Chaite

Shapiro-Wilk normality test

data: SRI\_chaite$`moisture%`

W = 0.74853, p-value = 0.0003105

> shapiro.test(SRI\_chaite$`height (cm)`)

Shapiro-Wilk normality test

data: SRI\_chaite$`height (cm)`

W = 0.94529, p-value = 0.356

> shapiro.test(SRI\_chaite$`tiller no`)

Shapiro-Wilk normality test

data: SRI\_chaite$`tiller no`

W = 0.88474, p-value = 0.03139

> shapiro.test(SRI\_chaite$`Days of maturity`)

Shapiro-Wilk normality test

data: SRI\_chaite$`Days of maturity`

W = 0.86569, p-value = 0.01512

> shapiro.test(SRI\_chaite$`Days of harvest`)

Shapiro-Wilk normality test

data: SRI\_chaite$`Days of harvest`

W = 0.5665, p-value = 3.207e-06

> shapiro.test(SRI\_chaite$`Yield (mt/ha)`)

Shapiro-Wilk normality test

data: SRI\_chaite$`Yield (mt/ha)`

W = 0.94583, p-value = 0.3634

> shapiro.test(SRI\_chaite$`Grain panicle`)

Shapiro-Wilk normality test

data: SRI\_chaite$`Grain panicle`

W = 0.45794, p-value = 3.532e-07

> shapiro.test(SRI\_chaite$`1000 grain weight (gm)`)

Shapiro-Wilk normality test

data: SRI\_chaite$`1000 grain weight (gm)`

W = 0.8008, p-value = 0.001559

SRI1

|  |
| --- |
| hapiro.test(SRI1$paniclelength)  Shapiro-Wilk normality test  data: SRI1$paniclelength  W = 0.82963, p-value = 0.0009365  > shapiro.test(SRI1$filledgrain)  Shapiro-Wilk normality test  data: SRI1$filledgrain  W = 0.93289, p-value = 0.1132  > shapiro.test(SRI1$unfilledgrain)  Shapiro-Wilk normality test  data: SRI1$unfilledgrain  W = 0.88535, p-value = 0.01067  > shapiro.test(SRI1$tillerpersqm)  Shapiro-Wilk normality test  data: SRI1$tillerpersqm  W = 0.94179, p-value = 0.1788  > shapiro.test(SRI1$`1000 grain weight (gm)`)  Shapiro-Wilk normality test  data: SRI1$`1000 grain weight (gm)`  W = 0.81122, p-value = 0.000452  > shapiro.test(SRI1$`Grain Yield (mt/ha)`)  Shapiro-Wilk normality test  data: SRI1$`Grain Yield (mt/ha)`  W = 0.92209, p-value = 0.06499 |
|  |
| |  | | --- | | > | |

setwd("C:/Users/vijay/Desktop/SRI trichoderma")

SRI\_chaite <- read\_excel("C:/Users/vijay/Desktop/SRI trichoderma/SRI chaite.xlsx")

detach(SRI1)

attach(SRI\_chaite)

SRI\_chaite <- read\_csv("submitted/PEERJ/SRI\_chaite.csv")

attach(SRI\_chaite)

names(SRI\_chaite)

as.factor(Rep)

as.factor(`Main plot`)-> Seedtreat

as.factor(`Sub plot`)->Method

shapiro.test(SRI\_chaite$`moisture%`)

shapiro.test(SRI\_chaite$`height (cm)`)

shapiro.test(SRI\_chaite$`tiller no`)

shapiro.test(SRI\_chaite$`Days of maturity`)

shapiro.test(SRI\_chaite$`Days of harvest`)

shapiro.test(SRI\_chaite$`Yield (mt/ha)`)

shapiro.test(SRI\_chaite$`Grain panicle`)

shapiro.test(SRI\_chaite$`1000 grain weight (gm)`)