

One-way augmented design

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2023-11-16

One-way ANOVA & pairwise comparison post hoc tests in a non-resolvable augmented design.

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```
# (install &) load packages
pacman::p_load(
  conflicted,
  desplot,
  emmeans,
  ggtext,
  lme4,
  lmerTest,
  multcomp,
  multcompView,
  tidyverse)
```

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

1 Data

This example is taken from Chapter “3.7 Analysis of a non-resolvable augmented design” of the course material “Mixed models for metric data (3402-451)” by [Prof. Dr. Hans-Peter Piepho](#). It considers data published in Petersen (1994) from a yield trial laid out as an augmented design. The genotypes (**gen**) include 3 standards (**st**, **ci**, **wa**) and 30 new cultivars of interest. The trial was laid out in 6 blocks (**block**). The 3 standards are tested in each block, while each entry is tested in only one of the blocks. Therefore, the blocks are “*incomplete blocks*”.

1.1 Import

```
# data is available online:
path <- "https://raw.githubusercontent.com/SchmidtPaul/dsfair_quarto/master/data/Petersen1"
```

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

```
# A tibble: 48 x 5
   gen   yield block   row   col
  <chr> <dbl> <chr> <dbl> <dbl>
1 st     2972 I         1     1
2 14     2405 I         2     1
3 26     2855 I         3     1
4 ci     2592 I         4     1
5 17     2572 I         5     1
6 wa     2608 I         6     1
7 22     2705 I         7     1
8 13     2391 I         8     1
9 st     3122 II        1     2
10 ci    3023 II        2     2
# i 38 more rows
```

1.2 Format

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

```
dat <- dat %>%  
  mutate(across(c(gen, block), ~ 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(gen) %>%  
  dlookr::describe(yield) %>%  
  select(2:sd) %>%  
  arrange(desc(n), desc(mean))
```



```
# A tibble: 33 x 5  
   gen      n    na mean    sd  
   <fct> <int> <int> <dbl> <dbl>  
1 st         6     0 2759.  832.  
2 ci         6     0 2726.  711.  
3 wa         6     0 2678.  615.  
4 19         1     0 3643    NA  
5 11         1     0 3380    NA  
6 07         1     0 3265    NA  
7 03         1     0 3055    NA  
8 04         1     0 3018    NA  
9 01         1     0 3013    NA  
10 30        1     0 2955    NA  
# i 23 more rows
```

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

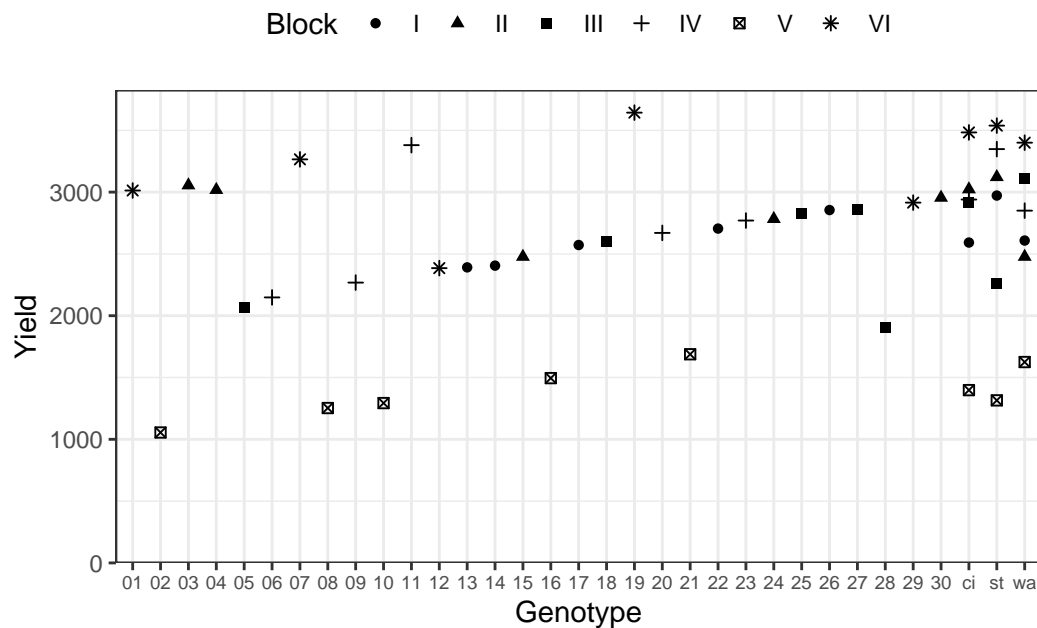
```
# A tibble: 6 x 5
  block      n    na mean    sd
  <fct> <int> <int> <dbl> <dbl>
1 VI         8     0 3205.  417.
2 II         8     0 2864.  258.
3 IV         8     0 2797.  445.
4 I          8     0 2638.  202.
5 III        8     0 2567.  440.
6 V          8     0 1390.  207.
```

Additionally, we can decide to plot our data. Note that we here define custom colors for the genotypes, where all unreplicated entries get a shade of green and all replicated checks get a shade of red.

```
greens30 <- colorRampPalette(c("#bce2cc", "#00923f"))(30)
oranges3 <- colorRampPalette(c("#e4572e", "#ad0000"))(3)
gen_cols <- set_names(c(greens30, oranges3), nm = levels(dat$gen))

ggplot(data = dat) +
  aes(
    y = yield,
    x = gen,
    shape = block
  ) +
  geom_point() +
  scale_x_discrete(
    name = "Genotype"
  ) +
  scale_y_continuous(
    name = "Yield",
    limits = c(0, NA),
    expand = expansion(mult = c(0, 0.05))
  ) +
  scale_color_manual(
    guide = "none",
    values = gen_cols
  ) +
  scale_shape_discrete(
    name = "Block"
  ) +
  guides(shape = guide_legend(nrow = 1)) +
```

```
theme_bw() +
theme(
  legend.position = "top",
  axis.text.x = element_text(size = 7)
)
```



Finally, since this is an experiment that was laid with a certain experimental design (= a non-resolvable augmented design) - it makes sense to also get a field plan. This can be done via `desplot()` from `{desplot}`.

```
desplot(
  data = dat,
  flip = TRUE, # row 1 on top, not on bottom
  form = gen ~ col + row, # fill color per cultivar
  col.regions = gen_cols, # custom fill colors
  out1 = block, # line between blocks
  text = gen, # 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

st	st	st
14	ci	18
26	04	27
ci	15	ci
17	30	25
wa	03	28
22	wa	05
13	24	wa
st	st	st
09	02	29
06	21	07
ci	wa	ci
wa	ci	01
20	10	wa
11	08	12
23	16	19

2 Model

Finally, we can decide to fit a linear model with **yield** as the response variable and **gen** as fixed effects, since our goal is to compare them to each other. Since the trial was laid out in blocks, we also need **block** effects in the model, but these can be taken either as a fixed or as random effects. Since our goal is to compare genotypes, we will determine which of the two models we prefer by comparing the average standard error of a difference (s.e.d.) for the comparisons between adjusted genotype means - the lower the s.e.d. the better.

```
# blocks as fixed (linear model)
mod_fb <- lm(yield ~ gen + block,
             data = dat)

mod_fb %>%
  emmeans(pairwise ~ "gen",
           adjust = "tukey") %>%
  pluck("contrasts") %>% # extract diffs
  as_tibble() %>% # format to table
```

```

pull("SE") %>% # extract s.e.d. column
mean() # get arithmetic mean

[1] 461.3938

# blocks as random (linear mixed model)
mod_rb <- lmer(yield ~ gen + (1 | block),
              data = dat)

mod_rb %>%
  emmeans(pairwise ~ "gen",
          adjust = "tukey",
          lmer.df = "kenward-roger") %>%
  pluck("contrasts") %>% # extract diffs
  as_tibble() %>% # format to table
  pull("SE") %>% # extract s.e.d. column
  mean() # get arithmetic mean

[1] 462.0431

```

As a result, we find that the model with fixed block effects has the slightly smaller s.e.d. and is therefore more precise in terms of comparing genotypes.

 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_fb)
ANOVA

```

Analysis of Variance Table

```

Response: yield
      Df    Sum Sq Mean Sq F value    Pr(>F)
gen      32 12626173   394568    4.331 0.0091056 **
block     5  6968486 1393697   15.298 0.0002082 ***
Residuals 10   911027    91103
---
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 ($p = 0.009^{**}$). Additionally, the block effects are also statistically significant ($p < .001^{***}$), 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_fb %>%
  emmeans(specs = ~ gen) %>% # adj. mean per genotype
  cld(adjust = "Tukey", Letters = letters) # compact letter display (CLD)

```

```
mean_comp
```

gen	emmean	SE	df	lower.CL	upper.CL	.group
12	1632	341	10	164	3100	a
06	1823	341	10	355	3291	a
28	1862	341	10	394	3330	a
09	1943	341	10	475	3411	a
05	2024	341	10	556	3492	a
29	2162	341	10	694	3630	a
01	2260	341	10	792	3728	a
15	2324	341	10	856	3792	a
02	2330	341	10	862	3798	a
20	2345	341	10	877	3813	a
13	2388	341	10	920	3856	a
14	2402	341	10	934	3870	a
23	2445	341	10	977	3913	a
07	2512	341	10	1044	3980	a
08	2528	341	10	1060	3996	a
18	2562	341	10	1094	4030	a

10	2568	341	10	1100	4036	a
17	2569	341	10	1101	4037	a
24	2630	341	10	1162	4098	a
wa	2678	123	10	2148	3208	a
22	2702	341	10	1234	4170	a
ci	2726	123	10	2195	3256	a
st	2759	123	10	2229	3289	a
16	2770	341	10	1302	4238	a
25	2784	341	10	1316	4252	a
30	2802	341	10	1334	4270	a
27	2816	341	10	1348	4284	a
26	2852	341	10	1384	4320	a
04	2865	341	10	1397	4333	a
19	2890	341	10	1422	4358	a
03	2902	341	10	1434	4370	a
21	2963	341	10	1495	4431	a
11	3055	341	10	1587	4523	a

Results are averaged over the levels of: block
 Confidence level used: 0.95
 Conf-level adjustment: sidak method for 33 estimates
 P value adjustment: tukey method for comparing a family of 33 estimates
 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.

It can be seen that while some genotypes have a higher yield than others, no differences are found to be statistically significant here. Accordingly, notice that *e.g.* for **gen 11**, which is the genotype with the highest adjusted yield mean (=3055), its lower confidence limit (=1587) includes **gen 12**, which is the genotype with the lowest adjusted yield mean (=1632).

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.

```
# reorder genotype factor levels according to adjusted mean
my_caption <- "Dots represent raw data. Red diamonds and error bars represent adjusted mean"

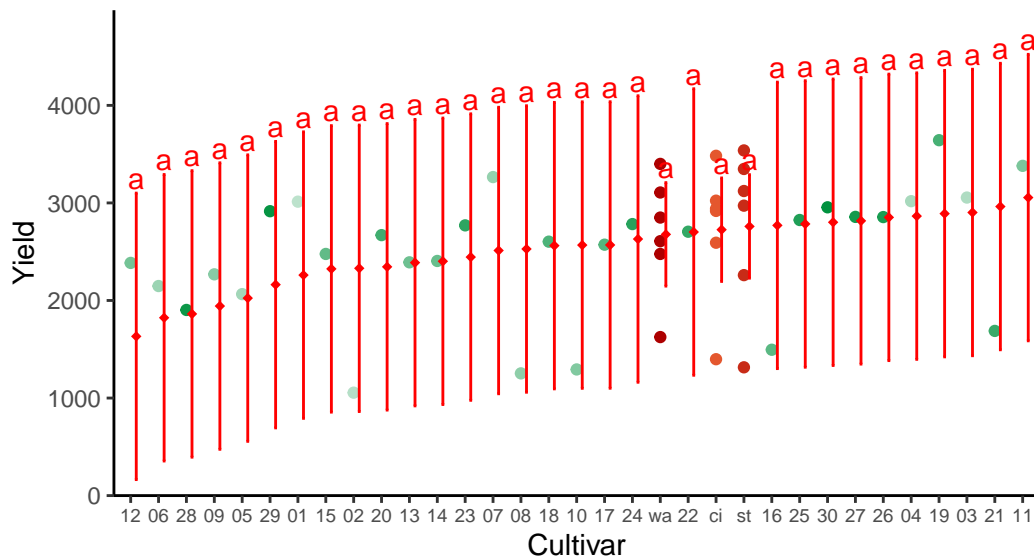
ggplot() +
```

```

# green/red dots representing the raw data
geom_point(
  data = dat,
  aes(y = yield, x = gen, color = gen)
) +
# red diamonds representing the adjusted means
geom_point(
  data = mean_comp,
  aes(y = emmean, x = gen),
  shape = 18,
  color = "red",
  position = position_nudge(x = 0.2)
) +
# red error bars representing the confidence limits of the adjusted means
geom_errorbar(
  data = mean_comp,
  aes(ymin = lower.CL, ymax = upper.CL, x = gen),
  color = "red",
  width = 0.1,
  position = position_nudge(x = 0.2)
) +
# red letters
geom_text(
  data = mean_comp,
  aes(y = upper.CL, x = gen, label = str_trim(.group)),
  color = "red",
  vjust = -0.2,
  position = position_nudge(x = 0.2)
) +
scale_color_manual(
  guide = "none",
  values = gen_cols
) +
scale_x_discrete(
  name = "Cultivar",
  limits = as.character(mean_comp$gen)
) +
scale_y_continuous(
  name = "Yield",
  limits = c(0, NA),
  expand = expansion(mult = c(0, 0.1))

```

```
) +
labs(caption = my_caption) +
theme_classic() +
theme(plot.caption = element_textbox_simple(margin = margin(t = 5)),
      plot.caption.position = "plot",
      axis.text.x = element_text(size = 7))
```



Dots represent raw data. Red diamonds 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.

5 Bonus

Here are some other things you would maybe want to look at for the analysis of this dataset.

5.1 Variance components

To extract variance components from our models, we unfortunately need different functions per model since only of of them is a mixed model and we used different functions to fit them.

```
# Residual Variance
summary(mod_fb)$sigma^2
```

```
[1] 91102.66
```

```
# Both Variance Components  
as_tibble(VarCorr(mod_rb))
```

```
# A tibble: 2 x 5  
  grp      var1      var2    vcov sdcov  
  <chr>   <chr>    <chr>   <dbl> <dbl>  
1 block (Intercept) <NA> 434198. 659.  
2 Residual <NA>      <NA> 91103. 302.
```

Petersen, Roger G. 1994. *Agricultural Field Experiments*. CRC Press. <https://doi.org/10.1201/9781482277371>.