Effect of treatments on leaves

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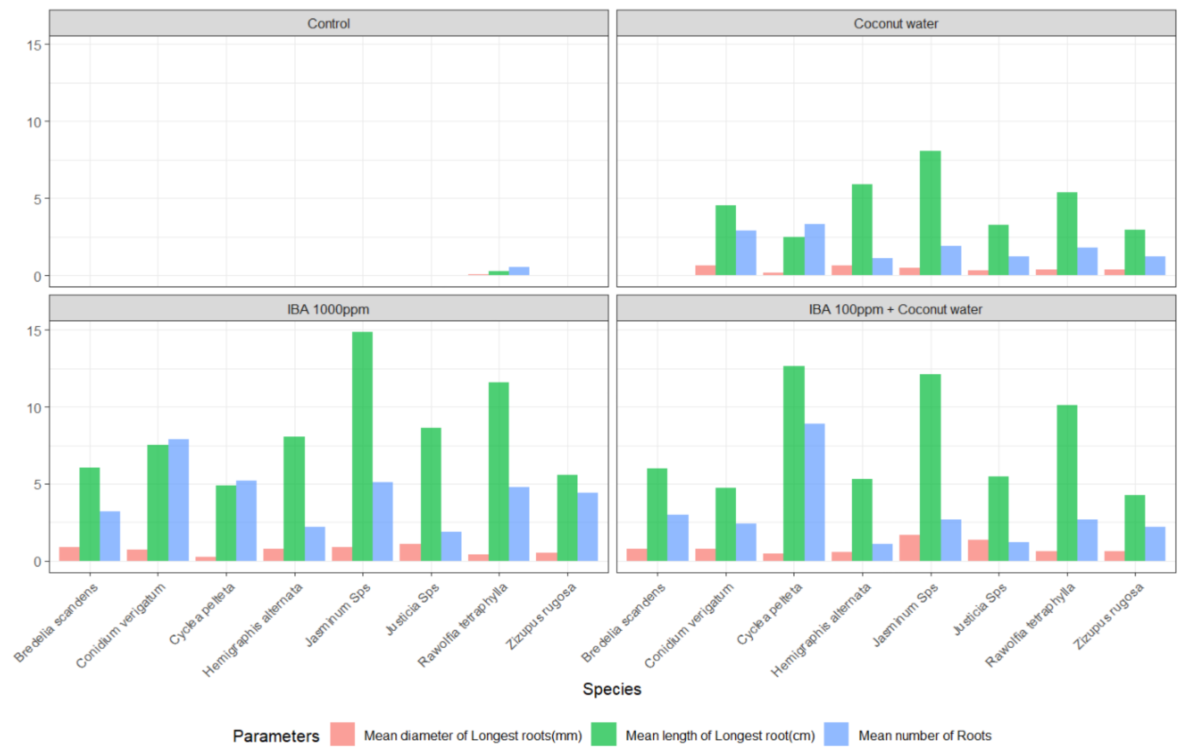
Effect of Treatments on leaves to produce roots

An experiment was conducted to find the rooting potential of the leaves mainly angiosperms to root when treated with different phyto-hormones.



- In the experiment, 4 treatments were applied on 8 different species, and the observations included:
  - Number of roots (`num_roots_n`).

  - Length of the longest root in centimeters (`lng_long_root_cm`).
  - Diameter of the longest root in millimeters (`dia_long_root_mm`).

Loading Required packages

```r
library(tidyverse)
library(gt)
```

Loading the data and formatting

The data is loaded as a dataframe and columns such as treatments(`Treatment`) and species(`Species`) are changes to factors as they are not suitable as strings.

```r
# Loading data
thesisdata <- read_csv("thesisdata.csv",
                       show_col_types = FALSE)
# formating data
ths_data <- thesisdata
ths_data$Treatment <- as.factor(ths_data$Treatment)
ths_data$Treatment <-
  factor(ths_data$Treatment,levels = c("Control",
                                       "Coconut water",
                                       "IBA 1000ppm",
                          "IBA 100ppm + Coconut water"))
ths_data$Species <- factor(ths_data$Species)

ths_data %>% head()
```

```
# A tibble: 6 x 5
  Species            Treatment num_roots_n lng_long_root_cm dia_long_root_mm
  <fct>              <fct>           <dbl>            <dbl>            <dbl>
1 Conidium verigatum Control             0                0                0
2 Conidium verigatum Control             0                0                0
3 Conidium verigatum Control             0                0                0
4 Conidium verigatum Control             0                0                0
5 Conidium verigatum Control             0                0                0
6 Conidium verigatum Control             0                0                0
```

- Confirming that only 8 species and 4 treatments are used in the experiment.

```r
treatments_and_species <- list(unique(ths_data$Treatment), unique(ths_data$Species))

treatments_and_species
```

```
[[1]]
[1] Control                     Coconut water
[3] IBA 1000ppm                 IBA 100ppm + Coconut water
Levels: Control Coconut water IBA 1000ppm IBA 100ppm + Coconut water

[[2]]
[1] Conidium verigatum    Rawolfia tetraphylla  Justicia Sps
[4] Zizupus rugosa        Jasminum Sps          Cyclea pelteta
[7] Bredelia scandens     Hemigraphis alternata
8 Levels: Bredelia scandens Conidium verigatum ... Zizupus rugosa
```

Aggregating data and formatting the results into a table.

The data is aggregated by the average of root lengths with standard deviation(SD)

```r
ths_data_1 <- ths_data %>% group_by(Species, Treatment) %>%
  summarise(avg_n_roots = mean(num_roots_n),
            SD_n_roots = sd(num_roots_n),
            avg_lng_root = mean(lng_long_root_cm),
            SD_lng_root = sd(lng_long_root_cm),
            avg_dia_root = mean(dia_long_root_mm),
            SD_dia_root = sd(dia_long_root_mm)) %>%
  # rounding of to 2 digits
  mutate(across(where(is.double), ~round(., digits = 2))) %>%
  # combining means and SD into a single column
  unite(avg_n_roots_SD, avg_n_roots, SD_n_roots, sep = " \u00b1 ") %>%
  unite(avg_lng_root_SD, avg_lng_root, SD_lng_root, sep = " \u00b1 ") %>%
  unite(avg_dia_root_SD, avg_dia_root, SD_dia_root, sep = " \u00b1 ") %>%
  # using 'gt' package to get a table
  gt(rowname_col = "Treatment") %>%
  tab_header(
    title = "Thesis Data of the Species",
    subtitle = "Influence of growth regulators on the root generation"
  ) %>%
  opt_align_table_header(align = "center") %>%
  cols_label( # renaming columns
```

```r
    avg_n_roots_SD = md("Mean number of roots \u00b1 SD"), #md is markdown language
    avg_lng_root_SD = md("Mean length of longest roots \u00b1 SD (cm)"),
    avg_dia_root_SD = md("Mean diameter of  longest roots \u00b1 SD (mm)")
  ) %>% # fixing columns width
  cols_width(Treatment ~ px(150),
             avg_n_roots_SD ~ px(150),
             avg_lng_root_SD ~ px(150),
             avg_dia_root_SD ~ px(150),
            ) %>%
  cols_align(align = "center")

ths_data_1
```

Thesis Data of the Species

Influence of growth regulators on the root generation

	Mean number of roots ± SD	Mean length of longest roots ± SD (cm)	M
Bredelia scandens			
Control	0 ± 0	0 ± 0	
Coconut water	0 ± 0	0 ± 0	
IBA 1000ppm	3.22 ± 0.44	6.06 ± 2.02	
IBA 100ppm + Coconut water	3 ± 0.5	6.02 ± 1.26	
Conidium verigatum			
Control	0 ± 0	0 ± 0	
Coconut water	2.89 ± 1.05	4.52 ± 1.1	
IBA 1000ppm	7.89 ± 3.62	7.52 ± 2.55	
IBA 100ppm + Coconut water	2.44 ± 0.88	4.74 ± 1.09	
Cyclea pelteta			
Control	0 ± 0	0 ± 0	
Coconut water	3.33 ± 0.71	2.48 ± 0.37	
IBA 1000ppm	5.22 ± 1.39	4.89 ± 1.17	
IBA 100ppm + Coconut water	8.89 ± 2.03	12.64 ± 3.23	
Hemigraphis alternata			
Control	0 ± 0	0 ± 0	
Coconut water	1.11 ± 0.33	5.89 ± 0.84	
IBA 1000ppm	2.22 ± 0.83	8.06 ± 1.58	
IBA 100ppm + Coconut water	1.11 ± 0.33	5.33 ± 1.93	
Jasminum Sps			

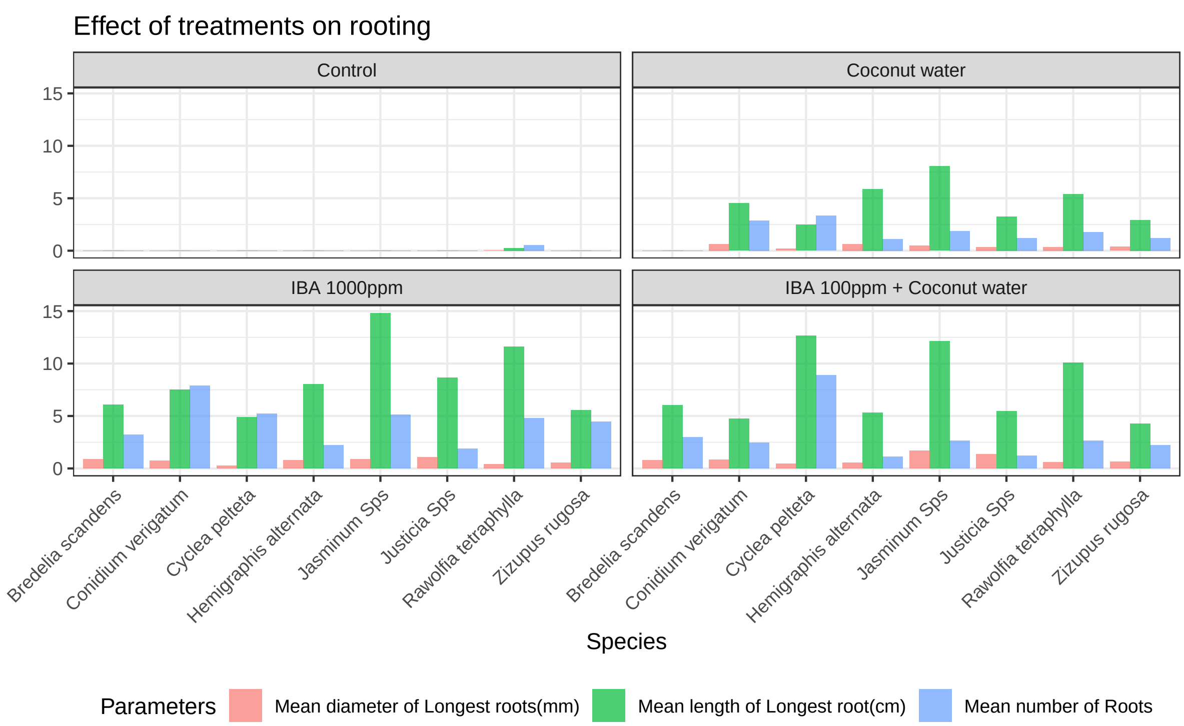
Control	0 ± 0	0 ± 0
Coconut water	1.89 ± 0.6	8.06 ± 0.88
IBA 1000ppm	5.11 ± 1.17	14.82 ± 1.59
IBA 100ppm + Coconut water	2.67 ± 1.22	12.12 ± 2.27
Justicia Sps		
Control	0 ± 0	0 ± 0
Coconut water	1.22 ± 0.44	3.28 ± 1.24
IBA 1000ppm	1.89 ± 0.78	8.64 ± 2.41
IBA 100ppm + Coconut water	1.22 ± 0.44	5.47 ± 1.84
Rawolfia tetraphylla		
Control	0.56 ± 1.13	0.26 ± 0.51
Coconut water	1.78 ± 0.97	5.4 ± 2.64
IBA 1000ppm	4.78 ± 2.17	11.59 ± 4.79
IBA 100ppm + Coconut water	2.67 ± 1.41	10.09 ± 2.34
Zizupus rugosa		
Control	0 ± 0	0 ± 0
Coconut water	1.22 ± 0.83	2.94 ± 1.34
IBA 1000ppm	4.44 ± 1.59	5.56 ± 2.08
IBA 100ppm + Coconut water	2.22 ± 0.67	4.26 ± 1.11

Plotting the data for better understanding.

- Plotting a bar graph to see how each treatment performed on each species.

```
ths_data |> summarise(avg_n_roots = mean(num_roots_n),
                      avg_lng_root = mean(lng_long_root_cm),
                      avg_dia_root = mean(dia_long_root_mm),
                      .by = c(Species, Treatment)) %>%
  rename("Mean number of Roots" = avg_n_roots,
         "Mean length of Longest root(cm)" = avg_lng_root,
         "Mean diameter of Longest roots(mm)" = avg_dia_root) %>%
  tidyr::pivot_longer(c("Mean number of Roots", "Mean length of Longest root(cm)",
                        "Mean diameter of Longest roots(mm)")) |>
  ggplot(aes(x = Species, y = value, fill = name)) +
  geom_col(alpha = 0.7, position = "dodge") +
  facet_wrap(~Treatment, ncol = 2) +
  theme_bw() + labs(y = " ", fill = "Parameters",
                    title = "Effect of treatments on rooting") +
```

```
theme(legend.position = "bottom",
      axis.text.x = element_text(angle = 45, hjust = 1))
```



- We can clearly see that *Control* treatment is not producing any roots in majority of the species.
- **IBA 1000ppm** is clearly showing most promising results in most of the species in the graph.

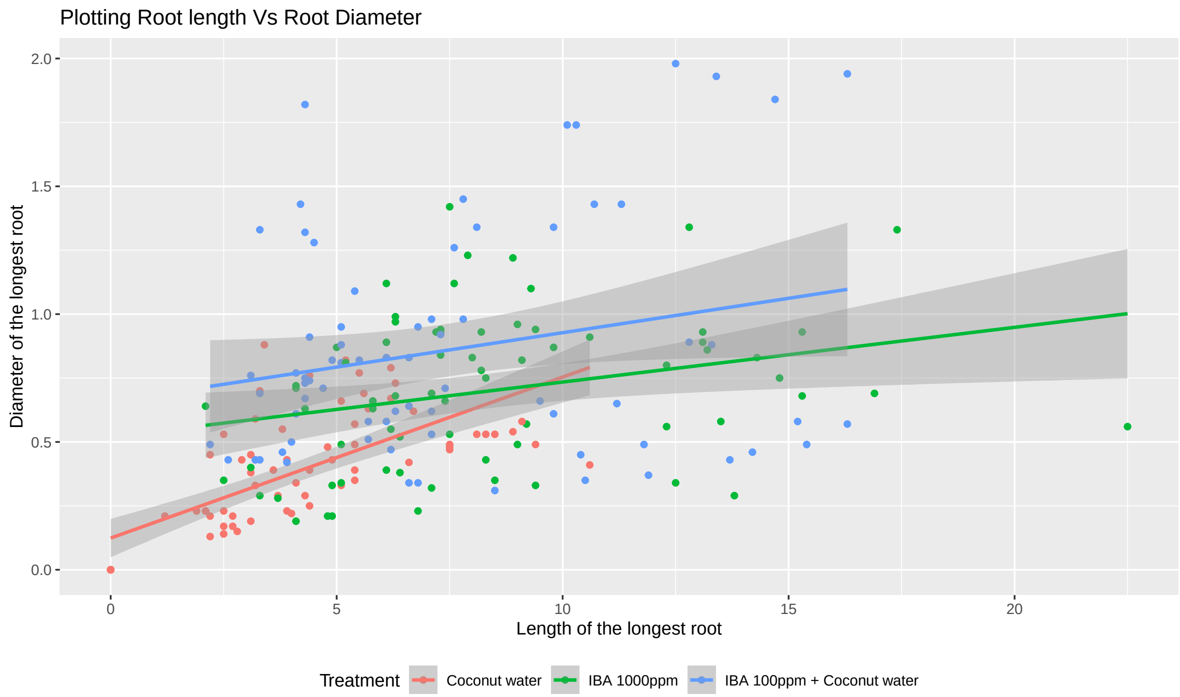
Finding corelation

We are going to filter out the control treatment as it is not significant at producing roots at all.

```
ths_data |> filter(Treatment!= "Control") |>
   ggplot(aes(x = lng_long_root_cm, y = dia_long_root_mm)) +
  geom_point(aes(color = Treatment)) +
  geom_smooth(method = "lm", aes(group = Treatment, color = Treatment)) +
  labs(title = "Plotting Root length Vs Root Diameter",
       x = "Length of the longest root",
```

```
        y = "Diameter of the longest root") +
    theme(legend.position = "bottom")
```

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



- The graph clearly shows that the `Coconut Water` treatment has the highest Slope.