

Randomized complete block design

true

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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(
  broom,
  conflicted,
  desplot,
  emmeans,
  ggtext,
  multcomp,
  multcompView,
  tidyverse)

# handle function conflicts
conflict_prefer("filter", "dplyr")
conflict_prefer("select", "dplyr")
```

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()`¹ to conveniently obtain descriptive summary tables. Here, we get can summarize per block and per cultivar.

```
dat %>%
  group_by(cultivar) %>%
  dlookr::describe(yield) %>%
  select(cultivar: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(block: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:

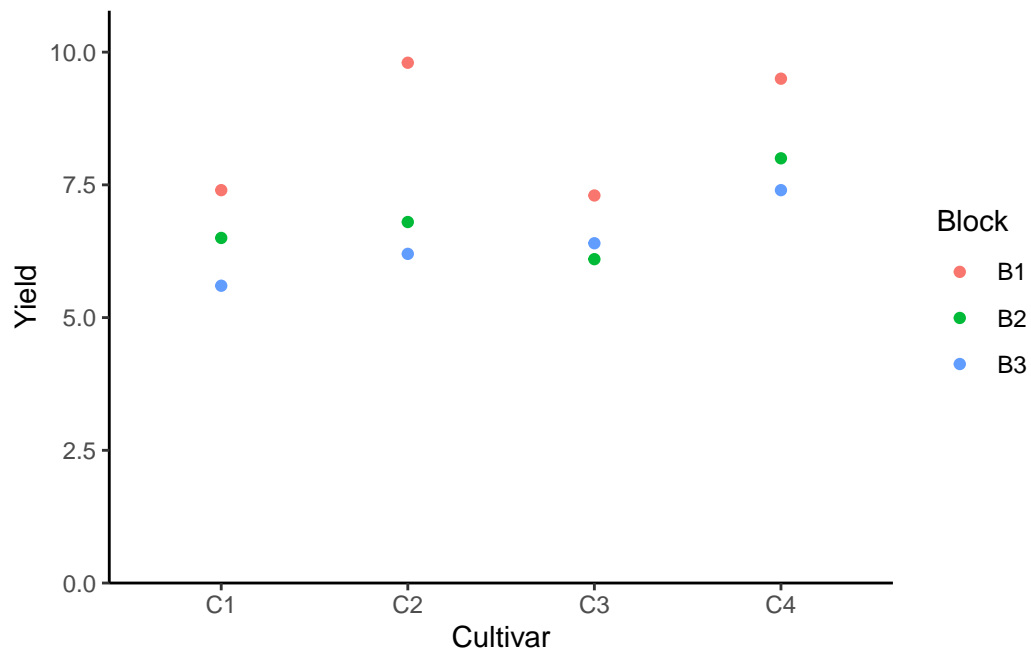
```
ggplot(data = dat) +
  aes(y = yield, x = cultivar, color = block) +
  geom_point() +
  scale_x_discrete(
    name = "Cultivar"
```

¹As described in the {dlookr} section of the Summary Article “Useful things”.

```

) +
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", # plot title
show.key = FALSE # hide legend
)

```

Field layout

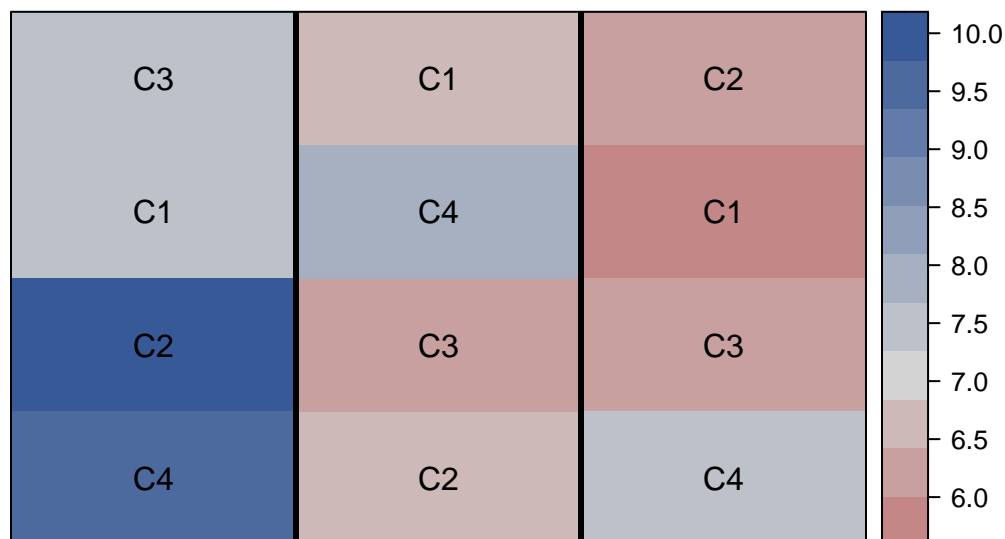
| | | |
|----|----|----|
| C3 | C1 | C2 |
| C1 | C4 | C1 |
| C2 | C3 | C3 |
| C4 | C2 | C4 |

```

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. # 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)
```

::: {.callout-caution icon="false"} ## Model assumptions should be checked at this point

2 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 different ($p = 0.037^*$). Additionally, the block effects are also statistically significant ($p = 0.008^{**}$), but this is only of secondary concern for us.

3 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(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 | ab |
| 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
P value adjustment: tukey method for comparing a family of 4 estimates
significance level used: alpha = 0.05
NOTE: If two or more means share the same grouping letter,
      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(

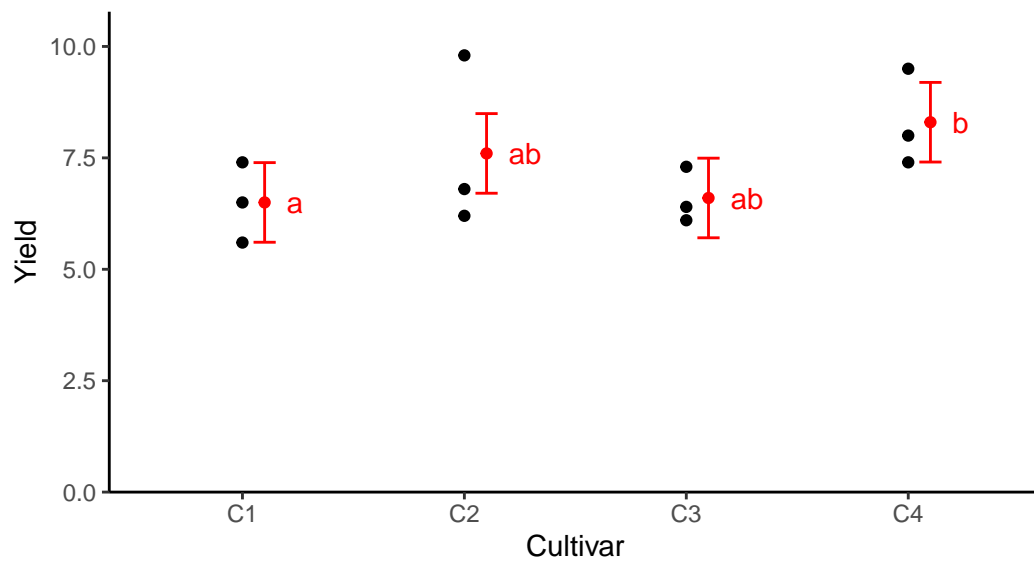
```



```

    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 Tukey-test.

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