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##Factorial Design
rm(list=ls())
Data1=read.csv("3^2 data.csv")
head(Data1)
library(dplyr)
Data_RBD_Con=Data1 %>%
mutate(across(!"Yield", as.factor))
model_CRD=aov(Yield~Nozzle_Type*Speed*Pressure, data = Data_RBD_Con)
summary(model_CRD)
TukeyHSD(model_CRD, "Nozzle_Type")
pairwise.t.test(Data_RBD_Con$Yield, Data_RBD_Con$Nozzle_Type, p.adjust.method =
"bonferroni")
TukeyHSD(model_CRD, "Speed")
pairwise.t.test(Data_RBD_Con$Yield, Data_RBD_Con$Speed, p.adjust.method =
"bonferroni")
TukeyHSD(model_CRD, "Pressure")
pairwise.t.test(Data_RBD_Con$Yield, Data_RBD_Con$Pressure, p.adjust.method =
"bonferroni")
par(mar = c(5, 8, 4, 2)) # Set margins for better label spacing
# Set custom x-axis limits (e.g., from -5 to +5)
plot(TukeyHSD(model_CRD, "Nozzle_Type"), las = 1, col = "pink")
plot(TukeyHSD(model_CRD, "Speed"), las = 1, col = "blue")
plot(TukeyHSD(model_CRD, "Pressure"), las = 1, col = "blue")
mean_data <- Data_RBD_Con %>%
group_by(Speed) %>%
summarise(mean_yield = mean(Yield))
attach(mean_data)
plot(mean_yield,Speed, data = mean_data, pch = 19, col = "blue",
xlab = "Speed", ylab = "Mean Yield", main = "Mean Yield by Speed")
mean_data <- Data_RBD_Con %>%
group_by(Speed) %>%
summarise(mean_yield = mean(Yield))
attach(mean_data)
plot(mean_yield,Speed, data = mean_data, pch = 19, col = "blue",
xlab = "Speed", ylab = "Mean Yield", main = "Mean Yield by Speed")
##Ancova
rm(list=ls())
getwd()
data<-data.frame(read.csv("ancova.csv"))
data
data$Potatos=as.factor(data$Potato)
av1=aov(X~Potatos,data=data)
av2=aov(Yield~Potatos,data=data)
summary(av1)
Txx=anova(av1)["Potatos","Sum Sq"]

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Exx=anova(av1)["Residuals","Sum Sq"]
Gxx=Txx+Exx
Tyy=anova(av2)["Potatos","Sum Sq"]
Eyy=anova(av2)["Residuals","Sum Sq"]
summary(av2)
Gyy=Tyy+Eyy
reg1=lm(Yield~Potatos+X,data=data)
reg2=lm(Yield~X,data=data)
b_hat=coef(reg1)["X"]
b_hat=coef(reg1)[5]# vector
b_2_hat=coef(reg2)[2]
Exy=Exx*b_hat
Gxy=Gxx*b_2_hat
Txy=Gxy-Exy
ancova_model <- aov(Yield ~ Potato + X, data = data)
summary(ancova_model)
# ---- Step 6: Check homogeneity of regression slopes ----
# Interaction term model
ancova_interaction <- aov(Yield ~ Potato * X, data = data)
summary(ancova_interaction)
# Compare models
anova(ancova_model, ancova_interaction)
# ---- Step 7: Diagnostic plots ----
par(mfrow = c(2, 2))
plot(ancova_model)
library(emmeans)
emmeans(ancova_model, "Potato")
##Confounding
data<-read.csv("onnesha_confounding.csv")
data
data_rbd= data %>%
mutate(across(! "Yield",as.factor))
model_rbd=aov(Yield~Block+N*P*K*D,data=data_rbd)
summary(model_rbd)
TukeyHSD(model_rbd,"N")
pairwise.t.test(data_rbd$Yield,data_rbd$N, p.adjust="bonferroni")
TukeyHSD(model_rbd,"P")
pairwise.t.test(data_rbd$Yield,data_rbd$P, p.adjust="bonferroni")
TukeyHSD(model_rbd,"K")
pairwise.t.test(data_rbd$Yield,data_rbd$K, p.adjust="bonferroni")
TukeyHSD(model_rbd,"D")
pairwise.t.test(data_rbd$Yield,data_rbd$D, p.adjust="bonferroni")
plot(TukeyHSD(model_rbd,"N"), las=1, col="blue")
plot(TukeyHSD(model_rbd,"P"), las=1, col="red")
plot(TukeyHSD(model_rbd,"K"), las=1, col="blue")

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plot(TukeyHSD(model_rbd,"D"), las=1, col="blue")
mean_data<-data_rbd %>%
group_by(N) %>%
summarise(mean_yield=mean(Yield))
attach(mean_data)
plot(mean_yield, N, data=mean_data, pch=1, X_lab="Nitrogen", y_lab="Mean Yield")
mean_data<-data_rbd %>%
group_by(P) %>%
summarise(mean_yield=mean(Yield))
attach(mean_data)
plot(mean_yield, P, data=mean_data, pch=1, X_lab="Potash", y_lab="Mean Yield")
##Lab 1st and 2nd class
## CRD
# Clear workspace
rm(list = ls())
# Read data
data <- read.csv("CRD_404.csv")
# View data
head(data)
# Convert treatment variables to factors
data$Treatment_A <- as.factor(data$Treatment_A)
data$Treatment_B <- as.factor(data$Treatment_B)
# Fit two-way ANOVA with interaction
model <- aov(Yield ~ Treatment_A * Treatment_B, data = data)
# Display ANOVA table
summary(model)
# Or if you prefer Type II or Type III SS (like Python's typ=2)
# install.packages("car")
library(car)
# Type II ANOVA (equivalent to typ=2 in statsmodels)
Anova(model, type = 2)
# Type III ANOVA (if your design is unbalanced)
Anova(model, type = 3)
# Optional: check interaction plots
interaction.plot(data$Treatment_A, data$Treatment_B, data$Yield,
main = "Interaction Plot",
xlab = "Treatment A", ylab = "Yield", col = 2:4, lwd = 2)
# Optional: diagnostic plots
par(mfrow = c(2, 2))
plot(model)
## RBD
data<-read.csv("RBD 1.csv")
data
block=as.factor(data$Block)
age_group= as.factor(data$Age_group)

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body_condition=as.factor(data$Body_condition)
protein_level= as.factor(data$Protein)
Model_RBD=aov(Body_weight~ block+age_group*body_condition*protein_level,
data=data)
summary(Model_RBD)
## RBD2
# Clear workspace
rm(list = ls())
# Read the data
data <- read.csv("RBD_404 - Copy.csv")
getwd()
# Convert categorical variables to factors
data$Block <- as.factor(data$Block)
data$Treatment_A <- as.factor(data$Treatment_A)
data$Treatment_B <- as.factor(data$Treatment_B)
# Fit the two-way ANOVA model with blocking and interaction
model <- aov(Yield ~ Block + Treatment_A * Treatment_B, data = data)
# Display ANOVA table (Type I SS by default)
summary(model)
# For Type II (same as typ=2 in Python's statsmodels)
# install.packages("car") # run once if not installed
library(car)
Anova(model, type = 2)
# Optional: Diagnostic plots
par(mfrow = c(2, 2))
plot(model)

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