Greg Finkelberg: HW07

Loading packages

```
library(ggplot2)
library(lme4)
library(Matrix)
library(tidyverse)
```

Trajectory plot

```
tlc.data <- read.table("C:/Users/Greg/Downloads/tlc-data.txt", quote="\"",
comment.char="")

new_col_names <- c("subject_ID", "group", "lead_level_baseline",
"lead_level_1week", "lead_level_4weeks", "lead_level_6weeks")

colnames(tlc.data) <- new_col_names

tlc_long <- tlc.data %>%
  gather(key = "week", value = "lead_level", lead_level_baseline,
  lead_level_1week, lead_level_4weeks, lead_level_6weeks)

tlc_long <- tlc_long %>%
  mutate(week = case_when(
   week == "lead_level_baseline" ~ 0,
   week == "lead_level_1week" ~ 1,
   week == "lead_level_4weeks" ~ 4,
   week == "lead_level_6weeks" ~ 6,
   TRUE ~ as.numeric(as.character(week))))

ggplot(tlc_long, aes(x = week, y = lead_level, group = subject_ID, color =
group)) +
  geom_line() +
  labs(x = "Week", y = "Lead Level", color = "Group") +
  ggtitle("Lead Level Trajectories by Group") +
  theme_minimal()
```

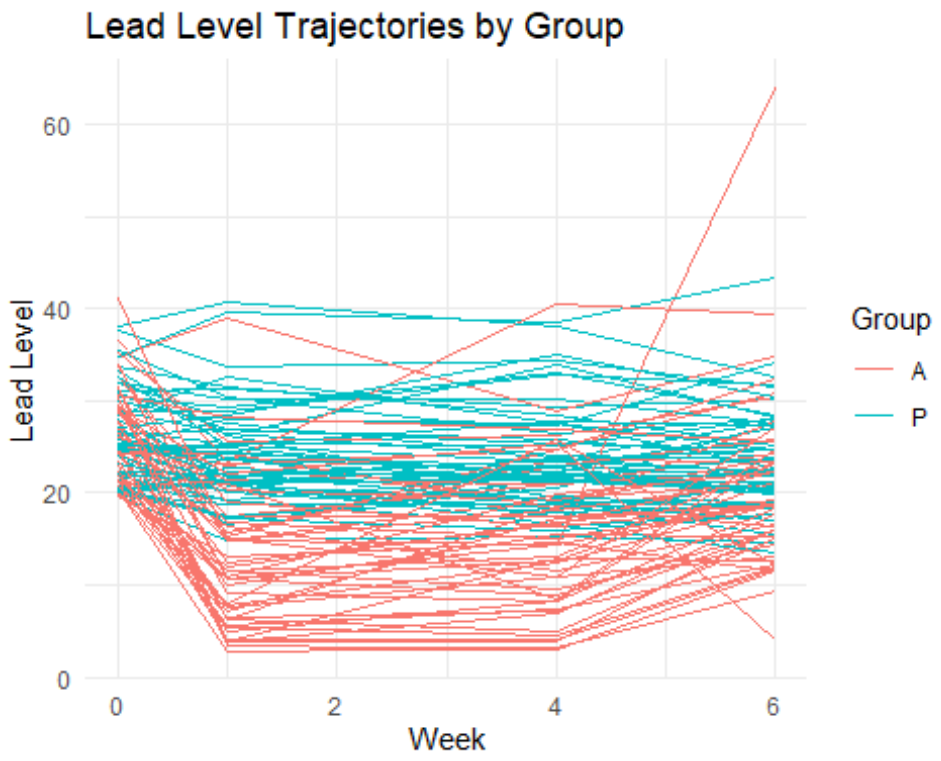

Figure 1.

Visually, it looks like the new agent is successful at reducing lead content in the blood up to about 4 weeks, when it starts to increase again. There also appears to be a lot more variability in the new agent group.

Mixed effect model (random intercept)

```
model <- lmer(lead_level ~ week + (1 | group), data = tlc_long)
summary(model)

Linear mixed model fit by REML ['lmerMod']
Formula: lead_level ~ week + (1 | group)
   Data: tlc_long

REML criterion at convergence: 2747.8

Scaled residuals:
    Min      1Q  Median      3Q     Max
-2.2810 -0.6373 -0.0570  0.5904  6.1681

Random effects:
 Groups   Name        Variance Std.Dev.
 group    (Intercept) 15.28    3.908
 Residual             55.78    7.469
Number of obs: 400, groups:  group, 2
```

```
Fixed effects:
            Estimate Std. Error t value
(Intercept)  22.9760     2.8218   8.142
week         -0.4010     0.1566  -2.561

Correlation of Fixed Effects:
     (Intr)
week -0.153
```

Overall, this model suggests that there is a significant decrease in lead levels over time (-0.401). The variance of 15.28 for the "group" variable indicates that there are differences in baseline lead levels between groups.

Mixed effect model (random intercept + random time variable)

```
mixed_model <- lmer(lead_level ~ week + (1 + week | group), data = tlc_long)

summary(mixed_model)

Linear mixed model fit by REML ['lmerMod']
Formula: lead_level ~ week + (1 + week | group)
   Data: tlc_long

REML criterion at convergence: 2747.7

Scaled residuals:
    Min      1Q  Median      3Q     Max
-2.2877 -0.6361 -0.0524  0.5973  6.1807

Random effects:
 Groups   Name        Variance  Std.Dev. Corr
 group    (Intercept) 14.418255 3.79714
          week         0.001638 0.04047  1.00
 Residual             55.779027 7.46854
Number of obs: 400, groups:  group, 2

Fixed effects:
            Estimate Std. Error t value
(Intercept)  22.9760     2.7448   8.371
week         -0.4010     0.1592  -2.519

Correlation of Fixed Effects:
     (Intr)
week 0.022
optimizer (nloptwrap) convergence code: 0 (OK)
boundary (singular) fit: see help('isSingular')
```

This model shows much of the same trends as the previous model. The rate of lead decline is the same (-0.401), however, this model provides additional information regarding the variability in this effect between groups.