

# Study\_1

Farid Anvari and Daniel Lakens

## Read in raw data

```
T1PANAS <- read.csv(file('PANAS_study1_T1_data_anon.csv'), stringsAsFactors = FALSE)

#to see and remove duplicate entries, keeping only the first entry for each
# unique Student ID
sum(duplicated(T1PANAS$StudentID)) #4 duplicates in T1 data

## [1] 4

T1PANAS <- T1PANAS[!duplicated(T1PANAS$StudentID),]
sum(duplicated(T1PANAS$StudentID)) #0 duplicates in T1 data after removing duplicates

## [1] 0

#to read in data for T2
T2PANAS <- read.csv(file('PANAS_study1_T2_data_anon.csv'), stringsAsFactors = FALSE)

#checking for duplicates from T2 data
sum(duplicated(T2PANAS$StudentID)) #0 duplicates in T2 data

## [1] 0

#renaming the PANAS variables so they reflect they are from T1
names(T1PANAS)[2:21] <- c("T1_PAattentive", "T1_PAinterested", "T1_PAalert", "T1_PAexcited",
                          "T1_PAenthusiastic", "T1_PAinspired", "T1_PAproud", "T1_PAdetermined",
                          "T1_PAstrong", "T1_PAactive", "T1_NAdistressed", "T1_NAupset",
                          "T1_NAhostile", "T1_NAirritable", "T1_NAscared", "T1_NAafraid",
                          "T1_NAashamed", "T1_NAguilty", "T1_NAnervous", "T1_NAjittery")

head(T1PANAS)

##   StudentID T1_PAattentive T1_PAinterested T1_PAalert T1_PAexcited
## 1   4127842             4             5             2             4
## 2   4059994             2             4             4             3
## 3   4142506             4             3             2             4
## 4   4184242             4             4             4             3
## 5   4142950             4             4             4             4
## 6   3906238             3             4             3             3
##   T1_PAenthusiastic T1_PAinspired T1_PAproud T1_PAdetermined T1_PAstrong
## 1                 5             2             4             4             2
## 2                 2             3             2             3             3
## 3                 4             3             3             4             3
## 4                 4             4             4             2             3
## 5                 4             4             4             4             4
## 6                 3             3             3             4             3
##   T1_PAactive T1_NAdistressed T1_NAupset T1_NAhostile T1_NAirritable
## 1           4             1             1             1             1
## 2           3             1             4             1             2
## 3           3             2             1             1             1
## 4           3             2             5             1             3
## 5           4             2             2             2             3
```

```
## 6      4      1      2      1      2
## T1_NAscared T1_NAafraid T1_NAashamed T1_NAgUILty T1_NAnervous
## 1      1      1      1      2      1
## 2      1      1      2      1      4
## 3      1      1      2      1      1
## 4      4      4      2      2      5
## 5      1      2      2      2      3
## 6      2      1      1      1      3
## T1_NAjittery
## 1      3
## 2      2
## 3      2
## 4      4
## 5      3
## 6      1
```

*#renaming variables from T2 to reflect they are from T2*

```
names(T2PANAS)[2:23] <- c( "T2_PAattentive", "T2_PAinterested", "T2_PAalert", "T2_PAexcited",
                           "T2_PAenthusiastic", "T2_PAinspired", "T2_PAproud", "T2_PAdetermined",
                           "T2_PAStrong", "T2_PAactive", "T2_NAdistressed", "T2_NAupset",
                           "T2_NAhostile", "T2_NAirritable", "T2_NAscared", "T2_NAafraid",
                           "T2_NAashamed", "T2_NAgUILty", "T2_NAnervous", "T2_NAjittery",
                           "globalPA", "globalNA")
```

```
head(T2PANAS)
```

```
## StudentID T2_PAattentive T2_PAinterested T2_PAalert T2_PAexcited
## 1 4176235      4      1      4      1
## 2 4004161      4      4      3      3
## 3 2849593      3      4      2      4
## 4 2678251      4      3      1      3
## 5 2327605      2      4      5      5
## 6 3937534      4      4      4      2
## T2_PAenthusiastic T2_PAinspired T2_PAproud T2_PAdetermined T2_PAStrong
## 1      1      2      1      4      2
## 2      3      4      2      4      2
## 3      4      2      4      2      3
## 4      4      3      5      3      1
## 5      5      4      4      4      4
## 6      3      3      3      4      3
## T2_PAactive T2_NAdistressed T2_NAupset T2_NAhostile T2_NAirritable
## 1      4      4      3      4      4
## 2      3      2      2      3      2
## 3      1      3      4      1      2
## 4      3      1      2      1      2
## 5      5      2      4      3      4
## 6      3      2      1      1      3
## T2_NAscared T2_NAafraid T2_NAashamed T2_NAgUILty T2_NAnervous
## 1      4      3      3      3      1
## 2      2      1      1      1      2
## 3      3      2      1      4      1
## 4      1      1      2      1      1
## 5      2      2      4      4      2
## 6      1      1      1      1      2
## T2_NAjittery globalPA globalNA
## 1      3      1      4
```

```
## 2          1          2          2
## 3          1          2          4
## 4          5          4          3
## 5          2          3          2
## 6          1          3          3
```

```
#to merge the data sets, matching T1 to T2 responses, by student ID,
# and matching only the first response for those with duplicate Student IDs using plyr package
PANASdata <- join(T1PANAS, T2PANAS, by = c("StudentID"), type="full")
```

```
#remove those with NA values (e.g., where there are T1 response but no T2) to keep only participants with
PANASdata <- PANASdata[complete.cases(PANASdata), ]
```

## Calculate Difference Scores

This uses a custom function written to calculate effect sizes and confidence interval for within designs.

```
#using subsetting to calculate mean of T1 and T2 PA and NA for each participant
PANASdata$T1_PA <- rowMeans(PANASdata[, grep('T1_PA', colnames(PANASdata))], na.rm=TRUE)
PANASdata$T1_NA <- rowMeans(PANASdata[, grep('T1_NA', colnames(PANASdata))], na.rm=TRUE)
PANASdata$T2_PA <- rowMeans(PANASdata[, grep('T2_PA', colnames(PANASdata))], na.rm=TRUE)
PANASdata$T2_NA <- rowMeans(PANASdata[, grep('T2_NA', colnames(PANASdata))], na.rm=TRUE)
```

```
#calculate difference score, from T1 to T2, for PA and NA for each participant
PANASdata$PA_change <- PANASdata$T2_PA - PANASdata$T1_PA
PANASdata$NA_change <- PANASdata$T2_NA - PANASdata$T1_NA
```

```
#Calculate all statistics for positive----
```

```
sum_data<-data.frame(t = numeric(0),
                     df = numeric(0),
                     p = numeric(0),
                     ci_lower_mean = numeric(0),
                     ci_upper_mean = numeric(0),
                     mean_1 = numeric(0),
                     mean_2 = numeric(0),
                     m_diff = numeric(0),
                     ci_l_m_diff = numeric(0),
                     ci_u_m_diff = numeric(0),
                     d_av = numeric(0),
                     d_av_unb = numeric(0),
                     s_av = numeric(0),
                     s_diff = numeric(0),
                     ci_l_d_av = numeric(0),
                     ci_u_d_av = numeric(0),
                     d_z = numeric(0),
                     d_z_unb = numeric(0),
                     ci_l_d_z = numeric(0),
                     ci_u_d_z = numeric(0),
                     N = numeric(0),
                     m1 = numeric(0),
                     m2 = numeric(0),
                     sd1 = numeric(0),
                     sd2 = numeric(0),
```

```

cor = numeric(0),
vi = numeric(0))
for(i in 1:5){
  temp <- t.test(PANASdata$PA_change[PANASdata$globalPA == i])
  sum_data[i,1] <- temp$statistic
  sum_data[i,2] <- temp$parameter
  sum_data[i,3] <- temp$p.value
  sum_data[i,4] <- temp$conf.int[1]
  sum_data[i,5] <- temp$conf.int[2]
  sum_data[i,6] <- temp$estimate[1]
  sum_data[i,7] <- temp$estimate[2]
  temp <- effect_size_d_paired(PANASdata$T1_PA[PANASdata$globalPA == i],
                                PANASdata$T2_PA[PANASdata$globalPA == i])

  sum_data[i,8] <- temp$m_diff
  sum_data[i,9] <- temp$ci_l_m_diff
  sum_data[i,10] <- temp$ci_u_m_diff
  sum_data[i,11] <- temp$d_av
  sum_data[i,12] <- temp$d_av_unb
  sum_data[i,13] <- temp$s_av
  sum_data[i,14] <- temp$s_diff
  sum_data[i,15] <- temp$ci_l_d_av
  sum_data[i,16] <- temp$ci_u_d_av
  sum_data[i,17] <- temp$d_z
  sum_data[i,18] <- temp$d_z_unb
  sum_data[i,19] <- temp$ci_l_d_z
  sum_data[i,20] <- temp$ci_u_d_z
  sum_data[i,21] <- temp$N
  sum_data[i,22] <- temp$m1
  sum_data[i,23] <- temp$m2
  sum_data[i,24] <- temp$sd1
  sum_data[i,25] <- temp$sd2
  sum_data[i,26] <- temp$cor
  sum_data[i,27] <- 1/sum_data$N[i] + sum_data$d_z[i]^2 / (2*sum_data$N[i]) #this is the formula for th
}

```

```

## Mean Difference      : -0.4333 95% CI [-1.0825;0.2158]
## Cohen's d_z_unb     : -0.5899 95% CI [-1.7299;0.2522]
## Cohen's d_av_unb    : -0.7084 95% CI [-1.8965;0.2765]
## s_diff: 0.6186, s_av: 0.5151, sd1: 0.6743, sd2: 0.2757, cor: 0.3981
## N = 6 pairs.Mean Difference      : -0.55 95% CI [-0.7463;-0.3537]
## Cohen's d_z_unb     : -0.9022 95% CI [-1.3146;-0.5433]
## Cohen's d_av_unb    : -0.9754 95% CI [-1.4023;-0.5795]
## s_diff: 0.5972, s_av: 0.5524, sd1: 0.5147, sd2: 0.5876, cor: 0.4193
## N = 38 pairs.Mean Difference     : -0.131 95% CI [-0.2815;0.0196]
## Cohen's d_z_unb     : -0.2661 95% CI [-0.5845;0.039]
## Cohen's d_av_unb    : -0.1908 95% CI [-0.4141;0.0277]
## s_diff: 0.4831, s_av: 0.6737, sd1: 0.5877, sd2: 0.7499, cor: 0.765
## N = 42 pairs.Mean Difference     : 0.1188 95% CI [0.0136;0.2241]
## Cohen's d_z_unb     : 0.2683 95% CI [0.0303;0.5144]
## Cohen's d_av_unb    : 0.1842 95% CI [0.0206;0.3505]
## s_diff: 0.438, s_av: 0.6381, sd1: 0.6617, sd2: 0.6136, cor: 0.7666
## N = 69 pairs.Mean Difference     : 0.3 95% CI [0.001;0.599]
## Cohen's d_z_unb     : 0.5254 95% CI [0.0017;1.1312]
## Cohen's d_av_unb    : 0.4669 95% CI [0.0015;0.9711]

```

```
## s_diff: 0.5398, s_av: 0.6075, sd1: 0.5939, sd2: 0.6209, cor: 0.6058
## N = 15 pairs.
```

```
sum_data_PA <- sum_data
```

```
#Calculate all statistics for negative----
```

```
sum_data<-data.frame(t = numeric(0),
                     df = numeric(0),
                     p = numeric(0),
                     ci_lower_mean = numeric(0),
                     ci_upper_mean = numeric(0),
                     mean_1 = numeric(0),
                     mean_2 = numeric(0),
                     m_diff = numeric(0),
                     ci_l_m_diff = numeric(0),
                     ci_u_m_diff = numeric(0),
                     d_av = numeric(0),
                     d_av_unb = numeric(0),
                     s_av = numeric(0),
                     s_diff = numeric(0),
                     ci_l_d_av = numeric(0),
                     ci_u_d_av = numeric(0),
                     d_z = numeric(0),
                     d_z_unb = numeric(0),
                     ci_l_d_z = numeric(0),
                     ci_u_d_z = numeric(0),
                     N = numeric(0),
                     m1 = numeric(0),
                     m2 = numeric(0),
                     sd1 = numeric(0),
                     sd2 = numeric(0),
                     cor = numeric(0),
                     vi = numeric(0))

for(i in 1:5){
  temp <- t.test(PANASdata$NA_change[PANASdata$globalNA == i])
  sum_data[i,1] <- temp$statistic
  sum_data[i,2] <- temp$parameter
  sum_data[i,3] <- temp$p.value
  sum_data[i,4] <- temp$conf.int[1]
  sum_data[i,5] <- temp$conf.int[2]
  sum_data[i,6] <- temp$estimate[1]
  sum_data[i,7] <- temp$estimate[2]
  temp <- effect_size_d_paired(PANASdata$T1_NA[PANASdata$globalNA == i],
                               PANASdata$T2_NA[PANASdata$globalNA == i])

  sum_data[i,8] <- temp$m_diff
  sum_data[i,9] <- temp$ci_l_m_diff
  sum_data[i,10] <- temp$ci_u_m_diff
  sum_data[i,11] <- temp$d_av
  sum_data[i,12] <- temp$d_av_unb
  sum_data[i,13] <- temp$s_av
  sum_data[i,14] <- temp$s_diff
  sum_data[i,15] <- temp$ci_l_d_av
  sum_data[i,16] <- temp$ci_u_d_av
```

```

sum_data[i,17] <- temp$d_z
sum_data[i,18] <- temp$d_z_unb
sum_data[i,19] <- temp$ci_l_d_z
sum_data[i,20] <- temp$ci_u_d_z
sum_data[i,21] <- temp$N
sum_data[i,22] <- temp$m1
sum_data[i,23] <- temp$m2
sum_data[i,24] <- temp$sd1
sum_data[i,25] <- temp$sd2
sum_data[i,26] <- temp$cor
sum_data[i,27] <- 1/sum_data$N[i] + sum_data$d_z[i]^2 / (2*sum_data$N[i]) #this is the formula for th
}

```

```

## Mean Difference      : -0.52 95% CI [-0.7652;-0.2748]
## Cohen's d_z_unb     : -1.1105 95% CI [-1.8912;-0.5153]
## Cohen's d_av_unb    : -0.7615 95% CI [-1.2528;-0.3414]
## s_diff: 0.4427, s_av: 0.6456, sd1: 0.7298, sd2: 0.5488, cor: 0.7962
## N = 15 pairs.Mean Difference      : -0.2967 95% CI [-0.4041;-0.1893]
## Cohen's d_z_unb     : -0.7044 95% CI [-1.0033;-0.4309]
## Cohen's d_av_unb    : -0.5167 95% CI [-0.7298;-0.3135]
## s_diff: 0.4158, s_av: 0.5668, sd1: 0.6167, sd2: 0.512, cor: 0.7436
## N = 60 pairs.Mean Difference      : -0.1 95% CI [-0.2079;0.0079]
## Cohen's d_z_unb     : -0.2567 95% CI [-0.5439;0.02]
## Cohen's d_av_unb    : -0.1464 95% CI [-0.307;0.0113]
## s_diff: 0.3837, s_av: 0.6729, sd1: 0.6774, sd2: 0.6685, cor: 0.8375
## N = 51 pairs.Mean Difference      : 0.2763 95% CI [0.1033;0.4493]
## Cohen's d_z_unb     : 0.5143 95% CI [0.1848;0.873]
## Cohen's d_av_unb    : 0.4008 95% CI [0.1421;0.6713]
## s_diff: 0.5263, s_av: 0.6754, sd1: 0.6457, sd2: 0.7039, cor: 0.699
## N = 38 pairs.Mean Difference      : 0.55 95% CI [-0.2993;1.3993]
## Cohen's d_z_unb     : 0.5723 95% CI [-0.2683;1.7011]
## Cohen's d_av_unb    : 0.5666 95% CI [-0.2425;1.5375]
## s_diff: 0.8093, s_av: 0.8174, sd1: 0.784, sd2: 0.8495, cor: 0.5115
## N = 6 pairs.

```

```
sum_data_NA <- sum_data
```

## Plot the distributions

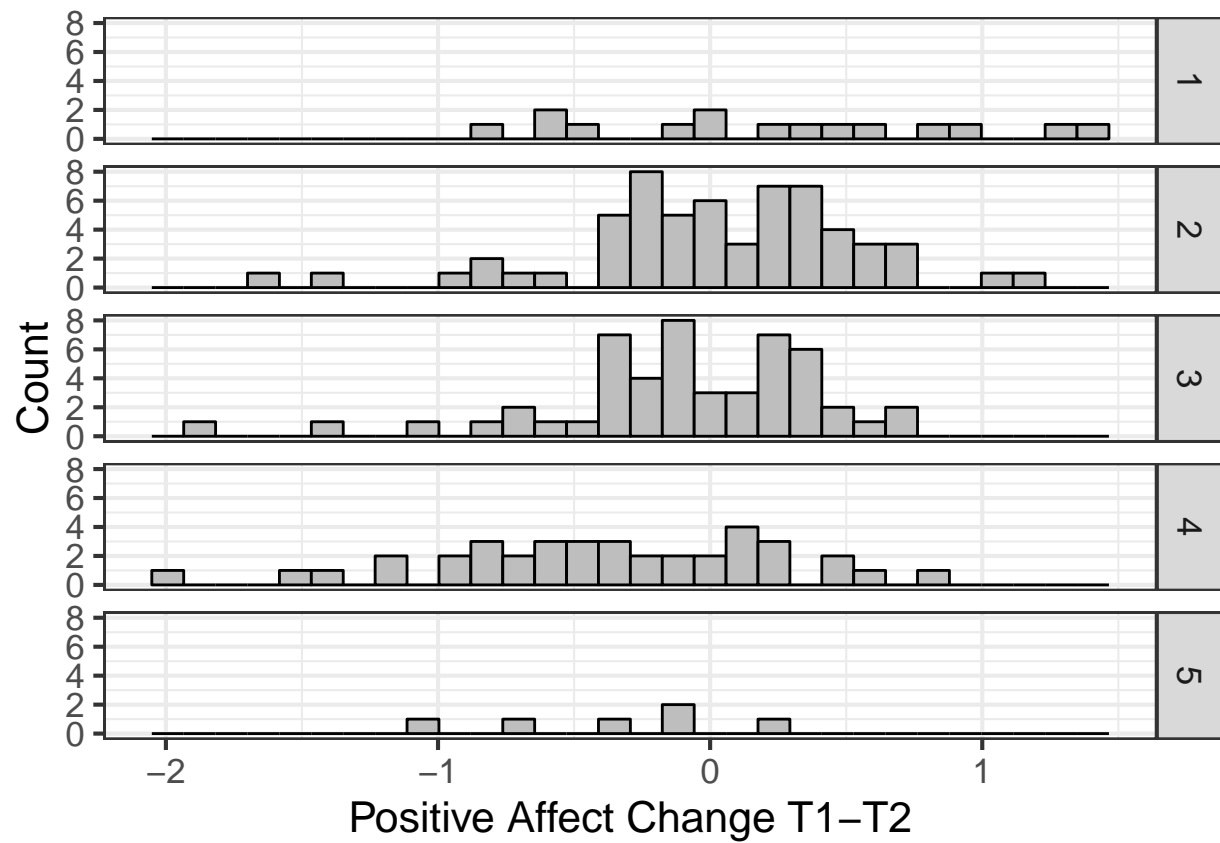
Note that these plots are not in the manuscript.

```

#Plot the data----
#For positive
ggplot(PANASdata, aes(PA_change)) +
  geom_histogram(colour = "black", fill = "grey") +
  xlab("Positive Affect Change T1-T2") + ylab("Count") +
  theme_bw(base_size = 16) +
  facet_grid(rows = vars(PANASdata$globalNA))

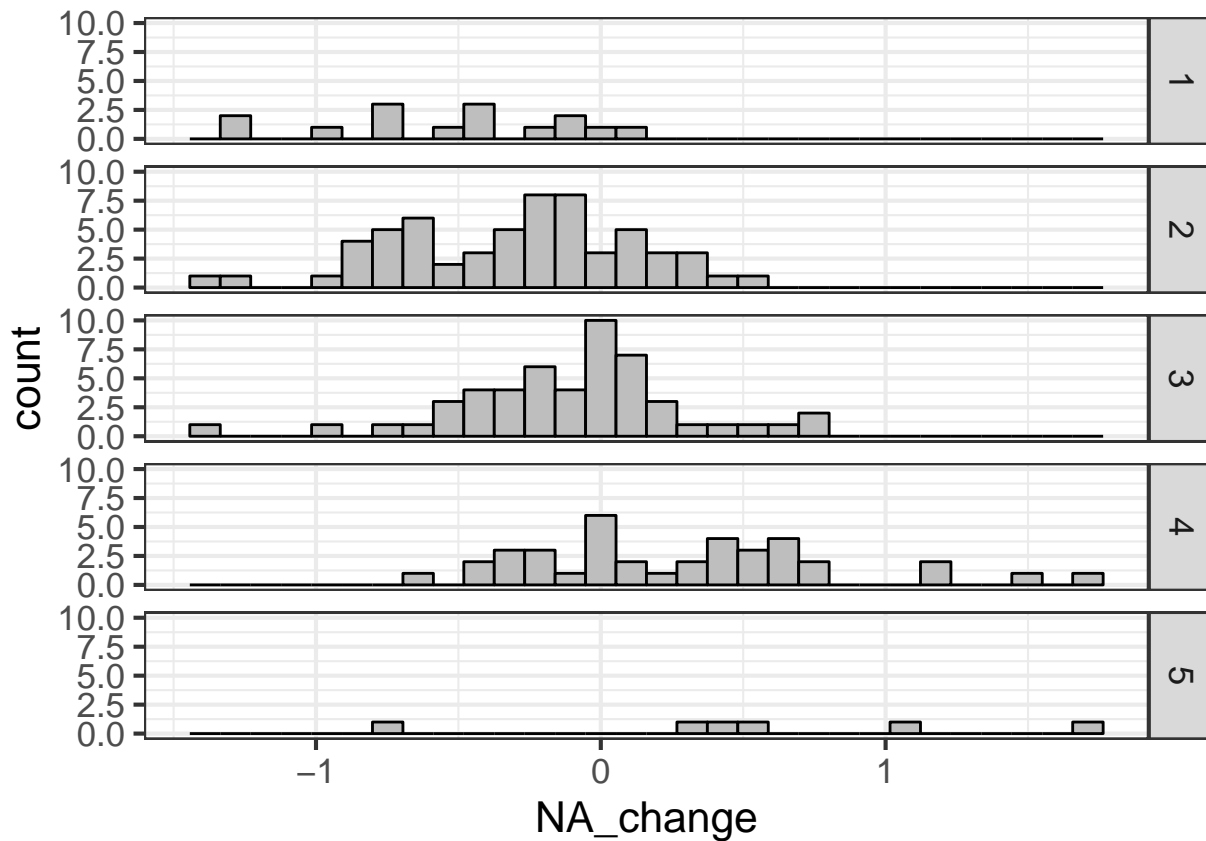
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
#For negative
ggplot(PANASdata, aes(NA_change)) +
  geom_histogram(colour = "black", fill = "grey") +
  theme_bw(base_size = 16) +
  facet_grid(rows = vars(PANASdata$globalNA))
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



## Summary Stats Table

The first 5 lines are for the positive affect conditions (who answered 1 to 5 on the global transition question), the bottom 5 lines are for the negative affect groups.

*#Create summary stats table*

```
sum_data <- rbind(sum_data_PA, sum_data_NA)
round(sum_data[,c(21,8,9,10,17,19,20,11,15,16)],2)
```

##	N	m_diff	ci_l_m_diff	ci_u_m_diff	d_z	ci_l_d_z	ci_u_d_z	d_av
## 1	6	-0.43	-1.08	0.22	-0.70	-1.73	0.25	-0.84
## 2	38	-0.55	-0.75	-0.35	-0.92	-1.31	-0.54	-1.00
## 3	42	-0.13	-0.28	0.02	-0.27	-0.58	0.04	-0.19
## 4	69	0.12	0.01	0.22	0.27	0.03	0.51	0.19
## 5	15	0.30	0.00	0.60	0.56	0.00	1.13	0.49
## 6	15	-0.52	-0.77	-0.27	-1.17	-1.89	-0.52	-0.81
## 7	60	-0.30	-0.40	-0.19	-0.71	-1.00	-0.43	-0.52
## 8	51	-0.10	-0.21	0.01	-0.26	-0.54	0.02	-0.15
## 9	38	0.28	0.10	0.45	0.53	0.18	0.87	0.41
## 10	6	0.55	-0.30	1.40	0.68	-0.27	1.70	0.67
##		ci_l_d_av	ci_u_d_av					
## 1		-1.90	0.28					
## 2		-1.40	-0.58					
## 3		-0.41	0.03					
## 4		0.02	0.35					
## 5		0.00	0.97					



```
## 6      -1.25      -0.34
## 7      -0.73      -0.31
## 8      -0.31       0.01
## 9       0.14       0.67
## 10     -0.24       1.54
```

We add a TOTAL line in the summary graph, which is based on combining the 2 little change groups (the people who answer 2 and 4). For this, we need to recode the data in one group (otherwise the differences in both groups which are in opposite directions cancel each other out). Then we calculate the means and sd, and perform a t-test in R to get the CI.

```
#And the combined means for the little change individuals:
PANASdata$PA_change_rec <- PANASdata$T2_PA - PANASdata$T1_PA
PANASdata$NA_change_rec <- PANASdata$T2_NA - PANASdata$T1_NA

#Need to flip around the scores from group 2 (which are in the opposite direction)
PANASdata$PA_change_rec <- ifelse(PANASdata$globalPA == 2 | PANASdata$globalPA == 1,
                                  PANASdata$PA_change_rec * -1,
                                  PANASdata$PA_change_rec * 1)

PANASdata$NA_change_rec <- ifelse(PANASdata$globalNA == 2 | PANASdata$globalNA == 1,
                                  PANASdata$NA_change_rec * -1,
                                  PANASdata$NA_change_rec * 1)

#Mean only for little change group: positive
mean(PANASdata$PA_change_rec[PANASdata$globalPA == 2 | PANASdata$globalPA == 4])

## [1] 0.2719626

sd(PANASdata$PA_change_rec[PANASdata$globalPA == 2 | PANASdata$globalPA == 4])

## [1] 0.5390058

t.test(PANASdata$PA_change_rec[PANASdata$globalPA == 2 | PANASdata$globalPA == 4])

##
## One Sample t-test
##
## data: PANASdata$PA_change_rec[PANASdata$globalPA == 2 | PANASdata$globalPA == 4]
## t = 5.2192, df = 106, p-value = 8.995e-07
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## 0.1686541 0.3752711
## sample estimates:
## mean of x
## 0.2719626

#Mean only for little change group: negative
mean(PANASdata$NA_change_rec[PANASdata$globalNA == 2 | PANASdata$globalNA == 4])

## [1] 0.2887755

sd(PANASdata$NA_change_rec[PANASdata$globalNA == 2 | PANASdata$globalNA == 4])

## [1] 0.4592425

t.test(PANASdata$NA_change_rec[PANASdata$globalNA == 2 | PANASdata$globalNA == 4])

##
```

```
## One Sample t-test
##
## data: PANASdata$NA_change_rec[PANASdata$globalNA == 2 | PANASdata$globalNA == 4]
## t = 6.2249, df = 97, p-value = 1.23e-08
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## 0.1967032 0.3808478
## sample estimates:
## mean of x
## 0.2887755
```

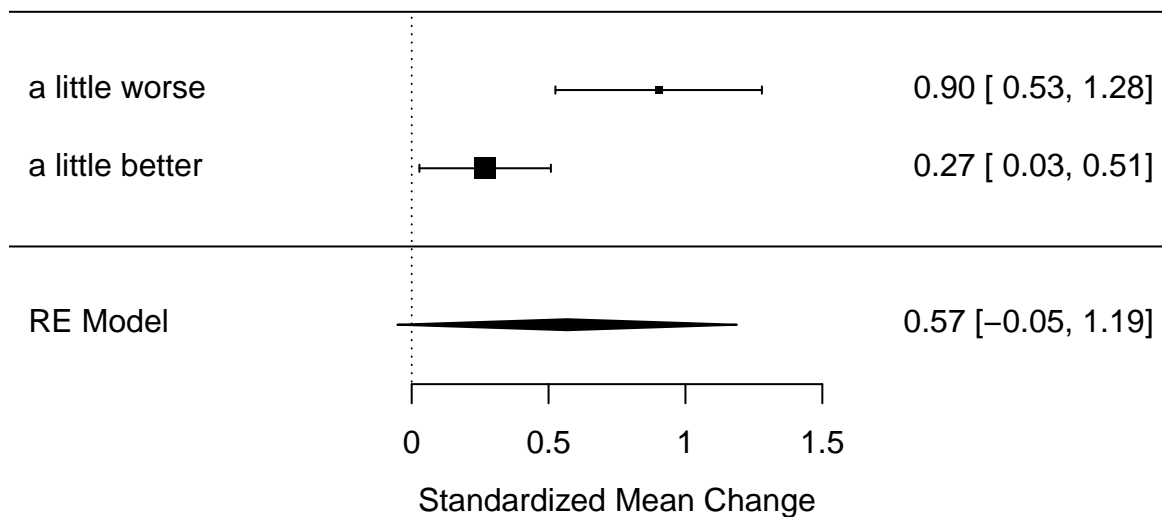
## Meta-Analytic Approach

Although we originally planned (and pre-registered) to simply follow the ‘combine the 2 slightly changed groups’ analysis approach, upon consideration and after looking at the data from both studies, we changed our mind. Combining these 2 groups assumes 1) the effect sizes are similar, and 2) the standard deviations are similar. That might be true, but we believe for now it is too strong an assumption to make. An alternative solution is to not simply combine the two groups, but to meta-analyze them using a random effects meta-analysis. We can explore heterogeneity, and after several datasets have been collected, decide if effect sizes and sd’s are similar or not.

```
# We can perform a meta-analysis based on this data for dz.----
# We can use the escalc function - which reports a bias corrected version of dz (so the estimates are s
#for positive:
g <- escalc(ni = sum_data_PA$N, m1i = sum_data_PA$m1, m2i = sum_data_PA$m2, sd1i = sum_data_PA$sd1, sd2i = sum_data_PA$sd2)
# We reverse the direction of the effect for individuals in group 2 by using abs(yi)
result <- rma(abs(yi), vi, data=g[c(2,4),], slab = c("a little worse", "a little better"))
result

##
## Random-Effects Model (k = 2; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 0.1749 (SE = 0.2841)
## tau (square root of estimated tau^2 value): 0.4182
## I^2 (total heterogeneity / total variability): 87.05%
## H^2 (total variability / sampling variability): 7.72
##
## Test for Heterogeneity:
## Q(df = 1) = 7.7206, p-val = 0.0055
##
## Model Results:
##
## estimate se zval pval ci.lb ci.ub
## 0.5679 0.3165 1.7945 0.0727 -0.0524 1.1881 .
##
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

forest(result)
```

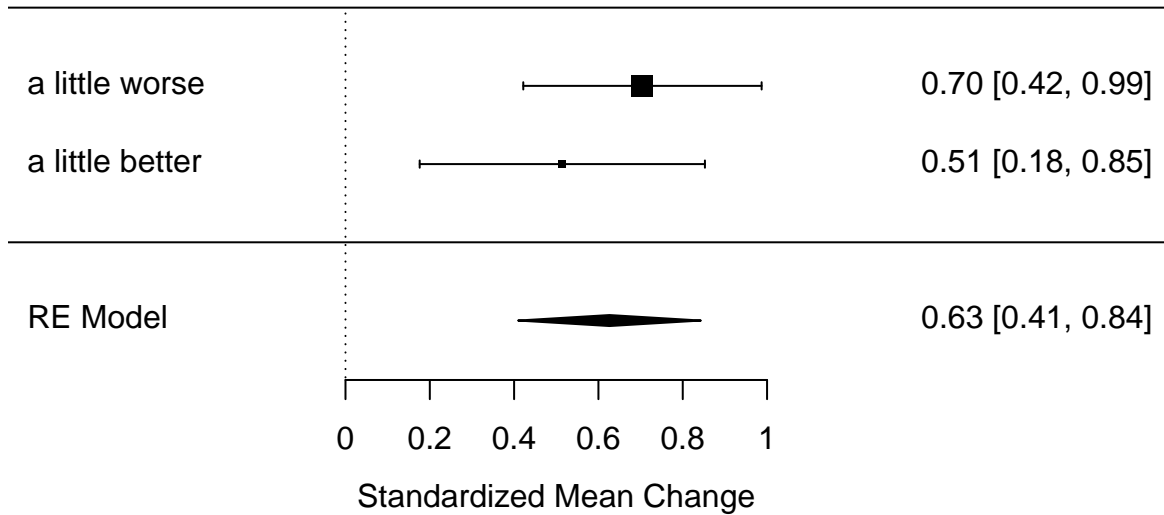


*#for negative:*

```
g <- escalc(ni = sum_data_NA$N, m1i = sum_data_NA$m1, m2i = sum_data_NA$m2, sd1i = sum_data_NA$sd1, sd2i = sum_data_NA$sd2)
# We reverse the direction of the effect for individuals in group 2 by using abs(yi)
result <- rma(abs(yi), vi, data=g[c(2,4),], slab = c("a little worse", "a little better"))
result
```

```
##
## Random-Effects Model (k = 2; tau^2 estimator: REML)
##
## tau^2 (estimated amount of total heterogeneity): 0 (SE = 0.0358)
## tau (square root of estimated tau^2 value): 0
## I^2 (total heterogeneity / total variability): 0.00%
## H^2 (total variability / sampling variability): 1.00
##
## Test for Heterogeneity:
## Q(df = 1) = 0.7144, p-val = 0.3980
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.6262 0.1107 5.6583 <.0001 0.4093 0.8432 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
forest(result)
```



```
#We can also meta-analyze d_av (treating the 2 scores as independent)----
```

```
# For positive
```

```
g <- escalc(n1i = sum_data_PA$N, n2i = sum_data_PA$N, m1i = sum_data_PA$m1, m2i = sum_data_PA$m2, sd1i =
```

```
# We reverse the direction of the effect for individuals in group 2 by using abs(yi)
```

```
result <- rma(abs(yi), vi, data=g[c(2,4),])
```

```
result
```

```
##
```

```
## Random-Effects Model (k = 2; tau^2 estimator: REML)
```

```
##
```

```
## tau^2 (estimated amount of total heterogeneity): 0.2762 (SE = 0.4529)
```

```
## tau (square root of estimated tau^2 value): 0.5256
```

```
## I^2 (total heterogeneity / total variability): 86.24%
```

```
## H^2 (total variability / sampling variability): 7.27
```

```
##
```

```
## Test for Heterogeneity:
```

```
## Q(df = 1) = 7.2683, p-val = 0.0070
```

```
##
```

```
## Model Results:
```

```
##
```

```
## estimate se zval pval ci.lb ci.ub
```

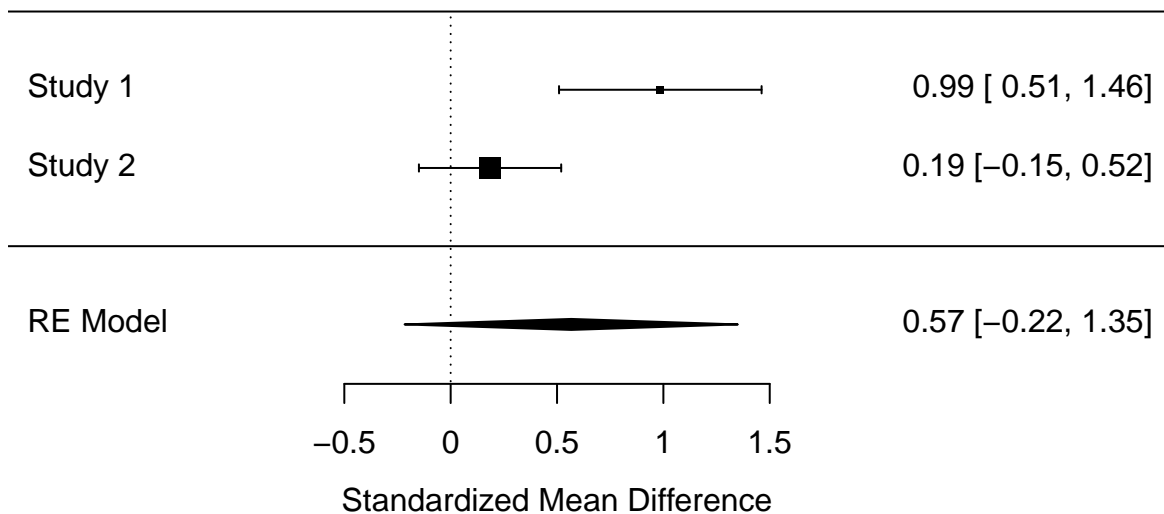
```
## 0.5667 0.3997 1.4177 0.1563 -0.2168 1.3502
```

```
##
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
forest(result)
```



```
# For negative
```

```
g <- escalc(n1i = sum_data_NA$N, n2i = sum_data_NA$N, m1i = sum_data_NA$m1, m2i = sum_data_NA$m2, sd1i =
```

```
# We reverse the direction of the effect for individuals in group 2 by using abs(yi)
```

```
result <- rma(abs(yi), vi, data=g[c(2,4),])
```

```
result
```

```
##
```

```
## Random-Effects Model (k = 2; tau^2 estimator: REML)
```

```
##
```

```
## tau^2 (estimated amount of total heterogeneity): 0 (SE = 0.0623)
```

```
## tau (square root of estimated tau^2 value): 0
```

```
## I^2 (total heterogeneity / total variability): 0.00%
```

```
## H^2 (total variability / sampling variability): 1.00
```

```
##
```

```
## Test for Heterogeneity:
```

```
## Q(df = 1) = 0.1504, p-val = 0.6982
```

```
##
```

```
## Model Results:
```

```
##
```

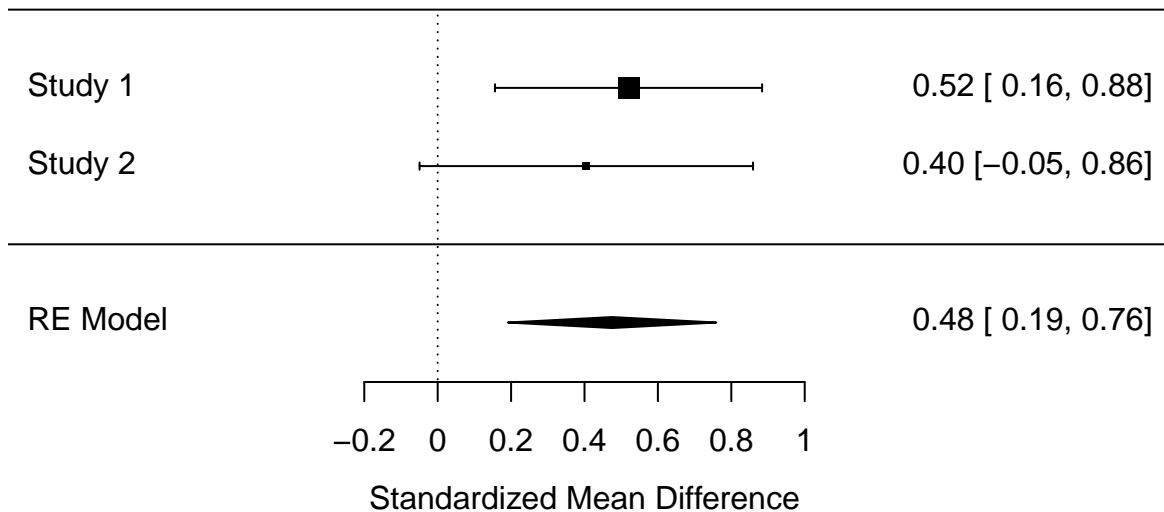
```
## estimate      se      zval      pval      ci.lb      ci.ub      **
##    0.4751    0.1449    3.2790    0.0010    0.1911    0.7591
```

```
##
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
forest(result)
```



Note the heterogeneity is substantial, increasing our doubt that simply combining these two groups is the best analytic approach.

Then the plot is produced (when saving, the resolution is better)

*#Create a graph showing individual change*

```
longPA = PANASdata
```

*#NOW WE MAKE IT LONG FORMAT and we only want those in the little changed PA group first*

```
longPA = melt(longPA[longPA$globalPA==2 | longPA$globalPA == 4,],
  measure.vars = c("T1_PA", "T2_PA") )
```

*#looking at the dataframe created, can see that each participant now has a  
# T1\_PA, and T2\_PA entry (i.e., in long format)*

```
longPA$globalPA = as.factor(longPA$globalPA)
```

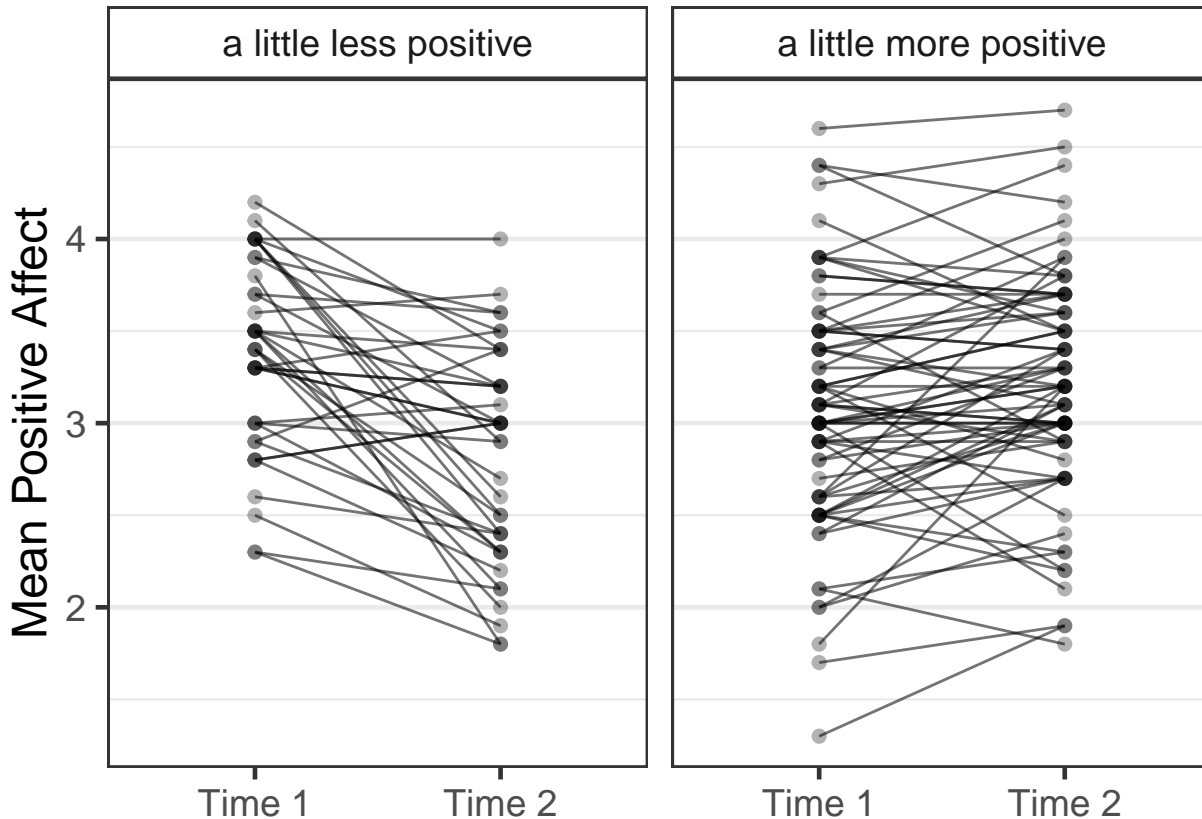
```
levels(longPA$globalPA) <- c("a little less positive", "a little more positive") #renaming the levels
```

```
plot1 <- ggplot(data = longPA, aes(x = variable, y = value)) +
  geom_point(size = 2, color = "black", alpha = 0.3) + #colour points by globalPA
  geom_path(aes(group = StudentID, alpha = 0.3)) + #spaghetti plot
  ylab("Mean Positive Affect") +
  xlab("Time") +
  theme_bw(base_size = 18) +
```

```

facet_grid(~ globalPA) +
theme(legend.position="none") +
scale_x_discrete(labels=c("T1_PA" = "Time 1", "T2_PA" = "Time 2")) +
theme(axis.title.x=element_blank(),
      strip.background =element_rect(fill="white"),
      panel.grid.major.x = element_blank())
plot1

```



```

#code to save the plot
# jpeg(file="plot1.jpg",width=2000,height=1400, units = "px", res = 300)
# plot1
# dev.off()

#now do the same for NA
longNA = PANASdata
longNA = melt(longNA[longNA$globalNA==2 | longNA$globalNA == 4,],
             measure.vars = c("T1_NA", "T2_NA") )

longNA$globalNA = as.factor(longNA$globalNA)
levels(longNA$globalNA) <- c("a little less negative", "a little more negative") #renaming the levels

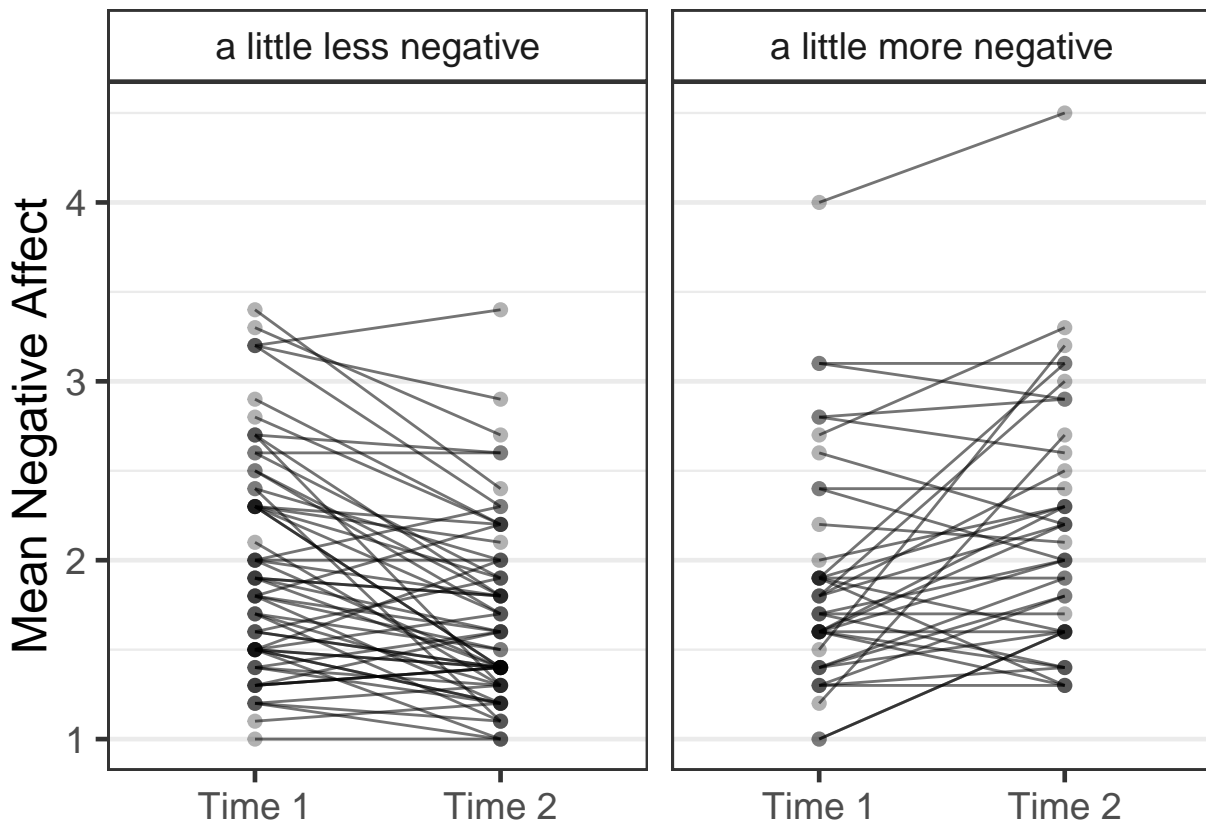
plot2 <- ggplot(data = longNA, aes(x = variable, y = value)) +
  geom_point(size = 2, color = "black", alpha = 0.3) + #colour points by globalPA
  geom_path(aes(group = StudentID, alpha = 0.3)) + #spaghetti plot
  ylab("Mean Negative Affect") +
  xlab("Time") +

```

```

theme_bw(base_size = 18) +
facet_grid(~ globalNA) +
theme(legend.position="none") +
scale_x_discrete(labels=c("T1_NA" = "Time 1", "T2_NA" = "Time 2")) +
theme(axis.title.x=element_blank(),
      strip.background =element_rect(fill="white"),
      panel.grid.major.x = element_blank())
plot2

```



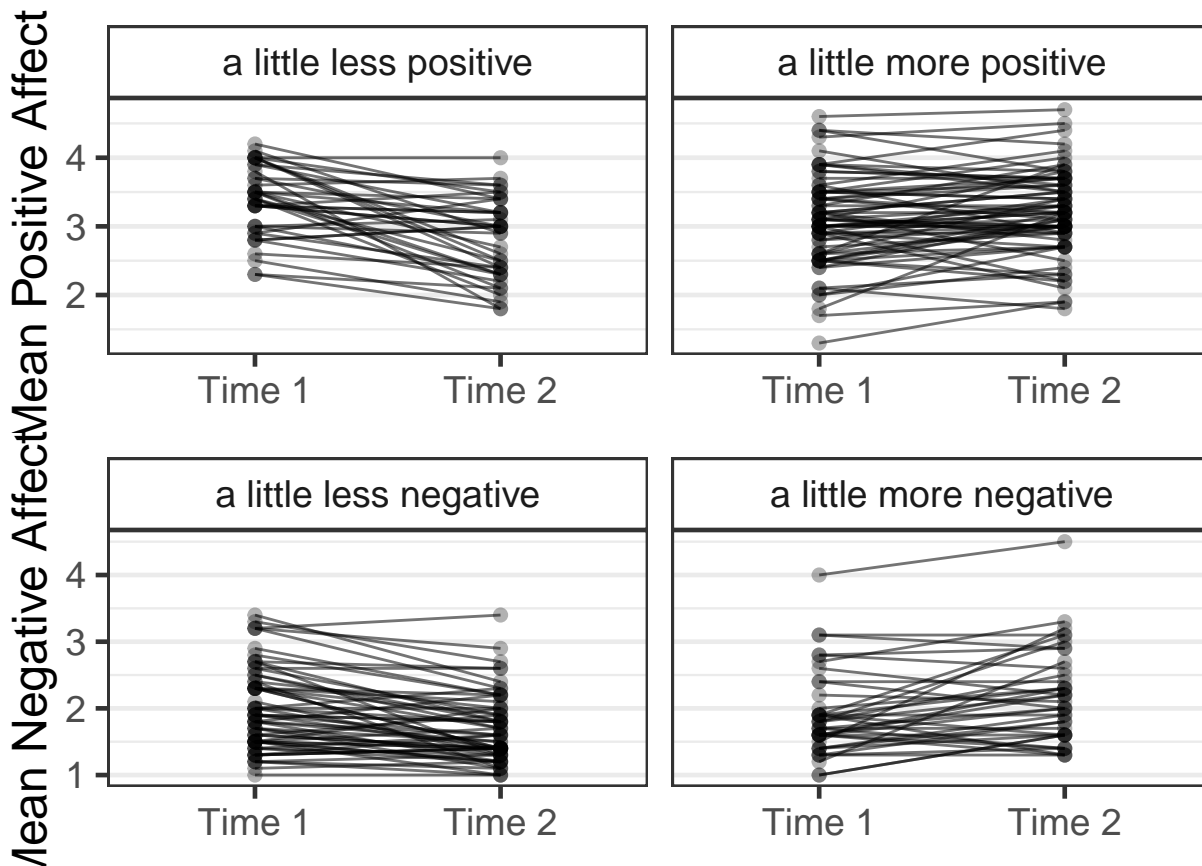
```

# jpeg(file="plot2.jpg",width=2000,height=1400, units = "px", res = 300)
# plot2
# dev.off()

#Save combined plot
grid.arrange(plot1, plot2, nrow = 2)

```





```
# jpeg(file="plot_grid.jpg",width=2000,height=2400, units = "px", res = 300)
# grid.arrange(plot1, plot2, nrow = 2)
# dev.off()
```

## Correlations

The code below replicates the text:

“In our study using the global transition question (Study 1), however, this was not the case, possibly due to the short interval before recall: the correlations of the global transition question responses with participant change scores (PA:  $r = .48$ ; NA:  $r = .52$ ) were larger than the correlation with T2 current state scores (PA:  $r = .32$ ,  $rdif = 0.17$ , 95% CI[0.03; 0.30], NA:  $r = .38$ ,  $rdif = 0.14$ , 95% CI[0; 0.28], Zou, 2007).”

We report the 95% CI following Zou, 2017.

```
##### correlations of global Qs, including with individual items
```

```
cor_PA_NA <- PANASdata[42:51]
cor(cor_PA_NA)
```

```
##          globalPA    globalNA    T1_PA    T1_NA
## globalPA    1.00000000 -0.66089239 -0.10169866  0.016280635
## globalNA   -0.660892392  1.00000000  0.07181701 -0.021716755
## T1_PA      -0.101698663  0.07181701  1.00000000 -0.093884383
## T1_NA       0.016280635 -0.02171675 -0.09388438  1.000000000
## T2_PA       0.317565370 -0.20390699  0.60926871 -0.007652072
```

```
## T2_NA      -0.296374781  0.38032640 -0.01269962  0.690474759
## PA_change  0.482677092 -0.31696684 -0.36546894  0.092474803
## NA_change  -0.402979801  0.51815823  0.10086089 -0.357489437
## PA_change_rec -0.185200584  0.08792447 -0.05956225  0.108577937
## NA_change_rec -0.009182971 -0.09727449 -0.12530603  0.094122084
##           T2_PA      T2_NA      PA_change      NA_change
## globalPA    0.3175653700 -0.29637478  0.48267709 -0.402979801
## globalNA    -0.2039069870  0.38032640 -0.31696684  0.518158229
## T1_PA       0.6092687066 -0.01269962 -0.36546894  0.100860893
## T1_NA       -0.0076520723  0.69047476  0.09247480 -0.357489437
## T2_PA       1.0000000000 -0.06822370  0.51544061 -0.078525753
## T2_NA       -0.0682237048  1.00000000 -0.06636067  0.428717619
## PA_change    0.5154406081 -0.06636067  1.00000000 -0.201174207
## NA_change   -0.0785257532  0.42871762 -0.20117421  1.000000000
## PA_change_rec 0.0234877568  0.10207686  0.09193781 -0.003818536
## NA_change_rec -0.0002019022  0.21846026  0.13517637  0.164497414
##           PA_change_rec NA_change_rec
## globalPA    -0.185200584 -0.0091829709
## globalNA     0.087924465 -0.0972744880
## T1_PA       -0.059562255 -0.1253060286
## T1_NA        0.108577937  0.0941220838
## T2_PA        0.023487757 -0.0002019022
## T2_NA        0.102076857  0.2184602595
## PA_change    0.091937812  0.1351763686
## NA_change   -0.003818536  0.1644974139
## PA_change_rec 1.000000000  0.1664900754
## NA_change_rec 0.166490075  1.0000000000
```

```
# Compare two correlations based on two dependent groups
# The correlations are overlapping
```

```
cocor(~PA_change + globalPA | T2_PA + globalPA, cor_PA_NA)
```

```
##
## Results of a comparison of two overlapping correlations based on dependent groups
##
## Comparison between r.jk (globalPA, PA_change) = 0.4827 and r.jh (globalPA, T2_PA) = 0.3176
## Difference: r.jk - r.jh = 0.1651
## Related correlation: r.kh = 0.5154
## Data: cor_PA_NA: j = globalPA, k = PA_change, h = T2_PA
## Group size: n = 170
## Null hypothesis: r.jk is equal to r.jh
## Alternative hypothesis: r.jk is not equal to r.jh (two-sided)
## Alpha: 0.05
##
## pearson1898: Pearson and Filon's z (1898)
## z = 2.4510, p-value = 0.0142
## Null hypothesis rejected
##
## hotelling1940: Hotelling's t (1940)
## t = 2.4853, df = 167, p-value = 0.0139
## Null hypothesis rejected
##
## williams1959: Williams' t (1959)
## t = 2.4655, df = 167, p-value = 0.0147
```

```

## Null hypothesis rejected
##
## olkin1967: Olkin's z (1967)
## z = 2.4510, p-value = 0.0142
## Null hypothesis rejected
##
## dunn1969: Dunn and Clark's z (1969)
## z = 2.4414, p-value = 0.0146
## Null hypothesis rejected
##
## hendrickson1970: Hendrickson, Stanley, and Hills' (1970) modification of Williams' t (1959)
## t = 2.4853, df = 167, p-value = 0.0139
## Null hypothesis rejected
##
## steiger1980: Steiger's (1980) modification of Dunn and Clark's z (1969) using average correlations
## z = 2.4333, p-value = 0.0150
## Null hypothesis rejected
##
## meng1992: Meng, Rosenthal, and Rubin's z (1992)
## z = 2.4264, p-value = 0.0153
## Null hypothesis rejected
## 95% confidence interval for r.jk - r.jh: 0.0380 0.3571
## Null hypothesis rejected (Interval does not include 0)
##
## hittner2003: Hittner, May, and Silver's (2003) modification of Dunn and Clark's z (1969) using a back
## z = 2.4306, p-value = 0.0151
## Null hypothesis rejected
##
## zou2007: Zou's (2007) confidence interval
## 95% confidence interval for r.jk - r.jh: 0.0324 0.2990
## Null hypothesis rejected (Interval does not include 0)
cocor(~NA_change + globalNA | T2_NA + globalNA, cor_PA_NA)

##
## Results of a comparison of two overlapping correlations based on dependent groups
##
## Comparison between r.jk (globalNA, NA_change) = 0.5182 and r.jh (globalNA, T2_NA) = 0.3803
## Difference: r.jk - r.jh = 0.1378
## Related correlation: r.kh = 0.4287
## Data: cor_PA_NA: j = globalNA, k = NA_change, h = T2_NA
## Group size: n = 170
## Null hypothesis: r.jk is equal to r.jh
## Alternative hypothesis: r.jk is not equal to r.jh (two-sided)
## Alpha: 0.05
##
## pearson1898: Pearson and Filon's z (1898)
## z = 1.9573, p-value = 0.0503
## Null hypothesis retained
##
## hottelling1940: Hotelling's t (1940)
## t = 1.9905, df = 167, p-value = 0.0482
## Null hypothesis rejected
##
## williams1959: Williams' t (1959)

```

```
## t = 1.9589, df = 167, p-value = 0.0518
## Null hypothesis retained
##
## olkin1967: Olkin's z (1967)
## z = 1.9573, p-value = 0.0503
## Null hypothesis retained
##
## dunn1969: Dunn and Clark's z (1969)
## z = 1.9481, p-value = 0.0514
## Null hypothesis retained
##
## hendrickson1970: Hendrickson, Stanley, and Hills' (1970) modification of Williams' t (1959)
## t = 1.9905, df = 167, p-value = 0.0482
## Null hypothesis rejected
##
## steiger1980: Steiger's (1980) modification of Dunn and Clark's z (1969) using average correlations
## z = 1.9442, p-value = 0.0519
## Null hypothesis retained
##
## meng1992: Meng, Rosenthal, and Rubin's z (1992)
## z = 1.9406, p-value = 0.0523
## Null hypothesis retained
## 95% confidence interval for r.jk - r.jh: -0.0017 0.3485
## Null hypothesis retained (Interval includes 0)
##
## hittner2003: Hittner, May, and Silver's (2003) modification of Dunn and Clark's z (1969) using a back
## z = 1.9424, p-value = 0.0521
## Null hypothesis retained
##
## zou2007: Zou's (2007) confidence interval
## 95% confidence interval for r.jk - r.jh: -0.0009 0.2780
## Null hypothesis retained (Interval includes 0)
```

## Exploratory results reported in the discussion

```
#####
#other (exploratory) analyses, and descriptive statistics----

### test of difference between the "little-changed" groups and the "same" group
#for PA
t.test(PANASdata$PA_change_rec[PANASdata$globalPA == 2 | PANASdata$globalPA == 4],
       PANASdata$PA_change_rec[PANASdata$globalPA == 3])

##
## Welch Two Sample t-test
##
## data: PANASdata$PA_change_rec[PANASdata$globalPA == 2 | PANASdata$globalPA == 4] and PANASdata$PA_change_rec[PANASdata$globalPA == 3]
## t = 4.4299, df = 83.171, p-value = 2.85e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.2220174 0.5838126
```

```

## sample estimates:
## mean of x mean of y
## 0.2719626 -0.1309524

mean(PANASdata$PA_change_rec[PANASdata$globalPA == 3])

## [1] -0.1309524

sd(PANASdata$PA_change_rec[PANASdata$globalPA == 3])

## [1] 0.483124

#for NA
t.test(PANASdata$NA_change_rec[PANASdata$globalNA == 2 | PANASdata$globalNA == 4],
       PANASdata$NA_change_rec[PANASdata$globalNA == 3])

##
## Welch Two Sample t-test
##
## data: PANASdata$NA_change_rec[PANASdata$globalNA == 2 | PANASdata$globalNA == 4] and PANASdata$NA_change_rec[PANASdata$globalNA == 3]
## t = 5.4771, df = 118.42, p-value = 2.465e-07
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.2482183 0.5293327
## sample estimates:
## mean of x mean of y
## 0.2887755 -0.1000000

mean(PANASdata$NA_change_rec[PANASdata$globalNA == 3])

## [1] -0.1

sd(PANASdata$NA_change_rec[PANASdata$globalNA == 3])

## [1] 0.3836665

#seems to be a bit of a difference between change scores for those who said
# they were a little less positive compared to those who were a little more positive
t.test(PANASdata$PA_change[PANASdata$globalPA == 2],
       PANASdata$PA_change[PANASdata$globalPA == 4])

##
## Welch Two Sample t-test
##
## data: PANASdata$PA_change[PANASdata$globalPA == 2] and PANASdata$PA_change[PANASdata$globalPA == 4]
## t = -6.0641, df = 59.337, p-value = 9.941e-08
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.8895156 -0.4481655
## sample estimates:
## mean of x mean of y
## -0.5500000 0.1188406

```

This is the end of the results reported in the main text.

# Exploratory Analyses Not Reported in the Main Text

## Analyzing Individual Results.

“We conducted exploratory analyses investigating individual variability. In total, 70 out of 107 individuals in the self-reported little change group for positive affect showed a change in positive affect that corresponded to the direction they indicated on the global transition question, 7 showed no change in positive affect, and 30 changed in the opposite direction (e.g., they said they felt a little more positive but their change scores were negative). For negative affect scores 66 out of 98 individuals in the little-changed group had change scores that were greater than zero on negative affect in the direction they indicated on the global transition question, 9 showed no change, and 23 had change scores going in the opposite direction to what they reported in the global transition questions.”

```
# Analysis of individual responses----
```

```
sum(PANASdata$PA_change_rec[PANASdata$globalPA == 2 | PANASdata$globalPA == 4] > 0)
```

```
## [1] 70
```

```
# 70/107 in the PA little-changed group showed change greater than zero  
# scale points in the direction they said they changed on the global Qs
```

```
sum(PANASdata$PA_change_rec[PANASdata$globalPA == 2 | PANASdata$globalPA == 4] == 0)
```

```
## [1] 7
```

```
# 7/107 in the PA little-changed group showed no change  
# scale points in the direction they said they changed on the global Qs
```

```
sum(PANASdata$PA_change_rec[PANASdata$globalPA == 2 | PANASdata$globalPA == 4] < 0)
```

```
## [1] 30
```

```
# 30/107 in the PA little-changed group showed change in the opposite direction to  
# what they said (e.g., said they felt a little more positive emotions but PA change  
# shows they got a little worse)
```

```
sum(PANASdata$NA_change_rec[PANASdata$globalNA == 2 | PANASdata$globalNA == 4] > 0)
```

```
## [1] 66
```

```
# 66/98 in the NA little-changed group showed change greater than or equal to zero  
# scale points in the direction they said they changed on the global Qs
```

```
sum(PANASdata$NA_change_rec[PANASdata$globalNA == 2 | PANASdata$globalNA == 4] == 0)
```

```
## [1] 9
```

```
# 9/98 in the NA little-changed group showed no change
```

```
sum(PANASdata$NA_change_rec[PANASdata$globalNA == 2 | PANASdata$globalNA == 4] < 0)
```

```
## [1] 23
```

```
# 23/98 in the NA little-changed group showed change in the opposite direction
```