Mixed-effects models
Solutions to Exercises

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Contents

Chapter 1

Mixed-effects models

1.10 Exercises

In these exercises, we use the following colour codes:

■ **Easy**: make sure you complete some of these before moving on. These exercises will follow examples in the text very closely.

♦ **Intermediate**: a bit harder. You will often have to combine functions to solve the exercise in two steps.

▲ **Hard**: difficult exercises! These exercises will require multiple steps, and significant departure from examples in the text.

We suggest you complete these exercises in an **R** markdown file. This will allow you to combine code chunks, graphical output, and written answers in a single, easy-to-read file.

1.10.1 PREF Canopy data

1. ♦ In the analysis of the `pref` data, use model selection (`AIC`, `anova`) to evaluate the importance of `species` and `dfromtop`.

```
library(lme4)

# read in data
pref <- read.csv("prefdata.csv")

# Random intercept only
lmer1 <- lmer(LMA ~ species + dfromtop + species:dfromtop + (1|ID), data=pref)

# Random intercept and slope
lmer2 <- lmer(LMA ~ species + dfromtop + species:dfromtop + (dfromtop|ID), data=pref)

# Compare models using AIC
# model 1 is more efficient (lower AIC due to fewer degrees of freedom)
AIC(lmer1, lmer2)

##       df      AIC
## lmer1  6 2251.997
```

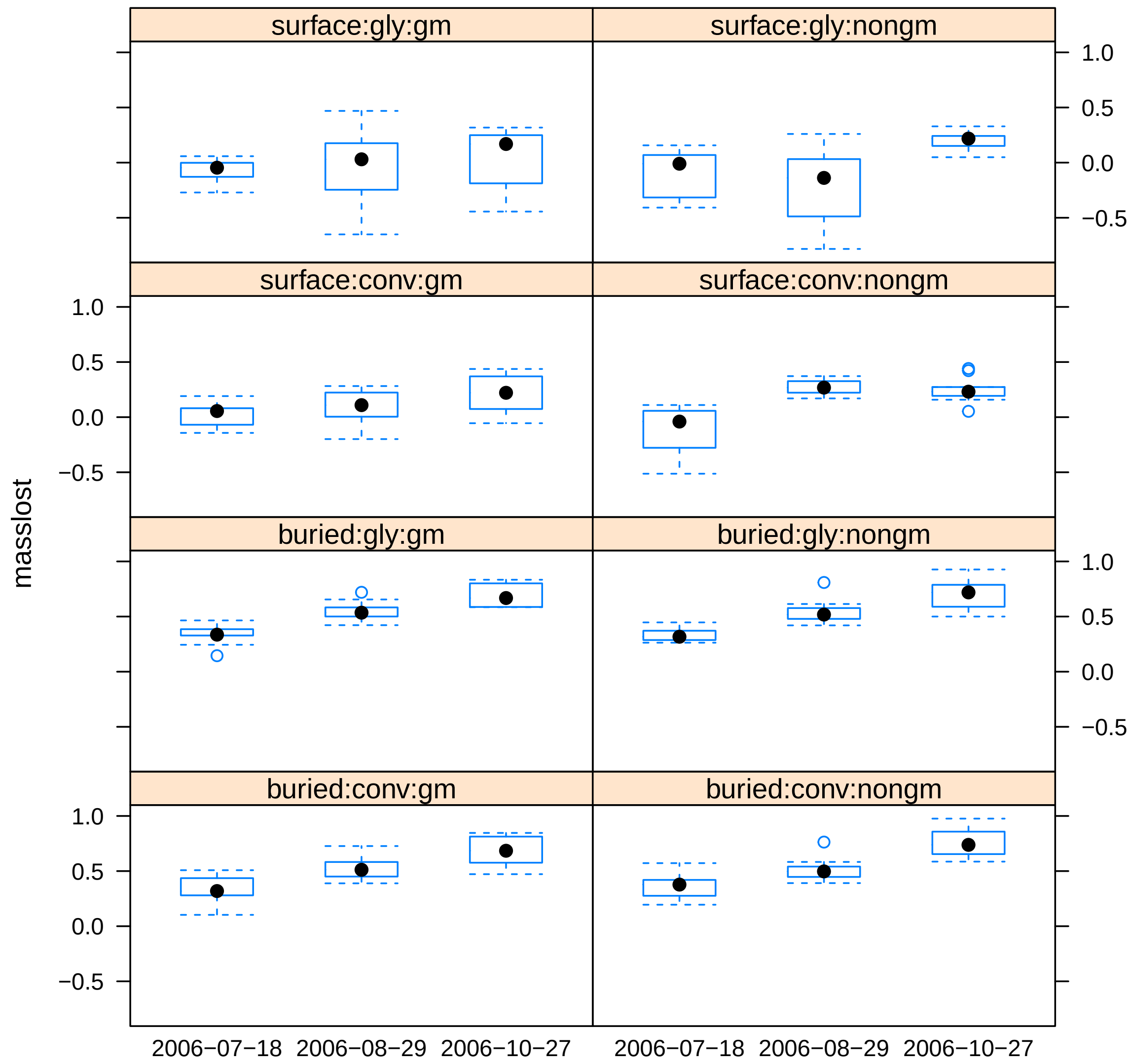
```
## lmer2  8 2255.735
# Evaluate the importance of the interaction between 'species' and 'dfromtop'
lmer1 <- lmer(LMA ~ species + dfromtop + species:dfromtop + (1|ID), data=pref)
lmer3 <- lmer(LMA ~ species + dfromtop + (1|ID), data=pref)
anova(lmer1, lmer3)  # P > 0.05 so interaction probably not important
## Data: pref
## Models:
## lmer3: LMA ~ species + dfromtop + (1 | ID)
## lmer1: LMA ~ species + dfromtop + species:dfromtop + (1 | ID)
##       Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## lmer3  5 2263.7 2281.2 -1126.8   2253.7
## lmer1  6 2263.2 2284.3 -1125.6   2251.2 2.4417      1     0.1182
AIC(lmer1, lmer3)  # there is not much difference, suggesting that the interaction is probably not
##       df      AIC
## lmer1  6 2251.997
## lmer3  5 2253.002
# Evaluate the importance of 'species' and 'dfromtop' as main effects
lmer3a <- lmer(LMA ~ dfromtop + (1|ID), data=pref, REML=F)
lmer3b <- lmer(LMA ~ species + (1|ID), data=pref, REML=F)
anova(lmer3, lmer3a)
## Data: pref
## Models:
## lmer3a: LMA ~ dfromtop + (1 | ID)
## lmer3: LMA ~ species + dfromtop + (1 | ID)
##        Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## lmer3a  4 2321.7 2335.8 -1156.9   2313.7
## lmer3   5 2263.7 2281.2 -1126.8   2253.7 60.085      1  9.085e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
anova(lmer3, lmer3b) # model fit significantly reduced by dropping either main effect
## Data: pref
## Models:
## lmer3b: LMA ~ species + (1 | ID)
## lmer3: LMA ~ species + dfromtop + (1 | ID)
##        Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
## lmer3b  4 2326.3 2340.4 -1159.2   2318.3
## lmer3   5 2263.7 2281.2 -1126.8   2253.7 64.678      1   8.82e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
AIC(lmer3, lmer3a, lmer3b) # model fit greatly reduced by dropping either main effect
##        df      AIC
## lmer3   5 2253.002
## lmer3a  4 2321.736
## lmer3b  4 2326.329
# Use Anova to compute p-values
library(car)
Anova(lmer3)
## Analysis of Deviance Table (Type II Wald chisquare tests)
```

```
##
## Response: LMA
##            Chisq Df Pr(>Chisq)
## species  152.913  1  < 2.2e-16 ***
## dfromtop  85.178  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

1.10.2 Litter decomposition data

1. ⧫ The `litter` data contain a factor (`variety`) describing whether the litter is derived from a genetically modified (`gm`) or conventional (`nongm`) soy variety. Plot the data to observe the effect of `variety`. Use `lmer` to test the effect of `variety`, in addition to the other significant variables, on litter decomposition.

```
# Read data and get summary
litter <- read.csv('masslost.csv')

# Change random effects (plot and block) to factors
litter$plot <- as.factor(litter$plot)
litter$block <- as.factor(litter$block)

# Represent date as number of days since the start of the experiment
library(lubridate)

##
## Attaching package:  'lubridate'

## The following object is masked from 'package:base':
##
##     date

litter$date <- as.Date(mdy(litter$date))
litter$date2 <- litter$date - as.Date('2006-05-23')

# look for treatment effects
library(lattice)
bwplot(masslost ~ factor(date) | profile:herbicide:variety, data=litter, layout=c(2,4))
```




```r
# there does not look to be much effect of 'variety' (look across two
# columns - 'layout' argument controls this)


library(lme4)
library(car)
m1 <- lmer(masslost ~ date2 + herbicide * profile * variety + (1|block/plot), data = litter)
Anova(m1)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: masslost
##                               Chisq Df Pr(>Chisq)
## date2                      140.2532  1  < 2.2e-16 ***
## herbicide                   12.8083  1  0.0003451 ***
## profile                    519.9182  1  < 2.2e-16 ***
## variety                      0.3391  1  0.5603610
```

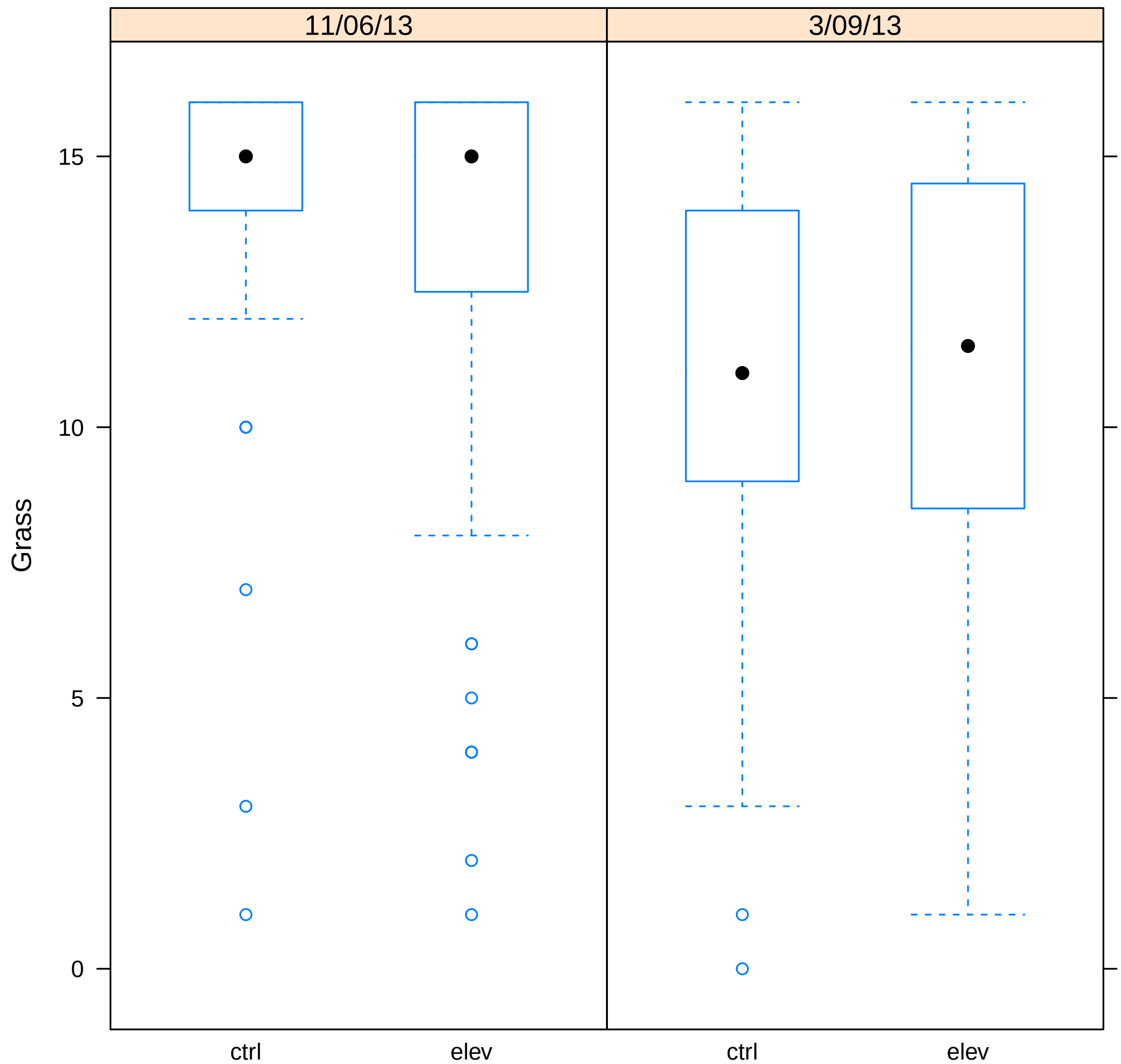
```
## herbicide:profile          11.7192  1  0.0006186 ***
## herbicide:variety            0.4603  1  0.4974986
## profile:variety              0.0760  1  0.7827760
## herbicide:profile:variety    0.0051  1  0.9430675
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

1.10.3 EucFACE ground cover data

The file `eucfaceGC.csv` contains estimates of plant and litter cover within the rings of the EucFACE experiment, evaluating forest ecosystem responses to elevated CO2, on two dates; the data description can be found in Section A.20 (p. 271).

1. ♦ Convert the variables indicating the nested sampling design to factors, then use `glmer` in `lme4` to test for an interaction between `Trt` and `Date` on `Grass` and `Litter` cover. Grass cover represents a frequency across a maximum of 16 points within a quadrat (use the `binomial` family), while litter cover represents counts (use the `poisson` family).

```
# read data
gc <- read.csv('eucfaceGC.csv')
str(gc)

## 'data.frame': 192 obs. of  8 variables:
##  $ Date   : Factor w/ 2 levels "11/06/13","3/09/13": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Ring   : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ Plot   : int  1 1 1 1 2 2 2 2 3 3 ...
##  $ Sub    : int  1 2 3 4 1 2 3 4 1 2 ...
##  $ Forbes: int  0 2 0 0 2 5 4 0 1 3 ...
##  $ Grass : int  16 14 16 16 15 16 16 16 16 13 ...
##  $ Litter: int  5 6 2 2 3 3 4 3 0 4 ...
##  $ Trt    : Factor w/ 2 levels "ctrl","elev": 2 2 2 2 2 2 2 2 2 2 ...

# convert random variables to factors
gc$Ring <- factor(gc$Ring)
gc$Plot <- factor(gc$Plot)
gc$Sub <- factor(gc$Sub)

## Grass data

# Plot variation associated with 'Trt' and date
bwplot(Grass ~ Trt | Date, data=gc)
```



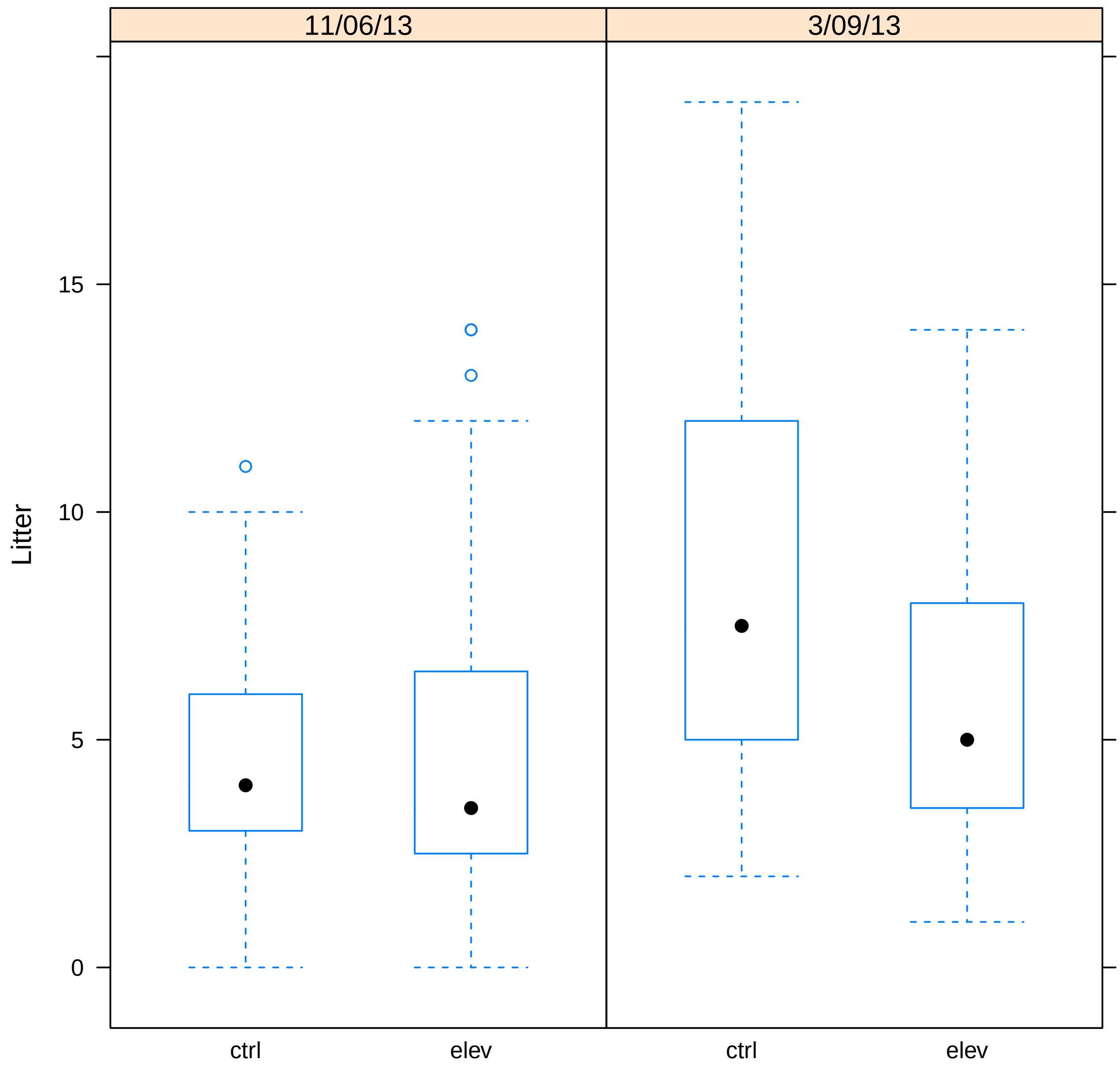

```
# Plot variation associated with plots and subplots
xyplot(Grass ~ Date | Ring, groups=Plot, data=eucface, pch=16, jitter.x=T)

## Error in eval(substitute(groups), data, environment(x)):  object 'eucface' not found

# fit model and test for effects
m1 <- glmer(cbind(Grass, 16-Grass) ~ Trt * Date + (1|Ring/Plot),
            data=gc, family=binomial)
summary(m1)

## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: cbind(Grass, 16 - Grass) ~ Trt * Date + (1 | Ring/Plot)
##    Data: gc
##
##      AIC      BIC   logLik deviance df.resid
##    844.8    864.3   -416.4    832.8      186
```

```
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -5.1405 -0.7560  0.4334  0.9890  4.1769
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  Plot:Ring (Intercept) 0.9969   0.9984
##  Ring      (Intercept) 0.7915   0.8897
## Number of obs: 192, groups:  Plot:Ring, 24; Ring, 6
##
## Fixed effects:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)            2.4440     0.6041   4.046 5.22e-05 ***
## Trtelev               -0.4079     0.8530  -0.478   0.6325
## Date3/09/13           -1.5946     0.1552 -10.278  < 2e-16 ***
## Trtelev:Date3/09/13    0.6155     0.2150   2.863   0.0042 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) Trtelv D3/09/
## Trtelev     -0.708
## Date3/09/13 -0.181  0.127
## Tr:D3/09/13  0.130 -0.166 -0.720
```

```
library(car)
Anova(m1)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: cbind(Grass, 16 - Grass)
##             Chisq Df Pr(>Chisq)
## Trt        0.0000  1   0.998208
## Date     140.2362  1  < 2.2e-16 ***
## Trt:Date   8.1946  1   0.004202 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Litter data

# Plot variation associated with 'Trt' and date
bwplot(Litter ~ Trt | Date, data=gc)
```




```
# Plot variation associated with plots and subplots
xyplot(Litter ~ Date | Ring, groups=Plot, data=eucface, pch=16, jitter.x=T)

## Error in eval(substitute(groups), data, environment(x)):  object 'eucface' not found

# fit model and test for effects
m2 <- glmer(Litter ~ Trt * Date + (1|Ring/Plot), data=gc, family=poisson)
summary(m2)

## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: Litter ~ Trt * Date + (1 | Ring/Plot)
##    Data: gc
##
##      AIC      BIC   logLik deviance df.resid
##    923.2    942.8   -455.6    911.2      186
##
```

```
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.22194 -0.66709  0.02852  0.54770  2.40787
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  Plot:Ring (Intercept) 0.1023   0.3199
##  Ring      (Intercept) 0.0867   0.2945
## Number of obs: 192, groups:  Plot:Ring, 24; Ring, 6
##
## Fixed effects:
##                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)            1.45991    0.20529   7.111 1.15e-12 ***
## Trtelev                0.01786    0.29009   0.062 0.950915
## Date3/09/13            0.62952    0.08334   7.554 4.22e-14 ***
## Trtelev:Date3/09/13 -0.42318    0.12015  -3.522 0.000428 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Trtelv D3/09/
## Trtelev      -0.707
## Date3/09/13 -0.265  0.187
## Tr:D3/09/13  0.184 -0.248 -0.694
```

```
library(car)
Anova(m2)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Litter
##             Chisq Df Pr(>Chisq)
## Trt        0.7057  1   0.400889
## Date      50.3420  1  1.292e-12 ***
## Trt:Date 12.4057  1   0.000428 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2. ▲ Following on from exercise 3, generate subsets to determine the sources of the interactions (i.e., does the treatment effect differ between the two dates or does the date effect differ between the two treatments?).

```
# still need to do
```