

Split-plot Analysis

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Introduction

- ▶ Split-plot design (RCBD)
- ▶ EDA
- ▶ Linear Mixed Model
- ▶ Means Comparison

Factors

Whole-plot: Irrigation

1. moist
2. saturated
3. flooded

Sub-plot: Fertilizer

1. 0
2. 50
3. 100
4. 150

Creating the design

```
sp <- FieldHub::split_plot(  
  wp = 3, # whole-plot  
  sp = 4, # sub-plot  
  reps = 3, # blocks  
  type = 2, # for RCBD  
  seed = 2023  
)
```

Field layout

Split Plot Design (RCBD) 12X3

ROWS	2 3	3 4	1 3
	2 4	3 1	1 4
	2 2	3 3	1 2
	2 1	3 2	1 1
	1 3	2 2	3 1
	1 2	2 4	3 3
	1 4	2 3	3 4
	1 1	2 1	3 2
	1 2	2 2	3 4
	1 3	2 3	3 1
	1 4	2 4	3 2
	1 1	2 1	3 3
COLUMNS			

Simulating effects of treatments

```
# effect of irrigation
split_plot$y_irr <- NA
split_plot$y_irr[split_plot$irrigation == "flooded"] <- 6
split_plot$y_irr[split_plot$irrigation == "saturated"] <- 12
split_plot$y_irr[split_plot$irrigation == "moist"] <- 15

# effect of fertilizer
split_plot$y_fert <- NA
split_plot$y_fert[split_plot$fertilizer == "0"] <- 5
split_plot$y_fert[split_plot$fertilizer == "50"] <- 8
split_plot$y_fert[split_plot$fertilizer == "100"] <- 10
split_plot$y_fert[split_plot$fertilizer == "150"] <- 12

# effect of interaction
split_plot$y_inter <- (
  split_plot$y_irr * split_plot$y_fert
) * 0.01
```

Simulating effects of blocks and error

```
# effect of block
split_plot$y_b <- NA
split_plot$y_b[split_plot$REP == 1] <- -10
split_plot$y_b[split_plot$REP == 2] <- 5
split_plot$y_b[split_plot$REP == 3] <- -5
split_plot$y_b[split_plot$REP == 4] <- -10

# effect of error
set.seed(2023)
split_plot$error <- rnorm(36, 0, 2.5)

# creating response
split_plot$y <- (
  split_plot$y_irr + split_plot$y_fert +
  split_plot$y_inter + split_plot$y_b + split_plot$error
)
```


EDA

```
with(split_plot, table(block))
```

block

1	2	3
12	12	12

```
with(split_plot, table(irrigation))
```

irrigation

moist	saturated	flooded
12	12	12

```
with(split_plot, table(fertilizer))
```

fertilizer

0	50	100	150
9	9	9	9

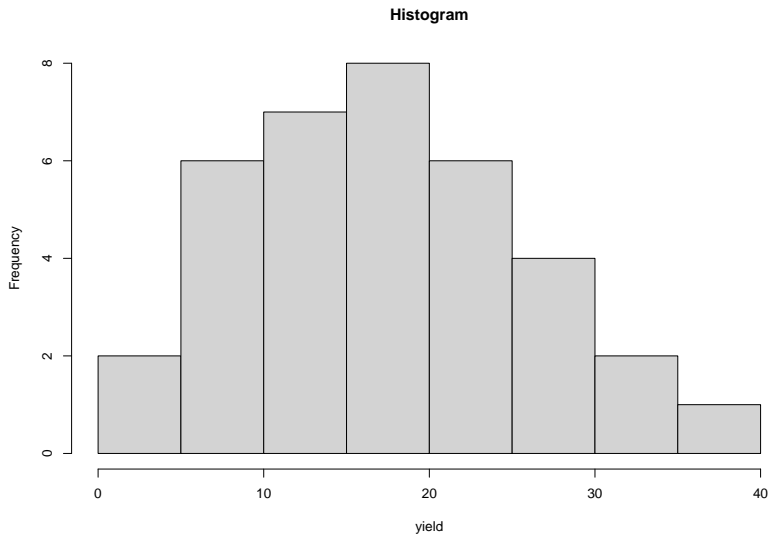
EDA

```
with(split_plot, addmargins(table(irrigation, fertilizer)))
```

	fertilizer				
irrigation	0	50	100	150	Sum
moist	3	3	3	3	12
saturated	3	3	3	3	12
flooded	3	3	3	3	12
Sum	9	9	9	9	36

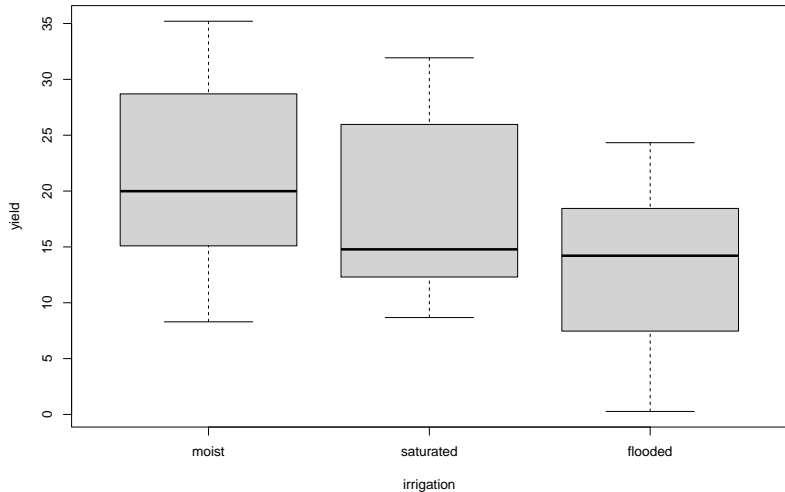
EDA

```
hist(split_plot$, main = 'Histogram', xlab = 'yield')
```



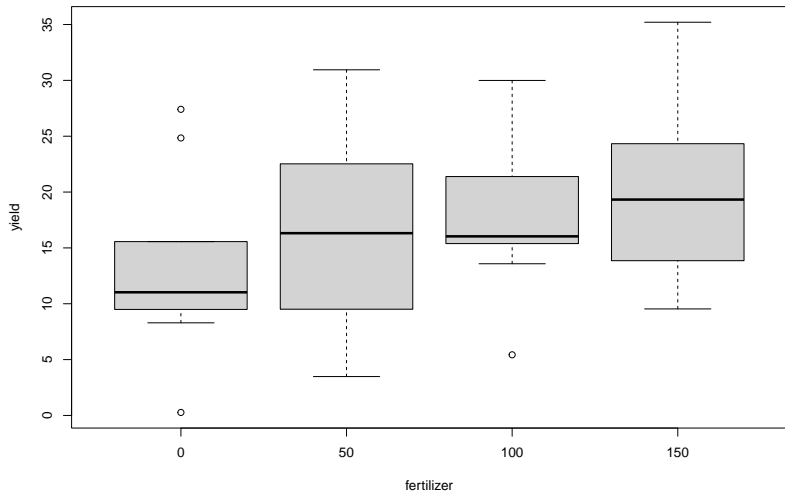
EDA

```
boxplot(y ~ irrigation, data = split_plot, ylab = 'yield')
```



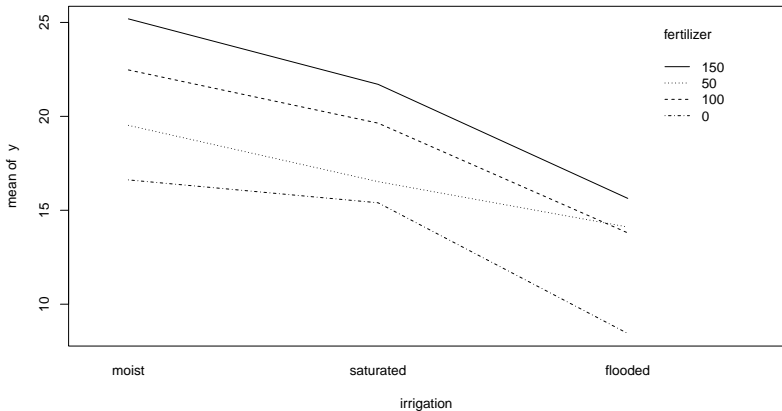
EDA

```
boxplot(y ~ fertilizer, data = split_plot, ylab = 'yield')
```



EDA

```
with(split_plot, interaction.plot(x.factor = irrigation,  
                                trace.factor = fertilizer,  
                                response = y))
```



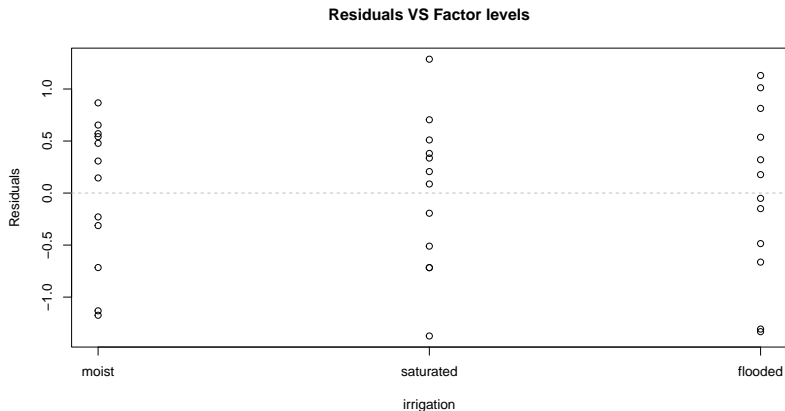
Model

```
mod.lme <- nlme::lme(  
  y ~ irrigation * fertilizer,  
  random = ~1|block/irrigation,  
  data = split_plot  
)  
res <- residuals(mod.lme, type = 'pearson')  
anova(mod.lme)
```

	numDF	denDF	F-value	p-value
(Intercept)	1	18	12.624677	0.0023
irrigation	2	4	12.401598	0.0193
fertilizer	3	18	22.922619	<.0001
irrigation:fertilizer	6	18	1.067825	0.4172

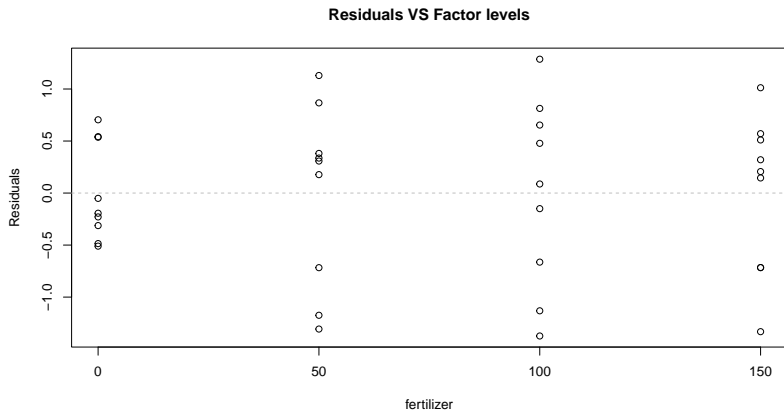
Model diagnostics

```
stripchart(res ~ mod.lme$data$irrigation, vertical = T, pch = 1,  
           xlab = 'irrigation', ylab = 'Residuals',  
           main = 'Residuals VS Factor levels')  
abline(h = 0, lty = 2, col = 'grey')
```



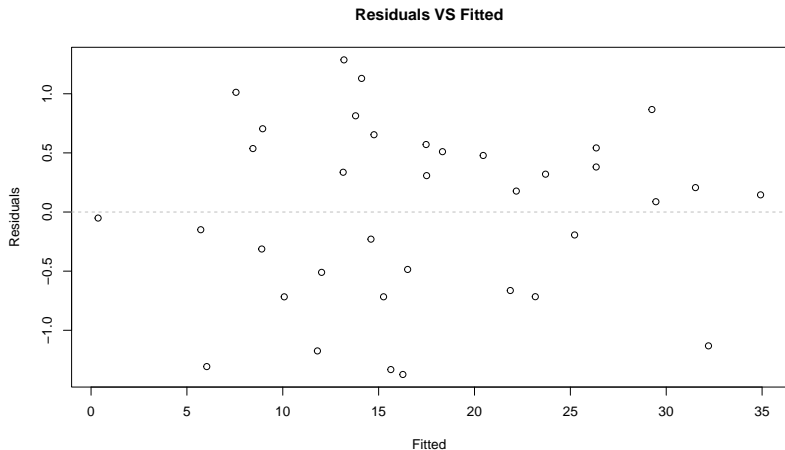
Model diagnostics

```
stripchart(res ~ mod.lme$data$fertilizer, vertical = T, pch = 1,  
           xlab = 'fertilizer', ylab = 'Residuals',  
           main = 'Residuals VS Factor levels')  
abline(h = 0, lty = 2, col = 'grey')
```



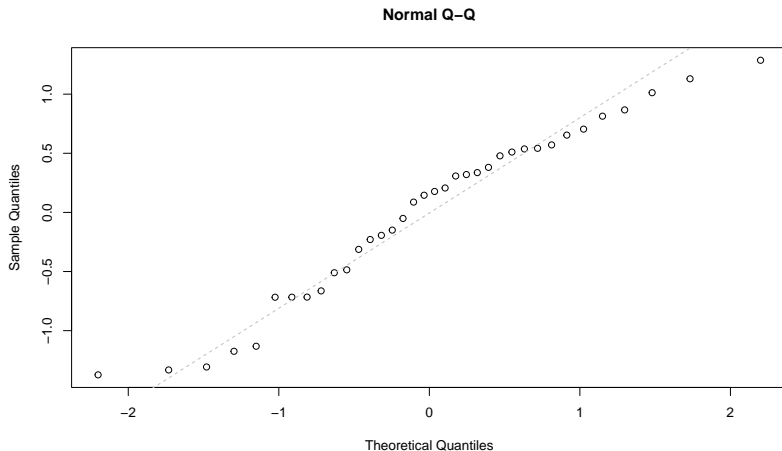
Model diagnostics

```
plot(res ~ fitted(mod.lme), main = 'Residuals VS Fitted',  
     xlab = 'Fitted', ylab = 'Residuals')  
abline(h = 0, lty = 2, col = 'grey')
```



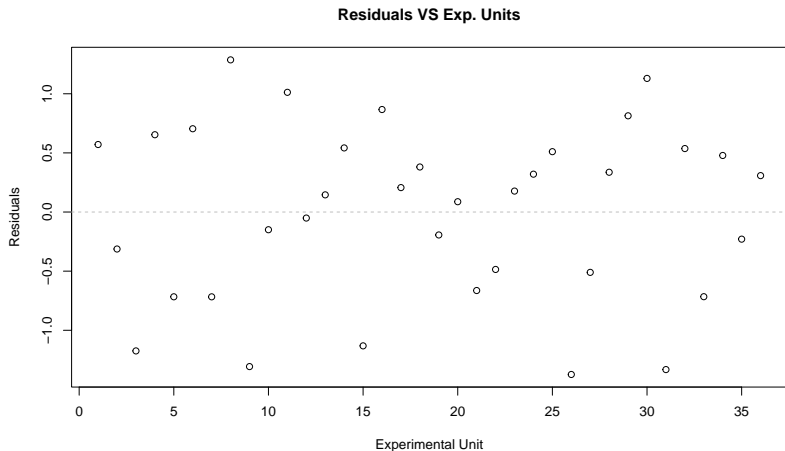
Model diagnostics

```
qqnorm(res, main = 'Normal Q-Q')  
qqline(res, lty = 2, col = 'grey')
```



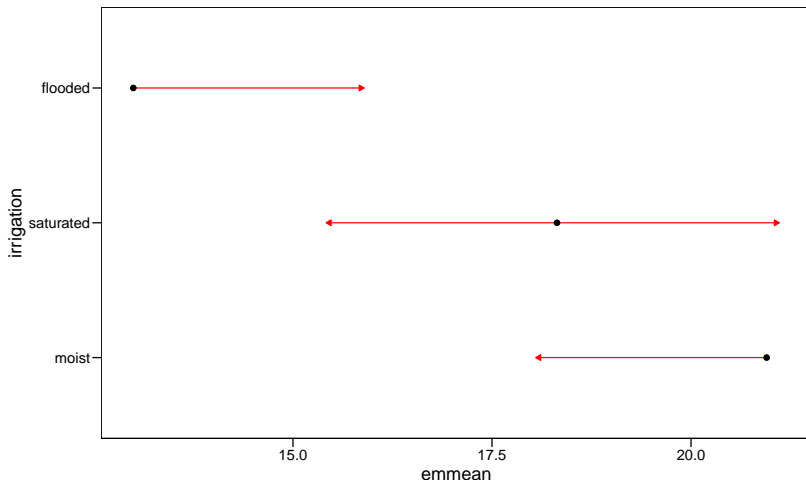
Model diagnostics

```
plot(res ~ split_plot$ID, main = 'Residuals VS Exp. Units',  
     xlab = 'Experimental Unit', ylab = 'Residuals')  
abline(h = 0, lty = 2, col = 'grey')
```



Means comparison

```
emm.irr <- emmeans::emmeans(mod.lme, pairwise ~ irrigation,  
                             adjust = "Tukey")  
plot(emm.irr, interval = F, comparisons = T)
```



Means comparisons

```
emm.fert <- emmeans::emmeans(mod.lme, pairwise ~ fertilizer,  
                             adjust = "Tukey")  
plot(emm.fert, interval = F, comparisons = T)
```

