Coding notes for Advanced Data Visualization

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```
#loading packages
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 1.9.3     v tidyr     1.3.1
## v purrr     1.0.2
## -- 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 errors
```

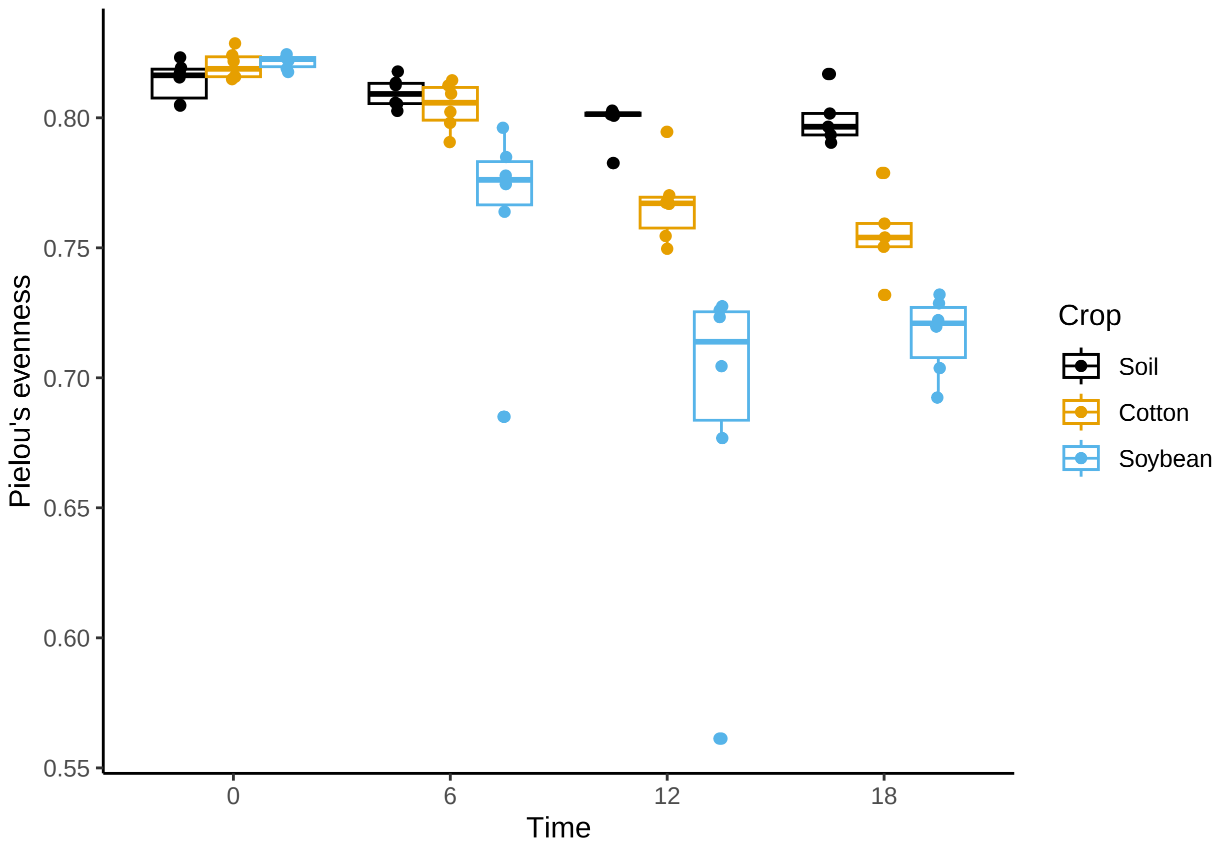
```
library(ggpubr)
library(ggrepel)

#loading color-blind palette
cbbPalette <- c("#000000", "#E69F00", "#56B4E9", "#009E73", "#F0E442", "#0072B2", "#D55E00", "#CC79A7")

#loading data in R
sample.data.bac <- read.csv("BacterialAlpha.csv", na.strings = "na")
sample.data.bac
```

```
##       Code    Crop Time_Point Replicate Water_Imbibed  shannon invsimpson
## 1    S01_13    Soil          0         1            NA 6.624921  210.72795
## 2    S02_16    Soil          0         2            NA 6.612413  206.86664
## 3    S03_19    Soil          0         3            NA 6.660853  213.01843
## 4    S04_22    Soil          0         4            NA 6.660671  204.69080
## 5    S05_25    Soil          0         5            NA 6.610965  200.25523
## 6    S06_28    Soil          0         6            NA 6.650812  199.32110
## 7    S61_32    Soil          6         1            NA 6.570679  200.23177
## 8    S62_35    Soil          6         2            NA 6.492227  171.27965
## 9    S63_38    Soil          6         3            NA 6.610986  192.08535
## 10   S64_41    Soil          6         4            NA 6.472259  163.99814
## 11   S65_44    Soil          6         5            NA 6.508824  181.69248
## 12   S66_47    Soil          6         6            NA 6.482495  176.90684
## 13  S121_51    Soil         12         1            NA 6.276073  126.56259
## 14  S122_54    Soil         12         2            NA 6.461118  152.98152
## 15  S123_57    Soil         12         3            NA 6.334648  138.92556
## 16  S124_60    Soil         12         4            NA 6.461988  171.13732
## 17  S125_63    Soil          12          5           NA 6.501973  172.97532
## 18  S126_66    Soil          12          6           NA 6.354387  142.61016
## 19  S181_70    Soil          18          1           NA 6.299381  142.64506
## 20  S182_74    Soil          18          2           NA 6.340644  145.48656
## 21  S183_78    Soil          18          3           NA 6.282807  150.39829
## 22  S184_82    Soil          18          4           NA 6.268316  141.14138
## 23  S186_90    Soil          18          6           NA 6.289000  140.45260
## 24   C01_11  Cotton           0          1       0.0042 6.618126  220.66218
## 25   C02_14  Cotton           0          2       0.0091 6.627206  211.03921
## 26   C03_17  Cotton           0          3       0.0013 6.616958  216.06631
## 27   C04_20  Cotton           0          4       0.0087 6.626465  215.93901
## 28   C05_23  Cotton           0          5       0.0075 6.642822  211.08960
## 29   C06_26  Cotton           0          6       0.0046 6.679131  216.31351
## 30   C61_30  Cotton           6          1       0.0580 6.454741  170.03639
## 31   C62_33  Cotton           6          2       0.0440 6.484032  172.35279
## 32   C63_36  Cotton           6          3       0.0569 6.517958  173.41489
## 33   C64_39  Cotton           6          4       0.0841 6.476069  167.13138
## 34   C65_42  Cotton           6          5       0.0535 6.569722  197.01186
## 35   C66_45  Cotton           6          6       0.0029 6.482145  172.96394
## 36  C121_49  Cotton          12          1       0.0651 5.944568   71.55607
## 37  C122_52  Cotton          12          2       0.0527 6.187755   96.43939
## 38  C123_55  Cotton          12          3       0.0675 6.129460   81.26646
## 39  C124_58  Cotton          12          4       0.0545 6.028523   75.49726
## 40  C125_61  Cotton          12          5       0.0623 6.148179   98.94468
## 41  C126_64  Cotton          12          6       0.0021 6.347332  150.05708
## 42  C181_68  Cotton          18          1       0.0034 6.301392  132.36230
## 43  C182_72  Cotton          18          2       0.0632 6.000205   83.90929
## 44  C183_76  Cotton          18          3       0.0514 5.981284   82.44127
## 45  C184_80  Cotton          18          4       0.0577 5.578566   50.73174
## 46  C185_84  Cotton          18          5       0.0554 6.064655   87.82732
## 47  SB01_12 Soybean           0          1       0.1664 6.644864  216.86110
## 48  SB02_15 Soybean           0          2       0.0942 6.615662  211.32573
## 49  SB03_18 Soybean           0          3       0.1248 6.693987  230.45439
## 50  SB04_21 Soybean           0          4       0.1150 6.647502  234.80343
## 51  SB05_24 Soybean           0          5       0.0993 6.605749  198.57265
## 52  SB06_27 Soybean           0          6       0.1005 6.640696  215.26494
## 53  SB61_31 Soybean           6          1       0.2308 6.044229   89.13912
## 54  SB62_34 Soybean           6          2       0.2603 6.437589  154.21624
## 55  SB63_37 Soybean           6          3       0.2111 6.194632   83.11681
## 56  SB64_40 Soybean           6          4       0.2808 6.117393   87.20257
## 57  SB65_43 Soybean           6          5       0.2712 5.439798   29.48338
## 58  SB66_46 Soybean           6          6       0.2887 6.195816  108.22394
## 59 SB121_50 Soybean          12          1       0.2822 4.393341   12.39587
## 60 SB122_53 Soybean          12          2       0.2557 5.630929   52.97931
## 61 SB123_56 Soybean          12          3       0.2982 5.579523   48.59842
## 62 SB124_59 Soybean          12          4       0.2489 5.406651   34.08685
## 63 SB125_62 Soybean          12          5       0.2573 5.863941   63.33020
## 64 SB126_65 Soybean          12          6       0.2285 5.738025   57.88780
## 65 SB181_69 Soybean          18          1       0.2528 5.671024   57.37726
## 66 SB182_73 Soybean          18          2       0.2706 5.489406   43.16854
## 67 SB183_77 Soybean          18          3       0.3196 5.713960   60.47882
## 68 SB184_81 Soybean          18          4       0.2437 5.467076   44.06798
## 69 SB185_85 Soybean          18          5       0.2461 5.729473   55.95864
## 70 SB186_89 Soybean          18          6       0.3010 5.556356   54.34527
##      simpson richness      even
## 1  0.9952545     3319 0.8171431
## 2  0.9951660     3079 0.8232216
## 3  0.9953056     3935 0.8046776
## 4  0.9951146     3922 0.8049774
## 5  0.9950064     3196 0.8192376
## 6  0.9949830     3481 0.8155427
## 7  0.9950058     3250 0.8125582
## 8  0.9941616     3170 0.8053387
## 9  0.9947940     3657 0.8057856
## 10 0.9939024     3177 0.8026420
## 11 0.9944962     2985 0.8134652
## 12 0.9943473     2770 0.8178151
## 13 0.9920988     3040 0.7825905
## 14 0.9934633     3192 0.8007927
## 15 0.9928019     2673 0.8027732
## 16 0.9941567     3180 0.8012745
## 17 0.9942188     3320 0.8019483
## 18 0.9929879     2773 0.8015438
## 19 0.9929896     2806 0.7934213
## 20 0.9931265     3047 0.7904155
## 21 0.9933510     2190 0.8168340
## 22 0.9929149     2488 0.8016534
## 23 0.9928802     2684 0.7965737
## 24 0.9954682     3076 0.8240330
## 25 0.9952615     3180 0.8217613
## 26 0.9953718     2938 0.8286233
## 27 0.9953691     3371 0.8157692
## 28 0.9952627     3435 0.8158938
## 29 0.9953771     3629 0.8148549
## 30 0.9941189     2767 0.8144250
## 31 0.9941979     3377 0.7980600
## 32 0.9942335     3804 0.7906489
## 33 0.9940167     3204 0.8022726
## 34 0.9949242     3250 0.8124399
## 35 0.9942184     3009 0.8093209
## 36 0.9860249     2779 0.7496447
## 37 0.9896308     3193 0.7668822
## 38 0.9876948     2859 0.7702042
## 39 0.9867545     2950 0.7545500
## 40 0.9898933     3018 0.7673379
## 41 0.9933359     2946 0.7945881
## 42 0.9924450     3266 0.7787840
## 43 0.9880824     2969 0.7504026
## 44 0.9878702     2636 0.7593336
## 45 0.9802885     2043 0.7318864
## 46 0.9886140     3113 0.7539969
## 47 0.9953888     3203 0.8232153
## 48 0.9952680     3055 0.8244294
## 49 0.9956607     3595 0.8176063
## 50 0.9957411     3253 0.8219646
## 51 0.9949641     3187 0.8188774
## 52 0.9953546     3190 0.8231136
## 53 0.9887816     2371 0.7777862
## 54 0.9935156     3248 0.7961603
## 55 0.9879687     2976 0.7744902
## 56 0.9885324     3006 0.7638754
## 57 0.9660826     2809 0.6850627
## 58 0.9907599     2680 0.7849191
## 59 0.9193280     2508 0.5612885
## 60 0.9811247     2403 0.7233538
## 61 0.9794232     2752 0.7044778
## 62 0.9706632     2946 0.6768294
## 63 0.9842097     3165 0.7275444
## 64 0.9827252     2705 0.7260697
## 65 0.9825715     2642 0.7197378
## 66 0.9768350     2773 0.6924349
## 67 0.9834653     2454 0.7320451
## 68 0.9773078     2365 0.7037462
## 69 0.9821297     2789 0.7221929
## 70 0.9815991     2050 0.7286456
```

```
#coding time-point and crop as factor (because we don't want it to be treated as continuous variable)
sample.data.bac$Time_Point <- as.factor(sample.data.bac$Time_Point)
sample.data.bac$Crop <- as.factor(sample.data.bac$Crop)

#viewing the structure of data
str(sample.data.bac)
```

```
## ’data.frame':    70 obs. of  10 variables:
##  $ Code         : chr  "S01_13" "S02_16" "S03_19" "S04_22" ...
##  $ Crop         : Factor w/ 3 levels "Cotton","Soil",..: 2 2 2 2 2 2 2 2 2 2 ...
##  $ Time_Point   : Factor w/ 4 levels "0","6","12","18": 1 1 1 1 1 1 2 2 2 2 ...
##  $ Replicate    : int  1 2 3 4 5 6 1 2 3 4 ...
##  $ Water_Imbibed: num  NA NA NA NA NA NA NA NA NA NA ...
##  $ shannon      : num  6.62 6.61 6.66 6.66 6.61 ...
##  $ invsimpson   : num  211 207 213 205 200 ...
##  $ simpson      : num  0.995 0.995 0.995 0.995 0.995 ...
##  $ richness     : int  3319 3079 3935 3922 3196 3481 3250 3170 3657 3177 ...
##  $ even         : num  0.817 0.823 0.805 0.805 0.819 ...
```

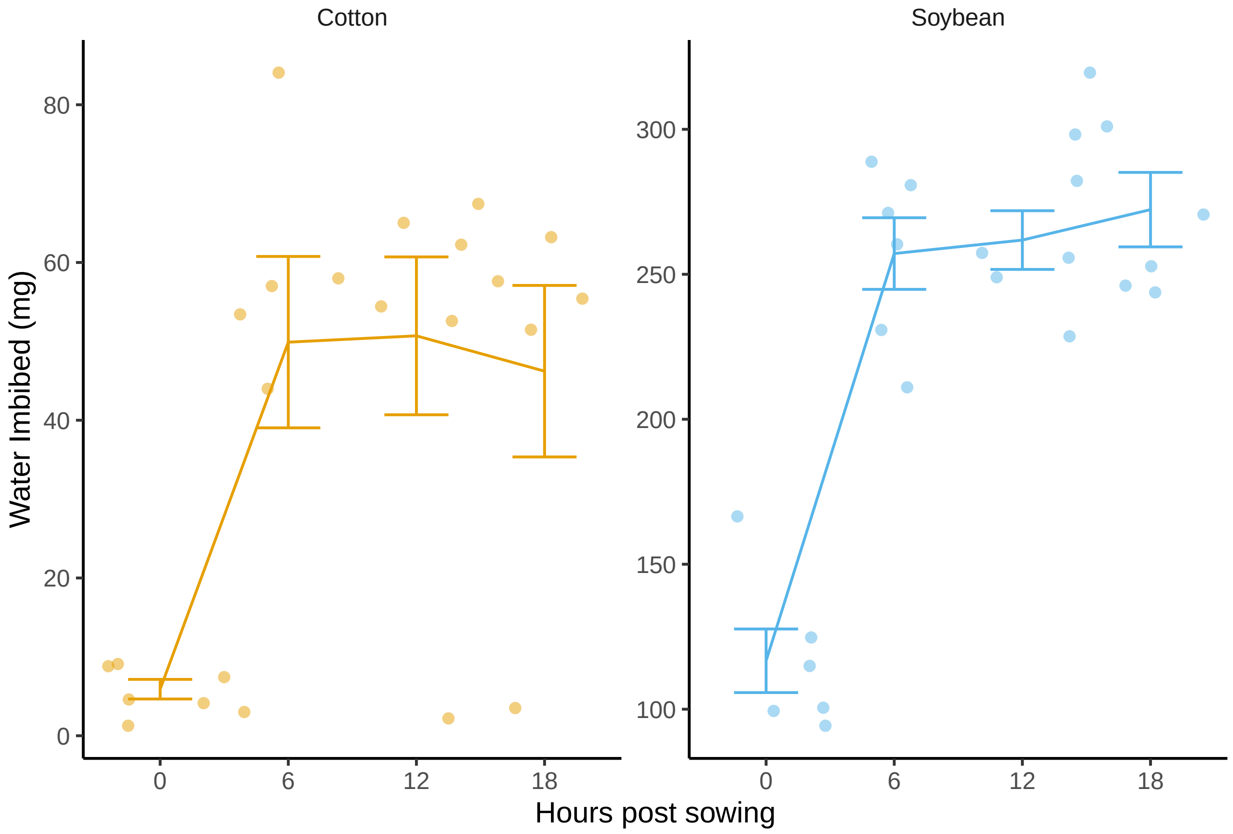
```
#changing the order of treatments to be plotted (default of ggplot is alphabetical order)
sample.data.bac$Crop <- factor (sample.data.bac$Crop, levels = c("Soil", "Cotton", "Soybean"))

#plotting boxplot

#Plot 1 - Bacterial Evenness

bac.even <- ggplot(sample.data.bac, aes(x=Time_Point, y= even, color= Crop)) +   #Timepoint as x axis a
  geom_boxplot(position = position_dodge()) +    #making boxplots side by side without overlapping
  geom_point(position = position_jitterdodge(0.05)) +   #filling the data points in boxplot without ove
  xlab("Time") +    #labelling X axis
  ylab("Pielou's evenness") +    #labelling Y axis
  scale_color_manual(values = cbbPalette) +   #choosing colorblind palette for colors of boxplot and da
  theme_classic()  #making the background of plot uniform/white
bac.even
```



```
#Plot 2 - A

#subsetting data to exclude soil data
sample.data.bac.no.soil <- subset(sample.data.bac, Crop!= "Soil")
sample.data.bac.no.soil
```

```
##         Code   Crop Time_Point Replicate Water_Imbibed  shannon invsimpson
## 24    C01_11 Cotton          0         1        0.0042 6.618126  220.66218
## 25    C02_14 Cotton          0         2        0.0091 6.627206  211.03921
## 26    C03_17 Cotton          0         3        0.0013 6.616958  216.06631
## 27    C04_20 Cotton          0         4        0.0087 6.626465  215.93901
## 28    C05_23 Cotton          0         5        0.0075 6.642822  211.08960
## 29    C06_26 Cotton          0         6        0.0046 6.679131  216.31351
## 30    C61_30 Cotton          6         1        0.0580 6.454741  170.03639
## 31    C62_33 Cotton          6         2        0.0440 6.484032  172.35279
## 32    C63_36 Cotton          6         3        0.0569 6.517958  173.41489
## 33    C64_39 Cotton          6         4        0.0841 6.476069  167.13138
## 34    C65_42 Cotton          6         5        0.0535 6.569722  197.01186
## 35    C66_45 Cotton          6         6        0.0029 6.482145  172.96394
## 36   C121_49 Cotton         12         1        0.0651 5.944568   71.55607
## 37   C122_52 Cotton         12         2        0.0527 6.187755   96.43939
## 38   C123_55 Cotton         12         3        0.0675 6.129460   81.26646
## 39   C124_58 Cotton         12         4        0.0545 6.028523   75.49726
## 40   C125_61 Cotton         12         5        0.0623 6.148179   98.94468
## 41   C126_64 Cotton         12         6        0.0021 6.347332  150.05708
## 42   C181_68 Cotton         18         1        0.0034 6.301392  132.36230
## 43  C182_72  Cotton         18         2        0.0632 6.000205   83.90929
## 44  C183_76  Cotton         18         3        0.0514 5.981284   82.44127
## 45  C184_80  Cotton         18         4        0.0577 5.578566   50.73174
## 46  C185_84  Cotton         18         5        0.0554 6.064655   87.82732
## 47  SB01_12 Soybean          0         1        0.1664 6.644864  216.86110
## 48  SB02_15 Soybean          0         2        0.0942 6.615662  211.32573
## 49  SB03_18 Soybean          0         3        0.1248 6.693987  230.45439
## 50  SB04_21 Soybean          0         4        0.1150 6.647502  234.80343
## 51  SB05_24 Soybean          0         5        0.0993 6.605749  198.57265
## 52  SB06_27 Soybean          0         6        0.1005 6.640696  215.26494
## 53  SB61_31 Soybean          6         1        0.2308 6.044229   89.13912
## 54  SB62_34 Soybean          6         2        0.2603 6.437589  154.21624
## 55  SB63_37 Soybean          6         3        0.2111 6.194632   83.11681
## 56  SB64_40 Soybean          6         4        0.2808 6.117393   87.20257
## 57  SB65_43 Soybean          6         5        0.2712 5.439798   29.48338
## 58  SB66_46 Soybean          6         6        0.2887 6.195816  108.22394
## 59 SB121_50 Soybean         12         1        0.2822 4.393341   12.39587
## 60 SB122_53 Soybean         12         2        0.2557 5.630929   52.97931
## 61 SB123_56 Soybean         12         3        0.2982 5.579523   48.59842
## 62 SB124_59 Soybean         12         4        0.2489 5.406651   34.08685
## 63 SB125_62 Soybean         12         5        0.2573 5.863941   63.33020
## 64 SB126_65 Soybean         12         6        0.2285 5.738025   57.88780
## 65 SB181_69 Soybean         18         1        0.2528 5.671024   57.37726
## 66 SB182_73 Soybean         18         2        0.2706 5.489406   43.16854
## 67 SB183_77 Soybean         18         3        0.3196 5.713960   60.47882
## 68 SB184_81 Soybean         18         4        0.2437 5.467076   44.06798
## 69 SB185_85 Soybean         18         5        0.2461 5.729473   55.95864
## 70 SB186_89 Soybean         18         6        0.3010 5.556356   54.34527
##      simpson richness      even
## 24 0.9954682     3076 0.8240330
## 25 0.9952615     3180 0.8217613
## 26 0.9953718     2938 0.8286233
## 27 0.9953691     3371 0.8157692
## 28 0.9952627     3435 0.8158938
## 29 0.9953771     3629 0.8148549
## 30 0.9941189     2767 0.8144250
## 31 0.9941979     3377 0.7980600
## 32 0.9942335     3804 0.7906489
## 33 0.9940167     3204 0.8022726
## 34 0.9949242     3250 0.8124399
## 35 0.9942184     3009 0.8093209
## 36 0.9860249     2779 0.7496447
## 37 0.9896308     3193 0.7668822
## 38 0.9876948     2859 0.7702042
## 39 0.9867545     2950 0.7545500
## 40 0.9898933     3018 0.7673379
## 41 0.9933359     2946 0.7945881
## 42 0.9924450     3266 0.7787840
## 43 0.9880824     2969 0.7504026
## 44 0.9878702     2636 0.7593336
## 45 0.9802885     2043 0.7318864
## 46 0.9886140     3113 0.7539969
## 47 0.9953888     3203 0.8232153
## 48 0.9952680     3055 0.8244294
## 49 0.9956607     3595 0.8176063
## 50 0.9957411     3253 0.8219646
## 51 0.9949641     3187 0.8188774
## 52 0.9953546     3190 0.8231136
## 53 0.9887816     2371 0.7777862
## 54 0.9935156     3248 0.7961603
## 55 0.9879687     2976 0.7744902
## 56 0.9885324     3006 0.7638754
## 57 0.9660826     2809 0.6850627
## 58 0.9907599     2680 0.7849191
## 59 0.9193280     2508 0.5612885
## 60 0.9811247     2403 0.7233538
## 61 0.9794232     2752 0.7044778
## 62 0.9706632     2946 0.6768294
## 63 0.9842097     3165 0.7275444
## 64 0.9827252     2705 0.7260697
## 65 0.9825715     2642 0.7197378
## 66 0.9768350     2773 0.6924349
## 67 0.9834653     2454 0.7320451
## 68 0.9773078     2365 0.7037462
## 69 0.9821297     2789 0.7221929
## 70 0.9815991     2050 0.7286456
```

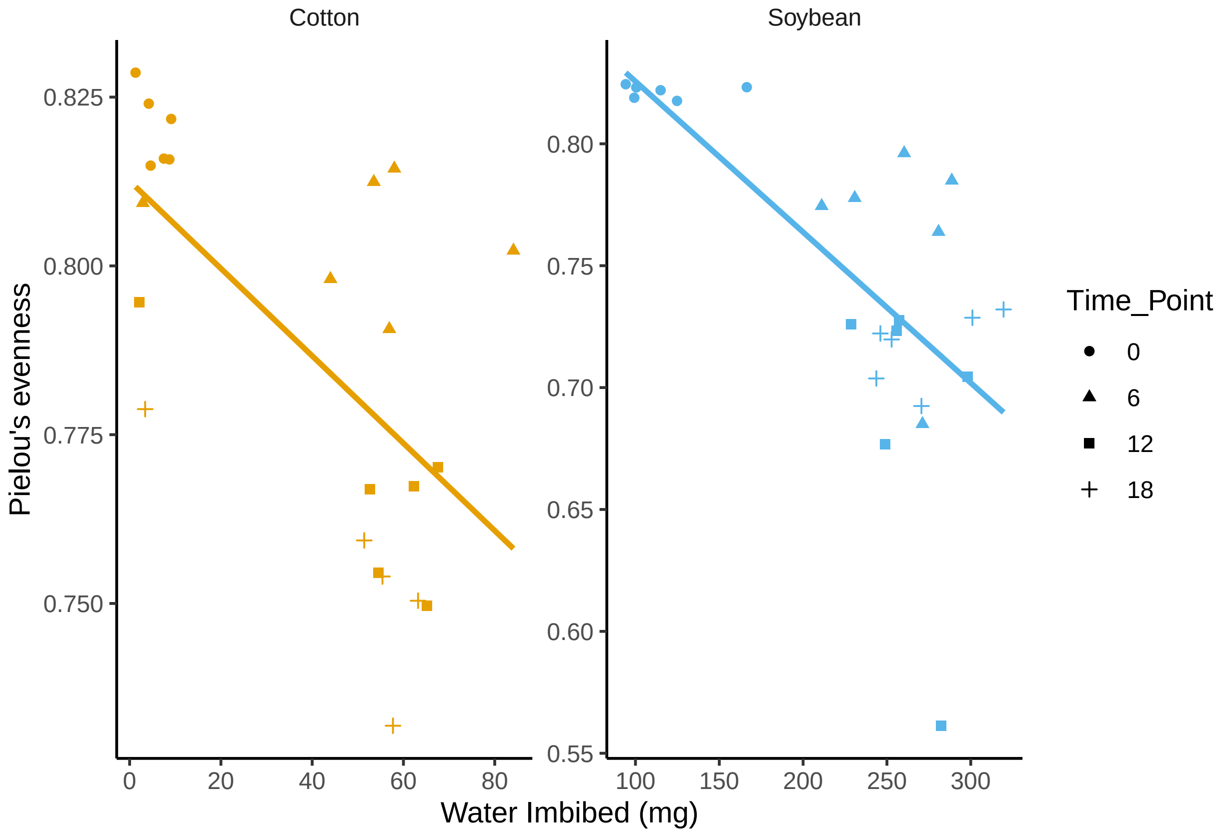
```
water.imbibed <- ggplot(sample.data.bac.no.soil, aes(Time_Point, 1000 * Water_Imbibed, color = Crop)) +
  geom_jitter(width = 0.5, alpha = 0.5) + #adding jitter points with transparency to show individual da
  stat_summary(fun = mean, geom = "line", aes(group = Crop)) + #adding lines to represent the mean valu
  stat_summary(fun.data = mean_se, geom = "errorbar", width = 0.5) + #adding error bars to represent th
  xlab("Hours post sowing") + #labelling x axis
  ylab("Water Imbibed (mg)") + #labelling y axis
  scale_color_manual(values = c(cbbPalette[[2]], cbbPalette[[3]]), name = "", labels = c("", "")) + #se
  theme_classic() + #using classic theme for the plot to make background plain white
  theme(strip.background = element_blank(), legend.position = "none") + #costumizing theme to remore st
  facet_wrap(~Crop, scales = "free") #creating separate panels for each crop and allowing free scales
water.imbibed
```



```
#Plot 3 -C

water.imbibed.cor <- ggplot(sample.data.bac.no.soil, aes (y= even, x = 1000 * Water_Imbibed, color = Cro
  geom_point(aes(shape = Time_Point)) + #adding points with different shapes based on time points
  geom_smooth(se=FALSE, method = lm) +  #adding a linear model smooth line without confidence interval
  xlab("Water Imbibed (mg)") + #labelling x axis
  ylab("Pielou's evenness") + #labelling y axis
  scale_color_manual(values = c(cbbPalette[[2]], cbbPalette[[3]]), name = "", labels = c("", "")) + #se
  theme_classic() + #using classic theme for the plot to make background plain white
  guides(color = "none") +
  theme(strip.background = element_blank(), legend.posion = "right") + #costumizing theme to remore str
  facet_wrap(~Crop, scales = "free") #creating separate panels for each crop and allowing free scales
water.imbibed.cor
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning in plot_theme(plot): The `legend.posion` theme element is not defined
## in the element hierarchy.
```

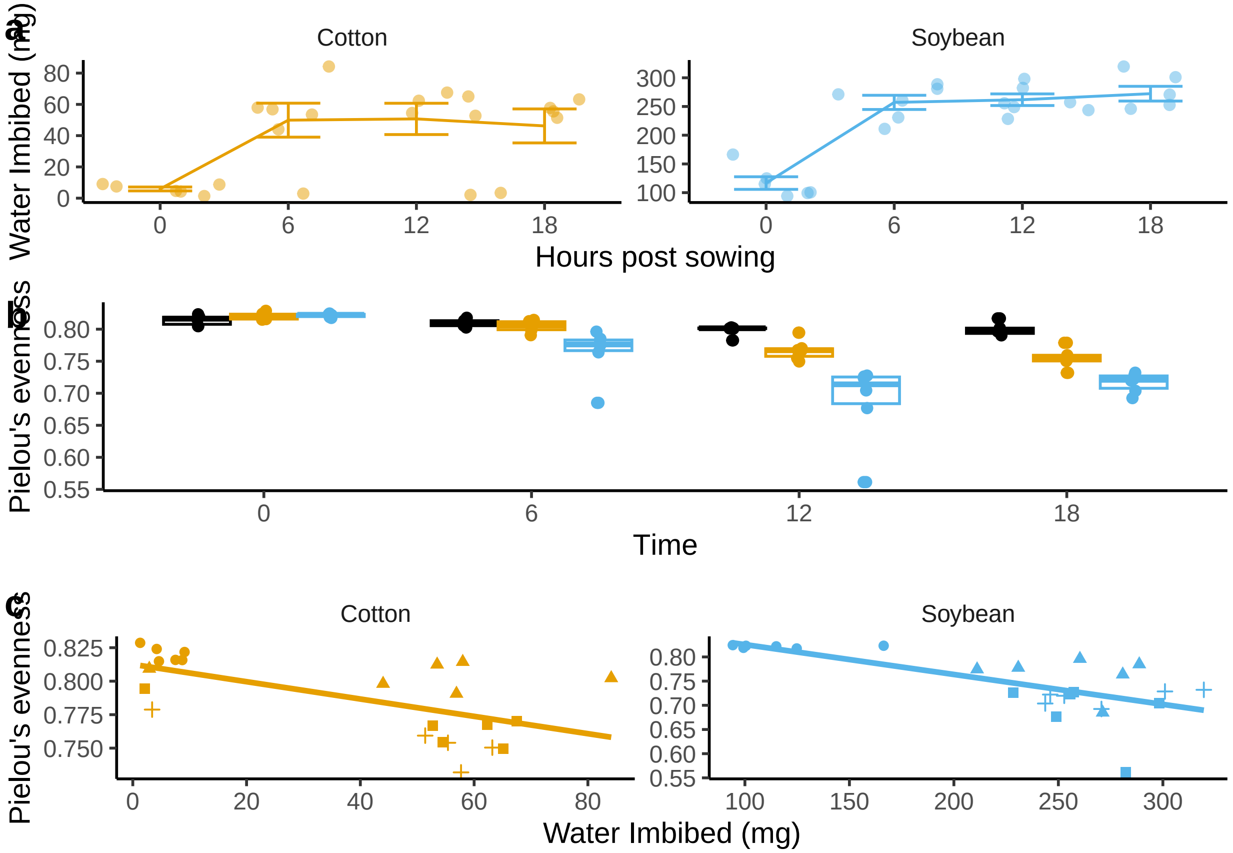


```
#Combining multiple figures into a single figure

figure2 <- ggarrange(
  water.imbibed, #first figure to plot
  bac.even,  #second figure to plot
  water.imbibed.cor,  #third figure to plot
  labels = "auto", #automatically labelling the plots as A, B ,C
  nrow = 3, #Arranging plots vertically in 3 rows
  ncol = 1, #Arranging plots in single column
  legend = FALSE #not including legend in the combined figure
)
```

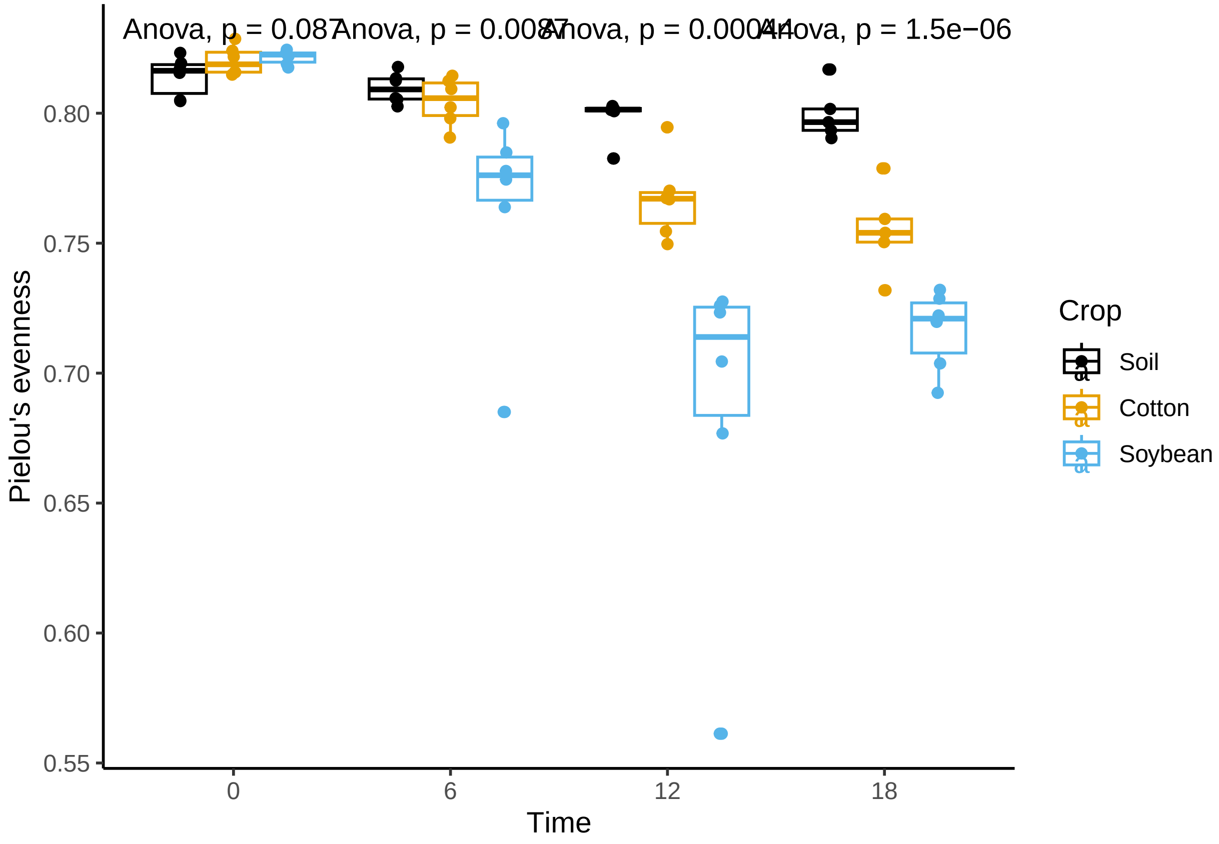
```
## ‘geom_smooth()‘ using formula = ’y ~ x’
```

```
## Warning in plot_theme(plot): The ‘legend.posion‘ theme element is not defined
## in the element hierarchy.
```

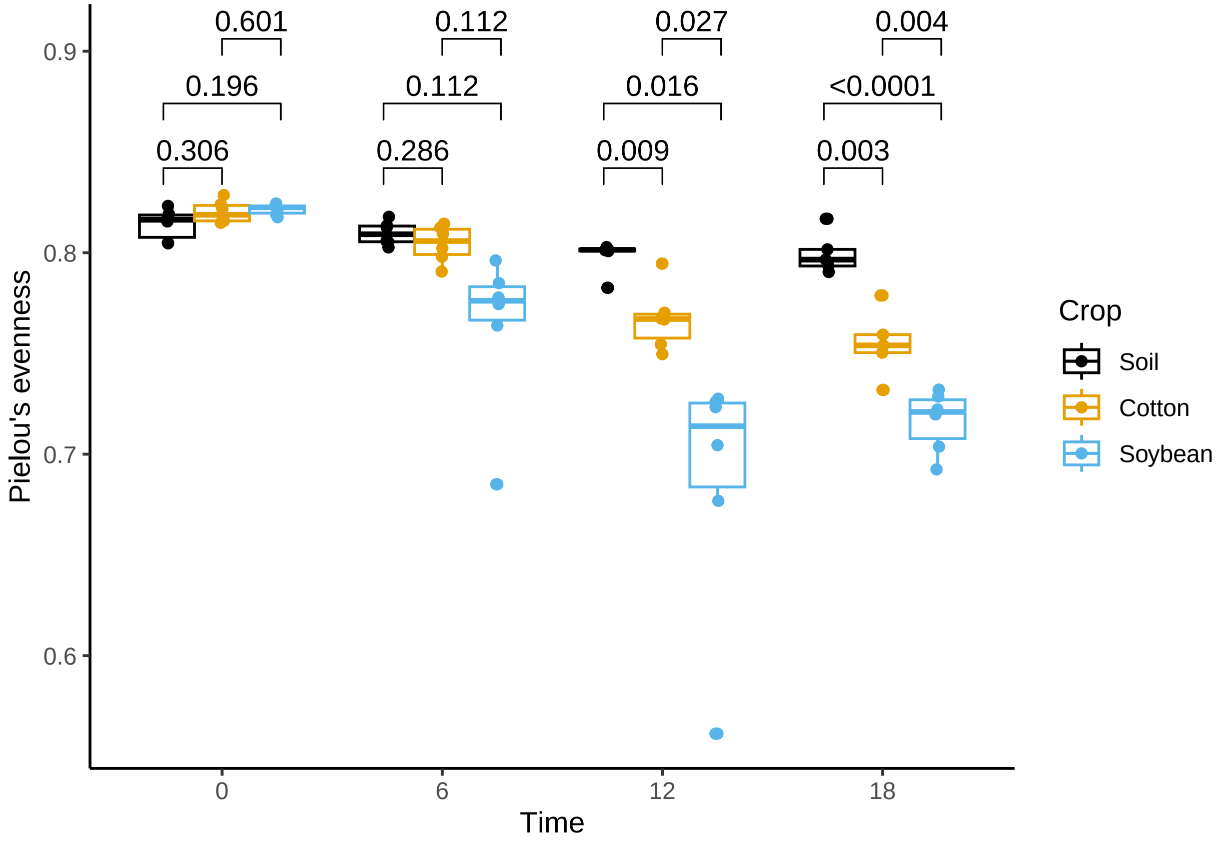
```
figure2
```



```
#ggpubr can integrate statistics in plot
# integrating statistics into plots for exploratory analyses


#applying anova to the groups
bac.even +
  stat_compare_means(method = "anova")
```



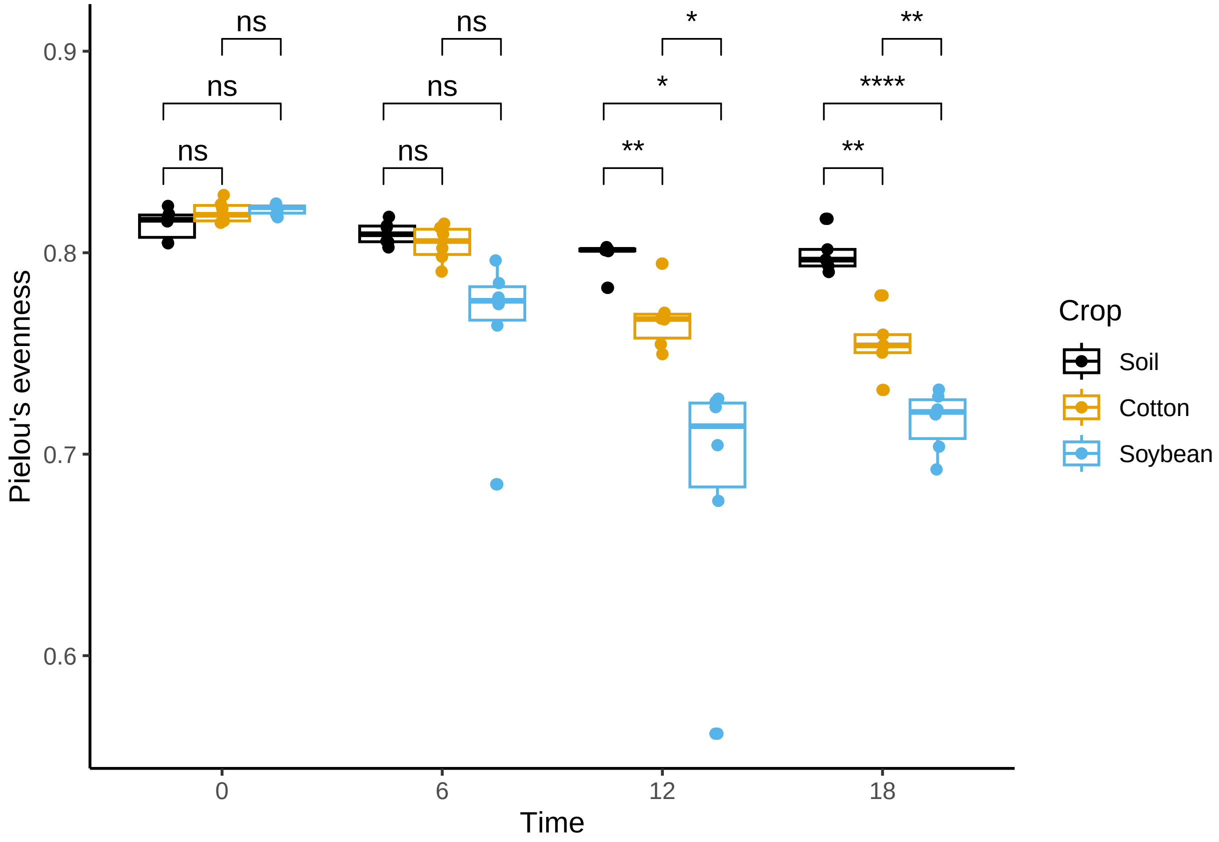
```r
#comparison within crop group at a single time point
bac.even +
  geom_pwc(aes(group = Crop), method = "t.test", label = "p.adj.format" )
```



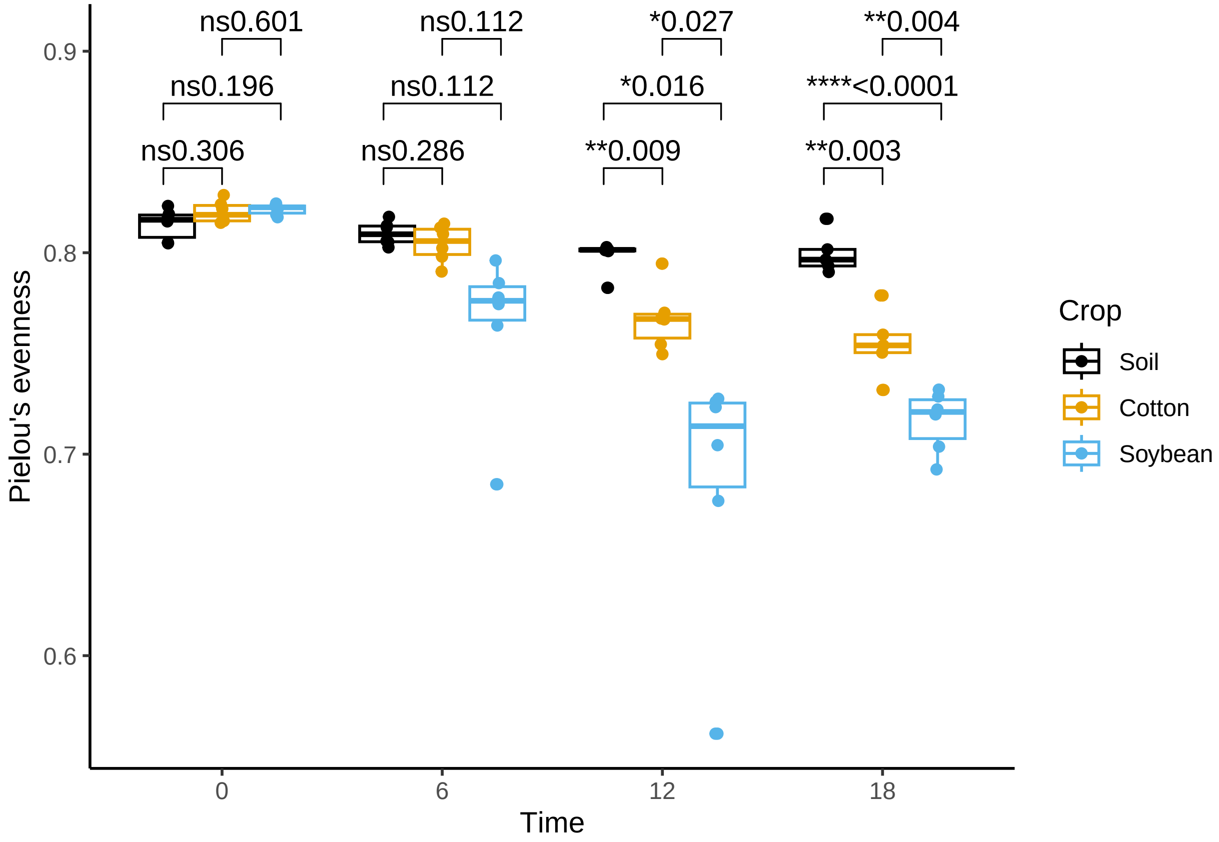
```
  geom_pwc(aes(group = Crop), method = "t.test", label = "p.adj.signif" ) #denoting significance levels
```

```
## mapping: group = ~Crop, legend.var = ~Crop
## geom_pwc: na.rm = FALSE, remove.bracket = FALSE, parse = FALSE
## stat_pwc: method = t.test, method.args = list(), ref.group = NULL, stat.label = p.adj.signif, y.posi
## position_identity
```

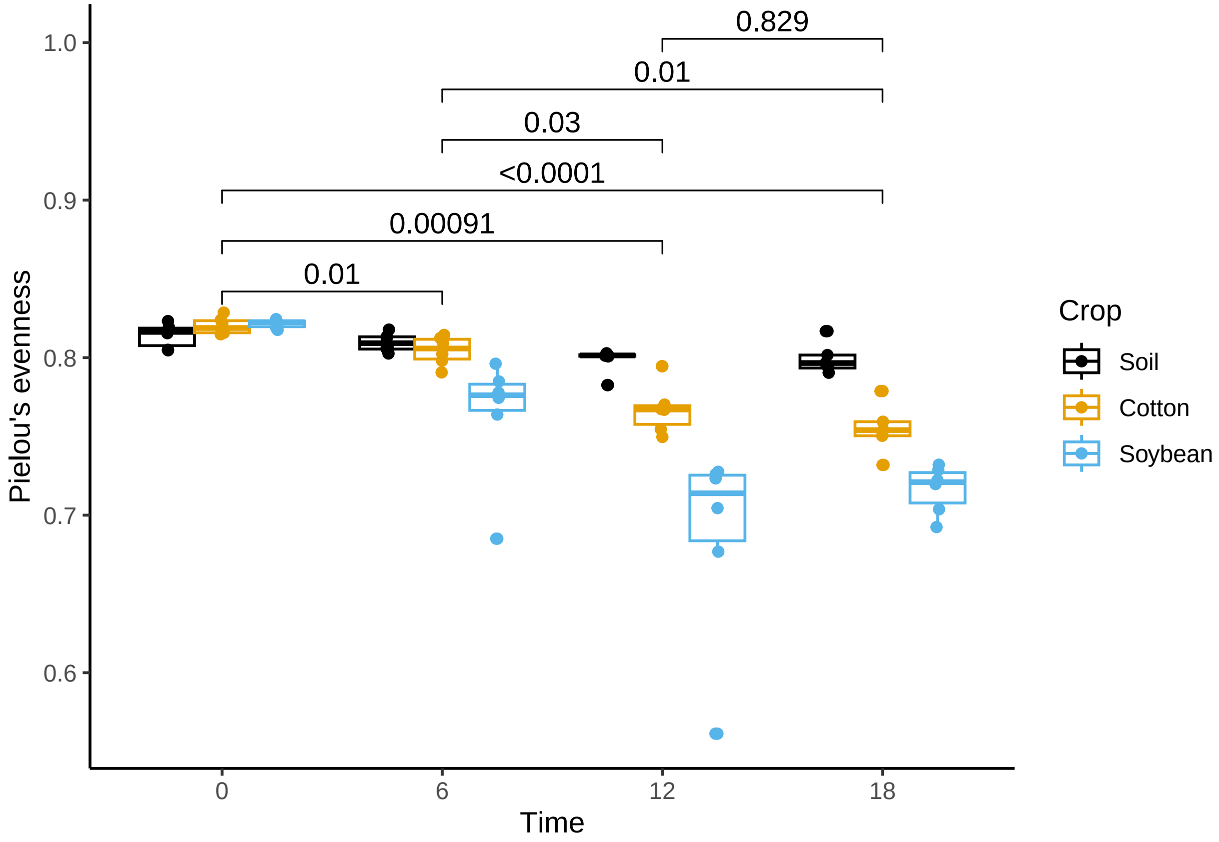
```
bac.even +
  geom_pwc(aes(group = Crop), method = "t.test", label = "p.adj.signif" ) #denoting significance levels
```



```
bac.even +
  geom_pwc(aes(group = Crop), method = "t.test", label = "{p.adj.signif}{p.adj.format}" ) #denoting sig
```



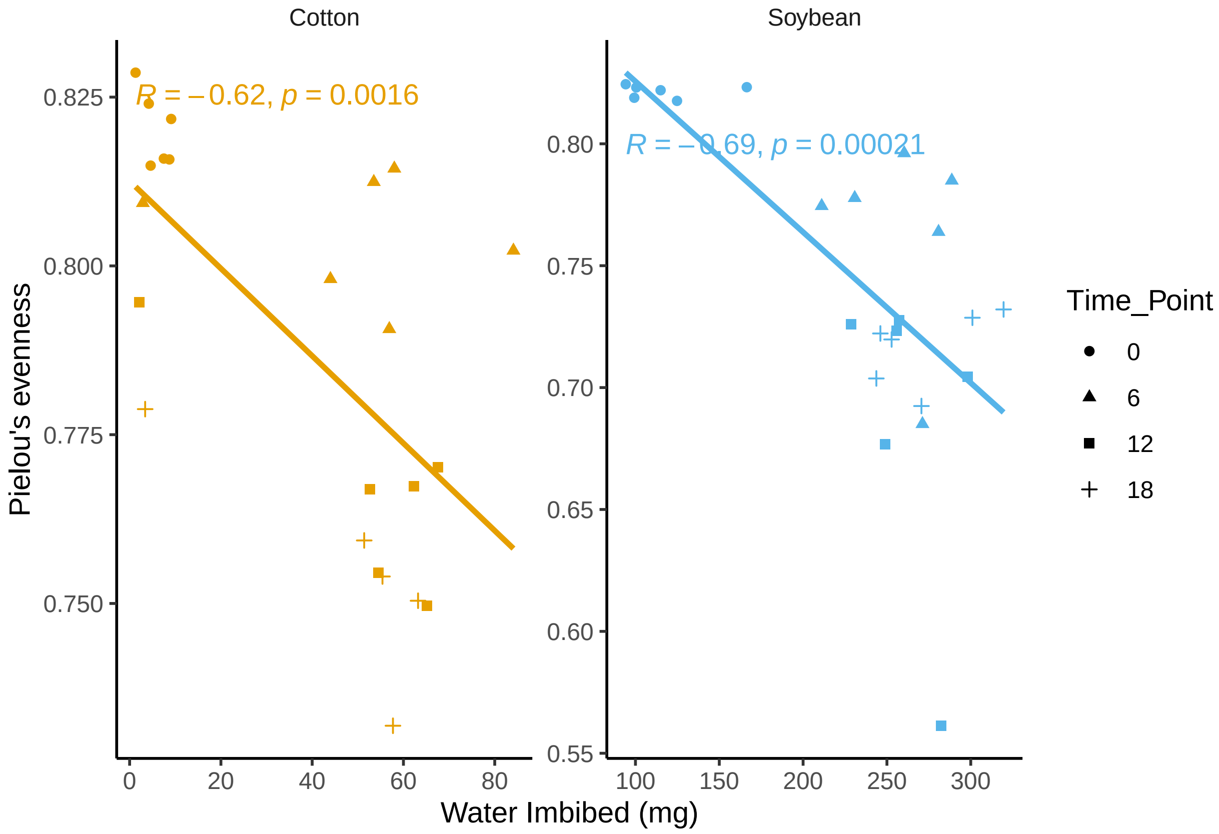
```
#comparison between time point (average evenness of all crops at certain time point compared with avera
bac.even +
  geom_pwc(aes(group = Time_Point), method = "t.test", label = "p.adj.format" )
```



```
#correlation
water.imbibed.cor +
  stat_cor()  #gives pearson's correlation
```

```
## ‘geom_smooth()‘ using formula = ’y ~ x’
```

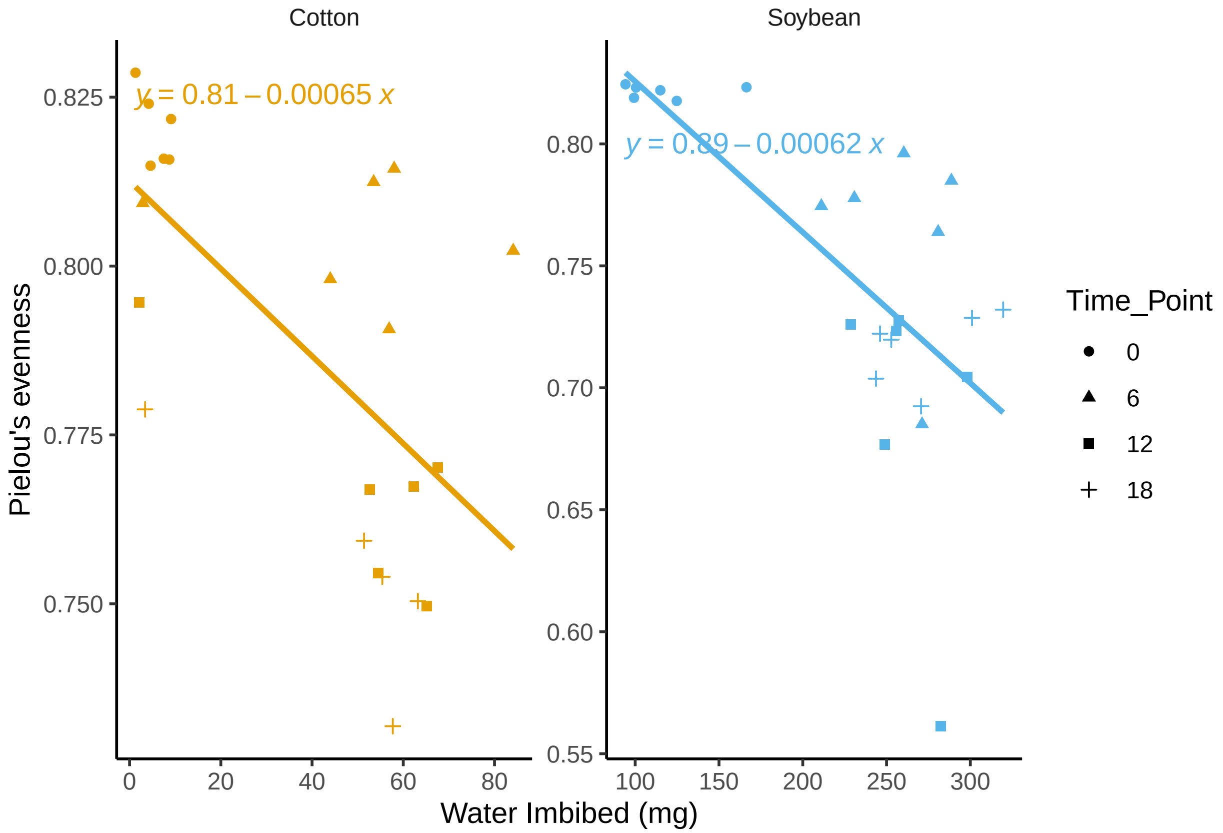
```
## Warning in plot_theme(plot): The ‘legend.posion‘ theme element is not defined
## in the element hierarchy.
```



```
water.imbibed.cor +
  stat_regline_equation() #gives regression line
```

```
## ‘geom_smooth()‘ using formula = ’y ~ x’
```

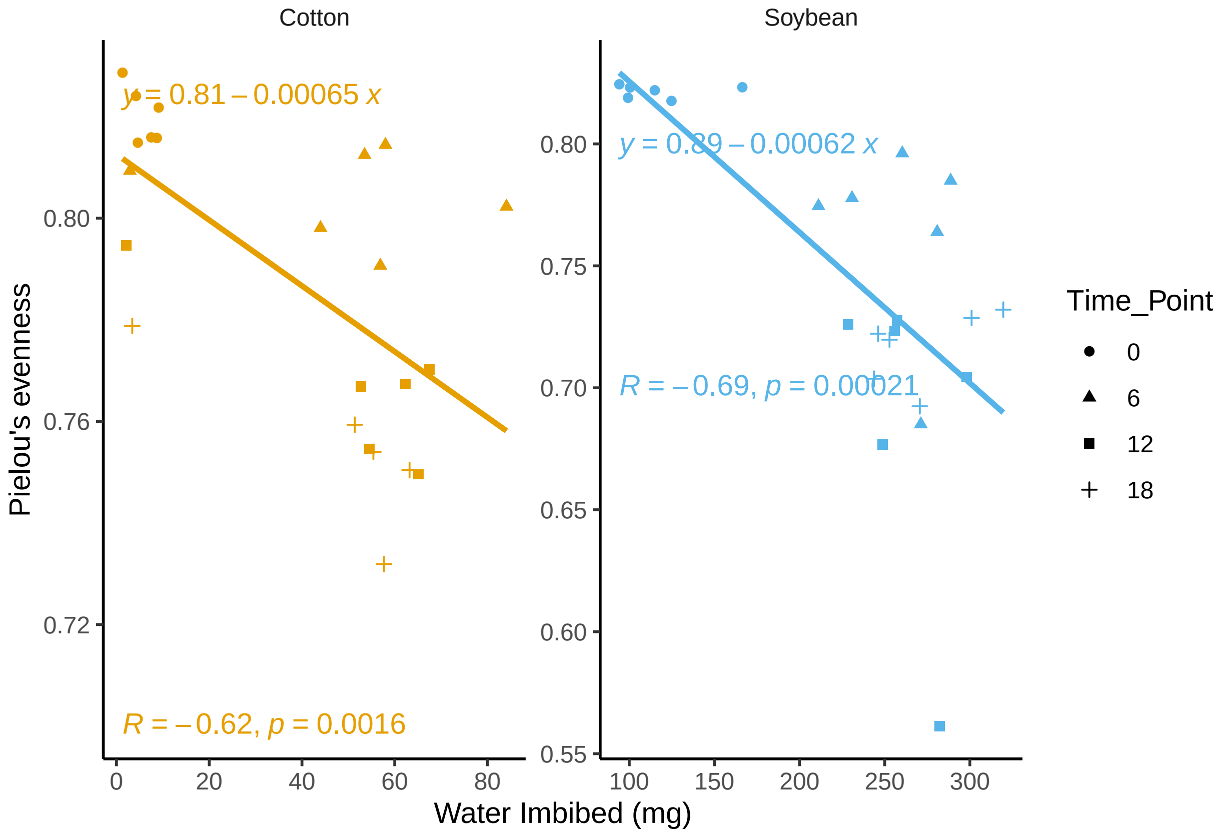
```
## Warning in plot_theme(plot): The ‘legend.posion‘ theme element is not defined
## in the element hierarchy.
```



```
water.imbibed.cor +
  stat_cor(label.y = 0.7) +
  stat_regline_equation()
```

```
## 'geom_smooth()' using formula = 'y ~ x'
```

```
## Warning in plot_theme(plot): The 'legend.posion' theme element is not defined
## in the element hierarchy.
```

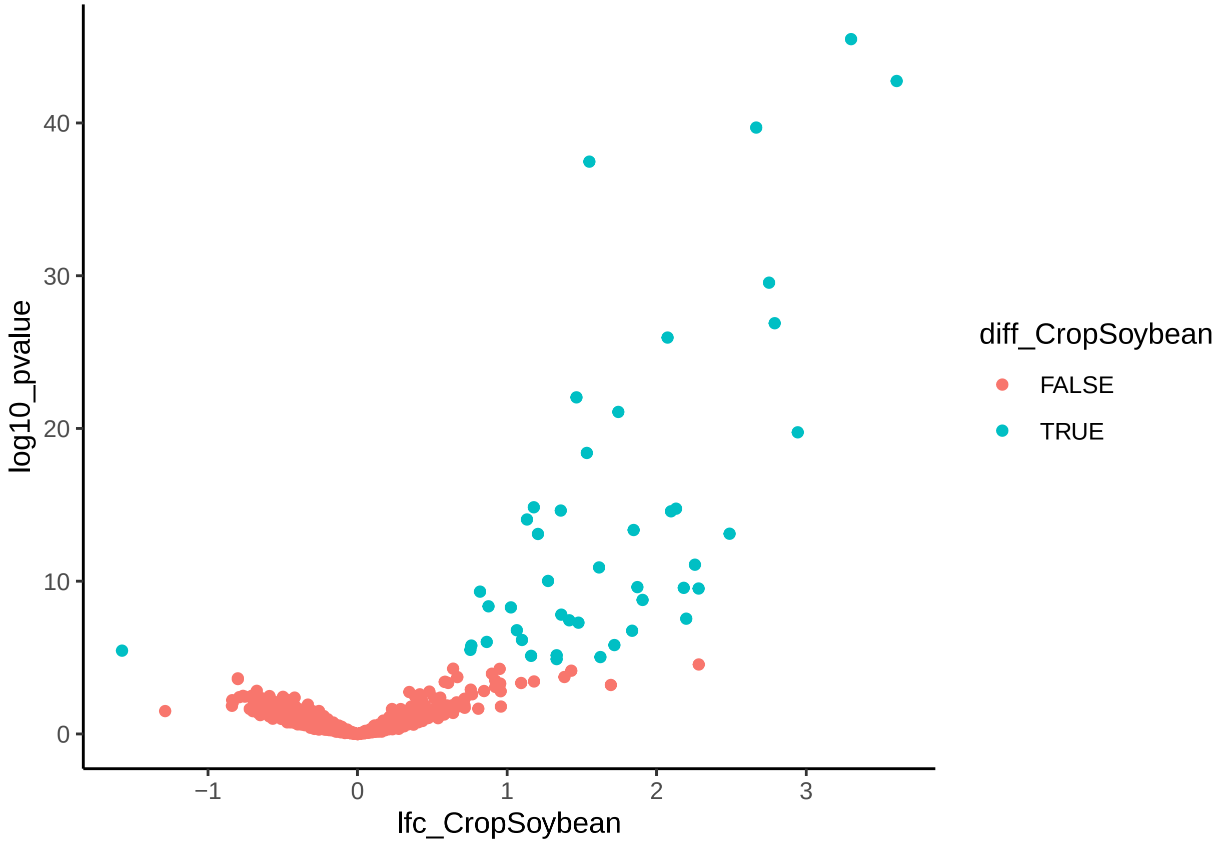


```
#Differential abundance test for plotting while emphasizing most significant points
diff_abundance <- read.csv("diff_abund.csv") #loading data in R

str(diff_abundance)
```

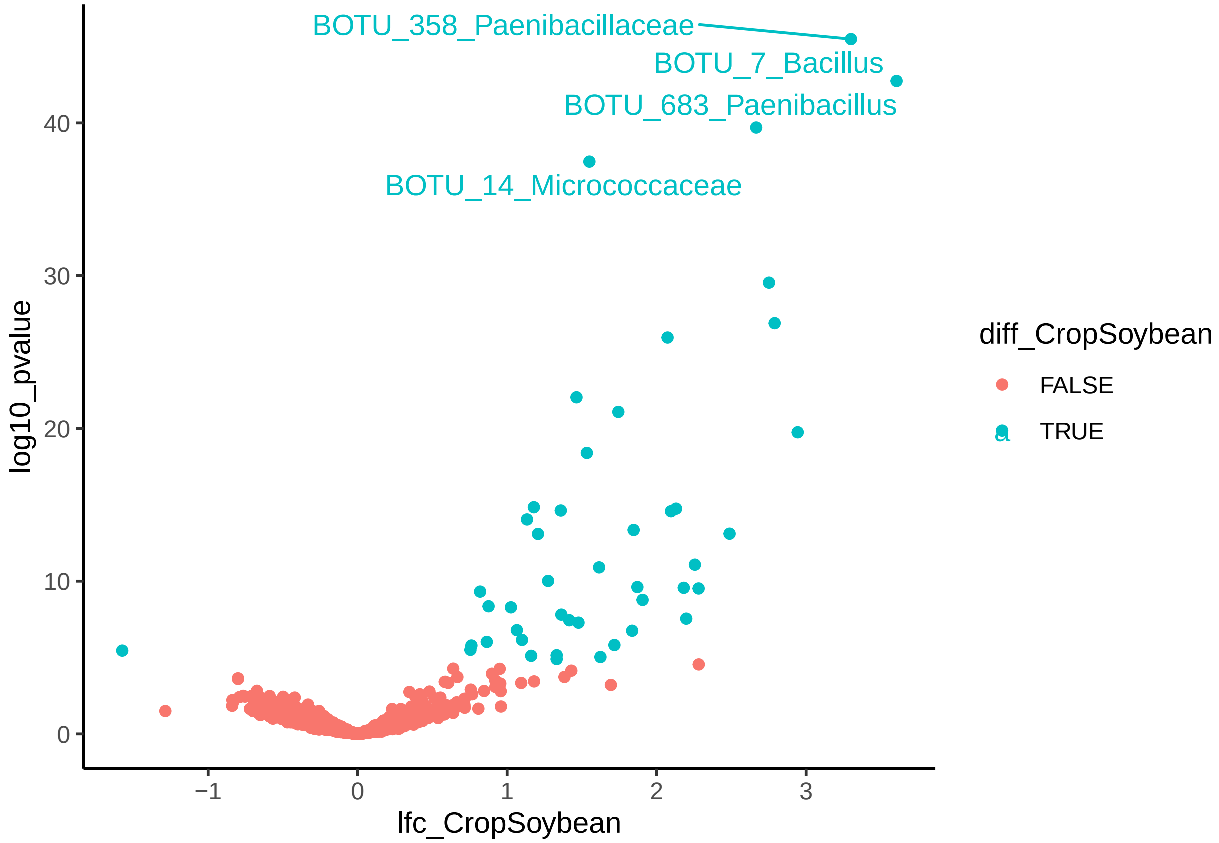
```
## ’data.frame’:    2375 obs. of  16 variables:
##  $ taxon           : chr  "BOTU_1387" "BOTU_1197" "BOTU_2475" "BOTU_1574" ...
##  $ lfc_CropCotton  : num  0.016 0.1019 -0.0503 0.1019 0.0791 ...
##  $ lfc_CropSoybean : num  -0.305 0.191 -0.0213 0.2592 0.9588 ...
##  $ p_CropCotton    : num  0.947 0.572 0.806 0.531 0.846 ...
##  $ p_CropSoybean   : num  0.193 0.28 0.915 0.103 0.016 ...
##  $ q_CropCotton    : num  1 1 1 1 1 1 1 1 1 1 ...
##  $ q_CropSoybean   : num  1 1 1 1 1 ...
##  $ diff_CropCotton : logi  FALSE FALSE FALSE FALSE FALSE FALSE ...
##  $ diff_CropSoybean: logi  FALSE FALSE FALSE FALSE FALSE FALSE ...
##  $ Kingdom         : chr  "Bacteria" "Bacteria" "Bacteria" "Bacteria" ...
##  $ Phylum          : chr  "Proteobacteria" "Proteobacteria" "Proteobacteria" "Proteobacteria" ...
##  $ Class           : chr  "Gammaproteobacteria" "Gammaproteobacteria" "Gammaproteobacteria" "Gammapro
##  $ Order           : chr  "Legionellales" "Diplorickettsiales" "Diplorickettsiales" "Diplorickettsial
##  $ Family          : chr  "Legionellaceae" "Diplorickettsiaceae" "Diplorickettsiaceae" "Diplorickett
##  $ Genus           : chr  "Legionella" "Aquicella" "Aquicella" "unidentified" ...
##  $ Label           : chr  "BOTU_1387_Legionella" "BOTU_1197_Aquicella" "BOTU_2475_Aquicella" "BOTU_15
```

```
diff_abundance$log10_pvalue <- -log10(diff_abundance$p_CropSoybean)  #adding column log10_pvalue in the
```

```
diff_abundance_label <- diff_abundance[diff_abundance$log10_pvalue>30,] #subsetting the dataset with lo

ggplot() +
  geom_point(data = diff_abundance, aes(x = lfc_CropSoybean, y = log10_pvalue, color = diff_CropSoybean
  theme_classic()    #using classic theme for the plot to make background plain white
```

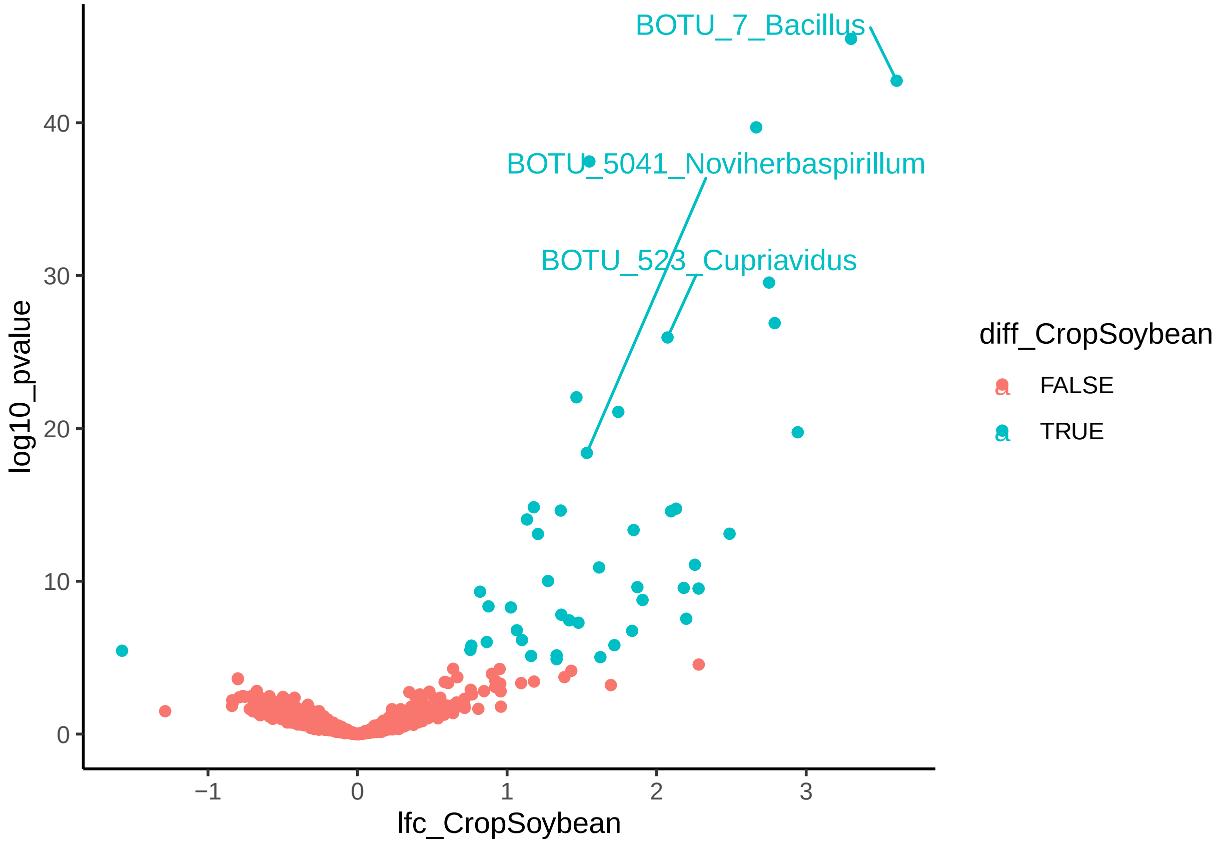


```
ggplot() +
  geom_point(data = diff_abundance, aes(x = lfc_CropSoybean, y = log10_pvalue, color = diff_CropSoybean
  theme_classic() +      #using classic theme for the plot to make background plain white
  geom_text_repel(data = diff_abundance_label, aes(x = lfc_CropSoybean, y = log10_pvalue, color = diff_
```

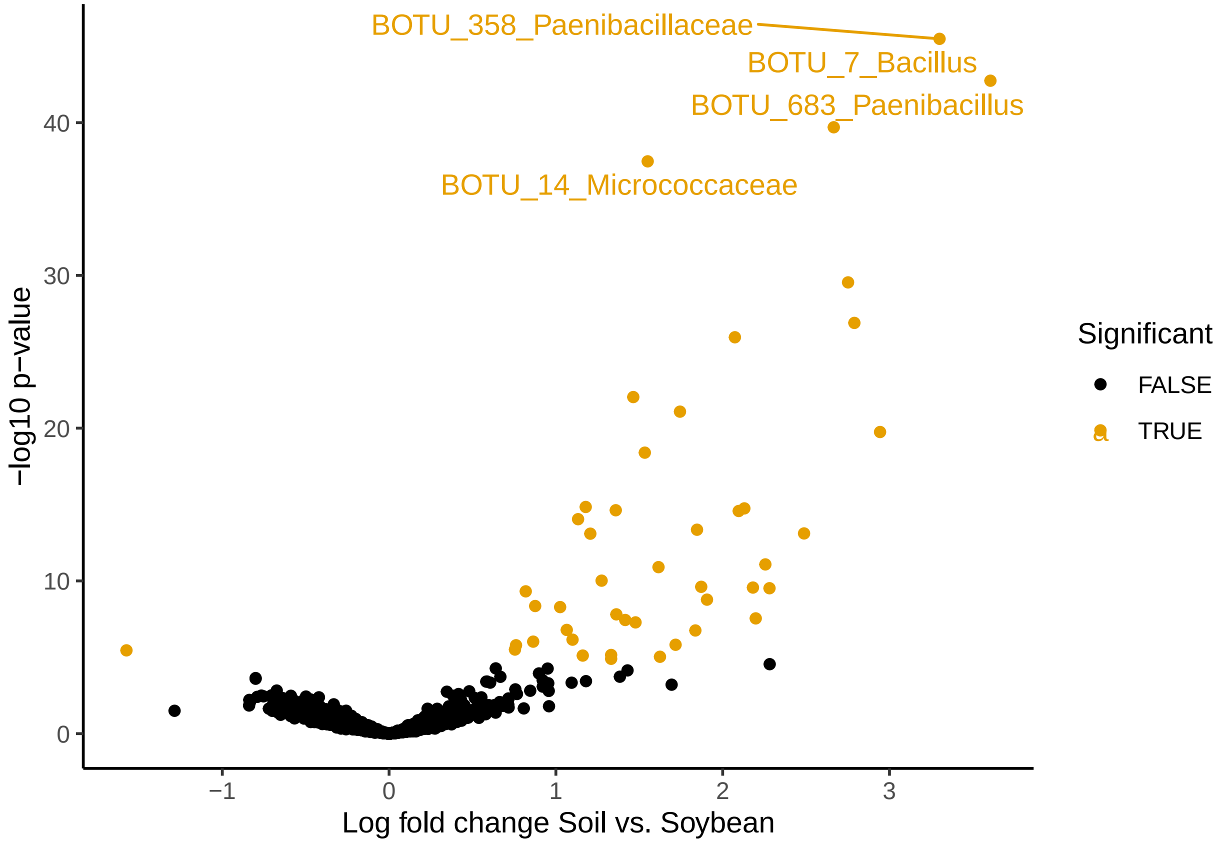


```r
#using all data points
ggplot() +
  geom_point(data = diff_abundance, aes(x = lfc_CropSoybean, y = log10_pvalue, color = diff_CropSoybean)
  theme_classic() + #using classic theme for the plot to make background plain white
  geom_text_repel(data = diff_abundance, aes(x = lfc_CropSoybean, y = log10_pvalue, color = diff_CropSoy
```

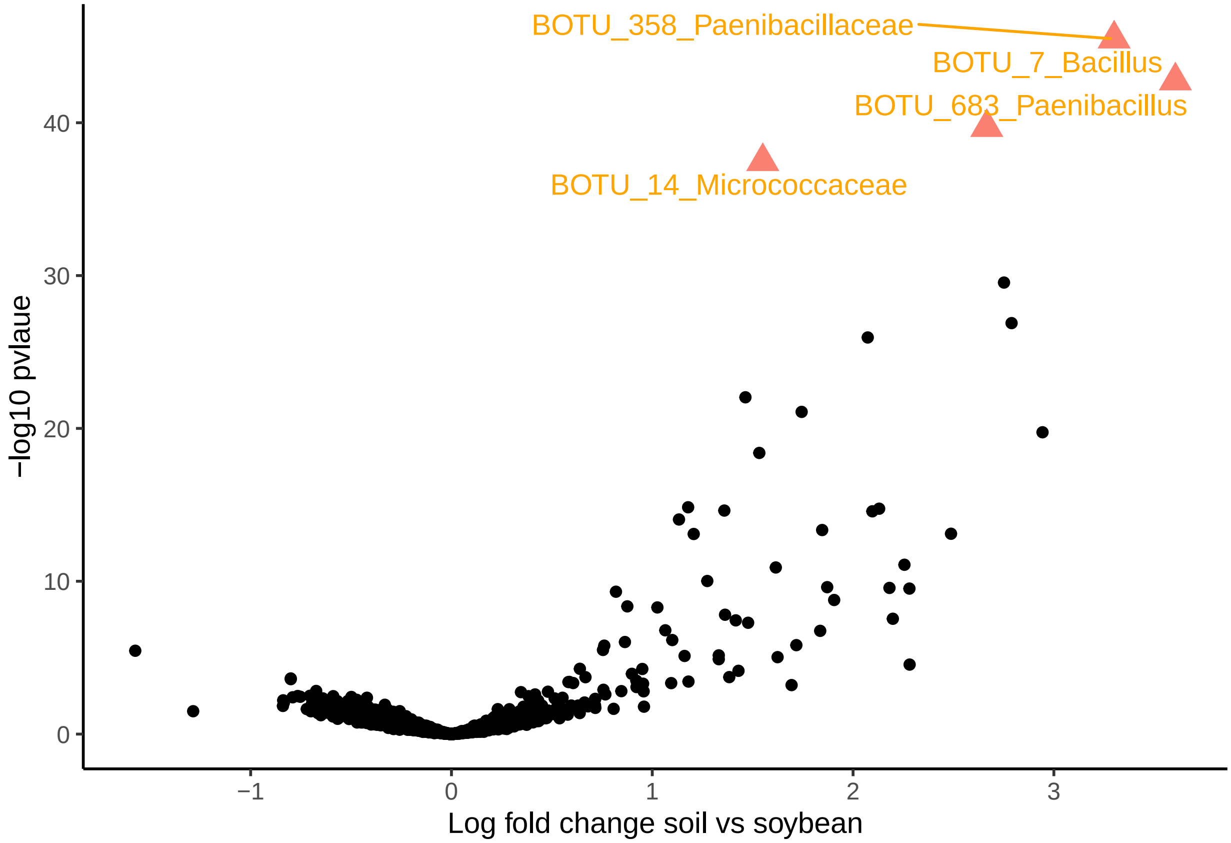
```
## Warning: ggrepel: 2372 unlabeled data points (too many overlaps). Consider
## increasing max.overlaps
```



```
volcano <- ggplot() +
  geom_point(data = diff_abundance, aes(x = lfc_CropSoybean, y = log10_pvalue, color = diff_CropSoybean
  geom_text_repel(data = diff_abundance_label, aes(x = lfc_CropSoybean, y = log10_pvalue, color = diff_
  scale_color_manual(values = cbbPalette, name = "Significant") +
  theme_classic() +
  xlab("Log fold change Soil vs. Soybean") +
  ylab("-log10 p-value")
volcano
```



```r
#using the same concept to emphasize only certain points as a different color and shape
ggplot() +
  geom_point(data = diff_abundance, aes(x = lfc_CropSoybean, y = log10_pvalue)) + #defining x as lfc cr
  geom_point(data = diff_abundance_label, aes(x = lfc_CropSoybean, y = log10_pvalue, color = diff_CropS
  theme_classic() +
  geom_text_repel(data = diff_abundance_label, aes(x = lfc_CropSoybean, y = log10_pvalue, color = diff_(
  scale_color_manual(values = cbbPalette, name = "Significant") +
  xlab("Log fold change soil vs soybean") +
  ylab("-log10 pvlaue")
```


BOTU_358_Paenibacillaceae
BOTU_7_Bacillus
BOTU_683_Paenibacillus
BOTU_14_Micrococcaceae
−log10 pvlaue
40
30
20
10
0
−1
0
1
2
3
Log fold change soil vs soybean