STAT 516 Lec 09

Randomized complete block designs

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In each block all levels of the factor are tried

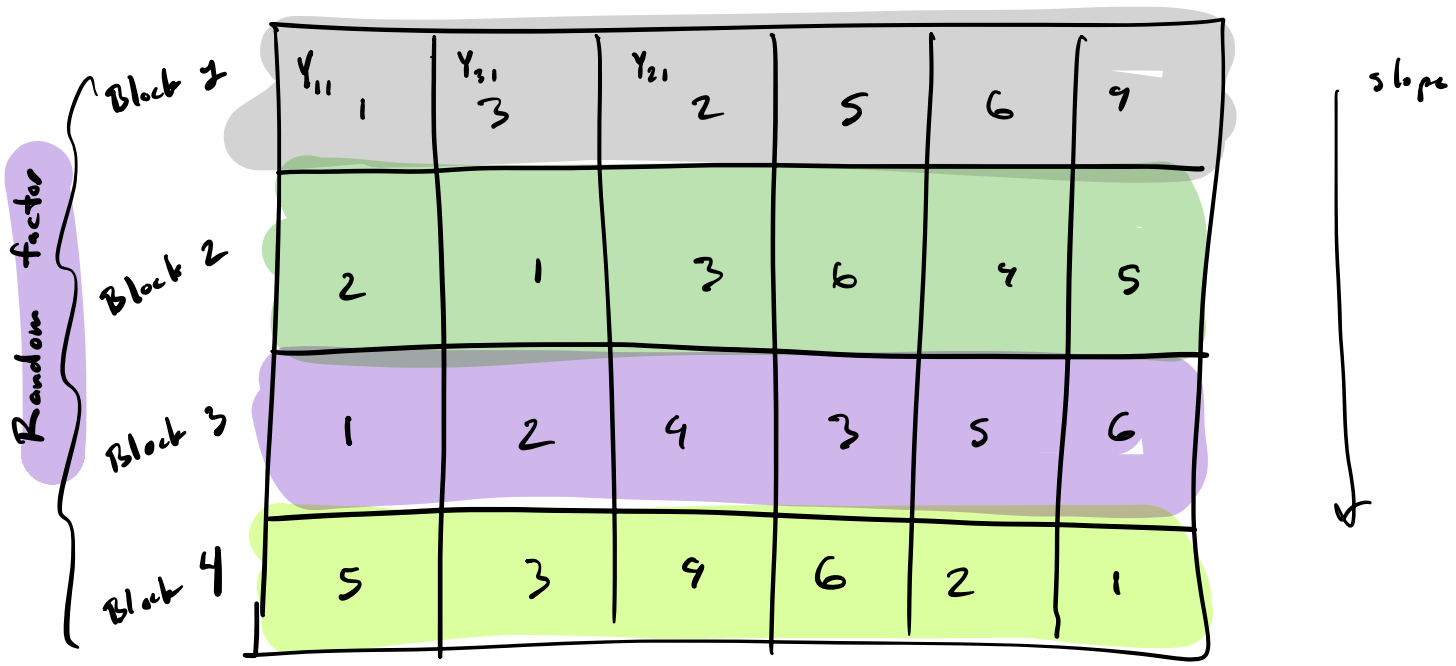
2025-04-08

"Fixed factor"

6 fertilization schedules for wheat

Response "nitrate content"

24 plots (EUs). Make blocks. Randomized in each block.



EUs not homogeneous → so we can group them.

Nitrogen fertilization data from Kuehl (2000)

Six nitrogen timing schedules in each of four plots in a field of wheat. Response is the nitrate content in stem tissue samples.

Display 8.1 Arrangement of Experimental Plots for the Wheat Experiment in a Randomized Complete Block Design

Irrigation Gradient ↓

Block 1	2	5	4	1	6	3
	40.89	37.99	37.18	34.98	34.89	42.07
Block 2	1	3	4	6	5	2
	41.22	49.42	45.85	50.15	41.99	46.69
Block 3	6	3	5	1	2	4
	44.57	52.68	37.61	36.94	46.65	40.23
Block 4	2	4	6	5	3	1
	41.90	39.20	43.29	40.45	42.91	39.97

Source: Dr. T. Doerge, Department of Soil and Water Science, University of Arizona.

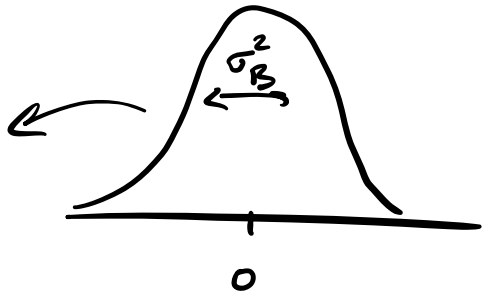
```
ntr <- c(40.89,37.99,37.18,34.98,34.89,42.07,
         41.22,49.42,45.85,50.15,41.99,46.69,
         44.57,52.68,37.61,36.94,46.65,40.23,
         41.90,39.20,43.29,40.45,42.91,39.97)
block <- as.factor(c(1,1,1,1,1,1,2,2,2,2,2,2,3,3,3,3,3,3,4,4,4,4,4,4))
trt <- as.factor(c(2,5,4,1,6,3,1,3,4,6,5,2,6,3,5,1,2,4,2,4,6,5,3,1))
```

Randomized complete block design (RCBD)

- EUs belong to blocks—groups of EUs homogeneous in some way.
- Each EU in a block is randomly assigned to a fixed treatment.
- All treatments appear exactly once[1] in each block.
- Purpose is to capture the between-block variability among the EUs.
- This helps us detect treatment effects with greater power.

[1] Can have replication, but many RCBDs do not.

Treatment effects model for the RCBD



Assume

i = level of factor

j = block

Block j effect

$$Y_{ij} = \mu + \tau_i + B_j + \varepsilon_{ij}, \quad \text{for } i = 1, \ldots, a, \quad j = 1, \ldots, b,$$

treatment i effect

Really like the interactions between Block x Trt.

where

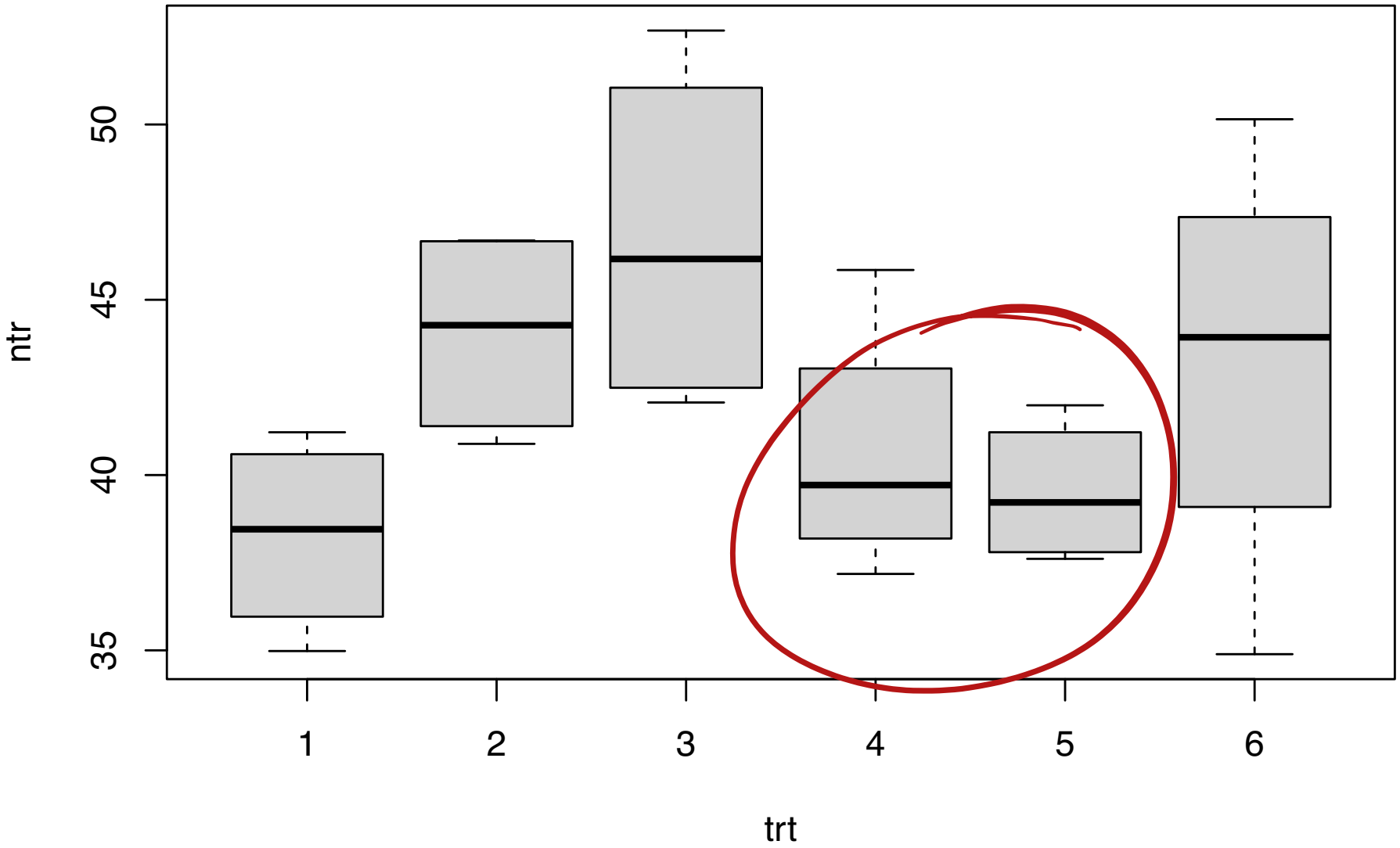
- Y_{ij} is the response of the EU in block j receiving treatment i.
- the τ_i are the fixed effects of the treatment.
- the B_j are independent Normal$(0, \sigma_B^2)$ random block effects.
- the ε_{ij} are independent Normal$(0, \sigma_\varepsilon^2)$ error/interaction terms.
- μ is an overall or baseline mean.

Define the cell means as

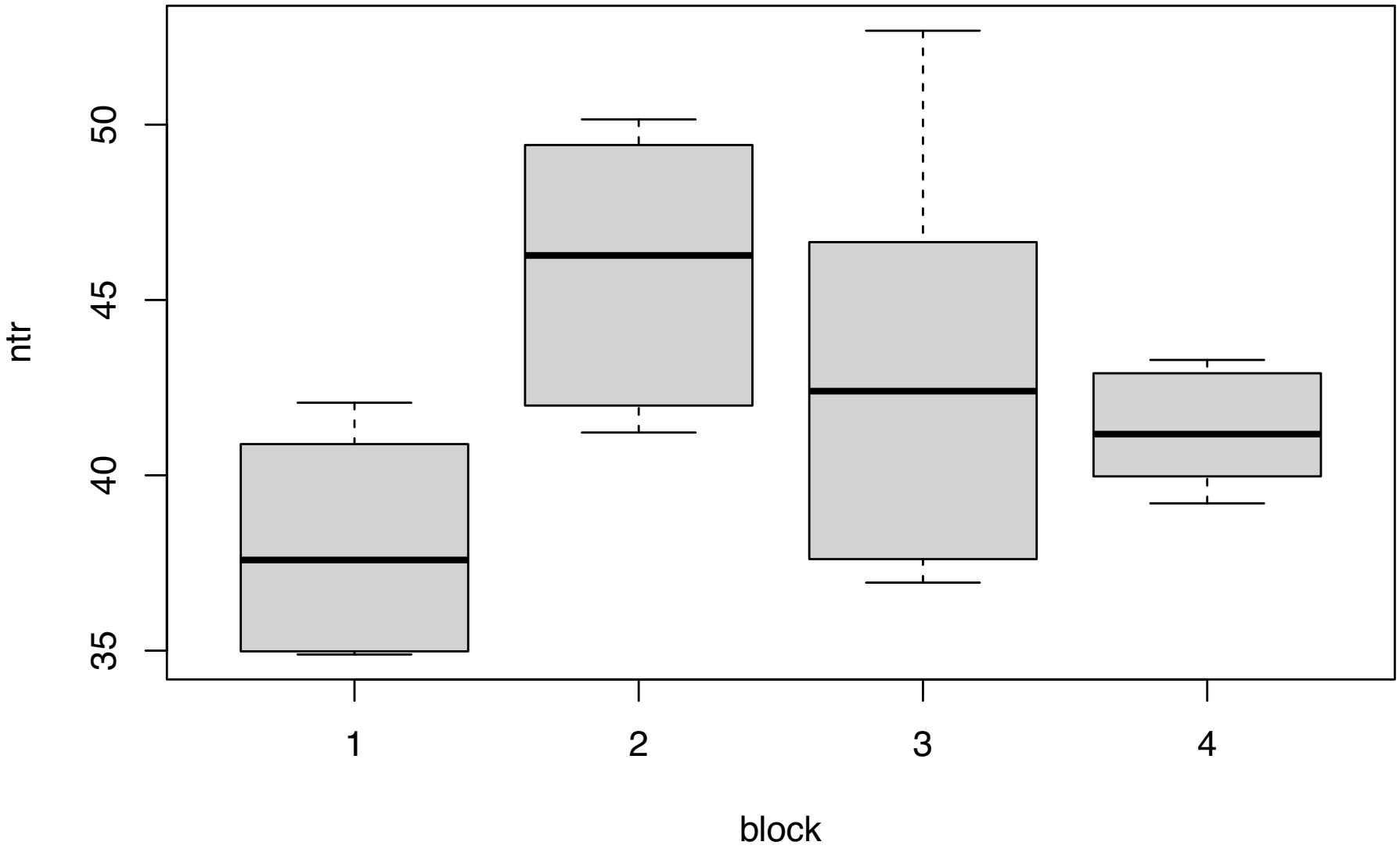
$$\mu_i = \mu + \tau_i, \quad i = 1, \ldots, a.$$

Nitrogen fertilization data (cont)

```
boxplot(ntr~trt)
```



```
boxplot(ntr~block)
```



Sums of squares for the RCBD

Decompose Variability in the Y_{ij}

Sum of squares	Symbol	Formula
Total	$\mathrm{SS}_{\mathrm{Tot}}$	$\sum_{i=1}^{a}\sum_{j=1}^{b}(Y_{ij}-\bar{Y}_{\cdot\cdot})^2$
Treatment	SS_{A}	$b\sum_{i=1}^{a}(\bar{Y}_{i\cdot}-\bar{Y}_{\cdot\cdot})^2$
Block	SS_{B}	$a\sum_{j=1}^{b}(\bar{Y}_{\cdot j}-\bar{Y}_{\cdot\cdot})^2$
Error	$\mathrm{SS}_{\mathrm{Error}}$	$\sum_{i=1}^{a}\sum_{j=1}^{b}(Y_{ij}-(\bar{Y}_{i\cdot}+\bar{Y}_{\cdot j}-\bar{Y}_{\cdot\cdot}))^2$

fitted value

- We can make the decomposition $\mathrm{SS}_{\mathrm{Tot}}=\mathrm{SS}_{\mathrm{A}}+\mathrm{SS}_{\mathrm{B}}+\mathrm{SS}_{\mathrm{Error}}$.
- The $\mathrm{SS}_{\mathrm{Error}}$ is really the interaction sum of squares $\mathrm{SS}_{\mathrm{AB}}$.
- But without replication, we cannot estimate an interaction.
- So the interaction serves as the error term.

ANOVA table for RCBD

Fertilizer: $a = 6$ $b = 4$ $n = 1$

Interaction serves as error

Source	Df	SS	MS	F value
A	$a-1$	SS_{A}	MS_{A}	$F_{\mathrm{A}} = \mathrm{MS}_{\mathrm{A}} / \mathrm{MS}_{\mathrm{Error}}$
B	$b-1$	SS_{B}	MS_{B}	$F_{\mathrm{B}} = \mathrm{MS}_{\mathrm{B}} / \mathrm{MS}_{\mathrm{Error}}$
Error	$(a-1)(b-1)$	$\mathrm{SS}_{\mathrm{Error}}$	$\mathrm{MS}_{\mathrm{Error}}$	
Total	$ab-1$	$\mathrm{SS}_{\mathrm{Tot}}$		

$abn - 1$

H_0: Fertilization schedule makes no difference.

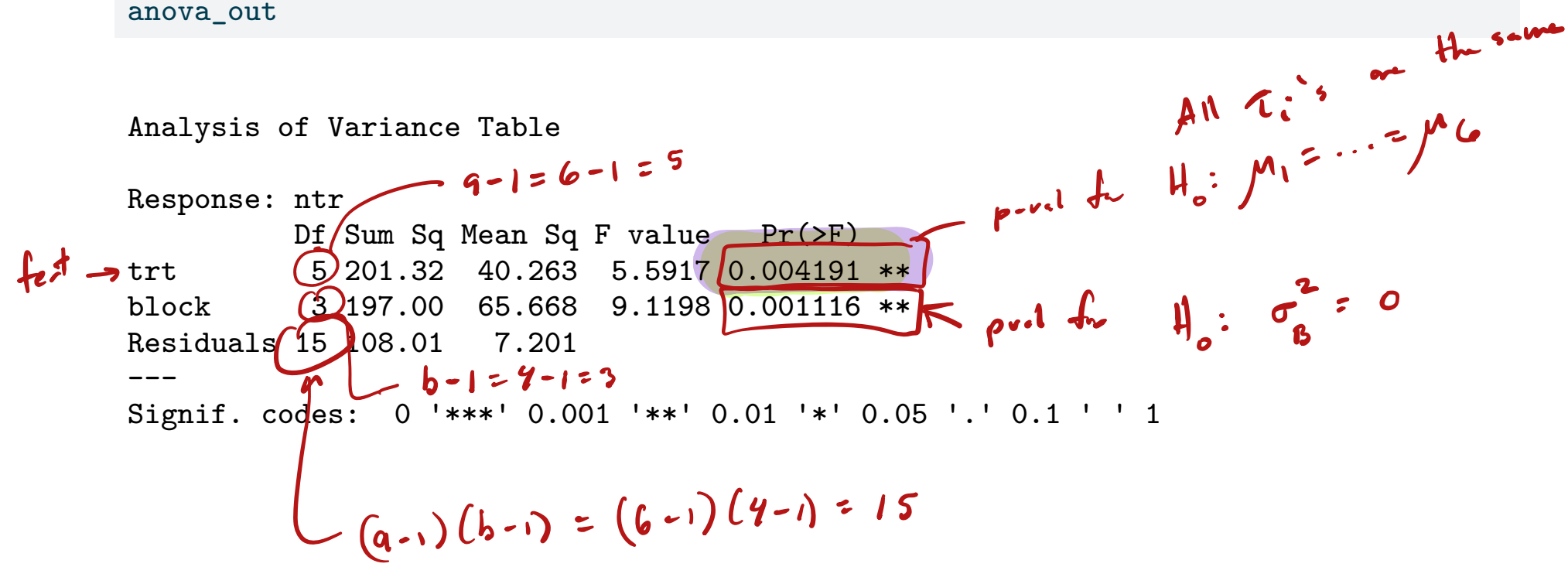
1. Reject H_0: $\mu_1 = \cdots = \mu_a$ if $F_{\mathrm{A}} > F_{a-1,(a-1)(b-1),\alpha}$.
2. Reject H_0: $\sigma_B^2 = 0$ if $F_{\mathrm{B}} > F_{b-1,(a-1)(b-1),\alpha}$.

H_0: The block has no effect

Nitrogen fertilization data (cont)

```
lm_out <- lm(ntr ~ trt + block) # do not include the interaction
anova_out <- anova(lm_out)
anova_out
```

```
Analysis of Variance Table

Response: ntr
          Df Sum Sq Mean Sq F value    Pr(>F)
trt        5 201.32  40.263  5.5917 0.004191 **
block      3 197.00  65.668  9.1198 0.001116 **
Residuals 15 108.01   7.201
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```r
y <- ntr
y.. <- predict(lm(ntr ~ 1))
yi. <- predict(lm(ntr ~ trt))
y.j <- predict(lm(ntr ~ block))

SSA <- sum((yi. - y..)^2)
SSB <- sum((y.j - y..)^2)
SSE <- sum((y - (yi. + y.j - y..))^2)

a <- 6
b <- 4

MSA <- SSA/(a-1)
MSB <- SSB/(b-1)
MSE <- SSE/((a-1)*(b-1))

FA <- MSA / MSE
FB <- MSB / MSE

pA <- 1 - pf(FA,a-1,(a-1)*(b-1))
pB <- 1 - pf(FB,b-1,(a-1)*(b-1))
```

Expected mean squares in the RCBD

Call σ^2_B and σ^2_ε "variance components".

Source	Df	Expected mean square
A	$a-1$	$b\theta^2_A + \sigma^2_\varepsilon$ ← E MS_{Trt}
B	$b-1$	$a\sigma^2_B + \sigma^2_\varepsilon$ ← E MS_{Block}
Error	$(a-1)(b-1)$	σ^2_ε ← E MS_{Error}

In the above $\theta^2_A = (a-1)^{-1}\sum_{i=1}^{a}(\mu_i - \bar{\mu}_\cdot)^2$.

Method of moments for variance components in RCBD

Set up equations

$$a\sigma_B^2 + \sigma_\varepsilon^2 \overset{\text{set}}{=} MS_{Block}$$

$$\sigma_\varepsilon^2 \overset{\text{set}}{=} MS_{Error}$$

solve for σ_B^2 and σ_ε^2

Equating $\mathrm{MS_B}$ and $\mathrm{MS_{Error}}$ with their expectations gives

- $\dot{\sigma}_\varepsilon^2 = \mathrm{MS_{Error}}$.
- $\dot{\sigma}_B^2 = \dfrac{\mathrm{MS_B} - \mathrm{MS_{Error}}}{a}$

May obtain $\dot{\sigma}_B^2 < 0$, so one should use REML estimation.

Nitrogen fertilization data (cont)

Obtain REML estimators of σ_B^2 and σ_ε^2 on the fertilization data.

```
library(lmerTest) # first time run install.packages("lmerTest")
lmer_out <- lmer(ntr ~ trt + (1|block))
lmer_out
```

```
Linear mixed model fit by REML ['lmerModLmerTest']
Formula: ntr ~ trt + (1 | block)
REML criterion at convergence: 101.5658
Random effects:
 Groups   Name        Std.Dev.
 block    (Intercept) 3.122
 Residual             2.683
Number of obs: 24, groups:  block, 4
Fixed Effects:
(Intercept)         trt2         trt3         trt4         trt5         trt6
     38.278        5.755        8.492        2.337        1.232        4.947
```

Obtain MoMs estimators for σ_B^2 and σ_ε^2 on the fertilization data.

```
sg_B <- sqrt((MSB - MSE)/a)
sg_e <- sqrt(MSE)
```

We have $\dot{\sigma}_B = 3.122$ and $\dot{\sigma}_\varepsilon = 2.683$.

Variances of some means and difference in means

Contrast	Variance	MoM variance estimator
$\bar{Y}_{i.}$	$\frac{1}{b}(\sigma_B^2 + \sigma_\varepsilon^2)$	$\frac{2}{ab}[\mathrm{MS_B} + (b-1)\,\mathrm{MS_{Error}}]$
$\bar{Y}_{i.} - \bar{Y}_{i'.}$	$\frac{2}{b}\sigma_\varepsilon^2$	$\frac{2}{b}\,\mathrm{MS_{Error}}$

Some (unadjusted) CIs in RCB split plot design

Target	$(1-\alpha)100\%$ confidence interval
μ_i	$\bar{Y}_{i.} \pm t_{\nu^*,\alpha/2}\sqrt{\mathrm{MS}_{\mathrm{B}} + (b-1)\,\mathrm{MS}_{\mathrm{Error}}}\sqrt{\frac{2}{ab}}$
$\mu_i - \mu_{i'}$	$\bar{Y}_{i.} - \bar{Y}_{i'.} \pm t_{(a-1)(b-1),\alpha/2}\sqrt{\mathrm{MS}_{\mathrm{Error}}}\sqrt{\frac{2}{b}}$

In the above $\nu^* = \dfrac{\mathrm{MS}_{\mathrm{B}} + (b-1)\,\mathrm{MS}_{\mathrm{Error}}}{\frac{\mathrm{MS}_{\mathrm{B}}^2}{(b-1)} + \frac{(b-1)^2\,\mathrm{MS}_{\mathrm{Error}}^2}{(a-1)(b-1)}}$ à la Satterthwaite[2].

[2] a degrees of freedom approximation when one has not exactly a t-distribution.

Nitrogen fertilization data (cont)

Unadjusted CIs with `ls_means()` from R package `lmerTest`

```
ls_means(lmer_out)
```

```
Least Squares Means table:

     Estimate Std. Error  df t value   lower   upper  Pr(>|t|)
trt1  38.2775     2.0582 6.8  18.597 33.3789 43.1761 4.505e-07 ***
trt2  44.0325     2.0582 6.8  21.393 39.1339 48.9311 1.767e-07 ***
trt3  46.7700     2.0582 6.8  22.724 41.8714 51.6686 1.179e-07 ***
trt4  40.6150     2.0582 6.8  19.733 35.7164 45.5136 3.033e-07 ***
trt5  39.5100     2.0582 6.8  19.196 34.6114 44.4086 3.646e-07 ***
trt6  43.2250     2.0582 6.8  21.001 38.3264 48.1236 2.000e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

  Confidence level: 95%
  Degrees of freedom method: Satterthwaite
```

```r
ls_means(lmer_out, pairwise = TRUE)
```

```
Least Squares Means table:

            Estimate Std. Error df t value    lower    upper  Pr(>|t|)
trt1 - trt2  -5.7550     1.8974 15 -3.0330  -9.7993  -1.7107 0.0083887 **
trt1 - trt3  -8.4925     1.8974 15 -4.4758 -12.5368  -4.4482 0.0004443 ***
trt1 - trt4  -2.3375     1.8974 15 -1.2319  -6.3818   1.7068 0.2369413
trt1 - trt5  -1.2325     1.8974 15 -0.6496  -5.2768   2.8118 0.5257996
trt1 - trt6  -4.9475     1.8974 15 -2.6075  -8.9918  -0.9032 0.0198026 *
trt2 - trt3  -2.7375     1.8974 15 -1.4427  -6.7818   1.3068 0.1696521
trt2 - trt4   3.4175     1.8974 15  1.8011  -0.6268   7.4618 0.0918200 .
trt2 - trt5   4.5225     1.8974 15  2.3835   0.4782   8.5668 0.0308031 *
trt2 - trt6   0.8075     1.8974 15  0.4256  -3.2368   4.8518 0.6764617
trt3 - trt4   6.1550     1.8974 15  3.2438   2.1107  10.1993 0.0054516 **
trt3 - trt5   7.2600     1.8974 15  3.8262   3.2157  11.3043 0.0016523 **
trt3 - trt6   3.5450     1.8974 15  1.8683  -0.4993   7.5893 0.0813776 .
trt4 - trt5   1.1050     1.8974 15  0.5824  -2.9393   5.1493 0.5689729
trt4 - trt6  -2.6100     1.8974 15 -1.3755  -6.6543   1.4343 0.1891597
trt5 - trt6  -3.7150     1.8974 15 -1.9579  -7.7593   0.3293 0.0691104 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

  Confidence level: 95%
  Degrees of freedom method: Satterthwaite
```

Multiple comparisons of treatment means in the RCBD

Compare μ_4 and μ_5:

$\bar{Y}_{4.} - \bar{Y}_{5.} \pm q_{6,15,0.05} \cdot 2.683 \cdot \sqrt{\frac{1}{4}}$

$q_{6,15,0.05}$: qtukey(0.95, 6, 15) = 4.595

$\hat{\sigma}^2_\varepsilon = MS_{Error}$

- Tukey's for comparing all pairs of means among $\mu_1, \ldots, \mu_a$:

Compare $\mu_i - \mu_{i'}$

$$\bar{Y}_{i.} - \bar{Y}_{i'.} \pm q_{a,(a-1)(b-1),\alpha} \sqrt{\text{MS}_{\text{Error}}} \sqrt{\frac{1}{b}}, \quad 1 \le i < i' \le a.$$

Tukey's; $\hat{\sigma}_\varepsilon$; 6; 15

- Dunnett's for comparing $\mu_1, \ldots, \mu_{a-1}$ to a baseline μ_a:

$$\bar{Y}_{i.} - \bar{Y}_{a.} \pm d_{a,(a-1)(b-1),\alpha} \sqrt{\text{MS}_{\text{Error}}} \sqrt{\frac{2}{b}}, \quad i = 1, \ldots, a-1.$$

Nitrogen fertilization data (cont)

Compare all pairs of fertilizers with Tukey's CIs for mean differences.

```
alpha <- 0.05
a <- 6
b <- 4
MSE <- anova_out$`Mean Sq`[3]
se <- sqrt(MSE) * sqrt(2/b)
me <- qtukey(1-alpha,a,(a-1)*(b-1)) / sqrt(2) * se
ntr_means <- aggregate(ntr, by = list(trt), mean)$x

CIs <- matrix(NA,choose(a,2),2)
comp <- numeric(choose(a,2))

k <- 1
for(i in 1:(a-1))
  for(j in (i+1):a){ # double loop takes us through all pairs

    dij <- ntr_means[i] - ntr_means[j]
    CIs[k,] <- c(dij - me, dij + me)
    comp[k] <- paste(i,"-",j)
    k <- k + 1

  }

colnames(CIs) <- c("lower","upper")
rownames(CIs) <- comp
```

```
round(CIs,3)
```

```
        lower  upper
1 - 2 -11.920  0.410
1 - 3 -14.657 -2.328
1 - 4  -8.502  3.827
1 - 5  -7.397  4.932
1 - 6 -11.112  1.217
2 - 3  -8.902  3.427
2 - 4  -2.747  9.582
2 - 5  -1.642 10.687
2 - 6  -5.357  6.972
3 - 4  -0.010 12.320
3 - 5   1.095 13.425
3 - 6  -2.620  9.710
4 - 5  -5.060  7.270
4 - 6  -8.775  3.555
5 - 6  -9.880  2.450
```

$$\binom{6}{2} = \frac{6 \cdot 5}{2} = 15$$

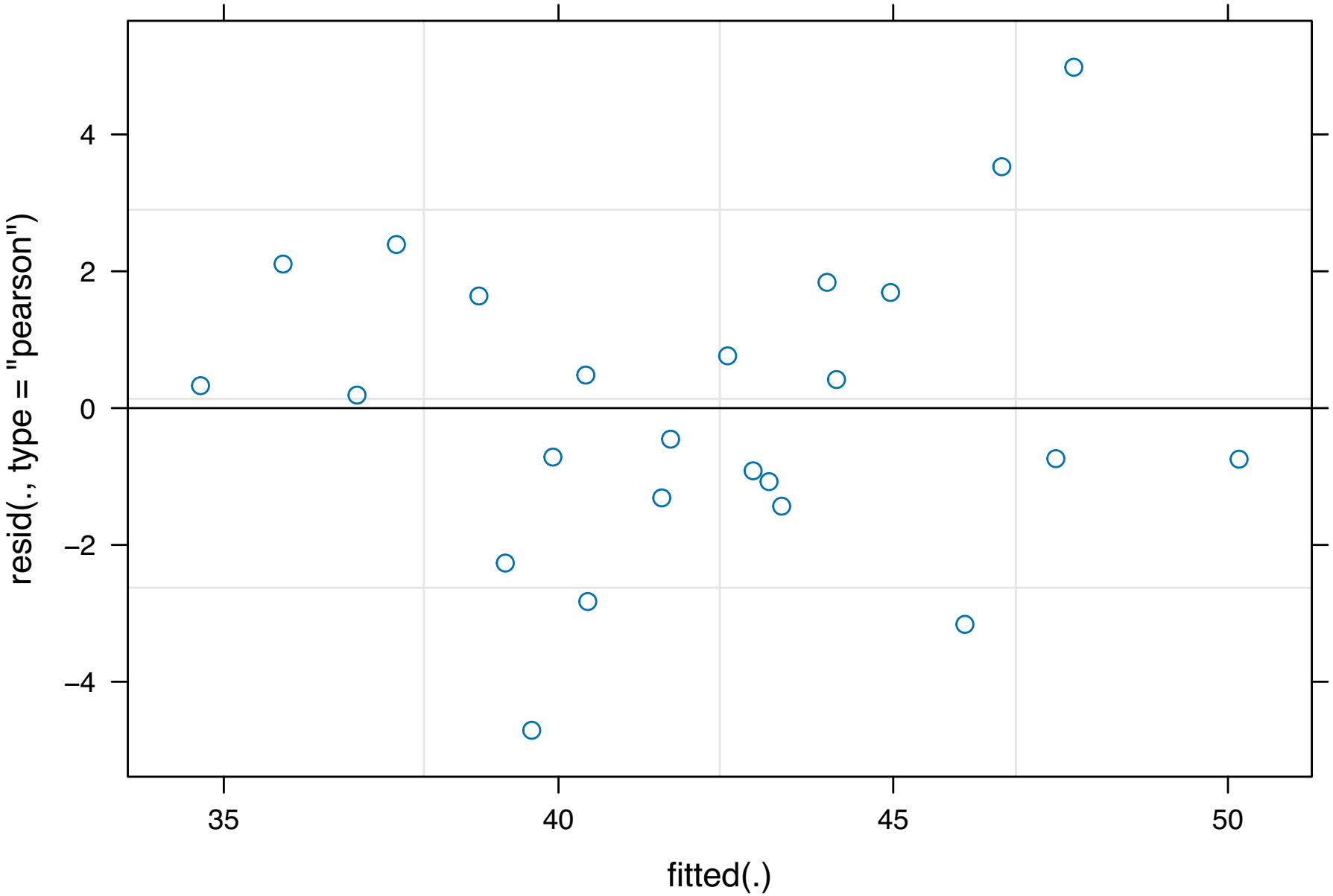
Compare all fertilizers to fertilizer 1 using Dunnett's method.

```
alpha <- 0.05
a <- 6
b <- 4
MSE <- anova_out$`Mean Sq`[3]
me <- 2.82 * sqrt(MSE) * sqrt(2/b) # value 2.82 from Dunnett's table
ntr_means <- aggregate(ntr, by = list(trt), mean)$x

CIs <- matrix(NA,a-1,2)

k <- 1
for(i in 2:a){

  di <- ntr_means[i] - ntr_means[1]
  CIs[k,] <- c(di - me,di + me)
  k <- k + 1

}

colnames(CIs) <- c("lower","upper")
rownames(CIs) <- paste(2:a,"- 1")
```

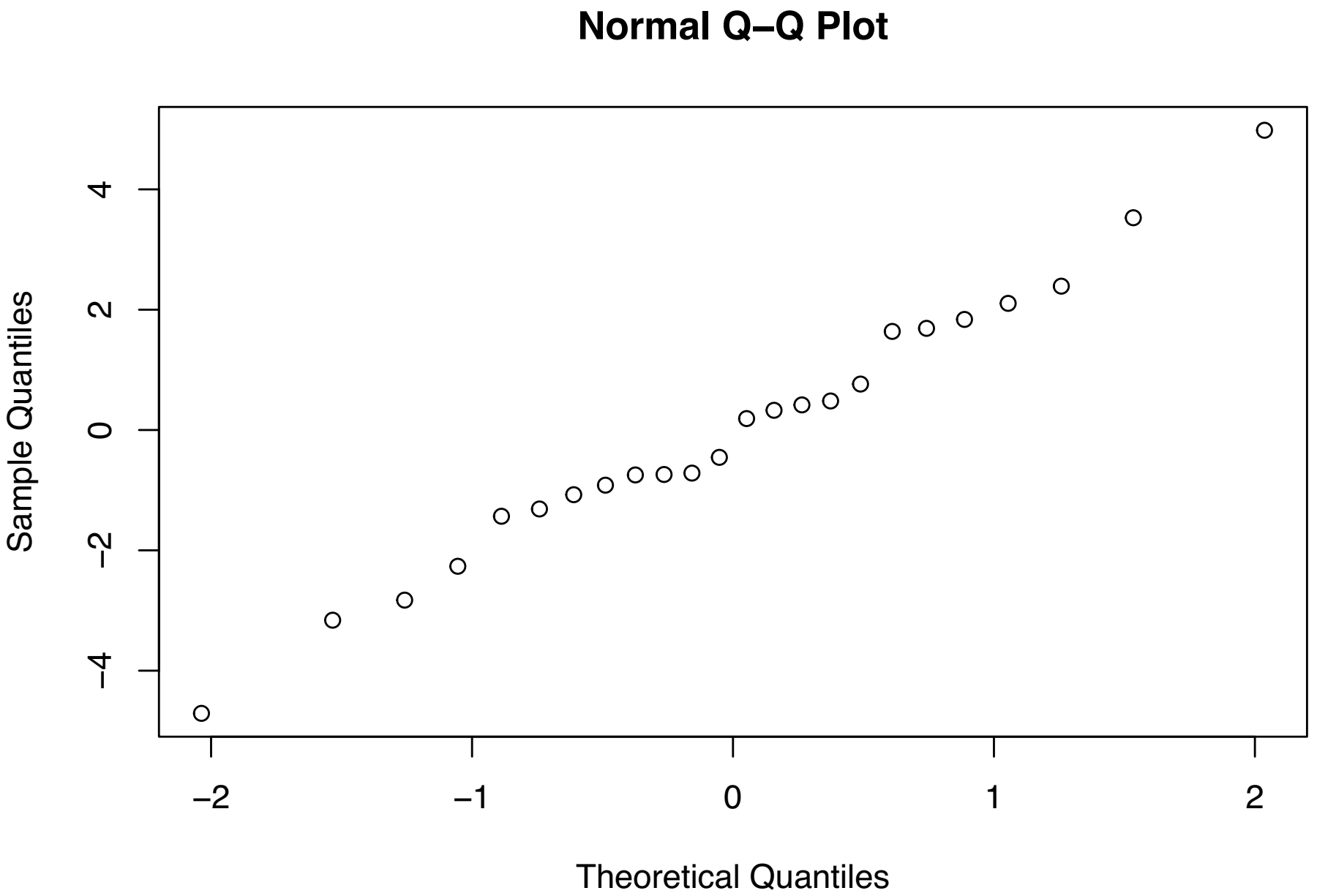
```r
round(CIs,3)
```

```
       lower  upper
2 - 1  0.404 11.106
3 - 1  3.142 13.843
4 - 1 -3.013  7.688
5 - 1 -4.118  6.583
6 - 1 -0.403 10.298
```

```
plot(lmer_out)
```



```r
yhat <- predict(lmer_out)
ehat <- ntr - yhat
qqnorm(ehat)
```



Ignoring the blocks in the nitrogen data

If we ignore the blocks, the design looks like a one-way ANOVA:

Treatment	1	2	3	4	5	6
	34.98	40.89	42.07	37.18	37.99	34.89
	41.22	46.69	49.42	45.85	41.99	50.15
	36.94	46.65	52.68	40.23	37.61	44.57
	39.97	41.90	43.29	39.20	40.45	43.29

Suppose we fit $Y_{ij} = \mu + \tau_i + \varepsilon_{ij}$, $i = 1, 2, 3, 4, 5, 6$, $j = 1, 2, 3, 4$.

We lose power to detect a treatment effect!

```
anova(lm(ntr ~ trt))
```

```
Analysis of Variance Table

Response: ntr
          Df Sum Sq Mean Sq F value  Pr(>F)
trt        5 201.32  40.263  2.3761 0.08024 .
Residuals 18 305.01  16.945
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

looks like there is no treatment effect...

Skin response data, Mohr, Wilson, and Freund (2021)

Galvanic skin responses of five subjects under shock and noise stimuli.

each subject is a block

		SUBJECT				
Noise	Shock	1	2	3	4	5
40	0.25	3	7	9	4	1
40	0.50	5	11	13	8	3
40	0.75	9	12	14	11	5
40	1.00	6	11	12	7	4
80	0.25	5	10	10	6	3
80	0.50	6	12	15	9	5
80	0.75	18	18	15	13	9
80	1.00	7	15	14	9	7

```
skin <- data.frame(resp = c(3,7,9,4,1,5,11,13,8,3,9,12,14,11,5,6,11,12,7,4,5,
                            10,10,6,3,6,12,15,9,5,18,18,15,13,9,7,15,14,9,7),
                   noise = as.factor(c(rep(40,20),rep(80,20))),
                   shock = as.factor(rep(c(rep(.25,5),rep(.5,5),
                                           rep(.75,5),rep(1,5)),2)),
                   subj = as.factor(rep(1:5,8)))
```

```r
head(skin,n=20)
```

```
   resp noise shock subj
1     3    40  0.25    1
2     7    40  0.25    2
3     9    40  0.25    3
4     4    40  0.25    4
5     1    40  0.25    5
6     5    40   0.5    1
7    11    40   0.5    2
8    13    40   0.5    3
9     8    40   0.5    4
10    3    40   0.5    5
11    9    40  0.75    1
12   12    40  0.75    2
13   14    40  0.75    3
14   11    40  0.75    4
15    5    40  0.75    5
16    6    40     1    1
17   11    40     1    2
18   12    40     1    3
19    7    40     1    4
20    4    40     1    5
```

Treatment effects model for two-way factorial RCBD

Assume

$$Y_{ijk} = \mu + \tau_i + \gamma_j + (\tau\gamma)_{ij} + C_k + \varepsilon_{ijk},$$

for $i = 1, \ldots, a$, $j = 1, \ldots, b$, and $k = 1, \ldots, c$, where

- Y_{ijk} is the response in block k under treatment combination $i \times j$.
- μ is an overall or baseline mean.
- the τ_i are fixed effects for factor A.
- the γ_j are fixed effects for factor B.
- the $(\tau\gamma)_{ij}$ are effects for the A×B interaction.
- the C_k are independent Normal$(0, \sigma_C^2)$ block effects.
- the ε_{ijk} are independent Normal$(0, \sigma_\varepsilon^2)$ error terms.

Define the cell means as

$$\mu_{ij} = \mu + \tau_i + \gamma_j + (\tau\gamma)_{ij}, \quad i = 1, \ldots, a, \quad j = 1, \ldots, b.$$

Sums of squares for the two-way factorial RCBD

Sum of squares	Symbol	Formula
Total	$\mathrm{SS}_{\mathrm{Tot}}$	$\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{k=1}^{c}(Y_{ijk}-\bar{Y}_{...})^2$
A	SS_{A}	$bc\sum_{i=1}^{a}(\bar{Y}_{i..}-\bar{Y}_{...})^2$
B	SS_{B}	$ac\sum_{j=1}^{b}(\bar{Y}_{.j.}-\bar{Y}_{...})^2$
AB	$\mathrm{SS}_{\mathrm{AB}}$	$c\sum_{i=1}^{a}\sum_{j=1}^{b}(Y_{ij.}-(\bar{Y}_{i..}+\bar{Y}_{.j.}-\bar{Y}_{...}))^2$
C	SS_{C}	$ab\sum_{k=1}^{c}(\bar{Y}_{..k}-\bar{Y}_{...})^2$
Error	$\mathrm{SS}_{\mathrm{Error}}$	$\mathrm{SS}_{\mathrm{Tot}}-(\mathrm{SS}_{\mathrm{A}}+\mathrm{SS}_{\mathrm{B}}+\mathrm{SS}_{\mathrm{AB}}+\mathrm{SS}_{\mathrm{C}})$

- Then we have $\mathrm{SS}_{\mathrm{Tot}}=\mathrm{SS}_{\mathrm{A}}+\mathrm{SS}_{\mathrm{B}}+\mathrm{SS}_{\mathrm{AB}}+\mathrm{SS}_{\mathrm{C}}+\mathrm{SS}_{\mathrm{Error}}$.
- The error $\mathrm{SS}_{\mathrm{Error}}$ is really the interaction sum of squares $\mathrm{SS}_{\mathrm{Trt}\times C}$.
- Again, without replication, we cannot estimate this interaction.
- So the interaction serves as the error term.

ANOVA table for two-way factorial RCBD

Source	Df	SS	MS	F value
A	$a-1$	SS_{A}	MS_{A}	$F_{\mathrm{A}} = \mathrm{MS}_{\mathrm{A}} / \mathrm{MS}_{\mathrm{Error}}$
B	$b-1$	SS_{B}	MS_{B}	$F_{\mathrm{B}} = \mathrm{MS}_{\mathrm{B}} / \mathrm{MS}_{\mathrm{Error}}$
AB	$(a-1)(b-1)$	$\mathrm{SS}_{\mathrm{AB}}$	$\mathrm{MS}_{\mathrm{AB}}$	$F_{\mathrm{AB}} = \mathrm{MS}_{\mathrm{B}} / \mathrm{MS}_{\mathrm{Error}}$
C	$c-1$	SS_{C}	MS_{C}	$F_{\mathrm{C}} = \mathrm{MS}_{\mathrm{C}} / \mathrm{MS}_{\mathrm{Error}}$
Error	$(ab-1)(c-1)$	$\mathrm{SS}_{\mathrm{Error}}$	$\mathrm{MS}_{\mathrm{Error}}$	
Total	$abc-1$	$\mathrm{SS}_{\mathrm{Tot}}$		

No. factor A main effects

1. Reject H_0: $\mu_{1.} = \cdots = \mu_{a.}$ if $F_{\mathrm{A}} > F_{a-1,(ab-1)(c-1),\alpha}$.
2. Reject H_0: $\mu_{.1} = \cdots = \mu_{.b}$ if $F_{\mathrm{B}} > F_{b-1,(ab-1)(c-1),\alpha}$.
3. Reject H_0: $\mu_{ij} = \bar{\mu}_{i.} + \bar{\mu}_{.j} - \bar{\mu}_{..}$ $\forall ij$ if $F_{\mathrm{AB}} > F_{(a-1)(b-1),(ab-1)(c-1),\alpha}$.
4. Reject H_0: $\sigma_C^2 = 0$ if $F_{\mathrm{C}} > F_{c-1,(ab-1)(c-1),\alpha}$.

No. factor B main fx

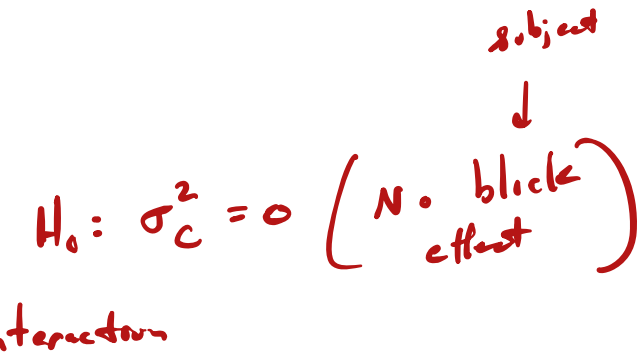
No. A×B interaction

No. block effect

Skin response data (cont)

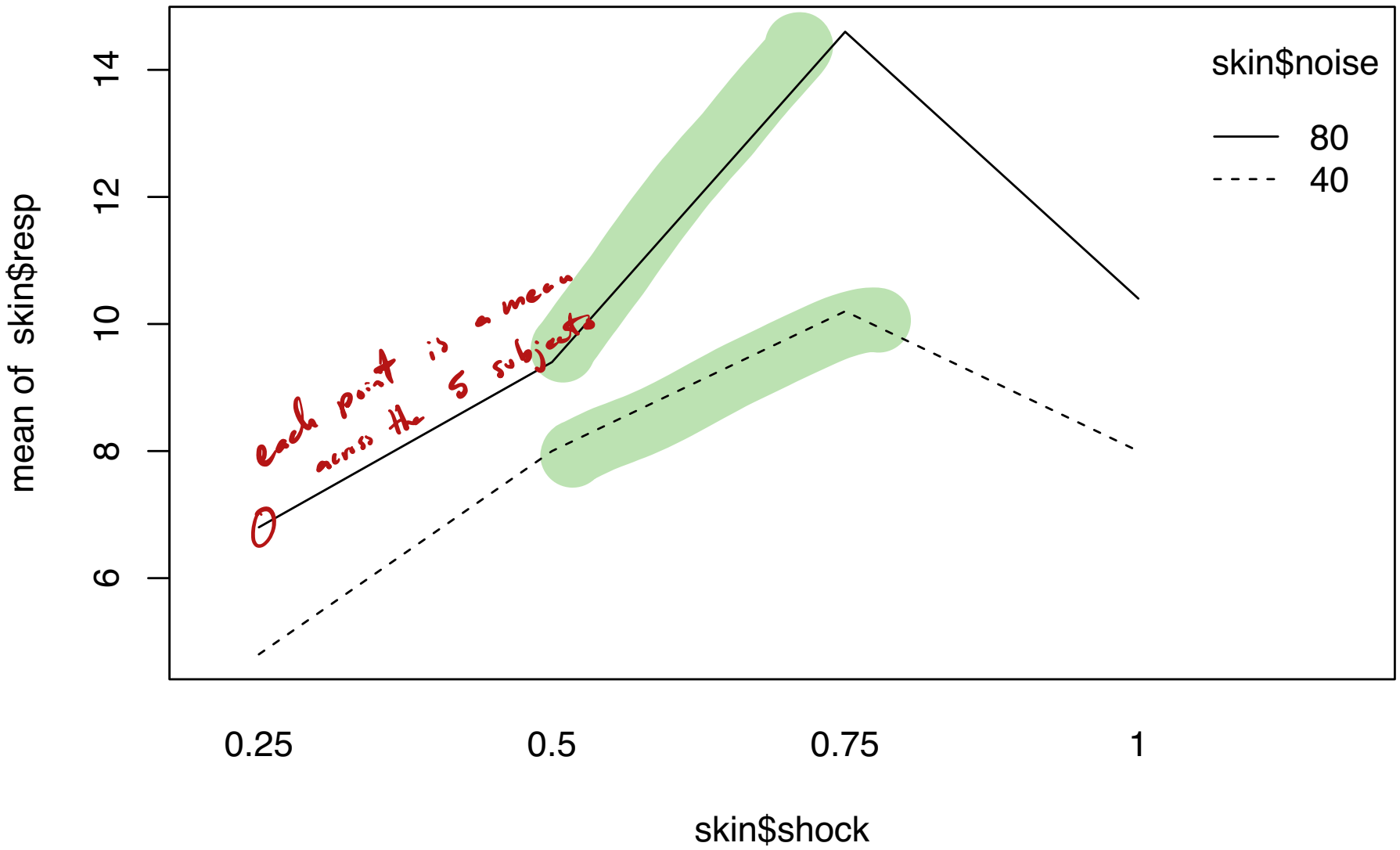
```
lm_out <- lm(resp ~ noise + shock + noise:shock + subj, data = skin)
anova(lm_out)
```

```
Analysis of Variance Table

Response: resp
            Df Sum Sq Mean Sq F value    Pr(>F)
noise        1  65.02  65.025 28.3819 1.134e-05 ***
shock        3 219.27  73.092 31.9028 3.564e-09 ***
subj         4 361.85  90.463 39.4848 3.975e-11 ***
noise:shock  3  12.67   4.225  1.8441    0.1621
Residuals   28  64.15   2.291
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```r
y <- skin$resp
y... <- predict(lm(resp ~ 1,data = skin))
yi.. <- predict(lm(resp ~ noise,data=skin))
y.j. <- predict(lm(resp ~ shock,data=skin))
y..k <- predict(lm(resp ~ subj,data=skin))
yij. <- predict(lm(resp ~ noise + shock + noise:shock,data=skin))

SSA <- sum((yi.. - y...)^2)
SSB <- sum((y.j. - y...)^2)
SSC <- sum((y..k - y...)^2)
SSAB <- sum((yij. - (yi.. + y.j. - y...))^2)
SST <- sum((y - y...)^2)
SSE <- SST - (SSA + SSB + SSC + SSAB)

a <- 2
b <- 4
c <- 5

MSA <- SSA/(a-1)
MSB <- SSB/(b-1)
MSC <- SSC/(c-1)
MSAB <- SSAB/((a-1)*(b-1))
MSE <- SSE/((a*b-1)*(c-1))

FA <- MSA / MSE
FB <- MSB / MSE
FAB <- MSAB / MSE
FC <- MSC / MSE

pA <- 1 - pf(FA,a-1,(a*b-1)*(c-1))
pB <- 1 - pf(FB,b-1,(a*b-1)*(c-1))
pAB <- 1 - pf(FAB,(a-1)*(b-1),(a*b-1)*(c-1))
pC <- 1 - pf(FC,c-1,(a*b-1)*(c-1))
```

```
interaction.plot(skin$shock,skin$noise,skin$resp)
```



Expected mean squares in factorial RCBD

Source	Df	Expected mean square
A	$a-1$	$bc\theta_A^2 + \sigma_\varepsilon^2$
B	$b-1$	$ac\theta_B^2 + \sigma_\varepsilon^2$
AB	$(a-1)(b-1)$	$c\theta_{AB}^2 + \sigma_\varepsilon^2$
C	$c-1$	$ab\sigma_C^2 + \sigma_\varepsilon^2$
Error	$(ab-1)(c-1)$	σ_ε^2

In the above

- $\theta_A^2 = (a-1)^{-1}\sum_{i=1}^{a}(\bar{\mu}_{i.} - \bar{\mu}_{..})^2$
- $\theta_B^2 = (b-1)^{-1}\sum_{j=1}^{b}(\bar{\mu}_{.j} - \bar{\mu}_{..})^2$
- $\theta_{AB}^2 = [(a-1)(b-1)]^{-1}\sum_{i=1}^{a}\sum_{j=1}^{b}(\mu_{ij} - (\bar{\mu}_{i.} + \bar{\mu}_{.j} - \bar{\mu}_{..}))^2$

MoMs for variance components in two-way factorial RCBD

- Equating MS_{C} and $\mathrm{MS}_{\mathrm{Error}}$ with their expectations gives

$$\dot{\sigma}_C^2 = \frac{\mathrm{MS}_{\mathrm{C}} - \mathrm{MS}_{\mathrm{Error}}}{ab} \quad \text{and} \quad \dot{\sigma}_\varepsilon^2 = \mathrm{MS}_{\mathrm{Error}} \,.$$

- May obtain $\dot{\sigma}_C^2 < 0$, so one should use REML estimation.

Skin response data (cont)

Obtain REML estimators of σ_C^2 and σ_ε^2 on the skin response data.

```
lmer_out <- lmer(resp ~ noise + shock + noise:shock + (1|subj), data = skin)
lmer_out
```

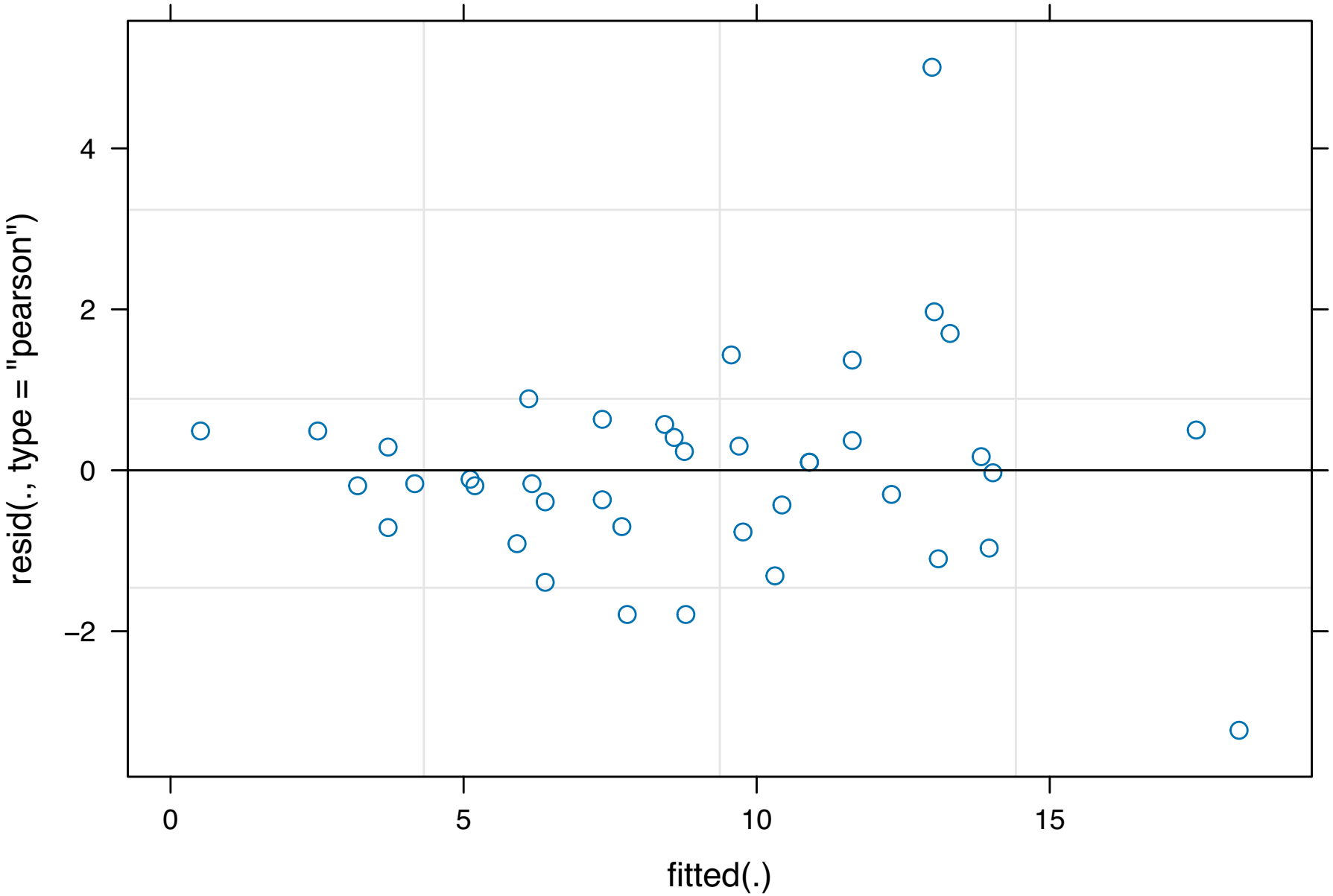
```
Linear mixed model fit by REML ['lmerModLmerTest']
Formula: resp ~ noise + shock + noise:shock + (1 | subj)
   Data: skin
REML criterion at convergence: 144.9199
Random effects:
 Groups   Name        Std.Dev.
 subj     (Intercept) 3.320
 Residual             1.514
Number of obs: 40, groups:  subj, 5
Fixed Effects:
      (Intercept)            noise80           shock0.5          shock0.75
              4.8                2.0                3.2                5.4
           shock1  noise80:shock0.5 noise80:shock0.75     noise80:shock1
              3.2               -0.6                2.4                0.4
```

Obtain MoMs estimators for σ_C^2 and σ_ε^2 on the skin response data.

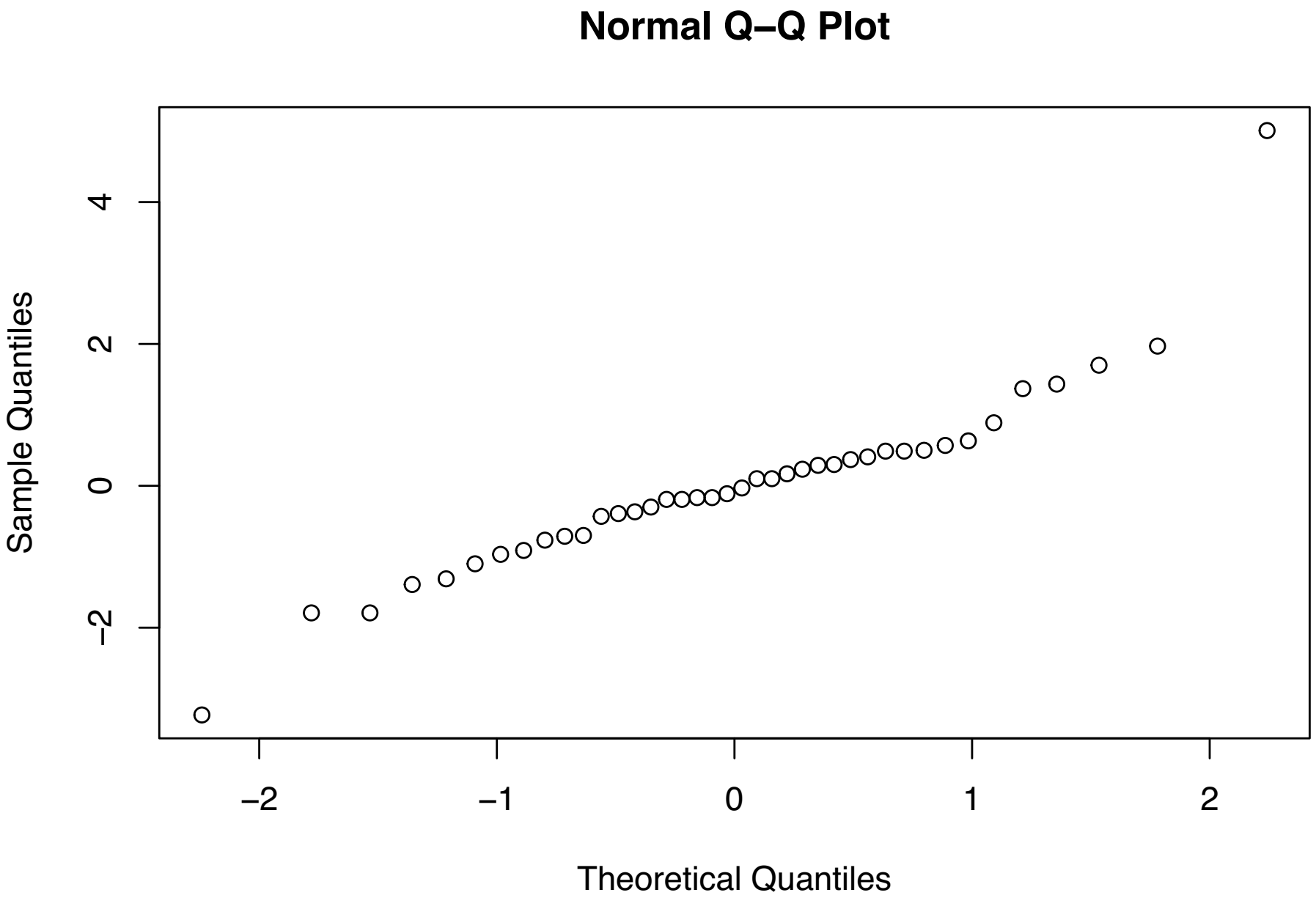
```
sg_C <- sqrt((MSC - MSE)/(a*b))
sg_e <- sqrt(MSE)
```

We have $\dot{\sigma}_C = 3.320$ and $\dot{\sigma}_\varepsilon = 1.514$.

```
plot(lmer_out)
```



```r
yhat <- predict(lmer_out)
ehat <- skin$resp - yhat
qqnorm(ehat)
```



References

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

Mohr, Donna L, William J Wilson, and Rudolf J Freund. 2021. *Statistical Methods*. Academic Press.