

# One-way randomized complete block design

Paul Schmidt

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One-way ANOVA & pairwise comparison post hoc tests in a randomized complete block design.

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```
# (install &) load packages
pacman::p_load(
  conflicted,
  desplot,
  emmeans,
  ggtext,
  multcomp,
  multcompView,
  tidyverse)

# handle function conflicts
conflicts_prefer(dplyr::filter)
conflicts_prefer(dplyr::select)
```

# 1 Data

This example is taken from Chapter “2 *Randomized complete block design*” of the course material “Mixed models for metric data (3402-451)” by [Prof. Dr. Hans-Peter Piepho](#). It considers data published in Clewer and Scarisbrick (2001) from a yield (t/ha) trial laid out as a randomized complete block design (3 blocks) with cultivar (4 cultivars) being the only treatment factor. Thus, we have a total of 12 plots.

## 1.1 Import

```
# data is available online:
path <- "https://raw.githubusercontent.com/SchmidtPaul/dsfair_quarto/master/data/Clewer&Sc

dat <- read_csv(path) # use path from above
dat

# A tibble: 12 x 5
  block cultivar yield   row   col
  <chr> <chr>    <dbl> <dbl> <dbl>
1 B1    C1         7.4    2     1
2 B1    C2         9.8    3     1
3 B1    C3         7.3    1     1
4 B1    C4         9.5    4     1
5 B2    C1         6.5    1     2
6 B2    C2         6.8    4     2
7 B2    C3         6.1    3     2
8 B2    C4          8     2     2
9 B3    C1         5.6    2     3
10 B3   C2         6.2    1     3
11 B3   C3         6.4    3     3
12 B3   C4         7.4    4     3
```

## 1.2 Format

Before anything, the columns `block` and `cultivar` should be encoded as factors, since R by default encoded them as character.

```
dat <- dat %>%
  mutate(across(c(block, cultivar), ~ as.factor(.x)))
```

## 1.3 Explore

We make use of `dlookr::describe()` to conveniently obtain descriptive summary tables. Here, we get can summarize per block and per cultivar.

```
dat %>%
  group_by(cultivar) %>%
  dlookr::describe(yield) %>%
  select(2:sd) %>%
  arrange(desc(mean))

# A tibble: 4 x 5
  cultivar     n    na mean    sd
  <fct>    <int> <int> <dbl> <dbl>
1 C4         3     0  8.3  1.08
2 C2         3     0  7.6  1.93
3 C3         3     0  6.6  0.624
4 C1         3     0  6.5  0.9
```

```
dat %>%
  group_by(block) %>%
  dlookr::describe(yield) %>%
  select(2:sd) %>%
  arrange(desc(mean))
```

```
# A tibble: 3 x 5
  block     n    na mean    sd
  <fct> <int> <int> <dbl> <dbl>
1 B1     4     0  8.5  1.33
2 B2     4     0  6.85 0.819
3 B3     4     0  6.4  0.748
```

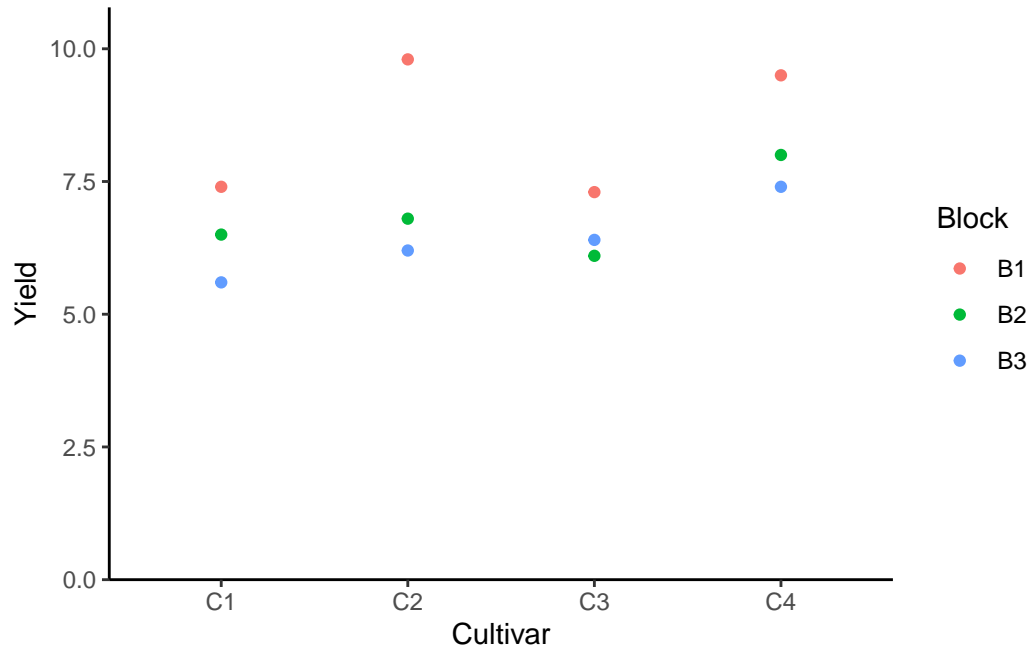
Additionally, we can decide to plot our data:

```
ggplot(data = dat) +
  aes(y = yield, x = cultivar, color = block) +
  geom_point() +
  scale_x_discrete(
    name = "Cultivar"
  ) +
  scale_y_continuous(
```

```

name = "Yield",
limits = c(0, NA),
expand = expansion(mult = c(0, 0.1))
) +
scale_color_discrete(
  name = "Block"
) +
theme_classic()

```



Finally, since this is an experiment that was laid with a certain experimental design (= a randomized complete block design; RCBD) - it makes sense to also get a field plan. This can be done via `desplot()` from `{desplot}`. We can even create a second field plan that gives us a feeling for the yields per plot.

```

desplot(
  data = dat,
  flip = TRUE, # row 1 on top, not on bottom
  form = cultivar ~ col + row, # fill color per cultivar
  out1 = block, # line between blocks
  text = cultivar, # cultivar names per plot
  cex = 1, # cultivar names: font size

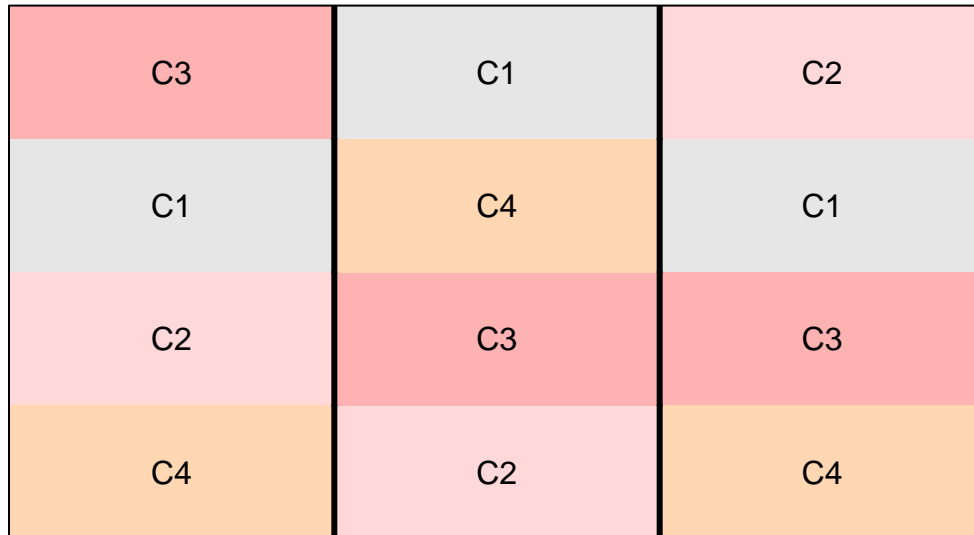
```

```

shorten = FALSE, # cultivar names: don't abbreviate
main = "Field layout: cultivars", # plot title
show.key = FALSE # hide legend
)

```

### Field layout: cultivars

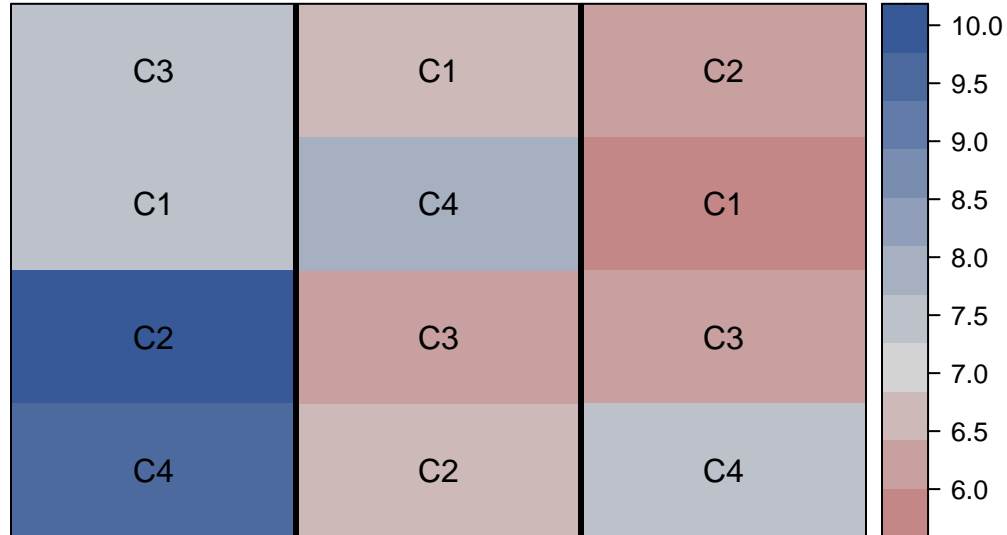


```

desplot(
  data = dat,
  flip = TRUE, # row 1 on top, not on bottom
  form = yield ~ col + row, # fill color according to yield
  out1 = block, # line between blocks
  text = cultivar, # cultivar names per plot
  cex = 1, # cultivar names: font size
  shorten = FALSE, # cultivar names: don't abbreviate
  main = "Yield per plot", # plot title
  show.key = FALSE # hide legend
)

```

## Yield per plot



Thus, C4 seems to be the most promising cultivar in terms of yield. Moreover, it can be seen that yields were generally higher in block B1 (left), compared to the other blocks.

## 2 Model

Finally, we can decide to fit a linear model with `yield` as the response variable and (fixed) `cultivar` and `block` effects.

```
mod <- lm(yield ~ cultivar + block, data = dat)
```

⚠ Model assumptions met? (click to show)

It would be at this moment (i.e. after fitting the model and before running the ANOVA), that you should check whether the model assumptions are met. Find out more in the [summary article “Model Diagnostics”](#)

## 3 ANOVA

Based on our model, we can then conduct an ANOVA:

```
ANOVA <- anova(mod)
ANOVA
```

```
Analysis of Variance Table
```

```
Response: yield
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
cultivar	3	6.63	2.21	5.525	0.036730 *
block	2	9.78	4.89	12.225	0.007651 **
Residuals	6	2.40	0.40		

```
---
```

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

Accordingly, the ANOVA's F-test found the cultivar effects to be statistically significant ( $p = 0.037^*$ ). Additionally, the block effects are also statistically significant ( $p = 0.008^{**}$ ), but this is only of secondary concern for us.

## 4 Mean comparison

Besides an ANOVA, one may also want to compare adjusted yield means between cultivars via post hoc tests (t-test, Tukey test etc.).

```
mean_comp <- mod %>%
  emmeans(specs = ~ cultivar) %>% # adj. mean per cultivar
  cld(adjust = "none", Letters = letters) # compact letter display (CLD)
```

```
mean_comp
```

cultivar	emmean	SE	df	lower.CL	upper.CL	.group
C1	6.5	0.365	6	5.61	7.39	a
C3	6.6	0.365	6	5.71	7.49	a
C2	7.6	0.365	6	6.71	8.49	ab
C4	8.3	0.365	6	7.41	9.19	b

```
Results are averaged over the levels of: block
```

```
Confidence level used: 0.95
```

```
significance level used: alpha = 0.05
```

```
NOTE: If two or more means share the same grouping symbol,
      then we cannot show them to be different.
```

```
      But we also did not show them to be the same.
```

Note that if you would like to see the underlying individual contrasts/differences between adjusted means, simply add `details = TRUE` to the `cld()` statement. Furthermore, check out the [Summary Article “Compact Letter Display”](#).

Finally, we can create a plot that displays both the raw data and the results, *i.e.* the comparisons of the adjusted means that are based on the linear model.

```
my_caption <- "Black dots represent raw data. Red dots and error bars represent adjusted m

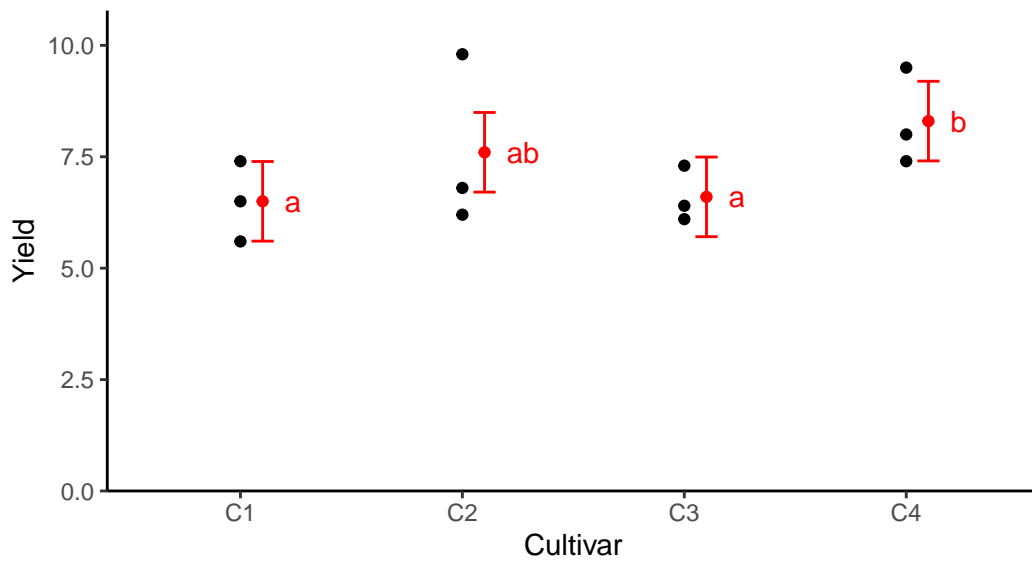
ggplot() +
  aes(x = cultivar) +
  # black dots representing the raw data
  geom_point(
    data = dat,
    aes(y = yield)
  ) +
  # red dots representing the adjusted means
  geom_point(
    data = mean_comp,
    aes(y = emmean),
    color = "red",
    position = position_nudge(x = 0.1)
  ) +
  # red error bars representing the confidence limits of the adjusted means
  geom_errorbar(
    data = mean_comp,
    aes(ymin = lower.CL, ymax = upper.CL),
    color = "red",
    width = 0.1,
    position = position_nudge(x = 0.1)
  ) +
  # red letters
  geom_text(
    data = mean_comp,
    aes(y = emmean, label = str_trim(.group)),
    color = "red",
    position = position_nudge(x = 0.2),
    hjust = 0
  ) +
  scale_x_discrete(
    name = "Cultivar"
  ) +
```



```

scale_y_continuous(
  name = "Yield",
  limits = c(0, NA),
  expand = expansion(mult = c(0, 0.1))
) +
scale_color_discrete(
  name = "Block"
) +
theme_classic() +
labs(caption = my_caption) +
theme(plot.caption = element_textbox_simple(margin = margin(t = 5)),
      plot.caption.position = "plot")

```



Black dots represent raw data. Red dots and error bars represent adjusted means with 95% confidence limits per cultivar. Means followed by a common letter are not significantly different according to the t-test.

Clewer, Alan G, and David H Scarisbrick. 2001. *Practical Statistics and Experimental Design for Plant and Crop Science*. Chichester, England: John Wiley & Sons.