

# STAT 516 Lec 08

One- and two-way random effects models

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## Fish net data from Dr. Longnecker's Notes

Strength of fish net material made from four randomly chosen machines.

	Strength Measurements: $y_{ij}$					
Machine	1	2	3	4	5	Mean: $\bar{y}_i$
1	128	127	129	126	128	127.6
2	121	120	123	122	125	122.2
3	126	125	127	125	124	125.4
4	125	126	129	128	127	127.0

```
y <- c(128,127,129,126,128,121,120,123,122,125,  
      126,125,127,125,124,125,126,129,128,127)  
machine <- as.factor(c(1,1,1,1,1,2,2,2,2,2,3,3,3,3,3,4,4,4,4,4))
```

Is there significant machine-to-machine variability?

# One-way random effects model

Suppose

$$Y_{ij} = \mu + A_i + \varepsilon_{ij}, \quad i = 1, \dots, a, \quad j = 1, \dots, n_i$$

where

- ▶  $Y_{ij}$  is the response of EU  $j$  in treatment group  $i$ .
- ▶ the  $A_i$  are independent  $\mathcal{N}(0, \sigma_A^2)$  rvs called random effects.
- ▶ the  $\varepsilon_{ij}$  are independent  $\mathcal{N}(0, \sigma_\varepsilon^2)$ .
- ▶ the  $A_i$  and the  $\varepsilon_{ij}$  are independent of each other.
- ▶  $\mu$  is the overall mean
- ▶ we call  $\sigma_A^2$  and  $\sigma_\varepsilon^2$  variance components.

Until now we have studied fixed-effects models.

Assume a balanced design, i.e.  $n_1 = \dots = n_a = n$ .

# Goals in the one-way random effects model

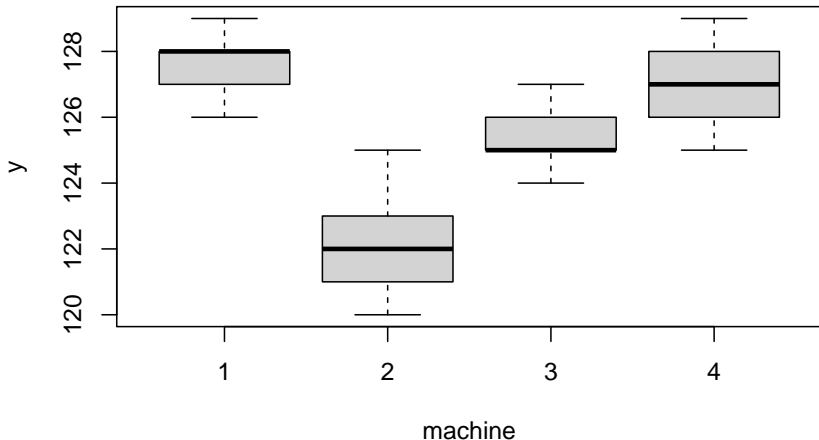
In the one-way random effects model we wish to

1. Visualize the data.
2. Decompose the variability in the  $Y_{ijk}$  into its sources.
3. Test  $H_0: \sigma_A^2 = 0$  versus  $H_1: \sigma_A^2 > 0$ .
4. Estimate the variance components  $\sigma_A^2$  and  $\sigma_\varepsilon^2$ .
5. Estimate the overall mean  $\mu$ .
6. “Predict” the realized values of  $A_1, \dots, A_a$ .
7. Check whether the model assumptions are satisfied.

## Fish net data (cont)

Side-by-side boxplots are a natural choice if the  $n_i$  are not too small.

```
boxplot(y~machine)
```



## Sums of squares for one-way random effects model

Sum of squares	Symbol	Formula
Total	$SS_{\text{Tot}}$	$\sum_{i=1}^a \sum_{j=1}^n (Y_{ij} - \bar{Y}_{..})^2$
Treatment	$SS_{\text{Trt}}$	$\sum_{i=1}^a n(\bar{Y}_{i.} - \bar{Y}_{..})^2$
Error	$SS_{\text{Error}}$	$\sum_{i=1}^a \sum_{j=1}^n (Y_{ij} - \bar{Y}_{i.})^2$

We have the decomposition  $SS_{\text{Tot}} = SS_{\text{Trt}} + SS_{\text{Error}}$ .

## Fish net data (cont)

Easiest way to obtain sums of squares:

```
lm_out <- lm(y ~ machine)

y.. <- mean(y)
SStot <- sum((y - y..)**2)
SSerror <- sum(lm_out$residuals**2)
SStrt <- SStot - SSerror
```

We obtain  $SS_{\text{Tot}} = 122.95$ ,  $SS_{\text{Trt}} = 87.75$ , and  $SS_{\text{Error}} = 35.2$ .

## ANOVA table for one-way random effects model

Obtain the MS values by dividing the SS values by the Df values.

Source	Df	SS	MS	F value
Treatment	$a - 1$	$SS_{\text{Trt}}$	$MS_{\text{Trt}}$	$F_{\text{test}} = MS_{\text{Trt}} / MS_{\text{Error}}$
Error	$a(n - 1)$	$SS_{\text{Error}}$	$MS_{\text{Error}}$	
Total	$an - 1$	$SS_{\text{Tot}}$		

We reject  $H_0: \sigma_A^2 = 0$  if  $F_{\text{test}} > F_{a-1, a(n-1), \alpha}$ .

The corresponding p-value is  $P(F > F_{\text{test}})$ , where  $F \sim F_{a-1, a(n-1), \alpha}$ .

**Discuss:** It can be shown that  $SS_{\text{Trt}}$  and  $SS_{\text{Error}}$  are independent and

$$\frac{SS_{\text{Trt}}}{n\sigma_A^2 + \sigma_\varepsilon^2} \sim \chi_{a-1}^2 \quad \text{and} \quad \frac{SS_{\text{Error}}}{\sigma_\varepsilon^2} \sim \chi_{a(n-1)}^2.$$

Show that  $F_{\text{test}} = \frac{MS_{\text{Trt}}}{MS_{\text{Error}}} \sim F_{a-1, a(n-1)}$  under  $H_0: \sigma_A^2 = 0$ .

## Fish net data (cont)

We obtain the ANOVA table just as we did in the fixed-effects case.

```
anova(lm_out)
```

```
Analysis of Variance Table
```

```
Response: y
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
machine	3	87.75	29.25	13.296	0.0001301 ***
Residuals	16	35.20	2.20		

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The small p-value indicates strong evidence against  $H_0: \sigma_A^2 = 0$ .

## Expected mean squares in one-way random-effects model

In models with random effects, we like to track how the variance components  $\sigma_A^2$  and  $\sigma_\varepsilon^2$  affect the expected values of the mean squares.

Source	Df	Expected mean square
Treatment	$a - 1$	$n\sigma_A^2 + \sigma_\varepsilon^2$
Error	$a(n - 1)$	$\sigma_\varepsilon^2$

## Method of moments for estimating $\sigma_A^2$ and $\sigma_\varepsilon^2$

The method of moments (MoM) is one way to estimate the variance components.

1. Set the observed mean squares equal to the expected mean squares:

$$MS_{\text{Trt}} \stackrel{\text{set}}{=} n\sigma_A^2 + \sigma_\varepsilon^2 \quad \text{and} \quad MS_{\text{Error}} \stackrel{\text{set}}{=} \sigma_\varepsilon^2$$

2. Solve these equations for  $\sigma_A^2$  and  $\sigma_\varepsilon^2$ , which gives

$$\dot{\sigma}_A^2 = \frac{MS_{\text{Trt}} - MS_{\text{Error}}}{n} \quad \text{and} \quad \dot{\sigma}_\varepsilon^2 = MS_{\text{Error}}.$$

MoM method is deprecated because it is possible to get  $\dot{\sigma}_A^2 < 0$ .

## Fish net data (cont)

Compute the MoM estimators  $\dot{\sigma}_A^2$  and  $\dot{\sigma}_\varepsilon^2$  for the fish net data.

```
n <- 5
a <- 4
MStrt <- SStrt / (a - 1)
MSerror <- SSerror / (a*(n-1))

sigma_e_mom <- sqrt(MSerror)
sigma_A_mom <- sqrt((MStrt - MSerror)/n)
```

We obtain  $\dot{\sigma}_A^2 = 5.41$  and  $\dot{\sigma}_\varepsilon^2 = 2.2$ .

# REML for estimating the variance components

- ▶ REML stands for restricted maximum likelihood.
- ▶ It is a recipe (beyond course) for estimating variance components.
- ▶ In the one-way random-effects model it results in

$$\hat{\sigma}_A^2 = \begin{cases} \dot{\sigma}_A^2 & \text{if } \dot{\sigma}_A^2 \geq 0 \\ 0 & \text{if } \dot{\sigma}_A^2 < 0 \end{cases} \quad \text{and} \quad \hat{\sigma}_\varepsilon^2 = \begin{cases} \dot{\sigma}_\varepsilon^2 & \text{if } \dot{\sigma}_A^2 \geq 0 \\ \frac{SS_{\text{Tot}}}{an - 1} & \text{if } \dot{\sigma}_A^2 < 0 \end{cases}$$

- ▶ Will always return a nonnegative estimate of  $\sigma_A^2$ .
- ▶ Same as MoM estimator if  $\dot{\sigma}_A^2 > 0$ .
- ▶ The “state of the art” is to use REML estimation.

## Fish net data (cont)

Use R package `lmerTest` to compute the REML estimates of  $\sigma_A^2$  and  $\sigma_\varepsilon^2$ .

```
# first time run install.packages("lmerTest")
library(lmerTest) # may need to run install.packages("Matrix") for this to work
lmer_out <- lmer(y ~ 1 + (1 | machine))
summary(lmer_out)
```

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
```

```
Formula: y ~ 1 + (1 | machine)
```

```
REML criterion at convergence: 79.7
```

```
Scaled residuals:
```

	Min	1Q	Median	3Q	Max
	-1.6531	-0.6884	-0.1019	0.4846	1.7179

```
Random effects:
```

Groups	Name	Variance	Std.Dev.
machine	(Intercept)	5.41	2.326
	Residual	2.20	1.483

```
Number of obs: 20, groups: machine, 4
```

```
Fixed effects:
```

	Estimate	Std. Error	df	t value	Pr(> t )
(Intercept)	125.550	1.209	3.000	103.8	1.97e-06 ***

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## Estimating $\mu$ and predicting $A_1, \dots, A_a$ .

- ▶ We estimate the overall mean  $\mu$  with  $\bar{Y}_{..}$ .
- ▶ We also wish to guess at the realized values of  $A_1, \dots, A_a$ .
- ▶ Call this *prediction* instead of estimation, because  $A_1, \dots, A_a$  are random variables rather than parameters with fixed values.
- ▶ A recipe (beyond course) for the best linear unbiased predictor yields

$$\hat{A}_i = \left( \frac{n\hat{\sigma}_A^2}{n\hat{\sigma}_A^2 + \hat{\sigma}_\varepsilon^2} \right) (\bar{Y}_{i.} - \bar{Y}_{..}) \quad \text{for } i = 1, \dots, a.$$

## Fish net data (cont)

Obtain the predicted values of  $A_1$ ,  $A_2$ ,  $A_3$ , and  $A_4$  for the fish net data.

```
yi. <- aggregate(y, by = list(machine = machine), mean)$x
# use MoMs, since sA2_dot > 0
Ahat <- (n * sigma_A_mom**2)/(n * sigma_A_mom**2 + sigma_e_mom**2) * (yi. - y..)
Ahat
```

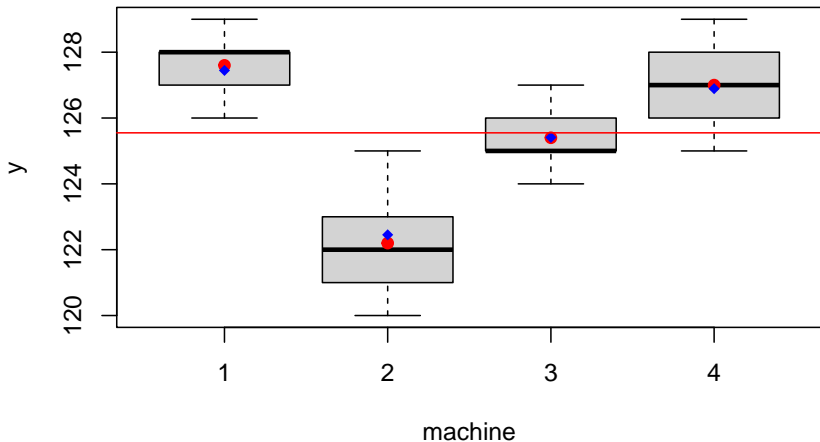
```
[1] 1.8958120 -3.0980342 -0.1387179 1.3409402
```

Can use `predict()` on the `lmer()` output to obtain the  $\hat{A}_i$  values:

```
predict(lmer_out, random.only = TRUE) # gives estimates of the A_i for each obs
```

1	2	3	4	5	6	7
1.8958120	1.8958120	1.8958120	1.8958120	1.8958120	-3.0980342	-3.0980342
8	9	10	11	12	13	14
-3.0980342	-3.0980342	-3.0980342	-0.1387179	-0.1387179	-0.1387179	-0.1387179
15	16	17	18	19	20	
-0.1387179	1.3409402	1.3409402	1.3409402	1.3409402	1.3409402	

```
boxplot(y~machine)
points(yi.~as.factor(levels(machine)),col="red",pch=19)
points((y.. + Ahat)~as.factor(levels(machine)),col="blue",pch=18)
abline(h = y..,col = "red")
```



## Confidence interval for the overall mean

- ▶ Under the one-way random effects model, we can show

$$\bar{Y}_{..} \sim \mathcal{N}\left(\mu, \frac{n\sigma_A^2 + \sigma_\varepsilon^2}{na}\right).$$

- ▶ From here, using  $\frac{SS_{\text{Trt}}}{n\sigma_A^2 + \sigma_\varepsilon^2} \sim \chi_{a-1}^2$ , we have

$$\frac{\bar{Y}_{..} - \mu}{\sqrt{MS_{\text{Trt}}/(na)}} \sim t_{a-1}.$$

- ▶ Thus a  $(1 - \alpha)100\%$  CI for  $\mu$  can be obtained as

$$\bar{Y}_{..} \pm t_{a-1, \alpha/2} \sqrt{\frac{MS_{\text{Trt}}}{an}}.$$

- ▶ `confint()` function on `lmer()` output uses another method.

## Fish net data (cont)

95% confidence interval for  $\mu$  in fish net example.

```
alpha <- 0.05
tval <- qt(1-alpha/2,a-1)
me <- tval * sqrt(MStrt/(a*n))
lo <- y.. - me
up <- y.. + me
c(lo,up)
```

```
[1] 121.7013 129.3987
```

Default confidence intervals from `confint()` function.

```
confint(lmer_out)
```

	2.5 %	97.5 %
.sig01	0.967975	5.093825
.sigma	1.087139	2.194122
(Intercept)	122.890054	128.209944

Wald-type CI  $Y_{..} \pm z_{\alpha/2} \sqrt{MS_{Trt} / (na)}$  on fish net data.

```
confint(lmer_out,method="Wald")
```

```
                2.5 %   97.5 %  
.sig01           NA     NA  
.sigma           NA     NA  
(Intercept) 123.1797 127.9203
```

```
zval <- qnorm(1-alpha/2)  
me <- zval * sqrt(MStrt/(a*n))  
lo <- y.. - me  
up <- y.. + me  
c(lo,up)
```

```
[1] 123.1797 127.9203
```

# Checking model assumptions

Validity of the methods in these slides depends on these assumptions:

1. The responses are normally distributed around the treatment means.  
(Check QQ plot of residuals)
2. The treatment means are normally distributed.  
(The number of groups  $a$  is often too small for this to be checked)
3. The response has the same variance in all treatment groups.  
(Check residuals vs fitted values plot)
4. The response values in each treatment group are independent.  
(No way to check; must trust experimental design)

## Fitted values and residuals in the random effects model

- ▶ Build fitted values from  $\hat{\mu}$  and the predictions  $\hat{A}_1, \dots, \hat{A}_a$  as

$$\hat{Y}_{ij} = \hat{\mu} + \hat{A}_i, \quad \text{for } i = 1, \dots, a, \quad j = 1, \dots, n.$$

- ▶ Our residuals then become

$$\hat{\varepsilon}_{ij} = Y_{ij} - \hat{Y}_{ij}, \quad \text{for } i = 1, \dots, a, \quad j = 1, \dots, n.$$

- ▶ These residuals are not simply the deviations of the responses around their treatment group means (as in fixed effects models)!
- ▶ So  $SS_{\text{Error}}$  is not the sum of squared residuals here.

Use `predict()` on the `lmer()` output to obtain the  $\hat{Y}_{ij} = \hat{\mu} + \hat{A}_i$ .

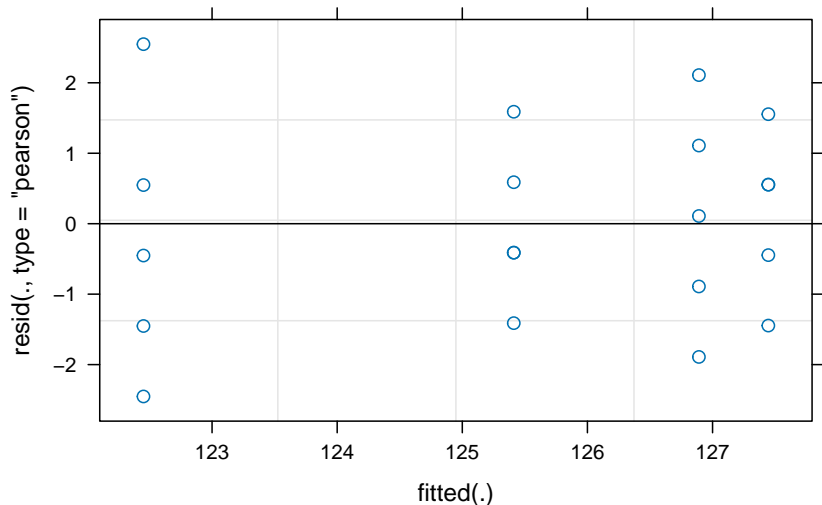
```
predict(lmer_out)
```

1	2	3	4	5	6	7	8
127.4458	127.4458	127.4458	127.4458	127.4458	122.4520	122.4520	122.4520
9	10	11	12	13	14	15	16
122.4520	122.4520	125.4113	125.4113	125.4113	125.4113	125.4113	126.8909
17	18	19	20				
126.8909	126.8909	126.8909	126.8909				

## Fish net data (cont)

Check the residuals vs fitted values plot: Use `plot()` on `lmer()` output.

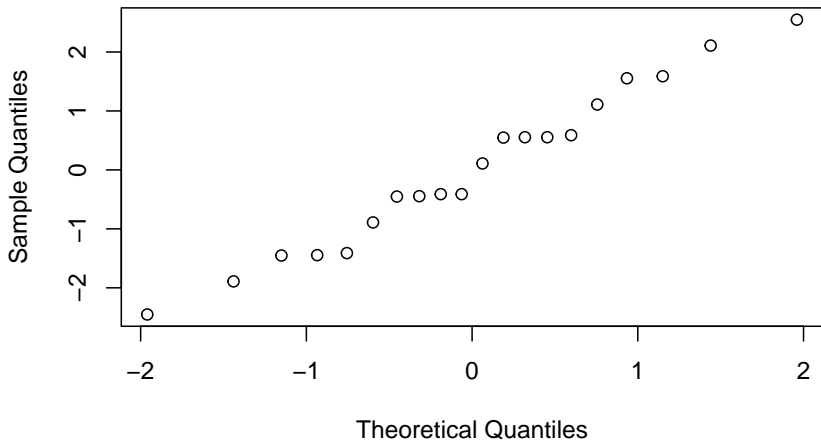
```
plot(lmer_out)
```



Check the normal q-q plot of the residuals:

```
yhat <- predict(lmer_out)
ehat <- y - yhat
qqnorm(ehat)
```

## Normal Q-Q Plot



# Triglyceride level data from Kuehl (2000)

Triglyceride levels in serum samples measured with 4 machines on 4 days.

Day	Machine			
	1	2	3	4
1	142.3, 144.0	148.6, 146.9	142.9, 147.4	133.8, 133.2
2	134.9, 146.3	145.2, 146.3	125.9, 127.6	108.9, 107.5
3	148.6, 156.5	148.6, 153.1	135.5, 138.9	132.1, 149.7
4	152.0, 151.4	149.7, 152.0	142.9, 142.3	141.7, 141.2

Source: Dr. J. Anderson, Beckman Instruments, Inc.

```
tg <- c(142.3, 144.0, 148.6, 146.9, 142.9, 147.4, 133.8, 133.2,  
        134.9, 146.3, 145.2, 146.3, 125.9, 127.6, 108.9, 107.5,  
        148.6, 156.5, 148.6, 153.1, 135.5, 138.9, 132.1, 149.7,  
        152.0, 151.4, 149.7, 152.0, 142.9, 142.3, 141.7, 141.2)  
days <- as.factor(c(rep(1,8), rep(2,8), rep(3,8), rep(4,8)))  
machine <- as.factor(c(1,1,2,2,3,3,4,4,1,1,2,2,3,3,4,4,  
                      1,1,2,2,3,3,4,4,1,1,2,2,3,3,4,4))
```

Machines randomly sampled. Regard days as randomly sampled.

## Two-way random effects model

Assume

$$Y_{ijk} = \mu + A_i + B_j + (AB)_{ij} + \varepsilon_{ijk}$$

for  $i = 1, \dots, a$ ,  $j = 1, \dots, b$ , and  $n = 1, \dots, n$ , where

- ▶  $A_i \stackrel{\text{ind}}{\sim} \mathcal{N}(0, \sigma_A^2)$
- ▶  $B_j \stackrel{\text{ind}}{\sim} \mathcal{N}(0, \sigma_B^2)$
- ▶  $(AB)_{ij} \stackrel{\text{ind}}{\sim} \mathcal{N}(0, \sigma_{AB}^2)$
- ▶  $\varepsilon_{ijk} \stackrel{\text{ind}}{\sim} \mathcal{N}(0, \sigma_\varepsilon^2)$
- ▶ the  $A_i$ ,  $B_j$ , and  $\varepsilon_{ijk}$  are all independent.
- ▶  $\mu$  is the overall mean.
- ▶ we call  $\sigma_A^2$ ,  $\sigma_B^2$ ,  $\sigma_{AB}^2$ , and  $\sigma_\varepsilon^2$  variance components.

Still assume a balanced design, that is  $n_{ij} = n$  for all  $i, j$ .

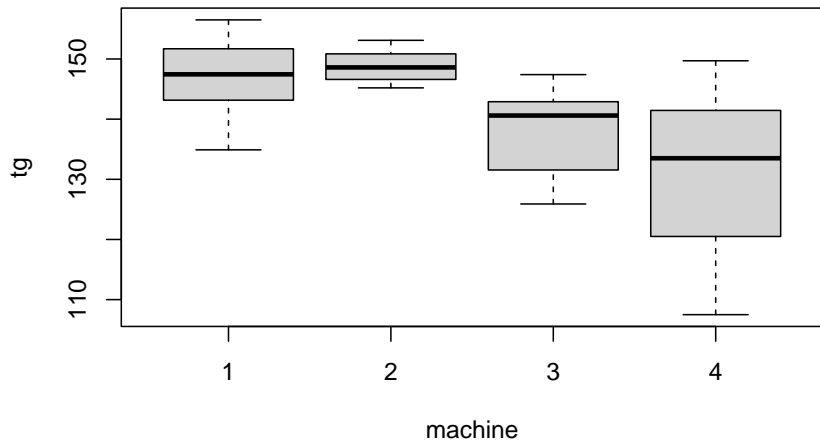
# Goals in the two-way random effects model

In the two-way random effects model we wish to

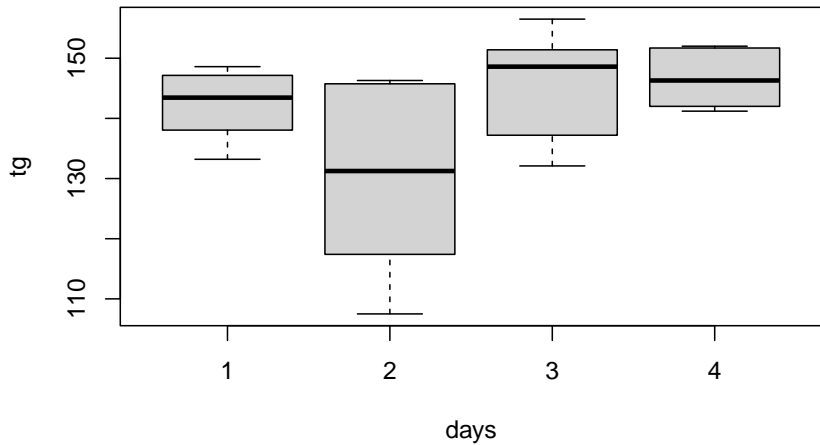
1. Visualize the data.
2. Decompose the variability in the  $Y_{ijk}$  into its sources.
3. Test whether  $\sigma_A^2$ ,  $\sigma_B^2$ , and  $\sigma_{AB}^2$  are equal to zero.
4. Estimate the variance components  $\sigma_A^2$ ,  $\sigma_B^2$ ,  $\sigma_{AB}^2$ , and  $\sigma_\varepsilon^2$ .
5. Estimate the overall mean  $\mu$ .
6. “Predict” the realized values of the random effects.
7. Check whether the model assumptions are satisfied.

# Triglyceride level data (cont)

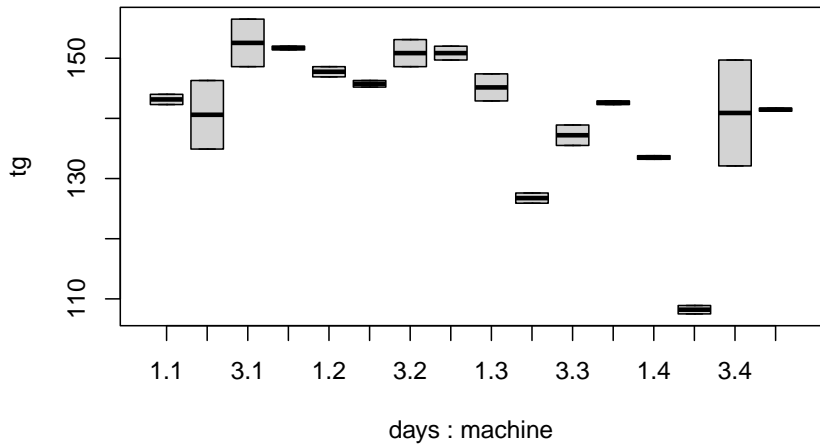
```
boxplot(tg-machine)
```



```
boxplot(tg~days)
```



```
boxplot(tg~days + machine)
```



## Sums of squares for the two-way random effects model

Sum of squares	Symbol	Formula
Total	$SS_{\text{Tot}}$	$\sum_{i=1}^a \sum_{j=1}^b \sum_{k=1}^n (Y_{ijk} - \bar{Y}_{...})^2$
A	$SS_A$	$nb \sum_{i=1}^a (\bar{Y}_{i..} - \bar{Y}_{...})^2$
B	$SS_B$	$na \sum_{j=1}^b (\bar{Y}_{.j.} - \bar{Y}_{...})^2$
AB	$SS_{AB}$	$n \sum_{i=1}^a \sum_{j=1}^b (\bar{Y}_{ij.} - (\bar{Y}_{i..} + \bar{Y}_{.j.} - \bar{Y}_{...}))^2$
Error	$SS_{\text{Error}}$	$\sum_{i=1}^a \sum_{j=1}^b \sum_{k=1}^n (Y_{ijk} - \bar{Y}_{ij.})^2$

We have the decomposition  $SS_{\text{Tot}} = SS_A + SS_B + SS_{AB} + SS_{\text{Error}}$ .

# Full ANOVA table for balanced two-way factorial design

Obtain the MS values by dividing the SS values by the Df values.

Source	Df	SS	MS	F value
A	$a - 1$	$SS_A$	$MS_A$	$F_A =$ $MS_A / MS_{AB}$
B	$b - 1$	$SS_B$	$MS_B$	$F_B =$ $MS_B / MS_{AB}$
AB	$(a - 1)(b - 1)$	$SS_{AB}$	$MS_{AB}$	$F_{AB} =$ $MS_{AB} / MS_{Error}$
Error	$ab(n - 1)$	$SS_{Error}$	$MS_{Error}$	
Total	$abn - 1$	$SS_{Tot}$		

1. Reject  $H_0: \sigma_A^2 = 0$  if  $F_A > F_{a-1, (a-1)(b-1), \alpha}$ .
2. Reject  $H_0: \sigma_B^2 = 0$  if  $F_B > F_{b-1, (a-1)(b-1), \alpha}$ .
3. Reject  $H_0: \sigma_{AB}^2 = 0$  if  $F_{AB} > F_{(a-1)(b-1), ab(n-1), \alpha}$ .

Note  $F_A$  and  $F_B$  are different from their fixed-effects counterparts!

## Expected mean squares in two-way random-effects model

We again tabulate the expected values of the mean squares:

Source	Df	Expected mean square
A	$a - 1$	$nb\sigma_A^2 + n\sigma_{AB}^2 + \sigma_\varepsilon^2$
B	$b - 1$	$na\sigma_B^2 + n\sigma_{AB}^2 + \sigma_\varepsilon^2$
AB	$(a - 1)(b - 1)$	$n\sigma_{AB}^2 + \sigma_\varepsilon^2$
Error	$a(n - 1)$	$\sigma_\varepsilon^2$

**Discuss:** Make F-stat by dividing by the MS having the same expectation under  $H_0$ .

## Triglyceride level data (cont)

Obtain  $p$ -values for testing whether the variance components are zero.

The `anova()` function on the `lm()` output only gives the correct F statistic and  $p$ -value for the interaction.

```
anova_out <- anova(lm(tg ~ days + machine + days:machine))
anova_out
```

Analysis of Variance Table

Response: tg

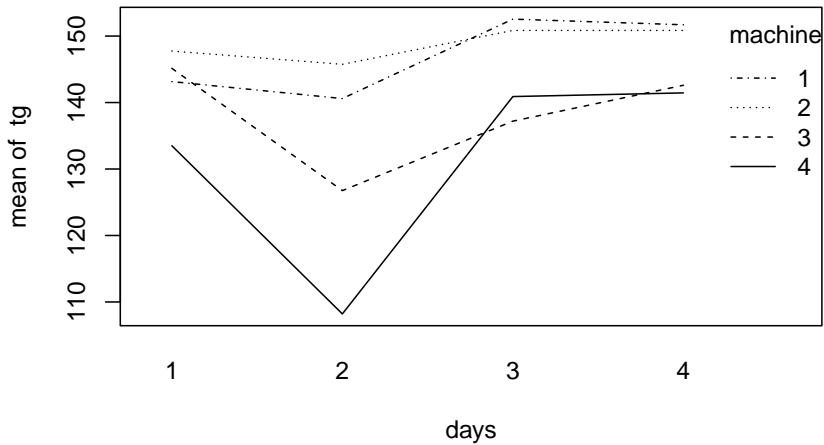
	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
days	3	1334.46	444.82	24.8569	2.907e-06	***
machine	3	1647.28	549.09	30.6836	7.192e-07	***
days:machine	9	786.04	87.34	4.8805	0.002936	**
Residuals	16	286.33	17.90			

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

From the  $p$ -value for  $H_0: \sigma_{AB}^2 = 0$ , we conclude there is interaction between the day and the machine. So machine performance does not appear to be consistent across days.

```
interaction.plot(days,machine,tg)
```



```
a <- 4
b <- 4
n <- 2
MSA <- anova_out$`Mean Sq`[1]
MSB <- anova_out$`Mean Sq`[2]
MSAB <- anova_out$`Mean Sq`[3]
FA <- MSA / MSAB
FB <- MSB / MSAB
pA <- 1 - pf(FA, a - 1, (a-1)*(b-1))
pB <- 1 - pf(FB, b - 1, (a-1)*(b-1))
```

For  $H_0: \sigma_A^2 = 0$  we obtain a p-value of 0.0248.

For  $H_0: \sigma_B^2 = 0$  we obtain a p-value of 0.0137.

There is significant machine-to-machine and day-to-day variation.

## Estimation of $\sigma_A^2$ , $\sigma_B^2$ , $\sigma_{AB}^2$ , and $\sigma_\varepsilon^2$

- ▶ Could use the MoM based on the table of expected mean squares.
- ▶ MoM can result in negative estimates of  $\sigma_A^2$ ,  $\sigma_B^2$ , or  $\sigma_{AB}^2$ .
- ▶ REML estimation is prescribed.
- ▶ Estimate  $\mu$  with the overall data mean  $\bar{Y}_{\dots}$ .

## Triglyceride level data (cont)

Obtain the REML estimators of  $\sigma_A^2$ ,  $\sigma_B^2$ ,  $\sigma_{AB}^2$ , and  $\sigma_\varepsilon^2$ .

Use `summary()` on the `lmer()` output.

```
lmer_out <- lmer(tg ~ 1 + (1|days) + (1|machine) + (1|days:machine))
summary(lmer_out)
```

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
```

```
Formula: tg ~ 1 + (1 | days) + (1 | machine) + (1 | days:machine)
```

```
REML criterion at convergence: 215
```

```
Scaled residuals:
```

	Min	1Q	Median	3Q	Max
	-1.84283	-0.35581	0.03485	0.20700	2.31766

```
Random effects:
```

Groups	Name	Variance	Std.Dev.
days:machine	(Intercept)	34.72	5.892
machine	(Intercept)	57.72	7.597
days	(Intercept)	44.69	6.685
Residual		17.90	4.230

```
Number of obs: 32, groups: days:machine, 16; machine, 4; days, 4
```

```
Fixed effects:
```

	Estimate	Std. Error	df	t value	Pr(> t )
(Intercept)	141.184	5.323	4.912	26.52	1.71e-06 ***

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## Prediction of realized values of random effects

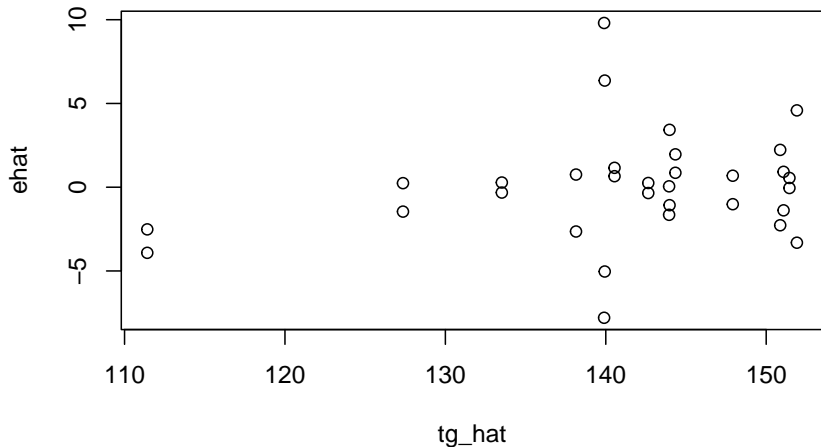
- ▶ We wish to guess at the values of  $A_i$ ,  $B_j$ , and  $(AB)_{ij}$  for all  $i, j$ .
- ▶ The formulas for the best linear unbiased predictors are complicated.
- ▶ The fitted values for the model are

$$\hat{Y}_{ijk} = \hat{\mu} + \hat{A}_i + \hat{B}_j + (\widehat{AB})_{ij}, \quad \text{for all } i, j, k$$

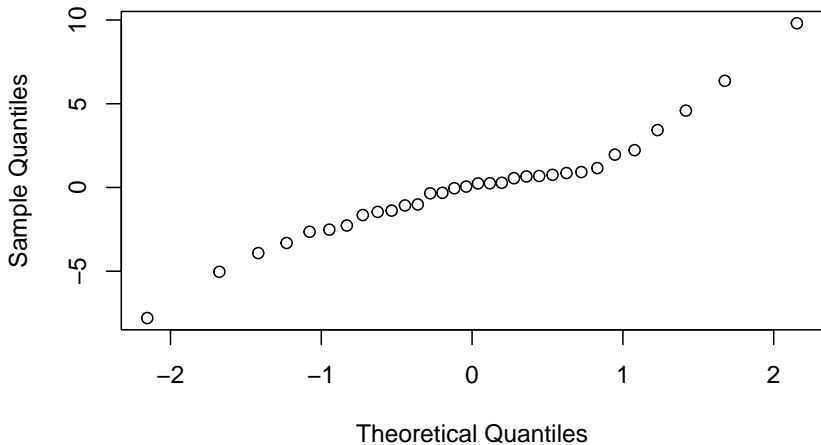
- ▶ Use `predict()` on the `lmer()` output to obtain these fitted values.
- ▶ The residuals are then  $Y_{ijk} - \hat{Y}_{ijk}$  for all  $i, j, k$ .
- ▶ Can then check diagnostic plots.

## Triglyceride level data (cont)

```
tg_hat <- predict(lmer_out)
ehat <- tg - tg_hat
plot(ehat ~ tg_hat)
```



## Normal Q-Q Plot



Both plots show some problems; interpret our results with caution.

# References

Kuehl, R. O. 2000. *Design of Experiments: Statistical Principles of Research Design and Analysis*. Duxbury/Thomson Learning.