

STAT 516 Lec 09

Randomized complete block designs

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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						
						<i>Irrigation Gradient</i> ↓
<i>Block 1</i>	2 40.89	5 37.99	4 37.18	1 34.98	6 34.89	3 42.07
<i>Block 2</i>	1 41.22	3 49.42	4 45.85	6 50.15	5 41.99	2 46.69
<i>Block 3</i>	6 44.57	3 52.68	5 37.61	1 36.94	2 46.65	4 40.23
<i>Block 4</i>	2 41.90	4 39.20	6 43.29	5 40.45	3 42.91	1 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(1,1,1,1,1,1,2,2,2,2,2,3,3,3,3,3,4,4,4,4,4,4))  
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 once¹ in each block.
- ▶ Purpose is to capture the between-block variability among the EUs.
- ▶ This helps us detect treatment effects with greater power.

¹Can have replication, but many RCBDs do not.

Treatment effects model for the RCBD

Assume

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

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 $\text{Normal}(0, \sigma_B^2)$ random block effects.
- ▶ the ε_{ij} are independent $\text{Normal}(0, \sigma_\varepsilon^2)$ error/interaction terms.
- ▶ μ is an overall or baseline mean.

Define the cell means as

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

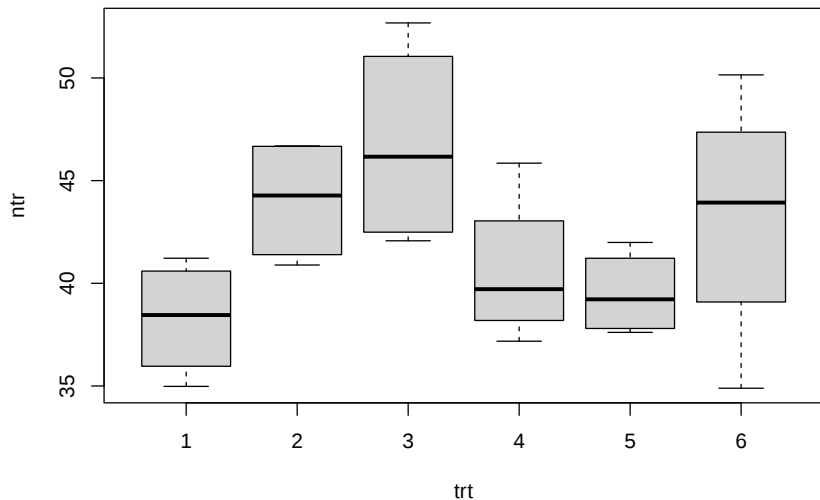
Goals in the RCBD

In the randomized complete block design we wish to

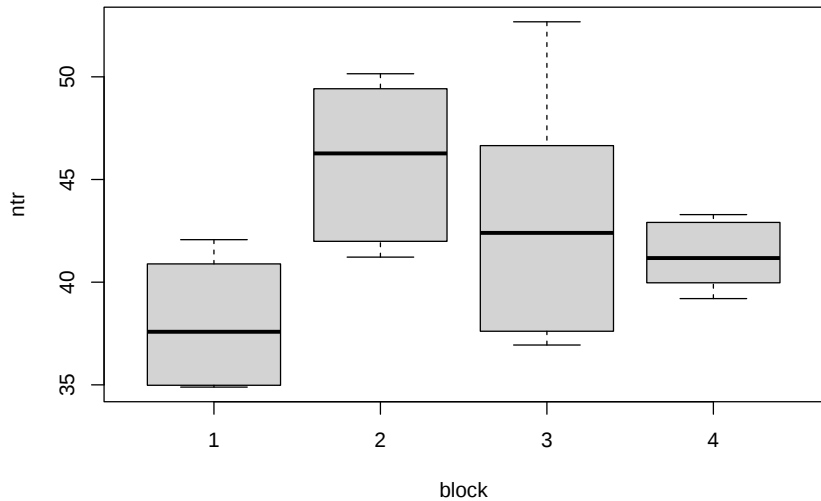
1. Visualize the data.
2. Decompose the variability in the Y_{ij} into its sources.
3. Estimate the variance components σ_B^2 and σ_ε^2 .
4. Test whether the treatment has any effect.
5. Make comparisons between treatment means.
6. Check whether the model assumptions are satisfied.

Nitrogen fertilization data (cont)

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



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



Sums of squares for the RCBD

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

- ▶ We can make the decomposition $SS_{\text{Tot}} = SS_A + SS_B + SS_{\text{Error}}$.
- ▶ The SS_{Error} is really the interaction sum of squares SS_{AB} .
- ▶ But without replication, we cannot estimate an interaction.
- ▶ So the interaction serves as the error term.

ANOVA table for RCBD

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

1. Reject $H_0: \mu_1 = \dots = \mu_a$ if $F_A > F_{a-1, (a-1)(b-1), \alpha}$.
2. Reject $H_0: \sigma_B^2 = 0$ if $F_B > F_{b-1, (a-1)(b-1), \alpha}$.

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

```

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

Source	Df	Expected mean square
A	$a - 1$	$b\theta_A^2 + \sigma_\varepsilon^2$
B	$b - 1$	$a\sigma_B^2 + \sigma_\varepsilon^2$
Error	$(a - 1)(b - 1)$	σ_ε^2

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

Method of moments for variance components in RCBD

Equating MS_B and MS_{Error} with their expectations gives

$$\blacktriangleright \dot{\sigma}_\varepsilon^2 = MS_{Error}.$$

$$\blacktriangleright \dot{\sigma}_B^2 = \frac{MS_B - MS_{Error}}{a}$$

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
$\bar{Y}_{i.}$	$\frac{1}{b}(\sigma_B^2 + \sigma_\varepsilon^2)$	$\frac{2}{ab}[\text{MS}_B + (b-1) \text{MS}_{\text{Error}}]$
$\bar{Y}_{i.} - \bar{Y}_{i' .}$	$\frac{2}{b}\sigma_\varepsilon^2$	$\frac{2}{b} \text{MS}_{\text{Error}}$

Some (unadjusted) CIs in RCB split plot design

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

In the above $\nu^* = \frac{MS_B + (b - 1) MS_{Error}}{\frac{MS_B^2}{(b-1)} + \frac{(b-1)^2 MS_{Error}^2}{(a-1)(b-1)}}$ à la Satterthwaite².

²a 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

```
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

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

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

- ▶ Dunnett's for comparing $\mu_2, \dots, \mu_a$ to a baseline μ_1 :

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

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

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

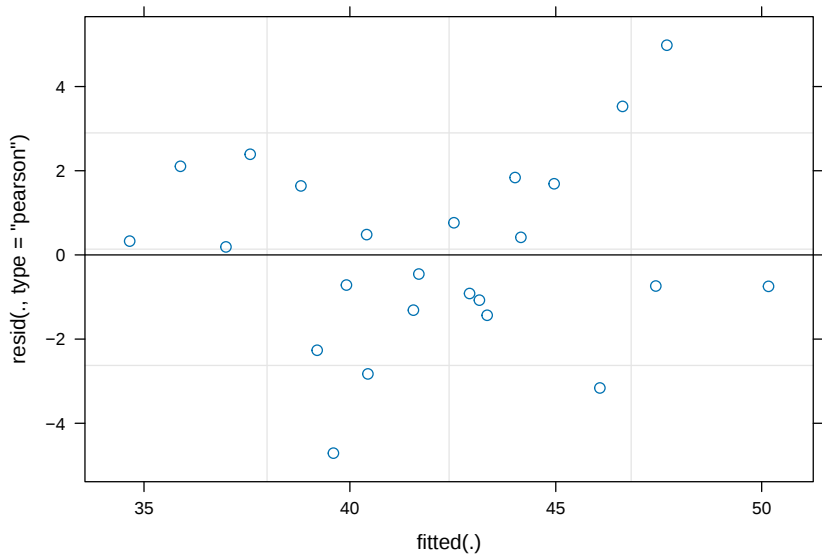
}

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

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

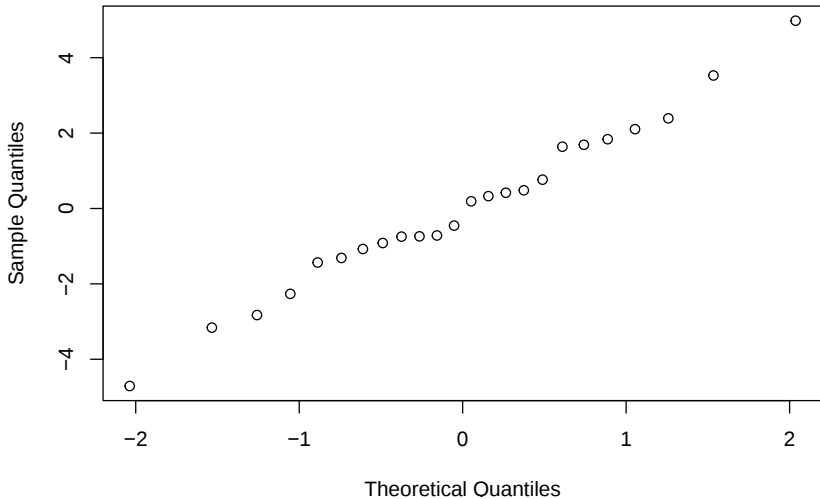
		lower	upper
2	- 1	0.404	11.106
3	- 1	3.142	13.843
4	- 1	-3.013	7.688
5	- 1	-4.118	6.583
6	- 1	-0.403	10.298

```
plot(lmer_out)
```



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

Normal Q-Q Plot



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

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

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

		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)))
```

```
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 $i = 1, \dots, a$, $j = 1, \dots, b$, and $k = 1, \dots, c$, 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 $\text{Normal}(0, \sigma_C^2)$ block effects.
- ▶ the ε_{ijk} are independent $\text{Normal}(0, \sigma_\varepsilon^2)$ error terms.

Define the cell means as

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

Sums of squares for the two-way factorial RCBD

Sum of squares	Symbol	Formula
Total	SS_{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	SS_{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	SS_{Error}	$SS_{\text{Tot}} - (SS_A + SS_B + SS_{AB} + SS_C)$

- ▶ Then we have $SS_{\text{Tot}} = SS_A + SS_B + SS_{AB} + SS_C + SS_{\text{Error}}$.
- ▶ The error SS_{Error} is really the interaction sum of squares $SS_{\text{Trt} \times C}$.
- ▶ 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	$F_A = MS_A / MS_{\text{Error}}$
B	$b - 1$	SS_B	MS_B	$F_B = MS_B / MS_{\text{Error}}$
AB	$(a - 1)(b - 1)$	SS_{AB}	MS_{AB}	$F_{AB} = MS_{AB} / MS_{\text{Error}}$
C	$c - 1$	SS_C	MS_C	$F_C = MS_C / MS_{\text{Error}}$
Error	$(ab - 1)(c - 1)$	SS_{Error}	MS_{Error}	
Total	$abc - 1$	SS_{Tot}		

1. Reject $H_0: \mu_{1.} = \dots = \mu_{a.}$ if $F_A > F_{a-1, (ab-1)(c-1), \alpha}$.
2. Reject $H_0: \mu_{.1} = \dots = \mu_{.b}$ if $F_B > F_{b-1, (ab-1)(c-1), \alpha}$.
3. R. $H_0: \mu_{ij} = \bar{\mu}_{i.} + \bar{\mu}_{.j} - \bar{\mu}_{..} \forall ij$ if $F_{AB} > F_{(a-1)(b-1), (ab-1)(c-1), \alpha}$.
4. Reject $H_0: \sigma_C^2 = 0$ if $F_C > F_{c-1, (ab-1)(c-1), \alpha}$.

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

```

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

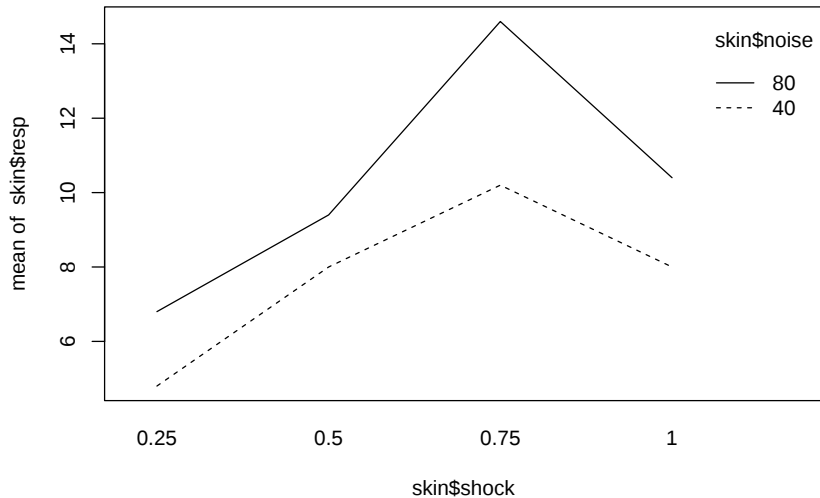
```

```

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

$$\blacktriangleright \theta_A^2 = (a - 1)^{-1} \sum_{i=1}^a (\bar{\mu}_{i.} - \bar{\mu}_{..})^2$$

$$\blacktriangleright \theta_B^2 = (b - 1)^{-1} \sum_{j=1}^b (\bar{\mu}_{.j} - \bar{\mu}_{..})^2$$

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

MoMs for variance components in two-way factorial RCBD

- ▶ Equating MS_C and MS_{Error} with their expectations gives

$$\dot{\sigma}_C^2 = \frac{MS_C - MS_{\text{Error}}}{ab} \quad \text{and} \quad \dot{\sigma}_\varepsilon^2 = MS_{\text{Error}} .$$

- ▶ 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:

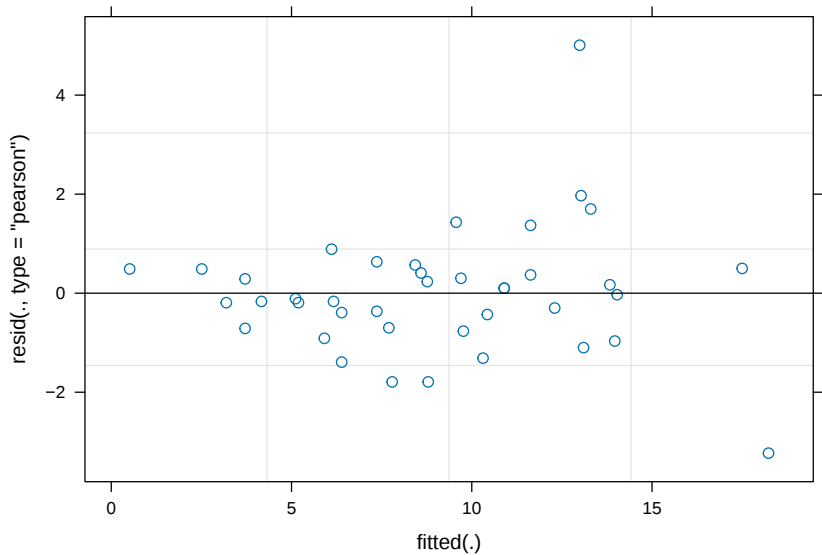
(Intercept)	noise80	shock0.5	shock0.75
4.8	2.0	3.2	5.4
shock1	noise80:shock0.5	noise80:shock0.75	noise80:shock1
3.2	-0.6	2.4	0.4

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)
```

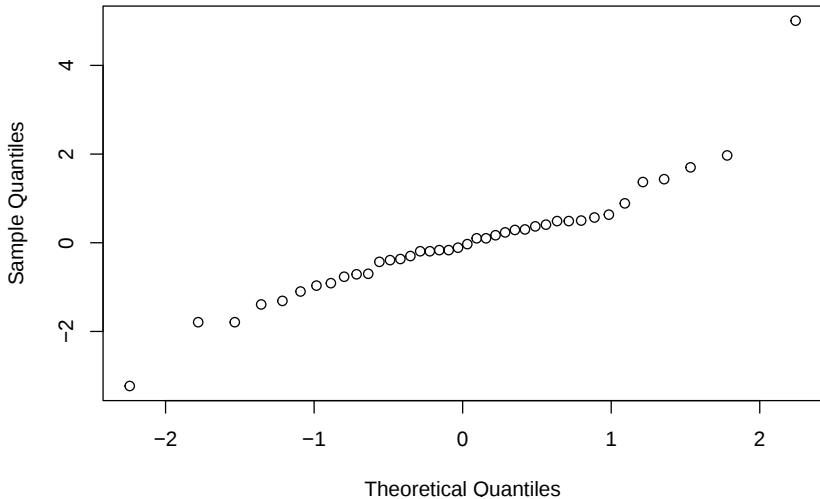
We have $\dot{\sigma}_C = 3.320$ and $\dot{\sigma}_\varepsilon = 1.514$.

```
plot(lmer_out)
```



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

Normal Q-Q Plot



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.