Assignment 2: ALDA

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1 Reading the Data

We are going to perform the analyses on two datasets: the original email dataset, and a sample dataset that contains resting state data from 91 participants.

```
> cell = read.csv("cell_withitems_complete.csv", header = TRUE, sep = ",")
> alda_sample = read.csv("alda_sample.csv", header = TRUE, sep = ",")
> head(cell)
```

```
  X  ID Days ItemNo Memorablity Accuracy Messages
1 1 103   17      1  11.0000000        1       19
2 2 103   14      2   7.4285717        1        6
3 3 103   68      3  30.7142870        1       11
4 4 103  279      4  21.0000000        0        3
5 5 103   52      5  30.0000000        1        4
6 6 103  203      6   0.5714285        0        2
  RecallBeforeHint Vividness GuessedMonth NumItems Month
1                1        10            1       30     1
2                3        10            1       30     1
3                1         9            3       30     3
4                5         5            9       30    10
5                1        10            2       30     2
6                4         9            7       30     7
  TimeJudgmentDistance
1                    0
2                    0
3                    0
4                    1
5                    0
6                    0
```

```
> head(alda_sample)
```

```
  ID group time    CON CON_SAL CON_SMN7    DAN DAN_CON
1  6    PD    4 0.1929  0.0708   0.0088 0.1619  0.1156
2  6    PD    5 0.1949  0.0862   0.0040 0.1677  0.1173
3  6    PD    6 0.1811  0.0916  -0.0037 0.2153  0.1636
4 29    PD    4 0.1594  0.0438  -0.0253 0.1749  0.0161
5 29    PD    5 0.0881  0.0446  -0.0288 0.1356  0.0377
6 34  CTRL    4 0.1372  0.0113  -0.0792 0.1659  0.0045
  DAN_SAL DAN_SMN7   DMN6 DMN6_CON DMN6_DAN DMN6_SAL
1  0.0739   0.0041 0.1775  -0.1162  -0.1184  -0.1264
2  0.0812   0.0204 0.1512  -0.0709  -0.1177  -0.1214
3  0.1133   0.0155 0.1733  -0.0994  -0.1215  -0.1622
```

```
4  0.0621   0.0121 0.2145   0.0199  -0.1355  -0.0815
5  0.0277   0.0444 0.1338   0.0311  -0.0819  -0.0237
6 -0.0075   0.0432 0.1250   0.0493  -0.0893  -0.0539
  DMN6_SMN7    SAL SAL_SMN7   SMN7 wave       date Exclude
1   -0.0257 0.2097   0.0695 0.0352    1 2011-01-07    keep
2   -0.0342 0.2036   0.0453 0.0504    2 2011-12-19    keep
3   -0.0295 0.2024   0.0443 0.0135    3 2012-11-12    keep
4   -0.0998 0.2337   0.0552 0.1104    1 2011-10-03    keep
5   -0.0655 0.1229   0.0465 0.0761    2 2012-10-16    keep
6   -0.0655 0.1432   0.0072 0.1226    1 2011-10-27    keep
  RSNdata RSNexclude RSNexcludeDevDem  CogDate_0
1       1       keep             keep 2006-12-08
2       1       keep             keep 2006-12-08
3       1       keep             keep 2006-12-08
4       1       keep          exclude 2007-11-27
5       1       keep          exclude 2007-11-27
6       1       keep             keep 2008-04-17
  CCIRtrio_MR_date_0 Dur_PDsx_0 PIBpos18 Neuro_Dx
1               <NA>         NA     PIB-      iPD
2               <NA>         NA     PIB-      iPD
3               <NA>         NA     PIB-      iPD
4               <NA>         NA     PIB-      iPD
5               <NA>         NA     PIB-      iPD
6               <NA>         NA     PIB-       HC
  NeuroCDR_0 NeuroCDR_1 NeuroCDR_2 NeuroCDR_3 NeuroCDR_4
1   PD CDR=0  PD CDR=.5  PD CDR=.5   PD CDR=0  PD CDR=.5
2   PD CDR=0  PD CDR=.5  PD CDR=.5   PD CDR=0  PD CDR=.5
3   PD CDR=0  PD CDR=.5  PD CDR=.5   PD CDR=0  PD CDR=.5
4   PD CDR=0   PD CDR=0       <NA>  PD CDR=.5  PD CDR=.5
5   PD CDR=0   PD CDR=0       <NA>  PD CDR=.5  PD CDR=.5
6   HC CDR=0       <NA>       <NA>       <NA>   HC CDR=0
  NeuroCDR_5 NeuroCDR_6 NeuroCDR_7 NeuroCDR_8  YOB    Sex
1  PD CDR=.5  PD CDR=.5  PD CDR=.5 PD CDR=0.5 1937 female
2  PD CDR=.5  PD CDR=.5  PD CDR=.5 PD CDR=0.5 1937 female
3  PD CDR=.5  PD CDR=.5  PD CDR=.5 PD CDR=0.5 1937 female
4   PD CDR=1  PD CDR=.5       <NA>       <NA> 1935   male
5   PD CDR=1  PD CDR=.5       <NA>       <NA> 1935   male
6       <NA>   HC CDR=0       <NA>       <NA> 1944 female
  Ethnicity Education APOEs APOE4 Orig_MCBP_30to60    Asyn
1 caucasian        14    33     0      -0.084801180      NA
2 caucasian        14    33     0      -0.084801180      NA
3 caucasian        14    33     0      -0.084801180      NA
4 caucasian        14    23     0       0.001760821 3356.47
5 caucasian        14    23     0       0.001760821 3356.47
6 caucasian        12    33     0       0.105326328      NA
     Abeta Total_Tau      week Cog_rest_datediff
1       NA        NA 0.0000000                NA
2       NA        NA 0.9479452                NA
3       NA        NA 1.8493151                NA
4 1273.076   357.214 0.0000000                NA
5 1273.076   357.214 1.0383562                NA
6       NA        NA 0.0000000                NA
```

In the CELL data, the DV is TimeJudgmentDistance, and the IV is Days. The question we're trying to ask is, whether the estimate of the month of the email is farther or closer to the actual month depending on how many days have passed since the email was written. In the resting state data, we will use DMN6 as a dependent variable, and time as the independent variable, and the research question is whether DMN6 increases or decreases as a functon of time.

2 Linear Model for All Subjects

We first run a linear model for all the subjects:

CELL data

```
> library(lme4)
> cell_lm1 = lm(data = cell, TimeJudgmentDistance ~ Days)
> summary(cell_lm1)
```

```
Call:
lm(formula = TimeJudgmentDistance ~ Days, data = cell)

Residuals:
    Min      1Q  Median      3Q     Max 
-3.4125 -1.4466 -0.7086  0.3640 10.3797 

Coefficients:
             Estimate Std. Error t value Pr(>|t|)    
(Intercept) 0.6125055  0.1550466   3.950 8.45e-05 ***
Days        0.0078212  0.0008296   9.428  < 2e-16 ***
---
Signif. codes:  
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.557 on 845 degrees of freedom
Multiple R-squared:  0.09518,	Adjusted R-squared:  0.09411 
F-statistic: 88.89 on 1 and 845 DF,  p-value: < 2.2e-16
```

The average intercept is 0.6125 and indicates the distance between the actual month and the participant's estimate at day 0, i.e. if the email was sent on the day of the test, the estimate is 0.6125 months off. The average slope is 0.0078, and indicates that for every 1-day change, the distance will increase by 0.0078 months. This is a weak but positive association.

Sample Data

```
> sample_lm1 = lm(data = alda_sample, DMN6 ~ time)
> summary(sample_lm1)
```

```
Call:
lm(formula = DMN6 ~ time, data = alda_sample)

Residuals:
     Min       1Q   Median       3Q      Max 
-0.20666 -0.07126 -0.01532  0.05281  0.32706 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept)  0.2171926  0.0092565  23.464   <2e-16 ***
time        -0.0003761  0.0036769  -0.102    0.919    
---
Signif. codes:  
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.09631 on 223 degrees of freedom
```

```
Multiple R-squared:  4.691e-05,	Adjusted R-squared:  -0.004437
F-statistic: 0.01046 on 1 and 223 DF,  p-value: 0.9186
```

The average intercept is 0.2172 and indicates the value of the DMN6 measure and time 0. The average slope is -0.00037, and indicates that for every 1-year change in time, the value of DMN6 decreases by 0.0003 units. This is a very weak negative association.

3 MLM with Random Intercept

CELL Data

```
> cell_mlm1 = lmer(data = cell, TimeJudgmentDistance ~ 1 + (1|ID))
> summary(cell_mlm1)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: TimeJudgmentDistance ~ 1 + (1 | ID)
   Data: cell

REML criterion at convergence: 4076.6

Scaled residuals:
    Min      1Q  Median      3Q     Max
-0.8575 -0.5833 -0.2994  0.0677  4.2154

Random effects:
 Groups   Name        Variance Std.Dev.
 ID       (Intercept) 0.1551   0.3939
 Residual             7.0646   2.6579
Number of obs: 847, groups:  ID, 44

Fixed effects:
            Estimate Std. Error t value
(Intercept)   1.8150     0.1098   16.52
```

Note that the intercept-only model only takes into account the differences across subjects. We can also calculate the ICC for this model:

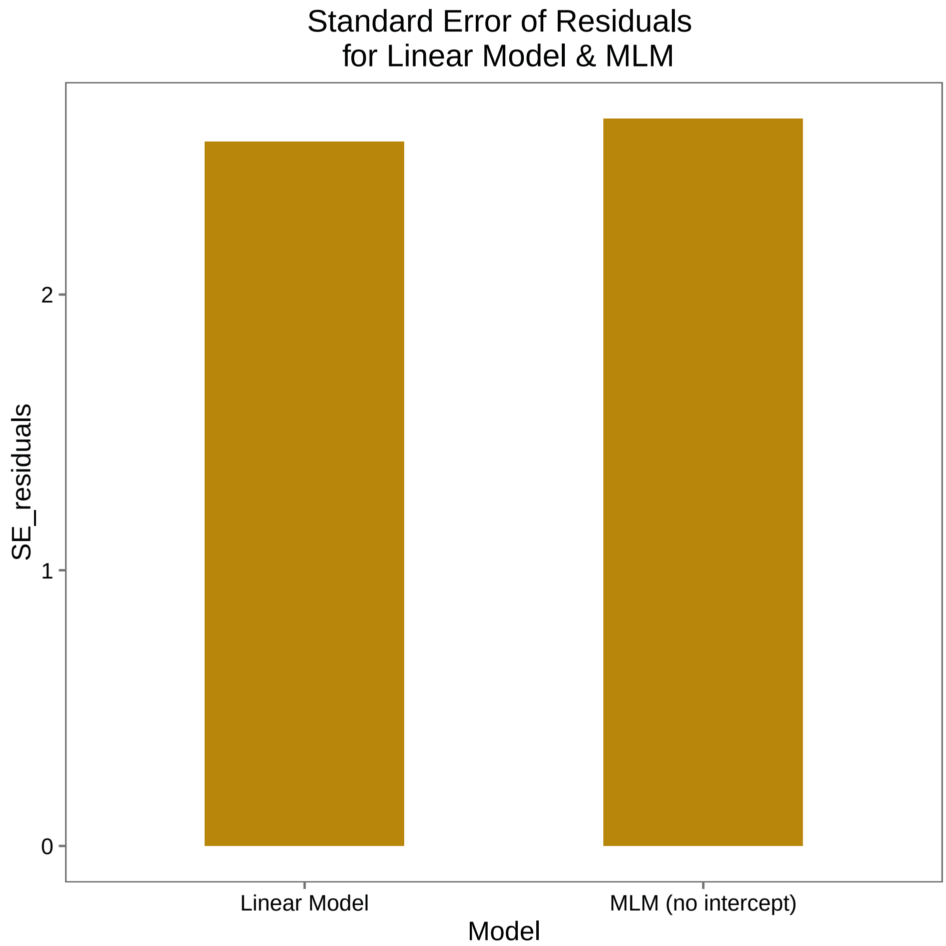
```
> cell_ICC = 0.1551/(0.1551+7.0646)
> print(cell_ICC)
```

```
[1] 0.02148289
```

Below, we compare the residual standard deviation from MLM1 to the residual standard error from the linear model.

```
> library(broom)
> library(ggplot2)
> library(ggthemes)
> cell_mlm1_fitted = augment(cell_mlm1, cell)
> cell_lm_fitted = augment(cell_lm1, cell)
> cell_residual_plot = matrix(nrow = 2, ncol = 2)
> colnames(cell_residual_plot) = c("Model", "SE_residuals")
> cell_residual_plot = as.data.frame(cell_residual_plot)
```

```
> cell_residual_plot$Model = c("Linear Model", "MLM (no intercept)")
> cell_residual_plot$SE_residuals = c(sd(cell_lm_fitted$.resid), sd(cell_mlm1_fitted$.resid))
> ggplot(cell_residual_plot, aes(x = Model, y = SE_residuals)) +
+   geom_bar(fill = "darkgoldenrod", stat = "identity", width = 0.5) +
+   theme_few()+
+   ggtitle("Standard Error of Residuals \n for Linear Model & MLM")
```



Note that the the residual SE is slightly larger in MLM1 (i.e. the intercept-only model), which means that there is more unexplained variance in the MLM than in the linear model.

Sample Data

```
> sample_mlm1 = lmer(data = alda_sample, DMN6 ~ 1 + (1|ID))
> summary(sample_mlm1)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: DMN6 ~ 1 + (1 | ID)
   Data: alda_sample

REML criterion at convergence: -514.7

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.83141 -0.53002 -0.05154  0.45287  2.99901

Random effects:
```

```
 Groups   Name        Variance Std.Dev.
 ID       (Intercept) 0.005944 0.07710
 Residual             0.002759 0.05253
Number of obs: 225, groups:  ID, 91

Fixed effects:
            Estimate Std. Error t value
(Intercept) 0.213057   0.008841    24.1
```

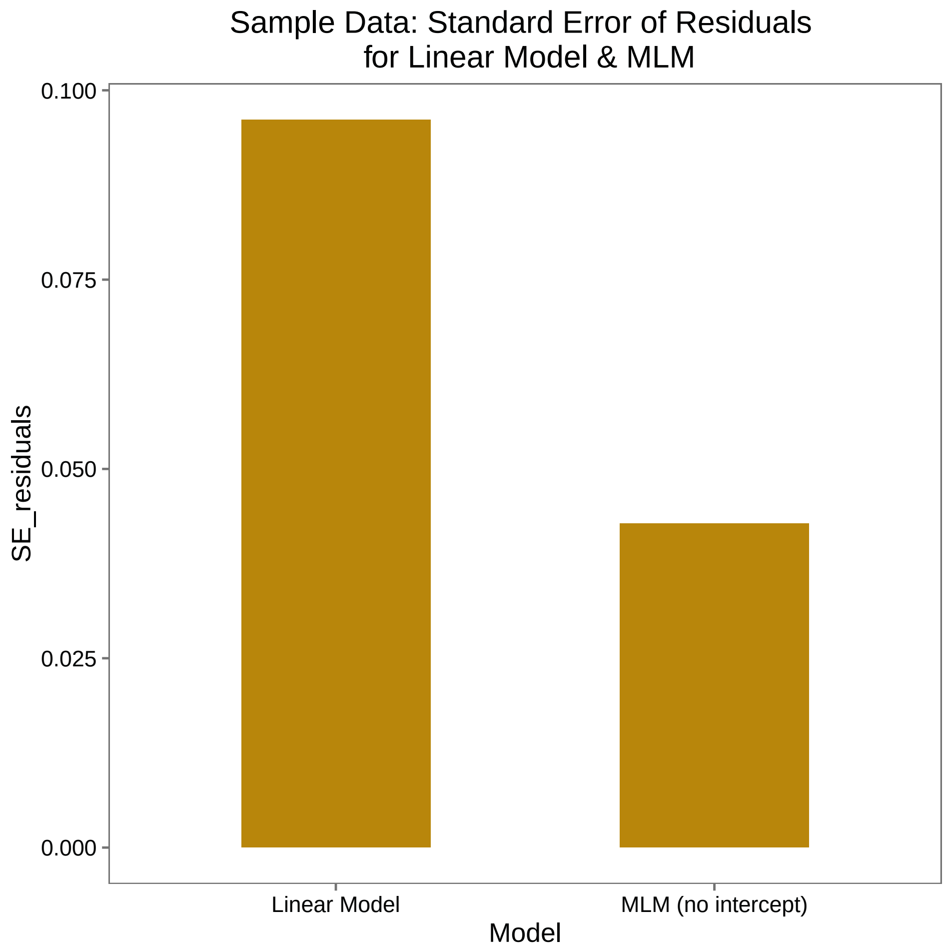
The ICC for this model is:

```
> sample_ICC = 0.005944/(0.005944 + 0.002759)
> print(sample_ICC)
```

```
[1] 0.6829829
```

Below, we compare the residual standard deviation from MLM1 to the residual standard error from the linear model.

```
> sample_mlm1_fitted = augment(sample_mlm1, alda_sample)
> sample_lm_fitted = augment(sample_lm1, alda_sample)
> sample_residual_plot = matrix(nrow = 2, ncol = 2)
> colnames(sample_residual_plot) = c("Model", "SE_residuals")
> sample_residual_plot = as.data.frame(sample_residual_plot)
> sample_residual_plot$Model = c("Linear Model", "MLM (no intercept)")
> sample_residual_plot$SE_residuals = c(sd(sample_lm_fitted$.resid), sd(sample_mlm1_fitted$.resid))
> ggplot(sample_residual_plot, aes(x = Model, y = SE_residuals)) +
+   geom_bar(fill = "darkgoldenrod", stat = "identity", width = 0.5) +
+   theme_few()+
+   ggtitle("Sample Data: Standard Error of Residuals \n for Linear Model & MLM")
```



In this case, the MLM residual standard error is much lower than the SE from the linear model.

4 Fixed Slope

CELL Data

We introduce a fixed slope term for Days in the model:

```
> cell_mlm2 = lmer(data = cell, TimeJudgmentDistance ~ Days + (1|ID))
> summary(cell_mlm2)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: TimeJudgmentDistance ~ Days + (1 | ID)
   Data: cell

REML criterion at convergence: 4002.1

Scaled residuals:
    Min      1Q  Median      3Q     Max
-1.4830 -0.5791 -0.2552  0.1900  4.2185

Random effects:
 Groups   Name        Variance Std.Dev.
 ID       (Intercept) 0.1891   0.4349
 Residual             6.3506   2.5200
Number of obs: 847, groups:  ID, 44
```

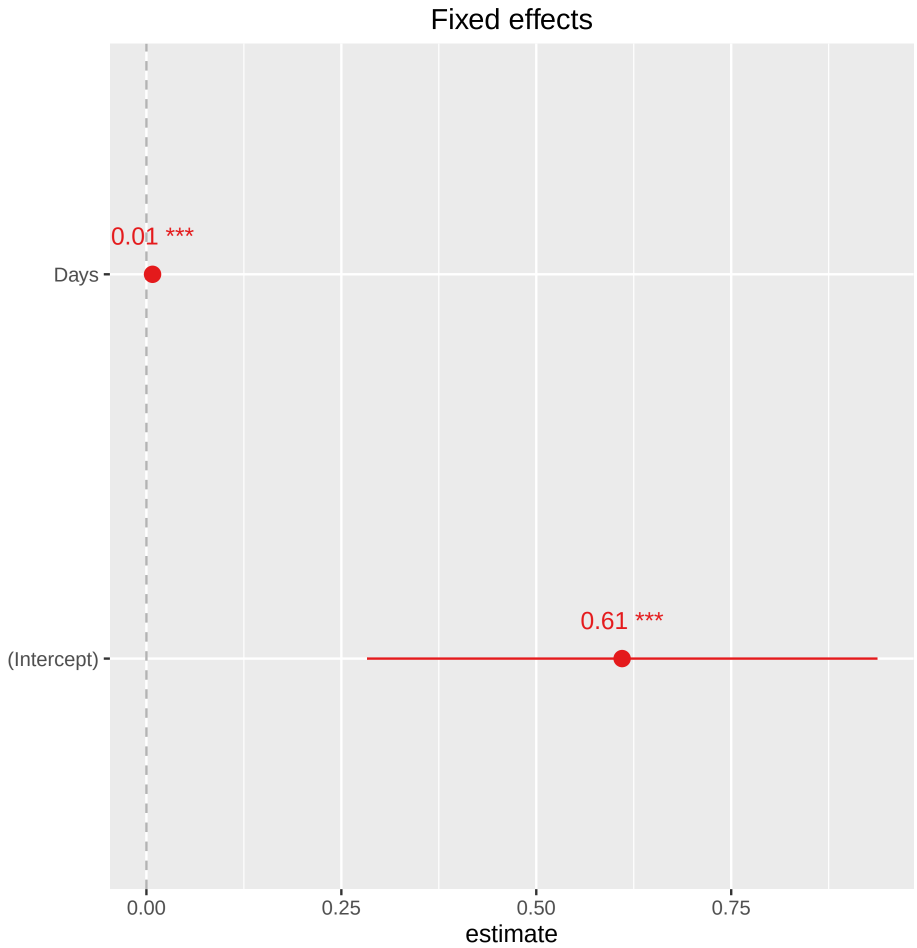
```
Fixed effects:
             Estimate Std. Error t value
(Intercept) 0.6100832  0.1668470   3.657
Days        0.0078864  0.0008239   9.572

Correlation of Fixed Effects:
     (Intr)
Days -0.754
```

Now, we have a fixed estimate of the change in TimeJudgmentDistance as a function of Days. This estimate is differnce from the previous estimate because now the regression line that we're fitting also has a slope. The intercept-only model fit parallel lines with slope 0 for each subject. This model fits lines with slope = 0.0078 for each subject. Note that the lines are still parallel, since this effect is fixed.

The residual standard error is now 6.35, in comparison to 7.06. Thus adding a predictor has reduced the residual standard error, or the unexplained variance in the model.

Below, we show the fixed effects estimates and the CIs around them using the sjPlot package (we can also use the confint function and manually make the plots):

```
> library(sjPlot)
> sjp.lmer(cell_mlm2, type = "fe")
```



Sample Data

```
> sample_mlm2 = lmer(data = alda_sample, DMN6 ~ time + (1|ID))
> summary(sample_mlm2)
```

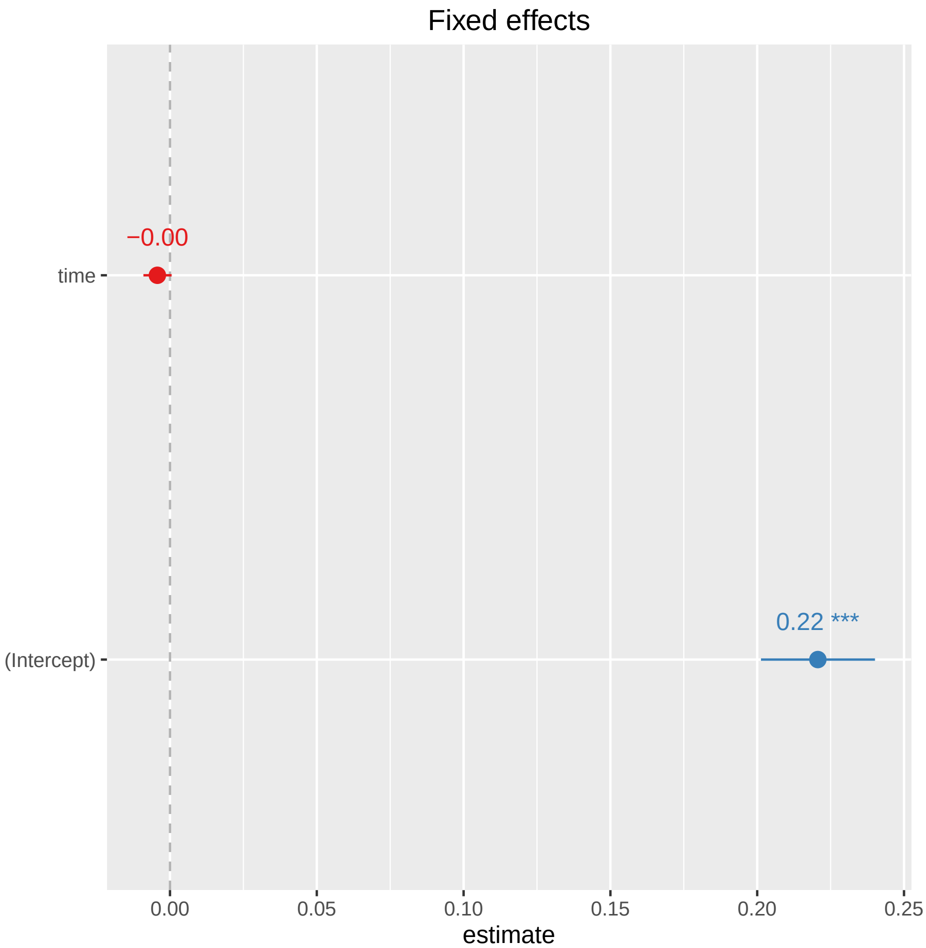
```
Linear mixed model fit by REML ['lmerMod']
Formula: DMN6 ~ time + (1 | ID)
   Data: alda_sample

REML criterion at convergence: -507.6

Scaled residuals:
    Min      1Q  Median      3Q     Max
-2.7370 -0.4612 -0.0904  0.4127  3.1761

Random effects:
 Groups   Name        Variance Std.Dev.
 ID       (Intercept) 0.006036 0.07769
 Residual             0.002699 0.05195
Number of obs: 225, groups:  ID, 91

Fixed effects:
             Estimate Std. Error t value
(Intercept)  0.220655   0.009857  22.385
time        -0.004297   0.002413  -1.781

Correlation of Fixed Effects:
     (Intr)
time -0.434
```

Just as in the previous case, this fixed effect estimate represents the slope of the regression line, and since there is only a fixed term for time and a random intercept for subject, each subject has the same slope but different intercepts i.e. the model produces a set of parallel lines with the slope = -0.00429.

The residual standard error is now 0.0026, and it was 0.0027 earlier. Thus, adding the new predictor has only slightly reduced the error variance.

Below, we plot the fixed effect:

```
> sjp.lmer(sample_mlm2, type = "fe")
```



5 Random Slope

CELL Data

We introduce a random slope term for Days in the model:

```
> cell_mlm3_1 = lmer(data = cell, TimeJudgmentDistance ~ Days + (Days|ID))
> summary(cell_mlm3_1)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: TimeJudgmentDistance ~ Days + (Days | ID)
   Data: cell

REML criterion at convergence: 3966

Scaled residuals:
    Min      1Q  Median      3Q     Max
-2.2453 -0.5440 -0.2062  0.1900  4.1650

Random effects:
 Groups   Name        Variance  Std.Dev. Corr
 ID       (Intercept) 7.344e-02 0.270989
          Days        3.124e-05 0.005589 -1.00
 Residual             5.877e+00 2.424338
Number of obs: 847, groups:  ID, 44
```

```
Fixed effects:
            Estimate Std. Error t value
(Intercept) 0.596585   0.153988   3.874
Days        0.008164   0.001184   6.898

Correlation of Fixed Effects:
     (Intr)
Days -0.739
convergence code: 0
Model failed to converge with max|grad| = 0.013951 (tol = 0.002, component 1)
Model is nearly unidentifiable: very large eigenvalue
 - Rescale variables?
```

```
> ##model fails to converge. we rescale Days.
>
> cell$zDays = scale(cell$Days, scale = TRUE, center = TRUE)
> cell_mlm3_2 = lmer(data = cell, TimeJudgmentDistance ~ zDays + (zDays|ID))
> summary(cell_mlm3_2)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: TimeJudgmentDistance ~ zDays + (zDays | ID)
   Data: cell

REML criterion at convergence: 3956.7

Scaled residuals:
    Min      1Q  Median      3Q     Max
-2.2453 -0.5440 -0.2062  0.1900  4.1650

Random effects:
 Groups   Name        Variance Std.Dev. Corr
 ID       (Intercept) 0.3478   0.5897
          zDays       0.3507   0.5922   1.00
 Residual             5.8774   2.4243
Number of obs: 847, groups:  ID, 44

Fixed effects:
            Estimate Std. Error t value
(Intercept)   1.8538     0.1242  14.927
zDays         0.8650     0.1254   6.898

Correlation of Fixed Effects:
      (Intr)
zDays 0.551
```

Introducing the random slope term allows each subject to have a different slope and intercept. In comparison to the previous model the residual variance is lower and therefore, we can say that more variance is being explained by this model. Hence, we keep the random slope. We can also compare the two models to see if the second model is a better fit:

```
> anova(cell_mlm2, cell_mlm3_2)
```

```
Data: cell
Models:
```

```
cell_mlm2: TimeJudgmentDistance ~ Days + (1 | ID)
cell_mlm3_2: TimeJudgmentDistance ~ zDays + (zDays | ID)
            Df    AIC    BIC  logLik deviance  Chisq Chi Df
cell_mlm2    4 3995.1 4014.1 -1993.5   3987.1
cell_mlm3_2  6 3963.7 3992.1 -1975.8   3951.7 35.407      2
            Pr(>Chisq)
cell_mlm2
cell_mlm3_2  2.049e-08 ***
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

This test tells us that the mlm3 fits the data better.

Sample Data

```
> sample_mlm3 = lmer(data = alda_sample, DMN6 ~ time + (time|ID))
> summary(sample_mlm3)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: DMN6 ~ time + (time | ID)
   Data: alda_sample

REML criterion at convergence: -512.8

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.43325 -0.42316 -0.04733  0.34412  2.72929

Random effects:
 Groups   Name        Variance Std.Dev. Corr
 ID       (Intercept) 0.005864 0.07658
          time        0.000180 0.01342  -0.09
 Residual             0.002135 0.04620
Number of obs: 225, groups:  ID, 91

Fixed effects:
             Estimate Std. Error t value
(Intercept)  0.222121   0.009504  23.372
time        -0.005727   0.002721  -2.105

Correlation of Fixed Effects:
     (Intr)
time -0.381
```

Just as before, the random slope term introduces a slope for each subject. The residual variance now is 0.002135, in comparison to 0.002699, which shows a slight decrease in the unexplained variance. We can also statistically test if this model is a better fit than the previous one:

```
> anova(sample_mlm2, sample_mlm3)
```

```
Data: alda_sample
Models:
sample_mlm2: DMN6 ~ time + (1 | ID)
sample_mlm3: DMN6 ~ time + (time | ID)
```

```
           Df     AIC    BIC logLik deviance  Chisq Chi Df
sample_mlm2  4 -517.47 -503.8 262.73  -525.47
sample_mlm3  6 -518.40 -497.9 265.20  -530.40 4.9342      2
           Pr(>Chisq)
sample_mlm2
sample_mlm3    0.08483 .
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

This shows that the new model is only a marginally better fit than the previous model. Thus, the random slopes do not add a lot, but we will still keep them.

6 Correlation between Intercept and Slope

The correlation between the slope and intercept tells us something about how a predictor might influence these variables, and essentially the regression line. For example, if the correlation between the slope and intercept is positive, then the predictor will move both in the same direction. On the other hand, if the slope and intercept have a negative correlation, then they will move in the opposite direction with the increase in the predictor.

For the CELL data, we see that the correlation between the slope and intercept is positive, i.e. the slope and intercept move in the same direction. For the sample data, the correlation is negative, i.e. the slope and intercept move in opposite directions.

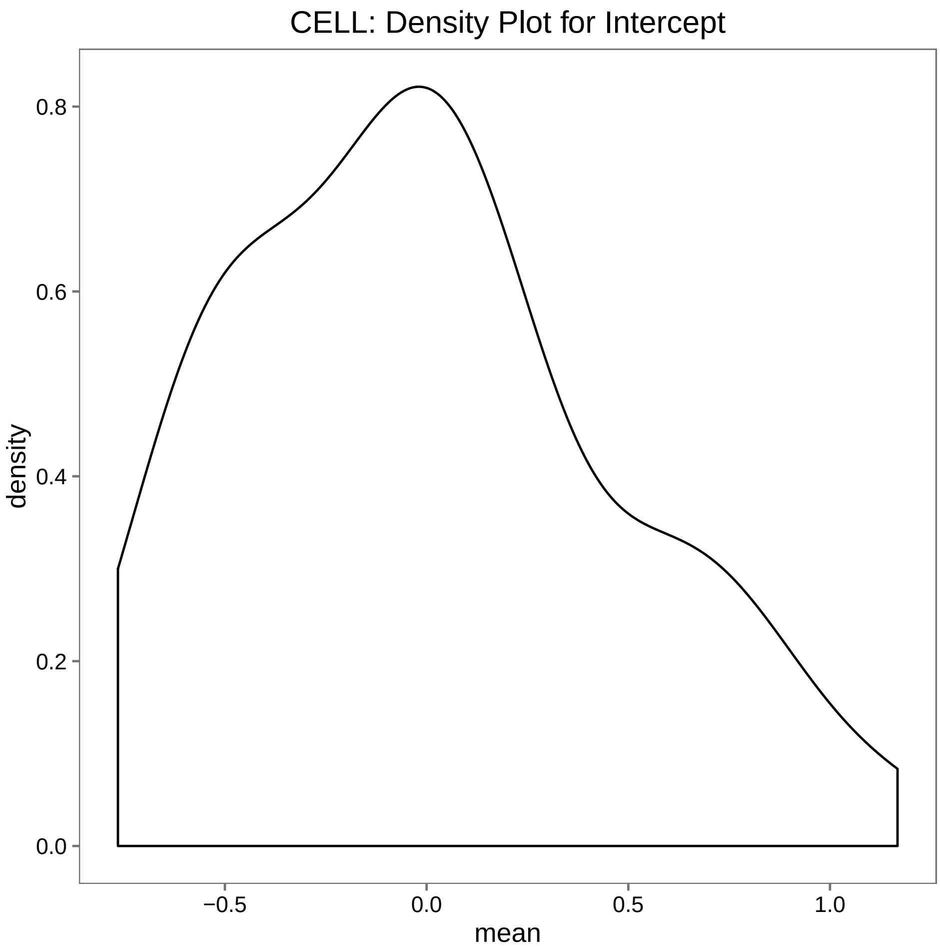
7 Density Plot of Random Effects

Below is the density plot for the random effects:

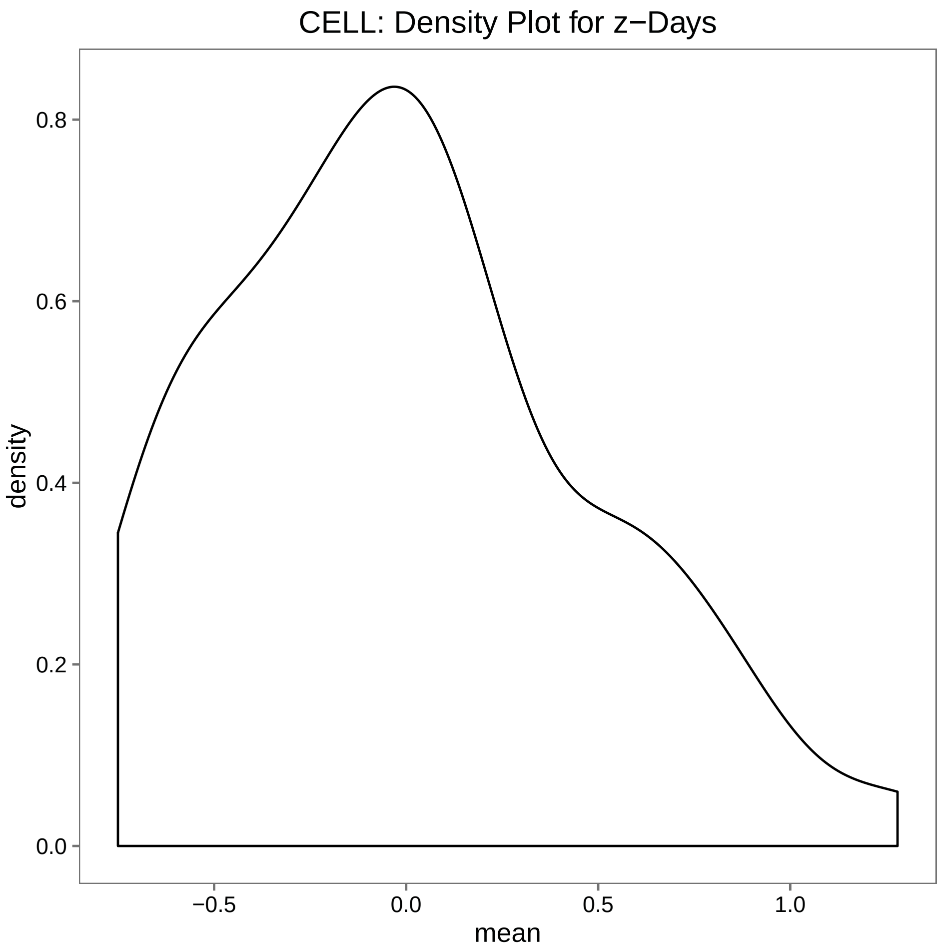
```
> library(merTools)
> cell_re.sim = REsim(cell_mlm3_2)
> sample_re.sim = REsim(sample_mlm3)
> cell_fe.sim = FEsim(cell_mlm3_2)
> sample_fe.sim = FEsim(sample_mlm3)
```

CELL data

```
> library(ggplot2)
> cell_g1 <- cell_re.sim %>%
+   filter(term == "(Intercept)")
> ggplot(cell_g1, aes(mean)) +
+   geom_density() +
+     theme_few()+
+   ggtitle("CELL: Density Plot for Intercept")
```

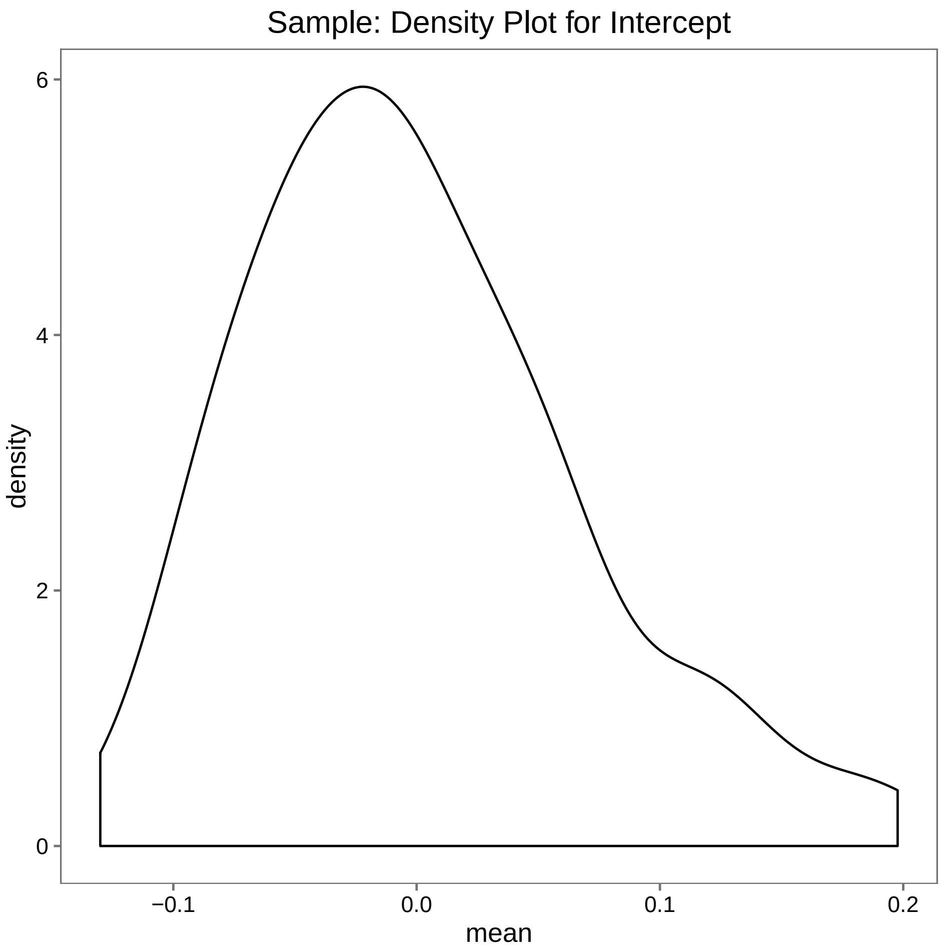



```
> cell_g2 <- cell_re.sim %>%
+   filter(term == "zDays")
> ggplot(cell_g2, aes(mean)) +
+   geom_density() +
+     theme_few()+
+   ggtitle("CELL: Density Plot for z-Days")
```

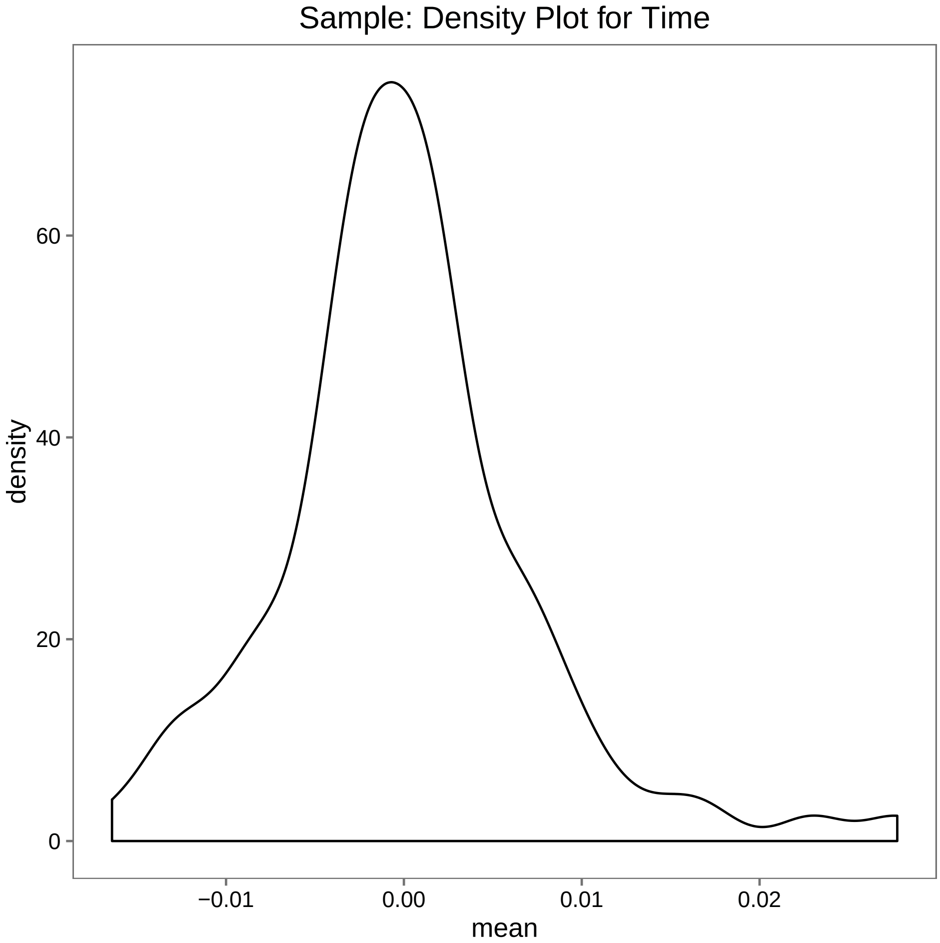


Sample data

```
> library(ggplot2)
> library(ggthemes)
> sample_g1 <- sample_re.sim %>%
+   filter(term == "(Intercept)")
> ggplot(sample_g1, aes(mean)) +
+   geom_density() +
+     theme_few()+
+   ggtitle("Sample: Density Plot for Intercept")
```



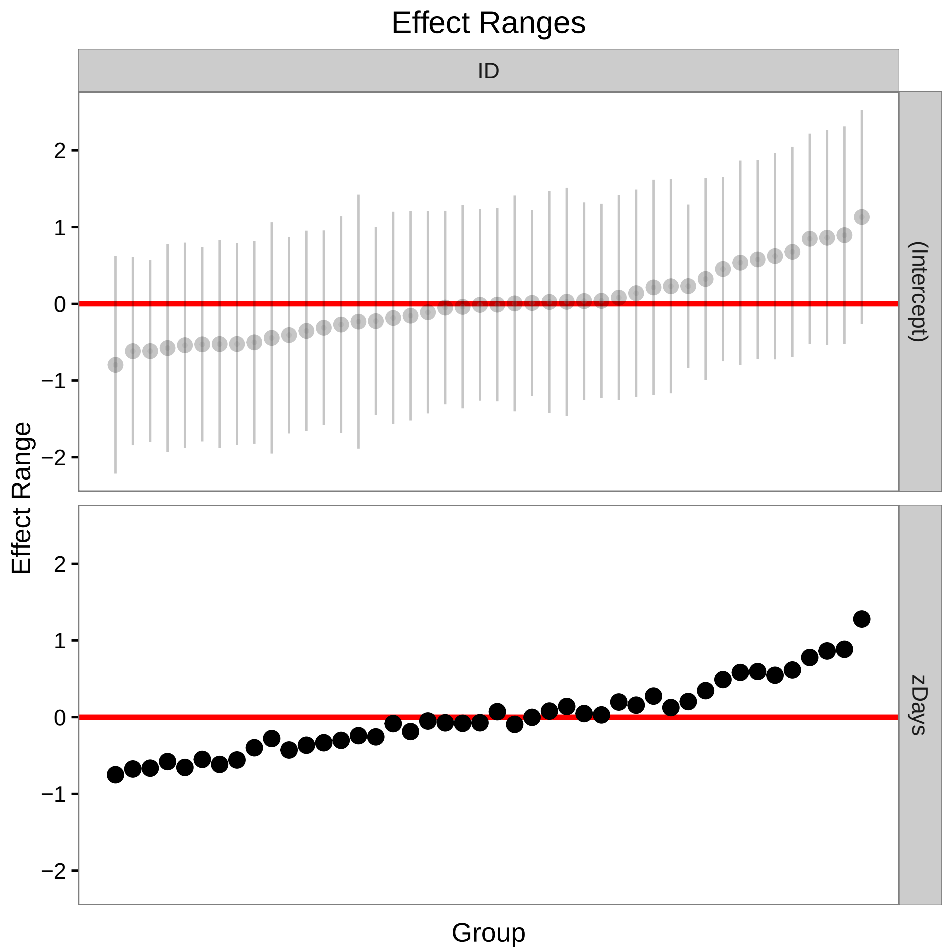

```
> sample_g2 <- sample_re.sim %>%
+   filter(term == "time")
> ggplot(sample_g2, aes(mean)) +
+   geom_density() +
+     theme_few()+
+   ggtitle("Sample: Density Plot for Time")
```



8 Caterpillar Plot of Random Effects

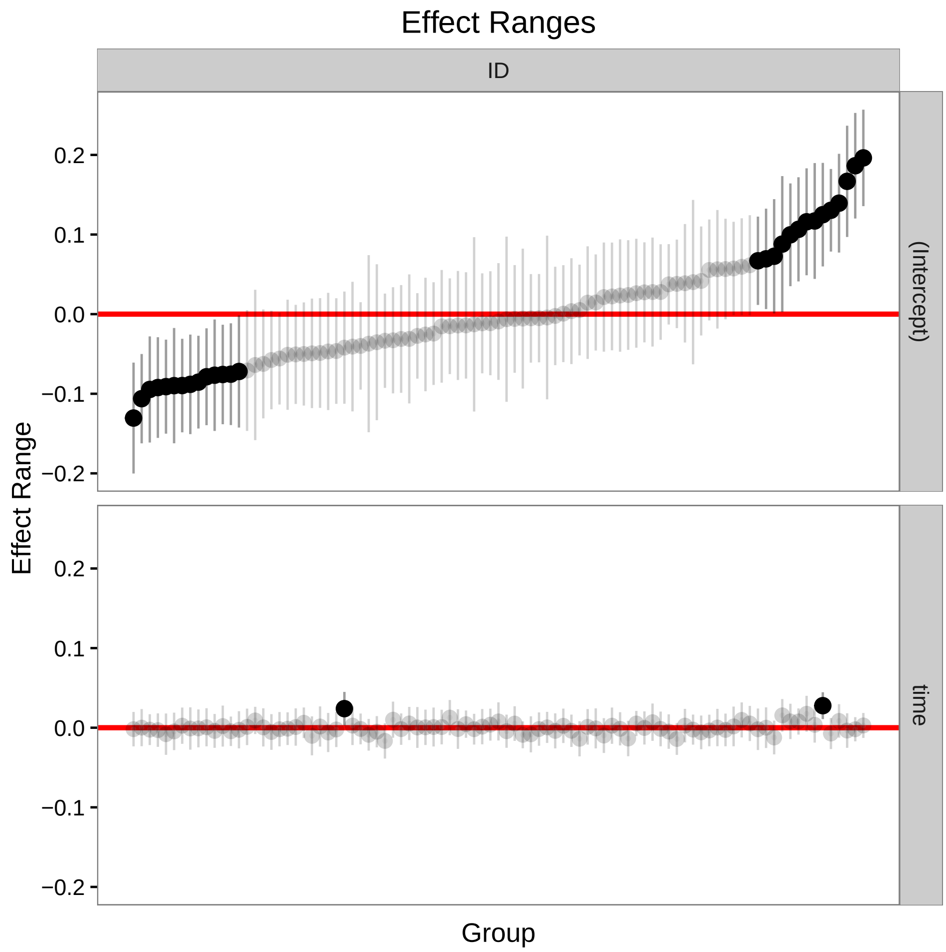
CELL data

```
> cell_p1 = plotREsim(cell_re.sim)
> cell_p1
```



Sample data

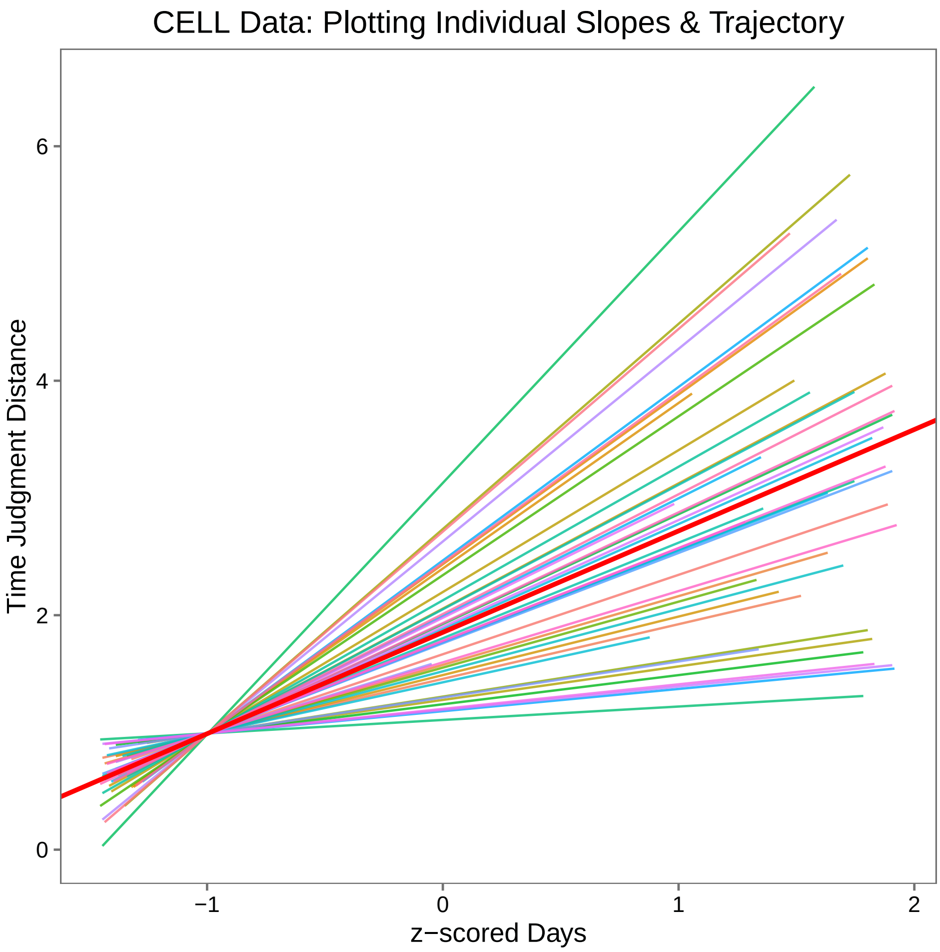
```
> sample_p1 = plotREsim(sample_re.sim)
> sample_p1
```



9 Plotting Trajectories

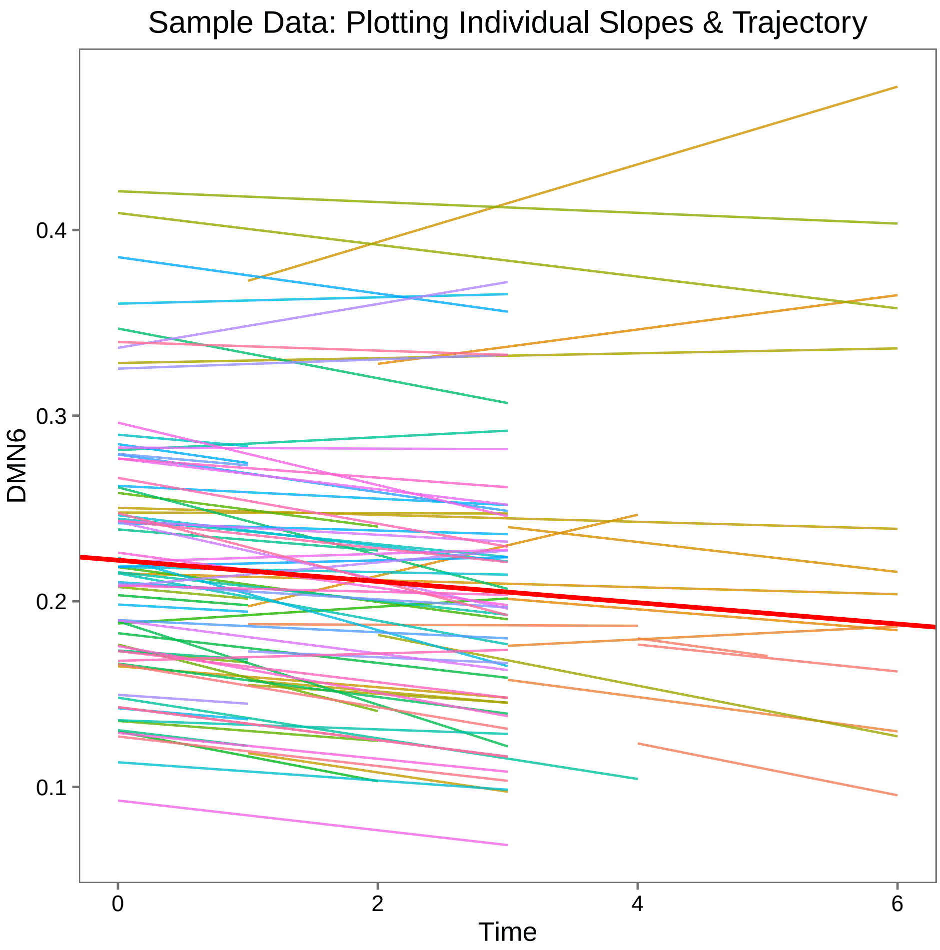
CELL data

```
> library(broom)
> cell_fittedvalues = augment(cell_mlm3_2, cell)
> cell_fittedvalues$ID = as.factor(cell_fittedvalues$ID)
> ggplot(cell_fittedvalues, aes(x = zDays, y = .fitted)) +
+   geom_line(aes(color = ID), show.legend = F, alpha = 0.8 ) +
+   geom_abline(slope = 0.8650, intercept = 1.8538,
+               color = "red", size = 1)+
+   theme_few()+
+   xlab("z-scored Days") + ylab("Time Judgment Distance") +
+   ggtitle("CELL Data: Plotting Individual Slopes & Trajectory")
```



Sample data

```
> library(broom)
> sample_fittedvalues = augment(sample_mlm3, alda_sample)
> sample_fittedvalues$ID = as.factor(sample_fittedvalues$ID)
> ggplot(sample_fittedvalues, aes(x = time, y = .fitted)) +
+   theme_few()+
+   geom_line(aes(color = ID), show.legend = F, alpha = 0.8 ) +
+   geom_abline(slope = -0.005727, intercept = 0.222121,
+               color = "red", size = 1)+
+   xlab("Time") + ylab("DMN6") +
+   ggtitle("Sample Data: Plotting Individual Slopes & Trajectory")
>
```


Sample Data: Plotting Individual Slopes & Trajectory
DMN6
0.4
0.3
0.2
0.1
0
2
4
6
Time