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BP

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1. Fv/Fm (szalka, concentration, yield) - yield.csv

* Kontola (brak hormonów ) - kontrola
* 2mg/ IAA 1mg/l K - alfa
* 2 mg/l IAA - beta
* 2 mg/l IAA 1 mg/l BAP - gamma
* 0,5 mg/l 2,4d 0,25mg/l bap - delta
* 2mg/l 2,4-D 1 mg/l BAP - epsilon
* 1 mg/l 2,4-D 0,5 mg/l BAP - dzeta

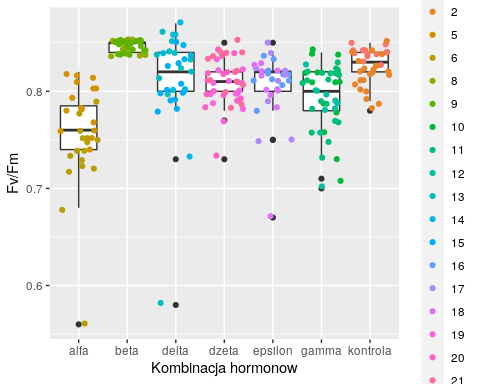
library(ggplot2)  
library(ggpubr)

## Loading required package: magrittr

yield = read.csv("./yield.csv")  
yield$szalka = as.factor(yield$szalka)  
yield$concentration = as.factor(yield$concentration)  
summary(yield)

## szalka concentration yield   
## 2 : 23 alfa :31 Min. :0.5600   
## 8 : 20 beta :38 1st Qu.:0.7900   
## 11 : 20 delta :33 Median :0.8200   
## 9 : 18 dzeta :43 Mean :0.8082   
## 6 : 16 epsilon :31 3rd Qu.:0.8400   
## 5 : 15 gamma :43 Max. :0.8700   
## (Other):143 kontrola:36

ggplot(data = yield) +   
 geom\_boxplot(aes(x=concentration, y=yield)) +  
 geom\_jitter(aes(x=concentration, y=yield, color=szalka)) +  
 xlab("Kombinacja hormonow") +   
 ylab("Fv/Fm")



* porownanie grup zapisane do pliku yield\_results.txt

kruskal.test(yield ~ concentration, data = yield)

##   
## Kruskal-Wallis rank sum test  
##   
## data: yield by concentration  
## Kruskal-Wallis chi-squared = 123.67, df = 6, p-value < 2.2e-16

results = compare\_means(yield ~ concentration, data = yield)  
write.table(results, "yield\_results.txt") # porownanie grup zapisane do pliku yield\_results.txt