

## Lab 9 – Split-plot Designs

October 15 & 16, 2018  
FANR 6750

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We apply treatments to two experimental units: whole-units and sub-units

Examples:

- Ag fields are sprayed with herbicides, and fertilizers are applied to plots within fields.
- Tenderizer is applied to roasts, and cooking times are applied to cores

We're interested in treatment effects at both levels

INTRO

AOV

LME

ASSIGNMENT

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### THE ADDITIVE MODEL

$$y_{ijk} = \mu + \alpha_i + \beta_j + \alpha\beta_{ij} + \gamma_k + \delta_{ik} + \varepsilon_{ijk}$$

The  $\alpha$ 's and  $\beta$ 's are fixed treatment effects. Note the interaction.

Because we want our inferences to apply to all roasts,  $\delta_{ik}$  is random. Specifically:

$$\delta_{ik} \sim \text{Normal}(0, \sigma_D^2)$$

We might treat block effects as random too:

$$\gamma_k \sim \text{Normal}(0, \sigma_C^2)$$

And as always,

$$\varepsilon_{ijk} \sim \text{Normal}(0, \sigma^2)$$

### THE MEAT DATA

It's important that you have variables for the whole unit (roast) and the block (carcass).

```
meatData <- read.csv("meatData.csv")
str(meatData)

## 'data.frame': 72 obs. of 5 variables:
## $ Wbscore : num 8.25 7.5 4.25 3.5 7.25 6.25 3.5 3.5 6.5 4.5 ...
## $ tenderizer: Factor w/ 3 levels "C","P","V": 1 1 1 1 3 3 3 3 2 2 ...
## $ time : int 30 36 42 48 30 36 42 48 30 36 ...
## $ carcass : int 1 1 1 1 1 1 1 1 1 1 ...
## $ roast : int 1 1 1 1 2 2 2 2 3 3 ...
```

Don't forget to convert to factors

```
meatData$time <- factor(meatData$time)
meatData$carcass <- factor(meatData$carcass)
meatData$roast <- factor(meatData$roast)
```

## CARCASS (BLOCK) EFFECTS AS FIXED

```
aov.meat1 <- aov(Wbscore ~ tenderizer * time + carcass +
  Error(roast), data=meatData)

summary(aov.meat1)

##
## Error: roast
##          Df Sum Sq Mean Sq F value    Pr(>F)
## tenderizer  2 20.715   10.358   190.00 1.11e-08 ***
## carcass     5   3.903    0.781    14.32 0.000276 ***
## Residuals  10   0.545    0.055
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Error: Within
##          Df Sum Sq Mean Sq F value    Pr(>F)
## time       3 170.08   56.69  656.62 < 2e-16 ***
## tenderizer:time 6   9.56    1.59   18.46 1.11e-10 ***
## Residuals   45   3.89    0.09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## USING lme INSTEAD OF aov

```
library(nlme)
lme.meat1 <- lme(Wbscore ~ tenderizer*time, data=meatData,
  correlation=corCompSymm(), # To make results same as aov()
  random = ~1|carcass/roast)
```

```
anova(lme.meat1)

##               numDF denDF   F-value p-value
## (Intercept)         1    45 2105.6140 <.0001
## tenderizer          2    10  190.0001 <.0001
## time                3    45  656.6222 <.0001
## tenderizer:time      6    45   18.4585 <.0001
```

The interaction is significant. (You can ignore the (Intercept) term)

## EXPLORING THE INTERACTION

Is the time effect significant for each level of tenderizer?

```
lme.meatP <- lme(Wbscore ~ time, data=meatData, random = ~1|carcass/roast,
  correlation=corCompSymm(), subset=tenderizer=="P")
lme.meatV <- lme(Wbscore ~ time, data=meatData, random = ~1|carcass/roast,
  correlation=corCompSymm(), subset=tenderizer=="V")
lme.meatC <- lme(Wbscore ~ time, data=meatData, random = ~1|carcass/roast,
  correlation=corCompSymm(), subset=tenderizer=="C")
```

Yes, it is

```
anova(lme.meatP, Terms="time")

## F-test for: time
##   numDF denDF  F-value p-value
## 1      3     15 126.6786 <.0001

anova(lme.meatV, Terms="time")

## F-test for: time
##   numDF denDF  F-value p-value
## 1      3     15 274.716 <.0001

anova(lme.meatC, Terms="time")

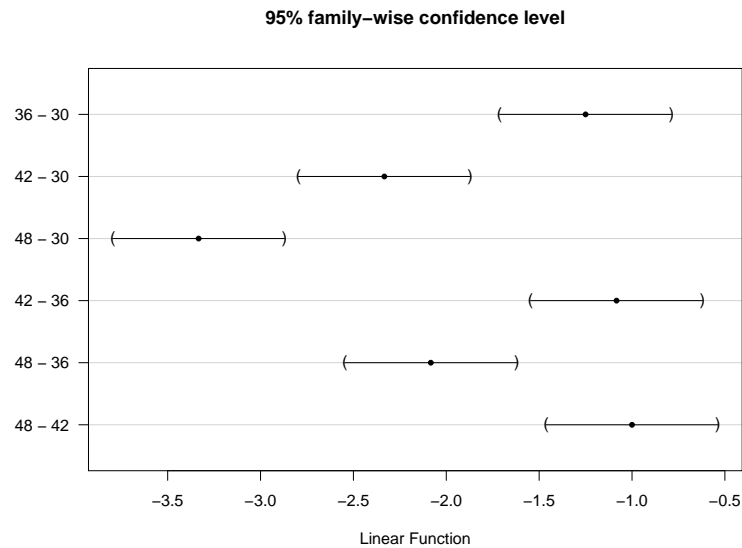
## F-test for: time
##   numDF denDF  F-value p-value
## 1      3     15 305.6551 <.0001
```

## MULTIPLE COMPARISONS USING glht

```
# install.packages("multcomp")
library(multcomp)
mcP <- glht(lme.meatP, linfct=mcp(time="Tukey"))
summary(mcP)

##
## Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
## Fit: lme.formula(fixed = Wbscore ~ time, data = meatData, random = ~1 |
##       carcass/roast, correlation = corCompSymm(), subset = tenderizer ==
##       "P")
##
## Linear Hypotheses:
##           Estimate Std. Error z value Pr(>|z|)
## 36 - 30 == 0   -1.250      0.180   -6.944 <1e-05 ***
## 42 - 30 == 0   -2.333      0.180  -12.961 <1e-05 ***
## 48 - 30 == 0   -3.333      0.180  -18.516 <1e-05 ***
## 42 - 36 == 0   -1.083      0.180   -6.018 <1e-05 ***
## 48 - 36 == 0   -2.083      0.180  -11.573 <1e-05 ***
## 48 - 42 == 0   -1.000      0.180   -5.555 <1e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)

# confint(mcP)
# plot(mcP)
```



## Design

- Sweet potato yield is studied in response to ( $a=3$ ) types of herbicide.
- Each herbicide is applied to 5 fields
- Each field is divided into 4 plots. Each plot is treated with one of ( $b=4$ ) fertilizers.

## Exercise

- (1) Import `yieldData.csv` and conduct the appropriate ANOVA using `aov` and `lme`.
- (2) Does the effect of herbicide depend on fertilizer?
- (3) Use Tukey's test to determine which fertilizers differ
- (4) State the null and alternative hypotheses, and summarize your results in 2-3 sentences.

Upload your self-contained script to ELC the day before your next lab.

<sup>1</sup>Nested and crossed is same as split-plot, but without the block