Split-plot Analysis

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Introduction

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

Factors

Whole-plot: Irrigation (in cm^3 / cm^3)

1. moist
2. saturated
3. flooded

Sub-plot: Fertilizer

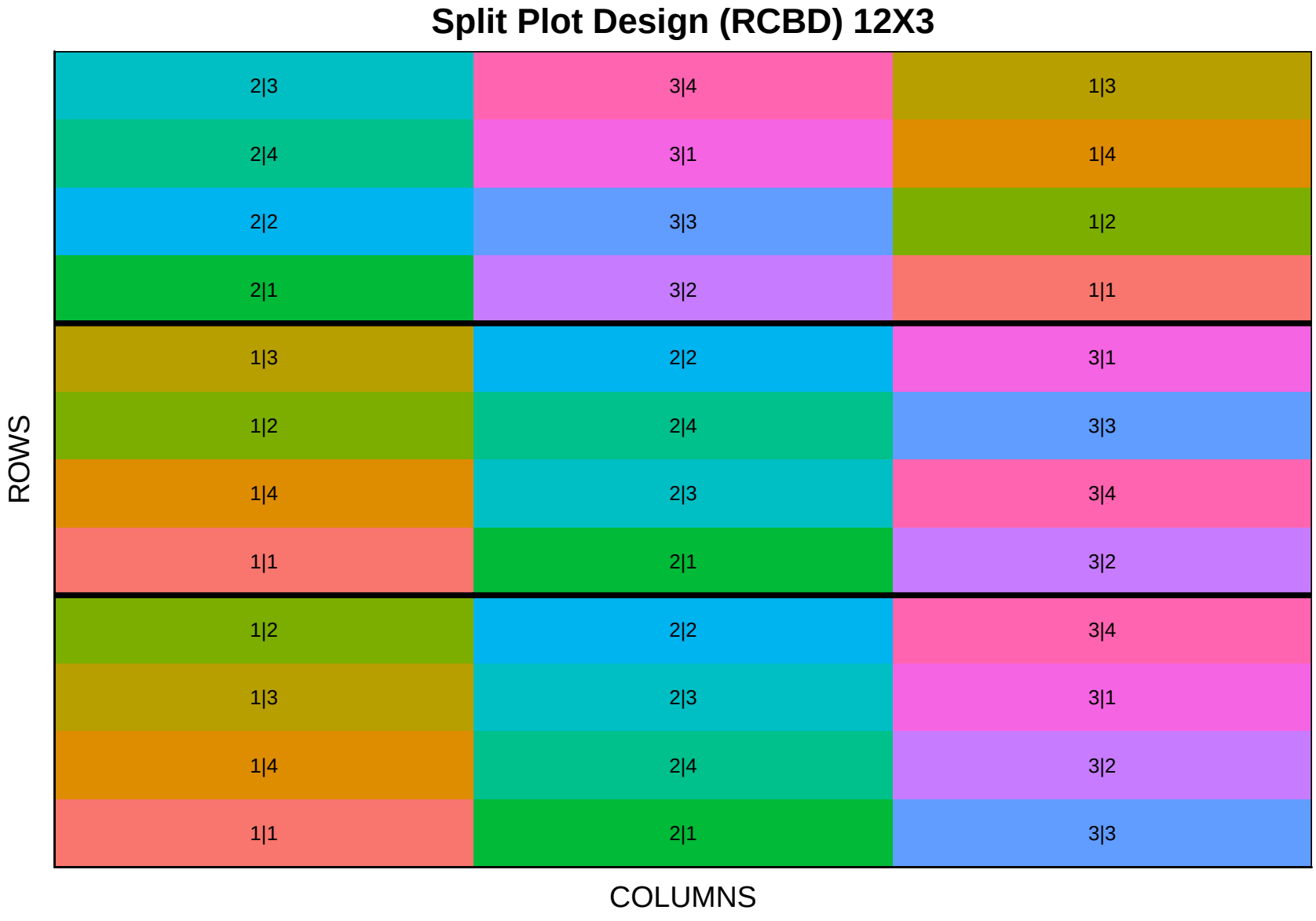
1. 0 kg/ha
2. 50 kg/ha
3. 100 kg/ha
4. 150 kg/ha

Response is the rice yield in Mg/ha

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



Simulating effects of treatments

```r
# 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

```r
# 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

# 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
```

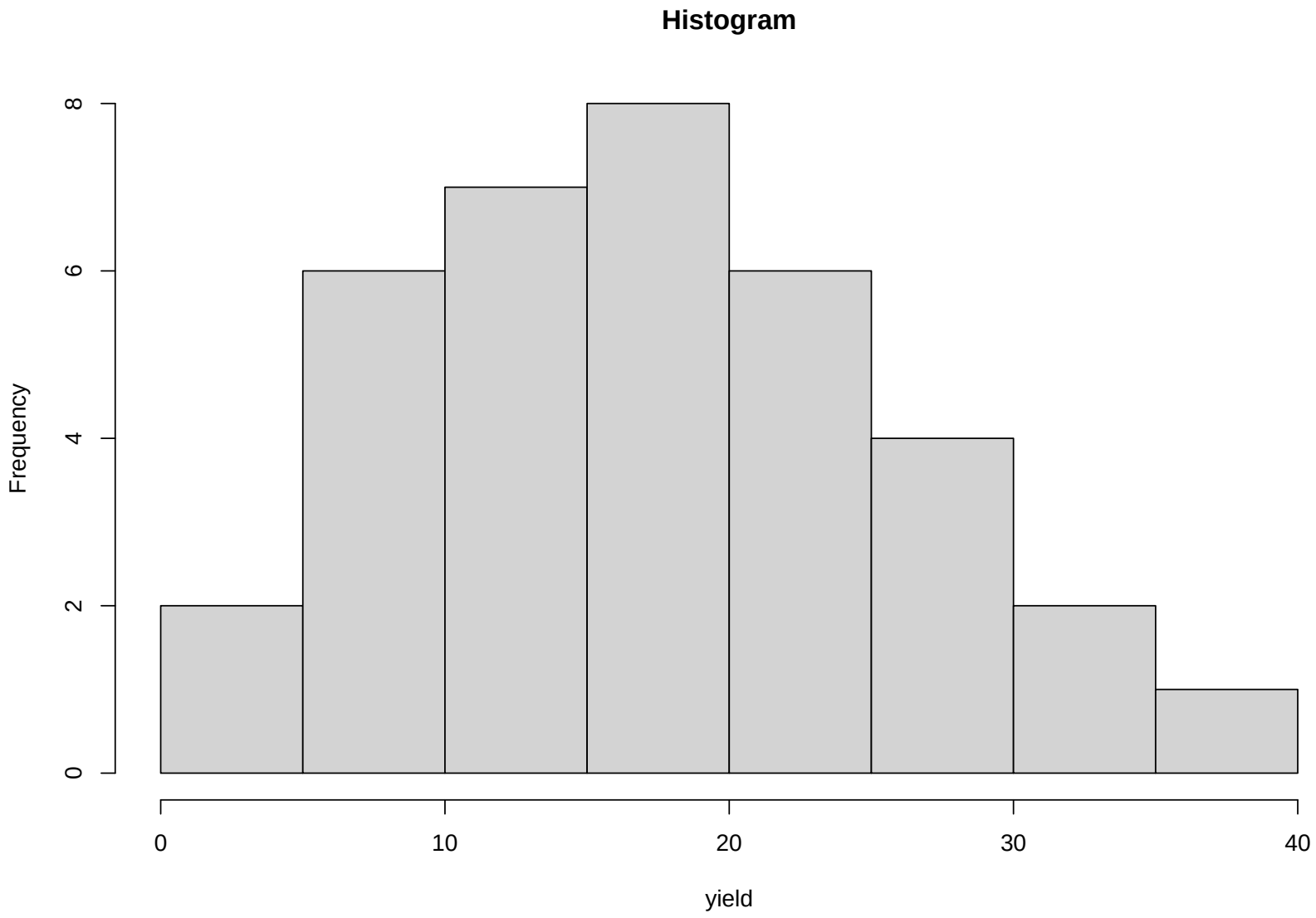
EDA

```
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
```

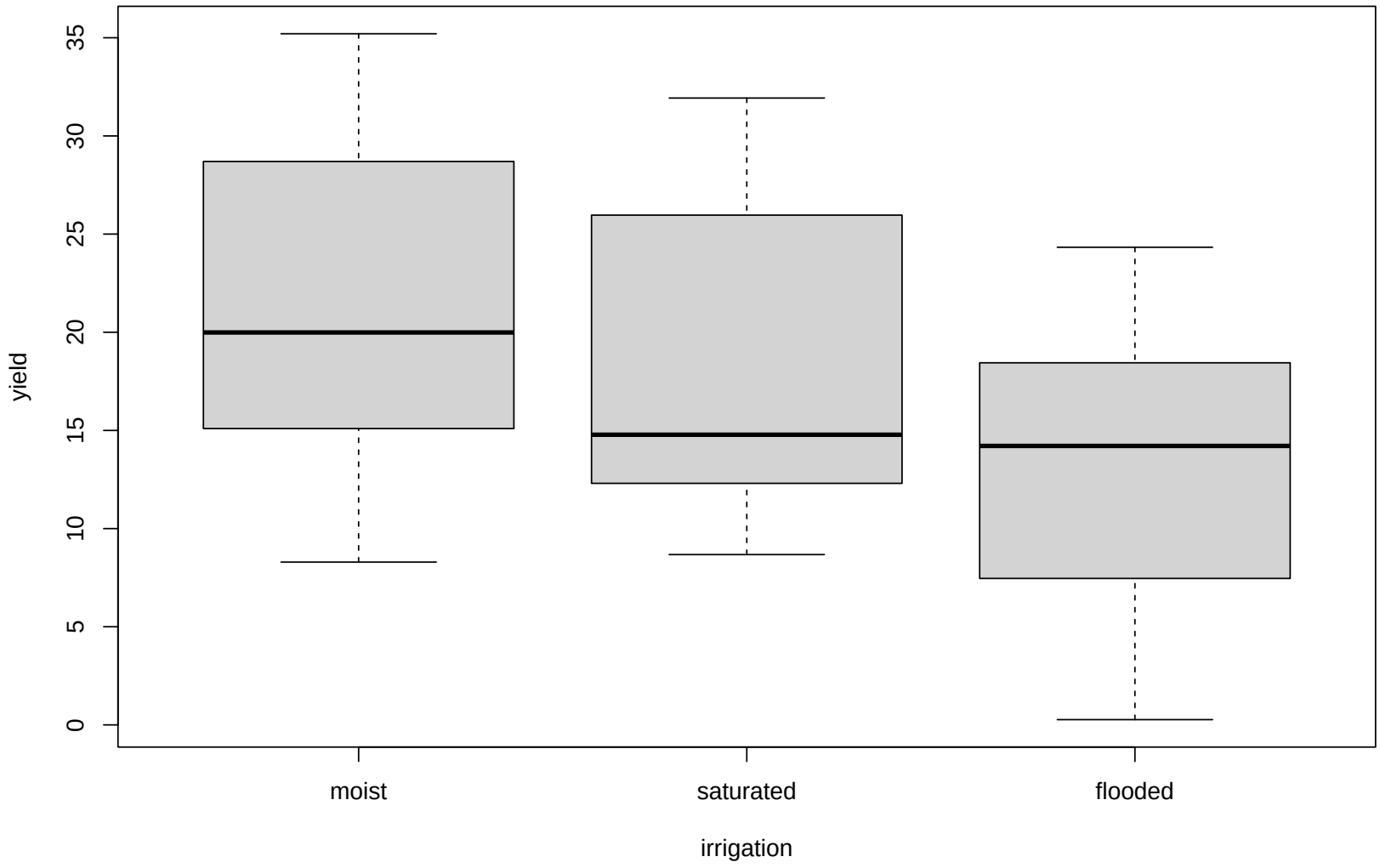
EDA

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



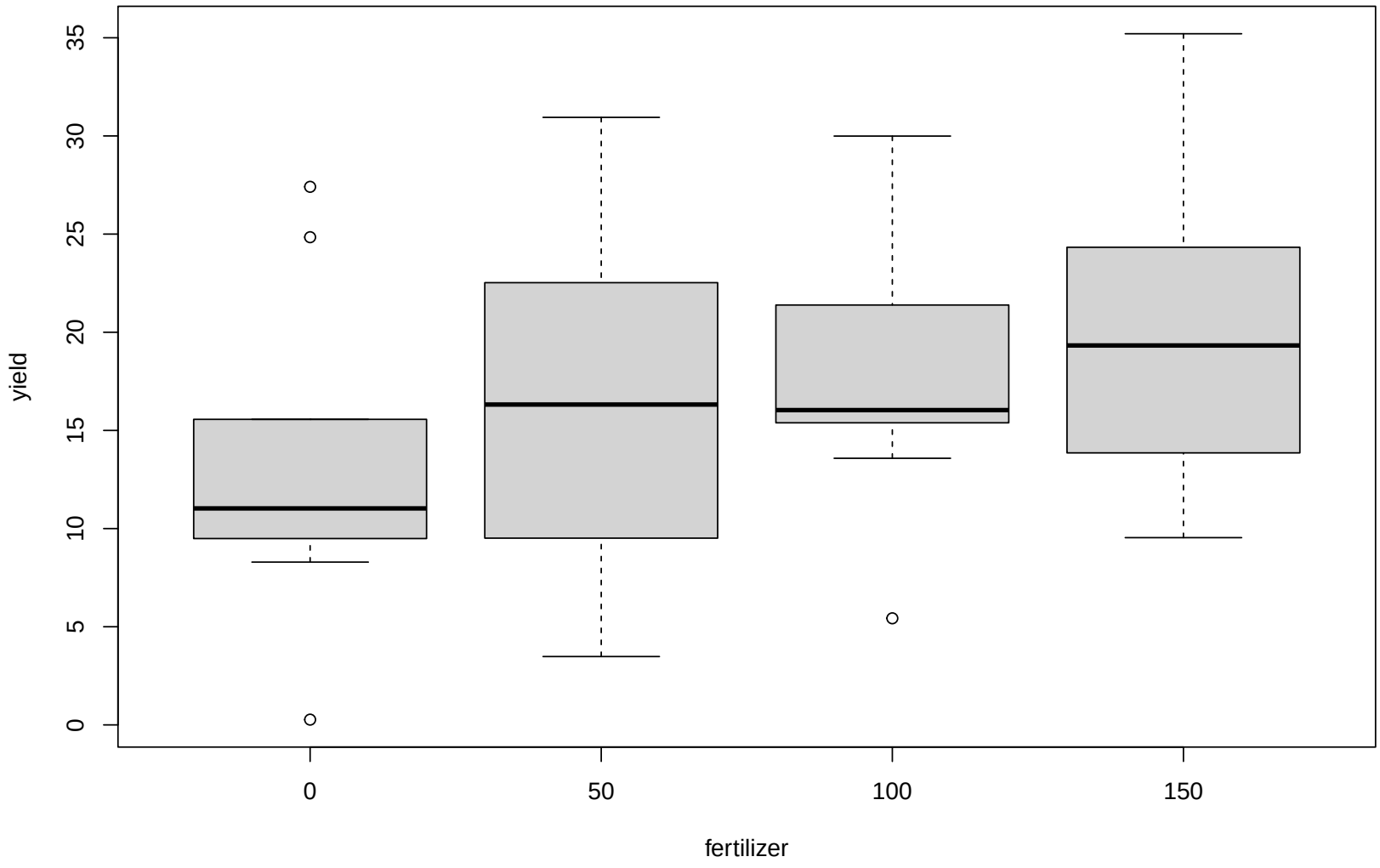
EDA

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



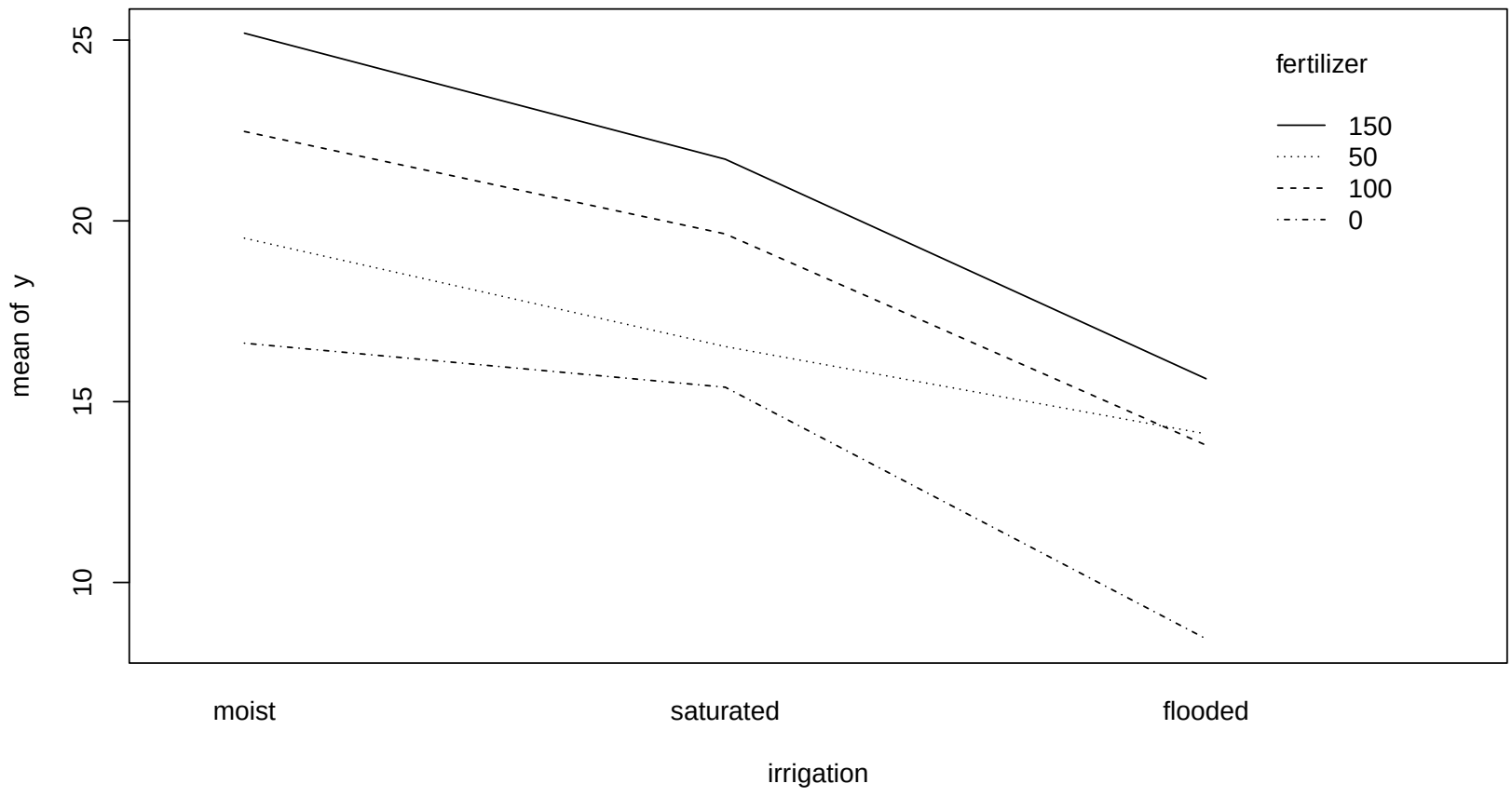
EDA

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



EDA

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



Model

$$y_{ijk} = \mu + b_i + \alpha_j + b_i\alpha_j + \beta_k + \alpha_j\beta_k + \varepsilon_{ijk},$$

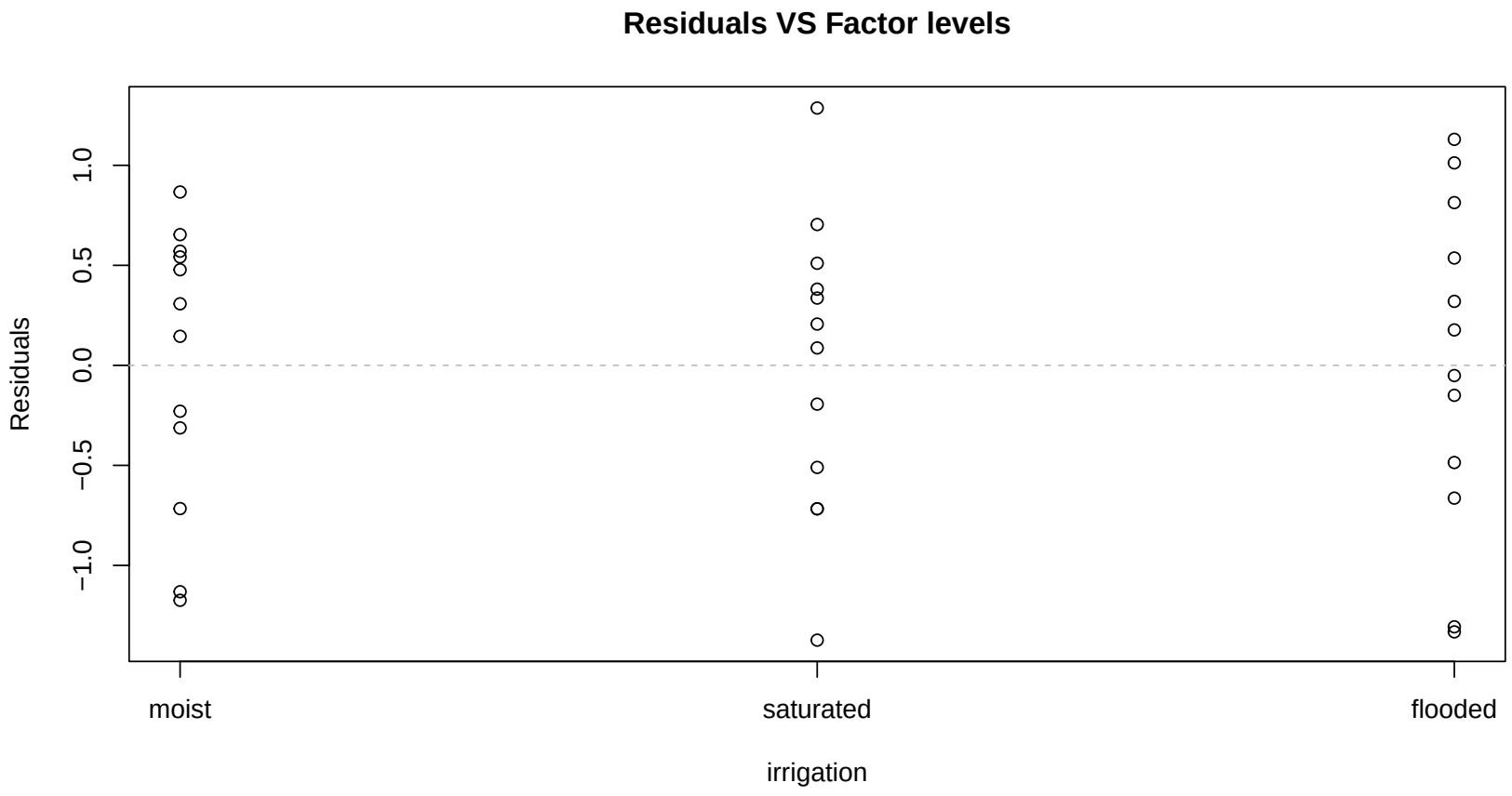
where y_{ijk} is the response, μ is the grand mean, b_i is the block (random), with $i = 1, 2, 3$, α_j is the irrigation term, with $j = 1, 2, 3$, $b_i\alpha_j$ is the interaction between block and irrigation (random), β_k is the fertilizer term, with $k = 1, 2, 3, 4$, $\alpha_j\beta_k$ is the interaction between irrigation and block, and ε_{ijk} is the residual term.

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

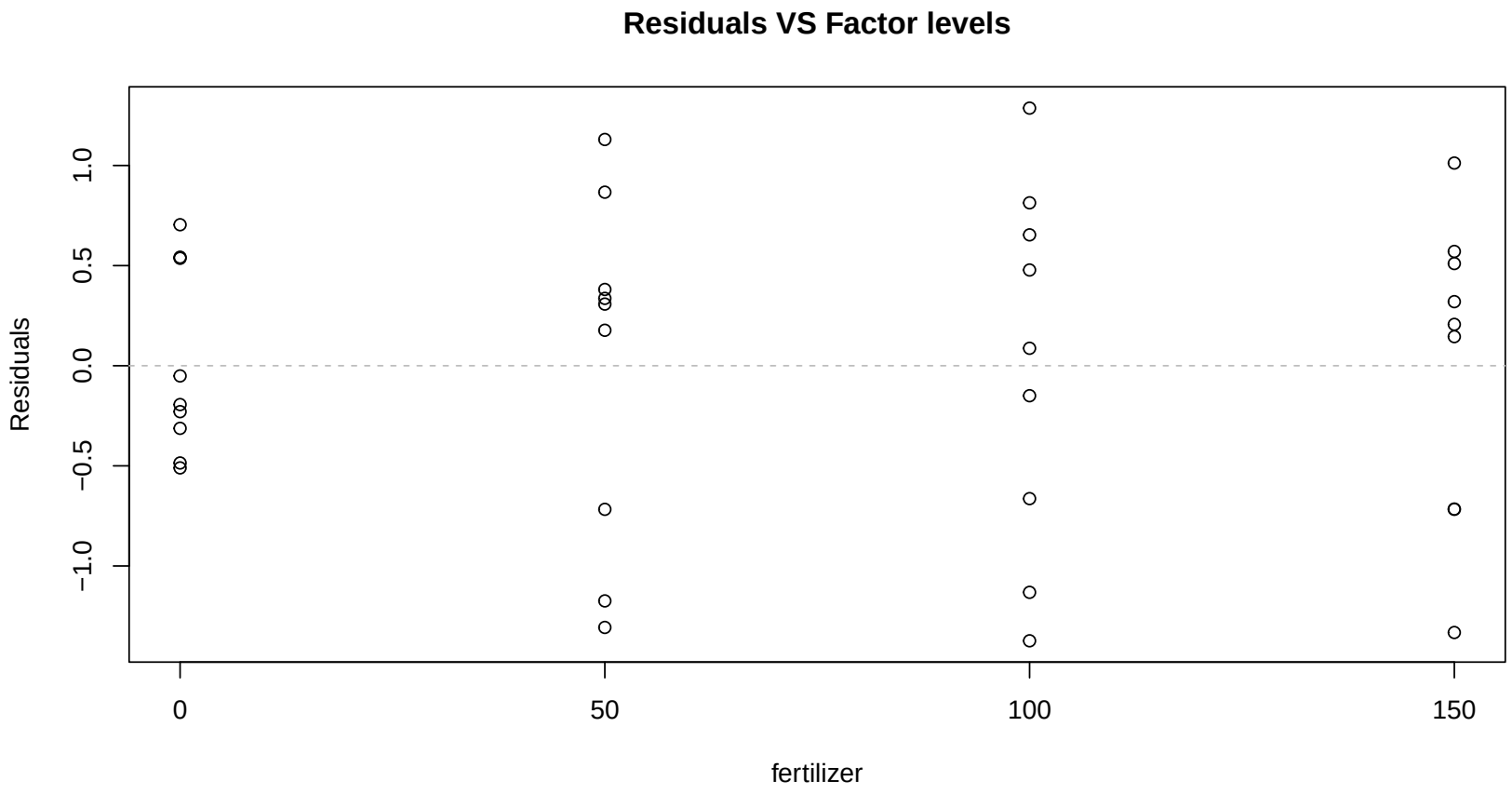
Model diagnostics

```
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')
```



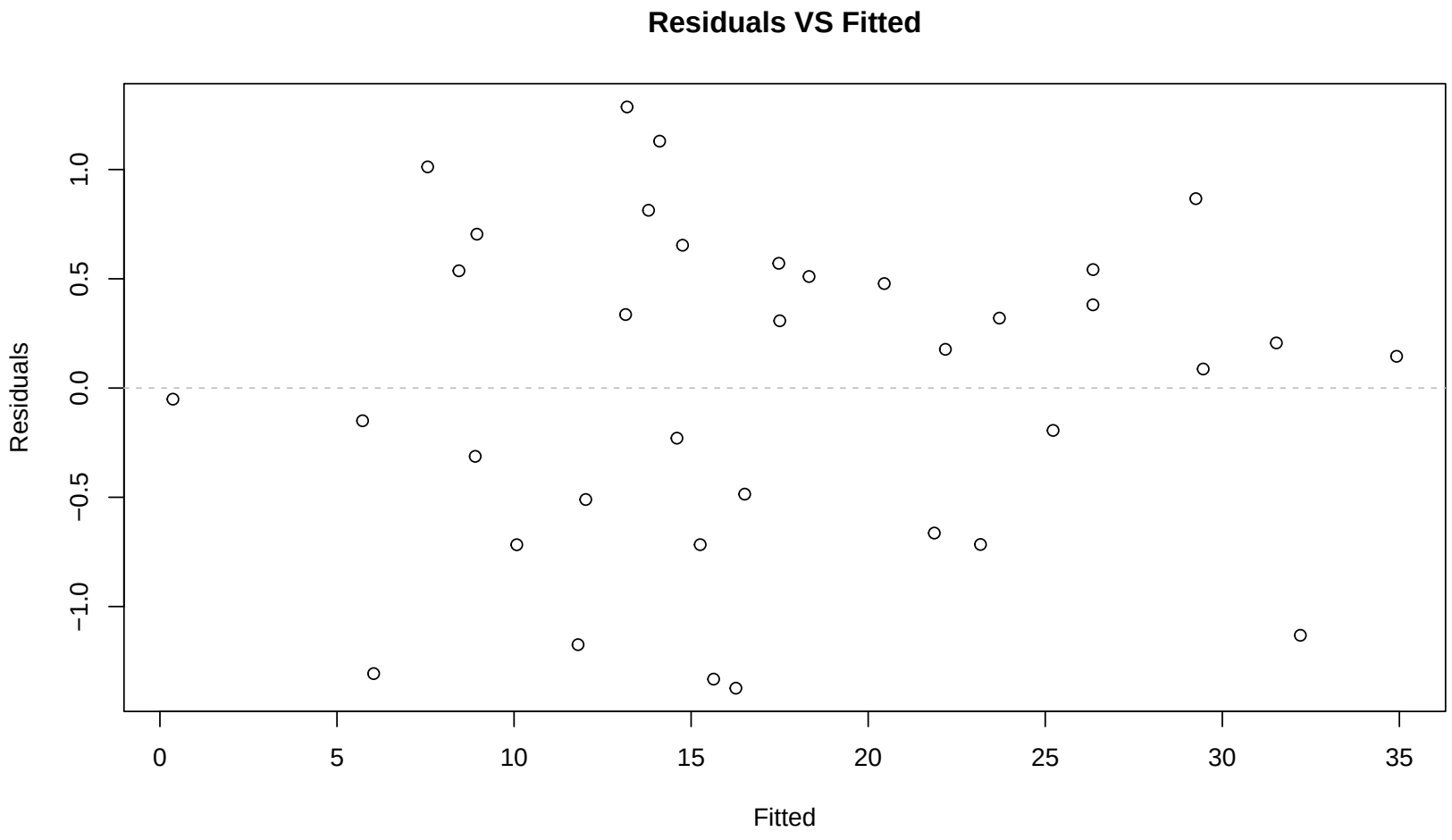
Model diagnostics

```
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')
```



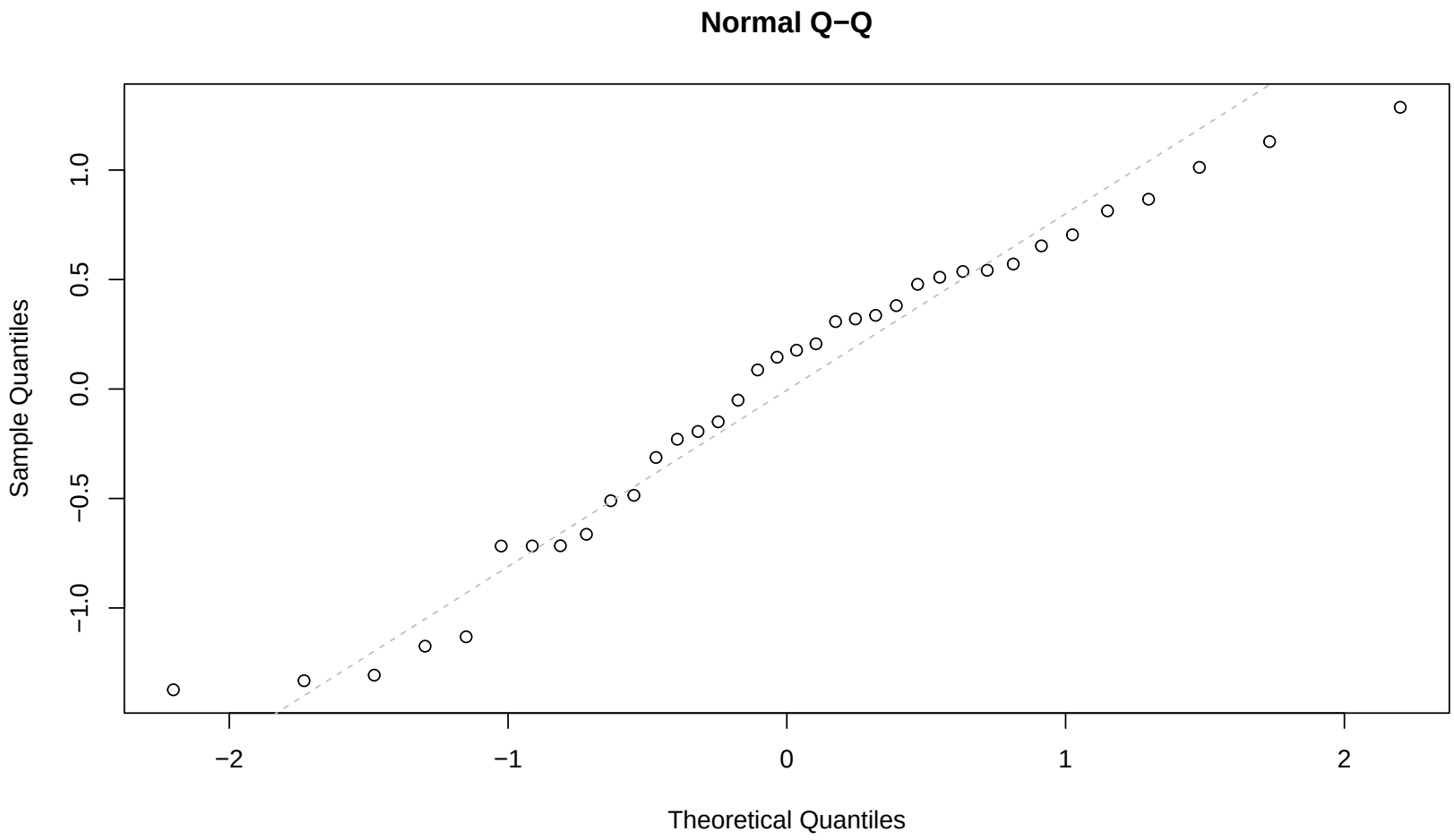
Model diagnostics

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



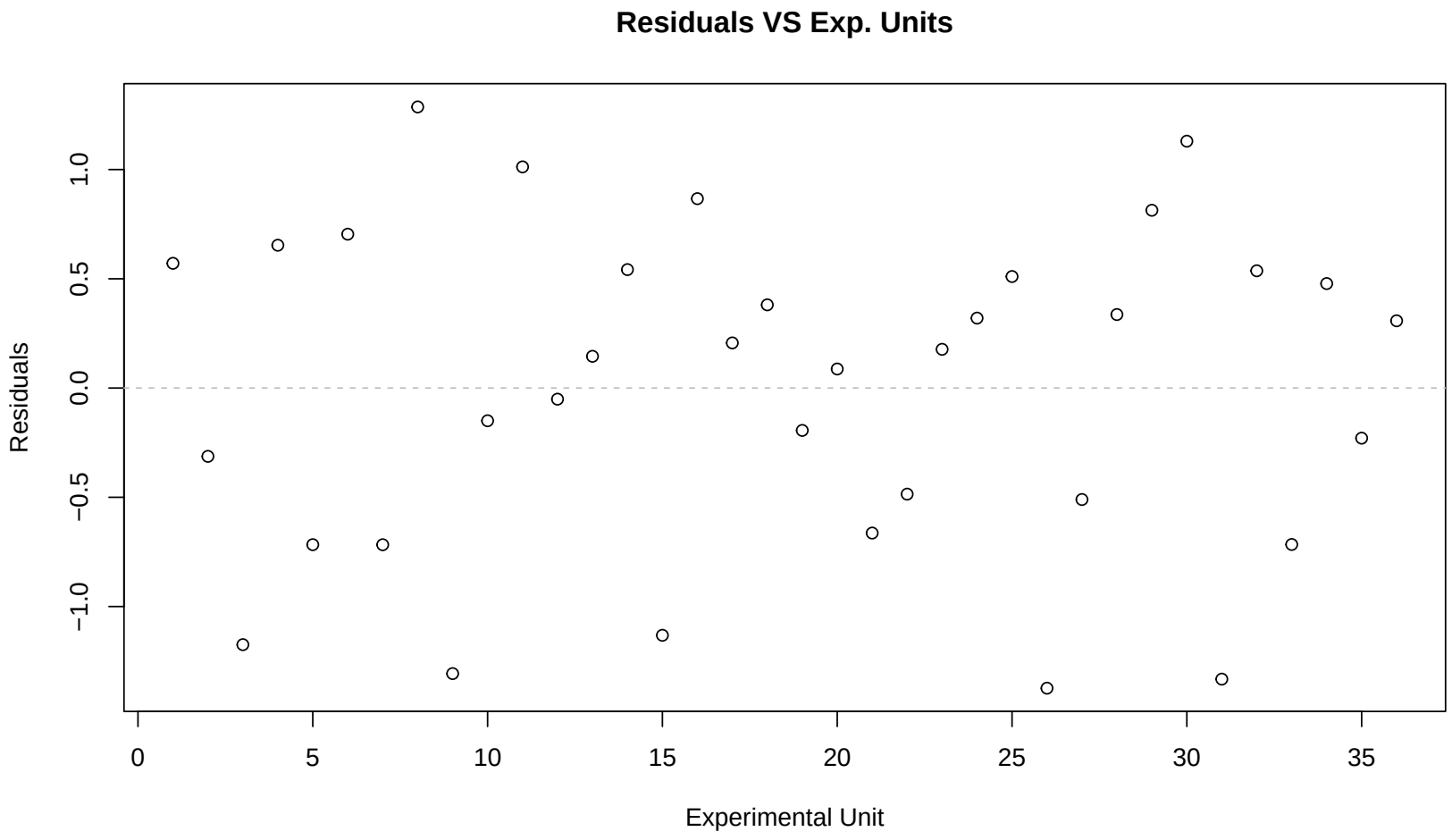
Model diagnostics

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



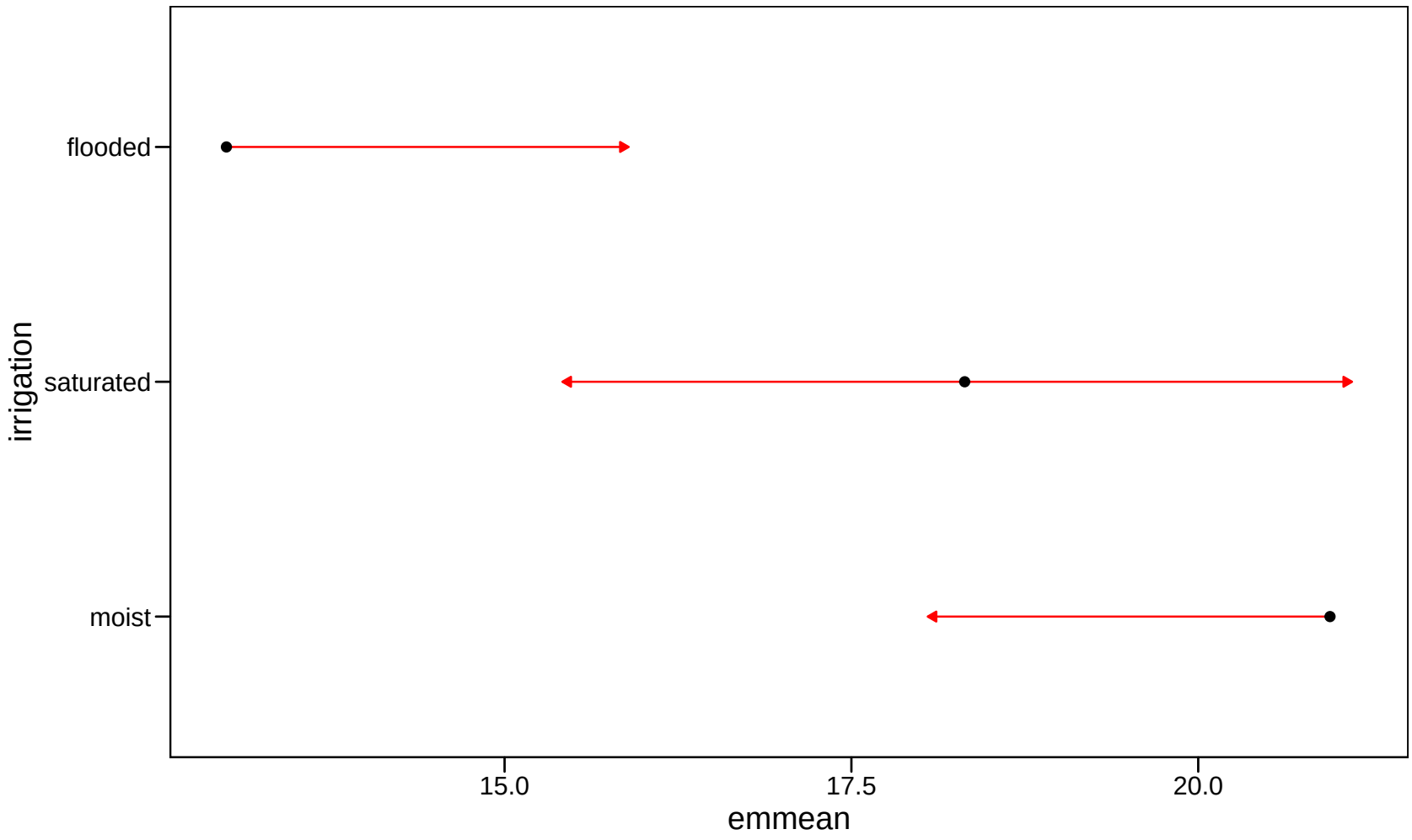
Model diagnostics

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



Means comparision

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



Means comparisions

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