<https://datatofish.com/create-dataframe-in-r/>

\_\_This did not work for me, file name not recognized\_\_

Filename is “C:/Users/ihear/OneDrive/Desktop/Lab work/R Scripts/Enzyme Synergy Results for R.csv”

You can create a dataframe by importing the data directly into R, then assigning it to a data frame (if it is a .csv file)

\*You have to include the .csv extension when importing csv files to R

\* A double backslash is used to avoid errors within R

mydata < - read.csv(“C:\\Users\\ihear\\OneDrive\\Desktop\\Lab work\\R Scripts\\Enzyme Synergy Results for R.csv”)

df <- data.frame(mydata)

print (df)

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**Help with TidyVerse**

<https://ggplot2.tidyverse.org/>

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library(ggplot2)

library(tidyverse)

**First, you need to format your data frame from wide format to long format. The following is an example using tidyverse to format the data frame.**

**Make a data.frame first (ended up not doing this part, transformed Excel file to data.frame)**

Enzyme <- c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15)

Cornstarch <- c(1.9, 11, 0, 8.2 , 7.8, 37, 34, 36, 41, 13, 100, 30, 42, 42, 62)

PotatoStarch <- c(4.5, 3.6, 0, 0, 2.2, 7.5, 6.3, 1, 3.8, 3.1, 5, 9.8, 6.6, 2.3, 3.4)

HighMaize <- c(22, 12, 8, 33, 31, 26, 64, 25, 63, 24, 59, 83, 67, 69, 94)

Versafibe <- c(8.7, 20, 1.8, 8.7, 16, 36, 16, 29, 39, 30, 47, 41, 35, 30, 29)

Df3 <- data.frame(Cornstarch, PotatoStarch, HighMaize, Versafibe)

Print (df)

library(tidyverse)

dt2 <- Df3 %>%

<https://stackoverflow.com/questions/47733031/how-to-plot-dataframe-in-r-as-a-heatmap-grid>

rownames\_to\_column() %>%

gather(colname, value, -rowname)

head(dt2)

# rowname colname value

# 1 tension tension NA

# 2 cluster tension 1.943113e+08

# 3 migraineNoAura tension 8.462798e+00

# 4 migraineAura tension 2.833333e+00

# 5 tension cluster 1.500000e+00

# 6 cluster cluster NA

**Now we are ready to use the ggplot2 to plot the heatmap using geom\_tile.**

ggplot(dt2, aes(x = rowname, y = colname, fill = value)) +

geom\_tile(plum)

**%>% is called the forward pipe operator in R. It provides a mechanism for chaining commands with a new forward-pipe operator, %>%. This operator will forward a value, or the result of an expression, into the next function call/expression. It is defined by the package magrittr (CRAN) and is heavily used by dplyr (CRAN)**

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**COLOR How to look at available colors R knows**

grDevices::colors()

<https://ggplot2.tidyverse.org/reference/aes_colour_fill_alpha.html>

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**Changing rownames and heatmap design in R: https://www.geeksforgeeks.org/how-to-change-row-names-of-dataframe-in-r/**

row.names(Df3) <- c("CB1", "CB2", "CB3", "CB4", "CB1+CB2", "CB1+CB3", "CB1+CB4", "CB2+CB3", "CB2+CB4", "CB3+CB4", "CB1+CB2+CB3", "CB1+CB2+CB4", "CB1+CB3+CB4", "CB2+CB3+CB4", "CB1+CB2+CB3+CB4")

dt2 <- Df3 %>%

+ rownames\_to\_column() %>%

+ gather(colname, value, -rowname)

>

<https://r-charts.com/correlation/heat-map-ggplot2/>

**Formatting heat maps**

**Customizing the border**

ggplot(dt4, aes(x = rowname, y = colname, fill = value)) +

geom\_tile(color = "white",

lwd = 1.5,

linetype = 1) +

coord\_fixed()

**Adding the values**

ggplot(dt5, aes(x = rowname, y = colname, fill = value)) +

geom\_tile(color = "black") +

geom\_text(aes(label = value), color = "white", size = 4) +

coord\_fixed()

**Changing the color and border**

ggplot(dt5, aes(x = rowname, y = colname, fill = value)) +

geom\_tile(color = "black", lwd = 1.0, linetype = 1) +

scale\_fill\_gradient(low = "white", high = "plum4") +

coord\_fixed()

**Change border, add the values, change the color**

ggplot(dt5, aes(x = rowname, y = colname, fill = value)) +

geom\_tile(color = "black", lwd = 1.0, linetype = 1) +

scale\_fill\_gradient(low = "white", high = "plum4") +

geom\_text(aes(label = value), color = "black", size = 4) +

coord\_fixed()

**Change width and height and title of the legend**

guides(fill = guide\_colourbar(barwidth = 0.5,

barheight = 20))

guides(fill = guide\_colourbar(title = "Title"))

Changing the order of rownames in the heatmap

a\_lot = df[df$value == 'A lot',]

df$Item = factor(df$Item, levels = a\_lot$Item[order(a\_lot$percent)])

Could just change the names of the rows?

row.names(Df6) <- c("1", "2", "3", "4", "5", "6", "7", "8", "9", "91", "92", "93", "94", "95", "96")

Script to make plot w text:

Dt8 <- Df6 %>%

+ rownames\_to\_column() %>%

+ gather(colname, value, -rowname)

ggplot(Dt9, aes(x = rowname, y = colname, fill = value)) +

geom\_tile(color = "black", lwd = 1.0, linetype = 1) +

scale\_fill\_gradient(low = "white", high = "plum4") +

geom\_text(aes(label = value), color = "black", size = 4) +

coord\_fixed()

Script without text:

ggplot(Dt9, aes(x = rowname, y = colname, fill = value)) +

geom\_tile(color = "black", lwd = 1.0, linetype = 1) +

scale\_fill\_gradient(low = "white", high = "plum4") +

guides(fill = guide\_colourbar(barwidth = 0.7,

barheight = 29))

coord\_fixed()

Enzyme <- c(“CB1”, “CB2”, “CB3”, CB4”, “CB1 + CB2”, “CB1 + CB3”, “CB1 + CB4”, “CB2 + CB3”, “CB2 + CB4”, “CB3 + CB4”, “CB1 + CB2 + CB3”, “CB1 + CB2 + CB4”, “CB1 + CB3 + CB4”, “CB2 + CB3 + CB4”, “CB1 + CB2 + CB3 + CB4”)

Cornstarch <- c(1.9 +- 0.26, 11 +- 0.29, 0, 8.2 +- 0.45, 7.8 +- 1.6, 37 +- 5.4, 34 +- 2.5, 36 +- 3.2, 41 +- 4.3, 13 +- 2.4, 100 +- 7.6, 30 +- 1.8, 42 +- 3.2, 42 +- 1, 62 +- 9.7)

PotatoStarch < - c(4.5 +- 0.78, 3.6 +- 1, 0, 0, 2.2 +- 0.34, 7.5 +- 0.39, 6.3 +- 1, 1 +- 0.22, 3.8 +- 2.1, 3.1 +- 1.2, 5 +- 0.81, 9.8 +- 3.8, 6.6 +- 1.6, 2.32 +- 0.97, 3.4 +- 0.59)

HighMaize <- c(22 +- 0.95, 12 +- 0.46, 8 +- 0.59, 33 +- 1.9, 31 +- 0.82, 26 +- 2.1, 64 +- 2.4, 25 +- 1.2, 63 +- 3.4, 24 +- 2.6, 59 +- 5.3, 83 +- 6, 67 +- 9.2, 69 +- 2.4,

94 +- 9.1)

Versafibe <- c(8.7 +- 1.6, 20 +- 0.61, 1.8 +- 0.22, 8.7 +- 0.67, 16 +- 1.4, 36 +- 3.5, 16 +- 4.2, 29 +- 4.3, 39 +- 8.2, 30 +- 3.5, 47 +- 0.67, 41 +- 2.2, 35 +- 3.9, 30 +- 4.2, 29 +- 7.7)