Light\_Spactrum

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The researcher has used light spectrum (as treatment with 3 different levels: Red, Blue, Control) for measure germination potential how they are significantly differing.  
\* He has measured different responses factors. Such as,

* Germinated\_seeds(%),
* Total\_seedling\_Length,
* Total\_Length,
* Leaf\_Length,
* Leaf\_Width.

(df <- read.table("Light\_Spectrum.csv", header = TRUE, sep = ","))

## Light\_Spectrum Germinated\_seeds... Total\_seedling\_Length Total\_Length  
## 1 Red 98 6.9925 12.10  
## 2 Red 96 6.9550 11.89  
## 3 Red 100 6.8100 11.99  
## 4 Blue 72 4.2950 15.55  
## 5 Blue 78 4.3000 15.33  
## 6 Blue 86 4.6300 15.48  
## 7 Control 84 7.3600 7.76  
## 8 Control 94 7.4950 7.94  
## 9 Control 90 7.6150 7.40  
## Leaf\_Length Leaf\_Width  
## 1 2.15 0.98  
## 2 2.26 1.08  
## 3 2.14 1.14  
## 4 2.98 1.19  
## 5 2.82 1.24  
## 6 3.01 1.31  
## 7 1.84 0.78  
## 8 2.17 1.02  
## 9 1.71 0.97

# 

# ANOVA Models

library(dplyr)  
Lights <- as.factor(df$Light\_Spectrum)  
x <- list(  
 df$Germinated\_seeds...,  
 df$Total\_seedling\_Length,   
 df$Total\_Length,   
 df$Leaf\_Length,  
 df$Leaf\_Width  
 )  
  
models <- function(x) {  
 ANOV <- vector("list", length(x))  
 for (i in seq\_along(x)) {  
 ANOV[[i]] <- anova(lm(x[[i]] ~ Lights))  
 }  
 ANOV  
}   
  
results <- models(x)  
names(results) <- c( "Germinated\_seeds...", "Total\_seedling\_Length",   
 "Total\_Length", "Leaf\_Length", "Leaf\_Width")  
results

## $Germinated\_seeds...  
## Analysis of Variance Table  
##   
## Response: x[[i]]  
## Df Sum Sq Mean Sq F value Pr(>F)   
## Lights 2 562.67 281.333 10.729 0.01043 \*  
## Residuals 6 157.33 26.222   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## $Total\_seedling\_Length  
## Analysis of Variance Table  
##   
## Response: x[[i]]  
## Df Sum Sq Mean Sq F value Pr(>F)   
## Lights 2 16.1268 8.0634 387.52 4.533e-07 \*\*\*  
## Residuals 6 0.1248 0.0208   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## $Total\_Length  
## Analysis of Variance Table  
##   
## Response: x[[i]]  
## Df Sum Sq Mean Sq F value Pr(>F)   
## Lights 2 90.518 45.259 1367.8 1.048e-08 \*\*\*  
## Residuals 6 0.199 0.033   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## $Leaf\_Length  
## Analysis of Variance Table  
##   
## Response: x[[i]]  
## Df Sum Sq Mean Sq F value Pr(>F)   
## Lights 2 1.7050 0.85248 35.969 0.0004562 \*\*\*  
## Residuals 6 0.1422 0.02370   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## $Leaf\_Width  
## Analysis of Variance Table  
##   
## Response: x[[i]]  
## Df Sum Sq Mean Sq F value Pr(>F)   
## Lights 2 0.15749 0.078744 9.0165 0.01556 \*  
## Residuals 6 0.05240 0.008733   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

So according to these results we can conclude that outputs by hypothetically as,

Null hypothesis (H0) :- There is same effect of 3 type of light spacrtrum on four different factors.

Alternative hypothesis (H1) :-The effects on four different factors are not all the same. (At least on pair of light spactrum are different).

p\_val <- vector("double", length(results))  
concl <- vector("double", length(results))  
for (i in seq\_along(results)) {  
 p\_val[[i]] <- results[[i]][[5]][1]  
 concl[[i]] <- ifelse(p\_val[[i]] < 0.05, "Significant", "Not\_Significant")  
}  
  
P\_Results <- tribble(  
 ~Factor,  
 "Germinated\_seeds...", "Total\_seedling\_Length",   
 "Total\_Length", "Leaf\_Length", "Leaf\_Width"  
) %>%  
 mutate(P\_Values = p\_val, Conclusions = concl)

(P\_Results)

## # A tibble: 5 x 3  
## Factor P\_Values Conclusions  
## <chr> <dbl> <chr>   
## 1 Germinated\_seeds... 0.0104 Significant  
## 2 Total\_seedling\_Length 0.000000453 Significant  
## 3 Total\_Length 0.0000000105 Significant  
## 4 Leaf\_Length 0.000456 Significant  
## 5 Leaf\_Width 0.0156 Significant

In above graph we can see 3 type of lights spactrum have significantly different on all different factors. *(All p\_values are less than the alpha (0.05) value)*

# Mean Comparisons

comparisions <- function(x) {  
 comp <- vector("list", length(x))  
 for (i in seq\_along(x)) {  
 comp[[i]] <- TukeyHSD(aov(lm(x[[i]] ~ Lights)))  
 }  
 comp  
}   
mean\_com <- comparisions(x)  
names(mean\_com) <- c( "Germinated\_seeds...", "Total\_seedling\_Length",   
 "Total\_Length", "Leaf\_Length", "Leaf\_Width")  
mean\_com

## $Germinated\_seeds...  
## Tukey multiple comparisons of means  
## 95% family-wise confidence level  
##   
## Fit: aov(formula = lm(x[[i]] ~ Lights))  
##   
## $Lights  
## diff lwr upr p adj  
## Control-Blue 10.666667 -2.162053 23.49539 0.0956406  
## Red-Blue 19.333333 6.504614 32.16205 0.0085771  
## Red-Control 8.666667 -4.162053 21.49539 0.1759680  
##   
##   
## $Total\_seedling\_Length  
## Tukey multiple comparisons of means  
## 95% family-wise confidence level  
##   
## Fit: aov(formula = lm(x[[i]] ~ Lights))  
##   
## $Lights  
## diff lwr upr p adj  
## Control-Blue 3.0816667 2.7202901 3.4430432 0.0000007  
## Red-Blue 2.5108333 2.1494568 2.8722099 0.0000017  
## Red-Control -0.5708333 -0.9322099 -0.2094568 0.0068416  
##   
##   
## $Total\_Length  
## Tukey multiple comparisons of means  
## 95% family-wise confidence level  
##   
## Fit: aov(formula = lm(x[[i]] ~ Lights))  
##   
## $Lights  
## diff lwr upr p adj  
## Control-Blue -7.753333 -8.209044 -7.297622 0.0e+00  
## Red-Blue -3.460000 -3.915711 -3.004289 1.1e-06  
## Red-Control 4.293333 3.837622 4.749044 5.0e-07  
##   
##   
## $Leaf\_Length  
## Tukey multiple comparisons of means  
## 95% family-wise confidence level  
##   
## Fit: aov(formula = lm(x[[i]] ~ Lights))  
##   
## $Lights  
## diff lwr upr p adj  
## Control-Blue -1.0300000 -1.4156761 -0.6443239 0.0004367  
## Red-Blue -0.7533333 -1.1390094 -0.3676572 0.0023508  
## Red-Control 0.2766667 -0.1090094 0.6623428 0.1494900  
##   
##   
## $Leaf\_Width  
## Tukey multiple comparisons of means  
## 95% family-wise confidence level  
##   
## Fit: aov(formula = lm(x[[i]] ~ Lights))  
##   
## $Lights  
## diff lwr upr p adj  
## Control-Blue -0.3233333 -0.55745337 -0.08921329 0.0128978  
## Red-Blue -0.1800000 -0.41412004 0.05412004 0.1221952  
## Red-Control 0.1433333 -0.09078671 0.37745337 0.2247583

In here we can conclude what group exactly differ from the control group. That is in hypothetically *(Reject H0 when p\_value is less than the alpha(0.05) value)*

H0 :- mean(i) = mean(control)

H1 :- mean(i) != mean(control ) for some i, (mean(i): mean of each treatment)

According to these results we can see basically,

+Two types of factor levels are significantly different from the control group *("Total\_seedling\_Length", "Total\_Length")* and

+Two types of factor levels are not significantly different from the control group *("Germinated\_seeds(%)", "Leaf\_Width")*.

+In *("Leaf\_Length")* factor Blue light spectrum is signifficantly different from the control group and Red light spectrum is not.

|  |  |  |
| --- | --- | --- |
| Factor | Light spectrum | From Control Group |
| Germinated\_seeds(%) | Red | Sgnificantly Not Different |
| - | Blue | Sgnificantly Not Different |
| Total\_seedling\_Length | Red | Sgnificantly Different |
| - | Blue | Sgnificantly Different |
| Total\_Length | Red | Sgnificantly Different |
| - | Blue | Sgnificantly Different |
| Leaf\_Lengt | Red | Sgnificantly Not Different |
| - | Blue | Sgnificantly Different |
| Leaf\_Width | Red | Sgnificantly Not Different |
| - | Blue | Sgnificantly Not Different |