Class 05: Data Visualization with GGPLOT

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Week 4 Data Visualization Lab

Install the package ggplot2

install.packages("ggplot2")

Anytime I want to use this package I need to load it

library(ggplot2)

View(cars)

A quick base R plot - this is not a ggplot2

plot(cars)

Our first ggplot

We need data + aes + geoms

ggplot(data=cars) + aes(x=speed, y=dist) + geom_point()

p <- ggplot(data=cars) + aes(x=speed, y=dist) + geom_point()

Add a line geom with geom_line()

p + geom_line()

Add a trend line close to the data

p + geom_smooth()

p + geom_smooth(method= "lm")

#————#

Read in our drug expression data

url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url) head(genes)

Q. How many genes are in this dataset

nrow(genes)

ncol(genes)

Q. how many 'up' regulated genes

table(genes$State)

Q. What fraction of genes is up-regulated

round((table(genes$State) / nrow(genes)) * 100, 2)

Let's make a first plot attempt

g <- ggplot(data=genes) + aes(x=Condition1, y=Condition2, col=State) + geom_point()

g

Add some color

g + scale_color_manual(values=c("blue", "gray", "red")) + labs(title = "Gene Expression changes", x ="Control (no drug)") + theme_bw()