

Preliminary Results

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Load packages

```
# Add additional packages you need
library(psych)
library(here) # makes reading data more consistent
library(tidyverse) # for data manipulation and plotting
library(haven) # for importing SPSS/SAS/Stata data
library(lme4) # for multilevel analysis
library(lattice) # for dotplot (working with lme4)
library(sjPlot) # for plotting effects
library(MuMIn) # for computing r-squared
library(r2mlm) # for computing r-squared
library(broom.mixed) # for summarizing results
library(modelsummary) # for making tables
library(dplyr)
library(skimr)
library(readxl)
library(mediation)
library(lmerTest)
```

Import Data

Read data and define two variables of interest treated: patient in the treatment group (intervention group) and in the post period anysymptom: has any symptom using the Geriatric Depression Scale - Short Form (GDS-SF)

```
# Read in the data from the Web
mydata <- read_excel("MatchedData.xlsx")
mydata$treated = mydata$treatment * mydata$post
mydata$anysymptom = ifelse(mydata$Depression_Scale > 0, 1, 0)
```

Intraclass Correlations (ICC)

1. Proportion of variance due to the higher (subclass) level
2. Average correlation between observations (patient) in the same cluster (subclass) s8q7: On how many of the last SEVEN DAYS did you test your blood sugar? subclass: Matched pair label using MatchIt package with propensity score and nearest one to one matching (most similar patient in intervention group to control group)

```
ran_int <- lmer(s8q7 ~ 1 + (1 | subclass), data = mydata)
summary(ran_int)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: s8q7 ~ 1 + (1 | subclass)
## Data: mydata
##
## REML criterion at convergence: 2722.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.2967 -0.7441 -0.3392  0.4867  2.1061
##
## Random effects:
## Groups Name Variance Std.Dev.
## subclass (Intercept) 0.6298  0.7936
## Residual 5.6393  2.3747
## Number of obs: 584, groups: subclass, 146
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 2.1096 0.1182 145.0000 17.85 <2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
variance_components <- as.data.frame(VarCorr(ran_int))
between_var <- variance_components$vcov[1]
within_var <- variance_components$vcov[2]
(icc <- between_var / (between_var + within_var))
```

```
## [1] 0.1004635
```

Test Random Slope

Since we used the matched data (with propensity score), we started with a simple model and tested random slope. Model equations: Lv-1:

$$s8q7_{ij} = \beta_{0j} + e_{ij}$$

Lv-2:

$$\beta_{0j} = \gamma_{00} + \gamma_{01} \text{treated}_j + u_{0j}$$

```
# First, no random slopes
m0 <- lmer(s8q7 ~ treated + (1 | subclass), data = mydata)
summary(m0)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: s8q7 ~ treated + (1 | subclass)
## Data: mydata
##
```

```
## REML criterion at convergence: 2700.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.6882 -0.7045 -0.3819  0.4678  2.2817
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
## subclass (Intercept) 0.6993   0.8363
## Residual              5.3612   2.3154
## Number of obs: 584, groups: subclass, 146
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   1.8402     0.1305 212.1027  14.10 < 2e-16 ***
## treated       1.0776     0.2213 437.0000   4.87 1.56e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr)
## treated -0.424
```

Then test random slopes

```
m1 <- lmer(s8q7 ~ treated + (treated| subclass), data = mydata)
summary(m1)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: s8q7 ~ treated + (treated | subclass)
##   Data: mydata
##
## REML criterion at convergence: 2697.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.3854 -0.6425 -0.3310  0.4679  2.3083
##
## Random effects:
##   Groups   Name      Variance Std.Dev. Corr
## subclass (Intercept) 0.9923   0.9962
##          treated     2.0386   1.4278  -0.41
## Residual              4.8539   2.2032
## Number of obs: 584, groups: subclass, 146
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   1.8402     0.1337 145.0005  13.762 < 2e-16 ***
## treated       1.0776     0.2414 144.9996   4.463 1.61e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr)
```

| | MLM | Linear regression |
|--------------------------|------------------|-------------------|
| (Intercept) | 1.840 (0.134) | 1.840 (0.118) |
| treated | 1.078 (0.241) | 1.078 (0.235) |
| sd__(Intercept) | 0.996 | |
| cor__(Intercept).treated | -0.413 | |
| sd__treated | 1.428 | |
| sd__Observation | 2.203 | |
| Num.Obs. | | 584 |
| R2 | | 0.035 |
| R2 Adj. | | 0.033 |
| AIC | 2709.1 | 2713.3 |
| BIC | 2735.3 | 2726.4 |
| Log.Lik. | -1348.546 | -1353.667 |
| F | | 20.990 |
| REMLcrit | 2697.093 | |

```
## treated -0.468
```

```
ranova(m1) #
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## s8q7 ~ treated + (treated | subclass)
##               npar logLik   AIC   LRT Df Pr(>Chisq)
## <none>              6 -1348.5 2709.1
## treated in (treated | subclass)  4 -1350.4 2708.9 3.786  2    0.1506
```

It is not statistically significant at 0.05 alpha level (on the boundary (0.075) after we divided the p-value by 2).

Compare with Conventional Method (lm)

```
m_lm <- lm(s8q7 ~ treated, data = mydata)
msummary(list("MLM" = m1,
              "Linear regression" = m_lm))
```

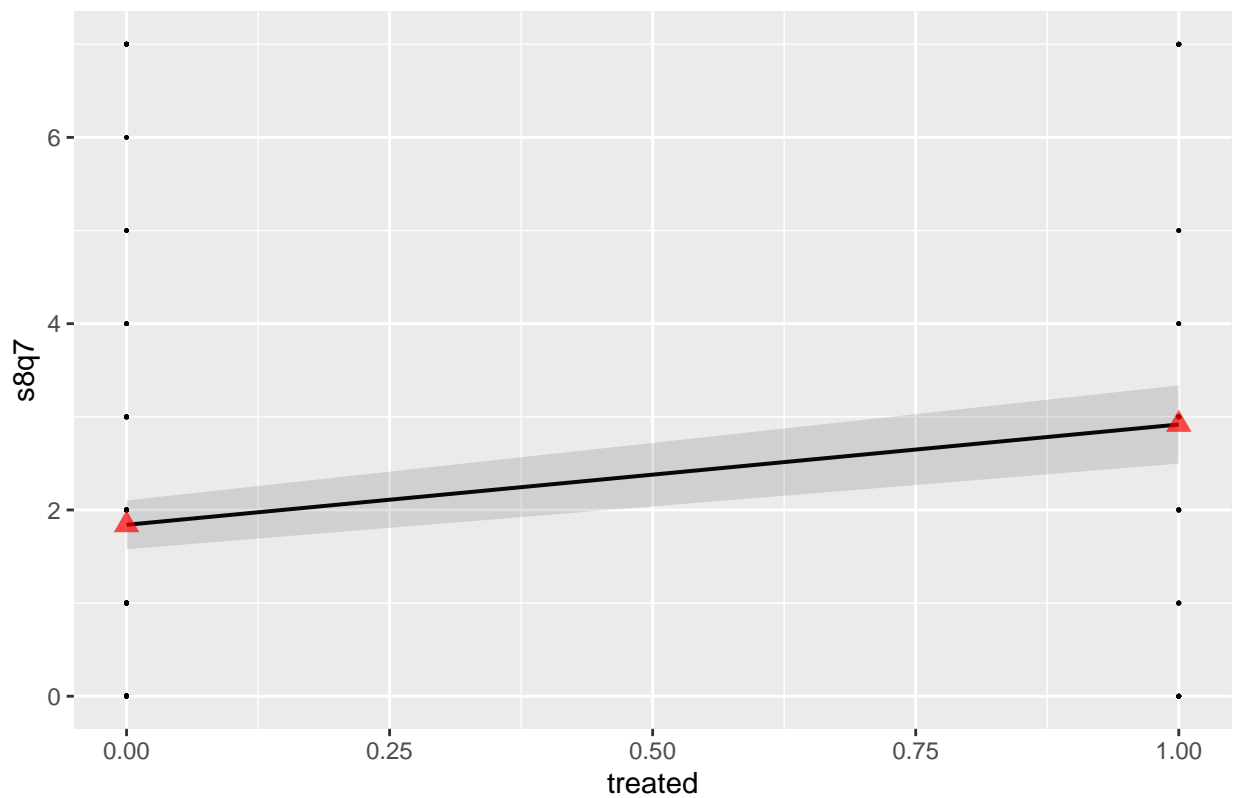
We found that using the conventional method would underestimate the standard error terms. This indicates the importance of considering multilevel structure.

Association between Receiving Digital Intervention and Weekly Number of Blood Sugar Testing

```

# Plot first 10 items
sjPlot::plot_model(m1, type = "pred", terms = "treated",
                   show.data = TRUE, title = "",
                   dot.size = 0.5) +
# Add the group means
stat_summary(data = mydata, aes(x = treated, y = s8q7),
            fun = mean, geom = "point",
            col = "red",
            shape = 17,
            # use triangles
            size = 3,
            alpha = 0.7)

```



This plots shows that receiving digital intervention would increase number of blood sugar testing among older adults in Taiwan.

Is Depression Symptom A Mediator?

```

detach_package <- function(pkg, character.only = FALSE)
{
  if(!character.only)
  {
    pkg <- deparse(substitute(pkg))
  }
}

```

```

search_item <- paste("package", pkg, sep = ":")
while(search_item %in% search())
{
  detach(search_item, unload = TRUE, character.only = TRUE)
}
}
detach_package(lmerTest)

fit.totaleffect <- lmer(s8q7 ~ treated+(treated| subclass), data = mydata)
summary(fit.totaleffect)

```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: s8q7 ~ treated + (treated | subclass)
## Data: mydata
##
## REML criterion at convergence: 2697.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.3854 -0.6425 -0.3310  0.4679  2.3083
##
## Random effects:
## Groups Name Variance Std.Dev. Corr
## subclass (Intercept) 0.9923 0.9962
## treated 2.0386 1.4278 -0.41
## Residual 4.8539 2.2032
## Number of obs: 584, groups: subclass, 146
##
## Fixed effects:
## Estimate Std. Error t value
## (Intercept) 1.8402 0.1337 13.762
## treated 1.0776 0.2414 4.463
##
## Correlation of Fixed Effects:
## (Intr)
## treated -0.468

```

```

fit.mediator <- lmer(anysymptom ~treated+(treated| subclass), data = mydata)
summary(fit.mediator)

```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: anysymptom ~ treated + (treated | subclass)
## Data: mydata
##
## REML criterion at convergence: 704.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.7735 -1.2704  0.4439  0.6117  0.9582
##
## Random effects:
## Groups Name Variance Std.Dev. Corr

```

```
## subclass (Intercept) 0.017252 0.13135
##           treated      0.006025 0.07762 0.06
## Residual              0.175799 0.41928
## Number of obs: 584, groups: subclass, 146
##
## Fixed effects:
##           Estimate Std. Error t value
## (Intercept)  0.73973    0.02279  32.454
## treated      -0.01370    0.04058  -0.338
##
## Correlation of Fixed Effects:
##           (Intr)
## treated -0.429
```

```
fit.dv <- lmer(s8q7 ~ anysymptom + treated+(treated| subclass), data = mydata)
summary(fit.dv)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: s8q7 ~ anysymptom + treated + (treated | subclass)
## Data: mydata
##
## REML criterion at convergence: 2698.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.3821 -0.6443 -0.3284  0.4719  2.3127
##
## Random effects:
## Groups Name Variance Std.Dev. Corr
## subclass (Intercept) 0.9972 0.9986
##           treated      2.0510 1.4321 -0.41
## Residual              4.8576 2.2040
## Number of obs: 584, groups: subclass, 146
##
## Fixed effects:
##           Estimate Std. Error t value
## (Intercept)  1.86660    0.21599  8.642
## anysymptom   -0.03571    0.22914  -0.156
## treated       1.07714    0.24170  4.456
##
## Correlation of Fixed Effects:
##           (Intr) anysym
## anysymptom -0.785
## treated     -0.300 0.013
```

```
results <- mediate(fit.mediator, fit.dv, treat='treated', mediator='anysymptom')
summary(results)
```

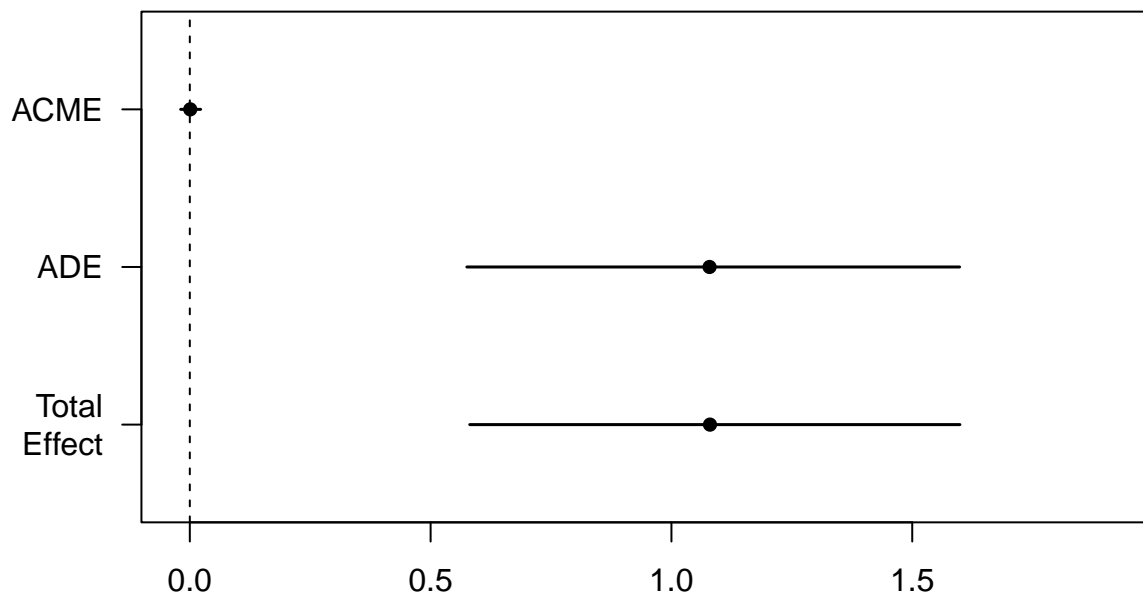
```
##
## Causal Mediation Analysis
##
## Quasi-Bayesian Confidence Intervals
##
```

```

## Mediator Groups: subclass
##
## Outcome Groups: subclass
##
## Output Based on Overall Averages Across Groups
##
##           Estimate 95% CI Lower 95% CI Upper p-value
## ACME           0.000911   -0.018959      0.02   0.95
## ADE            1.079138    0.575228      1.60 <2e-16 ***
## Total Effect    1.080049    0.581247      1.60 <2e-16 ***
## Prop. Mediated  0.000156   -0.020052      0.02   0.95
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Sample Size Used: 584
##
##
## Simulations: 1000

```

```
plot(summary(results))
```



Since ACME (average causal mediation effects) is not statistically significant, it shows that depression symptom may not be a good mediator.