Day6 exercise solutions

Ali Movasati, Isabelle Cretton, Tristan Koning

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```
# Set global code chunk options
knitr::opts_chunk$set(warning = FALSE)
```

```
# load required libraries
library(skimr)
library(ggplot2)
library(ggpubr)
library(magrittr)
library(tidyr)
library(dplyr)
library(tibble)
library(lme4)
library(lattice)
library(reshape2)


# define functions
`%notin%` <- Negate(`%in%`)
```

Problem 1

1.A)

```
# Load data
hearing <-  read.table(file = "data/hearing.txt", sep = "\t", header = TRUE)
hearing <- within(hearing, {
  ListID <- factor(ListID, levels = c("List1", "List2", "List3", "List4"))
})
skim(hearing)
```

Table 1: Data summary

Name	hearing
Number of rows	96
Number of columns	3
Column type frequency:	
factor	1
numeric	2
Group variables	None

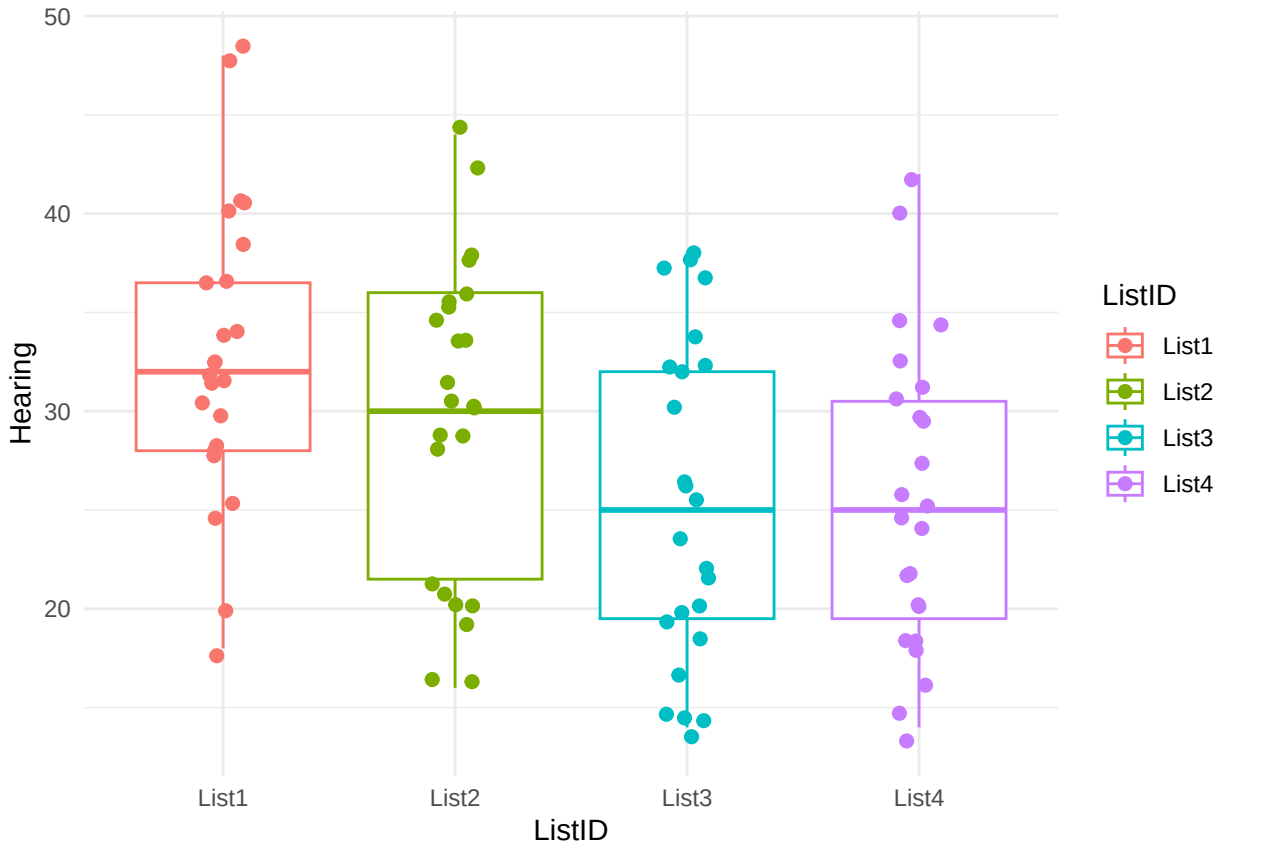
Variable type: factor

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
ListID	0	1	FALSE	4	Lis: 24, Lis: 24, Lis: 24, Lis: 24

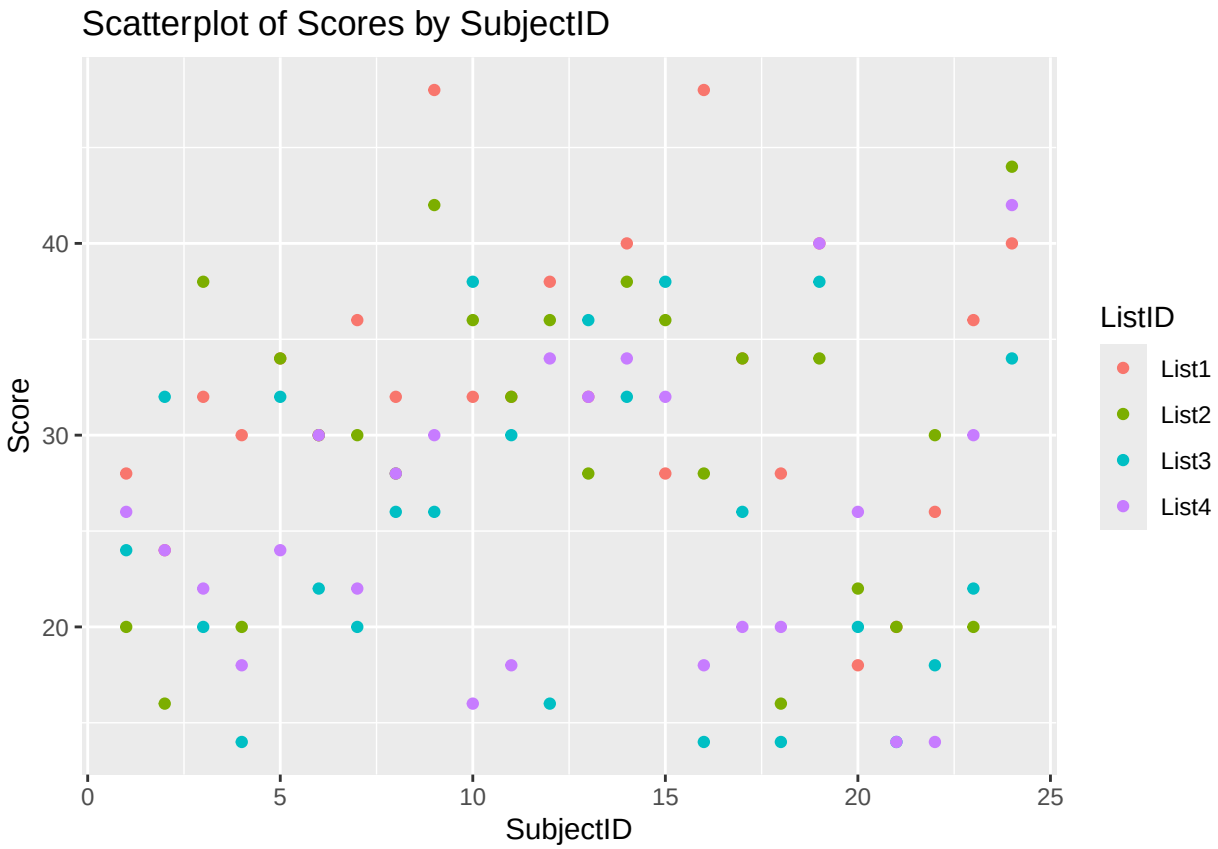
Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
SubjectID	0	1	12.50	6.96	1	6.75	12.5	18.25	24	
Hearing	0	1	28.31	8.37	14	20.00	30.0	34.00	48	

```
# Graphical summeries
# Boxplot of scores by ListID
hearing %>% ggplot(aes(x = ListID, y = Hearing, color = ListID)) +
        geom_boxplot() +
        geom_jitter(width = 0.1, aes(color = factor(ListID)), size = 2) +
        theme_minimal()
```




```
# Scatterplot of subjectids on hearing scores
ggplot(hearing, aes(x = SubjectID, y = Hearing, color = ListID)) +
  geom_point() +
  labs(title = "Scatterplot of Scores by SubjectID", x = "SubjectID", y = "Score")
```



1.B)

```
model_A <- lm(Hearing ~ ListID, data = hearing)
sum_model_A <- summary(model_A)
```

« comments »

Only 11.01% of variability in hearing measures are explained by different lists

We have enough evidence to state that the mean hearing score for List 3 and 4 are different than list 1, while for list 2 we cannot state that!

1.C)

```
# fit the mixed model
lm_mixed <- lmer(Hearing ~ 1 + ListID + (1|SubjectID), data = hearing)

sum_model_mixed <- summary(lm_mixed)

print(sum_model_mixed)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: Hearing ~ 1 + ListID + (1 | SubjectID)
##    Data: hearing
##
## REML criterion at convergence: 635.4
##
```

```
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.86533 -0.56158 -0.01092  0.63222  2.69167
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  SubjectID (Intercept) 26.04    5.103
##  Residual              36.33    6.027
## Number of obs: 96, groups:  SubjectID, 24
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)   32.750      1.612  20.315
## ListIDList2   -3.083      1.740  -1.772
## ListIDList3   -7.500      1.740  -4.311
## ListIDList4   -7.167      1.740  -4.119
##
## Correlation of Fixed Effects:
##             (Intr) LsIDL2 LsIDL3
## ListIDList2 -0.540
## ListIDList3 -0.540  0.500
## ListIDList4 -0.540  0.500  0.500
```

```
# fit the model without ListID (null model)
lm_mixed_null <- lmer(Hearing ~ (1 | SubjectID), data = hearing)

sum_model_mixed_null <- summary(lm_mixed_null)

# Likelihood ratio test
anova(lm_mixed_null, lm_mixed)
```

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

```
## Data: hearing
## Models:
## lm_mixed_null: Hearing ~ (1 | SubjectID)
## lm_mixed: Hearing ~ 1 + ListID + (1 | SubjectID)
##               npar    AIC    BIC  logLik deviance Chisq Df Pr(>Chisq)
## lm_mixed_null    3 674.22 681.91 -334.11   668.22
## lm_mixed         6 657.70 673.09 -322.85   645.70 22.52  3  5.083e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

« comments »

The more complex model with ListID as a fixed effect is significantly more accurate at representing the data than the simpler model.

1.D)

Both models from 1.B and 1.C have the same estimates.

Exercise 2

(a)

```
termites <- read.table(file = "data/termites.txt", sep = " ", header = TRUE)
# Remove NA entries
termites <- termites %>% select_if(~ !any(is.na(.)))

# EDA
skim(termites)
```

Table 4: Data summary

Name	termites
Number of rows	16
Number of columns	15
Column type frequency:	
numeric	15
Group variables	None

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
dish	0	1	8.50	4.76	1	4.75	8.5	12.25	16	
dose	0	1	7.50	2.58	5	5.00	7.5	10.00	10	
day1	0	1	25.00	0.00	25	25.00	25.0	25.00	25	
day2	0	1	23.94	1.88	18	24.00	24.5	25.00	25	
day4	0	1	19.00	6.63	4	15.50	22.5	23.25	25	
day5	0	1	15.56	7.51	3	9.00	19.0	21.25	24	
day6	0	1	13.81	7.79	1	6.75	17.0	20.25	22	
day7	0	1	12.62	7.49	1	4.75	16.0	18.25	22	
day8	0	1	11.31	7.60	0	2.75	14.0	18.00	21	
day10	0	1	10.31	7.27	0	2.75	13.0	16.00	20	
day11	0	1	9.50	7.00	0	1.75	12.5	15.00	18	
day12	0	1	8.38	6.23	0	1.75	11.0	12.25	18	
day13	0	1	7.81	5.88	0	1.75	10.0	11.50	17	
day14	0	1	7.50	5.83	0	1.00	9.0	11.50	17	
day15	0	1	6.81	5.56	0	0.75	7.5	11.25	16	

(b)

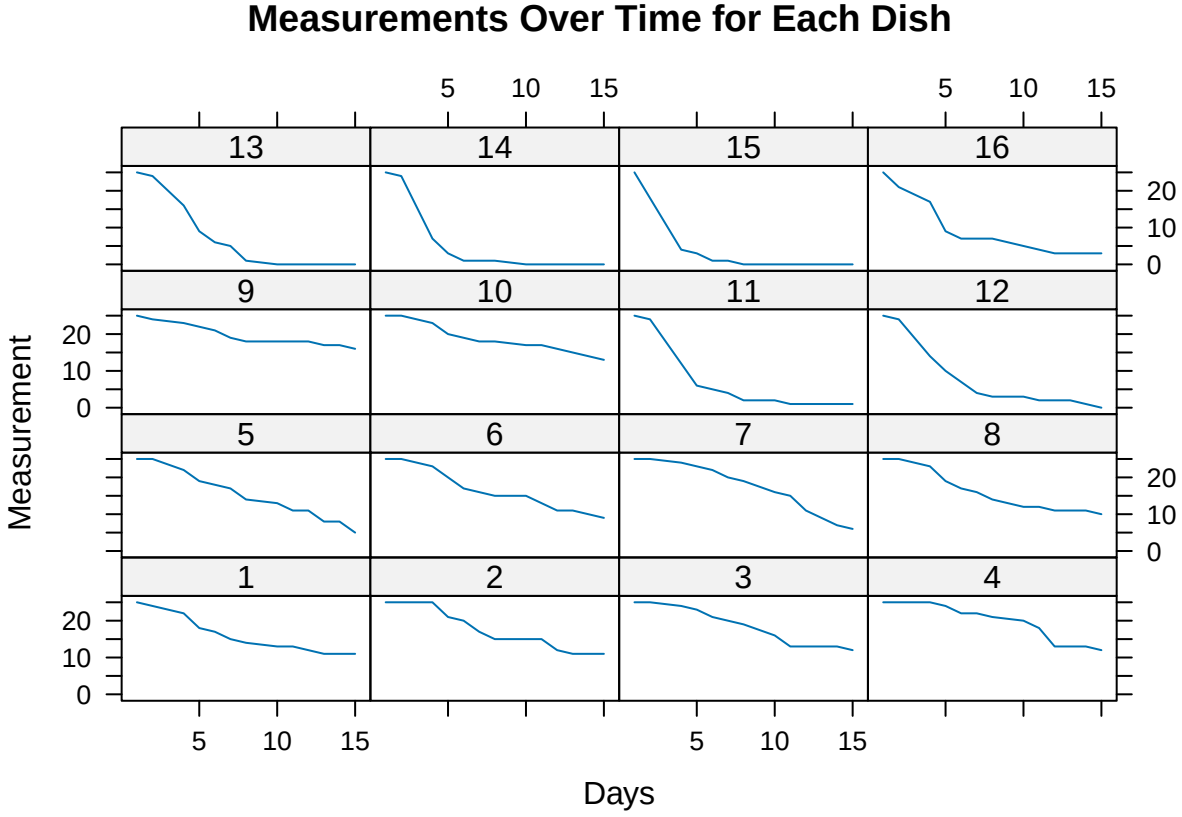
```
# Reshape data
termites <- melt(termites, id.vars = c("dish", "dose"),
                 variable.name = "day",
                 value.name = "measurement")
str(termites)
```

```
## 'data.frame':    208 obs. of  4 variables:
##  $ dish       : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ dose       : int  5 5 5 5 5 5 5 5 10 10 ...
```

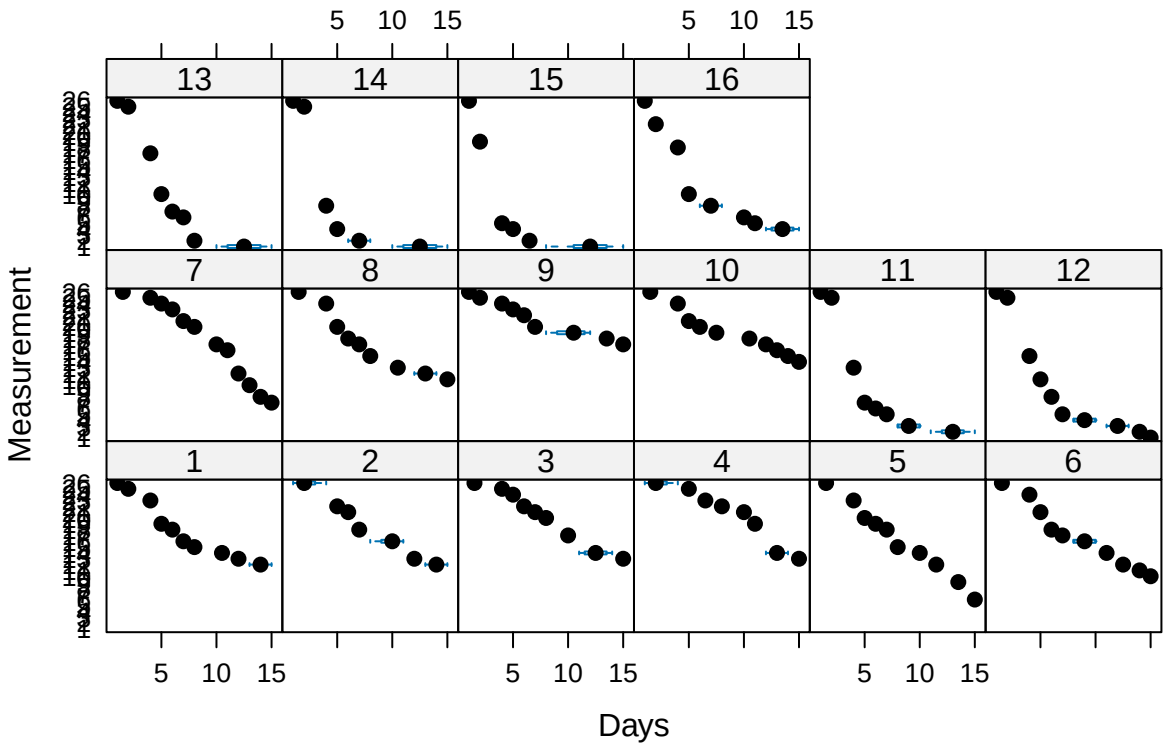
```
##  $ day        : Factor w/ 13 levels "day1","day2",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ measurement: int  25 25 25 25 25 25 25 25 25 25 ...
```

```
# Convert day to numeric
termites$day <- as.numeric(gsub("day", "", as.character(termites$day)))

# Graphical EDA
lattice::xyplot(measurement ~ as.numeric(gsub("day", "", day)) | as.factor(dish),
       data = termites, type = "l",
       layout = c(4, 4),
       main = "Measurements Over Time for Each Dish",
       xlab = "Days", ylab = "Measurement")
```




```
# bwplot of measurements distribution across days
lattice::bwplot(measurement ~ as.numeric(gsub("day", "", day)) | as.factor(dish),
       data = termites,
       main = "Measurement Distribution Across Days",
       xlab = "Days", ylab = "Measurement")
```



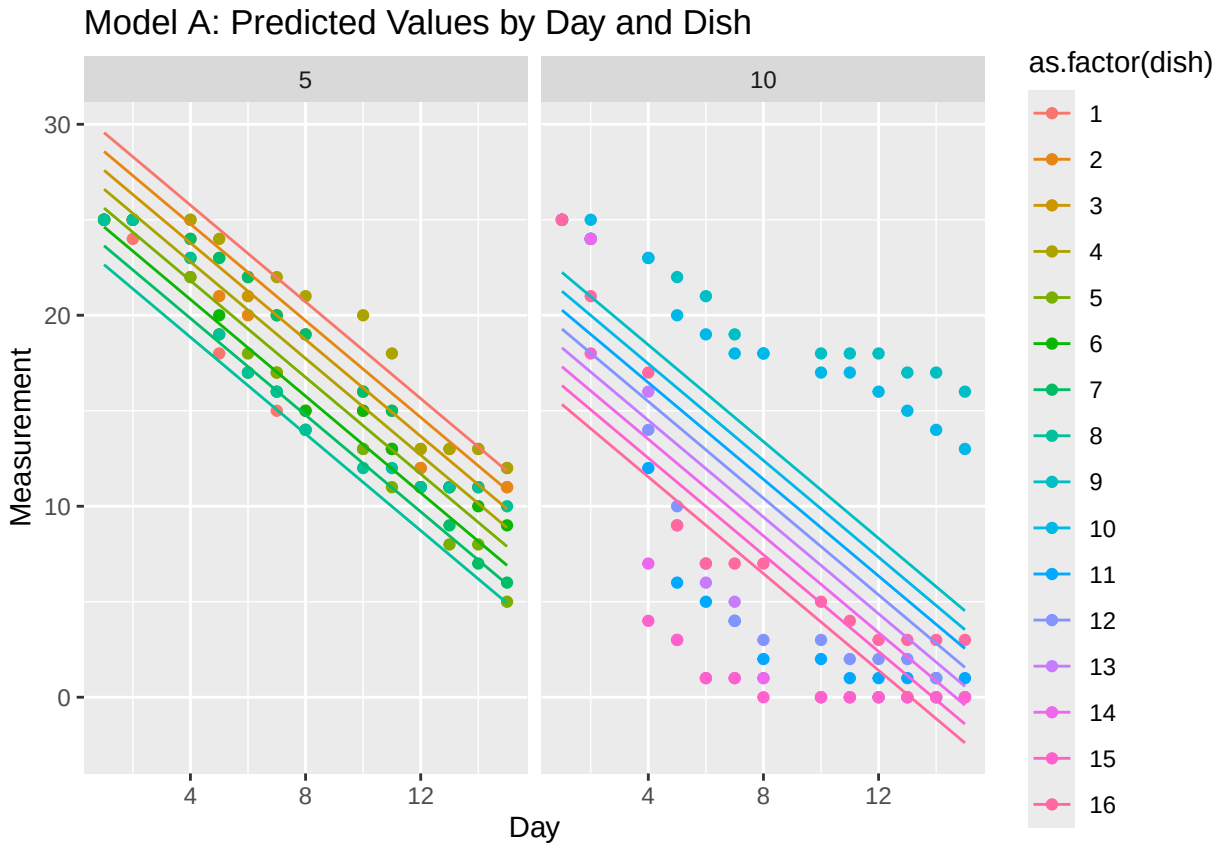
(c)

```
# Fit a linear model
model_A <- lm(measurement ~ dose + day + dish, data = termites)
summary(model_A)
```

```
##
## Call:
## lm(formula = measurement ~ dose + day + dish, data = termites)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -9.9783 -3.1681  0.1416  3.3309 11.4765
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 31.23290    1.30944  23.852  < 2e-16 ***
## dose         0.11676    0.26441   0.442    0.659
## day         -1.26588    0.07451 -16.989  < 2e-16 ***
## dish        -0.98764    0.14340  -6.887  6.9e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.739 on 204 degrees of freedom
## Multiple R-squared:  0.6928, Adjusted R-squared:  0.6883
## F-statistic: 153.4 on 3 and 204 DF,  p-value: < 2.2e-16
```

```r
termites$predicted_A <- predict(model_A)

# Plot model
ggplot(termites, aes(x = as.numeric(gsub("day", "", day)), y = measurement, color = as.factor(dish))) +
  facet_wrap(~dose) +
  geom_point() +
  geom_line(aes(y = predicted_A)) +
  labs(title = "Model A: Predicted Values by Day and Dish", x = "Day", y = "Measurement")
```



« comments »

It is problematic to use dish as a dependent variable, as repeated measurements are taken on the same dish. This violates the assumption of independence of observations.

(d)

```r
# Fit a linear mixed model
model_B <- lmer(measurement ~ dose + day + (1 | dish), data = termites)
summary(model_B)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: measurement ~ dose + day + (1 | dish)
##    Data: termites
##
## REML criterion at convergence: 1137.6
##
## Scaled residuals:
```

```
##     Min      1Q  Median      3Q     Max
## -2.0822 -0.5606 -0.0373  0.4065  3.4749
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  dish     (Intercept) 18.66    4.320
##  Residual             10.97    3.312
## Number of obs: 208, groups:  dish, 16
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept) 34.68963    3.51844   9.859
## dose        -1.46346    0.44167  -3.313
## day         -1.26588    0.05208 -24.305
##
## Correlation of Fixed Effects:
##      (Intr) dose
## dose -0.941
## day  -0.123  0.000
```

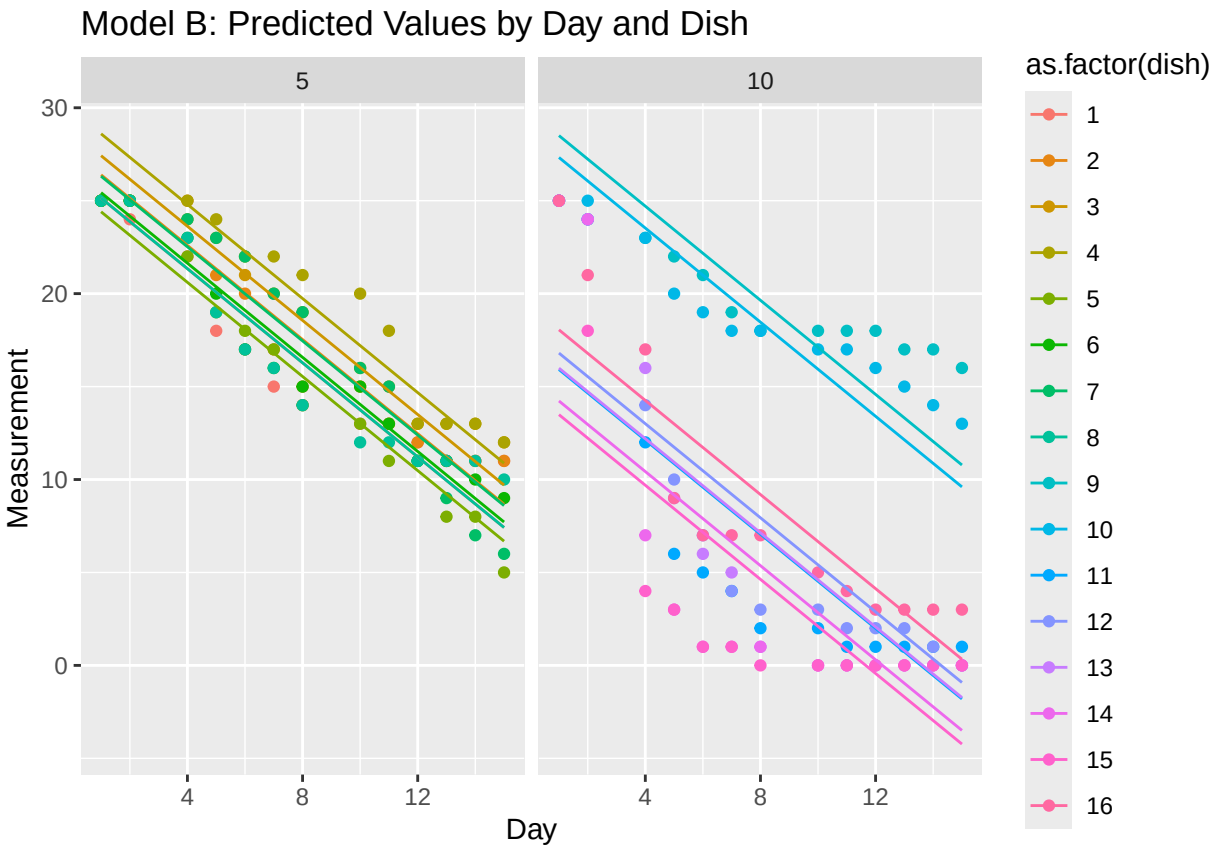
```
confint(model_B, method = "boot", nsim = 100, oldNames = FALSE)
```

```
## Computing bootstrap confidence intervals ...
```

```
##                           2.5 %    97.5 %
## sd_(Intercept)|dish  2.401195  5.976705
## sigma                2.988105  3.619098
## (Intercept)         26.619185 41.345871
## dose                -2.362734 -0.593798
## day                 -1.377440 -1.146994
```

```
termites$predicted_B <- predict(model_B)

# Plot model
ggplot(termites, aes(x = as.numeric(gsub("day", "", day)), y = measurement, color = as.factor(dish))) +
  facet_wrap(~dose) +
  geom_point() +
  geom_line(aes(y = predicted_B)) +
  labs(title = "Model B: Predicted Values by Day and Dish", x = "Day", y = "Measurement")
```



« comments »

The linear mixed model is more appropriate for this data as it accounts for the repeated measurements taken on the same dish, this can also be seen visually in the plots, where each prediction in model_B seem to be closer to the actual measurements compared to model_A. Dose now seems highly correlated with the measurements whereas in model_A it was not significant.

(e)

```
# Fit a linear mixed model
model_C <- lmer(measurement ~ dose + day + (day | dish) + day, data = termites)
```

```
## boundary (singular) fit: see help('isSingular')
```

```
summary(model_C)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: measurement ~ dose + day + (day | dish) + day
##    Data: termites
##
## REML criterion at convergence: 1115.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.47711 -0.51473  0.04884  0.42996  2.89506
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
```

```
##  dish     (Intercept) 4.77731  2.1857
##           day         0.06521  0.2554   1.00
##  Residual             9.66642  3.1091
## Number of obs: 208, groups:  dish, 16
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept) 32.49049    2.18765  14.852
## dose        -1.17024    0.27571  -4.245
## day         -1.26588    0.08041 -15.743
##
## Correlation of Fixed Effects:
##      (Intr) dose
## dose -0.945
## day   0.085  0.000
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
confint(model_C, method = "boot", nsim = 100, oldNames = FALSE)
```

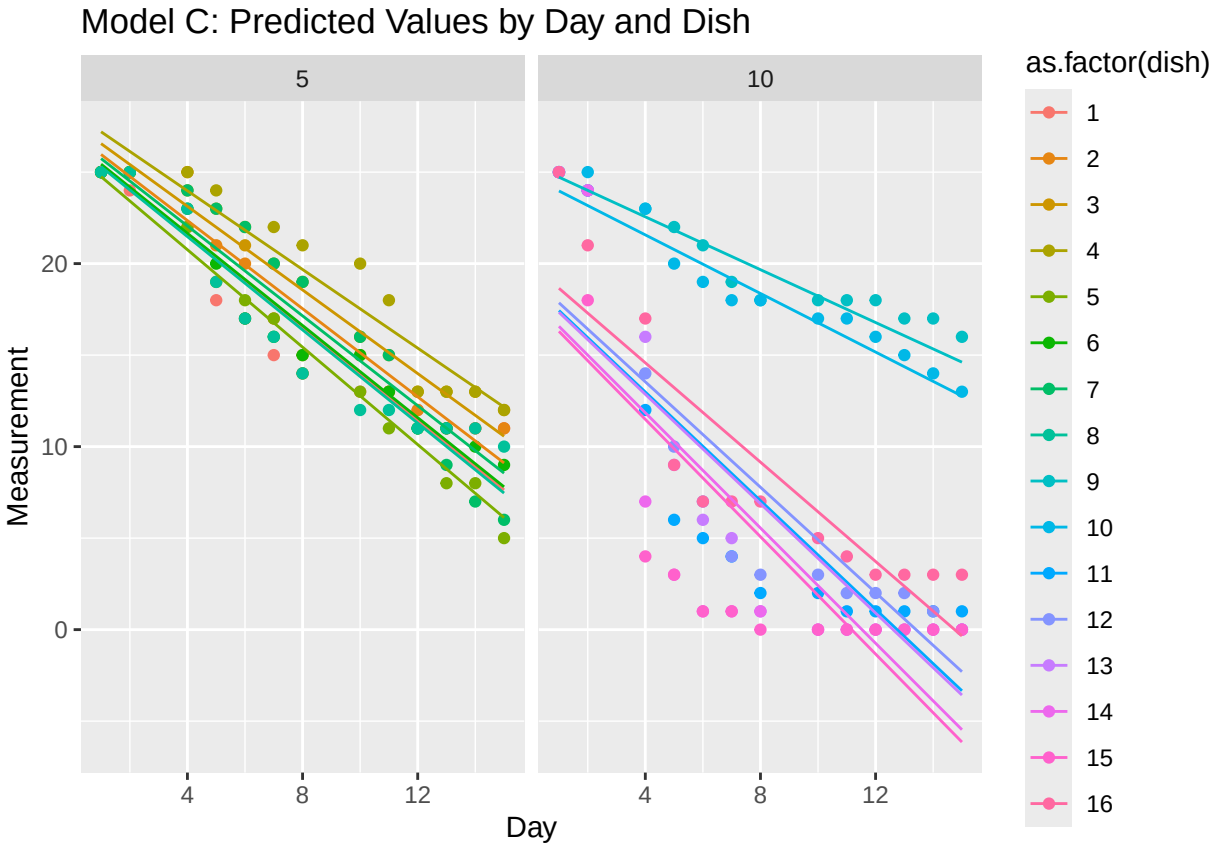
```
## Computing bootstrap confidence intervals ...
```

```
##
## 63 message(s): boundary (singular) fit: see help('isSingular')
## 6 warning(s): Model failed to converge with max|grad| = 0.00229635 (tol = 0.002, component 1) (and o
```

```
##                                2.5 %     97.5 %
## sd_(Intercept)|dish       0.8969791  3.5973036
## cor_day.(Intercept)|dish  0.2866130  1.0000000
## sd_day|dish               0.1047442  0.4031702
## sigma                     2.6913453  3.3509691
## (Intercept)              27.0896362 36.7670619
## dose                     -1.7582204 -0.4625347
## day                      -1.4443375 -1.0804296
```

```
termites$predicted_C <- predict(model_C)

# Plot model
ggplot(termites, aes(x = as.numeric(gsub("day", "", day)), y = measurement, color = as.factor(dish))) +
  facet_wrap(~dose) +
  geom_point() +
  geom_line(aes(y = predicted_C)) +
  labs(title = "Model C: Predicted Values by Day and Dish", x = "Day", y = "Measurement")
```



« comments »

Again, this model seems to be more accurate than the previous models.

(f)

```
boostrap_ci <- function(data, formula, parameter, N = 1000, conf = 0.90) {
  estimates <- numeric(N)

  for (i in 1:N) {
    resample <- data[sample(nrow(data), replace = TRUE), ]
    model <- lmer(formula, data = resample)
    estimates[i] <- fixef(model)[[parameter]]
  }

  return(quantile(estimates, c((1 - conf) / 2, 1 - (1 - conf) / 2)))
}

ci <- boostrap_ci(termites, measurement ~ dose + day + (1 | dish) + day, "dose")
ci
```

```
##        5%       95%
## -1.619785 -1.293684
```

« comments »

The 90% confidence interval excludes 0, therefore we can say that dose significantly impact survival!