# Longitudinal Data: Repeated Measures

Mixed Models 1

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Oct 25, 2018

#### Read in data

```
dat1 = read csv("deeks_ex1.csv")
## Parsed with column specification:
## cols(
## id = col_integer(),
## cd4 = col_integer(),
## binage = col_integer()
## )
tbl df(dat1)
## # A tibble: 594 x 3
       id cd4 binage
     <int> <int> <int>
##
       1 45
     1 119
## 3 2 196
## 4 2 369
## 5 4 29
## 6 4 137
## 7 5 84
     5 93
## 9
     7 246
                  0
     7 439
## # ... with 584 more rows
```

# Binary time-independent variable (balanced

data)

#### Random Intercept Model

```
# random intercept
lme_1 <- lmer(cd4 - binage + (1 | id), data = dat1)
summary(lme_1)</pre>
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: cd4 ~ binage + (1 | id)
##
     Data: dat1
##
## REML criterion at convergence: 7445.8
##
## Scaled residuals:
## Min 1Q Median
                                   Max
                             3Q
## -2.7471 -0.3915 -0.1013 0.3812 3.3980
##
## Random effects:
## Groups Name
                      Variance Std.Dev.
          (Intercept) 24883 157.74
## id
## Residual
                       5095 71.38
## Number of obs: 594, groups: id. 297
##
## Fixed effects:
            Estimate Std. Error t value
## (Intercept) 225.90 13.39 16.871
## binage 24.24 19.23 1.261
##
## Correlation of Fixed Effects:
        (Intr)
## binage -0.696
```

## 0.830038

```
library(sjstats)
# ICC - var(b0i)/(var(b0i)+var(eij))
icc(lme_1)
##
## Linear mixed model
##
## Family : gaussian (identity)
## Formula: cd4 ~ binage + (1 | id)
##
   ICC (id): 0.8300
##
AIC(lme_1)
## [1] 7453.81
# Now do by grabbing relevant objects
rand_vars1 <- re var(lme_1)
rand vars1
         Within-group-variance: 5095.062
##
        Between-group-variance: 24882.595 (id)
##
rand vars1[2]/(rand vars1[1] + rand vars1[2])
## id_tau.00
```

#### Random intercept and slope model

```
# random slope - try it, it won't work (not identifiable,
# why) lme_1b <- lmer(cd4 ~ (binage/id), data=dat1)</pre>
```

Binary time-dependent variable (balanced data)

#### Read in data

```
dat2 = read csv("deeks_ex2.csv")
## Parsed with column specification:
## cols(
## id = col_integer(),
## cd4 = col_integer(),
## medvl = col_integer()
## )
tbl df(dat2)
## # A tibble: 142 x 3
##
       id cd4 medvl
     <int> <int> <int>
##
     16 449
     16 226
## 3 18 294
## 4 18 138
## 5 21 132
## 6 21 132
## 7 26 324
## 8
     26 500
                   0
## 9
     30 216
       30 254
## # ... with 132 more rows
```

#### Random Intercept Model

```
# random intercept
lme_2 <- lmer(cd4 ~ medvl + (1 | id), data = dat2)
summary(lme_2)</pre>
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: cd4 ~ medvl + (1 | id)
     Data: dat2
##
## REML criterion at convergence: 1808.9
##
## Scaled residuals:
      Min 1Q Median
                                    Max
## -2.0055 -0.4830 -0.0936 0.4303 3.2651
##
## Random effects:
## Groups Name
                       Variance Std.Dev.
## id
           (Intercept) 23820 154.34
## Residual
                        8960 94.66
## Number of obs: 142, groups: id, 71
##
## Fixed effects:
             Estimate Std. Error t value
## (Intercept) 310.66 21.49 14.458
## medvl
           -48.28 15.89 -3.039
##
## Correlation of Fixed Effects:
        (Intr)
## medvl -0.370
```

```
# ICC - var(b0i)/(var(b0i)+var(eij))
icc(lme_2)
##
## Linear mixed model
##
## Family : gaussian (identity)
## Formula: cd4 ~ medvl + (1 | id)
##
##
   ICC (id): 0.7267
AIC(lme 2)
## [1] 1816.93
# Now do by grabbing relevant objects
rand_vars2 <- re var(lme_2)
rand_vars2
##
         Within-group-variance: 8960.088
##
        Between-group-variance: 23820.260 (id)
rand vars2[2]/(rand vars2[1] + rand vars2[2])
```

```
## id_tau.00
## 0.7266628
```

#### Random intercept and slope model

```
# random slope also not identifiable here lme_2b <- lmer(cd4
# ~ (medvl/id), data=dat2)</pre>
```

Continuous time-dependent variables (very unbalanced data)

#### Read in data

1 74

1 95

1 120

1 209

1 137

375

NA

## # ... with 11,290 more rows

## 5

## 8

## 9

## 10

##

## 6

2.70

2.70

2.70

2.70

2.70

2.70

2.70

2.50

NΑ

NΑ

NΑ

NΑ

1.17

2.38

```
dat3 = read csv("deeks ex3.csv")
## Parsed with column specification:
## cols(
## id = col_integer(),
## cd4 = col_integer(),
## logvlbase = col double().
## logvlchange = col_double()
## )
tbl_df(dat3)
## # A tibble: 11,300 x 4
##
           cd4 logvlbase logvlchange
##
     <int> <int>
                  <db1>
                              <db1>
   1
        1 45
                2.70
                               0
##
                2.70
        1 119
##
                             2.52
## 3 1 113
                2.70
                              NA
```

#### Random Intercept Model

```
# random intercept
lme_3 <- lmer(cd4 ~ logvlbase + logvlchange + (1 | id), data = dat3)
summary(lme_3)</pre>
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: cd4 ~ logvlbase + logvlchange + (1 | id)
##
     Data: dat3
##
## REML criterion at convergence: 87637.8
##
## Scaled residuals:
      Min
               1Q Median
                                     Max
## -4.7739 -0.5248 -0.0489 0.4548 8.6669
##
## Random effects:
## Groups
            Name
                       Variance Std.Dev.
            (Intercept) 35011 187.1
## id
## Residual
                       11750 108.4
## Number of obs: 7053, groups: id, 406
##
## Fixed effects:
              Estimate Std. Error t value
##
## (Intercept) 506.539 34.484 14.689
## logvlbase -52.051 8.141 -6.393
## logvlchange -53.463 1.855 -28.815
##
## Correlation of Fixed Effects:
##
             (Intr) lgvlbs
## logvlbase -0.961
## logvlchange -0.146 0.184
```

```
# ICC - var(b0i)/(var(b0i)+var(eij))
icc(lme 3)
## Linear mixed model
##
## Family : gaussian (identity)
## Formula: cd4 ~ logvlbase + logvlchange + (1 | id)
##
##
   TCC (id): 0.7487
AIC(lme 3)
## [1] 87647.77
# Now do by grabbing relevant objects
rand_vars3 <- re_var(lme_3)
rand vars3
```

```
## Within-group-variance: 11749.751
## Between-group-variance: 35010.755 (id)
```

### Random intercept and slope model

```
# random slope also not identifiable here
lme_3b <- lmer(cd4 - logvlbase + logvlchange + (logvlchange |
   id), data = dat3)
summary(lme_3b)</pre>
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: cd4 ~ logvlbase + logvlchange + (logvlchange | id)
     Data: dat3
##
##
## REML criterion at convergence: 87345.9
##
## Scaled residuals:
      Min
              10 Median
                              30
                                     Max
## -5.1119 -0.5016 -0.0558 0.4388 9.0926
##
## Random effects:
## Groups Name
                       Variance Std.Dev. Corr
## id
           (Intercept) 27039 164.43
            logvlchange 1703 41.27
##
                                        -0.59
                       10979 104.78
## Residual
## Number of obs: 7053, groups: id, 406
##
## Fixed effects:
              Estimate Std. Error t value
## (Intercept) 553.885
                          28.978 19.114
                       6.955 -9.588
## logvlbase -66.685
## logvlchange -54.153
                       2.982 -18.160
##
## Correlation of Fixed Effects:
##
            (Intr) lgvlbs
## logvlbase -0.956
## logvlchange -0.167 0.080
```

##

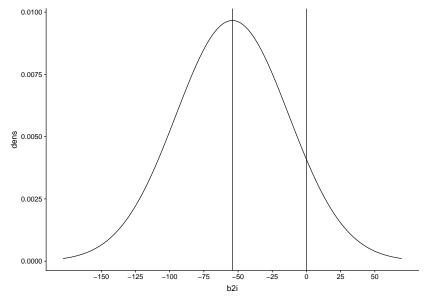
```
icc(lme_3b)
## Caution! ICC for random-slope-intercept models usually not meaningful. See 'Note' in `?icc`.
##
## Linear mixed model
##
## Family : gaussian (identity)
## Formula: cd4 ~ logvlbase + logvlchange + (logvlchange | id)
##
##
   ICC (id): 0.7112
AIC(lme 3b)
## [1] 87359.87
rand_vars3b <- re var(lme_3b)
rand vars3b
##
         Within-group-variance: 10978.987
##
        Between-group-variance: 27038.505 (id)
```

Random-slope-variance: 1703.276 (id.logvlchange)

Slope-Intercept-covariance: -3976.494 (id.(Intercept))

## Slope-Intercept-correlation: -0.586 (id)

Reporting the estimated distribution of associations from random coefficients model.



# Which model does one choose (3 or 3b)?

```
## df AIC ## lme_3 5 87647.77 ## lme_3b 7 87359.87
```

- The random intercept and slope model has lower AIC and thus fits the data relatively better than the random intercept model alone.