#this is in class activity - chisom

install.packages(c("dplyr", "lattice", "psych", "psychTools"))

library(psychTools)

library(psych)

library(dplyr)

library(lattice)

data(sai)

force(sai)

# MERGE DATA INTO CAFFEINE VARIABLE = DRUG AND CONTROL/NORESPONSE GROUPS = PLACEBO

sai <- mutate(sai,grouped\_study = recode(study,"AGES" = "DRUG","CITY"="DRUG","EMIT"="DRUG","SALT"="DRUG","XRAY"="DRUG","Cart" = "PLACEBO","Fast"="PLACEBO","Shed"="PLACEBO", "Raft"="PLACEBO","Shop"="PLACEBO"))

#FILTER DRUG AND PLACEBO VARIABLE INTO NEW VECTOR

sai\_filtered <- filter(sai, grouped\_study %in% c("DRUG", "PLACEBO"))

# figuring out what new function in CRAN to introduce in our code

# Define the function

test\_normality\_by\_group <- function(data, group\_col, variables) {

# Load necessary libraries

library(dplyr)

# Create an empty list to store results

result\_list <- list()

# Loop through each variable in the 'variables' list

for (var in variables) {

result <- data %>%

filter(get(group\_col) == "DRUG") %>%

group\_by(get(group\_col)) %>%

summarise(

shapiro\_p = shapiro.test(get(var))$p.value,

.groups = "drop"

)

# Store results in the list

result\_list[[var]] <- result

}

# Return the results list

return(result\_list)

}

# Example usage:

# test\_normality\_by\_group(sai\_2filtered, "grouped\_study", c("anxious", "another\_variable"))