# R_markdown_class_assignment

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## Contents

## Link to the manuscript

Plant Disease

####Take the code you wrote for coding challenge 3, question 5, and incorporate it into your R markdown file. Some of you have already been doing this, which is great! Your final R markdown file should have the following elements.

####At the top of the document, make a clickable link to the manuscript where these data are published. The link is here:

- Noel, Z.A., Roze, L.V., Breunig, M., Trail, F. 2022. Endophytic fungi as promising biocontrol agent to protect wheat from Fusarium graminearum head blight. Plant Disease. https://doi.org/10.1094/PDIS-06-21-1253-RE

####Read the data using a relative file path with na.strings option set to "na". This means you need to put the Mycotoxin.csv file we have used for the past two weeks into your directory, which git tracks.

```
####Load the data
mycotoxin<-read.csv("Data_Visualization/MycotoxinData.csv", na.string="na")
####Load library
library(ggplot2)
library(ggpubr)
####Load cbbPalette
cbbPalette <- c("#000000", "#E69F00", "#56B4E9", "#009E73", "#F0E442", "#0072B2", "#D55E00", "#CC79A7")
```

####Make a separate code chunk for the figures plotting the DON data, 15ADON, and Seedmass, and one for the three combined using ggarrange.
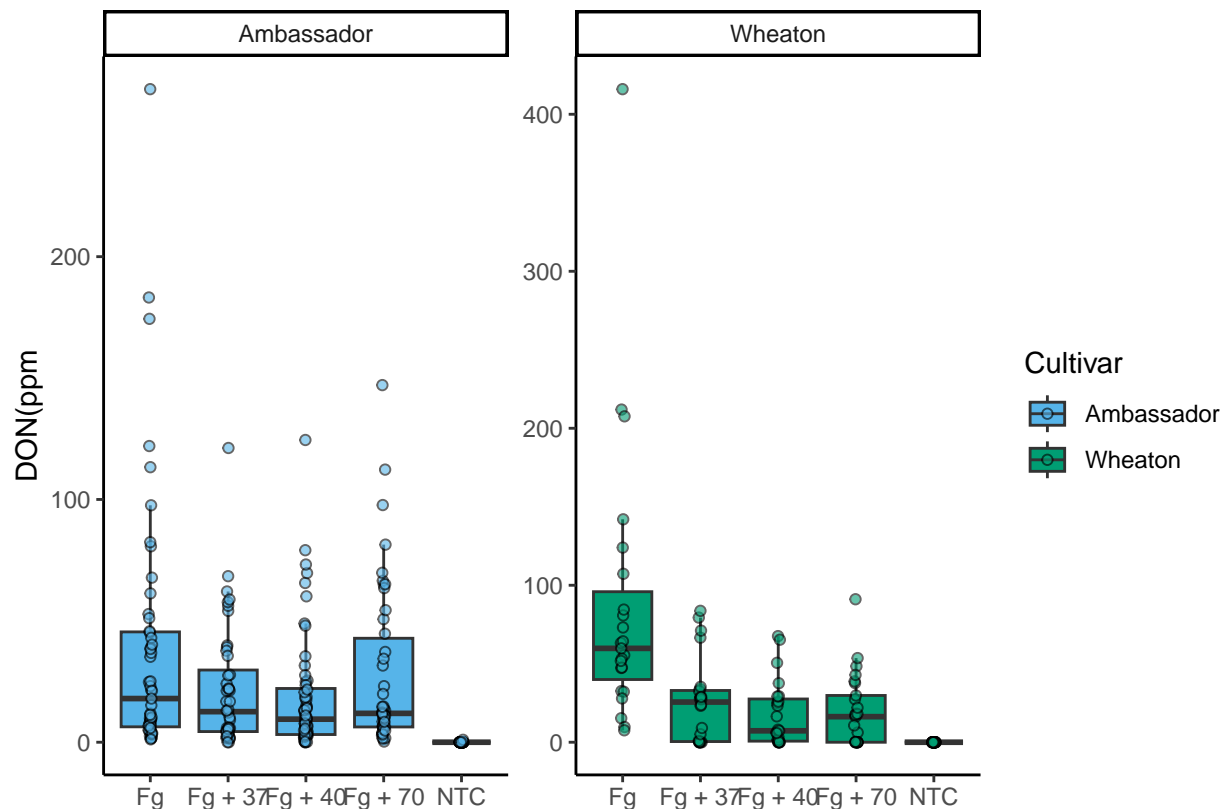
# DON

```
## Warning: Removed 8 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

```
## Warning: Removed 8 rows containing missing values or values outside the scale range
## ('geom_point()').
```

## X15DON

```
####Change the y-variable to plot X15ADON and MassperSeed_mg. The y-axis label should now be "15ADON" a
mycotoxin.X15ADON<-ggplot(mycotoxin,aes(Treatment,X15ADON, fill=Cultivar))+    #define asthetics x-axis
  geom_boxplot(outlier.shape=NA)+
  geom_point(position=position_jitterdodge(0.05), shape=21, alpha=0.6)+
  xlab("")+
  ylab("15ADON")+   #label y-axis as 15ADON
  scale_fill_manual(values=cbbPalette[c(3,4)])+
  theme_classic()+
  facet_wrap(~Cultivar, scales="free")
mycotoxin.X15ADON
```

```
## Warning: Removed 10 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

```
## Warning: Removed 10 rows containing missing values or values outside the scale range
## ('geom_point()').
```
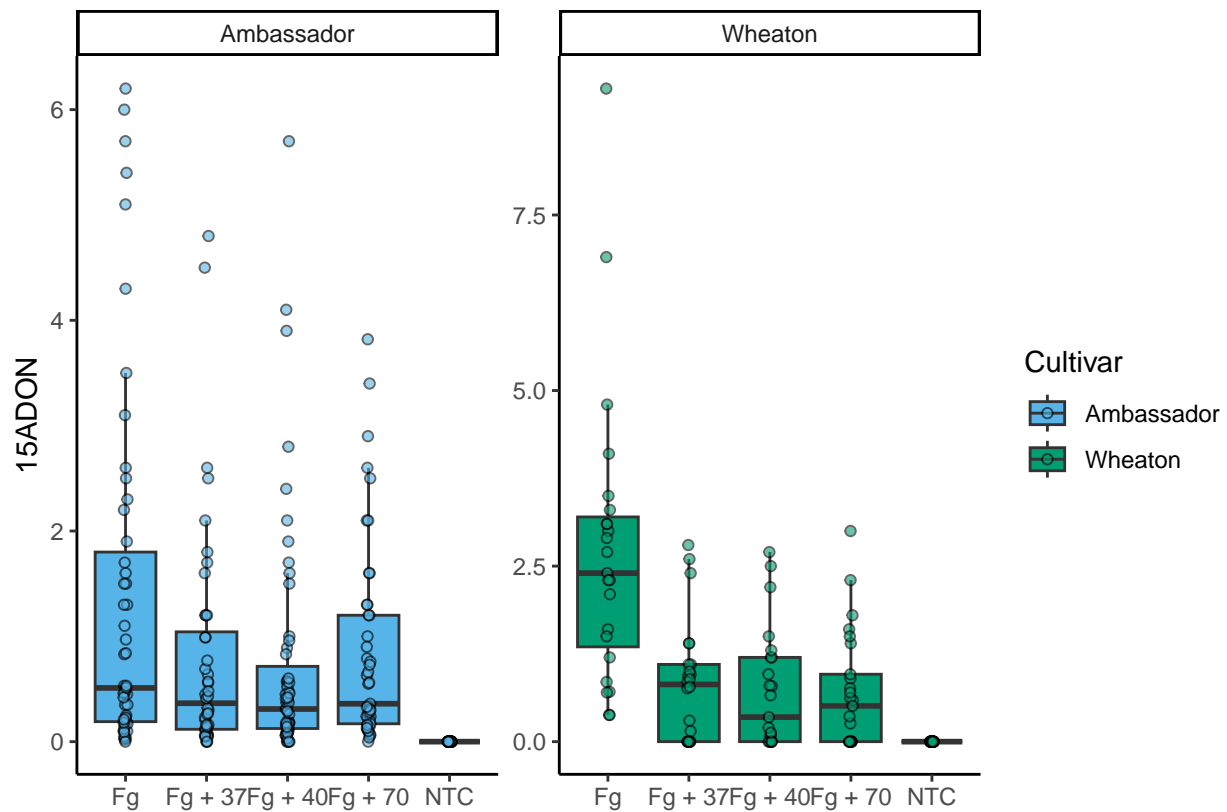


## MassperSeed

```
mycotoxin.seed<-ggplot(mycotoxin,aes(Treatment,MassperSeed_mg, fill=Cultivar))+    #define asthetics x-
  geom_boxplot(outlier.shape=NA)+
  geom_point(position=position_jitterdodge(0.05), shape=21, alpha=0.6)+
  xlab("")+
  ylab("Seed Mass (mg)")+ #label y axis as Seed Mass (mg)
  scale_fill_manual(values=cbbPalette[c(3,4)])+
  theme_classic()+
  facet_wrap(~Cultivar, scales="free")
mycotoxin.seed
```

```
## Warning: Removed 2 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

```
## Warning: Removed 2 rows containing missing values or values outside the scale range
## ('geom_point()').
```
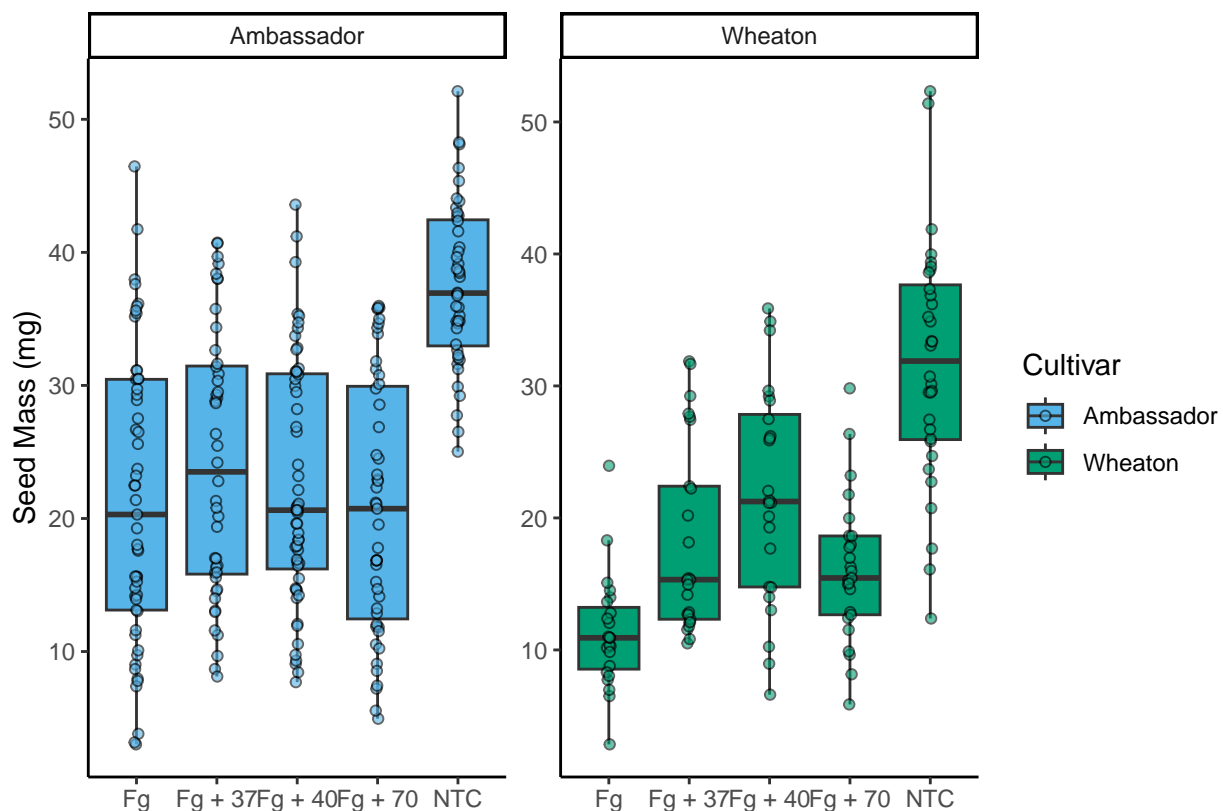


## Combine fig

```
####Use geom_pwc() to add t.test pairwise comparisons to the three plots made above. Save each plot as
mycotoxin.DON.significance<-mycotoxin.DON+
geom_pwc(aes(group=Treatment), method="t.test", label = "{p.adj.format}{p.adj.signif}", hide.ns=T)    #
mycotoxin.DON.significance
```

```
## 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()').
```
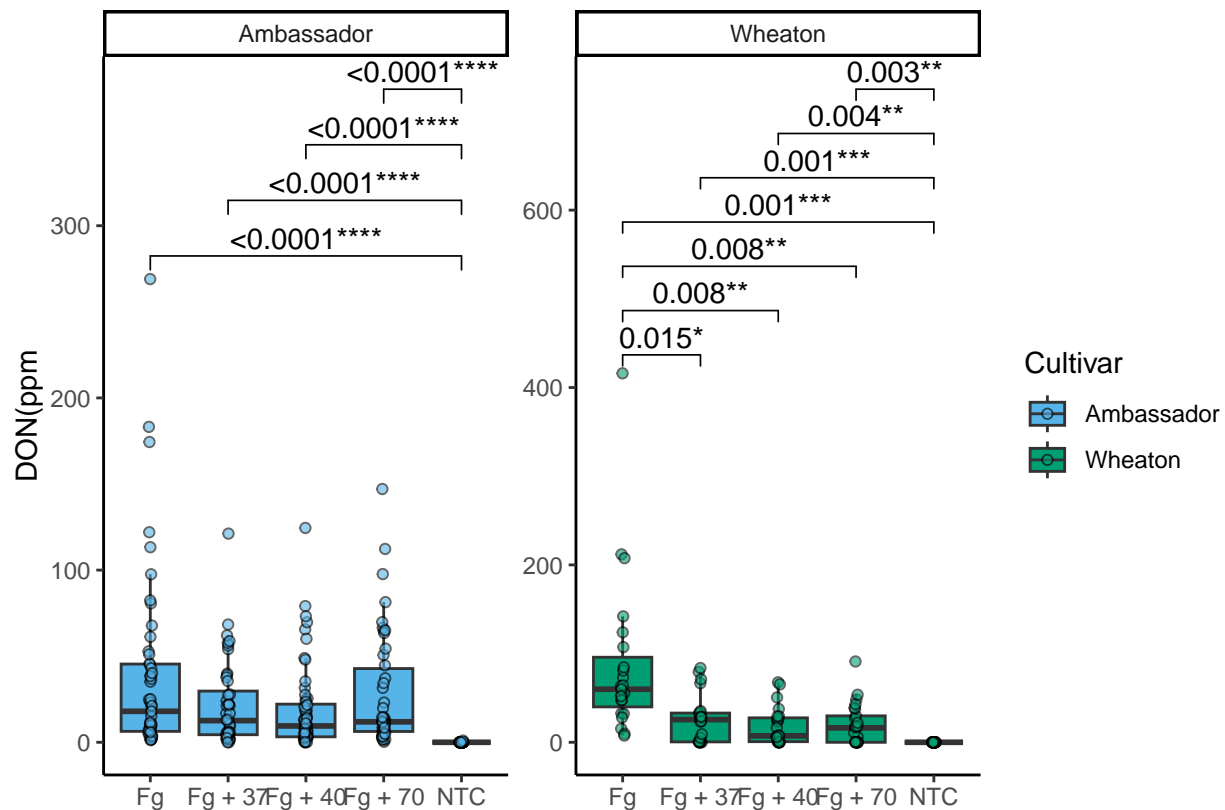


```
mycotoxin.X15ADON.significance<-mycotoxin.X15ADON+
geom_pwc(aes(group=Treatment), method="t.test", label = "{p.adj.format}{p.adj.signif}", hide.ns=T)
mycotoxin.X15ADON.significance
```

```
## Warning: Removed 10 rows containing non-finite outside the scale range
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```

```
## 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()').
```

```
mycotoxin.seed.significance<-mycotoxin.seed+
geom_pwc(aes(group=Treatment), method="t.test", label = "{p.adj.format}{p.adj.signif}", hide.ns=T)
mycotoxin.seed.significance
```

```
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```

```
## 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()').
```
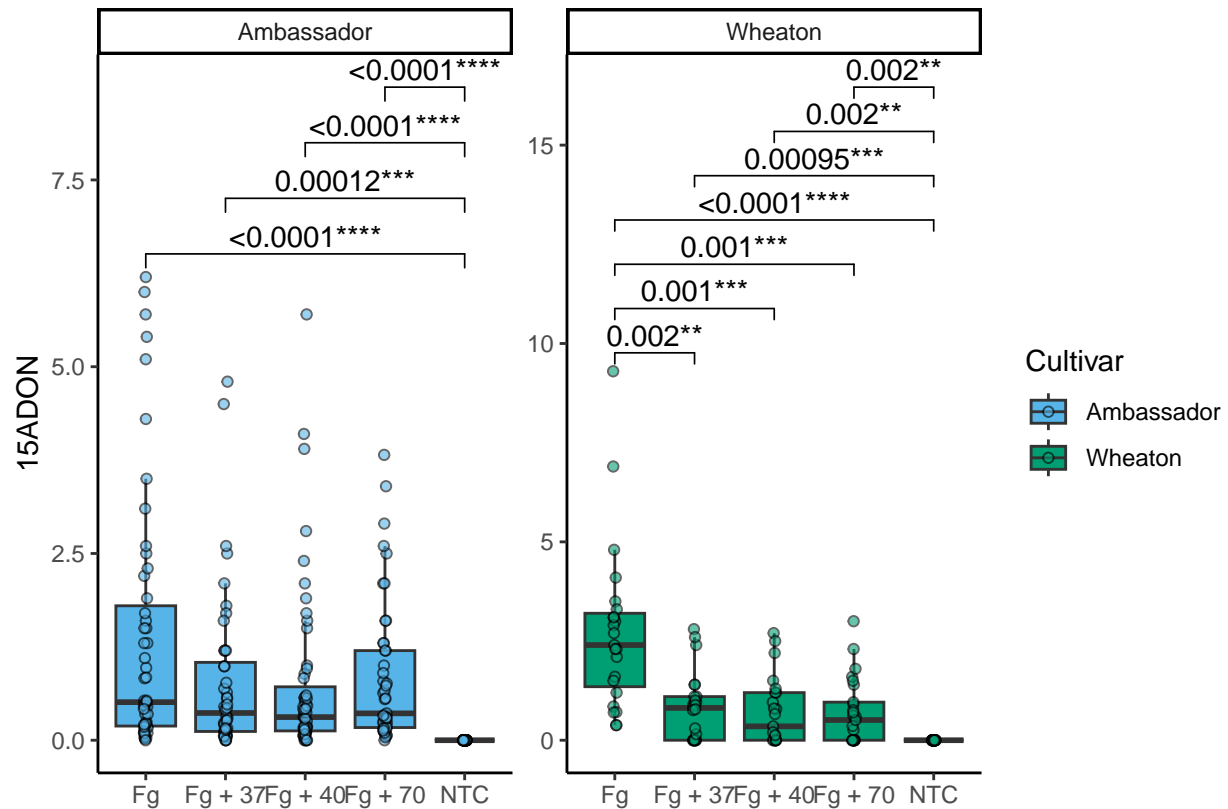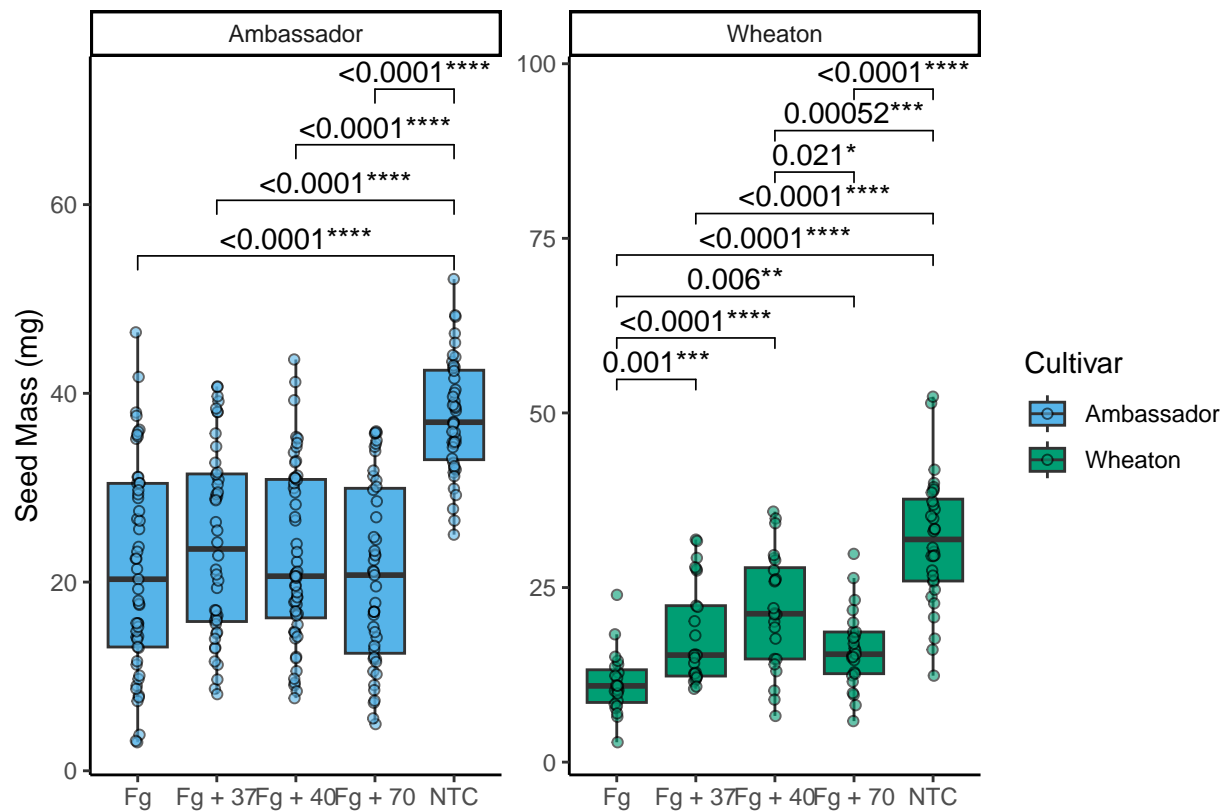
```
#Combining all the figures into one.
fig2 <- ggarrange(
        mycotoxin.DON.significance,   # First plot
        mycotoxin.X15ADON.significance,   # Second plot
        mycotoxin.seed.significance,   # Third plot
        labels = c("A","B","C"),   # label the plots A, B and C
        nrow = 1,   # Arrange the plots in 3 rows
        ncol = 3,   # Arrange the plots in 1 column
        common.legend = T #include a legend in the combined figure
      )
```

```
## Warning: Removed 8 rows containing non-finite outside the scale range
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## 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
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```
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## Warning: Removed 10 rows containing missing values or values outside the scale range
## ('geom_point()').

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## ('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()').
```

```
fig2
```