P8131 HW8

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Load packages

```
library(tidyverse)
library(readxl)
library(gee)
library(lme4)
library(nlme)
```

Problem 1

Import data

```
data =
  read_excel("HW8-HEALTH.xlsx") %>%
  janitor::clean_names() %>%
  mutate(
    id = factor(id),
    time = factor(time),
    txt = factor(txt),
    health = factor(health),
    agegroup = factor(agegroup)
  )
```

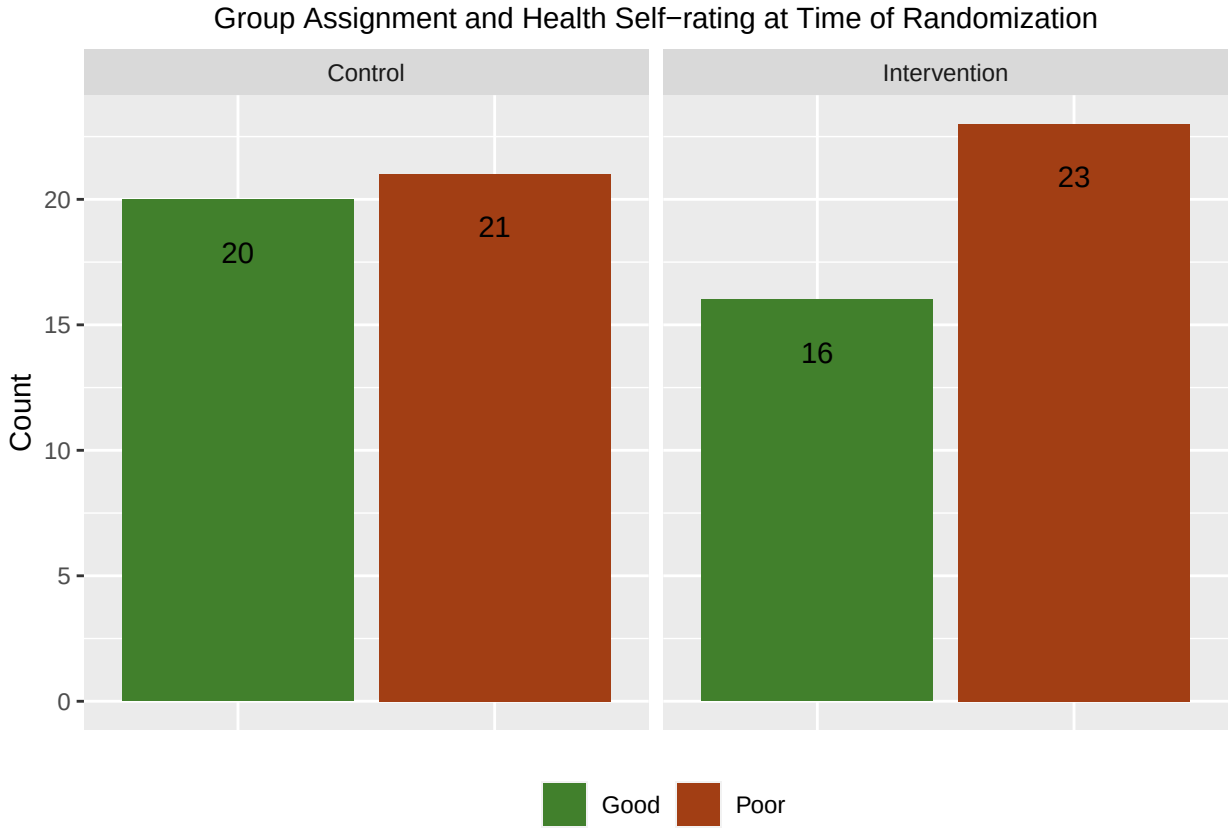
a) **Interpret and discuss the bivariate, cross-sectional relationship between group assignment and health self-rating.**

Samples that were given the control treatment (no educational intervention) had a more even-split health responses, where as lower proportion of samples in the intervention treatment reported good health. By count, there are more samples who reported poor health in the intervention group than the control group, even when the total sample count in the control group (41) exceeds that of the intervention group (39). While the treatment assignments were random, the baseline status for the 2 groups are not equivalent, and the discrepancy could impact study conclusions when the unobservable differences between groups are ignored.

The benefit of having longitudinal data is it could control for those time-invariant differences. Having multiple observations per individual allows us to base estimates on the variation within individuals. However, the correlation among the observations from an individual must be taken into account.

```
# plot the response counts for both the control and the intervention group
data %>%
  filter(
    time == "1"
  ) %>%
  group_by(txt, health) %>%
  summarize(count = n()) %>%
```

```
ggplot(aes(x = health, y = count, fill = health)) +
geom_col() +
scale_fill_manual(labels = c("Good", "Poor"), values = c("#41802C", "#A23E14")) +
facet_grid(cols = vars(txt)) +
geom_text(aes(label = count), vjust = 3) +
labs(
  title = "Group Assignment and Health Self-rating at Time of Randomization",
  y = "Count"
) +
theme(
  axis.title.x = element_blank(),
  axis.text.x = element_blank(),
  axis.ticks.x = element_blank(),
  legend.title = element_blank(),
  legend.position = "bottom",
  plot.title = element_text(size = 11, hjust = 0.5)
)
```



b) **Interpret health status over time using a GEE model**

The non-parametric GEE model averages over all individuals to make a population inference by making assuming a within-subject covariance structure. For example, according to the summary estimates, compared to the population that reported "poor" health as its baseline response, the "good" health population has a 1.82 increase in log odds of reporting another good health response by the second month's visit, while adjusting for treatment and age group.

```
# Create a new column showing baseline health rating, and a new column representing good health as 1, p
```

```r
data_bl =
  data %>%
  pivot_wider(
    names_from = time,
    values_from = health
  ) %>%
  pivot_longer(
    `2`:`4`,
    names_to = "time",
    values_to = "health"
  ) %>%
  rename("baseline" = `1`) %>%
  mutate(
    time = factor(time),
    baseline = factor(baseline, levels = c("Poor", "Good")),
    health = factor(health, levels = c("Poor", "Good")),
    nhealth = as.numeric(health == "Good")
  )
```

```r
gee_fit = gee(nhealth ~ baseline + txt + time + agegroup,
              data = data_bl,
              family = "binomial",
              id = id,
              corstr = "unstructured",
              scale.fix = FALSE)
```

```
## Beginning Cgee S-function, @(#) geeformula.q 4.13 98/01/27
```

```
## running glm to get initial regression estimate
```

```
##     (Intercept)    baselineGood txtIntervention           time3           time4
##      -1.5199450       1.7192117       2.0042708       0.2575654       0.2366989
##   agegroup25-34     agegroup35+
##       1.1968673       1.3958656
```

```r
summary(gee_fit)
```

```
##
##  GEE:  GENERALIZED LINEAR MODELS FOR DEPENDENT DATA
##  gee S-function, version 4.13 modified 98/01/27 (1998)
##
## Model:
##  Link:                      Logit
##  Variance to Mean Relation: Binomial
##  Correlation Structure:     Unstructured
##
## Call:
## gee(formula = nhealth ~ baseline + txt + time + agegroup, id = id,
##     data = data_bl, family = "binomial", corstr = "unstructured",
##     scale.fix = FALSE)
##
## Summary of Residuals:
##         Min          1Q      Median          3Q         Max
## -0.97980130 -0.20060701  0.09442344  0.18344971  0.83995062
##
##
```

```
## Coefficients:
##                   Estimate Naive S.E.    Naive z Robust S.E.  Robust z
## (Intercept)     -1.6578607  0.6014505 -2.7564377   0.4533989 -3.656517
## baselineGood     1.8164161  0.5978966  3.0380103   0.5113296  3.552339
## txtIntervention  2.1022271  0.5954429  3.5305269   0.5362768  3.920041
## time3            0.2753559  0.4747047  0.5800572   0.3368572  0.817426
## time4            0.2863563  0.4083916  0.7011809   0.4161352  0.688133
## agegroup25-34    1.3345925  0.5860828  2.2771400   0.5043829  2.645991
## agegroup35+      1.4112905  0.9740226  1.4489299   0.7855584  1.796544
##
## Estimated Scale Parameter:  1.486693
## Number of Iterations:  4
##
## Working Correlation
##           [,1]      [,2]      [,3]
## [1,] 1.0000000 0.1794182 0.5602284
## [2,] 0.1794182 1.0000000 0.2104116
## [3,] 0.5602284 0.2104116 1.0000000
```

c) **Generalized Linear Mixed Model** GLMM is an extension of generalized linear models to include both fixed and random effects on a subject level, and therefore its interpretation is similar. Reading from our summary, compared to an individual that reported "poor" health as its baseline response, a "good" health individual has a 2.81 increase in log odds of reporting another good health response by the second month's visit, while adjusting for treatment and age group.

```
glmm_fit = glmer(nhealth ~ baseline + txt + time + agegroup + (1 | id),
                 family = 'binomial', data = data_bl)
summary(glmm_fit)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: nhealth ~ baseline + txt + time + agegroup + (1 | id)
##    Data: data_bl
##
##      AIC      BIC   logLik deviance df.resid
##    186.5    212.9    -85.3    170.5      191
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4477 -0.2302  0.1443  0.2763  1.9348
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  id     (Intercept) 5.871    2.423
## Number of obs: 199, groups:  id, 78
##
## Fixed effects:
##                 Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -2.6142     1.0227  -2.556  0.01058 *
## baselineGood      2.8084     0.9990   2.811  0.00494 **
## txtIntervention   3.4540     1.0919   3.163  0.00156 **
## time3             0.4390     0.5592   0.785  0.43243
## time4             0.3546     0.6212   0.571  0.56806
## agegroup25-34     2.2779     1.0248   2.223  0.02623 *
```

```
## agegroup35+       1.9878     1.3960   1.424  0.15446
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) bslnGd txtInt time3  time4  a25-34
## baselineGod -0.671
## txtIntrvntn -0.673  0.456
## time3       -0.320  0.089  0.114
## time4       -0.230  0.023  0.057  0.420
## agegrp25-34 -0.661  0.386  0.402  0.067  0.015
## agegroup35+ -0.445  0.277  0.209  0.021 -0.004  0.392
```

Our model fits random intercepts per individual, and it adds or subtracts from the marginal intercept β_0 in the fixed effect. This makes a GLMM model inherently different, because a covariance model is estimated, not assumed under some structure. Furthermore, there is an added random factor with respect to each subject at the cost of computation power.

```
random.effects(glmm_fit)
```

```
## $id
##     (Intercept)
## 101  0.26955372
## 102 -0.76222542
## 103  0.60941107
## 104  0.03540812
## 105 -0.32144511
## 106  2.09061966
## 107  1.51432407
## 109  0.03540812
## 110  1.75639618
## 111  0.03540812
## 112 -2.34516556
## 113 -0.58147296
## 114  0.39929206
## 116  0.48651928
## 117 -2.47119883
## 118 -0.92735696
## 119  0.30609132
## 120 -1.59110159
## 121 -0.58147296
## 122  0.39929206
## 123  0.57906666
## 124 -2.78772464
## 125  0.20442269
## 126  1.29416594
## 127  0.26955372
## 128 -2.77400155
## 129  1.37787703
## 130 -0.58147296
## 131 -2.81263283
## 132 -0.58147296
## 133  1.37787703
## 134 -0.58147296
## 135 -4.46986571
```

```
## 136  1.18290863
## 137  0.26955372
## 138  1.82565052
## 139 -3.84571226
## 140  1.75639618
## 141 -1.99802581
## 142  0.30609132
## 143 -1.68610509
## 145  0.30250211
## 201  1.16545575
## 202  0.60941107
## 203 -1.68610509
## 204  0.88671151
## 205  0.20442269
## 206 -0.58147296
## 207  2.28086128
## 208  0.03540812
## 209  0.20178800
## 210 -1.59110159
## 211  0.30609132
## 213  1.29416594
## 601 -1.86094379
## 602  0.60941107
## 603 -1.37702527
## 604  0.26955372
## 605 -0.76222542
## 606 -5.56869974
## 607  0.61578065
## 608  0.39929206
## 609  0.60941107
## 610  0.39929206
## 611  1.18290863
## 612 -1.72050125
## 613  0.20178800
## 614  0.19132583
## 615  0.39929206
## 616  0.60941107
## 617  0.60941107
## 618  1.37787703
## 619 -0.26905010
## 620  0.26955372
## 621  0.03540812
## 622 -0.30163868
## 624 -0.50113922
## 625  0.39929206
##
## with conditional variances for "id"
```