```r
library(ggplot2)
library(ez)
library(car)
library(MOTE)
library(BayesFactor)
library(cowplot)
library(reshape2)
options(scipen = 999)
setwd("C:/Users/jel7c5/OneDrive - University of Missouri/John PhD Mizzou/Research/EP/Resting-state funct
#setwd("C:/Users/jel7c5/Desktop/adhd200")
theme = theme(panel.grid.major = element_blank(),
              panel.grid.minor = element_blank(),
              panel.background = element_blank(),
              axis.line = element_line(colour = "black"),
              legend.key = element_rect(fill = "white"),
              text = element_text(size = 15))

ITI_data = read.csv('ITI_data_combined.csv')
NT_data = read.csv('NT_data_combined.csv')
ITI_data_sd = read.csv('ITI_data_combined_sd.csv')
colnames(ITI_data) = c('ID','ITI','TYPE')
colnames(NT_data) = c('ID','NT','TYPE')
colnames(ITI_data_sd) = c('ID','ITI','TYPE')
ITI_data$partno = 1:nrow(ITI_data)
NT_data$partno = 1:nrow(NT_data)
ITI_data_sd$partno = 1:nrow(ITI_data_sd)

ITI_data$sex = NA
ITI_data$diag = NA
for(x in 1:nrow(ITI_data)){
  if(ITI_data$TYPE[x] == 'fa'){
    ITI_data$sex[x] = 'F'
    ITI_data$diag[x] = 'A'
  } else if(ITI_data$TYPE[x] == 'fc'){
    ITI_data$sex[x] = 'F'
    ITI_data$diag[x] = 'C'
  } else if(ITI_data$TYPE[x] == 'ma'){
    ITI_data$sex[x] = 'M'
    ITI_data$diag[x] = 'A'
  } else if(ITI_data$TYPE[x] == 'mc') {
    ITI_data$sex[x] = 'M'
    ITI_data$diag[x] = 'C'
  }
}

ITI_data_sd$sex = NA
ITI_data_sd$diag = NA
for(x in 1:nrow(ITI_data_sd)){
  if(ITI_data_sd$TYPE[x] == 'fa'){
    ITI_data_sd$sex[x] = 'F'
    ITI_data_sd$diag[x] = 'A'
  } else if(ITI_data_sd$TYPE[x] == 'fc'){
    ITI_data_sd$sex[x] = 'F'
```

```r
      ITI_data_sd$diag[x] = 'C'
    } else if(ITI_data_sd$TYPE[x] == 'ma'){
      ITI_data_sd$sex[x] = 'M'
      ITI_data_sd$diag[x] = 'A'
    } else if(ITI_data_sd$TYPE[x] == 'mc') {
      ITI_data_sd$sex[x] = 'M'
      ITI_data_sd$diag[x] = 'C'
    }
}

NT_data$sex = NA
NT_data$diag = NA
for(x in 1:nrow(NT_data)){
    if(NT_data$TYPE[x] == 'fa'){
      NT_data$sex[x] = 'F'
      NT_data$diag[x] = 'A'
    } else if(NT_data$TYPE[x] == 'fc'){
      NT_data$sex[x] = 'F'
      NT_data$diag[x] = 'C'
    } else if(NT_data$TYPE[x] == 'ma'){
      NT_data$sex[x] = 'M'
      NT_data$diag[x] = 'A'
    } else if(NT_data$TYPE[x] == 'mc'){
      NT_data$sex[x] = 'M'
      NT_data$diag[x] = 'C'
    }
}

ITI_data$sex = factor(ITI_data$sex)
ITI_data$diag = factor(ITI_data$diag)

ITI_data_sd$sex = factor(ITI_data_sd$sex)
ITI_data_sd$diag = factor(ITI_data_sd$diag)

NT_data$sex = factor(NT_data$sex)
NT_data$diag = factor(NT_data$diag)

FO_comb_dat = read.csv('hmm2_frac_occ_common.csv')


ITI_data$sub = FO_comb_dat$sub
ITI_data_sd$sub = FO_comb_dat$sub
NT_data$sub = FO_comb_dat$sub

## link up sites
sitez = read.csv('ID_site.csv')
FO_comb_dat$site = 'x'
for(x in 1:nrow(FO_comb_dat)){
  id = FO_comb_dat$sub[x]
  FO_comb_dat$site[x] = as.character(subset(sitez, ScanDirID == id)$Site2[1])
}
ITI_data$site = FO_comb_dat$site
NT_data$site = FO_comb_dat$site
```

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ITI_data_sd$site = FO_comb_dat$site

zscores = scale(ITI_data$ITI)
ITI_noout = subset(ITI_data, abs(zscores) < 3)

zscoress = scale(ITI_data_sd$ITI)
ITI_noout_sd = subset(ITI_data_sd, abs(zscoress) < 3)

zscores2 = scale(NT_data$NT)
NT_noout = subset(NT_data, abs(zscores2) < 3)

zscores3 = scale(FO_comb_dat$FO)
FO_noout = subset(FO_comb_dat, abs(zscores3) < 3)

ITI_noout$sex = factor(ITI_noout$sex, levels = c('F','M'), labels = c('Female','Male'))
ITI_noout$diag = factor(ITI_noout$diag, levels = c('A','C'), labels = c('ADHD','Control'))

ITI_noout_sd$sex = factor(ITI_noout_sd$sex, levels = c('F','M'), labels = c('Female','Male'))
ITI_noout_sd$diag = factor(ITI_noout_sd$diag, levels = c('A','C'), labels = c('ADHD','Control'))

NT_noout$sex = factor(NT_noout$sex, levels = c('F','M'), labels = c('Female','Male'))
NT_noout$diag = factor(NT_noout$diag, levels = c('A','C'), labels = c('ADHD','Control'))
```

Age

```r
library(dplyr)
p_kki = read.csv('KKI/KKI_phenotypic.csv')
p_kki$site2 = 'KKI'
p_nyu = read.csv('NYU/NYU_phenotypic.csv')
p_nyu$site2 = 'NYU'
p_peking1 = read.csv('Peking_1/Peking_1_phenotypic.csv')
p_peking1$site2 = 'Peking_1'
p_peking2 = read.csv('Peking_2/Peking_2_phenotypic.csv')
p_peking2$site2 = 'Peking_2'
p_peking3 = read.csv('Peking_3/Peking_3_phenotypic.csv')
p_peking3$site2 = 'Peking_3'
p_ohsu = read.csv('OHSU/OHSU_phenotypic.csv')
p_ohsu$site2 = 'OHSU'
p_neuroimage = read.csv('NeuroIMAGE/NeuroIMAGE_phenotypic.csv')
p_neuroimage$site2 = 'NEUROIMAGE'

phenotypic = rbind(p_kki,p_nyu,p_peking1,p_peking2,p_peking3,
                   p_ohsu,p_neuroimage)

phenotypic2 = phenotypic[,c('ScanDirID','site2','Age')]
colnames(phenotypic2) = c('sub','site','age')



ITI_2 = ITI_noout %>% full_join(phenotypic2, by=c('site','sub'))
ITI_3 = ITI_2[complete.cases(ITI_2), ]
```

```
ITI_2_sd = ITI_noout_sd %>% full_join(phenotypic2, by=c('site','sub'))
ITI_3_sd = ITI_2_sd[complete.cases(ITI_2_sd),]

NT_2 = NT_noout %>% full_join(phenotypic2, by=c('site','sub'))
NT_3 = NT_2[complete.cases(NT_2),]


## check if experimental groups differ on the covariate
ezANOVA(data = ITI_3,
        wid = partno,
        between = .(sex, diag),
        dv = age,
        type = 3)
```

```
## $ANOVA
##      Effect DFn DFd        F          p p<.05        ges
## 2       sex   1 896 16.606377 0.0000500769     * 0.018196648
## 3      diag   1 896  6.599970 0.0103588816     * 0.007312176
## 4 sex:diag   1 896  3.508956 0.0613632926       0.003900968
##
## $`Levene's Test for Homogeneity of Variance`
##   DFn DFd      SSn      SSd        F          p p<.05
## 1   3 896 28.72852 2264.906 3.788348 0.01021015     *
```

```
ezANOVA(data = ITI_3_sd,
        wid = partno,
        between = .(sex, diag),
        dv = age,
        type = 3)
```

```
## $ANOVA
##      Effect DFn DFd        F          p p<.05        ges
## 2       sex   1 894 16.315845 0.00005821904     * 0.017923279
## 3      diag   1 894  6.754593 0.00950470686     * 0.007498816
## 4 sex:diag   1 894  3.383269 0.06619276393       0.003770149
##
## $`Levene's Test for Homogeneity of Variance`
##   DFn DFd      SSn      SSd        F          p p<.05
## 1   3 894 28.70746 2273.748 3.762433 0.01057965     *
```

```
ezANOVA(data = NT_3,
        wid = partno,
        between = .(sex, diag),
        dv = age,
        type = 3) # This violates the independence assumption between teh covariate and treatment effec
```

```
## $ANOVA
##      Effect DFn DFd        F          p p<.05        ges
## 2       sex   1 897 16.453954 0.00005418415     * 0.018012899
## 3      diag   1 897  6.682132 0.00989524333     * 0.007394339
## 4 sex:diag   1 897  3.428057 0.06442597013       0.003807141
##
## $`Levene's Test for Homogeneity of Variance`
##   DFn DFd      SSn      SSd        F          p p<.05
## 1   3 897 28.81572 2274.202 3.788537 0.01020716     *
```

```
## so advice is to not run ancova with age.


## However, check for it anyway to see if main conclusions change
ezANOVA(data = ITI_3,
        wid = partno,
        between = .(sex, diag),
        between_covariates = .(age),
        dv = ITI,
        type = 3)

## $ANOVA
##     Effect DFn DFd          F          p p<.05          ges
## 2      sex   1 896 4.74425801 0.02965634     * 0.00526704219
## 3     diag   1 896 0.05163493 0.82029424       0.00005762495
## 4 sex:diag   1 896 0.30005734 0.58398290       0.00033477332
##
## $`Levene's Test for Homogeneity of Variance`
##   DFn DFd       SSn     SSd        F         p p<.05
## 1   3 896 0.2459688 35.2234 2.085622 0.1005617
ezANOVA(data = ITI_3_sd,
        wid = partno,
        between = .(sex, diag),
        between_covariates = .(age),
        dv = ITI,
        type = 3)

## $ANOVA
##     Effect DFn DFd          F          p p<.05          ges
## 2      sex   1 894 2.83893996 0.09235390       0.0031654959
## 3     diag   1 894 4.19039529 0.04094551     * 0.0046653753
## 4 sex:diag   1 894 0.02383816 0.87733226       0.0000266639
##
## $`Levene's Test for Homogeneity of Variance`
##   DFn DFd       SSn      SSd        F         p p<.05
## 1   3 894 0.5069975 112.7723 1.339737 0.2601235
ezANOVA(data = NT_3,
        wid = partno,
        between = .(sex, diag),
        between_covariates = .(age),
        dv = NT,
        type = 3)

## $ANOVA
##     Effect DFn DFd            F          p p<.05            ges
## 2      sex   1 897 6.15934193637 0.01325411     * 0.00681977326743
## 3     diag   1 897 0.02144739421 0.88359963       0.00002390956679
## 4 sex:diag   1 897 0.00008397991 0.99269028       0.00000009362308
##
## $`Levene's Test for Homogeneity of Variance`
##   DFn DFd        SSn      SSd        F         p p<.05
## 1   3 897 0.02026379 1.593205 3.802947 0.01000768     *
```