

#####ANALYSIS OVERVIEW FOR DUNN ET AL JCCP PREVENT SECONDARY ANALYSIS PAPER MAIN ARTICLE

Variable Names

#TrialID: Unique anonymised identifier for participant

#NumberOfMBCTSessionsAttended: number of MBCT sessions attended (out of a maximum of 8)

#CatMedicationUse: if participants continued with or discontinued use of ADM: 0 continued, 1 discontinued

#group2: treatment allocation: MADM = 0, MBCT = 1

#site_dummy1: dummy codes site: 1 if site 1, 0 if elsewhere

#site_dummy2: dummy codes site: 1 if site 2, 0 if elsewhere

#site_dummy3: dummy codes site: 1 if site 3, 0 if elsewhere

#timetoevent: days to relapse/recurrence (if occurred) or final follow up (if did not occur) from baseline assessment for overall sample

#eventstatus: if relapse/recurrence occurred: no = 0, yes = 1

#ContentmentBL: baseline score on DPES contentment

#JoyBL: baseline score on DPES joy

#Contentment@1: post treatment on DPES contentment

#Joy@1: post treatment on DPES joy

#jc_complete: If complete DPES data was available at baseline and post: 0 = no, 1 = yes

#sym: If participants had residual depression symptoms at baseline on Hamilton Depression Rating Scale: 0 = asymptomatic, 1 = symptomatic

#HAMD_TotalR: Hamilton Depression Rating Scale score at baseline assessment

#HAMD_Total1: Hamilton Depression Rating Scale score at post treatment assessment

#Age: age of participants (in years)

#Gender: gender of participant: 0 = male, 1 = female

#ethnic_recode: ethnicity of participant: 0 = white british, 1 = any other (CHECK)

#AbuseSubGroup: history of childhood abuse: 0 = no, 1 = yes

#ComorbiditiesPresentatBL: number of comorbid diagnoses at baseline assessment

#BLFFMQ_Total: FFMQ mindfulness total score at baseline assessment

#@1FFMQ_Total: FFMQ mindfulness total score at post treatment assessment

#BLSCIDAgeOnset: Age of first onset of depression (coded on the SCID interview)

#BLSCIDNoEpi: Number of prior depression episodes (coded on the SCID interview)

#episode_split: episodes split into ≤ 5 episodes (coded 0) or >5 episodes (coded 1), based on SCID interview

#relapse_mediate: if participants in mediation sample relapsed after post treatment: 0 = no, 1 = yes

#time_to_relapse_mediate: days to relapse/recurrence from post treatment (if occurred) or final follow up (if did not occur) for mediation sample

#BLFormalMeditation: extent of formal meditation practice at intake assessment: from 0 not at all to 3 regularly and more days than not

#@1FormalMeditation: extent of formal meditation practice at post treatment assment: from 0 not at all to 3 regularly and more days than not

#timetorelapse_posttreatment: days to relapse/recurrence (if occurred) or till post-treatment assessment (if did not occur) by end of post-treatment assessment

#relapse_posttreatment: if a relapse occurred by end of post-treatment assessment: 0 = no, 1 = yes

#valid_mediate2 dummy: variable to select 266 participants eligible for mediation analysis: 1 = include, blank = exclude

#meds_time1_merge_recode: if medications were continued or stopped/reduced by post-treatment assessment: 0 = continued, 1 = stopped/reduced

#Main article

#1. relapse up until post treatment assessment (Cox regression)

#2. relapse across entire follow up window (Cox regression)

#3. Change in PA from pre to post treatment (linear regression), with and without adjusting for confounders, imputed

#4. Paired t change in pre to post change in PA for each arm seperately and pooled sample

#5. does PA at intake predict risk of RR, with and without adjusting for confounders, and when including group by PA interaction

#6. mediation analysis on those folks with complete data who had not relapsed at post (n=266)

#unique imputation run for each analysis

LOAD UP DATA, TRIM OUT VALUES AND COMPUTE VARIABLES##

###if need to update R

#install.packages("installr")

#library(installr)

#to then update R type: updateR()

###clear working directory

rm(list=ls())

```
####install packages if required
```

```
#install.packages("bmlm")
```

```
#install.packages("MatchIt")
```

```
#install.packages("lmtest")
```

```
#install.packages("sandwich")
```

```
#install.packages("survminer")
```

```
#install.packages("contsurvplot")
```

```
#install.packages("pammtools")
```

```
#install.packages("mice")
```

```
#install.packages("frailtypack")
```

```
#install.packages("mediation")
```

```
#install.packages("car")
```

```
#install.packages("MKmisc")
```

```
#load relevant packages
```

```
library(bmlm)
```

```
library(rlang)
```

```
library(tidyverse)
```

```
library(haven)
```

```
library(MatchIt)
```

```
library(lmtest)
```

```
library(sandwich)
```

```
library(survival)
```

```
library(survminer)
```

```
library(contsurvplot)
```

```
library(pammtools)
```

```
library(mice)
```

```
library(frailtypack)
```

```
library(mediation)
```

```
library(car)
```

```
#library(MKmisc)
```

```
#### set working directory where data is stored
```

```
#for home
```

```
setwd("C:/Users/Barney/Desktop/JCCP DPES revisions")
```

```
#for work
```

```
#setwd("C:/Users/bdd202/JCCP DPES revisions/")
```

```
#### Load the csv data and prepare it for use
```

```
#specify filename of data file
```

```
filename1<-"Dunn et al JCCP secondary analysis of PREVENT trial data.csv"
```

```
#load in data
```

```
PREVENT_data1 <- read.csv(filename1) %>%
```

```
  mutate(group2 = as_factor(group2),
```

```
         sym = as_factor(sym),
```

```
         Gender = as_factor(Gender),
```

```
         ethnic_recode = as_factor(ethnic_recode)
```

```
  ) %>%
```

```
  zap_formats() %>%
```

```
  zap_widths()
```

```
#should create file with 424 observations of 35 variables
```

```
#create variables
```

```
PREVENT_data1$DPESBLJoyContentment_check <- PREVENT_data1$JoyBL + PREVENT_data1$ContentmentBL
```

```
PREVENT_data1$DPES.1JoyContentment_check <- PREVENT_data1$Joy.1 + PREVENT_data1$Contentment.1
```

```
PREVENT_data1$JCchange <- PREVENT_data1$DPES.1JoyContentment_check -
```

```
PREVENT_data1$DPESBLJoyContentment_check
```

```
PREVENT_data1$HAMDCchange <- PREVENT_data1$HAMD_Total1 - PREVENT_data1$HAMD_TotalR
```

```
PREVENT_data1$FFMQchange <- PREVENT_data1$X.1FFMQ_Total - PREVENT_data1$BLFFMQ_Total
```

```
#label group variable
```

```
PREVENT_data1$group_name<- car::recode(PREVENT_data1$group2,
```

```
    "'0' = 'ADM';
```

```
    '1' = 'MBCT')"
```

```
PREVENT_data1$group_name<-as.factor(PREVENT_data1$group_name)
```

```
#####1. relapse up until post treatment assessment (Cox regression)
```

```
#no imputation required as complete data available
```

```
fit_outcome1b<-coxph(Surv(timetorelapse_posttreatment, relapse_posttreatment)~ group2 + site_dummy1 +  
site_dummy2 + site_dummy3 + sym, data=PREVENT_data1)
```

```
summary(fit_outcome1b)
```

```
#70 events, n=424
```

```
#group beta term: exp(beta) 0.51 (0.31, 0.83), p<.01
```

```
#exp(beta) = hazard ratio
```

```
#####2. relapse across entire follow up window (Cox regression)
```

```
#no imputation required as complete data available
```

```
fit_outcome1<-coxph(Surv(timetoevent, eventstatus)~ group2 + site_dummy1 + site_dummy2 + site_dummy3  
+ sym, data=PREVENT_data1)
```

```
summary(fit_outcome1)
```

```
#194 events, n = 424
```

```
#group term: exp(beta)0.89 (0.67, 1.18), p=.43
```

```
#####3. Change in PA from pre to post treatment (linear regression), with and without adjusting for  
confounders, imputed
```

```
#open dataframe with 424 rows
```

```
linear_frame2<-data.frame(ID=1:424)
```

```
linear_frame2$timetoevent<-PREVENT_data1$timetoevent
```

```
linear_frame2$eventstatus<-PREVENT_data1$eventstatus
```

```
linear_frame2$jcbl<-PREVENT_data1$DPESBLJoyContentment_check
```

```
linear_frame2$jc.1<-PREVENT_data1$DPES.1JoyContentment_check
```

```
linear_frame2$group2<-PREVENT_data1$group2
```

```
linear_frame2$site_dummy1<- PREVENT_data1$site_dummy1
```

```
linear_frame2$site_dummy2<-PREVENT_data1$site_dummy2
```

```
linear_frame2$site_dummy3<-PREVENT_data1$site_dummy3
```

```
linear_frame2$HAMD_TotalR<-PREVENT_data1$HAMD_TotalR
```

```
linear_frame2$BLFFMQ_Total<-PREVENT_data1$BLFFMQ_Total
```

```

linear_frame2$sym<-PREVENT_data1$sym

linear_frame2$ComorbiditiesPresentatBL<-PREVENT_data1$ComorbiditiesPresentatBL

linear_frame2$Age<-PREVENT_data1$Age

linear_frame2$Gender<-PREVENT_data1$Gender

linear_frame2$AbuseSubGroup<-PREVENT_data1$AbuseSubGroup

linear_frame2$CatMedicationUse<-PREVENT_data1$CatMedicationUse

linear_frame2$episode_split<-PREVENT_data1$episode_split

linear_frame2$BLSCIDAgeOnset<-PREVENT_data1$BLSCIDAgeOnset

linear_frame2$BLFormalMeditation <-PREVENT_data1$BLFormalMeditation

#imputed

summary(linear_frame2$jcb1) # 16 missing (4%)

summary(linear_frame2$jcb.1) # 77 missing (18%)


#dropping id

linear_frame2<- subset(linear_frame2, select = -c(ID))


#selected 20 imp runs

seed_value = 4956767

runs_for_imp2<-20

imp_data2 <-mice(linear_frame2, m=runs_for_imp2, maxit=50, seed=seed_value)

#without covariates

modelFit_mi2<-with(imp_data2, lm(jcb.1 ~ group2 +jcb1 + site_dummy1 + site_dummy2 + site_dummy3 +sym))

summary(pool(modelFit_mi2))

#group 2.84 (0.66), p<.001

#r does not produce 95% CIs on imputed data set, so calculating manually

lowerci_modelFit_mi2<- 2.84 - (0.66*1.96) #1.55

upperci_modelFit_mi2<- 2.84 + (0.66*1.96) #4.13


#with covariates

modelFit_mi2b<-with(imp_data2, lm(jcb.1 ~ group2 +jcb1 + site_dummy1 + site_dummy2 + site_dummy3 +sym +
BLSCIDAgeOnset + BLFormalMeditation + episode_split + CatMedicationUse+ AbuseSubGroup
+ComorbiditiesPresentatBL + Age + Gender + BLFFMQ_Total + HAMD_TotalR))

summary(pool(modelFit_mi2b))

#group = 1.78 (SE=0.71), p=.01

#r does not produce 95% CIs on imputed data set, so calculating manually

```

```
lowerci_modelFit_mi2b<- 1.78 - (0.71*1.96) #0.38
```

```
upperci_modelFit_mi2b<- 1.78 + (0.71*1.96) #3.17
```

```
#####4. Paired t change in pre to post change in PA for each arm separately and pooled sample
```

```
#open dataframe with 424 rows
```

```
linear_frame2b<-data.frame(ID=1:424)
```

```
linear_frame2b$jcbl<-PREVENT_data1$DPESBLJoyContentment_check
```

```
linear_frame2b$jc.1<-PREVENT_data1$DPES.1JoyContentment_check
```

```
linear_frame2b$group2<-PREVENT_data1$group2
```

```
linear_frame2b$site_dummy1<- PREVENT_data1$site_dummy1
```

```
linear_frame2b$site_dummy2<-PREVENT_data1$site_dummy2
```

```
linear_frame2b$site_dummy3<-PREVENT_data1$site_dummy3
```

```
linear_frame2b$HAMD_TotalR<-PREVENT_data1$HAMD_TotalR
```

```
linear_frame2b$BLFFMQ_Total<-PREVENT_data1$BLFFMQ_Total
```

```
linear_frame2b$sym<-PREVENT_data1$sym
```

```
linear_frame2b$ComorbiditiesPresentatBL<-PREVENT_data1$ComorbiditiesPresentatBL
```

```
linear_frame2b$Age<-PREVENT_data1$Age
```

```
linear_frame2b$Gender<-PREVENT_data1$Gender
```

```
linear_frame2b$AbuseSubGroup<-PREVENT_data1$AbuseSubGroup
```

```
linear_frame2b$CatMedicationUse<-PREVENT_data1$CatMedicationUse
```

```
linear_frame2b$episode_split<-PREVENT_data1$episode_split
```

```
linear_frame2b$BLSCIDAgeOnset<-PREVENT_data1$BLSCIDAgeOnset
```

```
linear_frame2b$BLFormalMeditation <-PREVENT_data1$BLFormalMeditation
```

```
#dropping id
```

```
linear_frame2b<- subset(linear_frame2b, select = -c(ID))
```

```
#pooled across groups
```

```
seed_value = 4956767
```

```
runs_for_imp2<-20
```

```
imp_data_tpooled <-mice(linear_frame2b, m=runs_for_imp2, maxit=50, seed=seed_value)
```

```
modelFit_mi_tpooled<-with(imp_data_tpooled, t.test(jcbl, jc.1,paired=TRUE, alternative="two.sided"))
```

```
pooled_t_impute<-summary(modelFit_mi_tpooled)
```

```

mean(pooled_t_impute$estimate)
mean(pooled_t_impute$conf.low)
mean(pooled_t_impute$conf.high)
mean(pooled_t_impute$statistic)
mean(pooled_t_impute$p.value)
#t=3.95, est = 1.29 (0.65 to 1.93), p<.001
#manually computing d
sd_pooled_t_impute <-((1.93 - 0.65)/3.92)*sqrt(424)
d_pooled_t_impute <-1.29/sd_pooled_t_impute

#MADM group only
PREVENT_data1_MADM_impute<-subset(linear_frame2b,group2==0) #gets to 212 folks in M-ADM
PREVENT_data1_MADM_impute<-subset(PREVENT_data1_MADM_impute, select = -group2)
seed_value = 4956767
runs_for_imp2<-20
imp_data_tMADM <-mice(PREVENT_data1_MADM_impute, m=runs_for_imp2, maxit=50, seed=seed_value)
modelFit_mi_tMADM<-with(imp_data_tMADM, t.test(jcbl, jc.1,paired=TRUE, alternative="two.sided"))
MADM_t_impute<-summary(modelFit_mi_tMADM)
mean(MADM_t_impute$estimate)
mean(MADM_t_impute$conf.low)
mean(MADM_t_impute$conf.high)
mean(MADM_t_impute$statistic)
mean(MADM_t_impute$p.value)
#t=0.64, p=.56, est = -0.28 (-1.12, 0.56)
#manually computing d
sd_MADM_t_impute <-((0.56 - -1.12)/3.92)*sqrt(212)
d_MADM_t_impute <- -0.28/sd_MADM_t_impute #d= -0.04

#MBCT group only
PREVENT_data1_MBCT_impute<-subset(linear_frame2b,group2==1) #gets to 212 folks in MBCT
PREVENT_data1_MBCT_impute<-subset(PREVENT_data1_MBCT_impute, select = -group2)

```

```

seed_value = 4956767

runs_for_imp2<-20

imp_data_tMBCT <-mice(PREVENT_data1_MBCT_impute, m=runs_for_imp2, maxit=50, seed=seed_value)

modelFit_mi_MBCT<-with(imp_data_tMBCT, t.test(jcbl, jc.1,paired=TRUE, alternative="two.sided"))

MBCT_t_impute<-summary(modelFit_mi_MBCT)

mean(MBCT_t_impute$estimate)

mean(MBCT_t_impute$conf.low)

mean(MBCT_t_impute$conf.high)

mean(MBCT_t_impute$statistic)

mean(MBCT_t_impute$p.value)

#t=6.19, p<.001, est = 2.93 (2.00, 3.87)

#manually computing d

sd_MBCT_t_impute <-((3.87 - 2.00)/3.92)*sqrt(212)

d_MBCT_t_impute <- -2.93/sd_MBCT_t_impute #d= 0.42

```

#####5. does PA at intake predict risk of RR, with and without adjusting for confounders, and when including group by PA interaction

```

#open dataframe with 82 rows

linear_frame<-data.frame(ID=1:424)

linear_frame$timetoevent<-PREVENT_data1$timetoevent

linear_frame$eventstatus<-PREVENT_data1$eventstatus

linear_frame$jcbl<-PREVENT_data1$DPESBLJoyContentment_check

linear_frame$group2<-PREVENT_data1$group2

linear_frame$site_dummy1<- PREVENT_data1$site_dummy1

linear_frame$site_dummy2<-PREVENT_data1$site_dummy2

linear_frame$site_dummy3<-PREVENT_data1$site_dummy3

linear_frame$sym<-PREVENT_data1$sym

linear_frame$Age<-PREVENT_data1$Age

linear_frame$Gender<-PREVENT_data1$Gender

linear_frame$AbuseSubGroup<-PREVENT_data1$AbuseSubGroup

linear_frame$CatMedicationUse<-PREVENT_data1$CatMedicationUse

linear_frame$ComorbiditiesPresentatBL <-PREVENT_data1$ComorbiditiesPresentatBL

linear_frame$episode_split<-PREVENT_data1$episode_split

linear_frame$BLSCIDAgeOnset<-PREVENT_data1$BLSCIDAgeOnset

```

```

linear_frame$BLFFMQ_Total<-PREVENT_data1$BLFFMQ_Total

linear_frame$HAMD_TotalR<-PREVENT_data1$HAMD_TotalR

linear_frame$BLFormalMeditation <-PREVENT_data1$BLFormalMeditation

summary(PREVENT_data1$DPESBLJoyContentment_check) # 16 missing (4%)

#want > missing %, so selected 10


#dropping id

linear_frame<- subset(linear_frame, select = -c(ID))


#imputed

#imputing missing data

seed_value = 4956767

runs_for_imp<-10

imp_data_PApred <-mice(linear_frame, m=runs_for_imp, maxit=50, seed=seed_value)

#without covariates

modelFit_mi_PApred<-with(imp_data_PApred, coxph(Surv(timetoevent, eventstatus)~ jcbl+ group2 +
site_dummy1 + site_dummy2 + site_dummy3 + sym))

summary(pool(modelFit_mi_PApred))

#jcbl beta = -0.04284062 (SE = 0.01036629, p<.001)

#manually converting to HR (95% CI), via exponentiation of beta term

exp_modelFit_mi_PApred <- exp(-0.04284062) #0.96

lowerci_modelFit_mi_PApred <- exp( -0.04284062 -(0.01036629*1.96)) #0.94

upperci_modelFit_mi_PApred <- exp( -0.04284062 + (0.01036629*1.96)) #0.98

#with covariates

modelFit_mi_PApred_cov<-with(imp_data_PApred, coxph(Surv(timetoevent, eventstatus)~ jcbl + group2 +
site_dummy1 + site_dummy2 + site_dummy3 +sym + BLSCIDAgeOnset + BLFormalMeditation + episode_split +
CatMedicationUse+ AbuseSubGroup +ComorbiditiesPresentatBL + Age + Gender + BLFFMQ_Total +
HAMD_TotalR))

summary(pool(modelFit_mi_PApred_cov))

#jcbl beta =-0.048400929 (SE = 0.012124952, p<.001)

#manually converting to HR (95% CI), via exponentiation of beta term

exp_modelFit_mi_PApred_cov <- exp(-0.048400929) #0.95

lowerci_modelFit_mi_PApred_cov <- exp( -0.048400929 -(0.012124952*1.96)) #0.93

upperci_modelFit_mi_PApred_cov <- exp( -0.048400929 + (0.012124952*1.96)) #0.98

```

```

#generate graph of baseline PA predicting time to RR

PREVENT_data1$PA <- PREVENT_data1$DPESBLJoyContentment_check

fita_plot<-coxph(Surv(timetoevent, eventstatus)~ group_name + site_dummy1 + site_dummy2 + site_dummy3
+ sym + PA, data=PREVENT_data1, x=TRUE)

summary(fita_plot)

plot_surv_area(time="timetoevent",
               status="eventstatus",
               variable="PA",
               data=PREVENT_data1,
               model=fita_plot,
               bins=4,
               start_color = "black",
               end_color = "grey")+
ylim(0,1)+
theme(text = element_text(size=20), # axis number font size
      axis.title = element_text(size=20)) # axis title font size

###exploratory moderation

#without covariates

modelFit_mi_PApred_mod<-with(imp_data_PApred, coxph(Surv(timetoevent, eventstatus)~ jcb1*group2 +
site_dummy1 + site_dummy2 + site_dummy3 + sym))

summary(pool(modelFit_mi_PApred_mod))

#int 0.02089640 (SE = 0.02043643), p = .31

#manually converting to HR (95% CI), via exponentiation of beta term

exp_modelFit_mi_PApred_mod <- exp(0.02089640) #1.02

lowerci_modelFit_mi_PApred_mod <- exp( 0.02089640 -(0.02043643*1.96)) #0.98

upperci_modelFit_mi_PApred_mod <- exp( 0.02089640 + (0.02043643*1.96)) #1.06


#6. mediation analysis on those folks with complete data who had not relapsed at post (n=266)

# 266 sample of folks with valid survival data and complete PA data

```

#research question: does change in positive affect during mindfulness course mediate protective effects on subsequent depressive relapse?

#time = time to depressive relapse from time one assessment (in days, using right censoring if no event)

#event = if a relapse occurred from time one assessment (0 no, 1 yes)

#exp = treatment group (0= maintenance anti-depressants, 1 = MBCT-TS)

#M = mediator (levels of positive affect at time one)

#cov1 = dummy variable coding recruitment (0,1)

#cov2 = dummy variable coding recruitment (0,1)

#cov3 = dummy variable coding recruitment (0,1)

#cov4 = intake depression severity (0 no residual symptom, 1 some residual symptoms), using sym variable

#cov5 = intake levels of positive affect

#cov6 = catmedicationuse

#cov7 = HAMD baseline

#cov8 = FFMQ baseline

#cov9 = Age

#cov10 = gender

#cov11 = comorbidities baseline

#cov12 = episodesplit (3 - 5; > 5)

#cov13 = age of onset

#cov15 = baseline formal mediation experience

#cov16 = abusesubgroup

#cov17 = HAMD total one

#cov18 = FFMQ total one

#cov19 = formal mediation at time one

##(cov14 was other hours meditation (no longer included as skewed))

```
linear_frame4<-data.frame(ID=1:424)
```

```
linear_frame4$time<-PREVENT_data1$time_to_relapse_mediate
```

```
linear_frame4$event<-PREVENT_data1$relapse_mediate
```

```
linear_frame4$M<-PREVENT_data1$DPES.1JoyContentment_check
```

```
linear_frame4$exp<-PREVENT_data1$group2
```

```
linear_frame4$cov1<- PREVENT_data1$site_dummy1
```

```
linear_frame4$cov2<-PREVENT_data1$site_dummy2
```

```
linear_frame4$cov3<-PREVENT_data1$site_dummy3
```

```
linear_frame4$cov4<-PREVENT_data1$sym
```

```

linear_frame4$cov5<-PREVENT_data1$DPESBLJoyContentment_check
linear_frame4$cov6 <-PREVENT_data1$meds_time1_merge_recode
linear_frame4$cov7<-PREVENT_data1$HAMD_TotalR
linear_frame4$cov8<-PREVENT_data1$BLFFMQ_Total
linear_frame4$cov9<-PREVENT_data1$Age
linear_frame4$cov10<-PREVENT_data1$Gender
linear_frame4$cov11 <-PREVENT_data1$ComorbiditiesPresentatBL
linear_frame4$cov12<-PREVENT_data1$episode_split
linear_frame4$cov13<-PREVENT_data1$BLSCIDAgeOnset
linear_frame4$cov15 <-PREVENT_data1$BLFormalMeditation
linear_frame4$cov16<-PREVENT_data1$AbuseSubGroup
linear_frame4$cov17<-PREVENT_data1$HAMD_Total1
linear_frame4$cov18<-PREVENT_data1$X.1FFMQ_Total
linear_frame4$cov19 <-PREVENT_data1$X.1FormalMeditation #automatically renamed as R does not like
@symbol
linear_frame4$jc_complete <-PREVENT_data1$jc_complete
linear_frame4$valid_mediate2 <-PREVENT_data1$valid_mediate2
linear_frame4$Sessions<-PREVENT_data1$NumberofMBCTSessionsAttended
#for main mediation analysis
linear_frame4<-subset(linear_frame4,jc_complete==1) #only those with complete PA
#for medication sub group analysis
linear_frame4_MBCT_med<-subset(linear_frame4,linear_frame4$exp==1)
linear_frame4<-subset(linear_frame4,valid_mediate2==1) #only those with complete PA
#is there a difference in change in PA between groups?
#no covariates
mediation_mediation_model1b<-lm(M ~ exp + cov1 + cov2 + cov3 + cov4 + cov5, data=linear_frame4)
summary(mediation_mediation_model1b)
confint(mediation_mediation_model1b)
#exp = 2.65 (SE=.72), p<.0001, 95% CI = 1.23 to 4.06
#with covariates
mediation_mediation_model1_covb<-lm(M ~ exp + cov1 + cov2 + cov3 + cov4 + cov5 + cov7 + cov8 + cov9
+cov10 + cov11 + cov12 + cov13+cov15+cov16, linear_frame4)
summary(mediation_mediation_model1_covb)
confint(mediation_mediation_model1_covb)
#exp = 2.91 (SE=.72), p<.001, 95% CI = 1.49 to 4.34

```

```

# is there a difference in RR between groups (report exp term)

fita_plot<-coxph(Surv(time,event)~ exp+ cov1 + cov2 + cov3 + cov4 + cov5, data=linear_frame4)

summary(fita_plot)

#exp term: p=0.53, HR 1.14 (0.75, 1.72)

#exploratory analysis for footnote 2 (change in risk of RR in those who had stopped/tapered versus continued
with meds by post treatment assessment

mediation_outcome_model1_medication<-coxph(Surv(time,event) ~ cov6+exp + cov1 + cov2 + cov3 + cov4 ,
linear_frame4)

summary(mediation_outcome_model1_medication)

confint(mediation_outcome_model1_medication)

#1.43 (0.84, 2.45), p=.19


#does change in PA predict RR?

#no covariates

#without group interaction term

mediation_outcome_model1b2<-survreg(Surv(time,event) ~ M + exp + cov1 + cov2 + cov3 + cov4 + cov5,
data=linear_frame4, dist="weibull", robust=TRUE)

summary(mediation_outcome_model1b2)

confint(mediation_outcome_model1b2)

#0.0413 (0.0195)(0.00309346 to 0.07956769), p=.03

#with group interaction term

mediation_outcome_model1b<-survreg(Surv(time,event) ~ M*exp + cov1 + cov2 + cov3 + cov4 + cov5,
data=linear_frame4, dist="weibull", robust=TRUE)

summary(mediation_outcome_model1b)

confint(mediation_outcome_model1b)

#int: 0.05491 (0.03556)(-0.01488476, 0.12461096), p=.12

#generate graph of baseline PA predicting time to RR

#label group variable

linear_frame4$group<- car::recode(linear_frame4$exp,

      "'0' = 'ADM';

      '1' = 'MBCT'")

linear_frame4$group<-as.factor(linear_frame4$group)

fita_plot<-coxph(Surv(time,event)~ M*group + group+ cov1 + cov2 + cov3 + cov4 + cov5,
data=linear_frame4,x=TRUE)

summary(fita_plot)

plot_surv_area(time="time",

```

```

status="event",
variable="M",
group="group",
data=linear_frame4,
model=fita_plot,
bins=4,
legend.title ="ChangePA",
start_color = "black",
end_color = "grey")+
ylim(0,1)+

theme(text = element_text(size=20), # axis number font size
      axis.title = element_text(size=20)) # axis title font size

#feeding this into mediate

#no interaction term

set.seed(20210825)

mediation_estimate1b<-mediate(mediation_mediation_model1b, mediation_outcome_model1b2, boot=
FALSE, sims=10000, treat="exp", mediator="M")

summary(mediation_estimate1b) #written summary of effects
plot(mediation_estimate1b) #graphical summary of effects

#ACME control, p=.04 261 (95% CI 9, 721)
#ACME treated, p=.04, 184 (95% CI 9, 483)
#ACME average, p=.04, 223 (95% CI 9, 589)

#with interaction term

set.seed(20210825)

mediation_estimate1b<-mediate(mediation_mediation_model1b, mediation_outcome_model1b, boot= FALSE,
sims=10000, treat="exp", mediator="M")

summary(mediation_estimate1b) #written summary of effects
plot(mediation_estimate1b) #graphical summary of effects

#ACME control, p=.74 66 (95% CI -231, 483)
#ACME treated, p<.01, 341 (95% CI 53, 894)
#ACME average, p =.06, 203 (-7 to 553)

test.TMint(mediation_estimate1b, conf.level=.95)

#p=.24

#with covariates (this time including catmeduse, FFMQ at 1 HAMD at 1, and med practice at t1)

#11 missing post med practice variable

```

```

sum(is.na(linear_frame4$cov19))

linear_frame4b <- na.omit(linear_frame4)

#with covariates

#note mediator model not with HAMD total one, FFMQ total one, post med practice, or catmedicationuse, as
these occur after event

mediation_mediation_model1_covb<-lm(M ~ exp + cov1 + cov2 + cov3 + cov4 + cov5 + cov7 + cov8 + cov9
+cov10 + cov11 + cov12 + cov13+cov15+cov16, linear_frame4b)

summary(mediation_mediation_model1_covb)

confint(mediation_mediation_model1_covb)

#exp = 2.91 (SE=.73), p<.001, 95% CI = 1.47 to 4.36

#without interaction term

mediation_outcome_model1_covb2<-survreg(Surv(time,event) ~ M + exp + cov1 + cov2 + cov3 + cov4 + cov5
+cov6 + cov7 + cov8 + cov9 +cov10 + cov11 + cov12 + cov13+cov15 +cov16 +cov17 + cov18 +cov19,
linear_frame4b, dist="weibull", robust=TRUE)

summary(mediation_outcome_model1_covb2)

confint(mediation_outcome_model1_covb2)

#mediator 0.056958 (SE = 0.02234)(.00 to 0.11), p = .04

#with interaction term

mediation_outcome_model1_covb<-survreg(Surv(time,event) ~ M*exp + cov1 + cov2 + cov3 + cov4 + cov5
+cov6 + cov7 + cov8 + cov9 +cov10 + cov11 + cov12 + cov13+cov15 +cov16 +cov17 + cov18 +cov19,
linear_frame4b, dist="weibull", robust=TRUE)

summary(mediation_outcome_model1_covb)

confint(mediation_outcome_model1_covb)

#mediator int 0.055848 (0.037178) (-0.02 to 0.13), p = .13

#feeding this into mediate

#no interaction term

set.seed(20210825)

mediation_estimate1b_cov<-mediate(mediation_mediation_model1_covb,
mediation_outcome_model1_covb2, boot= FALSE, sims=10000, treat="exp", mediator="M")

summary(mediation_estimate1b_cov) #written summary of effects

plot(mediation_estimate1b_cov) #graphical summary of effects

#when using post treatment med use

#ACME control, p=.04 633 (95% CI 11, 2060)

#ACME treated, p=.04, 613 (95% CI 10, 2001)

#ACME average, p=.04, 623 (95% CI 11, 2002)

#with interaction term

set.seed(20210825)

```

```
mediation_estimate1b_cov<-mediate(mediation_mediation_model1_covb, mediation_outcome_model1_covb,  
boot= FALSE, sims=10000, treat="exp", mediator="M")  
  
summary(mediation_estimate1b_cov) #written summary of effects  
  
plot(mediation_estimate1b_cov) #graphical summary of effects  
  
#ACME control, p=.50, 235 (95% CI -383, 1222)  
  
#ACME treated, p=.01, 1006 (95% CI 103, 3730)  
  
test.TMint(mediation_estimate1b_cov, conf.level=.95)  
  
#p=.18
```