# Multivariate Analysis for the Behavioral Sciences, Second Edition (Chapman and Hall/CRC, 2019)

# Examples of Chapter 11: Missing Values

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### Examples

# Table 11.1: Car Wash Data That Includes Missing Values

```
library("tidyr"); library("dplyr")
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
       filter, lag
##
## The following objects are masked from 'package:base':
##
       intersect, setdiff, setequal, union
WASH2 <- read.table("data/carwash2.txt", sep = ' ', header = TRUE)
glimpse(WASH2)
## Observations: 20
## Variables: 3
## $ Time <int> 46, 79, 63, 42, 44, 59, 27, 40, 30, 61, 50, 65, 70, 20, ...
## $ Age <int> NA, NA, 26, 34, NA, 26, 25, NA, 45, 31, 28, 34, 44, NA, ...
## $ Extro <int> 40, NA, NA, 43, 41, 42, NA, 30, 35, 48, 37, NA, NA, 28, ...
WASH2
      Time Age Extro
##
## 1
        46 NA
## 2
       79
           NA
                  NA
## 3
       63 26
                  NA
## 4
       42 34
                  43
## 5
       44 NA
                  41
## 6
       59
           26
                  42
## 7
       27
           25
                  NA
## 8
       40 NA
                  30
## 9
       30
           45
                  35
       61 31
## 10
                  48
## 11
       50
           28
                  37
## 12
       65 34
                  NA
## 13
       70 44
                  NA
## 14
       20 NA
                  28
## 15
       32 NA
                  34
           28
## 16
       65
                  44
## 17
       30
           50
                  33
        48 23
## 18
                  NA
## 19
       20 NA
                  NA
## 20
       56 NA
                  47
```

```
fit02 <- lm(Time ~ Age + Extro, data = WASH2)</pre>
summary(fit02)
##
## Call:
## lm(formula = Time ~ Age + Extro, data = WASH2)
## Residuals:
##
        4
                6
                        9
                             10
                                      11
                                              16
                                                      17
## -9.3856  0.6487 -2.5691  1.7053 -1.4362  6.6655  4.3713
##
## Coefficients:
##
              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 42.8029 38.6640
                                  1.107 0.3304
## Age
              -0.9939
                          0.3979 -2.498 0.0669 .
## Extro
                0.9855
                          0.6849
                                  1.439 0.2236
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.396 on 4 degrees of freedom
## (13 observations deleted due to missingness)
## Multiple R-squared: 0.8708, Adjusted R-squared: 0.8063
## F-statistic: 13.49 on 2 and 4 DF, p-value: 0.01668
```

```
#install.packages("mice")
library("mice")
## Loading required package: lattice
##
## Attaching package: 'mice'
## The following object is masked from 'package:tidyr':
##
##
      complete
## The following objects are masked from 'package:base':
##
      cbind, rbind
imp1_WASH2 <- mice(WASH2, method = "mean", m = 1, maxit = 1, seed = 2018)
##
## iter imp variable
   1
        1 Age Extro
fit12 <- with(imp1_WASH2,
             lm(Time ~ Age + Extro))
summary(fit12)
##
                                          statistic
           term
                    estimate std.error
                                                       p.value
## 1 (Intercept) -20.84188389 37.9367823 -0.54938460 0.58988618
## 2
            Age -0.05408842 0.5452381 -0.09920148 0.92213870
                 1.81191481 0.7339292 2.46878707 0.02445887
summary(fit12$analyses[[1]]) # single data: get the traditional summary
##
## Call:
## lm(formula = Time ~ Age + Extro)
##
## Residuals:
##
      Min
               1Q Median
                               3Q
                                      Max
## -27.350 -7.782 -3.656 7.789 31.650
##
## Coefficients:
               Estimate Std. Error t value Pr(>|t|)
##
## (Intercept) -20.84188 37.93678 -0.549
                                            0.5899
## Age
               -0.05409
                           0.54524 -0.099
                                             0.9221
## Extro
                1.81191
                           0.73393
                                    2.469
                                             0.0245 *
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 15.36 on 17 degrees of freedom
## Multiple R-squared: 0.2877, Adjusted R-squared: 0.2039
## F-statistic: 3.433 on 2 and 17 DF, p-value: 0.05593
```

```
library("mice")
imp2_WASH2 <- mice(WASH2, method = "pmm", m = 5, seed = 2018, print = TRUE)
##
   iter imp variable
##
##
       1 Age Extro
    1
##
    1
       2 Age Extro
##
    1
       3 Age Extro
##
      4 Age Extro
    1
##
      5 Age Extro
    1
##
    2
      1 Age Extro
##
    2
      2 Age Extro
##
    2
      3 Age Extro
##
    2
      4 Age Extro
##
    2
      5 Age Extro
##
    3
      1 Age Extro
##
    3
      2 Age Extro
      3 Age Extro
##
    3
##
    3
      4 Age Extro
   3
##
      5 Age Extro
##
   4
      1 Age Extro
      2 Age Extro
##
    4
##
   4
      3 Age Extro
##
    4
      4 Age Extro
      5 Age Extro
##
    4
##
    5
      1 Age Extro
   5
##
      2 Age Extro
##
    5
      3 Age Extro
##
    5
      4 Age Extro
       5 Age Extro
fit22 <- with(imp2_WASH2,</pre>
            lm(Time ~ Age + Extro))
summary(pool(fit22))
                                                    p.value
              estimate std.error statistic
                                               df
## (Intercept) -13.050709 45.9645422 -0.2839299 4.682013 0.78167580
## Age
            1.795865 0.9101368 1.9731811 3.587528 0.07381966
## Extro
```

## Beat the Blues Revisited (Again)

Using the Beat the Blues data introduced in Chapter 9 and revisited in Chapter 10:

```
BtB <- read.table("data/BtB.txt", header = TRUE, sep = '\t')</pre>
# to make sure that the factor levels are logical (esp. Treatment):
BtB <- within(BtB, {
      Drug <- factor(Drug, levels=c("No", "Yes")) # default</pre>
    Length <- factor(Length, levels=c("<6m", ">6m")) # default
 Treatment <- factor(Treatment, levels=c("TAU", "BtheB")) # NOT default!
})
glimpse(BtB); head(BtB); tail(BtB)
## Observations: 100
## Variables: 9
## $ Subject
              <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 1...
## $ Drug
              <fct> No, Yes, Yes, No, Yes, Yes, Yes, No, Yes, Yes, No, Y...
              ## $ Length
## $ Treatment <fct> TAU, BtheB, TAU, BtheB, BtheB, TAU, TAU, Bthe...
## $ BDIpre
              <int> 29, 32, 25, 21, 26, 7, 17, 20, 18, 20, 30, 49, 26, 3...
## $ BDI2m
              <int> 2, 16, 20, 17, 23, 0, 7, 20, 13, 5, 32, 35, 27, 26, ...
## $ BDI4m
              <int> 2, 24, NA, 16, NA, 0, 7, 21, 14, 5, 24, NA, 23, 36, ...
## $ BDI6m
              <int> NA, 17, NA, 10, NA, 0, 3, 19, 20, 8, 12, NA, NA, 27,...
## $ BDI8m
              <int> NA, 20, NA, 9, NA, 0, 7, 13, 11, 12, 2, NA, NA, 22, ...
    Subject Drug Length Treatment BDIpre BDI2m BDI4m BDI6m BDI8m
##
## 1
          1
              No
                    >6m
                              TAU
                                      29
                                             2
                                                   2
                                                        NA
## 2
          2
             Yes
                    >6m
                            BtheB
                                      32
                                            16
                                                  24
                                                        17
                                                              20
## 3
          3
             Yes
                    <6m
                              TAU
                                      25
                                            20
                                                  NA
                                                        NA
                                                              NA
## 4
          4
                    >6m
                                      21
                                            17
                                                  16
                                                        10
                                                               9
              No
                            BtheB
                    >6m
                                      26
                                            23
                                                              NA
## 5
          5
             Yes
                            BtheB
                                                  NA
                                                        NA
## 6
          6
             Yes
                    <6m
                            BtheB
                                       7
                                             0
                                                   0
                                                         0
                                                               0
      Subject Drug Length Treatment BDIpre BDI2m BDI4m BDI6m BDI8m
##
## 95
           95
                No
                      >6m
                              BtheB
                                        16
                                              11
                                                           2
## 96
                      >6m
           96
               Yes
                              BtheB
                                        16
                                              16
                                                    10
                                                          10
                                                                 8
## 97
           97
                      <6m
                                TAU
                                        28
                                              NA
                                                    NA
                                                          NA
                                                                NA
               Yes
                                              22
## 98
           98
                      >6m
                                        11
                                                     9
                                                                11
                No
                              BtheB
                                                          11
## 99
           99
                                        13
                                               5
                                                     5
                                                           0
                                                                 6
                No
                      <6m
                                TAU
## 100
                                TAU
                                        43
                                              NA
           100
               Yes
                      <6m
                                                    NA
                                                          NA
                                                                NA
# Convert data to long form for the analyses, adding Time:
BtBL <- gather(BtB, key = Visit, value = BDI, BDI2m, BDI4m, BDI6m, BDI8m) %>%
 mutate(Time = as.integer(substr(Visit, 4, 4)))
glimpse(BtBL); head(BtBL); tail(BtBL)
## Observations: 400
## Variables: 8
## $ Subject
              <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 1...
## $ Drug
              <fct> No, Yes, Yes, No, Yes, Yes, Yes, No, Yes, Yes, No, Y...
## $ Length
              ## $ Treatment <fct> TAU, BtheB, TAU, BtheB, BtheB, BtheB, TAU, TAU, Bthe...
## $ BDIpre
              <int> 29, 32, 25, 21, 26, 7, 17, 20, 18, 20, 30, 49, 26, 3...
```

```
## $ Visit
              <chr> "BDI2m", "BDI2m", "BDI2m", "BDI2m", "BDI2m", "BDI2m"...
## $ BDI
              <int> 2, 16, 20, 17, 23, 0, 7, 20, 13, 5, 32, 35, 27, 26, ...
## $ Time
              Subject Drug Length Treatment BDIpre Visit BDI Time
## 1
          1
              No
                   >6m
                             TAU
                                    29 BDI2m
                                               2
                                                   2
## 2
          2 Yes
                                    32 BDI2m
                                                   2
                   >6m
                           BtheB
                                             16
## 3
                             TAU
                                    25 BDI2m
                                                   2
          3
            Yes
                   <6m
                                             20
## 4
          4
                                    21 BDI2m
                                              17
                                                   2
              No
                   >6m
                           BtheB
## 5
          5 Yes
                   >6m
                           BtheB
                                    26 BDI2m
                                             23
                                                   2
                                                   2
## 6
          6 Yes
                                     7 BDI2m
                                              0
                   <6m
                           BtheB
      Subject Drug Length Treatment BDIpre Visit BDI Time
##
## 395
           95
               No
                     >6m
                             BtheB
                                      16 BDI8m
                                                3
                                                     8
## 396
                                      16 BDI8m
           96
              Yes
                     >6m
                             BtheB
                                                     8
## 397
           97
              Yes
                     <6m
                               TAU
                                      28 BDI8m
                                               NA
                                                     8
## 398
           98
               No
                     >6m
                             BtheB
                                      11 BDI8m
                                                11
                                                     8
## 399
           99
               No
                     <6m
                               TAU
                                      13 BDI8m
                                                6
                                                     8
## 400
                                      43 BDI8m
          100 Yes
                     <6m
                               TAU
                                               NA
                                                     8
```

```
library("mice")
imp1_BtB <- mice(BtBL, method = "mean", m = 1, maxit = 1, seed = 2019)</pre>
##
##
  iter imp variable
        1 BDI
##
   1
## Warning: Number of logged events: 1
fit0mean <- with(imp1_BtB,
                lm(BDI ~ BDIpre + Time + Treatment + Drug + Length))
summary(fit0mean)
##
                     estimate std.error statistic
              term
                                                        p.value
## 1
        (Intercept) 10.4971960 1.41511372 7.417917 7.372448e-13
            BDIpre 0.3563400 0.03866106 9.217025 1.859872e-18
              Time -0.6810893 0.17778482 -3.830975 1.484779e-04
## 4 TreatmentBtheB -2.6111204 0.83967818 -3.109668 2.009121e-03
## 5
           DrugYes -1.8077718 0.87095075 -2.075630 3.857633e-02
         Length>6m 2.3140858 0.81990676 2.822377 5.008494e-03
summary(fit0mean$analyses[[1]]) # single data: get the traditional summary
##
## Call:
## lm(formula = BDI ~ BDIpre + Time + Treatment + Drug + Length)
##
## Residuals:
##
                     Median
                                   3Q
       Min
                 1Q
                                           Max
## -22.1132 -4.6752 -0.2941 4.0395 30.9403
## Coefficients:
##
                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                             1.41511
                                      7.418 7.37e-13 ***
                 10.49720
## BDIpre
                  0.35634
                             0.03866
                                      9.217 < 2e-16 ***
## Time
                 -0.68109
                             0.17778 -3.831 0.000148 ***
## TreatmentBtheB -2.61112
                             0.83968 -3.110 0.002009 **
## DrugYes
                -1.80777
                             0.87095 -2.076 0.038576 *
## Length>6m
                  2.31409
                             0.81991
                                      2.822 0.005008 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 7.951 on 394 degrees of freedom
## Multiple R-squared: 0.269, Adjusted R-squared: 0.2597
                 29 on 5 and 394 DF, p-value: < 2.2e-16
## F-statistic:
```

```
imp2_BtB <- mice(BtBL, method = "pmm", m = 5, seed = 2020, print = FALSE)
## Warning: Number of logged events: 1
fit0mi <- with(imp2_BtB,</pre>
              lm(BDI ~ BDIpre + Time + Treatment + Drug + Length))
summary(pool(fit0mi))
                  estimate std.error statistic
                                                       df
                                                              p.value
## (Intercept)
                 11.237577 2.05663684 5.464055 26.40342 1.236282e-07
## BDIpre
                 0.342330 0.04662927 7.341525 223.77554 3.877343e-12
## Time
                 -0.956200 0.21465531 -4.454584 219.49920 1.327789e-05
## TreatmentBtheB -3.572554 1.52330496 -2.345265 10.57120 1.988848e-02
## DrugYes -2.322066 1.20899720 -1.920654 36.67885 5.604625e-02
## Length>6m
                 4.033926 1.07151103 3.764708 65.89928 2.131144e-04
```

```
# install.packages("lme4")
library("lme4")
## Loading required package: Matrix
##
## Attaching package: 'Matrix'
## The following object is masked from 'package:tidyr':
##
##
       expand
imp1_BtB <- mice(BtBL, method = "mean", m = 1, maxit = 1, seed = 2019)</pre>
##
##
   iter imp variable
    1
        1 BDI
## Warning: Number of logged events: 1
fit1mean <- with(imp1_BtB,
                 lmer(BDI ~ BDIpre + Time + Treatment + Drug + Length + (1 | Subject)))
summary(fit1mean)
##
               term
                      estimate std.error statistic
## 1
        (Intercept) 10.4971960 1.86230332 5.636674
## 2
            BDIpre 0.3563400 0.06142892 5.800850
              Time -0.6810893 0.12765705 -5.335305
## 4 TreatmentBtheB -2.6111204 1.33417245 -1.957109
            DrugYes -1.8077718 1.38386172 -1.306324
## 6
         Length>6m 2.3140858 1.30275745 1.776298
summary(fit1mean$analyses[[1]]) # single data: get the traditional summary
## Linear mixed model fit by REML ['lmerMod']
## Formula: BDI ~ BDIpre + Time + Treatment + Drug + Length + (1 | Subject)
##
## REML criterion at convergence: 2679.7
##
## Scaled residuals:
##
               1Q Median
      Min
                                3Q
                                       Max
## -2.6348 -0.5627 -0.0602 0.4319 4.2923
##
## Random effects:
## Groups Name
                         Variance Std.Dev.
## Subject (Intercept) 31.75
                                  5.635
## Residual
                         32.59
                                  5.709
## Number of obs: 400, groups: Subject, 100
##
## Fixed effects:
##
                  Estimate Std. Error t value
                            1.86230
## (Intercept)
                  10.49720
                                        5.637
## BDIpre
                  0.35634
                              0.06143
                                       5.801
## Time
                 -0.68109
                             0.12766 -5.335
                             1.33417 -1.957
## TreatmentBtheB -2.61112
```

```
-1.80777 1.38386 -1.306
## DrugYes
## Length>6m
             2.31409 1.30276 1.776
##
```

## Correlation of Fixed Effects:

(Intr) BDIpre Time TrtmBB DrugYs

## BDIpre -0.671 ## Time -0.343 0.000

## TretmntBthB -0.365 0.145 0.000

## DrugYes -0.086 -0.246 0.000 -0.311 ## Length>6m -0.243 -0.201 0.000 -0.048 0.181

```
imp2_BtB <- mice(BtBL, method = "pmm", m = 5, seed = 2020, print = FALSE)
## Warning: Number of logged events: 1
fit1mi <- with(imp2_BtB,</pre>
              lmer(BDI ~ BDIpre + Time + Treatment + Drug + Length + (1 | Subject)))
summary(pool(fit1mi))
                                                              p.value
                  estimate std.error statistic
                                                      df
## (Intercept)
                 11.237577 2.3320020 4.818854 41.55931 2.246766e-06
                 0.342330 0.0636655 5.377009 315.61685 1.476294e-07
## BDIpre
## Time
                 -0.956200 0.1828993 -5.228013 159.76439 3.123800e-07
## TreatmentBtheB -3.572554 1.7907569 -1.994997 19.70943 4.690280e-02
## DrugYes
              -2.322066 1.5541164 -1.494139 84.84596 1.361384e-01
## Length>6m
                 4.033926 1.4118211 2.857250 145.24565 4.557036e-03
```