Stat 445/545: Analysis of Variance and Experimental Design

Chapter 19: Two factor ANOVA—equal sample size

Instructor: Yan Lu

THE UNIVERSITY OF NEW MEXICO

ANOVA with two factors and replication

Consider an experiment on beetles' survival time under different insecticides and doses

- Four different insecticides and three different doses (low, medium, high) are interested
  ——There are twelve combinations
  ——Suppose each combination is replicated four times, which results in 48 observations.
- Response: the survival time of the beetles.
  —— time is measured in fractions of a 10 minute interval. (So 0.4 means 4 minutes.)
- The doses of high, medium, and low, are really ordinal (we don't know if they are equally spaced, but they can be ranked)
  —— ANOVA will treat them as qualitative, like having three different brands without knowing the rankings.

Crossing: Every level of Insecticides occurs within every level of doses.

	Dose			
Insecticides	1	2	3	
		$n_{ij} = 4$		
A	n_{11}	n_{12}	n_{13}	
B	n_{21}	n_{22}	n_{23}	
C	n_{31}	n_{32}	n_{33}	
D	n_{41}	n_{42}	n_{43}	
				48

General case:

- Factor A: a levels
- Factor B: b levels
- Treatment: one of the possible ab combinations of a level of factor A and a level of factor B

Some commonly used models:

- Complete factorial design: all ab treatment combinations are used.
- Fractional factorial design: only some of the ab treatment combinations are used or treatment combinations have been carefully selected
- Fixed effects model: both factors are fixed
- Random effects model: both factors are random
- Mixed effeccts model: One factor fixed, one factor random

Why using multifactor designs?

- When the factors don't interact with each other, the two-way ANOVA gives the same precision for the main effects of A and B, as a single factor study, but study two factors at once
- Can assess interaction between the factors that are not be assessed by one factor experiment
- Additional factors can be used to account for other sources of variation and provide a more sensitive test for the factor of interest.

Mean structure

	Factor B				
Factor A	1	2	$\cdots$	b	Row level means
1	μ_{11}	μ_{12}	$\cdots$	μ_{1b}	$\mu_{1.}$
2	μ_{21}	μ_{22}	$\cdots$	μ_{2b}	$\mu_{2.}$
$\vdots$	$\vdots$	$\vdots$	$\cdots$	$\vdots$	$\vdots$
a	μ_{a1}	μ_{a2}	$\cdots$	μ_{ab}	$\mu_{a.}$
Column level means	$\mu_{.1}$	$\mu_{.2}$	$\cdots$	$\mu_{.b}$	$\mu_{..}$

$$\mu_{i.} = \frac{1}{b}\sum_{j=1}^{b}\mu_{ij}, \quad \mu_{.j} = \frac{1}{a}\sum_{i=1}^{a}\mu_{ij}$$

$$\mu_{..} = \frac{1}{ab}\sum_{i=1}^{a}\sum_{j=1}^{b}\mu_{ij} = \frac{1}{a}\sum_{i=1}^{a}\mu_{i.} = \frac{1}{b}\sum_{j=1}^{b}\mu_{.j}$$

ANOVA with two factors and replication

```
beetles.long <- read.table
(file="~/Desktop/jenn/teaching/stat445545/data/beetle",
header = TRUE)
> head(beetles.long)
    dose insecticide number hours10
1    low           A     t1    0.31
2    low           B     t1    0.82
3    low           C     t1    0.43
4    low           D     t1    0.45
5 medium           A     t1    0.36
6 medium           B     t1    0.92
```

ANOVA with two factors and replication

```
> beetles.mean.di
     dose insecticide      m
1     low           A 0.4125
2     low           B 0.8800
3     low           C 0.5675
4     low           D 0.6100
5  medium           A 0.3200
6  medium           B 0.8150
7  medium           C 0.3750
8  medium           D 0.6675
9    high           A 0.2100
10   high           B 0.3350
11   high           C 0.2350
12   high           D 0.3250
```

ANOVA with two factors and replication

Balanced ANOVA examples have an advantage in interpretation

- marginal is calculated by average of the averages. For example, the average of low doses 0.618 is the average of the averages for each combination of low dose and insecticide $(0.413 + 0.880 + 0.568 + 0.610)/4 = 0.61775$.

Cell Means	Dose			
Insecticide	1	2	3	Insect marg
A	0.413	0.320	0.210	0.314
B	0.880	0.815	0.335	0.677
C	0.568	0.375	0.235	0.393
D	0.610	0.668	0.325	0.534
Dose marg	0.618	0.544	0.277	0.480

ANOVA with two factors and replication

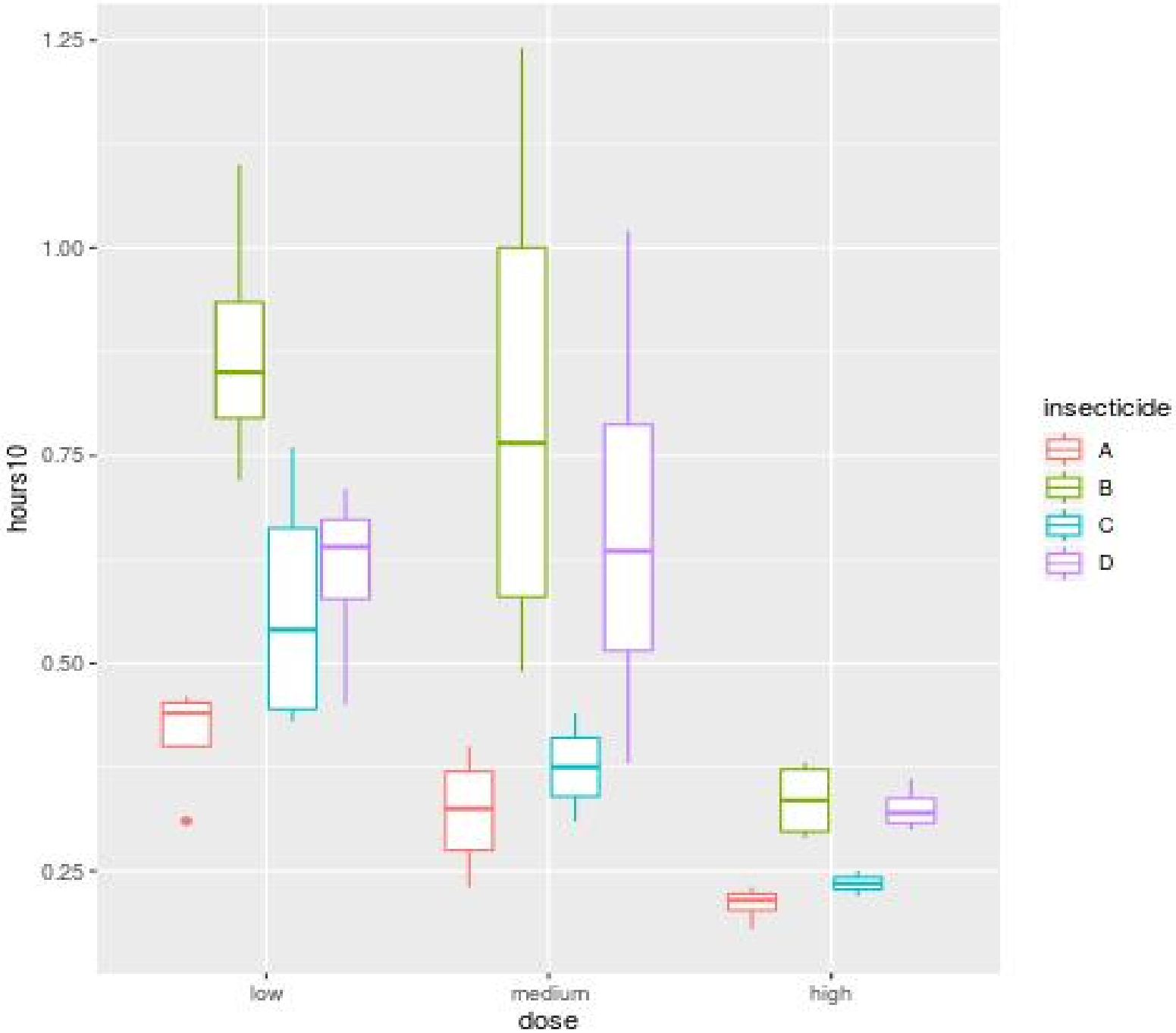
- Looking at the margins, the survival time was lowest for insecticides A and C.
- Higher doses also lead to lower survival times on average
- The survival times are not equally spaced—the difference in average survival times between doses 3 versus 2 is larger than for doses 2 versus 1

Cell Means	Dose			
Insecticide	1	2	3	Insect marg
A	0.413	0.320	0.210	0.314
B	0.880	0.815	0.335	0.677
C	0.568	0.375	0.235	0.393
D	0.610	0.668	0.325	0.534
Dose marg	0.618	0.544	0.277	0.480

You can do boxplots for looking at the responses for combinations of predictors.

```
library(ggplot2)
  p <- ggplot(beetles.long, aes(x = dose, y = hours10,
  colour = insecticide))
  p <- p + geom_boxplot()
  print(p)
```

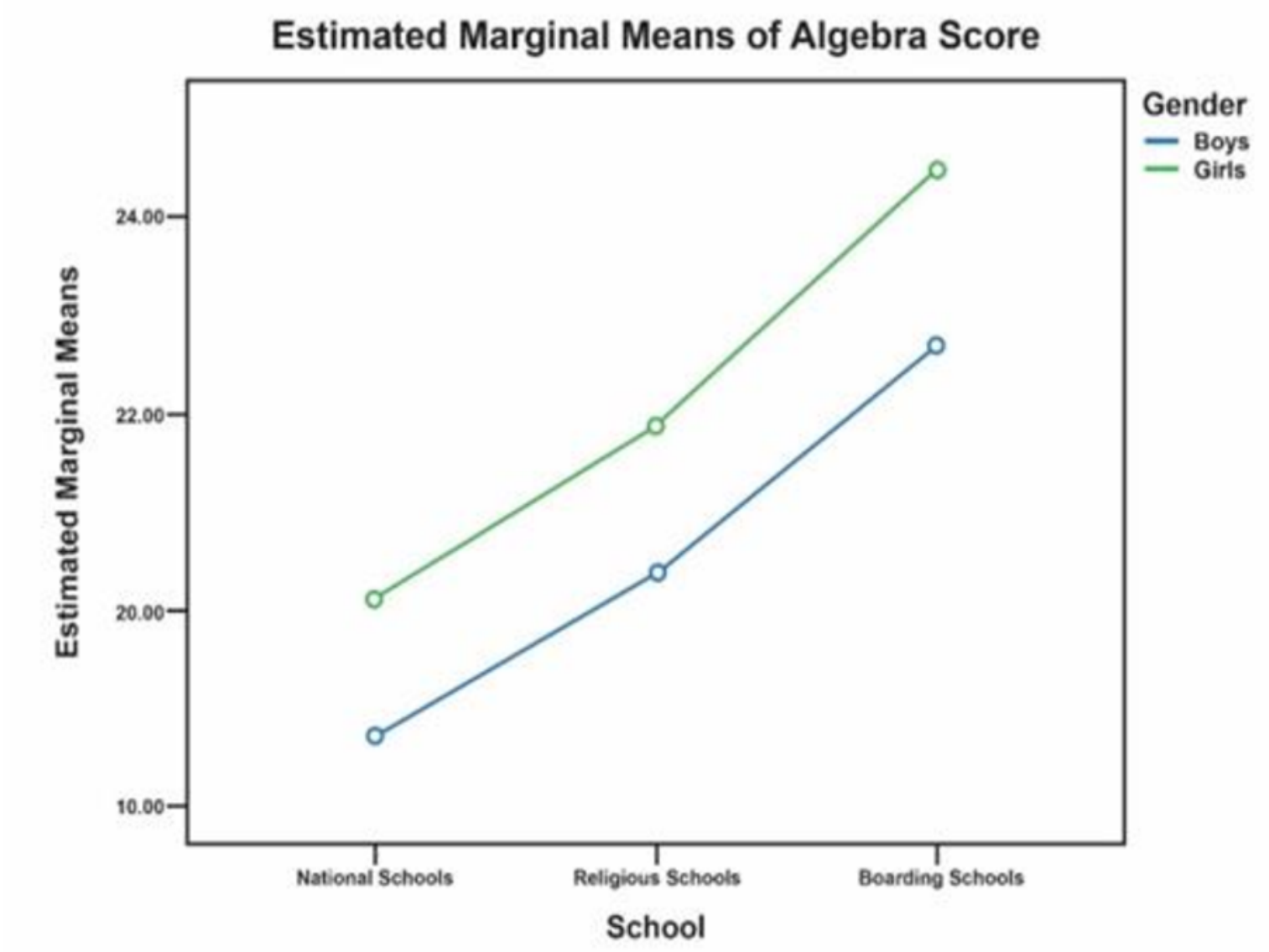
It looks like there are problems with the equal variances assumption! To make the assumptions not so badly violated, one possibility is to transform the data, such as using log of the survival times.


1.25
1.00
0.75
0.50
0.25
hours10
low
medium
high
dose
insecticide
A
B
C
D

Interactions

To understand interaction, suppose you (conceptually) plot the means in each row of the population table, giving what is known as the population mean profile plot. In practice, we plot the sample mean profile plot.

No interaction is present: if the plot has perfectly parallel profiles, as in the plot below for a 2×3 experiment. The levels of A and B do not interact.

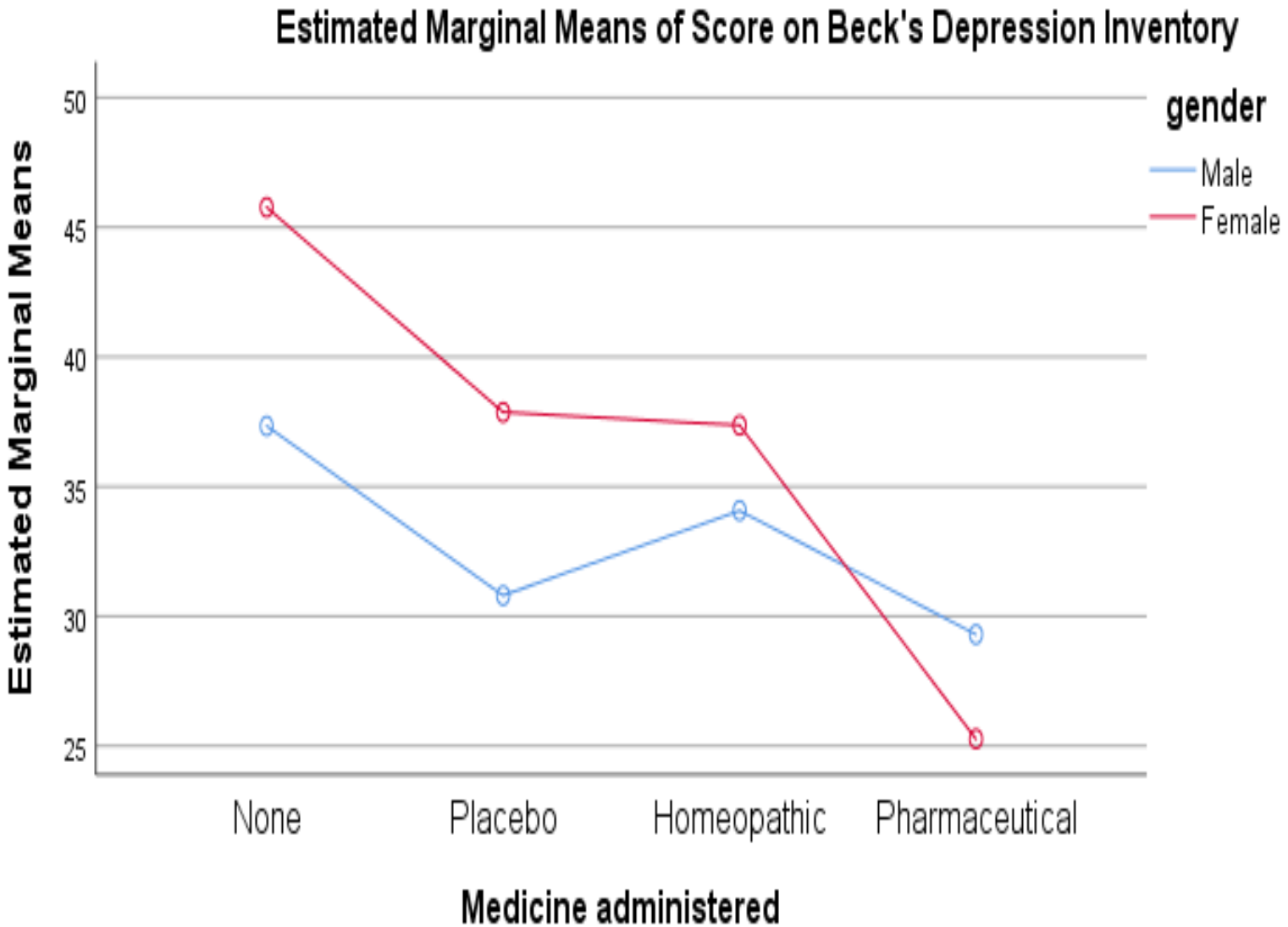


Parallel profiles

- $\mu_{ij} - \mu_{hj}$ is independent of j for each i and h
  ——-difference between levels of A does not depend on level of B
- $$\mu_{ij} - \bar{\mu}_{i\cdot} = \mu_{hj} - \bar{\mu}_{h\cdot} \text{ for all } i, j, h$$
- $$\mu_{ij} - \bar{\mu}_{i\cdot} = \bar{\mu}_{\cdot j} - \bar{\mu}_{\cdot\cdot} \text{ for all } i, j$$
- $$\mu_{ij} - \bar{\mu}_{i\cdot} - \bar{\mu}_{\cdot j} + \bar{\mu}_{\cdot\cdot} \text{ for all } i, j$$

  ——interaction effect $(\alpha\beta)_{ij} = 0$ for all i, j

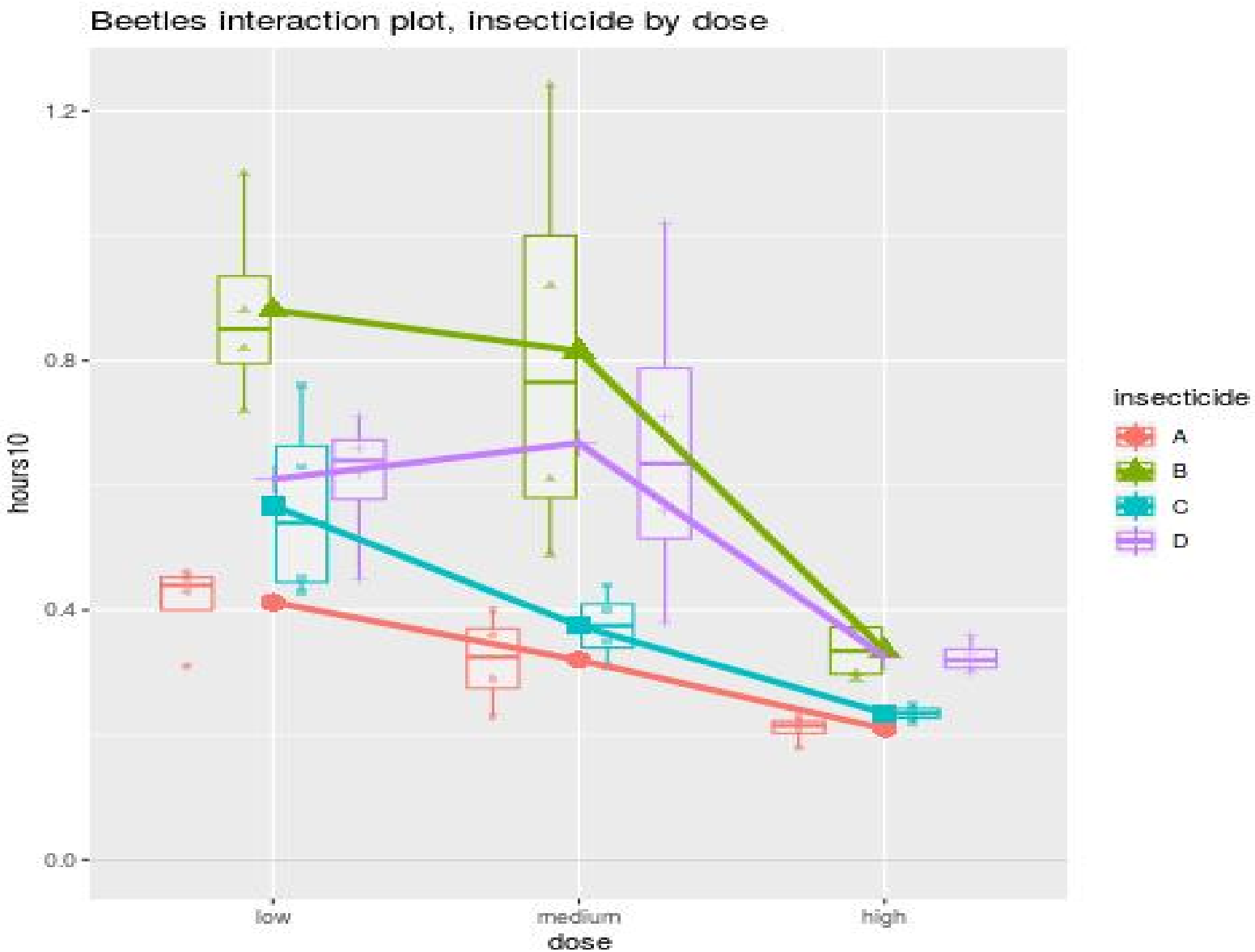
Interaction is present if the profiles are not perfectly parallel. An ex- ample of a profile plot for two-factor experiment (2×4) with interaction is given below.

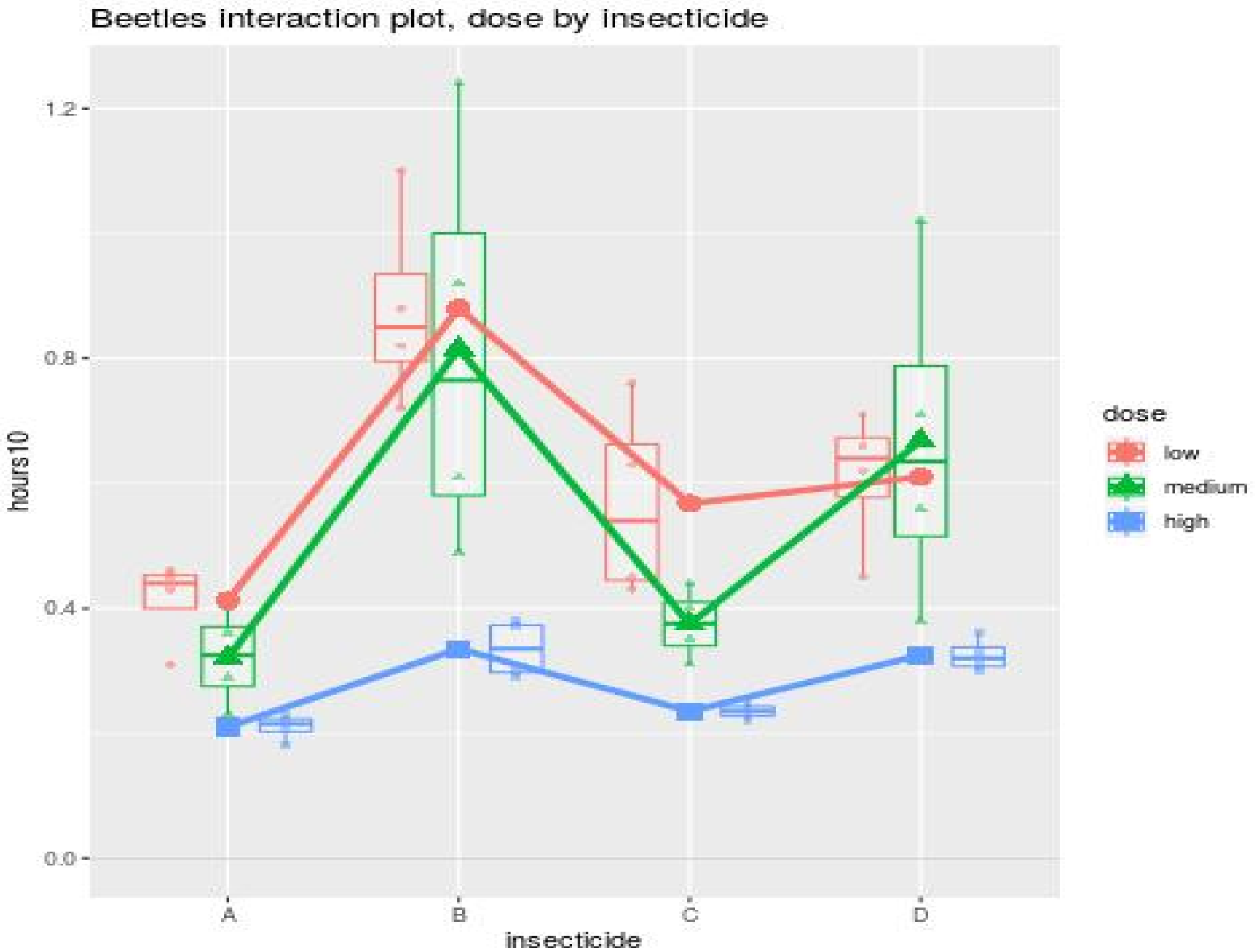


Comments on interactions:

- The roles of A and B can be reversed in the profile plots without changing the assessment of a presence or absence of interaction.
  ——It is often helpful to view the interaction plot from both perspectives.
- A qualitative check for interaction can be based on the sample means profile plot,
  ——but keep in mind that profiles of sample means are never perfectly parallel even when the factors do not interact in the population.
  ——The Interaction SS measures the extent of non-parallelism in the sample mean profiles.

Profile plots




Beetles interaction plot, dose by insecticide
1.2
0.8
0.4
0.0
hours10
A
B
C
D
insecticide
dose
low
medium
high

- The profile plots indicate that the main effects are significant ——the insecticides have noticeably different mean survival times averaged over doses, with insecticide A having the lowest mean survival time averaged over doses.
  ——higher doses tend to produce lower survival times.
- Interaction seems not significant.

Looking back at the table of cell means, the idea is the differences between columns are similar, and the differences between rows are similar.

—— For example, going from dose 1 to dose 2 (low to medium), the change in average survival for insecticide A is (0.413-0.320) = 0.093 (i.e., .93 minutes or 55 seconds), and the difference for insecticide B is (0.880 - 0.815) = 0.065 (i.e., 39 seconds). Given the variability in the data, the change going from low to medium doses is similar for insecticides A and B.

Cell Means	Dose			
Insecticide	1	2	3	Insect marg
A	0.413	0.320	0.210	0.314
B	0.880	0.815	0.335	0.677
C	0.568	0.375	0.235	0.393
D	0.610	0.668	0.325	0.534
Dose marg	0.618	0.544	0.277	0.480

ANOVA with interaction

Consider a balanced two-factor experiment with n responses at each combination of the a levels of factor A (F1), and with the b levels of factor B (F2). We express the ANOVA model in terms of cell (treatment) means μ_{ij} as

$$Y_{ijk} = \mu_{ij} + \varepsilon_{ijk}$$

- Y_{ijk} is the k th response at the i th level of A and the j th level of B.
- μ_{ij} are parameters, cell mean for treatment ij
- ε_{ijk} are independent $N(0, \sigma^2)$
- $i = 1, \cdots, a; j = 1, \cdots, b; k = 1, \cdots, n$

The Factor Effects or interaction model expresses the population means as

$$\mu_{ij} = \mu_{..} + \alpha_i + \beta_j + (\alpha\beta)_{ij}$$

- $\mu_{..}$ is a grand mean, $\mu_{..} = \sum_i \sum_j \mu_{ij}/ab$
- α_i is the effect for the ith level of F1
  ——$\alpha_i = \mu_{i.} - \mu_{..}, \sum_{i=1}^{a} \alpha_i = 0$
- β_j is the effect for the jth level of F2
  ——$\beta_j = \mu_{.j} - \mu_{..}, \sum_{j=1}^{b} \beta_j = 0$
- $(\alpha\beta)_{ij}$ is the interaction effect when factor A is at the ith level and factor B is at the jth level.

$$(\alpha\beta)_{ij} = \mu_{ij} - \mu_{i.} - \mu_{.j} + \mu_{..}$$

The interaction model is written as

$$Y_{ijk} = \mu_{..} + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \epsilon_{ijk}$$

where

- $\mu_{..}$ is a constant
- α_i are constants subject to the restriction $\sum \alpha_i = 0$
- β_j are constants subject to the restriction $\sum \beta_j = 0$
- $(\alpha\beta)_{ij}$ are constants subject to the restrictions:

$$\sum_i (\alpha\beta)_{ij} = 0, j = 1, \cdots, b$$

$$\sum_j (\alpha\beta)_{ij} = 0, i = 1, \cdots, a$$

- ε_{ijk} are independent $N(0, \sigma^2)$
- $i = 1, 2, \cdots, a, j = 1, 2, \cdots, b$ and $k = 1, 2, \cdots, n$.
  Informally,

  Response = Grand mean+F1 effect+F2 effect+F1-by-F2 interaction +residual.

Additive Model:
The model with no interaction is called an additive model or main effects model

$$Y_{ijk} = \mu_{..} + \alpha_i + \beta_j + \varepsilon_{ijk}$$

- $\mu_{..}$ is a constant
- α_i are constants subject to the restriction $\sum \alpha_i = 0$
- β_j are constants subject to the restriction $\sum \beta_j = 0$
- ε_{ijk} are independent $N(0, \sigma^2)$
- $i = 1, 2, \cdots, a, j = 1, 2, \cdots, b$ and $k = 1, 2, \cdots, n$.

Define

$$\bar{y}_{ij\cdot} = \frac{1}{n}\sum_{k=1}^{n} y_{ijk}$$

$$\bar{y}_{i\cdot\cdot} = \frac{1}{bn}\sum_{j=1}^{b}\sum_{k=1}^{n} Y_{ijk}$$

$$\bar{y}_{\cdot j\cdot} = \frac{1}{an}\sum_{i=1}^{a}\sum_{k=1}^{n} Y_{ijk}$$

$$\bar{y}_{\cdots} = \frac{1}{abn}\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{k=1}^{n} Y_{ijk}$$

Estimators:

Parameter	Estimator
$\mu_{..}$	$\bar{Y}_{...}$
α_i	$\bar{Y}_{i..} - \bar{Y}_{...}$
β_j	$\bar{Y}_{.j.} - \bar{Y}_{...}$
$(\alpha\beta)_{ij}$	$\bar{Y}_{ij.} - \bar{Y}_{i..} - \bar{Y}_{.j.} + \bar{Y}_{...}$
μ_{ij}	$\bar{Y}_{ij.}$

Breakdown the total sum of squares

$$Y_{ijk} - \bar{Y}_{...} = Y_{ij.} - \bar{Y}_{...} + Y_{ijk} - \bar{Y}_{ij.}$$

$Y_{ijk} - \bar{Y}_{...}$: total deviation
$Y_{ij.} - \bar{Y}_{...}$: deviation of estimated treatment mean around overall mean
$Y_{ijk} - \bar{Y}_{ij.}$: deviation around estimated treatment mean
Square both sides

$$\begin{aligned}\sum_i \sum_j \sum_k (Y_{ijk} - \bar{Y}_{...})^2 &= n \sum_i \sum_j (\bar{Y}_{ij.} - \bar{Y}_{...})^2 \\ &+ \sum_i \sum_j \sum_k (Y_{ijk} - \bar{Y}_{ij.})^2\end{aligned}$$

This is a one-way model approach, SSTO = SSTR + SSE

Assess the factor effects and interaction effects

$$Y_{ijk} - \bar{Y}_{...} = (Y_{i..} - \bar{Y}_{...}) + (\bar{Y}_{.j.} - \bar{Y}_{...}) + (Y_{ij.} - \bar{Y}_{i..} - \bar{Y}_{.j.} + \bar{Y}_{...}) + (Y_{ijk} - \bar{Y}_{ij.})$$

- $Y_{ijk} - \bar{Y}_{...}$: Total variability
- $Y_{i..} - \bar{Y}_{...}$: A main effect
- $\bar{Y}_{.j.} - \bar{Y}_{...}$: B main effect
- $Y_{ij.} - \bar{Y}_{i..} - \bar{Y}_{.j.} + \bar{Y}_{...}$: AB interaction effect
- $Y_{ijk} - \bar{Y}_{ij.}$: Deviation around estimated treatment mean

$$\begin{aligned}\sum_i \sum_j \sum_k (Y_{ijk} - \bar{Y}_{...})^2 &= nb \sum_i (Y_{i..} - \bar{Y}_{...})^2 \\ &+ na \sum_j (Y_{.j.} - \bar{Y}_{...})^2 \\ &+ n \sum_i \sum_j (Y_{ij.} - \bar{Y}_{i..} - \bar{Y}_{.j.} + \bar{Y}_{...})^2 \\ &+ \sum_i \sum_j \sum_k (Y_{ijk} - \bar{Y}_{ij.})^2\end{aligned}$$

$$SSTO = SSA + SSB + SSAB + SSE$$

$$SSTO = \sum_i \sum_j \sum_k (Y_{ijk} - \bar{Y}_{...})^2$$

$$SSA = bn \sum_i (Y_{i..} - \bar{Y}_{...})^2, SSB = an \sum_j (Y_{.j.} - \bar{Y}_{...})^2$$

$$SSAB = n \sum_i \sum_j (Y_{ij.} - \bar{Y}_{i..} - \bar{Y}_{.j.} + \bar{Y}_{...})^2, SSE = \sum_i \sum_j \sum_k (Y_{ijk} - \bar{Y}_{ij.})^2$$

ANOVA table for two-factor study with fixed factor levels and with balanced design.

Sources	df	SS	MS	E(MS)
A	a-1	SSA	$\frac{SSA}{a-1}$	$\sigma^2 + nb\frac{\sum(\mu_{i.} - \mu_{..})^2}{a-1}$
B	b-1	SSB	$\frac{SSB}{(b-1)}$	$\sigma^2 + na\frac{\sum(\mu_{.j} - \mu_{..})^2}{b-1}$
AB	(a-1)(b-1)	SSAB	$\frac{SSAB}{(a-1)(b-1)}$	$\sigma^2 + \frac{n\sum_i\sum_j(\mu_{ij} - \mu_{i.} - \mu_{.j} + \mu_{..})^2}{(a-1)(b-1)}$
Error	ab(n-1)	SSE	$\frac{SSE}{ab(n-1)}$	σ^2
SSTO	abn-1	SSTO		

- $\alpha_i = \mu_{i.} - \mu_{..} = 0 \rightarrow E[MSA] = E[MSE]$, Otherwise, $E[MSA] > E[MSE]$
- $\beta_j = \mu_{.j} - \mu_{..} = 0 \rightarrow E[MSB] = E[MSE]$, Otherwise, $E[MSB] > E[MSE]$
- $(\alpha\beta)_{ij} = \mu_{ij} - \mu_{i.} - \mu_{.j} + \mu_{..} = 0 \rightarrow E[MSAB] = E[MSE]$
  Otherwise, $E[MSAB] > E[MSE]$
- Suggests that F^* test statistics based on the ratios of MSA/MSE, MSB/MSE, $MSAB/MSE$ will provide info about the main effects and interactions of the two factors, with large values of the F^* indicating the presence of effects.

Test of no A effect

$$H_0 : \alpha_1 = \alpha_2 = \cdots = \alpha_a = 0$$

$$H_\alpha : \text{not all } \alpha_i \text{ equal to } 0$$

$$F_A^* = \frac{MSA}{MSE}$$

- Under H_0, F_A^* statistic is distributed as F with $a-1$ numerator degrees of freedom and $ab(n-1)$ denominator degrees of freedom.
- Reject H_0 if $F_A^* > F(1-\alpha; a-1, ab(n-1))$
  ——H_0 is rejected when the Factor A marginal means $\bar{Y}_{i\cdot\cdot}$ vary significantly relative to the within sample variation. Equivalently, H_0 is rejected when the sum of squared factor A effects (between sample variation) is large relative to the within sample variation.

Test of no Factor B effect

$$H_0 : \beta_1 = \beta_2 = \cdots = \beta_b = 0$$

$$H_\alpha : \text{not all } \beta_j \text{ equal to } 0$$

- Test statistic
$$F_B^* = \frac{MSB}{MSE}$$
- Under H_0, F_B^* statistic is distributed as F with $b-1$ numerator degrees of freedom and $ab(n-1)$ denominator degrees of freedom
- Reject H_0 if $F_B^* > F(1-\alpha; b-1, ab(n-1))$

Test of no interaction

$$H_0 : (\alpha\beta)_{11} = \cdots = (\alpha\beta)_{ab} = 0$$

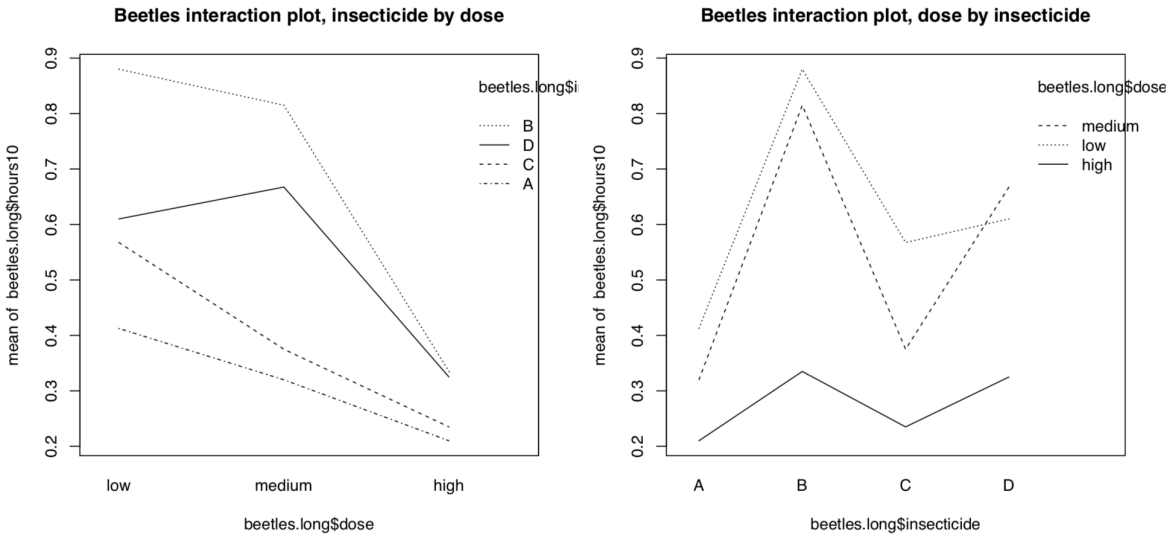
$$H_\alpha : \text{not all } (\alpha\beta)_{ij} \text{ equal to } 0$$

- Test statistic
$$F^*_{AB} = \frac{MSAB}{MSE}$$
- Under H_0, F^*_{AB} statistic is distributed as F with $(a-1)(b-1)$ numerator degrees of freedom and $ab(n-1)$ denominator degrees of freedom.
- Reject H_0 if $F^*_{AB} > F(1-\alpha; (a-1)(b-1), ab(n-1))$

ANOVA with interaction

When there are two factors, it is possible that the effect of one factor depends on the value of the other factor. For this example, this could mean that the effect of the dose depends on the insecticide.

```
> ##fit ANOVA model
> myfit <- aov(hours10~ dose*insecticide, data=beetles.long)
> summary(myfit) #ANOVA table
                 Df Sum Sq Mean Sq F value   Pr(>F)
dose              2 1.0330  0.5165  23.222 3.33e-07 ***
insecticide       3 0.9212  0.3071  13.806 3.78e-06 ***
dose:insecticide  6 0.2501  0.0417   1.874    0.112
Residuals        36 0.8007  0.0222
```




```
interaction.plot(beetles.long$dose, beetles.long$insecticide,
beetles.long$hours10 , main = "insecticide by dose")
interaction.plot(beetles.long$insecticide, beetles.long$dose,
beetles.long$hours10, main = "dose by insecticide")
```

ANOVA with interaction

The idea behind the plots is that we can see whether the effect of the insecticide depends on the dose, or similarly, whether the effect of the dose depends on the insecticide.

- In the left plot on the previous slide, there is a rank ordering of insecticides based on survival times.
  ——-Here lower survival times means a more effective insecticide, and for each dose, we appear to have that insecticide A has the lowest survival time, followed by C, then followed by D, and finally B.
- If there were a strong interaction between dose and insecticide, you might find that one insecticide is the most effective at low doses, while another is the the most effective at higher doses. In this case, the rank ordering of insecticides doesn't change much.

ANOVA with interaction

A statistical test for interaction is testing whether the lines in the interaction plot are parallel, taking into account variability in the data.

——This does not necessarily mean that the lines are straight, but that the spacing in between the lines doesn't change significantly from level to level of the factor on the horizontal axis.

—— An interaction can show up in the interaction plots either by curves crossing or by being significantly non-parallel.

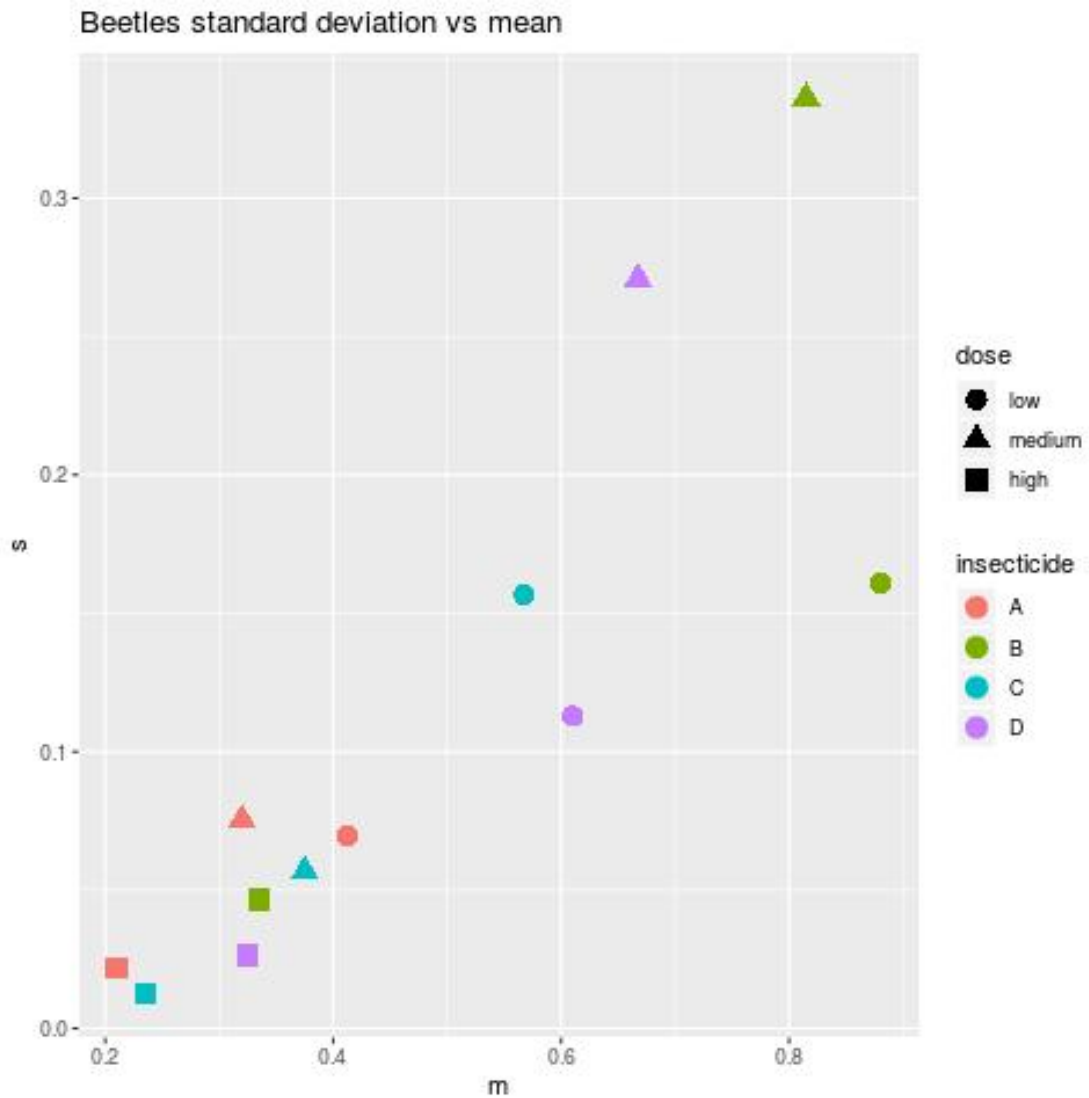
Comments:

- Always test the interaction first, can't really interpret the effects of factors A and B separately if interaction is significant.
  If there is an interaction present, A and B main effects should not be tested
- Interaction test at α_{AB}, A test at α_A, B test at α_B
  The family of these three tests has a level of significance that is at least at large as the largest of α_{AB}, α_A and α_B.
  Three tests are not independent, since each F-test has MSE as its denominator. Two ways to approximate the overall family level of significance
  Bonferroni's method,overall family level of significance $\leq \alpha_A + \alpha_B + \alpha_{AB}$
  Kimball's inequality family level of significance $\leq 1 - (1 - \alpha_A)(1 - \alpha_B)(1 - \alpha_{AB})$

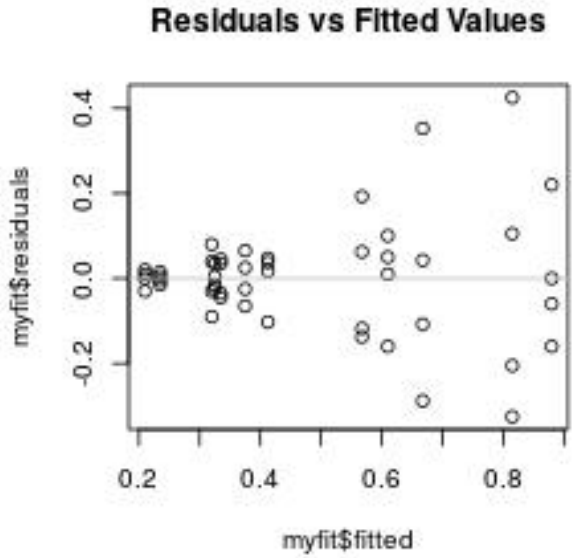
Example: $\alpha_A = \alpha_B = \alpha_{AB} = 0.05$ the family level of significance $\leq 1 - 0.95 * 0.95 * 0.95 = 0.143$

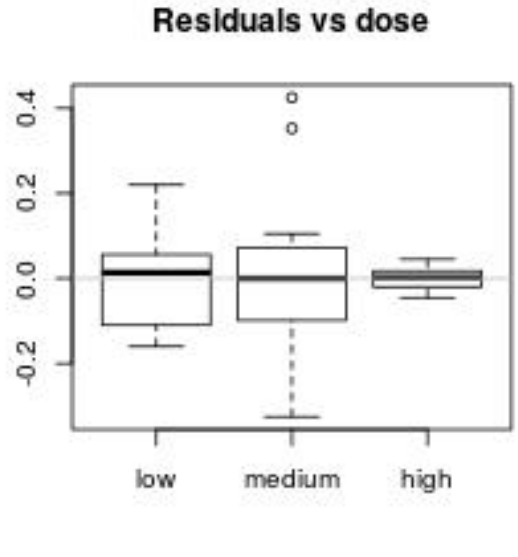
Diagnostics

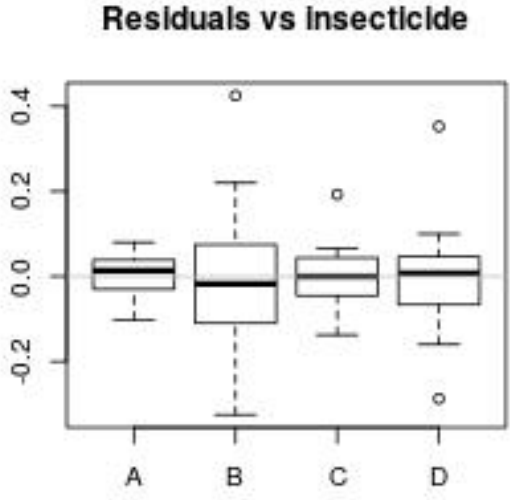
Plot of the standard deviation vs mean shows an increasing trend.

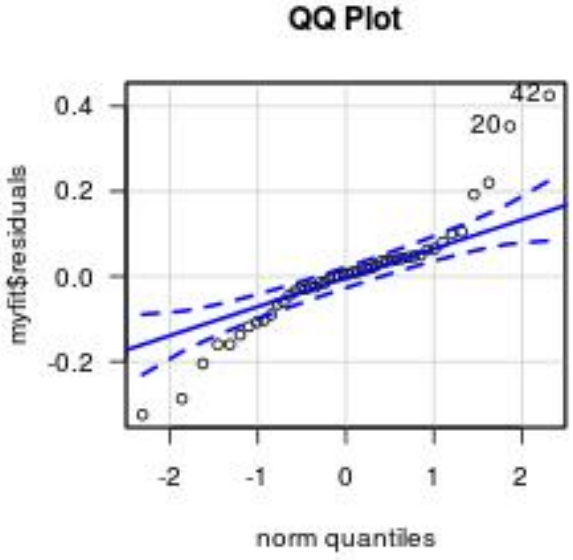


Diagnostic plots of the model with interactions









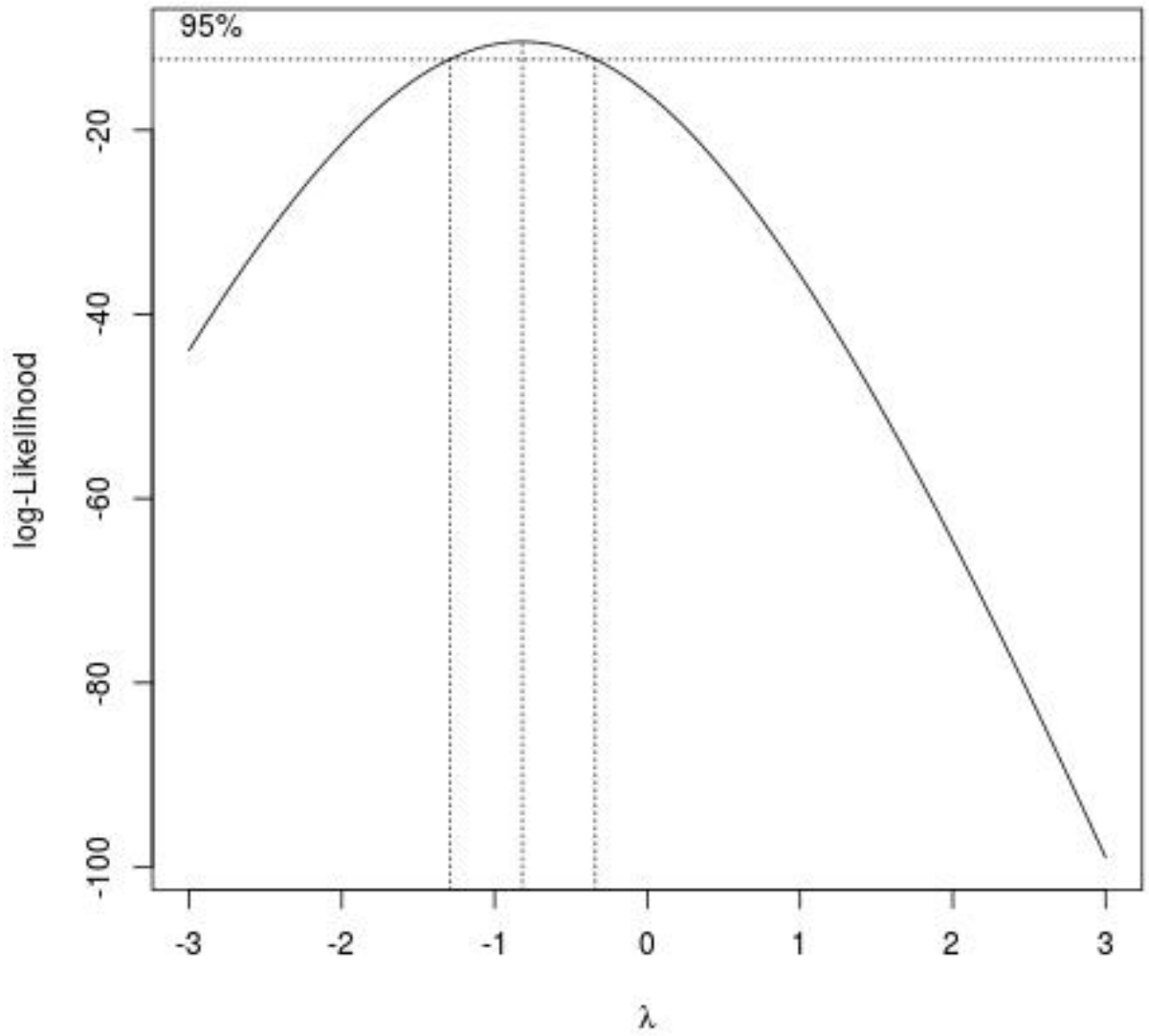
Diagnostic plots show the following features

- The normal quantile plot shows an "S" shape rather than a straight line, suggesting the residuals are not normal.
- The residuals vs the fitted (predicted) values show that the higher the predicted value the more variability (horn shaped). This could be seen from the plot of standard deviation v.s. mean.
- A couple of outliers shown in the residual vs dose plot and qq plot

Transformations

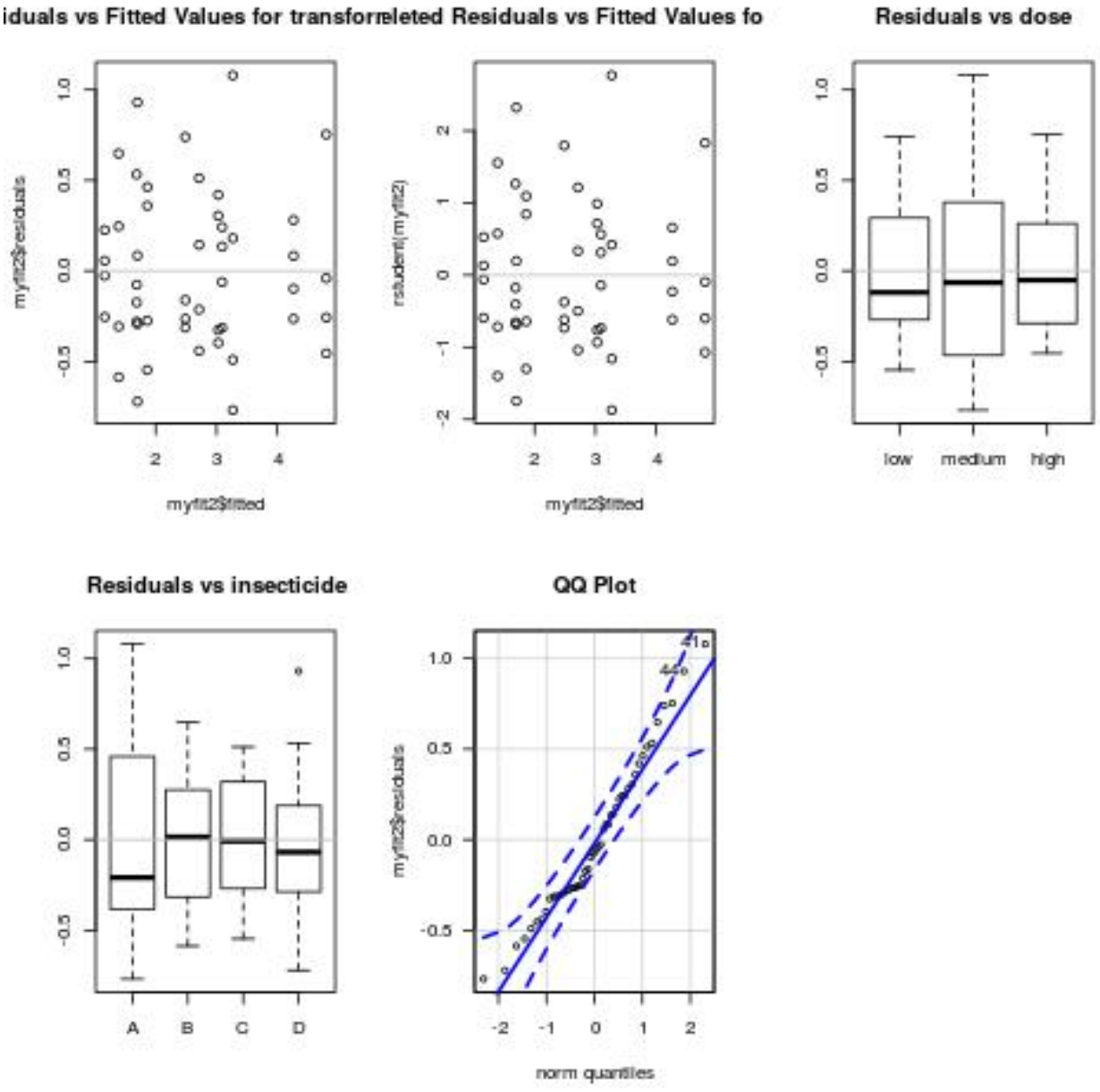
```
#transformation
par(mfrow=c(1,1))
library(MASS)
boxcox(myfit, lambda = seq(-3, 3, length = 10),
plotit = TRUE)
```

- $\lambda = -1$ is within the 95% confidence interval, we will try a transformation of $y^* = 1/y$
- the inverse survival time has a natural interpretation as the dying rate. For example, if you survive 2 hours, then 1/2 is the proportion of your remaining lifetime expired in the next hour.


95%
log-Likelihood
-20
-40
-60
-80
-100
-3
-2
-1
0
1
2
3
λ

```
##transformations on $y$
myfit2 <- aov(1/hours10 ~ dose*insecticide, data = beetles.
summary(myfit2)
> summary(myfit2)
                  Df Sum Sq Mean Sq F value   Pr(>F)
dose               2  34.88  17.439   72.64 2.31e-13 ***
insecticide        3  20.41   6.805   28.34 1.38e-09 ***
dose:insecticide   6   1.57   0.262    1.09    0.387
Residuals         36   8.64   0.240
```

Diagnostic plots of the transformed model



Diagnostic plots of the transformed model show the following features

- The normal quantile plot shows a rough straight line, suggesting the residuals are normal.
- The residuals vs the fitted (predicted) values show a random pattern.
- No outliers detected from the studentized deleted residual plot
- Normality assumption and constant variance assumption seem not violated.

Recall Additive Model: The model with no interaction is called an additive model or main effects model

$$Y_{ijk} = \mu_{..} + \alpha_i + \beta_j + \varepsilon_{ijk}$$

- $\mu_{..}$ is a constant
- α_i are constants subject to the restriction $\sum \alpha_i = 0$
- β_j are constants subject to the restriction $\sum \beta_j = 0$
- ε_{ijk} are independent $N(0, \sigma^2)$
- $i = 1, 2, \cdots, a, j = 1, 2, \cdots, b$ and $k = 1, 2, \cdots, n$.

Test of no Factor A effect

$$H_0 : \alpha_1 = \alpha_2 = \cdots = \alpha_a = 0$$

$$H_\alpha : \text{not all } \alpha_i \text{ equal to } 0$$

$$F_A^* = \frac{MSA}{MSE}$$

- Under H_0, F_A^* statistic is distributed as F with $a-1$ numerator degrees of freedom and $abn-a-b+1$ denominator degrees of freedom.
- Reject H_0 if $F_A^* > F(1-\alpha; a-1, abn-a-b+1)$

Test of no Factor B effect

$$H_0 : \beta_1 = \beta_2 = \cdots = \beta_b = 0$$

using an F test

$$H_\alpha : \text{not all } \beta_i \text{ equal to } 0$$

based on

$$F_B^* = \frac{MSB}{MSE}$$

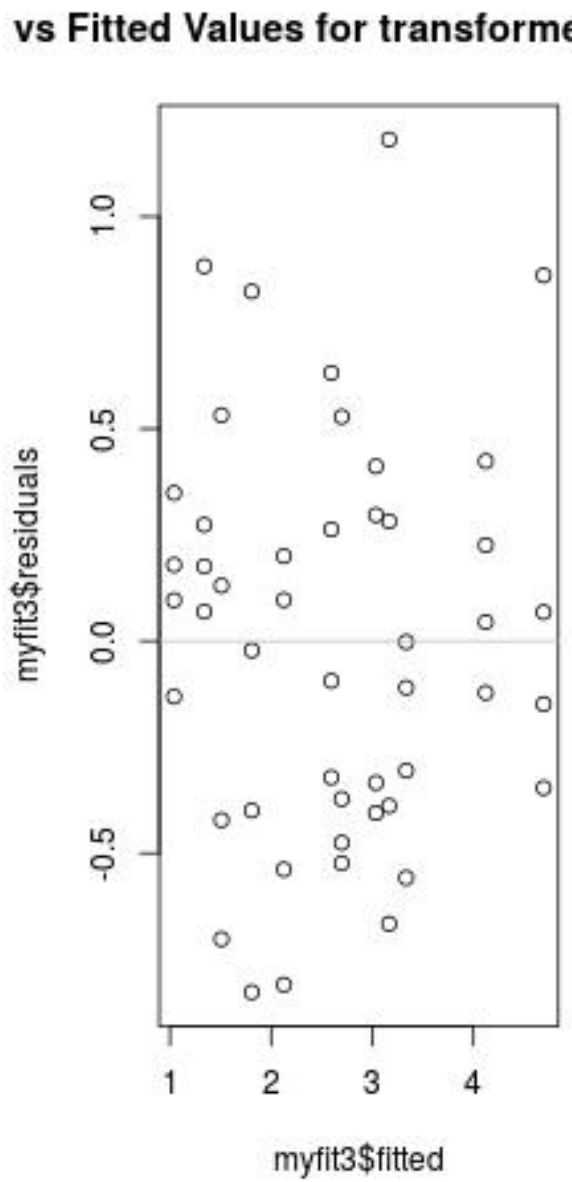
- Under H_0, F_B^* statistic is distributed as F with $b-1$ numerator degrees of freedom and $abn-a-b+1$ denominator degrees of freedom.
- Reject H_0 if $F_B^* > F(1-\alpha; b-1, abn-a-b+1)$

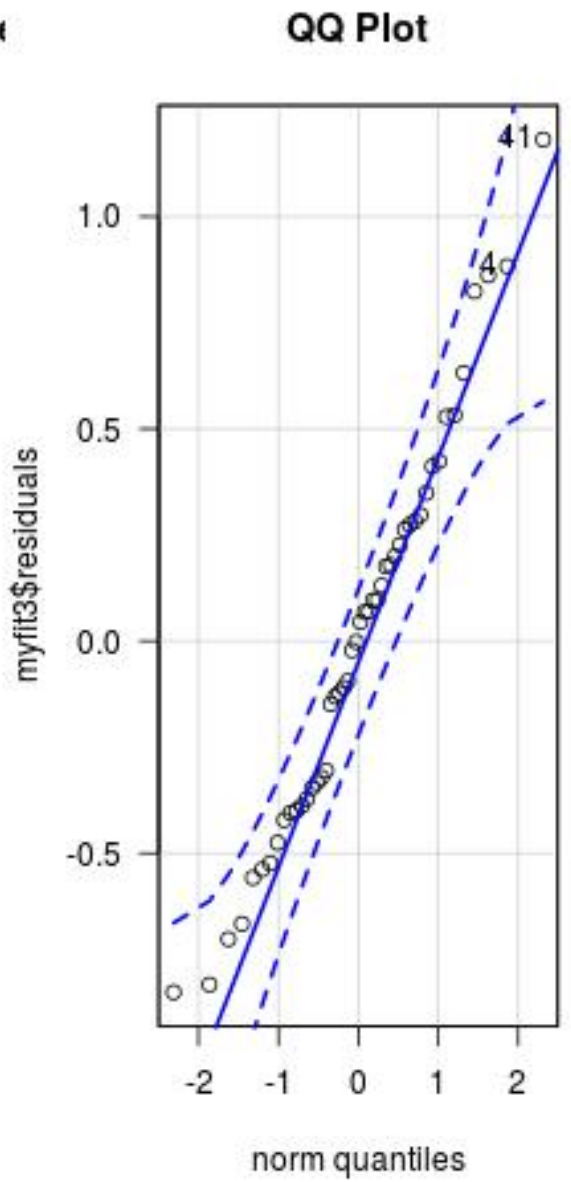
Comments: If there is an interaction, the F tests we did for additive model are conservative (don't reject often enough), since MSE includes interaction MS effect and may be too big.

Reduced Model: Drop the nonsignificant interaction term, refit model

```
> ##refit model without interaction term
>
> myfit3 <- aov(1/hours10 ~ dose+insecticide,
data = beetles.long)
> summary(myfit3)
             Df Sum Sq Mean Sq F value   Pr(>F)
dose          2  34.88  17.439   71.71 2.86e-14 ***
insecticide   3  20.41   6.805   27.98 4.19e-10 ***
Residuals    42  10.21   0.243
```

Diagnostic plots of the reduced transformed model





Diagnostic plots of the reduced transformed model show the following features

- The normal quantile plot shows a rough straight line, suggesting the residuals are normal.
- The residuals vs the fitted (predicted) values show a random pattern.
- No outliers detected from the studentized deleted residual plot.
- Normality assumption and constant variance assumption seem not violated.