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library(readxl)
finalexam <- read_excel("Waterfleas.xlsx", sheet = "data", na = "NA")

head(finalexam)
str(finalexam)
colnames(finalexam)

#install packages

install.packages("car")
install.packages("psych")
install.packages("carData")
install.packages("mvtnorm")

library(car)
library(carData)
library(psych)
library(lattice)
library(data.table)
library(plyr)
library(doBy)
library(afex)
library(multcomp)
library(lsmeans)
library(effects)
library(MASS)
library(plot3D)
library(rgl)
library(gmodels)

finalexam$LOG2_Fecundity=log2(finalexam$Fecundity)
finalexam

fit=aov(LOG2_Fecundity~ Hdepth, data=finalexam)
plot(allEffects(mod=fit))
summary(fit)

fit1=aov(LOG2_Fecundity~ Timeshift, data=finalexam)
plot(allEffects(mod=fit1))
summary(fit1)

riazmodel2=lm(LOG2_Fecundity~ Timeshift, data = finalexam)
summary(riazmodel2)

bwplot(LOG2_Fecundity~Hdepth, data=finalexam, fill="blue")
bwplot(LOG2_Fecundity~Timeshift, data=finalexam, fill="blue")
bwplot(LOG2_Fecundity~Timeshift|Hdepth, data=finalexam, fill="blue")

#Main effect ANOVA

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fit2=aov(LOG2_Fecundity~ Hdepth+ Timeshift, data=finalexam)
summary(fit2)

plot(allEffects(mod=fit2))

plot(effect(mod=fit2, term = "Timeshift"))
plot(effect(mod=fit2, term = "Hdepth"))


summary.lm(fit2)

AIC(fit2)
BIC(fit2)


#Full Factorial ANOVA
library(afex); set_treatment_contrasts()

fit3=aov(LOG2_Fecundity~ Hdepth+Timeshift+Hdepth:Timeshift, data=finalexam)
summary(fit3)
plot(allEffects(mod=fit3))
summary.lm(fit3)


AIC(fit)
AIC(fit1)
AIC(fit2)
AIC(fit3)


#Final MODEL *

riazmodell1=lm(LOG2_Fecundity~ Hdepth, data = finalexam)
summary(riazmodell1)


# Model diagnosis, outliers and influential observations for "final"
#mODEL Diagnosis
# variance are homogenous

leveneTest(finalexam$Fecundity, finalexam$Hdepth) # Levevtest for homogeneity

max(by(finalexam$Fecundity, finalexam$Hdepth,sd))^2/
min(by(finalexam$Fecundity, finalexam$Hdepth,sd))^2


residualPlots(riazmodell1)
#linearity cannot be assumed

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spreadLevelPlot(riazmodell)
# the plot suggests that variance increases

ncvTest(riazmodell)
# Based on ncvtest (Chisquare = 9.23212, Df = 1, p = 0.0023781).
# Formal test dont rejects constant variance, based on p value model is
statistically significant

studres.riazmodell=rstudent(riazmodell) # studentized residuals
hist(studres.riazmodell,
     probability=T,
     col="lightgrey",
     xlim=c(-6,6),
     breaks=12,
     main="Distribution of Studentized Residuals",
     xlab="Studentized residuals")
xfit=seq(-6,6,length=100)
yfit=dnorm(xfit) # normal fit
lines(xfit, yfit, col="red",lwd=2)

# The distribution looks very good
# The Shapiro Wilk's W test using linear regression model
shapiro.test(residuals(riazmodell))
# Formal test confirming normality since W (0.95055) > 0.9
# W = 0.95055, p-value = 0.01219

outlierTest(riazmodell) # observation 2 is an outlier
# No Studentized residuals with Bonferroni p < 0.05
# Largest |rstudent|:
# rstudent unadjusted p-value Bonferroni p
#2 -3.779943      0.00035901      0.022977

influenceIndexPlot(riazmodell,vars=c("Studentized","Bonf"))

influenceIndexPlot(riazmodell,vars="Cook") # but there are no influential
observations, so no problems there

# Conclusion

# The model "final" meets most of the assumptions, so we keep this model.

Anova(riazmodell, type = 3)
summary(riazmodell)

```

