Homework3

Ja-Yuan Pendley

2022-03-17

#Importing the pupae data pupae<- read.csv(“pupae.csv”) head(pupae)

#1 # Set colours for plotting The first colour will correspond to the first # level of CO2\_treatment, and so on. palette(c(“blue”, “red”)) plot(Frass ~ PupalWeight, col = CO2\_treatment, data = pupae, pch = 19) legend(“topleft”, levels(pupae$CO2\_treatment), col = palette(), pch = 19)

#2 plot(Frass ~ PupalWeight, col = CO2\_treatment, data = subset(pupae, CO2\_treatment == “280”), pch = 19) # windows() # optional, if not provided will display in Rstudio window plot(Frass ~ PupalWeight, col = CO2\_treatment, data = subset(pupae, CO2\_treatment == “400”), pch = 19)

#3 # windows() # optional, if not provided will display in Rstudio window plot(Frass ~ PupalWeight, col = CO2\_treatment, data = subset(pupae, CO2\_treatment == “400”), pch = 19) par(mfrow = c(1, 2)) plot(Frass ~ PupalWeight, col = CO2\_treatment, data = subset(pupae, T\_treatment == “ambient”), xlim = c(0, 0.5), ylim = c(0, 3.5), pch = 19) plot(Frass ~ PupalWeight, col = CO2\_treatment, data = subset(pupae, T\_treatment == “elevated”), xlim = c(0, 0.5), ylim = c(0, 3.5), pch = 19) par(mfrow = c(1, 1)) palette(c(“red”, “blue”)) plot(Frass ~ PupalWeight, col = CO2\_treatment, pch = c(1, 16)[T\_treatment], data = pupae, xlim = c(0, 0.5), ylim = c(0, 3.5)) # use a different symbol to distinguish from T treatment levels legend(“topleft”, levels(pupae$CO2\_treatment), pch = 3, title = "CO2 treatment", col = palette()) # use a different colour to distinguish from CO2 treatment levels legend("bottomleft", levels(pupae$T\_treatment), pch = c(1, 16), title = “T treatment”, col = “black”)

par(mfrow = c(1, 1)) plot(Frass ~ PupalWeight, col = CO2\_treatment, pch = c(3, 15)[T\_treatment], data = pupae) legend(“topleft”, c(“280ppm - Tamb”, “280ppm - Telev”, “400ppm - Tamb”, “400ppm - Telev”), pch = c(3, 15, 3, 15), col = c(palette()[1], palette()[1], palette()[2], palette()[2]), title = “CO2 - temp”)