Supplement 3

Exploratory analysis of predictors of study dropout by week 8

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Contents

We assessed four predictors of dropout (employment status, depression, study group allocation, and sex) from the study by week 8. Week 8 is the time point 2 weeks after the completion on the 6 week programme.

Import data

```
# Get data
## BPI
bpi <- read_rds('data-cleaned/bpi.rds') %>%
    select(ID, Pain_present.Wk8)

## Demographics
demo <- read_rds('data-cleaned/demographics.rds') %>%
    select(ID, Study_site, Group, Sex, Occupation)
```

```
## BDI
bdi <- read_rds('data-cleaned/bdi.rds') %>%
    select(ID, ends_with('BL'))
```

Quick look

```
glimpse(bpi)
```

```
## Observations: 160
## Variables: 2
## $ ID               <chr> "J1", "J3", "J4", "J5", "J6", "J7", "J9", "J1...
## $ Pain_present.Wk8 <chr> NA, NA, "Yes", NA, NA, NA, "Yes", "Yes", "Yes...
```

```
glimpse(demo)
```

```
## Observations: 160
## Variables: 5
## $ ID         <chr> "J1", "J3", "J4", "J5", "J6", "J7", "J9", "J10", "J...
## $ Study_site <chr> "U1", "U1", "U1", "U1", "U1", "U1", "U1", "U1", "U1...
## $ Group      <chr> "P", "T", "P", "P", "P", "T", "T", "T", "P", "T", "...
## $ Sex        <chr> "female", "female", "female", "female", "female", "...
## $ Occupation <chr> "employed", NA, "employed", "unemployed - looking f...
```

```
glimpse(bdi)
```

```
## Observations: 160
## Variables: 22
## $ ID                          <chr> "J1", "J3", "J4", "J5", "J6", "J7"...
## $ Sadness.BL                  <int> 1, 3, 0, 0, 2, 1, 0, 1, 3, 0, 3, N...
## $ Pessimism.BL                <int> 2, 3, 0, 1, 0, 0, 0, 0, 0, 1, 2, N...
## $ Past_failures.BL            <int> 2, 3, 0, 2, 1, 0, 0, 0, 2, 0, 0, N...
## $ Loss_of_pleasure.BL         <int> 2, 2, 1, 3, 2, 0, 1, 1, 2, 1, 0, N...
## $ Guilty_feelings.BL          <int> 2, 3, 0, 0, 1, 3, 0, 0, 2, 0, 0, N...
## $ Punishment_feelings.BL      <int> 3, 3, 0, 3, 3, 0, 0, 0, 3, 0, 0, N...
## $ Self_dislike.BL             <int> 1, 2, 0, 1, 1, 0, 0, 0, 2, 0, 0, N...
## $ Self_critical.BL            <int> 3, 3, 0, 3, 0, 0, 3, 0, 3, 0, 3, N...
## $ Suicidal.BL                 <int> 3, 1, 0, 0, 1, 0, 0, 0, 0, 0, 0, N...
## $ Crying.BL                   <int> 3, 1, 0, 0, 2, 2, 3, 0, 3, 0, 3, N...
## $ Agitation.BL                <int> 3, 1, 3, 2, 3, 3, 3, 3, 3, 0, 3, N...
## $ Loss_of_interest.BL         <int> 3, 1, 0, 1, 1, 0, 3, 0, 0, 0, 0, N...
## $ Indecisiveness.BL           <int> 2, 2, 0, 3, 2, 0, 1, 0, 0, 0, 0, N...
## $ Worthlessness.BL            <int> 2, 3, 1, 2, 2, 0, 0, 1, 0, 0, 0, N...
## $ Loss_of_energy.BL           <int> 1, 1, 0, 1, 0, 0, 2, 1, 2, 0, 2, N...
## $ Sleep.BL                    <int> 3, 0, 2, 1, 1, 2, 2, 2, 3, 2, 2, N...
## $ Irritability.BL             <int> 2, 3, 0, 1, 2, 3, 1, 0, 1, 0, 2, N...
## $ Appetite.BL                 <int> 1, 1, 0, 2, 0, 2, 0, 3, 3, 2, 0, N...
## $ Concentration_difficulty.BL <int> 3, 1, 0, 2, 1, 0, 2, 0, 0, 0, 0, N...
## $ Fatigue.BL                  <int> 2, 0, 0, 1, 0, 2, 1, 0, 3, 1, 2, N...
## $ Loss_of_interest_in_sex.BL  <int> 2, 1, 1, 3, 3, 2, 1, 1, 3, 1, 0, N...
```

Clean data

```
#################################################################
#                                                               #
#                            BPI                                #
#                                                               #
#################################################################
# Recode whether there is pain data at week 8 (data completeness)
bpi %<>%
    select(ID, Pain_present.Wk8) %>%
    mutate(coding = ifelse(is.na(Pain_present.Wk8),
                           yes = 'Data missing',
                           no = 'Data available')) %>%
    select(-Pain_present.Wk8)

#################################################################
#                                                               #
#                        Demographics                           #
#                                                               #
#################################################################
# Mutate new column to reclassify employment status into income grouping
# Employment status was recoded as stable income (employed or on a grant)
# or unstable income (all other categories, including being a student).
demo %<>%
    mutate(income_stability = case_when(
        Occupation == "employed" |
            Occupation == "unable to work - disability grant" ~ "Stable income",
        Occupation == "student/volunteer" |
            Occupation == "unemployed - looking for work" |
            Occupation == "unemployed - not looking for work" ~ "Unstable or no income"
        )) %>%
    select(ID, Study_site, Group, Sex, income_stability)

# Join with completeness ('bpi') data
demo %<>%
    left_join(bpi)

#################################################################
#                                                               #
#                            BDI                                #
#                                                               #
#################################################################
# Calculate BDI total score
bdi %<>%
    mutate_at(.vars = 2:22,
              .funs = as.integer) %>%
    mutate(Total.BL = rowSums(.[2:22]))

# Join with demo to get site info
bdi %<>%
    left_join(demo) %>%
    select(ID, Study_site, Total.BL)

# Convert total BDI scores into categories
```

```
## Site U1 used BDI II
## Site U2, R1, and R2 used BDI I
bdi %<>%
    mutate(bdi_category = case_when(
    Study_site == "U1" & Total.BL <= 13 ~ "none-minimal",
    Study_site == "U1" & Total.BL > 13 & Total.BL <= 19 ~ "mild",
    Study_site == "U1" & Total.BL > 19 & Total.BL <= 28 ~ "moderate-severe",
    Study_site == "U1" & Total.BL > 28 ~ "severe",
    Study_site != "U1" & Total.BL <= 9 ~ "none-minimal",
    Study_site != "U1" & Total.BL > 9 & Total.BL <= 18 ~ "mild",
    Study_site != "U1" & Total.BL > 18 & Total.BL <= 29 ~ "moderate-severe",
    Study_site != "U1" & Total.BL > 29 ~ "severe"))

# Convert bdi category into an ordered factor
bdi %<>% mutate(bdi_category = factor(bdi_category,
                                      levels = c("none-minimal",
                                                 "mild",
                                                 "moderate-severe",
                                                 "severe"),
                                      ordered = TRUE))
# Drop Site column
bdi %<>%
    select(-Study_site)

# Join with completeness ('bpi') data
bdi %<>%
    left_join(bpi)
```

Employment/income stability

Tabulate

(no stratification by study site)

```
demo %>% group_by(income_stability) %>%
    summarise(count = n()) %>%
    kable(., caption = 'Access to stable income',
          col.names = c('', 'Count'))
```

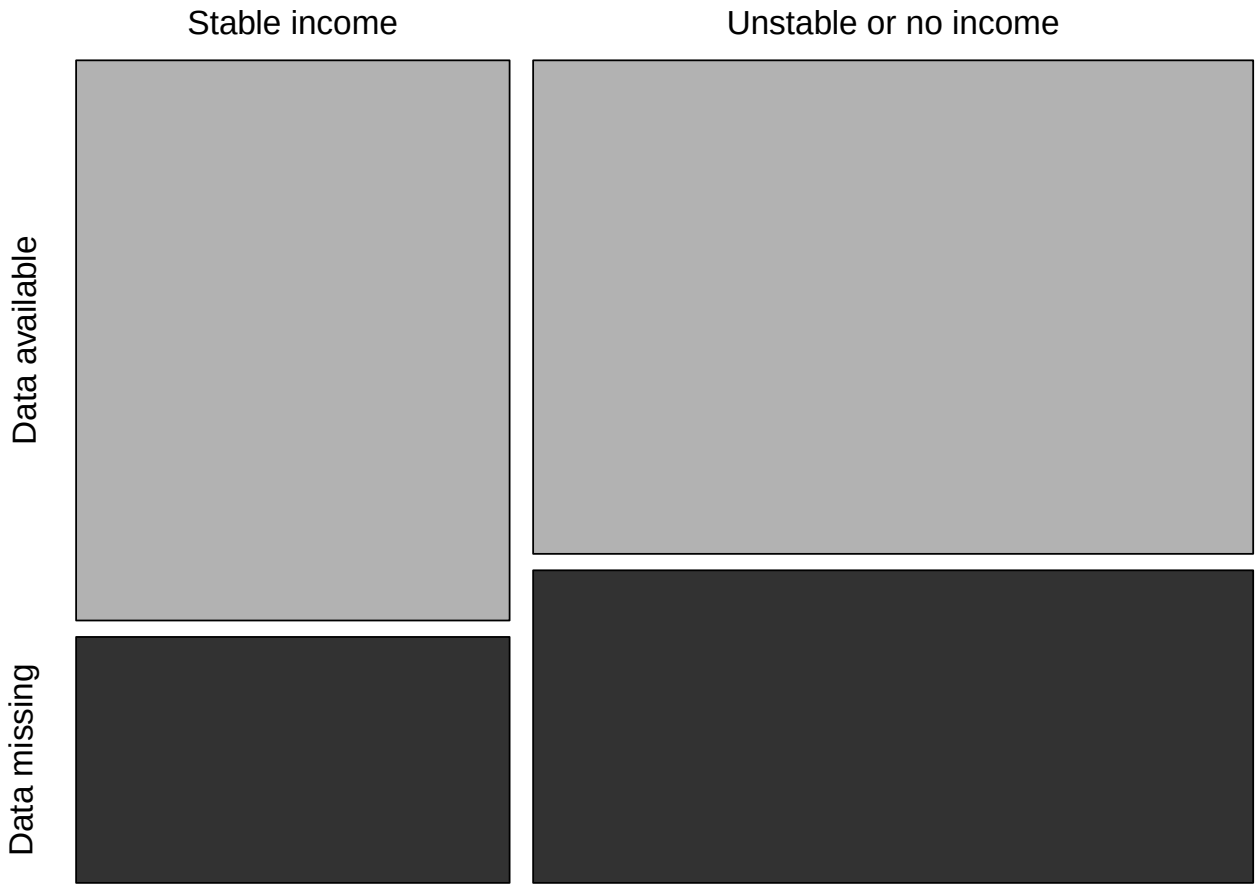
Table 1: Access to stable income

	Count
Stable income	59
Unstable or no income	98
NA	3

Null hypothesis significance testing (NHST)

```
# xtabulate the data
employ <- xtabs(~ income_stability + coding,
```

```
                data = demo)

# Produce mosaic plot
mosaicplot(employ,
           main = 'Income stability vs data completeness',
           xlab = '',
           ylab = '',
           cex = 1.2,
           color = c('#B2B2B2', '#323232'))
```




```
# Fishers exact test
kable(tidy(fisher.test(employ)),
      caption = 'Association between income stability and data completeness',
      col.names = c('Estimate', 'p-value',
                    'Lower 95% CI', 'Upper 95% CI',
                    'Method', 'Alternative'),
      digits = 3)
```

Table 2: Association between income stability and data completeness

Estimate	p-value	Lower 95% CI	Upper 95% CI	Method	Alternative
1.439	0.309	0.691	3.067	Fisher's Exact Test for Count Data	two.sided

---

Depression and anxiety

Tabulate

(no stratification by study site)

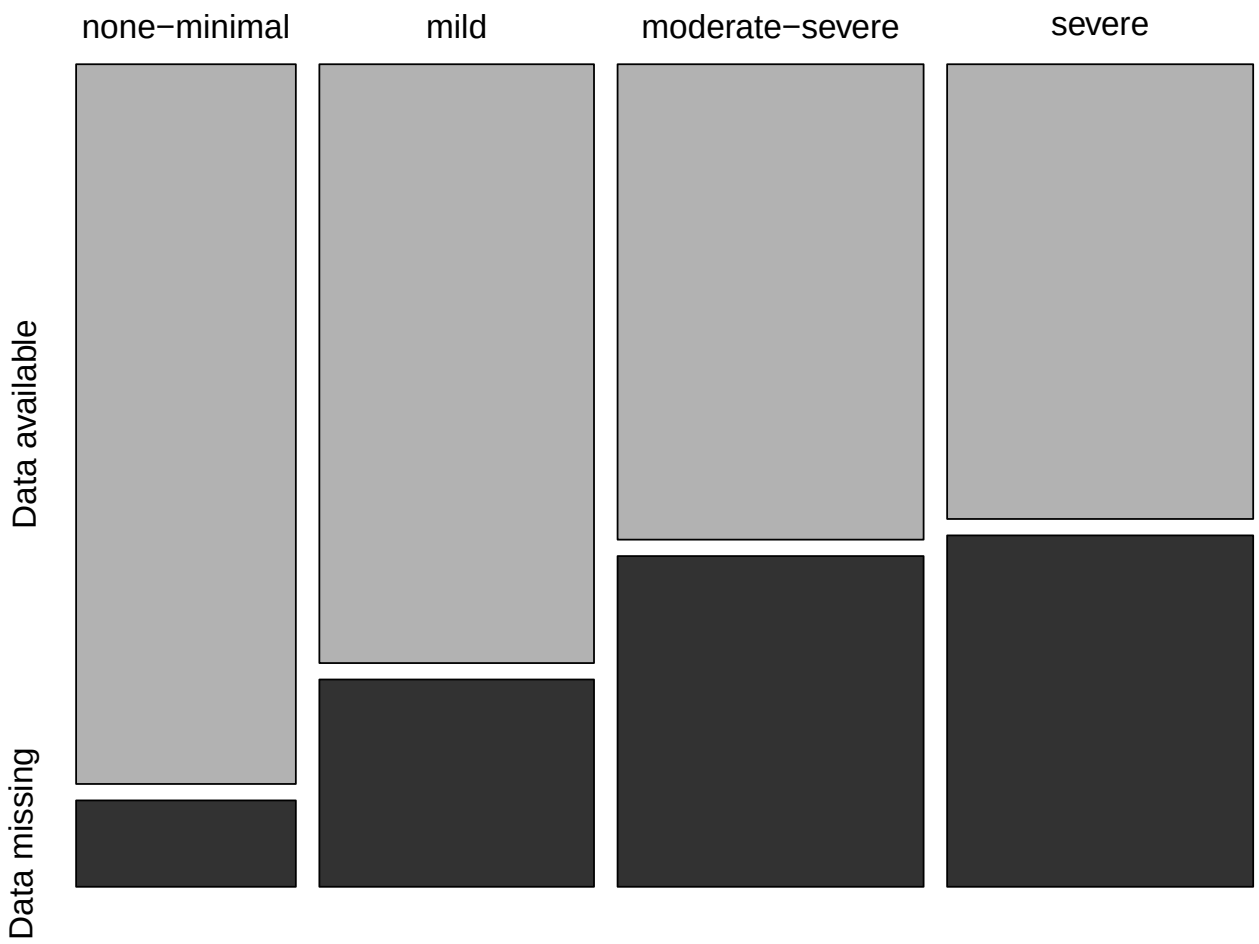
```
bdi %>% group_by(bdi_category) %>%
    summarise(count = n()) %>%
    kable(., caption = 'BDI severity category',
          col.names = c('', 'Count'))
```

Table 3: BDI severity category

	Count
none-minimal	28
mild	35
moderate-severe	39
severe	39
NA	19

Null hypothesis significance testing (NHST)

```
# xtabulate the data
depression <- xtabs(~ bdi_category + coding,
                    data = bdi)

# Produce mosaic plot
mosaicplot(depression,
           main = 'Depression severity vs data completeness',
           xlab = '',
           ylab = '',
           cex = 1.2,
           color = c('#B2B2B2', '#323232'))
```




```
# Logistic regression on ordered independent variable
model <- glm(factor(coding) ~ bdi_category,
             data = bdi,
             family = binomial(link = "logit"))

# Model summary
car::Anova(model)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: factor(coding)
##              LR Chisq Df Pr(>Chisq)
## bdi_category     11.4  3    0.00975 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Model summary
summary(model)
```

```
##
## Call:
## glm(formula = factor(coding) ~ bdi_category, family = binomial(link = "logit"),
##     data = bdi)
```

```
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.070  -1.028  -0.771   1.289   2.114
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)    -0.95047    0.21406  -4.440 8.99e-06 ***
## bdi_category.L  1.40543    0.47717   2.945  0.00323 **
## bdi_category.Q -0.47716    0.42812  -1.115  0.26504
## bdi_category.C -0.05176    0.37266  -0.139  0.88954
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 176.6  on 140  degrees of freedom
## Residual deviance: 165.2  on 137  degrees of freedom
##   (19 observations deleted due to missingness)
## AIC: 173.2
##
## Number of Fisher Scoring iterations: 4
```

```
# Print odds ratios
ci <- exp(confint(model))[c(-1, -4)]
oddR <- tibble('Item' = names(exp(coef(model))[-1]),
               'Odds ratio' = round(exp(coef(model))[-1], 3),
               'Lower 95% CI' = round(ci[1:3], 3),
               'Upper 95% CI' = round(ci[4:6], 3))

kable(oddR,
      caption = 'Odds ratio of regression coefficients')
```

Table 4: Odds ratio of regression coefficients

Item	Odds ratio	Lower 95% CI	Upper 95% CI
bdi_category.L	4.077	1.718	11.754
bdi_category.Q	0.621	0.252	1.393
bdi_category.C	0.950	0.575	1.968

Study group allocation

Tabulate

(no stratification by study site)

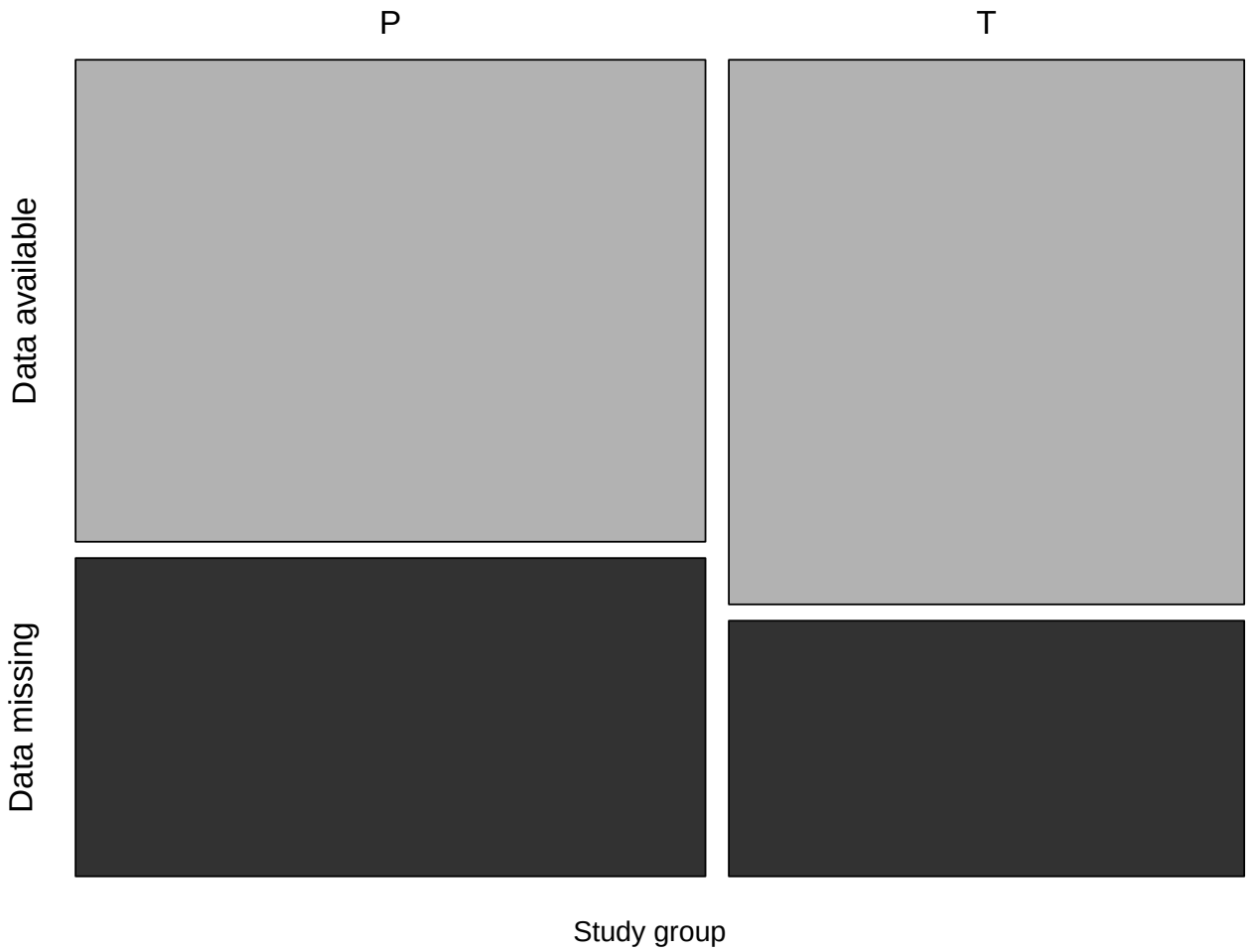
```
demo %>% group_by(Group) %>%
    summarise(count = n()) %>%
    kable(., caption = 'Study group allocation',
          col.names = c('', 'Count'))
```

Table 5: Study group allocation

	Count
P	88
T	72

Null hypothesis significance testing (NHST)

```
# xtabulate the data
group <- xtabs(~ Group + coding,
               data = demo)

# Produce mosaic plot
mosaicplot(group,
           main = 'Study group allocation vs data completeness',
           xlab = 'Study group',
           ylab = '',
           cex = 1.2,
           color = c('#B2B2B2', '#323232'))
```




```
# Fishers exact test
kable(tidy(fisher.test(group)),
      caption = 'Association between study group allocation and data completeness',
      col.names = c('Estimate', 'p-value',
                    'Lower 95% CI', 'Upper 95% CI',
                    'Method', 'Alternative'),
      digits = 3)
```

Table 6: Association between study group allocation and data completeness

Estimate	p-value	Lower 95% CI	Upper 95% CI	Method	Alternative
0.712	0.326	0.35	1.435	Fisher's Exact Test for Count Data	two.sided

Sex

Tabulate

(no stratification by study site)

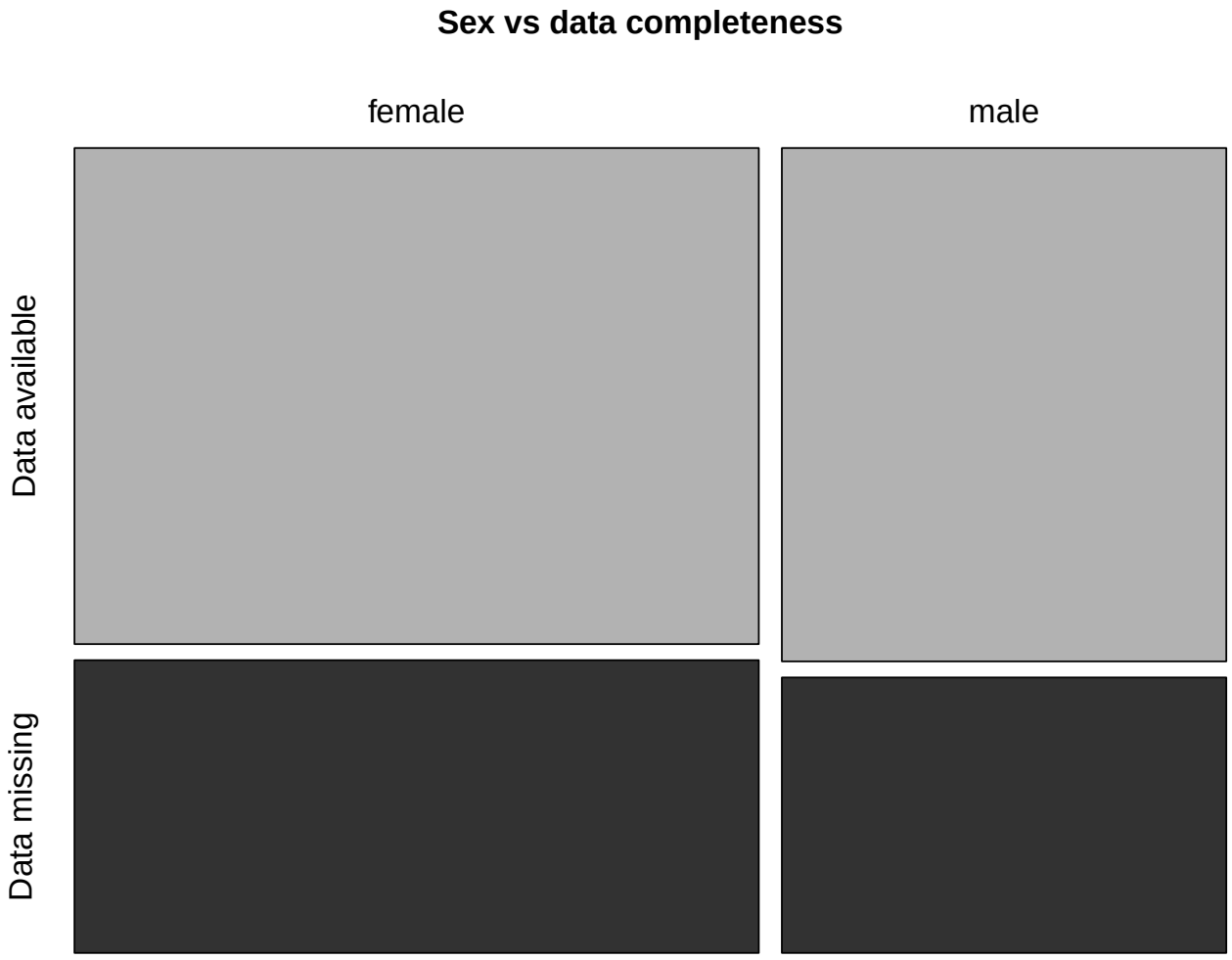
```
demo %>% group_by(Sex) %>%
    summarise(count = n()) %>%
    kable(., caption = 'Sex',
          col.names = c('', 'Count'))
```

Table 7: Sex

	Count
female	97
male	63

Null hypothesis significance testing (NHST)

```
# xtabulate the data
sex <- xtabs(~ Sex + coding,
               data = demo)

# Produce mosaic plot
mosaicplot(sex,
           main = 'Sex vs data completeness',
           xlab = '',
           ylab = '',
           cex = 1.2,
           color = c('#B2B2B2', '#323232'))
```




```
# Fishers exact test
kable(tidy(fisher.test(sex)),
      caption = 'Association between sex and data completeness',
      col.names = c('Estimate', 'p-value',
                    'Lower 95% CI', 'Upper 95% CI',
                    'Method', 'Alternative'),
      digits = 3)
```

Table 8: Association between sex and data completeness

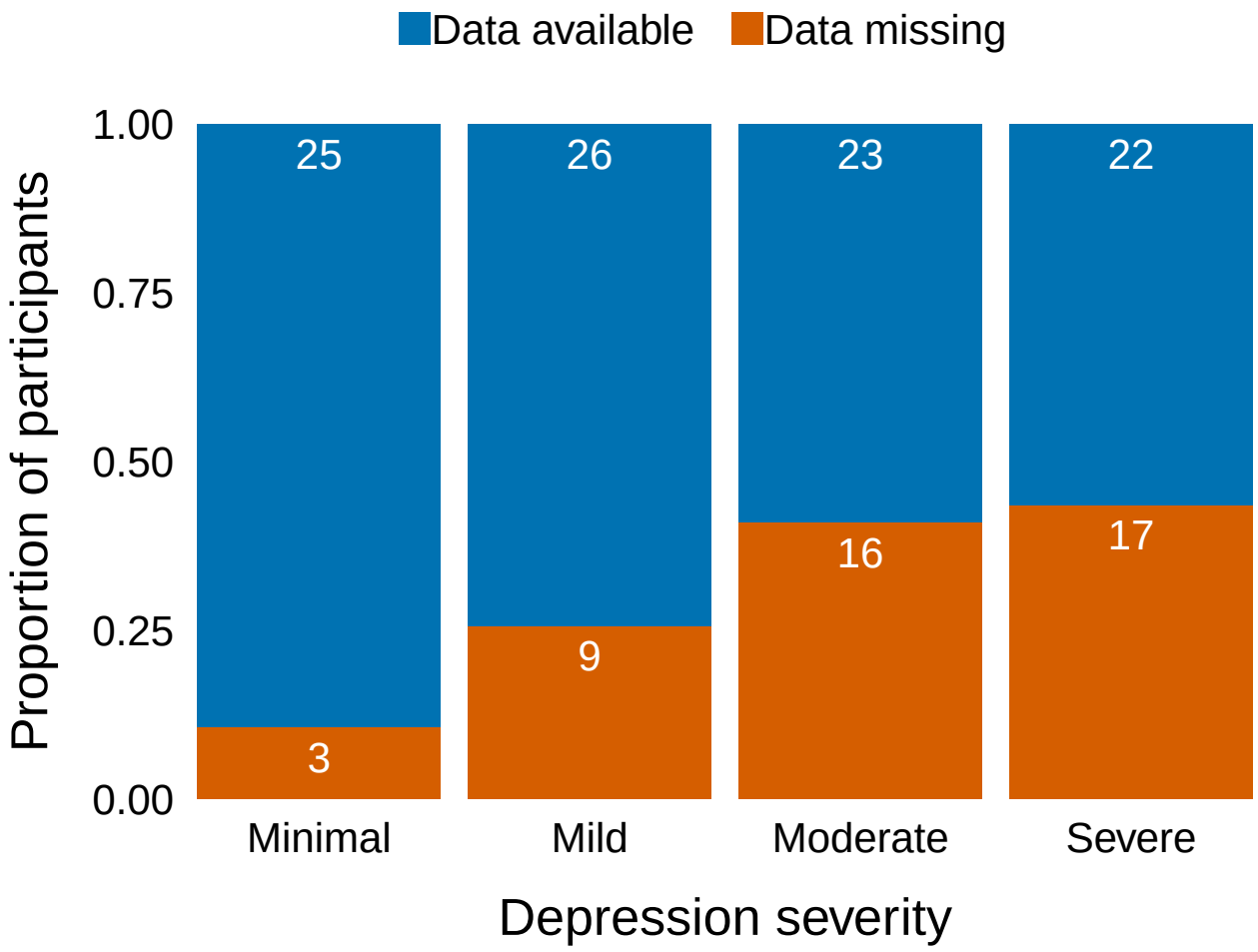
Estimate	p-value	Lower 95% CI	Upper 95% CI	Method	Alternative
0.91	0.867	0.442	1.85	Fisher's Exact Test for Count Data	two.sided

---

Summary

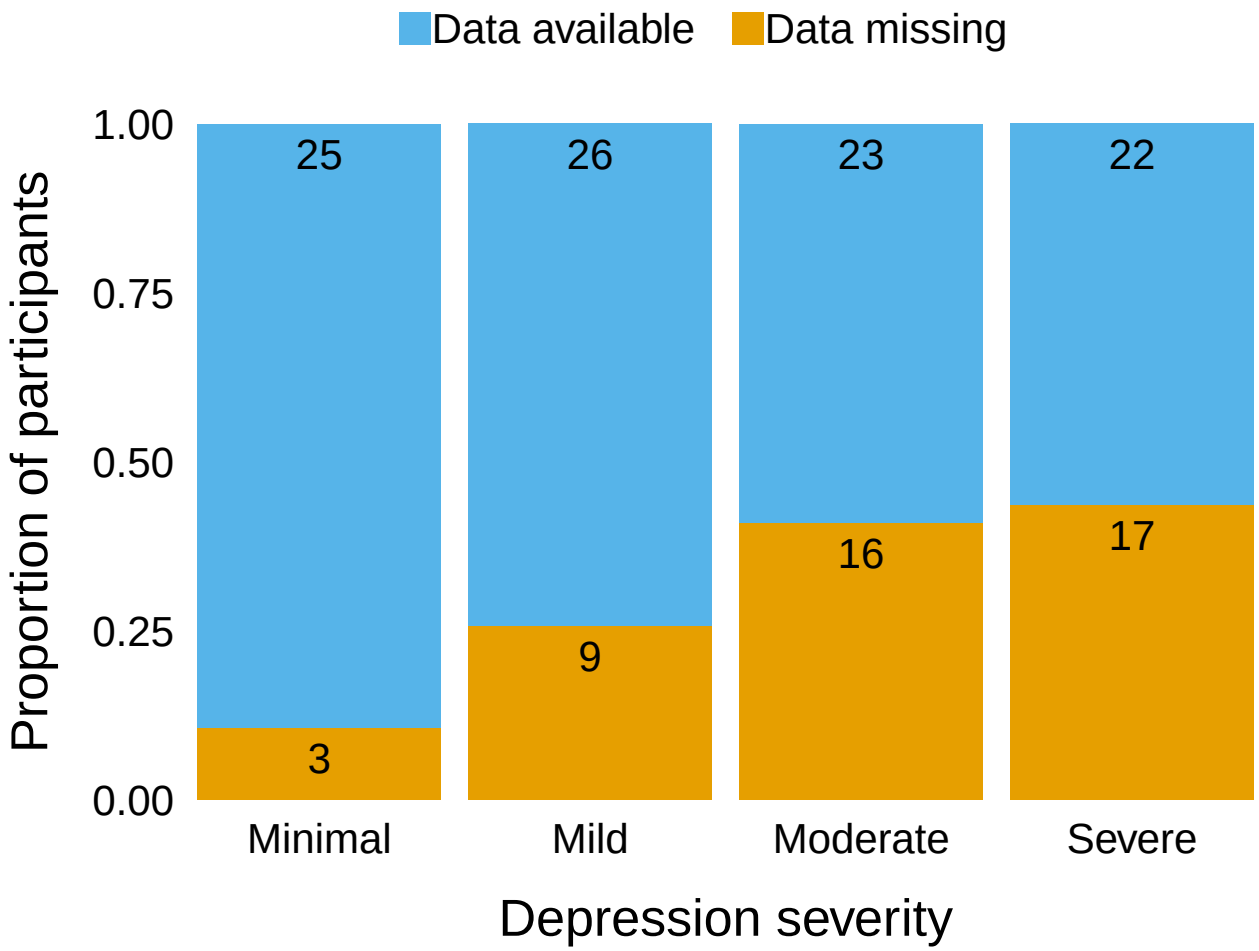
Income stability, sex, and group allocation did not predict whether or not an individual's data were present at 8 weeks. However, depression did: those with greater depression (on BDI) were more likely to have been lost to follow-up at the 8-week time point (main effect of depression severity: likelihood ratio = 11.31, df = 3, p = 0.01; OR for linear component of logistic regression = 4.01, 95% CI = 1.68 - 11.59).

```r
#-- Manuscript plot --#
# Plot of proportion of participants with missing data at each level of
# depression severity, as rated on the Beck's Depression Inventory.
# Numbers in the blocks show the absolute counts.
# Note: 19 participants are missing baseline BDI data, so n = 141

# Colour (dark)
p1 <- bdi %>%
    filter(!is.na(bdi_category)) %>%
    mutate(bdi_category = fct_recode(bdi_category,
                                     Minimal = 'none-minimal',
                                     Mild = 'mild',
                                     Moderate = 'moderate-severe',
                                     Severe = 'severe'),
           coding = case_when(
               coding == 'Data available' ~ 'Data available   ',
               coding == 'Data missing' ~ 'Data missing    '
               )) %>%
    ggplot(data = .) +
    aes(bdi_category,
        fill = coding) +
    geom_bar(position = position_fill()) +
    geom_text(stat = 'count',
              position = position_fill(),
              aes(label = ..count..),
              colour = '#FFFFFF',
              vjust = 1.5,
              size = 7.5) +
    labs(x = 'Depression severity',
         y = 'Proportion of participants') +
    scale_x_discrete(expand = c(0, 0)) +
    scale_y_continuous(expand = c(0, 0)) +
    scale_fill_manual(values = c('#0072B2', '#D55E00')) +
    theme_bw(base_size = 26) +
    theme(legend.position = 'top',
          legend.title = element_blank(),
          panel.border = element_blank(),
          panel.grid = element_blank(),
          axis.title.y = element_text(margin = margin(t = 0, r = 20, b = 0, l = 0)),
          axis.title.x = element_text(margin = margin(t = 20, r = 0, b = 0, l = 0)),
          axis.text = element_text(colour = '#000000'),
          axis.line = element_blank(),
          axis.ticks = element_blank()); p1
```



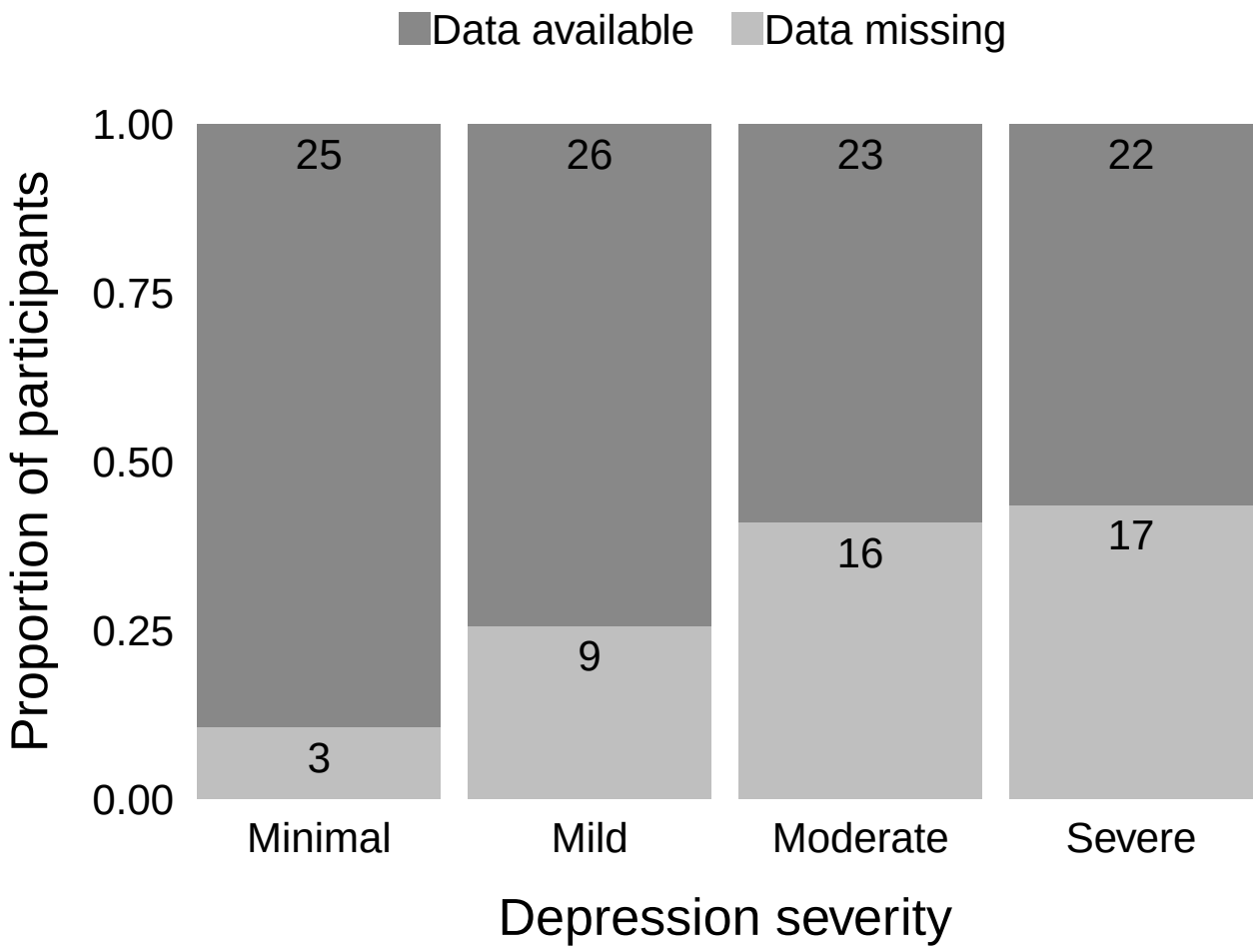

```
ggsave(filename = 'figures/figure-2_colourA.pdf',
       plot = p1,
       height = 8,
       width = 10,
       units = 'in')

# Colour (light)
p2 <- bdi %>%
    filter(!is.na(bdi_category)) %>%
    mutate(bdi_category = fct_recode(bdi_category,
                                     Minimal = 'none-minimal',
                                     Mild = 'mild',
                                     Moderate = 'moderate-severe',
                                     Severe = 'severe'),
           coding = case_when(
               coding == 'Data available' ~ 'Data available   ',
               coding == 'Data missing' ~ 'Data missing    '
               )) %>%
    ggplot(data = .) +
    aes(bdi_category,
        fill = coding) +
    geom_bar(position = position_fill()) +
    geom_text(stat = 'count',
              position = position_fill(),
```

```
            aes(label = ..count..),
            colour = '#000000',
            vjust = 1.5,
            size = 7.5) +
  labs(x = 'Depression severity',
       y = 'Proportion of participants') +
  scale_x_discrete(expand = c(0, 0)) +
  scale_y_continuous(expand = c(0, 0)) +
  scale_fill_manual(values = c('#56B4E9', '#E69F00')) +
  theme_bw(base_size = 26) +
  theme(legend.position = 'top',
        legend.title = element_blank(),
        panel.border = element_blank(),
        panel.grid = element_blank(),
        axis.title.y = element_text(margin = margin(t = 0, r = 20, b = 0, l = 0)),
        axis.title.x = element_text(margin = margin(t = 20, r = 0, b = 0, l = 0)),
        axis.text = element_text(colour = '#000000'),
        axis.line = element_blank(),
        axis.ticks = element_blank()); p2
```




```
ggsave(filename = 'figures/figure-2_colourB.pdf',
       plot = p2,
       height = 8,
```

```
       width = 10,
       units = 'in')

# Greyscale
p3 <- bdi %>%
    filter(!is.na(bdi_category)) %>%
    mutate(bdi_category = fct_recode(bdi_category,
                                     Minimal = 'none-minimal',
                                     Mild = 'mild',
                                     Moderate = 'moderate-severe',
                                     Severe = 'severe'),
           coding = case_when(
               coding == 'Data available' ~ 'Data available   ',
               coding == 'Data missing' ~ 'Data missing    '
               )) %>%
    ggplot(data = .) +
    aes(bdi_category,
        fill = coding) +
    geom_bar(position = position_fill()) +
    geom_text(stat = 'count',
              position = position_fill(),
              aes(label = ..count..),
              colour = '#000000',
              vjust = 1.5,
              size = 7.5) +
    labs(x = 'Depression severity',
         y = 'Proportion of participants') +
    scale_x_discrete(expand = c(0, 0)) +
    scale_y_continuous(expand = c(0, 0)) +
    scale_fill_manual(values = c('#888888', '#BFBFBF')) +
    theme_bw(base_size = 26) +
    theme(legend.position = 'top',
          legend.title = element_blank(),
          panel.border = element_blank(),
          panel.grid = element_blank(),
          axis.title.y = element_text(margin = margin(t = 0, r = 20, b = 0, l = 0)),
          axis.title.x = element_text(margin = margin(t = 20, r = 0, b = 0, l = 0)),
          axis.text = element_text(colour = '#000000'),
          axis.line = element_blank(),
          axis.ticks = element_blank()); p3
```




```
ggsave(filename = 'figures/figure-2_greyscale.pdf',
       plot = p3,
       height = 8,
       width = 10,
       units = 'in')
```

Session information

```
## R version 3.5.2 (2018-12-20)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Mojave 10.14.2
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_GB.UTF-8/en_GB.UTF-8/en_GB.UTF-8/C/en_GB.UTF-8/en_GB.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
```

```
##
## other attached packages:
##  [1] bindrcpp_0.2.2  knitr_1.21      broom_0.5.1     forcats_0.3.0
##  [5] stringr_1.3.1   dplyr_0.7.8     purrr_0.3.0     readr_1.3.1
##  [9] tidyr_0.8.2     tibble_2.0.1    ggplot2_3.1.0   tidyverse_1.2.1
## [13] magrittr_1.5
##
## loaded via a namespace (and not attached):
##  [1] tidyselect_0.2.5  xfun_0.4          haven_2.0.0
##  [4] lattice_0.20-38   carData_3.0-2     colorspace_1.4-0
##  [7] generics_0.0.2    htmltools_0.3.6   yaml_2.2.0
## [10] utf8_1.1.4        rlang_0.3.1       pillar_1.3.1
## [13] foreign_0.8-71    glue_1.3.0        withr_2.1.2.9000
## [16] modelr_0.1.2      readxl_1.2.0      bindr_0.1.1
## [19] plyr_1.8.4        munsell_0.5.0     gtable_0.2.0
## [22] cellranger_1.1.0  zip_1.0.0         rvest_0.3.2
## [25] evaluate_0.12     labeling_0.3      rio_0.5.16
## [28] curl_3.3          fansi_0.4.0       highr_0.7
## [31] Rcpp_1.0.0        scales_1.0.0      backports_1.1.3
## [34] jsonlite_1.6      abind_1.4-5       hms_0.4.2
## [37] digest_0.6.18     openxlsx_4.1.0    stringi_1.2.4
## [40] grid_3.5.2        cli_1.0.1         tools_3.5.2
## [43] lazyeval_0.2.1    car_3.0-2         crayon_1.3.4
## [46] pkgconfig_2.0.2   MASS_7.3-51.1     data.table_1.12.0
## [49] xml2_1.2.0        lubridate_1.7.4   assertthat_0.2.0
## [52] rmarkdown_1.11    httr_1.4.0        rstudioapi_0.9.0
## [55] R6_2.3.0          nlme_3.1-137      compiler_3.5.2
```