

Homework: Coding Notes Data Visualization 1

PLPA-5820 (Spring 2025)

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Instructions

Watch the videos associated with the introduction to data visualization in R and turn in your notes (R code).

Notes

I was familiar with the packages before. The demonstrated way to add significance letters was interesting, I'm used to doing differently but I think I'll start using this way.

I am unsure if the package `tidyplots` is known by you, but I think it is a good package for data visualization by people not familiar with `ggplot2`'s syntax. You can find more info at <https://tidyplots.org/>.

Adding significance letters to represent multiple pairwise comparisons of an ANOVA

```
# Load libraries
library(tidyverse)
```

```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
v dplyr      1.1.4      v readr      2.1.5
v forcats    1.0.0      v stringr    1.5.1
v ggplot2    3.5.1      v tibble     3.2.1
v lubridate  1.9.4      v tidyr      1.3.1
v purrr      1.0.4
-- Conflicts ----- tidyverse_conflicts() --
```

```
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become
```

```
library(lme4)
```

Loading required package: Matrix

Attaching package: 'Matrix'

The following objects are masked from 'package:tidyr':

expand, pack, unpack

```
library(emmeans)
```

Welcome to emmeans.

Caution: You lose important information if you filter this package's results.

See '? untidy'

```
library(multcomp)
```

Loading required package: mvtnorm

Loading required package: survival

Loading required package: TH.data

Loading required package: MASS

Attaching package: 'MASS'

The following object is masked from 'package:dplyr':

select

Attaching package: 'TH.data'

The following object is masked from 'package:MASS':

geyser

```
library(multcompView)

# Load data
STAND <- read.csv("Bull_richness.csv", na.strings = "na")

# Filter data
ave_stand <- STAND %>%
  group_by(Crop, Collection, Rep, Fungicide, Treatment) %>%
  summarize(
    ave_stand = mean(richness, na.rm=TRUE))
```

`summarise()` has grouped output by 'Crop', 'Collection', 'Rep', 'Fungicide'.
You can override using the `.groups` argument.

```
# Run ANOVA
lm <- lmer(ave_stand ~ Treatment * Crop * Fungicide + (1|Rep), data = ave_stand)
```

boundary (singular) fit: see help('isSingular')

```
# estimate lsmeans of variety within siteXyear
lsmeans <- emmeans(lm, ~ Treatment + Fungicide | Crop )

# contrast with Tukey adjustment
Results_lsmeansEC <- multcomp::cld(lsmeans, alpha = 0.05, reversed = TRUE,
                                   details = TRUE, Letters = letters)

Results_lsmeansEC
```

\$emmeans

Crop = Corn:

Treatment	Fungicide	emmean	SE	df	lower.CL	upper.CL	.group
No-till	F	12.92	1.52	70.3	9.88	16.0	a
No-till	C	12.19	1.52	70.3	9.16	15.2	a
Conv.	C	10.47	1.52	70.3	7.44	13.5	a
Conv.	F	7.36	1.52	70.3	4.32	10.4	a

Crop = Soy:

Treatment	Fungicide	emmean	SE	df	lower.CL	upper.CL	.group
Conv.	C	18.81	1.52	70.3	15.77	21.8	a
No-till	C	18.58	1.52	70.3	15.55	21.6	ab
No-till	F	13.15	1.52	70.3	10.12	16.2	bc

Conv.	F	12.14	1.52	70.3	9.10	15.2	c
-------	---	-------	------	------	------	------	---

Degrees-of-freedom method: kenward-roger

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 symbol,
then we cannot show them to be different.

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

\$comparisons

Crop = Corn:

contrast	estimate	SE	df	t.ratio	p.value
Conv. C - Conv. F	3.111	2.15	85	1.445	0.4754
(No-till C) - Conv. F	4.833	2.15	85	2.244	0.1197
(No-till C) - Conv. C	1.722	2.15	85	0.800	0.8543
(No-till F) - Conv. F	5.556	2.15	85	2.580	0.0553
(No-till F) - Conv. C	2.444	2.15	85	1.135	0.6690
(No-till F) - (No-till C)	0.722	2.15	85	0.335	0.9869

Crop = Soy:

contrast	estimate	SE	df	t.ratio	p.value
(No-till F) - Conv. F	1.014	2.15	85	0.471	0.9653
(No-till C) - Conv. F	6.444	2.15	85	2.993	0.0186
(No-till C) - (No-till F)	5.431	2.15	85	2.522	0.0637
Conv. C - Conv. F	6.667	2.15	85	3.096	0.0139
Conv. C - (No-till F)	5.653	2.15	85	2.625	0.0495
Conv. C - (No-till C)	0.222	2.15	85	0.103	0.9996

Degrees-of-freedom method: kenward-roger

P value adjustment: tukey method for comparing a family of 4 estimates

```
# Extracting the letters for the bars
sig.diff.letters <- data.frame(Results_lsmeansEC$emmeans$Crop,
                              Results_lsmeansEC$emmeans$Treatment,
                              Results_lsmeansEC$emmeans$Fungicide,
                              str_trim(Results_lsmeansEC$emmeans$.group))
colnames(sig.diff.letters) <- c("Crop",
                              "Treatment",
                              "Fungicide",
                              "Letters")
```

```
# for plotting with letters from significance test
ave_stand2 <- ave_stand %>%
  group_by(Crop, Treatment, Fungicide) %>%
  dplyr::summarize(
    ave_stand2 = mean(ave_stand, na.rm=TRUE),
    se = sd(ave_stand)/sqrt(4)) %>%
  left_join(sig.diff.letters)
```

`summarise()` has grouped output by 'Crop', 'Treatment'. You can override using the `.groups` argument.

Joining with `by = join_by(Crop, Treatment, Fungicide)`

```
### Stand bars ###
ggplot(ave_stand, aes(x = Crop, y = ave_stand)) +
  stat_summary(fun=mean, geom="bar") +
  stat_summary(fun.data = mean_se, geom = "errorbar", width = 0.5) +
  ylab("Richness") +
  geom_jitter(width = 0.02, alpha = 0.5) +
  geom_text(data = ave_stand2,
    aes(label = Letters, y = ave_stand2+(3*se)),
    vjust = -0.5) +
  xlab("")+
  theme_classic() +
  theme(
    strip.background = element_rect(color="white", fill="white",
                                     size=1.5, linetype="solid"),
    strip.text.x = element_text(size = 12, color = "black"),
    axis.text.x = element_text(angle = 45, vjust = 1, hjust=1)) +
  facet_wrap(~Treatment + Fungicide, scales = "free_y")
```

Warning: The `size` argument of `element_rect()` is deprecated as of ggplot2 3.4.0.
i Please use the `linewidth` argument instead.

