ALDA_HW3_EH

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```
library(lme4)

## Loading required package: Matrix

library(tidyverse)

## Loading tidyverse: ggplot2
## Loading tidyverse: tibble
## Loading tidyverse: tidyr
## Loading tidyverse: readr
## Loading tidyverse: purrr
## Loading tidyverse: dplyr

## Conflicts with tidy packages ----------------------------------------------

## expand(): tidyr, Matrix
## filter(): dplyr, stats
## lag():    dplyr, stats

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

PDS_data_2 <- read.csv(file =  "~/Documents/PDS_project/Longitudinal_project/datasets/PDS_long_final.csv
PDS_data_2$AGEMOSCAN <- as.numeric(PDS_data_2$AGEMOSCAN)
PDS_data_2$ADHDsum <- as.numeric(PDS_data_2$ADHDsum)
PDS_data_2$ADHD_INsum <- as.numeric(PDS_data_2$ADHD_INsum)
PDS_data_2$ADHD_HYIMsum<- as.numeric(PDS_data_2$ADHD_HYIMsum)
```

1. Run a series of models using a time-invariant nominal covariate. a) where the covariate only predicts the intercept b) predicts both intercept and slope c) is rescaled eg centering. For all models, how does your model change from model to model. What is your final model?

```r
#nominal covariate = sex
#a) where the covariate only predicts the intercept

mod.1 <- lmer(ADHDsum ~ agemo_converted + sex + (1|Subid_fMRI), data=PDS_data_2)
summary(mod.1)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: ADHDsum ~ agemo_converted + sex + (1 | Subid_fMRI)
##    Data: PDS_data_2
##
## REML criterion at convergence: 2732
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.4032 -0.4035 -0.1066  0.2421  4.6492
##
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  Subid_fMRI (Intercept) 8.908    2.985
##  Residual               3.959    1.990
## Number of obs: 554, groups:  Subid_fMRI, 209
##
## Fixed effects:
##                 Estimate Std. Error t value
## (Intercept)       8.5212     1.0937   7.791
## agemo_converted  -3.3747     0.5892  -5.727
## sex              -1.1163     0.4490  -2.486
##
## Correlation of Fixed Effects:
##             (Intr) agm_cn
## agem_cnvrtd -0.766
## sex         -0.640  0.040
```

```r
#b) predicts both intercept and slope
mod.2 <- lmer(ADHDsum ~ agemo_converted + sex + (agemo_converted|Subid_fMRI), data=PDS_data_2)
summary(mod.2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: ADHDsum ~ agemo_converted + sex + (agemo_converted | Subid_fMRI)
##    Data: PDS_data_2
##
## REML criterion at convergence: 2702.9
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.5203 -0.3163 -0.1150  0.2092  3.7891
```

```
##
## Random effects:
##  Groups     Name            Variance Std.Dev. Corr
##  Subid_fMRI (Intercept)     65.158   8.072
##             agemo_converted 14.427   3.798    -0.98
##  Residual                    3.468   1.862
## Number of obs: 554, groups:  Subid_fMRI, 209
##
## Fixed effects:
##                 Estimate Std. Error t value
## (Intercept)       8.7777     1.1559   7.594
## agemo_converted  -3.4633     0.6146  -5.635
## sex              -1.1862     0.4201  -2.823
##
## Correlation of Fixed Effects:
##             (Intr) agm_cn
## agem_cnvrtd -0.825
## sex         -0.558  0.027
```

```
#c) is rescaled eg centering
sex_c <- scale(PDS_data_2$sex, center = T, scale = F)
PDS_data_2$sex_c <- as.numeric(sex_c)
mod.3 <- lmer(ADHDsum ~ agemo_converted + sex_c + (agemo_converted|Subid_fMRI), data=PDS_data_2)
summary(mod.3)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## ADHDsum ~ agemo_converted + sex_c + (agemo_converted | Subid_fMRI)
##    Data: PDS_data_2
##
## REML criterion at convergence: 2702.9
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.5203 -0.3163 -0.1150  0.2092  3.7891
##
## Random effects:
##  Groups     Name            Variance Std.Dev. Corr
##  Subid_fMRI (Intercept)     65.158   8.072
##             agemo_converted 14.427   3.798    -0.98
##  Residual                    3.468   1.862
## Number of obs: 554, groups:  Subid_fMRI, 209
##
## Fixed effects:
##                 Estimate Std. Error t value
## (Intercept)       7.0189     0.9592   7.317
## agemo_converted  -3.4633     0.6146  -5.635
## sex_c            -1.1862     0.4201  -2.823
##
## Correlation of Fixed Effects:
##             (Intr) agm_cn
## agem_cnvrtd -0.976
## sex_c       -0.023  0.027
```

The model fit improves (explains more of the variance) when a time variable is added, showing that sex is a more useful predictor of ADHD symptoms when the slopes are allowed to vary by subject. Centering sex does not improve the model.

2. Introduce a time-invariant continuous covariate and run models a-c from #1.

```
#continuous covariate = SES (Income_to_Need_Scan)
#a) where the covariate only predicts the intercept

mod.4 <- lmer(ADHDsum ~ Income_to_Need_Scan + (1|Subid_fMRI), data=PDS_data_2)
summary(mod.4)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: ADHDsum ~ Income_to_Need_Scan + (1 | Subid_fMRI)
##    Data: PDS_data_2
##
## REML criterion at convergence: 2758.8
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.5855 -0.3508 -0.1653  0.2227  4.6363
##
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  Subid_fMRI (Intercept) 8.423    2.902
##  Residual               4.314    2.077
## Number of obs: 554, groups:  Subid_fMRI, 209
##
## Fixed effects:
##                     Estimate Std. Error t value
## (Intercept)           3.1860     0.3462   9.203
## Income_to_Need_Scan  -0.5099     0.1407  -3.624
##
## Correlation of Fixed Effects:
##             (Intr)
## Incm_t_Nd_S -0.771
```

```
#b) predicts both intercept and slope
mod.5 <- lmer(ADHDsum ~ agemo_converted + Income_to_Need_Scan + (agemo_converted|Subid_fMRI), data=PDS_d
summary(mod.5)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## ADHDsum ~ agemo_converted + Income_to_Need_Scan + (agemo_converted |
##     Subid_fMRI)
##    Data: PDS_data_2
##
## REML criterion at convergence: 2709.9
##
## Scaled residuals:
```

```
##      Min       1Q   Median       3Q      Max
## -3.5957 -0.3202 -0.1196  0.2055  3.7449
##
## Random effects:
##  Groups     Name            Variance Std.Dev. Corr
##  Subid_fMRI (Intercept)     66.683   8.166
##             agemo_converted 16.112   4.014    -0.98
##  Residual                    3.476   1.864
## Number of obs: 554, groups:  Subid_fMRI, 209
##
## Fixed effects:
##                     Estimate Std. Error t value
## (Intercept)           7.0188     0.9670   7.258
## agemo_converted      -3.1322     0.6459  -4.849
## Income_to_Need_Scan  -0.2420     0.1295  -1.869
##
## Correlation of Fixed Effects:
##             (Intr) agm_cn
## agem_cnvrtd -0.939
## Incm_t_Nd_S -0.018 -0.254
```

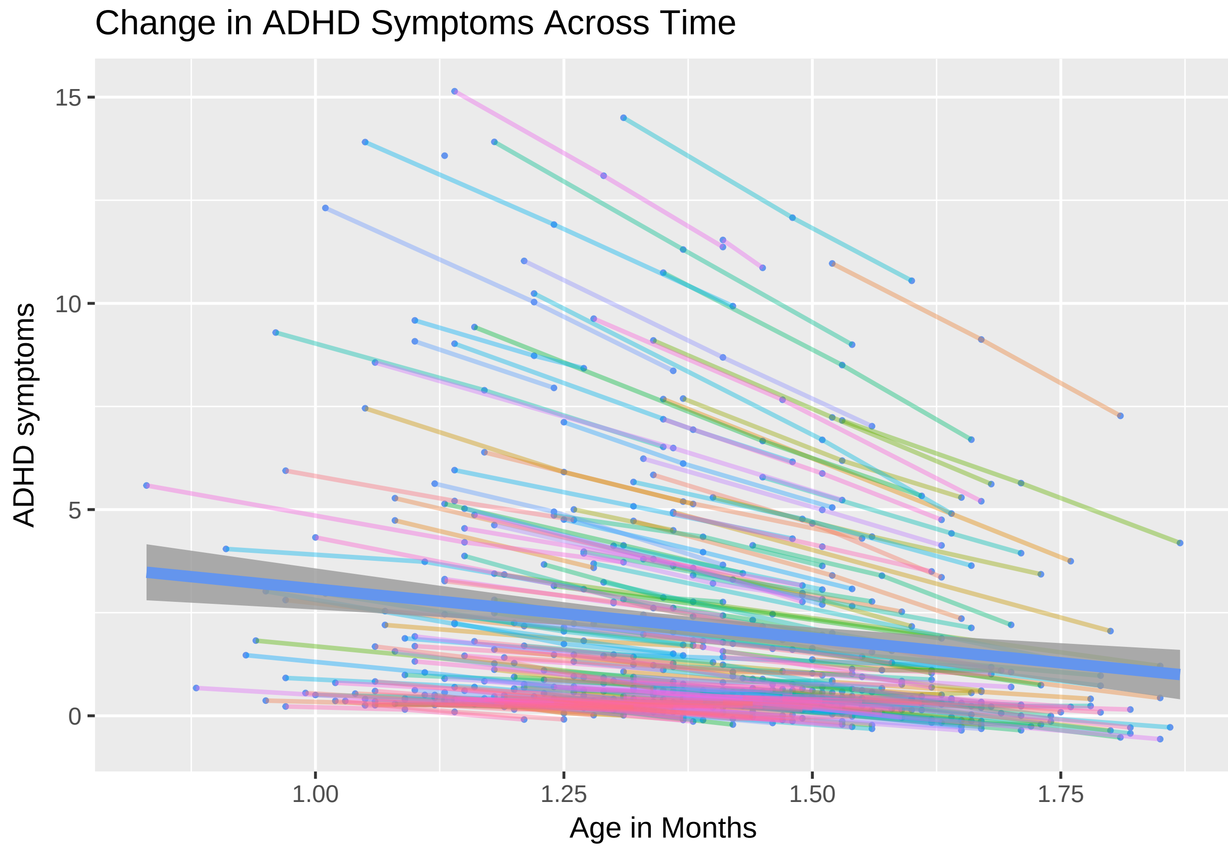
```
#c) is rescaled eg centering
Income_to_Need_Scan_c <- scale(PDS_data_2$ Income_to_Need_Scan , center = T, scale = F)
PDS_data_2$ Income_to_Need_Scan_c <- as.numeric(Income_to_Need_Scan_c)
mod.6 <- lmer(ADHDsum ~ agemo_converted + Income_to_Need_Scan_c + (agemo_converted|Subid_fMRI), data=PDS
summary(mod.6)
```

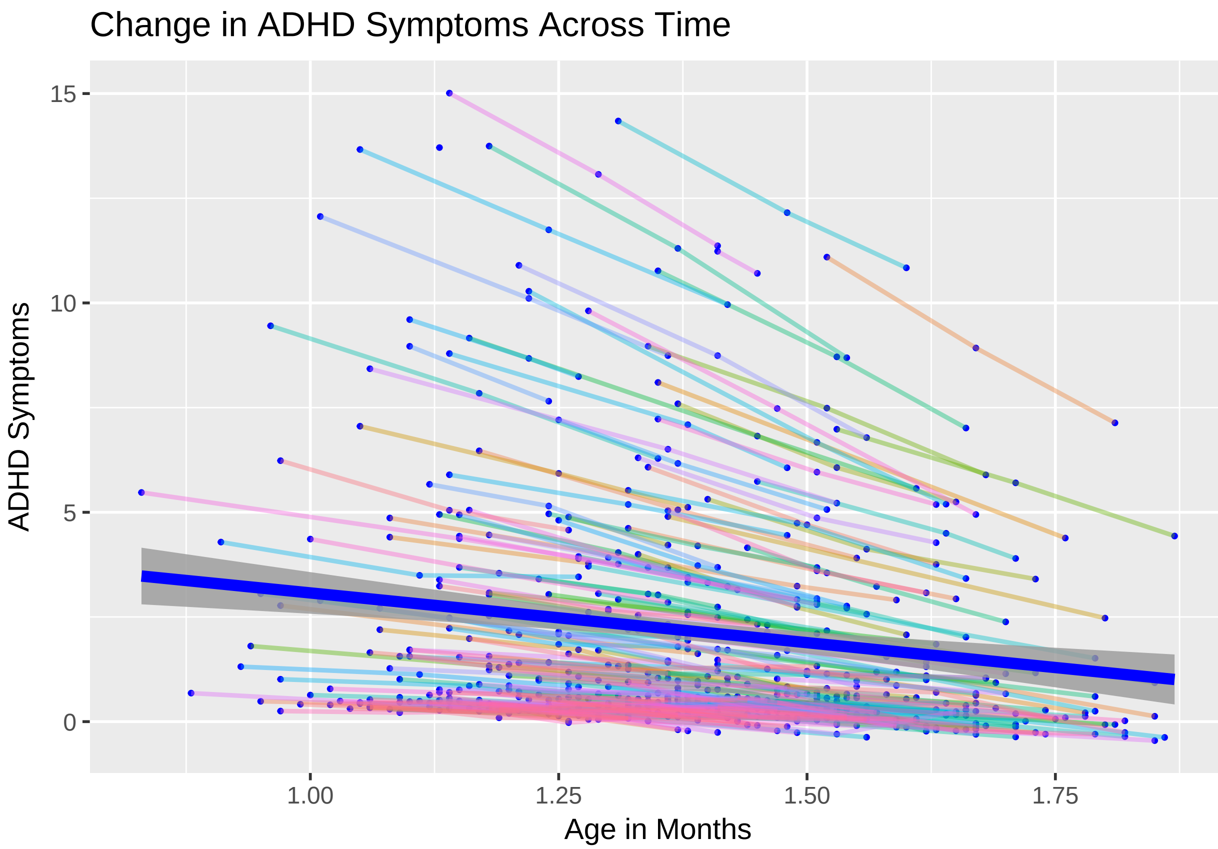
```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## ADHDsum ~ agemo_converted + Income_to_Need_Scan_c + (agemo_converted |
##     Subid_fMRI)
##    Data: PDS_data_2
##
## REML criterion at convergence: 2709.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.5957 -0.3202 -0.1196  0.2055  3.7449
##
## Random effects:
##  Groups     Name            Variance Std.Dev. Corr
##  Subid_fMRI (Intercept)     66.683   8.166
##             agemo_converted 16.112   4.014    -0.98
##  Residual                    3.476   1.864
## Number of obs: 554, groups:  Subid_fMRI, 209
##
## Fixed effects:
##                       Estimate Std. Error t value
## (Intercept)             6.5596     0.9934   6.603
## agemo_converted        -3.1322     0.6459  -4.849
## Income_to_Need_Scan_c  -0.2420     0.1295  -1.869
##
## Correlation of Fixed Effects:
##             (Intr) agm_cn
## agem_cnvrtd -0.977
```

```
## Incm_t_N_S_  0.230 -0.254
```

3. Graph both of your final models for the continuous and nominal models above.

Calculate confidence intervals around your estimates for your final models






```
## Computing profile confidence intervals ...

##                       2.5 %     97.5 %
## .sig01             5.894002 10.6846893
## .sig02            -1.000000 -0.9462445
## .sig03                   NA         NA
## .sigma                   NA         NA
## (Intercept)        5.124051  8.9261166
## agemo_converted   -4.695715 -2.2488878
## sex_c             -2.009822 -0.3610493

## Computing profile confidence intervals ...

##                           2.5 %      97.5 %
## .sig01                5.6991115 10.79504166
## .sig02               -1.0000000 -0.93767917
## .sig03                       NA          NA
## .sigma                       NA          NA
## (Intercept)           4.5999620  8.52969672
## agemo_converted      -4.4152518 -1.85632875
## Income_to_Need_Scan_c -0.5069412  0.02290092
```

4. Include both types of covariates in a single model. How does your interpretation of parameters change?

```r
mod.7 <- lmer(ADHDsum ~ agemo_converted + Income_to_Need_Scan_c + sex_c + (agemo_converted|Subid_fMRI),
summary(mod.7)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## ADHDsum ~ agemo_converted + Income_to_Need_Scan_c + sex_c + (agemo_converted |
##     Subid_fMRI)
##    Data: PDS_data_2
##
## REML criterion at convergence: 2701.8
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.4792 -0.3210 -0.1312  0.2327  3.8149
##
## Random effects:
##  Groups     Name            Variance Std.Dev. Corr
##  Subid_fMRI (Intercept)     69.497   8.336
##             agemo_converted 17.398   4.171    -0.98
##  Residual                    3.435   1.853
## Number of obs: 554, groups:  Subid_fMRI, 209
##
## Fixed effects:
##                         Estimate Std. Error t value
## (Intercept)               6.6245     0.9965   6.648
## agemo_converted          -3.1802     0.6476  -4.911
## Income_to_Need_Scan_c    -0.2444     0.1281  -1.907
## sex_c                    -1.1798     0.4150  -2.843
##
## Correlation of Fixed Effects:
##             (Intr) agm_cn I__N_S
## agem_cnvrtd -0.978
## Incm_t_N_S_  0.226 -0.250
## sex_c       -0.025  0.029 -0.007
```

```r
anova(mod.6, mod.7)
```

```
## refitting model(s) with ML (instead of REML)

## Data: PDS_data_2
## Models:
## mod.6: ADHDsum ~ agemo_converted + Income_to_Need_Scan_c + (agemo_converted |
## mod.6:     Subid_fMRI)
## mod.7: ADHDsum ~ agemo_converted + Income_to_Need_Scan_c + sex_c + (agemo_converted |
## mod.7:     Subid_fMRI)
##       Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## mod.6  7 2721.2 2751.4 -1353.6   2707.2
## mod.7  8 2715.2 2749.8 -1349.6   2699.2 8.0128      1   0.004645 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model 7 (including both covariates) appears to be a better fit since the AIC values are smaller.

5. If you have one available, introduce a time-varying covariate.

```
#time-varying covariate = MDD symptoms at each scan
mod.8 <- lmer(ADHDsum ~ agemo_converted + MDDCorescan + Income_to_Need_Scan_c + sex_c + (agemo_converte
summary(mod.8)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## ADHDsum ~ agemo_converted + MDDCorescan + Income_to_Need_Scan_c +
##     sex_c + (agemo_converted | Subid_fMRI)
##    Data: PDS_data_2
##
## REML criterion at convergence: 2637.8
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.2387 -0.4358 -0.0725  0.3033  3.4690
##
## Random effects:
##  Groups     Name            Variance Std.Dev. Corr
##  Subid_fMRI (Intercept)     34.80    5.899
##             agemo_converted  6.54    2.557    -0.98
##  Residual                    3.51    1.874
## Number of obs: 554, groups:  Subid_fMRI, 209
##
## Fixed effects:
##                       Estimate Std. Error t value
## (Intercept)            4.18752    0.92356   4.534
## agemo_converted       -2.31166    0.59687  -3.873
## MDDCorescan            0.55689    0.06316   8.817
## Income_to_Need_Scan_c -0.25229    0.12145  -2.077
## sex_c                 -1.04852    0.37086  -2.827
##
## Correlation of Fixed Effects:
##             (Intr) agm_cn MDDCrs I__N_S
## agem_cnvrtd -0.969
## MDDCorescan -0.271  0.134
## Incm_t_N_S_  0.213 -0.244  0.039
## sex_c       -0.038  0.038  0.029 -0.001
```

```
anova(mod.7, mod.8)
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: PDS_data_2
## Models:
## mod.7: ADHDsum ~ agemo_converted + Income_to_Need_Scan_c + sex_c + (agemo_converted |
## mod.7:     Subid_fMRI)
## mod.8: ADHDsum ~ agemo_converted + MDDCorescan + Income_to_Need_Scan_c +
## mod.8:     sex_c + (agemo_converted | Subid_fMRI)
##       Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
```

```
## mod.7  8 2715.2 2749.8 -1349.6   2699.2
## mod.8  9 2648.7 2687.6 -1315.4   2630.7 68.473      1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

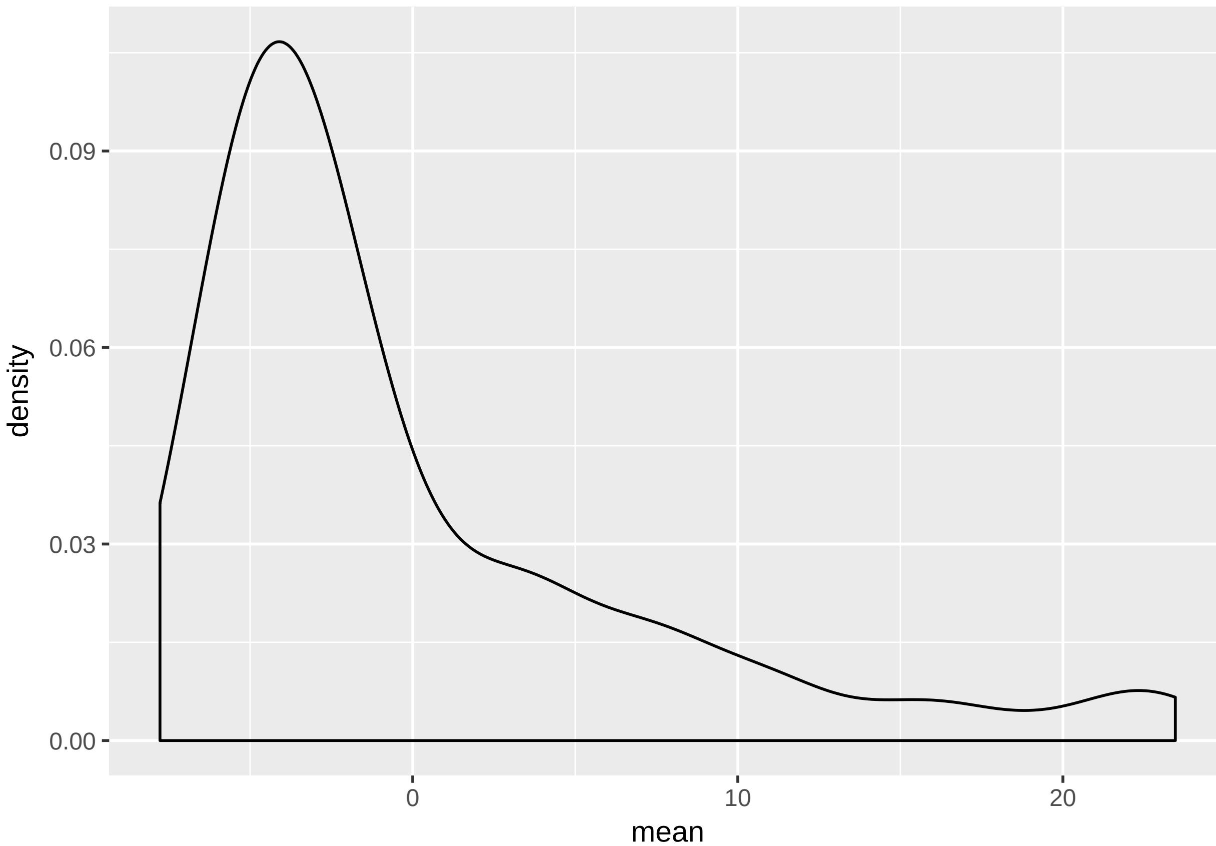
6. Create a density plot of the random effects from your final model.

```r
library(merTools)
re.sim <- REsim(mod.7)
head(re.sim)
```

```
##    groupFctr groupID        term      mean    median       sd
## 1 Subid_fMRI    L025 (Intercept) -4.906380 -4.984465 6.930962
## 2 Subid_fMRI    L027 (Intercept) 10.329766  9.927230 7.173690
## 3 Subid_fMRI    L029 (Intercept) -3.391491 -3.345723 6.809163
## 4 Subid_fMRI    L032 (Intercept) -4.507266 -4.827115 6.435547
## 5 Subid_fMRI    L039 (Intercept)  6.659549  6.837744 6.959220
## 6 Subid_fMRI    L041 (Intercept)  8.491120  8.879106 7.197817
```

```r
p.3 <- re.sim %>%
  filter(term == "(Intercept)")


ggplot(p.3, aes(mean)) +
  geom_density()
```


density
0.09
0.06
0.03
0.00
0
10
20
mean