R markdown coding challange

2025-02-27

Table of Contents

## R Markdown

# [Find data here](https://doi.org/10.1094/PDIS-06-21-1253-RE)

this is the code from coding challenge 3 question 5

library(knitr)  
library(rmarkdown)  
library(pandoc)

##   
## Attaching package: 'pandoc'

## The following objects are masked from 'package:rmarkdown':  
##   
## pandoc\_available, pandoc\_convert, pandoc\_version

library(tidyverse)

## ── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──  
## ✔ dplyr 1.1.4 ✔ readr 2.1.5  
## ✔ forcats 1.0.0 ✔ stringr 1.5.1  
## ✔ ggplot2 3.5.1 ✔ tibble 3.2.1  
## ✔ lubridate 1.9.4 ✔ tidyr 1.3.1  
## ✔ purrr 1.0.4

## ── Conflicts ────────────────────────────────────────── tidyverse\_conflicts() ──  
## ✖ dplyr::filter() masks stats::filter()  
## ✖ dplyr::lag() masks stats::lag()  
## ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors

library(ggrepel)  
library(ggpubr)  
library(tinytex)  
  
mycodata = read.csv("MycotoxinData.csv", na.strings = "na")  
View(mycodata)  
str(mycodata)

## 'data.frame': 375 obs. of 6 variables:  
## $ Treatment : chr "Fg" "Fg" "Fg" "Fg" ...  
## $ Cultivar : chr "Wheaton" "Wheaton" "Wheaton" "Wheaton" ...  
## $ BioRep : int 2 2 2 2 2 2 2 2 2 3 ...  
## $ MassperSeed\_mg: num 10.29 12.8 2.85 6.5 10.18 ...  
## $ DON : num 107.3 32.6 416 211.9 124 ...  
## $ X15ADON : num 3 0.85 3.5 3.1 4.8 3.3 6.9 2.9 2.1 0.71 ...

mycodata$Treatment=as.factor(mycodata$Treatment)  
mycodata$Cultivar=as.factor(mycodata$Cultivar)  
str(mycodata)

## 'data.frame': 375 obs. of 6 variables:  
## $ Treatment : Factor w/ 5 levels "Fg","Fg + 37",..: 1 1 1 1 1 1 1 1 1 1 ...  
## $ Cultivar : Factor w/ 2 levels "Ambassador","Wheaton": 2 2 2 2 2 2 2 2 2 2 ...  
## $ BioRep : int 2 2 2 2 2 2 2 2 2 3 ...  
## $ MassperSeed\_mg: num 10.29 12.8 2.85 6.5 10.18 ...  
## $ DON : num 107.3 32.6 416 211.9 124 ...  
## $ X15ADON : num 3 0.85 3.5 3.1 4.8 3.3 6.9 2.9 2.1 0.71 ...

cbbPalette <- c("#000000", "#E69F00", "#56B4E9", "#009E73", "#F0E442", "#0072B2", "#D55E00", "#CC79A7")  
colorchoice= c("#56B4E9","#009E73")

Graphs with DON

mycodata$Treatment2= factor(mycodata$Treatment, levels= c("NTC","Fg","Fg + 37","Fg + 40","Fg + 70")) #new column with correct order  
graph2= ggplot(mycodata, aes(x=Treatment2, y=DON, fill=Cultivar)) + #uses corrected order  
 geom\_boxplot(position=position\_dodge(0.5),outlier.color = "NA") +  
 xlab("") + ylab("DON (ppm)") +  
 geom\_point(pch=21, alpha=0.6, position=position\_jitterdodge(dodge.width=0.9)) +  
 scale\_fill\_manual(values= colorchoice)+  
 theme\_classic()+  
 facet\_wrap(~Cultivar)  
graph5= graph2 + geom\_pwc(aes(group=Treatment2, method= "t\_test", label= "p.adj.format"))

## Warning in geom\_pwc(aes(group = Treatment2, method = "t\_test", label =  
## "p.adj.format")): Ignoring unknown aesthetics: method

Graph with X15ADON

graph3= ggplot(mycodata, aes(x=Treatment2, y=X15ADON, fill=Cultivar)) +  
 geom\_boxplot(position=position\_dodge(0.5),outlier.color = "NA") +  
 xlab("") + ylab("15ADON") +  
 geom\_point(pch=21, alpha=0.6, position=position\_jitterdodge(dodge.width=0.9)) +  
 scale\_fill\_manual(values= colorchoice)+  
 theme\_classic()+  
 facet\_wrap(~Cultivar)  
graph6= graph3 + geom\_pwc(aes(group=Treatment2, method= "t\_test", label= "p.adj.format"))

## Warning in geom\_pwc(aes(group = Treatment2, method = "t\_test", label =  
## "p.adj.format")): Ignoring unknown aesthetics: method

graph4= ggplot(mycodata, aes(x=Treatment2, y=MassperSeed\_mg, fill=Cultivar)) +  
 geom\_boxplot(position=position\_dodge(0.5),outlier.color = "NA") +  
 xlab("") + ylab("Seed Mass (mg)") +  
 geom\_point(pch=21, alpha=0.6, position=position\_jitterdodge(dodge.width=0.9)) +  
 scale\_fill\_manual(values= colorchoice)+  
 theme\_classic()+  
 facet\_wrap(~Cultivar)  
graph7= graph4 + geom\_pwc(aes(group=Treatment2, method= "t\_test", label= "p.adj.format"))

## Warning in geom\_pwc(aes(group = Treatment2, method = "t\_test", label =  
## "p.adj.format")): Ignoring unknown aesthetics: method

ggarrange(graph5,graph6,graph7, ncol=3, nrow=1, common.legend = TRUE)

## Warning: Removed 8 rows containing non-finite outside the scale range  
## (`stat\_boxplot()`).

## Warning: Removed 8 rows containing non-finite outside the scale range  
## (`stat\_pwc()`).

## Warning: Removed 8 rows containing missing values or values outside the scale range  
## (`geom\_point()`).

## Warning: Removed 8 rows containing non-finite outside the scale range  
## (`stat\_boxplot()`).

## Warning: Removed 8 rows containing non-finite outside the scale range  
## (`stat\_pwc()`).

## Warning: Removed 8 rows containing missing values or values outside the scale range  
## (`geom\_point()`).

## Warning: Removed 10 rows containing non-finite outside the scale range  
## (`stat\_boxplot()`).

## Warning: Removed 10 rows containing non-finite outside the scale range  
## (`stat\_pwc()`).

## Warning: Removed 10 rows containing missing values or values outside the scale range  
## (`geom\_point()`).

## Warning: Removed 2 rows containing non-finite outside the scale range  
## (`stat\_boxplot()`).

## Warning: Removed 2 rows containing non-finite outside the scale range  
## (`stat\_pwc()`).

## Warning: Removed 2 rows containing missing values or values outside the scale range  
## (`geom\_point()`).

