

PDS_longitudinal_MLM

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Project Overview: Examine the time-varying relationship between brain network metric (global efficiency), and parent reported executive function scores across 3 waves of scan data.

Step 1. Examine using a time-varying co-variate in lme4 using the Conners EF raw score and network global efficiency (GE) in FPN, DAN, SAL, CON. Examine multiple time variables and covariates

Step 2. Compare GE to average within network connectivity. We would expect these to be very similar (no sig. difference)

Step 3. Examine the time-varying relationship between EF and ADHD symptoms (we would expect this to be very significant), and MDD symptoms (possibly sig.)

Data Management

```
#load lme4 package: lme4 provides functions for fitting and analyzing mixed models: linear (lmer),  
#generalized linear (glmer) and nonlinear (nlmer.)  
library(lme4)
```

```
## Loading required package: Matrix
```

```
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.2.0 --
```

```
## ✓ ggplot2 2.2.1      ✓ purrr   0.2.3  
## ✓ tibble  1.3.4      ✓ dplyr  0.7.4  
## ✓ tidyr   0.7.2      ✓ stringr 1.2.0  
## ✓ readr   1.1.1      ✓ forcats 0.2.0
```

```
## -- Conflicts ----- tidyverse_conflicts() --
```

```
## x tidyr::expand() masks Matrix::expand()  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag()    masks stats::lag()
```

```
library(broom)  
library(tidyr)  
library(merTools)
```

```
## Loading required package: arm
```

```
## Loading required package: MASS
```

```
##
```

```
## Attaching package: 'MASS'
```

```
## The following object is masked from 'package:dplyr':
```

```
##
```

```
##      select
```

```

##
## arm (Version 1.9-3, built: 2016-11-21)
## Working directory is /Users/elizabethhawkey/ejhawkey
library(semTools)

## Loading required package: lavaan
## This is lavaan 0.5-23.1097
## lavaan is BETA software! Please report any bugs.
##
## #####
## This is semTools 0.4-14
## All users of R (or SEM) are invited to submit functions or ideas for functions.
## #####

library(semPlot)
library(ggplot2)

#compute average efficiency metrics in SPSS prior to brining in dataset
#load in newest dataset from Rebecca Tillman
setwd("~/ejhawkey")
PDS_data_mlm <- read.csv("~/Documents/PDS_project/Longitudinal_project/datasets/PDS_long_9_8_17_MLM.csv")
#View(PDS_data_mlm)
#print(names(PDS_data_mlm))

#create a new variable to adjust age and EF to a scale that is closer to GE
#agemo_converted <- PDS_data_mlm$AGEMOSCAN/100
#CONP_EF_converted<- PDS_data_mlm$CONP_EF_T/100
#add back to dataframe
#PDS_data_mlm$agemo_converted <- as.numeric(agemo_converted)
#PDS_data_mlm$CONP_EF_converted <- as.numeric(CONP_EF_converted)

##Center predictor variables
#remember: centering is not the same as standardizing;
#centering creates a zero mean; use when you don't need the units to be the same; you are changing the v
#standardizing: converting to z-scores; units change, 1 unit is now 1 SD; so that you can compare the v

##mean center by subject (so write a for loop for each subject to mean center each )
BRIEFgects_scan_c <- scale(PDS_data_mlm$BRIEFgects_scan, center = T, scale = F)
CONP_EF_RAW_c <- scale(PDS_data_mlm$CONP_EF_RAW, center = T, scale = F)
CONT_EF_RAW_c <- scale(PDS_data_mlm$CONT_EF_RAW, center = T, scale = F)
CONP_EF_T_c <- scale(PDS_data_mlm$CONP_EF_T, center = T, scale = F)
AGEMOSCAN_c <- scale(PDS_data_mlm$AGEMOSCAN, center = T, scale = F)
FPN_GE_K1to5_c <- scale(PDS_data_mlm$FPN_GE_K1to5, center = T, scale = F)
FPN_GE_K6to10_c <- scale(PDS_data_mlm$FPN_GE_K6to10, center = T, scale = F)
SAL_GE_K1to5_c <- scale(PDS_data_mlm$SAL_GE_K1to5, center = T, scale = F)
SAL_GE_K6to10_c <- scale(PDS_data_mlm$SAL_GE_K6to10, center = T, scale = F)
DMN_GE_K1to5_c <- scale(PDS_data_mlm$DMN_GE_K1to5, center = T, scale = F)
DMN_GE_K6to10_c <- scale(PDS_data_mlm$DMN_GE_K6to10, center = T, scale = F)
CON_GE_K1to5_c <- scale(PDS_data_mlm$CON_GE_K1to5, center = T, scale = F)

```

```

CON_GE_K6to10_c <- scale(PDS_data_mlm$CON_GE_K6to10, center = T, scale = F)

#add the centered variables into the data frame
PDS_data_mlm$BRIEFgects_scan_c <- as.numeric(BRIEFgects_scan_c)
PDS_data_mlm$CONP_EF_RAW_c <- as.numeric(CONP_EF_RAW_c)
PDS_data_mlm$CONP_EF_T_c <- as.numeric(CONP_EF_T_c)
PDS_data_mlm$CONT_EF_RAW_c <- as.numeric(CONT_EF_RAW_c)
PDS_data_mlm$AGEMOSCAN_c <- as.numeric(AGEMOSCAN_c)
PDS_data_mlm$FPN_GE_K1to5_c <- as.numeric(FPN_GE_K1to5_c)
PDS_data_mlm$FPN_GE_K6to10_c <- as.numeric(FPN_GE_K6to10_c)
PDS_data_mlm$SAL_GE_K1to5_c <- as.numeric(SAL_GE_K1to5_c)
PDS_data_mlm$SAL_GE_K6to10_c <- as.numeric(SAL_GE_K6to10_c)
PDS_data_mlm$DMN_GE_K1to5_c <- as.numeric(DMN_GE_K1to5_c)
PDS_data_mlm$DMN_GE_K6to10_c <- as.numeric(DMN_GE_K6to10_c)
PDS_data_mlm$CON_GE_K1to5_c <- as.numeric(CON_GE_K1to5_c)
PDS_data_mlm$CON_GE_K6to10_c <- as.numeric(CON_GE_K6to10_c)

###center by person
#aggregate per subject all IVs and DVs
#cell_agg = cell %>% group_by(ID) %>%
# summarize(acc_mean = mean)

###subset for scan 2, 3
#PDS_data_mlm.2.3 <- subset(PDS_data_mlm, scan_wave == 2:3)
#PDS_data_mlm.3 <- subset(PDS_data_mlm, scan_wave == 3)

write.csv(PDS_data_mlm, file = "~/Documents/PDS_project/Longitudinal_project/datasets/PDS_long_final.csv")

PDS_data_mlm <- read.csv(file = "~/Documents/PDS_project/Longitudinal_project/datasets/PDS_long_09_9_17.csv")

##START FROM HERE FOR ANALYSES

```

setting up the models from class on 9/7

```
lmer(y ~ 1 + time + (1 + time | subjects), data = data)
```

```
lmer(y ~ time + (time|Subid), data = data) - both are equivalent
```

outside the parentheses: fixed effects

terms inside the parentheses (how we specify random effects 1 = not every indiv. will have the same intercept value)

pipe (|) denotes nesting variable (for us it is subject level identifier))

Global Efficiency models with Conners EF predicition GE

Salience Network

```
##SAL
mod.SAL.GE1a <- lmer(SAL_GE_K1to5 ~ ageo_converted + sex + (ageo_converted | Subid_fmRI), data=PDS_da
summary(mod.SAL.GE1a)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## SAL_GE_K1to5 ~ ageo_converted + sex + (ageo_converted | Subid_fmRI)
## Data: PDS_data_mlm
##
## REML criterion at convergence: -544
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.09870 -0.60107 -0.04002  0.58592  2.36779
##
## Random effects:
## Groups      Name                Variance Std.Dev. Corr
## Subid_fmRI (Intercept)          0.021682 0.14725
##              ageo_converted 0.002093 0.04574 -1.00
## Residual                        0.009317 0.09653
## Number of obs: 398, groups: Subid_fmRI, 188
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    0.265231   0.054846   4.836
## ageo_converted  0.008284   0.032892   0.252
## sex            -0.014624   0.015748  -0.929
##
## Correlation of Fixed Effects:
##              (Intr) agm_cn
## ageo_convrtd -0.892
## sex          -0.491  0.071
```

```
mod.SAL.GE1b <- lmer(SAL_GE_K1to5 ~ ageo_converted*CONP_EF_RAW_c + sex + (ageo_converted | Subid_fmRI)
summary(mod.SAL.GE1b)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## SAL_GE_K1to5 ~ ageo_converted * CONP_EF_RAW_c + sex + (ageo_converted |
## Subid_fmRI)
## Data: PDS_data_mlm
##
## REML criterion at convergence: -494.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.08698 -0.61426 -0.08281  0.58694  2.39595
##
## Random effects:
## Groups      Name                Variance Std.Dev. Corr
## Subid_fmRI (Intercept)          0.026694 0.1634
##              ageo_converted 0.003505 0.0592 -1.00
## Residual                        0.009293 0.0964
## Number of obs: 371, groups: Subid_fmRI, 185
```

```
##
## Fixed effects:
##
##           Estimate Std. Error t value
## (Intercept)      0.272655   0.057904   4.709
## agemo_converted    0.003052   0.034570   0.088
## CONP_EF_RAW_c      0.007283   0.014381   0.506
## sex               -0.014534   0.016104  -0.902
## agemo_converted:CONP_EF_RAW_c -0.004364   0.009843  -0.443
##
## Correlation of Fixed Effects:
##           (Intr) agm_cn CONP_E sex
## agem_cnvrted -0.902
## CONP_EF_RAW  0.050 -0.051
## sex          -0.502  0.105 -0.005
## a_:CONP_EF_ -0.068  0.060 -0.990  0.034

PDS_data_mlm.na.rm <- subset(PDS_data_mlm, SAL_GE_K1to5 > 0)
PDS_data_mlm.na <- subset(PDS_data_mlm.na.rm, CONP_EF_RAW_c > 0)

##just main effects alone; very similar to main effects in interaction model; no need to report this
#mod.SAL.GE1c <- lmer(SAL_GE_K1to5 ~ CONP_EF_RAW_c + (agemo_converted | Subid_fMRI), data=PDS_data_mlm.na)
#summary(mod.SAL.GE1c)

mod.SAL.GE2a <- lmer(SAL_GE_K6to10 ~ agemo_converted + sex + (agemo_converted | Subid_fMRI), data=PDS_data_mlm.na)
summary(mod.SAL.GE2a)

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## SAL_GE_K6to10 ~ agemo_converted + sex + (agemo_converted | Subid_fMRI)
## Data: PDS_data_mlm
##
## REML criterion at convergence: -489.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.0215 -0.5548  0.0386  0.5721  2.3160
##
## Random effects:
## Groups      Name                Variance Std.Dev. Corr
## Subid_fMRI (Intercept)          0.022500 0.15000
##              agemo_converted    0.002267 0.04761 -1.00
## Residual                        0.011218 0.10591
## Number of obs: 398, groups: Subid_fMRI, 188
##
## Fixed effects:
##           Estimate Std. Error t value
## (Intercept)      0.44757    0.05860   7.638
## agemo_converted    0.01460    0.03539   0.412
## sex               -0.01407    0.01640  -0.858
##
## Correlation of Fixed Effects:
##           (Intr) agm_cn
## agem_cnvrted -0.898
## sex          -0.484  0.075
```

```
mod.SAL.GE2b <- lmer(SAL_GE_K6to10 ~ agemo_converted*CONP_EF_RAW_c + sex + (agemo_converted | Subid_fMRI), data=PDS_data_mlm)
summary(mod.SAL.GE2b)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## SAL_GE_K6to10 ~ agemo_converted * CONP_EF_RAW_c + sex + (agemo_converted | Subid_fMRI)
## Data: PDS_data_mlm
##
## REML criterion at convergence: -445
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.61672 -0.54480  0.03041  0.59175  2.32272
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr
##   Subid_fMRI (Intercept)          0.019690 0.14032
##               agemo_converted 0.001826 0.04273  -1.00
## Residual                        0.011164 0.10566
## Number of obs: 371, groups: Subid_fMRI, 185
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)      0.4497230  0.0614000   7.324
## agemo_converted    0.0128016  0.0369537   0.346
## CONP_EF_RAW_c      0.0021860  0.0153192   0.143
## sex               -0.0130356  0.0168719  -0.773
## agemo_converted:CONP_EF_RAW_c -0.0008343  0.0105384  -0.079
##
## Correlation of Fixed Effects:
##              (Intr) agm_cn CONP_E sex
## agem_cnvrted -0.904
## CONP_EF_RAW  0.053 -0.057
## sex          -0.504  0.111  0.001
## a_:CONP_EF_ -0.070  0.065 -0.990  0.029
```

Cingulo-opercular Network

```
##CON
mod.CON.GE1a <- lmer(CON_GE_K1to5 ~ agemo_converted+ sex + (agemo_converted | Subid_fMRI), data=PDS_data_mlm)
summary(mod.CON.GE1a)
mod.CON.GE1b <- lmer(CON_GE_K1to5 ~ agemo_converted*CONP_EF_RAW_c + sex + (agemo_converted | Subid_fMRI), data=PDS_data_mlm)
summary(mod.CON.GE1b)

mod.CON.GE2 <- lmer(CON_GE_K6to10 ~ agemo_converted + sex + (agemo_converted | Subid_fMRI), data=PDS_data_mlm)
summary(mod.CON.GE2)
mod.CON.GE2 <- lmer(CON_GE_K6to10 ~ agemo_converted*CONP_EF_RAW_c + sex + (agemo_converted | Subid_fMRI), data=PDS_data_mlm)
summary(mod.CON.GE2)
```

Frontoparietal Network

```
##FPN
mod.FPN.GE1a <- lmer(FPN_GE_K1to5 ~ agemo_converted + sex + (agemo_converted | Subid_fmRI), data=PDS_da
summary(mod.FPN.GE1a)

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## FPN_GE_K1to5 ~ agemo_converted + sex + (agemo_converted | Subid_fmRI)
## Data: PDS_data_mlm
##
## REML criterion at convergence: -730.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.08844 -0.61478  0.01944  0.60214  2.64128
##
## Random effects:
## Groups      Name                Variance Std.Dev. Corr
## Subid_fmRI (Intercept)          0.0092707 0.09628
##              agemo_converted 0.0007024 0.02650 -1.00
## Residual                        0.0062424 0.07901
## Number of obs: 398, groups: Subid_fmRI, 188
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    0.14380    0.04298   3.345
## agemo_converted 0.07962    0.02607   3.055
## sex            -0.01056    0.01194  -0.885
##
## Correlation of Fixed Effects:
##              (Intr) agm_cn
## agem_cnvrted -0.899
## sex          -0.485  0.080

mod.FPN.GE1b <- lmer(FPN_GE_K1to5 ~ agemo_converted*CONP_EF_RAW_c + sex + (agemo_converted | Subid_fmRI)
summary(mod.FPN.GE1b)

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## FPN_GE_K1to5 ~ agemo_converted * CONP_EF_RAW_c + sex + (agemo_converted |
## Subid_fmRI)
## Data: PDS_data_mlm
##
## REML criterion at convergence: -669.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.08773 -0.60723  0.00627  0.55827  2.66373
##
## Random effects:
## Groups      Name                Variance Std.Dev. Corr
## Subid_fmRI (Intercept)          0.012782 0.11306
##              agemo_converted 0.001483 0.03851 -1.00
```

```

## Residual                      0.006060 0.07784
## Number of obs: 371, groups:  Subid_fMRI, 185
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)    0.159533   0.045320   3.520
## agemo_converted 0.072371   0.027254   2.655
## CONP_EF_RAW_c   0.011012   0.011304   0.974
## sex            -0.015002   0.012390  -1.211
## agemo_converted:CONP_EF_RAW_c -0.008624   0.007759  -1.111
##
## Correlation of Fixed Effects:
##      (Intr) agm_cn CONP_E sex
## agem_cnvrted -0.905
## CONP_EF_RAW  0.051 -0.055
## sex          -0.500  0.109 -0.002
## a_:CONP_EF_  -0.069  0.063 -0.990  0.031
mod.FPN.GE2a <- lmer(FPN_GE_K6to10 ~ agemo_converted + sex + (agemo_converted | Subid_fMRI), data=PDS_data)
summary(mod.FPN.GE2a)

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## FPN_GE_K6to10 ~ agemo_converted + sex + (agemo_converted | Subid_fMRI)
## Data: PDS_data_mlm
##
## REML criterion at convergence: -581.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.74403 -0.55408  0.06363  0.63074  2.69478
##
## Random effects:
## Groups      Name                Variance Std.Dev. Corr
## Subid_fMRI (Intercept)          0.038363 0.19587
##              agemo_converted 0.008528 0.09235  -1.00
## Residual                        0.009486 0.09740
## Number of obs: 398, groups:  Subid_fMRI, 188
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)    0.512876   0.052914   9.693
## agemo_converted -0.028985   0.032196  -0.900
## sex            -0.005981   0.013746  -0.435
##
## Correlation of Fixed Effects:
##      (Intr) agm_cn
## agem_cnvrted -0.913
## sex          -0.447  0.067
mod.FPN.GE2b <- lmer(FPN_GE_K6to10 ~ agemo_converted*CONP_EF_RAW_c + sex + (agemo_converted | Subid_fMRI))
summary(mod.FPN.GE2b)

## Linear mixed model fit by REML ['lmerMod']
## Formula:

```



```
## FPN_GE_K6to10 ~ agemo_converted * CONP_EF_RAW_c + sex + (agemo_converted |
##   Subid_fMRI)
##   Data: PDS_data_mlm
##
## REML criterion at convergence: -533.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6417 -0.5552  0.0494  0.6336  2.2102
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr
##   Subid_fMRI (Intercept)          0.05801  0.2408
##               agemo_converted 0.01556  0.1247  -1.00
##   Residual                        0.00910  0.0954
## Number of obs: 371, groups:  Subid_fMRI, 185
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)      0.531452   0.055958   9.497
## agemo_converted    -0.038139   0.033767  -1.129
## CONP_EF_RAW_c      0.017019   0.013957   1.219
## sex                -0.010917   0.014146  -0.772
## agemo_converted:CONP_EF_RAW_c -0.012420   0.009416  -1.319
##
## Correlation of Fixed Effects:
##              (Intr) agm_cn CONP_E sex
## agem_cnvrted -0.920
## CONP_EF_RAW  0.043 -0.036
## sex          -0.457  0.095 -0.022
## a_:CONP_EF_ -0.058  0.042 -0.992  0.052
##
#anova(mod.FPN.GE2a, mod.FPN.GE2b)
```

Default Mode Network

```
#DMN
mod.DMN.GE1a <- lmer(DMN_GE_K1to5 ~ agemo_converted + sex + (agemo_converted | Subid_fMRI), data=PDS_data,
summary(mod.DMN.GE1a)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## DMN_GE_K1to5 ~ agemo_converted + sex + (agemo_converted | Subid_fMRI)
##   Data: PDS_data_mlm
##
## REML criterion at convergence: -975.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.65695 -0.57365  0.04449  0.58988  2.09713
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr
##   Groups      Name                Variance Std.Dev. Corr
```

```

## Subid_fMRI (Intercept)      0.0052384 0.07238
##          agemo_converted 0.0004329 0.02081 -1.00
## Residual                    0.0033656 0.05801
## Number of obs: 398, groups: Subid_fMRI, 188
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    0.2637525  0.0315424   8.362
## agemo_converted -0.0168002  0.0191291  -0.878
## sex            0.0004801  0.0087403   0.055
##
## Correlation of Fixed Effects:
##              (Intr) agm_cn
## agem_cnvrted -0.900
## sex          -0.484  0.080
mod.DMN.GE1b <- lmer(DMN_GE_K1to5 ~ agemo_converted*CONP_EF_RAW_c + sex + (agemo_converted | Subid_fMRI)
summary(mod.DMN.GE1b)

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## DMN_GE_K1to5 ~ agemo_converted * CONP_EF_RAW_c + sex + (agemo_converted |
## Subid_fMRI)
## Data: PDS_data_mlm
##
## REML criterion at convergence: -895.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.77338 -0.56126  0.04098  0.60325  2.20264
##
## Random effects:
## Groups      Name                Variance Std.Dev. Corr
## Subid_fMRI (Intercept)          0.007770 0.08814
##          agemo_converted 0.001083 0.03291 -1.00
## Residual                    0.003333 0.05773
## Number of obs: 371, groups: Subid_fMRI, 185
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    0.2739016  0.0332929   8.227
## agemo_converted -0.0190568  0.0200576  -0.950
## CONP_EF_RAW_c    0.0004567  0.0083146   0.055
## sex            -0.0047747  0.0089782  -0.532
## agemo_converted:CONP_EF_RAW_c -0.0019124  0.0056966  -0.336
##
## Correlation of Fixed Effects:
##              (Intr) agm_cn CONP_E sex
## agem_cnvrted -0.908
## CONP_EF_RAW  0.051 -0.053
## sex          -0.494  0.109 -0.004
## a_:CONP_EF_ -0.068  0.060 -0.991  0.034
mod.DMN.GE2a <- lmer(DMN_GE_K6to10 ~ agemo_converted + sex + (agemo_converted | Subid_fMRI), data=PDS_d
summary(mod.DMN.GE2a)

```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## DMN_GE_K6to10 ~ agemo_converted + sex + (agemo_converted | Subid_fMRI)
##   Data: PDS_data_mlm
##
## REML criterion at convergence: -973.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.3742 -0.5055  0.0471  0.5745  2.0678
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr
##   Subid_fMRI (Intercept)          0.010158 0.10079
##               agemo_converted 0.001683 0.04103 -1.00
##   Residual                        0.003383 0.05817
## Number of obs: 398, groups:  Subid_fMRI, 188
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    0.4480889  0.0319818  14.011
## agemo_converted -0.0126473  0.0193613  -0.653
## sex            -0.0006492  0.0086645  -0.075
##
## Correlation of Fixed Effects:
##              (Intr) agm_cn
## agem_cnvrted -0.905
## sex          -0.466  0.071
mod.DMN.GE2b <- lmer(DMN_GE_K6to10 ~ agemo_converted*CONP_EF_RAW_c + sex + (agemo_converted | Subid_fMRI)
summary(mod.DMN.GE2b)

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## DMN_GE_K6to10 ~ agemo_converted * CONP_EF_RAW_c + sex + (agemo_converted |
##   Subid_fMRI)
##   Data: PDS_data_mlm
##
## REML criterion at convergence: -897.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5065 -0.5122  0.0589  0.5678  2.1866
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr
##   Subid_fMRI (Intercept)          0.013534 0.11633
##               agemo_converted 0.002807 0.05298 -1.00
##   Residual                        0.003292 0.05737
## Number of obs: 371, groups:  Subid_fMRI, 185
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    0.456022  0.033577  13.581
## agemo_converted -0.014991  0.020183  -0.743

```

```
## CONP_EF_RAW_c          0.004505   0.008369   0.538
## sex                    -0.004225   0.008869  -0.476
## agemo_converted:CONP_EF_RAW_c -0.004335   0.005688  -0.762
##
## Correlation of Fixed Effects:
##      (Intr) agm_cn CONP_E sex
## agem_cnvrted -0.912
## CONP_EF_RAW   0.047 -0.044
## sex           -0.479   0.102 -0.013
## a_:CONP_EF_   -0.063   0.050 -0.991   0.043
```

AVERAGE WITHIN CONNECTIVITY

```
##AVERAGE WITHIN CONNECTIVITY
```

```
mod.SAL <- lmer(SAL_SAL ~ agemo_converted*CONP_EF_RAW_c + sex + (agemo_converted | Subid_fmRI), data=PDS_data_mlm)
summary(mod.SAL)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## SAL_SAL ~ agemo_converted * CONP_EF_RAW_c + sex + (agemo_converted | Subid_fmRI)
## Data: PDS_data_mlm
##
## REML criterion at convergence: -883.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4651 -0.5010 -0.0209   0.4295   3.4810
##
## Random effects:
##   Groups       Name                Variance Std.Dev. Corr
##   Subid_fmRI (Intercept)          0.0088453 0.09405
##               agemo_converted 0.0007328 0.02707  -1.00
##   Residual                        0.0027615 0.05255
## Number of obs: 371, groups: Subid_fmRI, 185
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)      0.257832   0.034057   7.571
## agemo_converted    0.004046   0.019918   0.203
## CONP_EF_RAW_c      0.009031   0.008353   1.081
## sex              -0.001124   0.010253  -0.110
## agemo_converted:CONP_EF_RAW_c -0.004722   0.005735  -0.823
##
## Correlation of Fixed Effects:
##      (Intr) agm_cn CONP_E sex
## agem_cnvrted -0.884
## CONP_EF_RAW   0.052 -0.057
## sex           -0.530   0.100 -0.001
## a_:CONP_EF_   -0.074   0.069 -0.989   0.030
```

```
mod.CON <- lmer(CON_CON ~ agemo_converted*CONP_EF_RAW_c + sex + (agemo_converted | Subid_fmRI), data=PDS_data_mlm)
summary(mod.CON)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## CON_CON ~ ageo_converted * CONP_EF_RAW_c + sex + (ageo_converted |
##   Subid_fMRI)
##   Data: PDS_data_mlm
##
## REML criterion at convergence: -761.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.24763 -0.61400 -0.03926  0.57338  2.72470
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr
##   Subid_fMRI (Intercept)          0.006958 0.08342
##               ageo_converted      0.004157 0.06447  -0.89
##   Residual                        0.005233 0.07234
## Number of obs: 371, groups:  Subid_fMRI, 185
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)      0.264611   0.039382   6.719
## ageo_converted    0.016741   0.024454   0.685
## CONP_EF_RAW_c     0.016331   0.009932   1.644
## sex               0.005105   0.010246   0.498
## ageo_converted:CONP_EF_RAW_c -0.011294   0.006959  -1.623
##
## Correlation of Fixed Effects:
##              (Intr) agm_cn CONP_E sex
## ageo_cnvrted -0.913
## CONP_EF_RAW  0.065 -0.079
## sex          -0.500  0.127  0.020
## a_:CONP_EF_ -0.080  0.085 -0.991  0.009
```

```
mod.DMN <- lmer(DMN_DMN ~ ageo_converted*CONP_EF_RAW_c + sex + (ageo_converted | Subid_fMRI), data=PDS_data_mlm)
summary(mod.DMN)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## DMN_DMN ~ ageo_converted * CONP_EF_RAW_c + sex + (ageo_converted |
##   Subid_fMRI)
##   Data: PDS_data_mlm
##
## REML criterion at convergence: -1259.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.27762 -0.61604 -0.02704  0.60562  2.52505
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr
##   Subid_fMRI (Intercept)          0.0030692 0.05540
##               ageo_converted      0.0007106 0.02666  -0.89
##   Residual                        0.0011441 0.03382
## Number of obs: 371, groups:  Subid_fMRI, 185
```

```
##
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)      0.157631  0.020369   7.739
## agemo_converted  -0.015406  0.012258  -1.257
## CONP_EF_RAW_c     0.002410  0.005071   0.475
## sex               0.003865  0.005664   0.682
## agemo_converted:CONP_EF_RAW_c -0.001872  0.003497  -0.535
##
## Correlation of Fixed Effects:
##           (Intr) agm_cn CONP_E sex
## agem_cnvrted -0.901
## CONP_EF_RAW  0.051 -0.058
## sex          -0.507  0.109  0.005
## a_:CONP_EF_  -0.070  0.067 -0.990  0.024

mod.FPN <- lmer(FPN_FPN ~ agemo_converted*CONP_EF_RAW_c + sex + (agemo_converted | Subid_fmRI), data=PDS_data_mlm)
summary(mod.FPN)

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## FPN_FPN ~ agemo_converted * CONP_EF_RAW_c + sex + (agemo_converted | Subid_fmRI)
## Data: PDS_data_mlm
##
## REML criterion at convergence: -981.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.2278 -0.6449 -0.0344  0.5288  3.7249
##
## Random effects:
## Groups      Name                Variance Std.Dev. Corr
## Subid_fmRI (Intercept)          0.003612  0.06010
##              agemo_converted  0.000293  0.01712  -1.00
## Residual                        0.002694  0.05191
## Number of obs: 371, groups: Subid_fmRI, 185
##
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)      0.127715  0.029356   4.351
## agemo_converted    0.054127  0.017773   3.045
## CONP_EF_RAW_c     0.011249  0.007349   1.531
## sex              -0.002554  0.007931  -0.322
## agemo_converted:CONP_EF_RAW_c -0.007223  0.005064  -1.426
##
## Correlation of Fixed Effects:
##           (Intr) agm_cn CONP_E sex
## agem_cnvrted -0.907
## CONP_EF_RAW  0.055 -0.060
## sex          -0.500  0.114  0.003
## a_:CONP_EF_  -0.072  0.067 -0.990  0.027
```

ADHD

```
#ADHDsum; parent
mod.ADHD1 <- lmer(ADHDsum ~ agemo_converted + (agemo_converted | Subid_fMRI), data=PDS_data_mlm)
summary(mod.ADHD1)

## Linear mixed model fit by REML ['lmerMod']
## Formula: ADHDsum ~ agemo_converted + (agemo_converted | Subid_fMRI)
## Data: PDS_data_mlm
##
## REML criterion at convergence: 2710.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.6327 -0.2992 -0.1134  0.2267  3.8075
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr
##   Subid_fMRI (Intercept)          62.240   7.889
##                   agemo_converted  13.172   3.629   -0.98
## Residual                        3.509   1.873
## Number of obs: 554, groups: Subid_fMRI, 209
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    6.9537    0.9551   7.280
## agemo_converted -3.4153    0.6125  -5.576
##
## Correlation of Fixed Effects:
##              (Intr)
## agem_cnvrted -0.975

anova(mod.ADHD1)

## Analysis of Variance Table
##              Df Sum Sq Mean Sq F value
## agemo_converted  1  109.1   109.1   31.09

mod.ADHD2 <- lmer(ADHDsum ~ agemo_converted*CONP_EF_RAW_c + (agemo_converted | Subid_fMRI), data=PDS_data_mlm)
summary(mod.ADHD2)

## Linear mixed model fit by REML ['lmerMod']
## Formula: ADHDsum ~ agemo_converted * CONP_EF_RAW_c + (agemo_converted | Subid_fMRI)
## Data: PDS_data_mlm
##
## REML criterion at convergence: 2459.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.9581 -0.4592 -0.0437  0.2843  4.0425
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr
##   Subid_fMRI (Intercept)          33.127   5.756
```

```

##          agemo_converted  7.844   2.801   -0.98
## Residual                3.005   1.733
## Number of obs: 540, groups:  Subid_fmRI, 207
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)         5.3957    0.8137   6.631
## agemo_converted      -2.3724    0.5403  -4.391
## CONP_EF_RAW_c         1.0882    0.2063   5.275
## agemo_converted:CONP_EF_RAW_c -0.4231    0.1412  -2.997
##
## Correlation of Fixed Effects:
##      (Intr) agm_cn CONP_E
## agem_cnvrted -0.981
## CONP_EF_RAW -0.024  0.017
## a_:CONP_EF_  0.007  0.001 -0.987
mod.ADHD3 <- lmer(ADHDsum ~ agemo_converted*CONP_EF_RAW_c + sex + (agemo_converted | Subid_fmRI), data=
summary(mod.ADHD3)

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## ADHDsum ~ agemo_converted * CONP_EF_RAW_c + sex + (agemo_converted |
##      Subid_fmRI)
##      Data: PDS_data_mlm
##
## REML criterion at convergence: 2458.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.9219 -0.4606 -0.0455  0.3180  4.0525
##
## Random effects:
##      Groups      Name      Variance Std.Dev. Corr
##      Subid_fmRI (Intercept)  33.893   5.822
##                  agemo_converted  8.212   2.866   -0.98
##      Residual                2.984   1.727
## Number of obs: 540, groups:  Subid_fmRI, 207
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)         6.0381    0.9641   6.263
## agemo_converted      -2.4155    0.5423  -4.454
## CONP_EF_RAW_c         1.0959    0.2066   5.305
## sex                  -0.3939    0.3198  -1.232
## agemo_converted:CONP_EF_RAW_c -0.4344    0.1416  -3.067
##
## Correlation of Fixed Effects:
##      (Intr) agm_cn CONP_E sex
## agem_cnvrted -0.858
## CONP_EF_RAW -0.005  0.015
## sex          -0.534  0.055 -0.027
## a_:CONP_EF_ -0.025  0.005 -0.986  0.059

```



```
#ADHD_INsum
```

```
mod.ADHDIN <- lmer(ADHD_INsum ~ agemo_converted*CONP_EF_RAW_c + (agemo_converted | Subid_fmRI), data=PDS_data_mlm)  
summary(mod.ADHDIN)
```

```
## Linear mixed model fit by REML ['lmerMod']  
## Formula:  
## ADHD_INsum ~ agemo_converted * CONP_EF_RAW_c + (agemo_converted |  
## Subid_fmRI)  
## Data: PDS_data_mlm  
##  
## REML criterion at convergence: 2068.8  
##  
## Scaled residuals:  
## Min 1Q Median 3Q Max  
## -2.3455 -0.4954 -0.0532 0.3735 3.7233  
##  
## Random effects:  
## Groups Name Variance Std.Dev. Corr  
## Subid_fmRI (Intercept) 5.8255 2.4136  
## agemo_converted 0.9531 0.9763 -0.97  
## Residual 1.7579 1.3259  
## Number of obs: 540, groups: Subid_fmRI, 207  
##  
## Fixed effects:  
## Estimate Std. Error t value  
## (Intercept) 3.1260 0.5358 5.834  
## agemo_converted -1.1501 0.3702 -3.107  
## CONP_EF_RAW_c 0.6682 0.1438 4.648  
## agemo_converted:CONP_EF_RAW_c -0.2039 0.1001 -2.037  
##  
## Correlation of Fixed Effects:  
## (Intr) agm_cn CONP_E  
## agem_cnvrted -0.983  
## CONP_EF_RAW -0.005 -0.003  
## a_:CONP_EF_ -0.010 0.019 -0.987
```

```
#ADHD_HYIMsum
```

```
mod.ADHDHY <- lmer(ADHD_HYIMsum ~ agemo_converted*CONP_EF_RAW_c + (agemo_converted | Subid_fmRI), data=PDS_data_mlm)  
summary(mod.ADHDHY)
```

```
## Linear mixed model fit by REML ['lmerMod']  
## Formula:  
## ADHD_HYIMsum ~ agemo_converted * CONP_EF_RAW_c + (agemo_converted |  
## Subid_fmRI)  
## Data: PDS_data_mlm  
##  
## REML criterion at convergence: 1725.7  
##  
## Scaled residuals:  
## Min 1Q Median 3Q Max  
## -3.2427 -0.3113 -0.0439 0.1398 4.6298  
##  
## Random effects:  
## Groups Name Variance Std.Dev. Corr
```

```

## Subid_fMRI (Intercept)      11.4162  3.3788
##           agemo_converted  3.1925  1.7867   -0.98
## Residual                    0.7183  0.8475
## Number of obs: 540, groups: Subid_fMRI, 207
##
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)      2.21178    0.42437   5.212
## agemo_converted  -1.18262    0.28029  -4.219
## CONP_EF_RAW_c     0.51754    0.10554   4.904
## agemo_converted:CONP_EF_RAW_c -0.27074    0.07215  -3.752
##
## Correlation of Fixed Effects:
##           (Intr) agm_cn CONP_E
## agem_cnvrted -0.982
## CONP_EF_RAW -0.026  0.020
## a_:CONP_EF_  0.010 -0.002 -0.987
##EF and MDD
mod.MDD1 <- lmer(MDDCorescan ~ agemo_converted + (agemo_converted | Subid_fMRI), data=PDS_data_mlm)
summary(mod.MDD1)

## Linear mixed model fit by REML ['lmerMod']
## Formula: MDDCorescan ~ agemo_converted + (agemo_converted | Subid_fMRI)
## Data: PDS_data_mlm
##
## REML criterion at convergence: 2317.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.2069 -0.6170 -0.1288  0.5123  2.7024
##
## Random effects:
## Groups      Name                Variance Std.Dev. Corr
## Subid_fMRI (Intercept)      13.878    3.725
##           agemo_converted   3.798    1.949   -0.98
## Residual                    1.901    1.379
## Number of obs: 591, groups: Subid_fMRI, 211
##
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)      3.8699    0.5656   6.842
## agemo_converted  -1.2434    0.3813  -3.261
##
## Correlation of Fixed Effects:
##           (Intr)
## agem_cnvrted -0.984
mod.MDD2 <- lmer(MDDCorescan ~ agemo_converted*CONP_EF_RAW_c + (agemo_converted | Subid_fMRI), data=PDS_data_mlm)
summary(mod.MDD2)

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## MDDCorescan ~ agemo_converted * CONP_EF_RAW_c + (agemo_converted |
## Subid_fMRI)

```

```

## Data: PDS_data_mlm
##
## REML criterion at convergence: 2099.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.1061 -0.5844 -0.1804  0.4935  2.8090
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr
##   Subid_fmRI (Intercept)          14.958   3.868
##               agemo_converted     5.718   2.391   -0.98
##   Residual                        1.833   1.354
## Number of obs: 547, groups: Subid_fmRI, 209
##
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)          3.1888    0.5777   5.520
## agemo_converted       -0.7543    0.4011  -1.881
## CONP_EF_RAW_c         0.3904    0.1537   2.540
## agemo_converted:CONP_EF_RAW_c -0.1573    0.1072  -1.468
##
## Correlation of Fixed Effects:
##           (Intr) agm_cn CONP_E
## agem_cnvrted -0.988
## CONP_EF_RAW -0.003 -0.005
## a_:CONP_EF_ -0.009  0.017 -0.990
mod.MDD3 <- lmer(MDDCorescan ~ agemo_converted*CONP_EF_RAW_c + sex + (agemo_converted | Subid_fmRI), da
summary(mod.MDD3)

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## MDDCorescan ~ agemo_converted * CONP_EF_RAW_c + sex + (agemo_converted |
##   Subid_fmRI)
## Data: PDS_data_mlm
##
## REML criterion at convergence: 2100.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.1028 -0.5809 -0.1792  0.4916  2.8045
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr
##   Subid_fmRI (Intercept)          14.944   3.866
##               agemo_converted     5.698   2.387   -0.98
##   Residual                        1.833   1.354
## Number of obs: 547, groups: Subid_fmRI, 209
##
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)          3.15263    0.65342   4.825
## agemo_converted       -0.75334    0.40191  -1.874
## CONP_EF_RAW_c         0.39004    0.15375   2.537

```

```

## sex                0.02342    0.18350    0.128
## agemo_converted:CONP_EF_RAW_c -0.15678    0.10727   -1.461
##
## Correlation of Fixed Effects:
##          (Intr) agm_cn CONP_E sex
## agem_cnvrted -0.899
## CONP_EF_RAW  0.000 -0.005
## sex          -0.466  0.058 -0.007
## a_:CONP_EF_  -0.024  0.019 -0.990  0.035
##Next do GE predicting ADHD
#ADHDsum

mod.ADHD.SAL1 <- lmer(ADHDsum ~ agemo_converted*SAL_GE_K1to5_c + (agemo_converted | Subid_fmRI), data=P
summary(mod.ADHD.SAL1)

## Linear mixed model fit by REML ['lmerMod']
## Formula: ADHDsum ~ agemo_converted * SAL_GE_K1to5_c + (agemo_converted |
##      Subid_fmRI)
##      Data: PDS_data_mlm
##
## REML criterion at convergence: 1845.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6257 -0.2927 -0.1150  0.1581  3.6139
##
## Random effects:
##      Groups      Name                Variance Std.Dev. Corr
##      Subid_fmRI (Intercept)          113.583  10.658
##                  agemo_converted    43.387   6.587  -0.97
##      Residual                        2.727   1.651
## Number of obs: 378, groups: Subid_fmRI, 187
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)      6.6736     1.3393   4.983
## agemo_converted    -3.3436     0.9036  -3.700
## SAL_GE_K1to5_c    -12.7613     8.0186  -1.591
## agemo_converted:SAL_GE_K1to5_c   8.2396     5.6013   1.471
##
## Correlation of Fixed Effects:
##          (Intr) agm_cn SAL_GE
## agem_cnvrted -0.986
## SAL_GE_K15_  0.067 -0.070
## a_:SAL_GE_K -0.060  0.064 -0.990
mod.ADHD.SAL2 <- lmer(ADHDsum ~ agemo_converted*SAL_GE_K6to10_c + (agemo_converted | Subid_fmRI), data=I
summary(mod.ADHD.SAL2)

## Linear mixed model fit by REML ['lmerMod']
## Formula: ADHDsum ~ agemo_converted * SAL_GE_K6to10_c + (agemo_converted |
##      Subid_fmRI)
##      Data: PDS_data_mlm
##

```

```

## REML criterion at convergence: 1845.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6404 -0.2939 -0.1165  0.1500  3.5757
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr
##   Subid_fMRI (Intercept)          113.559  10.656
##               agemo_converted    43.226   6.575  -0.97
##   Residual                        2.701   1.643
## Number of obs: 378, groups:  Subid_fMRI, 187
##
## Fixed effects:
##                                Estimate Std. Error t value
## (Intercept)                   6.7061     1.3359   5.020
## agemo_converted                -3.3654     0.9006  -3.737
## SAL_GE_K6to10_c              -14.7008     7.2566  -2.026
## agemo_converted:SAL_GE_K6to10_c  9.8375     5.0698   1.940
##
## Correlation of Fixed Effects:
##              (Intr) agm_cn SAL_GE
## agem_cnvrted -0.986
## SAL_GE_K610  0.046 -0.049
## a_:SAL_GE_K -0.038  0.040 -0.990
mod.ADHD.CON1 <- lmer(ADHDsum ~ agemo_converted*CON_GE_K1to5_c + (agemo_converted | Subid_fMRI), data=P
summary(mod.ADHD.CON1)

## Linear mixed model fit by REML ['lmerMod']
## Formula: ADHDsum ~ agemo_converted * CON_GE_K1to5_c + (agemo_converted |
##      Subid_fMRI)
##      Data: PDS_data_mlm
##
## REML criterion at convergence: 1842.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.5591 -0.3052 -0.1436  0.2244  3.4844
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr
##   Subid_fMRI (Intercept)          118.531  10.887
##               agemo_converted    45.681   6.759  -0.97
##   Residual                        2.713   1.647
## Number of obs: 378, groups:  Subid_fMRI, 187
##
## Fixed effects:
##                                Estimate Std. Error t value
## (Intercept)                   6.6656     1.3486   4.943
## agemo_converted                -3.3411     0.9096  -3.673
## CON_GE_K1to5_c                 8.4251     7.8572   1.072
## agemo_converted:CON_GE_K1to5_c -7.3307     5.4178  -1.353
##
## Correlation of Fixed Effects:

```

```

##          (Intr) agm_cn CON_GE
## agem_cnvrted -0.986
## CON_GE_K15_  0.034 -0.034
## a_:CON_GE_K -0.025  0.025 -0.992

mod.ADHD.CON2 <- lmer(ADHDsum ~ agemo_converted*CON_GE_K6to10_c + (agemo_converted | Subid_fmRI), data=
summary(mod.ADHD.CON2)

## Linear mixed model fit by REML ['lmerMod']
## Formula: ADHDsum ~ agemo_converted * CON_GE_K6to10_c + (agemo_converted |
##      Subid_fmRI)
##      Data: PDS_data_mlm
##
## REML criterion at convergence: 1844
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6066 -0.2956 -0.1413  0.2055  3.5780
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr
##   Subid_fmRI (Intercept)          118.482  10.885
##               agemo_converted    45.470   6.743  -0.97
##   Residual                        2.733   1.653
## Number of obs: 378, groups: Subid_fmRI, 187
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)         6.6755     1.3491  4.948
## agemo_converted      -3.3518     0.9094 -3.686
## CON_GE_K6to10_c       5.7149     6.4892  0.881
## agemo_converted:CON_GE_K6to10_c -5.3275     4.5155 -1.180
##
## Correlation of Fixed Effects:
##          (Intr) agm_cn CON_GE
## agem_cnvrted -0.987
## CON_GE_K610  0.037 -0.040
## a_:CON_GE_K -0.029  0.032 -0.991

mod.ADHD.FPN1 <- lmer(ADHDsum ~ agemo_converted*FPN_GE_K1to5_c + (agemo_converted | Subid_fmRI), data=
summary(mod.ADHD.FPN1)

## Linear mixed model fit by REML ['lmerMod']
## Formula: ADHDsum ~ agemo_converted * FPN_GE_K1to5_c + (agemo_converted |
##      Subid_fmRI)
##      Data: PDS_data_mlm
##
## REML criterion at convergence: 1846.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.5701 -0.2936 -0.1106  0.1474  3.5753
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr

```

```

## Subid_fmRI (Intercept)      114.553  10.703
##          agemo_converted  43.968   6.631   -0.97
## Residual                    2.765   1.663
## Number of obs: 378, groups: Subid_fmRI, 187
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)      6.6543    1.3585   4.898
## agemo_converted  -3.3385    0.9174  -3.639
## FPN_GE_K1to5_c   -10.1347   11.4920  -0.882
## agemo_converted:FPN_GE_K1to5_c  6.6190    8.1353   0.814
##
## Correlation of Fixed Effects:
##          (Intr) agm_cn FPN_GE
## agem_cnvrted -0.986
## FPN_GE_K15_   0.079 -0.073
## a_:FPN_GE_K  -0.062  0.055 -0.992

mod.ADHD.FPN2 <- lmer(ADHDsum ~ agemo_converted*FPN_GE_K6to10_c + (agemo_converted | Subid_fmRI), data=
summary(mod.ADHD.FPN2)

## Linear mixed model fit by REML ['lmerMod']
## Formula: ADHDsum ~ agemo_converted * FPN_GE_K6to10_c + (agemo_converted |
##          Subid_fmRI)
## Data: PDS_data_mlm
##
## REML criterion at convergence: 1847.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6231 -0.2934 -0.1155  0.1477  3.5395
##
## Random effects:
## Groups      Name              Variance Std.Dev. Corr
## Subid_fmRI (Intercept)      114.704  10.710
##          agemo_converted  43.864   6.623   -0.97
## Residual                    2.749   1.658
## Number of obs: 378, groups: Subid_fmRI, 187
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)      6.9490    1.3444   5.169
## agemo_converted  -3.5376    0.9072  -3.900
## FPN_GE_K6to10_c   -5.3058    8.9830  -0.591
## agemo_converted:FPN_GE_K6to10_c  3.0923    6.4517   0.479
##
## Correlation of Fixed Effects:
##          (Intr) agm_cn FPN_GE
## agem_cnvrted -0.986
## FPN_GE_K610  -0.025  0.024
## a_:FPN_GE_K  0.015 -0.014 -0.992

mod.ADHD.DMN1 <- lmer(ADHDsum ~ agemo_converted*DMN_GE_K1to5_c + (agemo_converted | Subid_fmRI), data=
summary(mod.ADHD.DMN1)

```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: ADHDsum ~ agemo_converted * DMN_GE_K1to5_c + (agemo_converted |
##   Subid_fMRI)
##   Data: PDS_data_mlm
##
## REML criterion at convergence: 1844.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.5241 -0.2913 -0.1255  0.1742  3.5417
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr
##   Subid_fMRI (Intercept)          118.225  10.873
##             agemo_converted    45.747   6.764  -0.97
##   Residual                        2.735   1.654
## Number of obs: 378, groups:  Subid_fMRI, 187
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)         6.9080     1.3493   5.120
## agemo_converted      -3.5090     0.9112  -3.851
## DMN_GE_K1to5_c      -15.0607    16.5491  -0.910
## agemo_converted:DMN_GE_K1to5_c   8.9484    11.5538   0.775
##
## Correlation of Fixed Effects:
##              (Intr) agm_cn DMN_GE
## agem_cnvrted -0.986
## DMN_GE_K15_  -0.011  0.006
## a_:DMN_GE_K   0.007 -0.001 -0.993
```

```
mod.ADHD.DMN2 <- lmer(ADHDsum ~ agemo_converted*DMN_GE_K6to10_c + (agemo_converted | Subid_fMRI), data=
summary(mod.ADHD.DMN2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: ADHDsum ~ agemo_converted * DMN_GE_K6to10_c + (agemo_converted |
##   Subid_fMRI)
##   Data: PDS_data_mlm
##
## REML criterion at convergence: 1845.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.5687 -0.2897 -0.1311  0.1713  3.5598
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr
##   Subid_fMRI (Intercept)          117.461  10.838
##             agemo_converted    45.129   6.718  -0.97
##   Residual                        2.749   1.658
## Number of obs: 378, groups:  Subid_fMRI, 187
##
## Fixed effects:
##
##              Estimate Std. Error t value
## (Intercept)         6.8706     1.3478   5.098
```



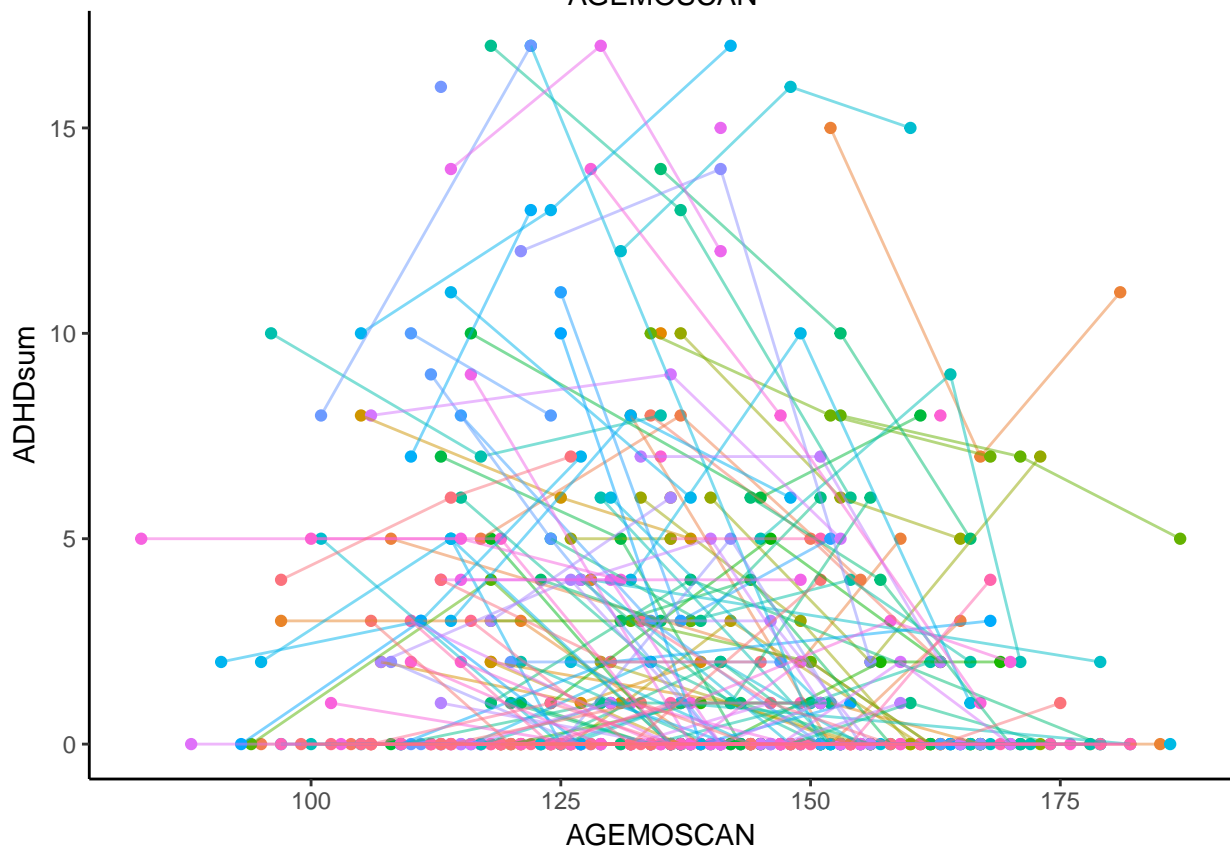
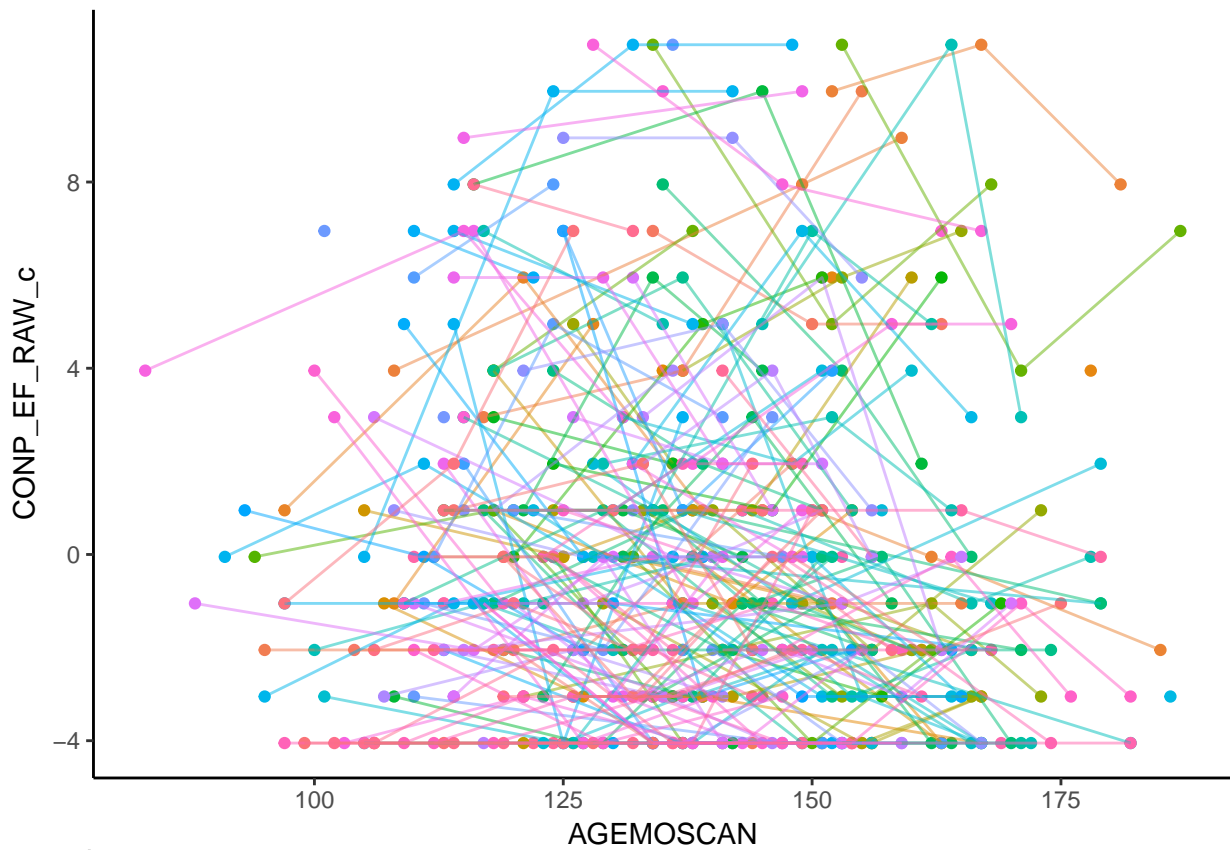
```

## agemo_converted          -3.4836      0.9092  -3.831
## DMN_GE_K6to10_c         -7.7708     15.5929  -0.498
## agemo_converted:DMN_GE_K6to10_c  4.1805     10.9244   0.383
##
## Correlation of Fixed Effects:
##      (Intr) agm_cn DMN_GE
## agem_cnvrted -0.986
## DMN_GE_K610 -0.010  0.007
## a_:DMN_GE_K  0.007 -0.004 -0.992

##output sig. models together in one table; break it up by analysis type?
#library(sjPlot)
#sjt.lm(mod.ADHD.SAL1 , mod.ADHD.SAL2, file = "sjt.ADHD.SAL.doc")
#sjt.lm(adhdmodel1, adhdmodel2, adhdmodel3, adhdmodel4, adhdmodel5, file = "sjt_adhd.doc")

```

Data Visualization



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.

Additional analyses: Teacher

```
#ADHDsum; teacher
#PDS_data_mlm_T_na <- subset(PDS_data_mlm, CONT_EF_RAW >= 0)

#mod.T.ADHD0 <- lm(ADHDsum ~ CONT_EF_RAW + sex, data = PDS_data_mlm_teacher)
#summary(mod.T.ADHD0)
#mod.T.ADHD1 <- lmer(ADHDsum ~ agemo_converted + (1 | Subid_fMRI), data=PDS_data_mlm_T_na)
#summary(mod.T.ADHD1)
#mod.T.ADHD2 <- lmer(ADHDsum ~ CONT_EF_RAW + (agemo_converted | Subid_fMRI), data = PDS_data_mlm_T_na)
#summary(mod.T.ADHD2)
#mod.T.ADHD3 <- lmer(ADHDsum ~ agemo_converted*CONT_EF_RAW + sex + (agemo_converted | Subid_fMRI), data=
#summary(mod.T.ADHD3)
#this isn't working
```