Lab 4

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Introduction

Being social inherently means having relationships. Whether they be romantic relationships, familial, occupational, or virtual, having and maintain relationships is the basis of being social. Humans are remarkably social creatures, as we can track information about our own relationships, and the relationships of others. It has been proposed that the ability to track the relationships between different individuals allows humans to live in large social groups (Dunbar & Shultz, 2007). The importance of social relationships is highlighted in theories of a need to belong, where having social connections is described as a fundamental desire of humans (Baumeister & Leary, 1995).

Having social relationships has been implicated in a variety of mental and health outcomes. Maintaining daily interactions with people has been implicated in better emotional well-being (Reis et al., 2000). Perceived social isolation can be a risk factor for depression, and a decrease in cognitive performance and executive functioning (Cacioppo & Hawkley, 2009; DiNapoli et al., 2014). Social relationships are also an important part of successful aging. Older adults who have more social relationships and engage in social activities are more likely to have better cognitive functioning (Barnes et al., 2007; Yaffe et al., 2009), and less likely to develop dementia (Fratiglioni et al., 2004) than older adults who were less social. In rodent literature, environmental enrichness (EE) is a term used to describe animal housing environments which contain either more toys or bedding, hereby referred to as physical EE, or communal housing environments in which multiple animals are kept in a single cage, hereby referred to as social enrichness. Social enrichness has been shown to lead to better task performance, compared to physical EE (Elliott & Grunberg, 2005), and an increase in neural plasticity (Branchi, 2009). Social enrichness is analogous to the literature in humans on greater social relationships and health outcomes.

In an effort to combat the spread of COVID-19, entire communities have had to enter into quarantines and lockdowns and practice "social distancing" from other individuals outside of their household. Interestingly, this provides for a unique opportunity to study a lack of social enrichness in humans. In a typical day, individuals experience a variety of relationships including with people in their family, work, local communities, and across social media. With the lockdown policies that have been enacted to decrease the spread of COVID-19, the number of possible relationships that individuals interact with daily, and the variety of possible relationships, has drastically decreased. Some people may be able to experience a large number and variety of relationships, but the format of interaction may be different (i.e. video conferencing with co-workers and friends). The quality of relationships is also an important feature to consider, as higher-quality relationships in older adults has been shown to have better well-being (Merz & Huxhold, 2010). Therefore, the valence of social relationships that individuals do still experience in person with social distancing should be considered, as they may experience strains with individuals spending more time together than typical. This also be more true for some relationships than others as the relationship between an individual and their in-laws might cause more conflict the relationship between an individual and their roommates.

The present study will aim to discover what impact social distancing, and thereby a deficit in social enrichness with an exclusive increase in activity with certain relationships, will have on mental well-being. Social enrichness in this study was measured as social relationship diversity. In a previous study by our group, the overarching dimensions and categories that people use to understand social relationships (i.e. social relationship knowledge) were explored by having individuals rate social relationship on an extensive list of previously report dimensions that were thought to be important for social relationships. Principal component analysis reveal that the dimensions of formality, activeness, valence, and negotiation were the most important dimensions. Social relationship categories were derived by using clustering techniques, which indicated that social relationships can be grouped into the categories of positive, negative, distant, transactional, and occupational (Fig. 1). In the present study, social relationship diversity was measured as the total distance between relationships that individuals experienced, based on each relationships representation within the four-dimensional space. We hypothesized that (1) individuals who report increased time with relationships at home that they perceive to be negative will result in worse well-being, and (2) greater social relationship diversity would result in better mental well-being over the course of an extended lockdown. The results of this study will be informative in whether a four-dimensional space of social relationship knowledge is related to real world phenomenon of social enrichness. It would also provide guidance in how individuals may increase their mental well-being by increasing their social networks to interact with more diverse connections.
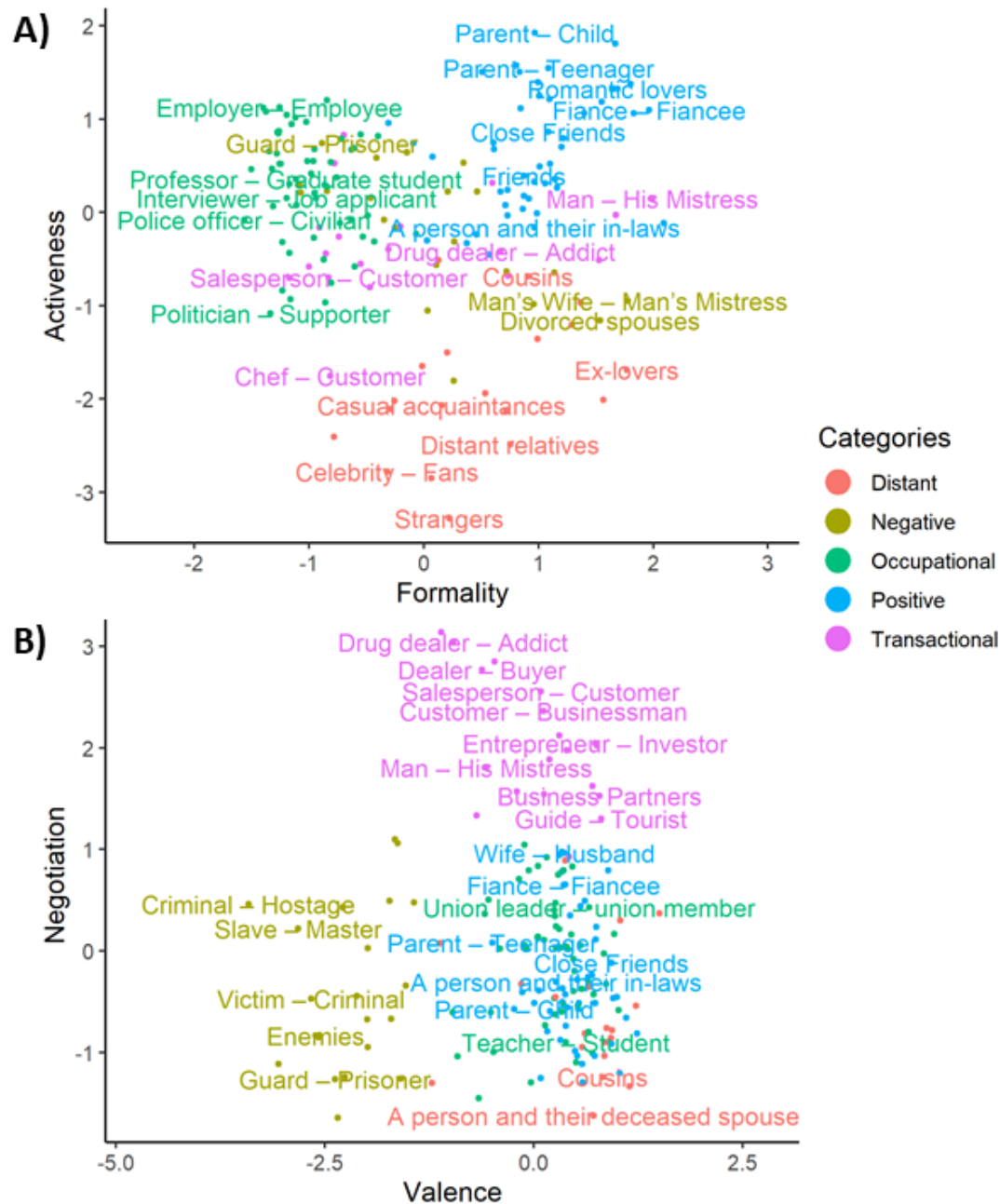
Figure 1. Social relationship dimensions and categories. (A) Relationships are plotted against the dimensions of formality and activeness, with color depicting their corresponding category. (B) Relationships are plotted against the dimensions of valence and negotiation. For visualization purposes, not all relationships are shown.

Methods

Data Source

Participants were recruited from Amazon Mechnical Turk (mTurk). mTurk is hosted by Amazon and provides an online platform for individuals (mTurkers) to partake in surveys. Use of mTurk has become popular in psychology research, as it allows for larger sample sizes than what can be typically collected in a lab setting. A link to the survey was posted on mTurk using turkprime.com. The use of "bots" to pose as real participants has been an issue with mTurk, and turkprime has a system that catches and excludes some of these bots. Participants from across the United States were eligible to take the survey at three time points during the beginning of the COVID-19 pandemic, from March to May 2020. An additional eligibility criteria was that participants must have learned English as their first language. This is due to cultural differences in social relationships, which we believe exist but are unable to directly address. Data was collected at three time points. Only individuals who completed the first time point were invited to participate at the second and third time points. All of the survey data for the first time point was collected within one day. At the second and third time points, the survey was opened and participants were invite to complete the survey again. The survey remained open for one week to allow individuals to complete the survey. The second survey was opened three weeks after the first survey was completed, and the third survey was opened four weeks after the second survey was completed. In this way, the time between surveys differed for each participant. Individuals who missed the second time were still allowed to complete the third time point. In total, 767 participants completed the survey at the first time point, 501 at the second time point, and 365 at the third time point (Table 1). The level 1 unit of analysis is observations and the level 2 unit of analysis is individuals.

Dropped Cases

Cases were dropped for two possible non-compliance reasons. The first is if participants failed attention check questions which were designed to easily reveal whether participants are attending to the survey. These questions were simple and had clear answers such as "which of the following is most likely the color red?" (e.g. strawberries). Participants who failed even one attention check question (of two) were excluded. The second way a participant might have been excluded is if they did not follow directions in how to format their responses for free response questions or did not answer all the questions. This was done so that the response coding could more easily be done by the researchers. In total 647 observations were dropped, with 234 individuals dropped due to noncompliance.

Table 1. Sample size at each time point and exclusion criteria stage.

Wave	Original responses	Excluding attention check failures	Excluding directions failures
1	767	753	467
2	501	463	289
3	365	360	230

Unique individuals   767   754   533

Variables

   This study includes variables that can be grouped as predictors, outcomes, and nuisance variables. The outcome we measured was a latent factor of mental well-being, derived from measures of anxiety, behavioral/emotional control, depression, calm-positive affect, and happy/positive affect. These variables are one-item questions that have collectively been shown to be detective of mental health illnesses (Berwick et al., 1991). The five variables were measured by asking participants whether they felt each factor much less, less, about the same, more, or much more in the past week. The predictors of interest were social relationship features, which included the total number of unique social relationships, the quality of immediate network (IN) (i.e. individuals who lived in their home) social relationships they experienced in the past week, and social relationship diversity. Participants were asked to report each person they interacted with in the past week, and their relationship to that person, resulting in their number of relationships (i.e. 10 relationships), and variety of relationship (i.e. 5 unique relationships) reported. They were also asked to rate how positive or negative each relationship was on a scale of one to five (later rescored to -2 to +2) indicating very negative, negative, neutral, positive, or very positive, and how much time they spent with each relationship. These two pieces of information for relationships in one's IN were used to calculate a variable of "IN time-weighted valence" by multiplying the valence score of relationships by the number of hours spent with each relationship, and dividing by the total number of relationships. Social relationship diversity was calculated by first matching each reported social relationship to our database of social relationships from our previous study. Then the scores for each social relationship dimension of formality, activeness, valence, and negotiation, was pulled. These four scores for each relationship were used to calculate the Euclidean distance between all relationships an individual reported. The social relationship distances were summed together for the variable of social relationship diversity. For example, if an individual only interacted with people who were only one's friends, these relationships would be tightly clustered in the four-dimensional space of social relationship knowledge (Fig. 1). Therefore, they would have low social relationship diversity. However, if an individual interacted with many different people, such as their family members, friends, co-workers, and strangers in public, the would be sampling from a large area in the social relationship knowledge space and therefore have high social relationship diversity.

   Nuisance variables were boredom, ability to do their interests (i.e. hobbies), their ability to do normal routine, and physical well-being, measured by a report of how they feel similar to the mental well-being questions. An additional nuisance variable was total distance traveled in the past week, which served as a measure of physical EE. The observation level variables were the social relationship feature variables, the nuisance variables, and time point. These observational level variables were aggregated as averages of the observations for each participant, then person-centered as we wished to know the pure within-person effects, except for time point. The individual level variables were the participant means for the predictors, the outcome, and the nuisance variables. All variables were standardized, except for time point.

Analysis and Estimation Technique

Multi-level linear regression was used as the analysis technique as this was a longitudinal analysis. In addition, multilevel modeling was the appropriate analysis since we were interested ~~in individual differences in growth curves, related to the impact of social relationships features to mental well-being over the course of the COVID-19 pandemic~~. Full maximum likelihood estimation was used as there were two to three time points per individual.

Results

Summary Statistics

Table 2. Summary statistics. All variables were z-standardized. IN = Immediate network, PC = person-centered, M = person-level mean.

Measure	Mean	Standard Deviation
Mental well-being (z)	0	1.00
# of unique relationships PC (z)	0	1.00
IN time-weighted valence PC (z)	0	1.00
Relationship diversity PC (z)	0	1.00
Total distance traveled PC (z)	0	1.00
Boredom PC (z)	0	1.00
Ability to do interests PC (z)	0	1.00
Ability to do normal routine PC (z)	0	1.00
General physical health PC (z)	0	1.00
# of unique relationships M (z)	0.05	0.99
IN time-weighted valence M (z)	0.03	0.94
Relationship diversity M (z)	0.01	0.96
Total distance traveled M (z)	-0.02	0.96
Boredom M (z)	-0.01	0.87
Ability to do interests M (z)	-0.02	0.94
Ability to do normal routine M (z)	0.02	0.93
General physical health M (z)	0.04	0.98

Table 2. Regression table for within and between model of mental well-being.

	Dependent variable:
	Mental well-being
Observation Level	
# of unique relationships PC (z)	-0.035
	(0.026)
IN time-weighted valence PC (z)	0.040[*]
	(0.020)
Relation diversity PC (z)	0.062
	(0.070)
Time point	0.184[***]
	(0.029)
Total distance traveled PC (z)	-0.020
	(0.020)
Boredom PC (z)	-0.059[**]
	(0.021)
Ability to do interests PC (z)	0.018
	(0.021)
Ability to do normal routine PC (z)	0.088[***]
	(0.021)
General physical health PC (z)	0.034
	(0.020)
Person Level	
# of unique relationships M (z)	-0.050
	(0.044)
IN time-weighted valence M (z)	0.106[**]
	(0.037)
Relation diversity M (z)	0.008
	(0.045)
Total distance traveled M (z)	-0.188[***]
	(0.039)
Boredom M (z)	0.018
	(0.037)
Ability to do interests M (z)	0.159[***]
	(0.039)
Ability to do normal routine M (z)	0.109[*]
	(0.041)
General physical health M (z)	0.150[***]
	(0.036)
Relation diversity PC (z) * Time point	-0.017
	(0.032)
Constant	-0.323[***]
	(0.059)

Observations	986
Log Likelihood	-1,209.268
Akaike Inf. Crit.	2,460.535
Bayesian Inf. Crit.	2,563.302

Note: *p<0.05; **p<0.005; ***p<0.001

z-standardized indicated in parentheses by variable name. Standard errors in are parentheses. IN = Immediate network, PC = person-centered, M = person-level mean.

Write-up

A latent variable of mental well-being was used as the outcome in a within- and between-subjects model. Holding all else constant, Person-centered immediate network time-weighted relationship valence significantly predictive of mental well-being, when comparing two observations from the same individual (β=0.04, *p*<.05; Table 2). A standard deviation increase in IN time-weighted valence predicted a 0.04 standard deviation increase in mental well-being. The other features of social relationships, total number of unique social relationships and social relationship diversity, were not significantly predictive of mental well-being. For the person-level effects, while holding all other variables constant, time-weighted relationship valence was significantly predictive of mental well-being, where a standard deviation increase was predictive of a 0.11 increase in mental well-being (Table 2). While time point was significantly predictive of mental well-being (β=0.18, *p*<.001), the interaction between time point and social relationship diversity was not significant (Table 2, Fig. 2).
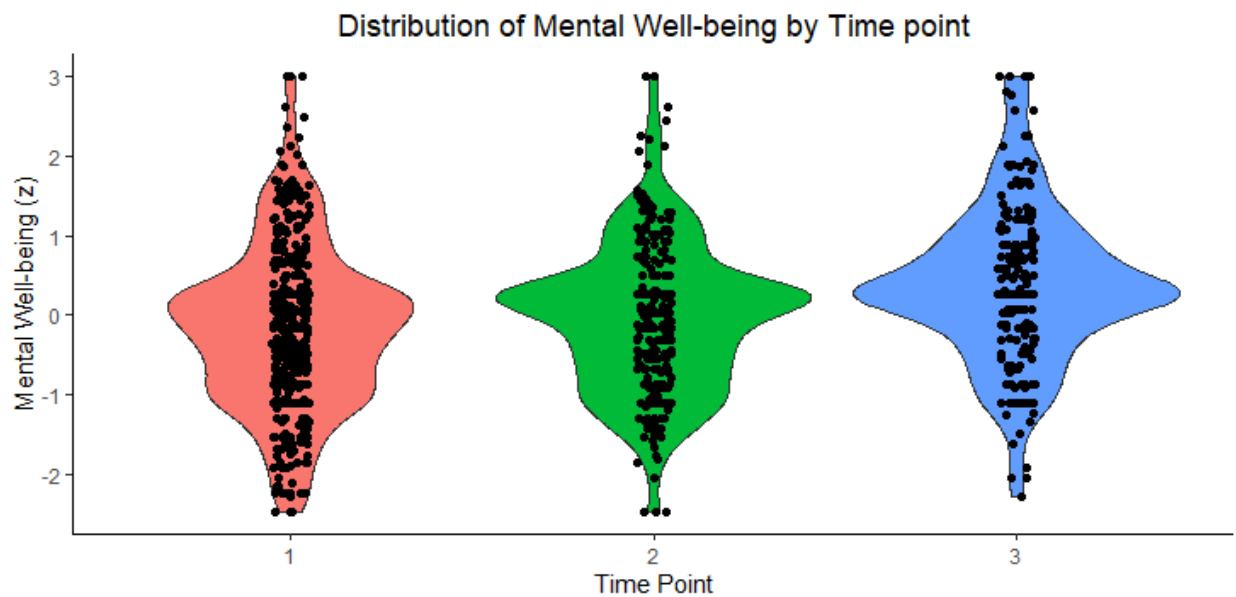
Figure 2. Interaction between social relationship diversity and time point on mental well-being.
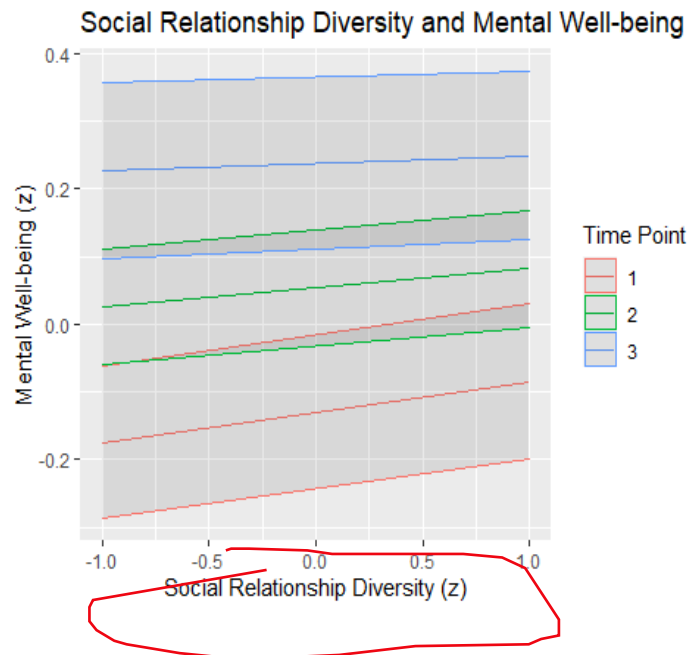
Figure 3. Distribution of mental well-being.

Discussion

Overall, our hypotheses were not supported, in that features of social relationships were not predictive of mental well-being during the COVID-19 pandemic lockdowns. Although social relationship valence was predictive of mental well-being, social relationship diversity was not. In addition, many of the nuisance variables were significantly predictive of mental well-being (Table 2), and much more so than social relationship valence. These results indicate that a lack of social relationship diversity was not a major contributor to mental well-being during the pandemic.

A limitation of this study is that it may be that individuals did not experience much change in mental well-being. The distribution of mental well-being scores seemed to have slightly increased over the two months this study was conducted (Fig. 3). Although many other have reported negative outcomes in health and mental well-being over the course of the pandemic, our results were not indicative of that. It may have been that this study was conducted over the early part of the pandemic before individuals felt "quarantine fatigue" and serious decreases in mental well-being. Perhaps if participants were sampled for additional time points, more variability in mental well-being would have been reported. This was not done in the present study due to participant attrition, where a 50% decrease in participant was seen between time points one and three.

Another limitation of this study was that we were unable to determine the directionality between social relationship valence and mental well-being. In our current analysis, we found that social relationship valence was predictive of mental well-being, but the opposite may be true as well. Due to limitations in the study design, we were not able to investigate causality by using a lagged variable. This is because social relationship valence was measured by asking participants to rate the valence of their relationships during the past week, and each time point was three to four weeks apart, meaning that a lagged variable would be measuring features from nearly a month ago. Had we directed individuals to rate their social relationships at their current time, and then survey participants with shorter gaps in time, we may have had better justification for creating a lagged variable social relationship valence to pinpoint the directionality of its relationship to mental well-being.

Appendix

Data Source

```
# Import data
responses_excluded <-
read.csv('/Users/Administrator/Google_Drive/olson_lab/projects/social_distancing/survey_data/responses_excluded.csv')
```

```
socdist_data <- responses_excluded %>% select(AmazonIdentifier, AN_URels, IN_valw,
AN_reldiv_sum, dist_total, anxiety, depression, behav_emo_control, pos_affect_calm,
pos_affect_happy, bored, do_interests, regulation, routine, health, wave)

names(socdist_data)[names(socdist_data)=='AmazonIdentifier'] <- 'ID'
```

Dropped Cases

```
# Drop cases that have any missing data
socdist_data <- socdist_data[rowSums(is.na(socdist_data)) == 0,]
socdist_data %>% group_by(wave) %>% summarise(count = n_distinct(ID))

## `summarise()` ungrouping output (override with `.groups` argument)

## # A tibble: 3 x 2
##    wave count
##   <dbl> <int>
## 1     1   467
## 2     2   289
## 3     3   230

length(unique(socdist_data$ID))

## [1] 533
```

Variables

Latent variable

```
wellb_mod_mg <- 'Wellb =~ NA*anxiety + pos_affect_calm + depression + pos_affect_happy +
behav_emo_control
            Wellb ~~ 1*Wellb'

wellb_configural_res <- sem(wellb_mod_mg, socdist_data, estimator='wlsmv')
socdist_data$wellb_lv <- as.numeric(predict(wellb_configural_res))

# Reverse score mental well-being variable so it is easier to interpret (higher score means better
mental well-being)
```

```
socdist_data$wellb_lv <- socdist_data$wellb_lv * -1
```

```
# Set wave as a factor variable
socdist_data$wave <- as.numeric(socdist_data$wave)
```

Subsetting due to missingness

```
socdist_data_ss <- subset(socdist_data, !is.na(AN_URels) & !is.na(IN_valw) &
!is.na(AN_reldiv_sum) & !is.na(wellb_lv))
nrow(socdist_data_ss)
```

```
## [1] 986
```

```
length(unique(socdist_data_ss$ID))
```

```
## [1] 533
```

Aggregation and centering

```
socdist_data_ss<-group_by(socdist_data_ss, ID)
socdist_data_ss<-mutate(socdist_data_ss,
          AN_URels.mean = mean(AN_URels,na.rm=TRUE),
          IN_valw.mean = mean(IN_valw,na.rm=TRUE),
          AN_reldiv_sum.mean = mean(AN_reldiv_sum,na.rm=TRUE),
          wellb_lv.mean = mean(wellb_lv, na.rm=TRUE),
          dist_total.mean = mean(dist_total,na.rm=TRUE),
          bored.mean = mean(bored,na.rm=TRUE),
          do_interests.mean = mean(do_interests,na.rm=TRUE),
          regulation.mean = mean(regulation,na.rm=TRUE),
          routine.mean = mean(routine,na.rm=TRUE),
          health.mean = mean(health,na.rm=TRUE),
          coobs=n())

socdist_data_ss <- ungroup(socdist_data_ss)
socdist_data_ss$AN_URels.pc <- socdist_data_ss$AN_URels -
socdist_data_ss$AN_URels.mean
socdist_data_ss$IN_valw.pc <- socdist_data_ss$IN_valw - socdist_data_ss$IN_valw.mean
socdist_data_ss$AN_reldiv_sum.pc <- socdist_data_ss$AN_reldiv_sum -
```

```r
socdist_data_ss$AN_reldiv_sum.mean
socdist_data_ss$wellb_lv.pc <- socdist_data_ss$wellb_lv - socdist_data_ss$wellb_lv.mean
socdist_data_ss$dist_total.pc <- socdist_data_ss$dist_total - socdist_data_ss$dist_total.mean
socdist_data_ss$bored.pc <- socdist_data_ss$bored - socdist_data_ss$bored.mean
socdist_data_ss$do_interests.pc <- socdist_data_ss$do_interests -
socdist_data_ss$do_interests.mean
socdist_data_ss$regulation.pc <- socdist_data_ss$regulation - socdist_data_ss$regulation.mean
socdist_data_ss$routine.pc <- socdist_data_ss$routine - socdist_data_ss$routine.mean
socdist_data_ss$health.pc <- socdist_data_ss$health - socdist_data_ss$health.mean

# Standardize
socdist_data_ss$AN_URels.pc_z <- as.numeric(scale(socdist_data_ss$AN_URels.pc))
socdist_data_ss$IN_valw.pc_z <- as.numeric(scale(socdist_data_ss$IN_valw.pc))
socdist_data_ss$AN_reldiv_sum.pc_z <- as.numeric(scale(socdist_data_ss$AN_reldiv_sum.pc))
socdist_data_ss$wellb_lv_z <- as.numeric(scale(socdist_data_ss$wellb_lv))
socdist_data_ss$dist_total.pc_z <- as.numeric(scale(socdist_data_ss$dist_total.pc))
socdist_data_ss$bored.pc_z <- as.numeric(scale(socdist_data_ss$bored.pc))
socdist_data_ss$do_interests.pc_z <- as.numeric(scale(socdist_data_ss$do_interests.pc))
socdist_data_ss$regulation.pc_z <- as.numeric(scale(socdist_data_ss$regulation.pc))
socdist_data_ss$routine.pc_z <- as.numeric(scale(socdist_data_ss$routine.pc))
socdist_data_ss$health.pc_z <- as.numeric(scale(socdist_data_ss$health.pc))


socdist_data_ss[, 16:ncol(socdist_data_ss)] <- lapply(16:ncol(socdist_data_ss), function(x)
as.numeric(socdist_data_ss[[x]]))

# Create person-level dataframe
socdist_data_pl <- group_by(socdist_data_ss, ID)
socdist_data_pl <- filter(socdist_data_pl[c('ID','AN_URels.mean', 'IN_valw.mean',
'AN_reldiv_sum.mean', 'wellb_lv.mean', 'dist_total.mean', 'bored.mean', 'do_interests.mean',
'regulation.mean', 'routine.mean', 'health.mean')], row_number(ID)==1)

socdist_data_pl$AN_URels.mean_z <- as.numeric(scale(socdist_data_pl$AN_URels.mean))
socdist_data_pl$IN_valw.mean_z <- as.numeric(scale(socdist_data_pl$IN_valw.mean))
socdist_data_pl$AN_reldiv_sum.mean_z <-
```

```
as.numeric(scale(socdist_data_pl$AN_reldiv_sum.mean))
socdist_data_pl$dist_total.mean_z <- as.numeric(scale(socdist_data_pl$bored.mean))
socdist_data_pl$bored.mean_z <- as.numeric(scale(socdist_data_pl$dist_total.mean))
socdist_data_pl$do_interests.mean_z <- as.numeric(scale(socdist_data_pl$do_interests.mean))
socdist_data_pl$regulation.mean_z <- as.numeric(scale(socdist_data_pl$regulation.mean))
socdist_data_pl$routine.mean_z <- as.numeric(scale(socdist_data_pl$routine.mean))
socdist_data_pl$health.mean_z <- as.numeric(scale(socdist_data_pl$health.mean))

socdist_data_pl_merge <- socdist_data_pl[c('ID', 'AN_URels.mean_z', 'IN_valw.mean_z',
'AN_reldiv_sum.mean_z', 'dist_total.mean_z', 'bored.mean_z', 'do_interests.mean_z',
'regulation.mean_z', 'routine.mean_z', 'health.mean_z')]

socdist_data_ss <- merge(socdist_data_ss, socdist_data_pl_merge, by="ID")
```

Summary Statistics

```
describe(socdist_data_ss)

describe(socdist_data_pl)
```

Analysis and Estimation Technique

Empty model

```
model1 <- lmer(wellb_lv_z ~ 1 + (1|ID), data=socdist_data_ss)
summary(model1)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: wellb_lv_z ~ 1 + (1 | ID)
##    Data: socdist_data_ss
##
## REML criterion at convergence: 2651.4
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -2.4417 -0.5260  0.0525  0.4224  3.7163
```

```
##
## Random effects:
##  Groups   Name         Variance Std.Dev.
##  ID       (Intercept) 0.5340   0.7308
##  Residual             0.4804   0.6931
## Number of obs: 986, groups:  ID, 533
##
## Fixed effects:
##              Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)  -0.01156    0.03946 502.30017  -0.293     0.77
```

Within- and Between-person model

```
model2 <- lmer(wellb_lv_z ~ AN_URels.pc_z + IN_valw.pc_z + AN_reldiv_sum.pc_z +
               wave + wave*AN_reldiv_sum.pc_z +
               dist_total.pc_z +
               bored.pc_z + do_interests.pc_z +
               routine.pc_z + health.pc_z +
               AN_URels.mean_z + IN_valw.mean_z +
               AN_reldiv_sum.mean_z + dist_total.mean_z +
               bored.mean_z + do_interests.mean_z +
               routine.mean_z + health.mean_z +
               (1 | ID),
        data=socdist_data_ss, REML=FALSE)

summary(model2)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: wellb_lv_z ~ AN_URels.pc_z + IN_valw.pc_z + AN_reldiv_sum.pc_z +
##     wave + wave * AN_reldiv_sum.pc_z + dist_total.pc_z + bored.pc_z +
##     do_interests.pc_z + routine.pc_z + health.pc_z + AN_URels.mean_z +
##     IN_valw.mean_z + AN_reldiv_sum.mean_z + dist_total.mean_z +
##     bored.mean_z + do_interests.mean_z + routine.mean_z + health.mean_z +
##     (1 | ID)
##     Data: socdist_data_ss
```

```
##
##      AIC      BIC   logLik deviance df.resid
##   2460.5   2563.3  -1209.3   2418.5      965
##
## Scaled residuals:
##     Min     1Q  Median     3Q     Max
## -2.6937 -0.4709  0.0157  0.4421  3.2231
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  ID       (Intercept) 0.4064   0.6375
##  Residual             0.3890   0.6237
## Number of obs: 986, groups:  ID, 533
##
## Fixed effects:
##                    Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)        -0.323148   0.059341 927.118105  -5.446 6.61e-08 ***
## AN_URels.pc_z      -0.034501   0.025922 450.229108  -1.331  0.18388
## IN_valw.pc_z        0.040215   0.020047 443.388411   2.006  0.04547 *
## AN_reldiv_sum.pc_z  0.061879   0.069897 720.914180   0.885  0.37630
## wave                0.183647   0.028578 600.835238   6.426 2.67e-10 ***
## dist_total.pc_z    -0.019758   0.020160 443.942696  -0.980  0.32759
## bored.pc_z         -0.059489   0.020784 444.545892  -2.862  0.00441 **
## do_interests.pc_z   0.018212   0.020803 443.053145   0.875  0.38180
## routine.pc_z        0.088032   0.021118 446.912230   4.169 3.68e-05 ***
## health.pc_z         0.034399   0.019995 442.754593   1.720  0.08607 .
## AN_URels.mean_z    -0.049902   0.043967 497.877006  -1.135  0.25693
## IN_valw.mean_z      0.105761   0.037060 539.956140   2.854  0.00449 **
## AN_reldiv_sum.mean_z 0.007874  0.044582 520.356228   0.177  0.85988
## dist_total.mean_z  -0.187876   0.038654 533.035877  -4.860 1.54e-06 ***
## bored.mean_z        0.018412   0.037299 613.672338   0.494  0.62174
## do_interests.mean_z 0.159478   0.039435 555.359857   4.044 6.00e-05 ***
## routine.mean_z      0.108732   0.040603 558.404600   2.678  0.00763 **
```

```
## health.mean_z           0.150065   0.036416 516.944073   4.121 4.40e-05 ***
## AN_reldiv_sum.pc_z:wave -0.016870   0.031966 768.849893  -0.528  0.59782
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation matrix not shown by default, as p = 19 > 12.
## Use print(x, correlation=TRUE)  or
##     vcov(x)       if you need it
```

Results Table

```
class(model1) <- "lmerMod"
class(model2) <- "lmerMod"

stargazer(model1, model2, type="text",
      out =
"/Users/Administrator/Google_Drive/courses/Hierarchical_Linear_Modeling/labs/lab_04/regressi
on_table.html",star.cutoffs=c(.05, .005, .001),
      covariate.labels = c("# of unique relationships PC",
                  "IN time-weighted valence PC",
                  "Relation diversity PC",
                  "Time point",
                  "Total distance traveled PC",
                  "Boredom PC",
                  "Ability to do interests PC",
                  "Ability to do normal routine PC",
                  "General physical health PC",
                  "# of unique relationships M",
                  "IN time-weighted valence M",
                  "Relation diversity M",
                  "Total distance traveled M",
                  "Boredom M",
                  "Ability to do interests M",
                  "Ability to do normal routine M",
```

```
            "General physical health M",
            "Relation diversity PC * Time point"),
    dep.var.labels = c("Mental well-being"),
    title = "Table 3. Regression table for the empty, within and between, and the cross-level
interaction models. ",
    notes="All variables are z-standardized. Standard errors in are parentheses. IN =
Immediate network, PC = person-centered, M = person-level mean.")
```

Graph

Interaction plot

```
model2_eff<-effect("AN_reldiv_sum.pc_z:wave",model2,
          xlevels=list(AN_reldiv_sum.pc_z=c(-1,1), wave=c(1,2,3)))
model2_eff_df <- data.frame(model2_eff)
model2_eff_df$AN_reldiv_sum.pc_zf <- factor(model2_eff_df$AN_reldiv_sum.pc_z,
                  labels=c("-1 SD", "+1 SD"))
model2_eff_df$wavef <- factor(model2_eff_df$wave,
                  labels=c("1", "2", "3"))
model2_eff_df
```

```
##   AN_reldiv_sum.pc_z wave        fit        se       lower       upper
## 1                 -1    1 -0.17469753 0.05720677 -0.286961259 -0.06243381
## 2                  1    1 -0.08468067 0.05840249 -0.199290909  0.02992957
## 3                 -1    2  0.02582000 0.04388686 -0.060304461  0.11194447
## 4                  1    2  0.08209627 0.04407788 -0.004403042  0.16859559
## 5                 -1    3  0.22633754 0.06611294  0.096596169  0.35607891
## 6                  1    3  0.24887322 0.06354231  0.124176493  0.37356994
##   AN_reldiv_sum.pc_zf wavef
## 1               -1 SD     1
## 2               +1 SD     1
## 3               -1 SD     2
## 4               +1 SD     2
## 5               -1 SD     3
## 6               +1 SD     3
```

```r
ggplot(model2_eff_df, aes(x=AN_reldiv_sum.pc_z, y=fit, color=wavef)) +
  geom_line() +
  geom_ribbon(aes(ymin=lower, ymax=upper), alpha=.1) +
  ggtitle("Social Relationship Diversity and Mental Well-being") +
  xlab("Social Relationship Diversity (z)") +
  ylab("Mental Well-being (z)") +
  labs(color="Time Point")
```

Distribution of Outcome

```r
socdist_data_ss$wavef <- factor(socdist_data_ss$wave)
ggplot(socdist_data_ss, aes(x = wavef, y=wellb_lv_z, fill=wavef)) +
  geom_violin() +
  geom_jitter(width=0.05) +
  theme_classic() +
  labs(title = "Distribution of Mental Well-being by Time point",
       x="Time Point", y = "Mental Well-being (z)") +
  theme(legend.position = "none", plot.title = element_text(hjust = 0.5))
```