ART 65 (69.1)
second-line ART 24 (25.5)
no ART 5 ( 5.3)
CD4_uptodate (median [IQR]) 410.50 [244.75, 570.50] PSS_BL (mean (sd)) 5.05 (1.89)
PIS_BL (mean (sd)) 5.32 (2.39)
bdi_BL (mean (sd)) 24.26 (12.65)
se6_BL (mean (sd)) 6.90 (2.31)
State_of_health.BL (mean (sd)) 58.12 (21.02)
eq5d_index_BL (mean (sd)) 0.61 (0.19)
Stratified by Sex male p test
n 63
Age (mean (sd)) 36.76 (4.76) 0.005
Education_category (%) 0.511
0-7 years 18 (29.0)
8-12 years 44 (71.0)
More than 12 years 0 ( 0.0)
SOS_mnemonic = lhl (%) 19 (40.4) <0.001
Years_on_ART (mean (sd)) 3.92 (2.05) 0.550
HIV_mx (%) 0.101
first-line ART 50 (80.6)
second-line ART 12 (19.4)
no ART 0 ( 0.0)
CD4_uptodate (median [IQR]) 335.00 [210.50, 491.75] 0.142 nonnorm PSS_BL (mean (sd)) 5.00 (2.56) 0.886
PIS_BL (mean (sd)) 4.76 (2.88) 0.222
bdi_BL (mean (sd)) 13.62 (11.44) <0.001
se6_BL (mean (sd)) 6.98 (2.16) 0.845
State_of_health.BL (mean (sd)) 62.08 (21.42) 0.285
eq5d_index_BL (mean (sd)) 0.64 (0.20) 0.282

```



```
# Save output to txt
```

```
tab1Mat <- print(table1, nonnormal = biomarker, quote = FALSE, noSpaces = TRUE, printToggle = FALSE, va
## Save to a CSV file
write.csv(tab1Mat, file = "myTable1.csv")

read.csv("myTable1.csv")
```

```

X                                female
1 n 97 2 Age (mean (sd)) 34.23 (5.97) 3 Education_category (%)
4 0-7 years 26 (27.1) 5 8-12 years 68 (70.8) 6 More than 12 years 2 (2.1) 7 SOS_mnemonic = lhl (%) 59
(89.4) 8 Years_on_ART (mean (sd)) 3.46 (3.03) 9 HIV_mx (%)
10 first-line ART 65 (69.1) 11 second-line ART 24 (25.5) 12 no ART 5 (5.3) 13 CD4_uptodate (median
[IQR]) 410.50 [244.75, 570.50] 14 PSS_BL (mean (sd)) 5.05 (1.89) 15 PIS_BL (mean (sd)) 5.32 (2.39) 16
bdi_BL (mean (sd)) 24.26 (12.65) 17 se6_BL (mean (sd)) 6.90 (2.31) 18 State_of_health.BL (mean (sd))
58.12 (21.02) 19 eq5d_index_BL (mean (sd)) 0.61 (0.19) male p test 1 63
2 36.76 (4.76) 0.005
3 0.511
4 18 (29.0)
5 44 (71.0)
6 0 (0.0)
7 19 (40.4) <0.001
8 3.92 (2.05) 0.550
9 0.101
10 50 (80.6)
11 12 (19.4)
12 0 (0.0)
13 335.00 [210.50, 491.75] 0.142 nonnorm 14 5.00 (2.56) 0.886
15 4.76 (2.88) 0.222
16 13.62 (11.44) <0.001
17 6.98 (2.16) 0.845
18 62.08 (21.42) 0.285
19 0.64 (0.20) 0.282
```

```
library(ztable)
options(ztable.type="pdf")
z <- ztable(tab1Mat, align="ccccc")

rgroup <- c("", "Demographics", "HIV management", "Study outcomes")
n.rgroup <- c(1, 6, 6, 6)
z <- addrgroup(z, rgroup=rgroup, n.rgroup=n.rgroup, cspan.rgroup=1)
print(z)
```

female

male

p

test

n

97

63

Demographics

Age (mean (sd))

34.23 (5.97)

36.76 (4.76)

0.005

Education_category (%)

0.511

0-7 years

26 (27.1)

18 (29.0)

8-12 years

68 (70.8)

44 (71.0)

More than 12 years

2 (2.1)

0 (0.0)

SOS_mnemonic = lhl (%)

59 (89.4)

19 (40.4)

<0.001

HIV management

Years_on_ART (mean (sd))

3.46 (3.03)

3.92 (2.05)

0.550

HIV_mx (%)

0.101

first-line ART

65 (69.1)

50 (80.6)

second-line ART

24 (25.5)

12 (19.4)

no ART

5 (5.3)

0 (0.0)
 CD4_uptodate (median [IQR])
 410.50 [244.75, 570.50]
 335.00 [210.50, 491.75]
 0.142
 nonnorm
 Study outcomes
 PSS_BL (mean (sd))
 5.05 (1.89)
 5.00 (2.56)
 0.886
 PIS_BL (mean (sd))
 5.32 (2.39)
 4.76 (2.88)
 0.222
 bdi_BL (mean (sd))
 24.26 (12.65)
 13.62 (11.44)
 <0.001
 se6_BL (mean (sd))
 6.90 (2.31)
 6.98 (2.16)
 0.845
 State_of_health.BL (mean (sd))
 58.12 (21.02)
 62.08 (21.42)
 0.285
 eq5d_index_BL (mean (sd))
 0.61 (0.19)
 0.64 (0.20)
 0.282

Session information

```
## R version 3.4.3 (2017-11-30)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: OS X El Capitan 10.11.6
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.4/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] ztable_0.1.5      tableone_0.9.2      labelled_1.0.1
## [4] data.table_1.10.4-3 bindrcpp_0.2        magrittr_1.5
## [7] skimr_1.0.1        forcats_0.3.0       stringr_1.3.0
## [10] dplyr_0.7.4        purrr_0.2.4         readr_1.1.1
## [13] tidyr_0.8.0        tibble_1.4.2        ggplot2_2.2.1.9000
## [16] tidyverse_1.2.1
##
## loaded via a namespace (and not attached):
## [1] Rcpp_0.12.16      lubridate_1.7.3     lattice_0.20-35
## [4] class_7.3-14      zoo_1.8-1           assertthat_0.2.0
## [7] rprojroot_1.3-2   digest_0.6.15       psych_1.7.8
## [10] R6_2.2.2          cellranger_1.1.0    plyr_1.8.4
## [13] backports_1.1.2   survey_3.33-2       evaluate_0.10.1
## [16] e1071_1.6-8       httr_1.3.1          highr_0.6
## [19] pillar_1.2.1      rlang_0.2.0         lazyeval_0.2.1
## [22] readxl_1.0.0      rstudioapi_0.7      Matrix_1.2-12
## [25] rmarkdown_1.9     splines_3.4.3       foreign_0.8-69
## [28] pander_0.6.1      munsell_0.4.3       broom_0.4.3
## [31] compiler_3.4.3    modelr_0.1.1        pkgconfig_2.0.1
## [34] mnormt_1.5-5      htmltools_0.3.6     tidyselect_0.2.4
## [37] crayon_1.3.4      MASS_7.3-49         grid_3.4.3
## [40] nlme_3.1-131.1    jsonlite_1.5         gtable_0.2.0
## [43] scales_0.5.0.9000 cli_1.0.0            stringi_1.1.7
## [46] reshape2_1.4.3    xml2_1.2.0          tools_3.4.3
## [49] glue_1.2.0        hms_0.4.2           parallel_3.4.3
## [52] survival_2.41-3   yaml_2.1.18         colorspace_1.3-2
## [55] rvest_0.3.2       knitr_1.20          bindr_0.1.1
## [58] haven_1.1.1
```