class05

Pham Vo

2/7/2022

View(cars)

install.packages(“ggplot2”) library(ggplot2) p <- ggplot(cars) + aes(x=speed, y=dist) + geom\_point()

p

p + geom\_smooth() p + geom\_smooth(method=“lm”)

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

#Look at first 6 lines head(genes)

View(genes)

#Q. how many genes are there in the list? nrow(genes)

#Q. how many genes are upregulated? table(genes$State)

#Q. What fraction of genes are up, down etc. round((table(genes$State)/nrow(genes))\*100, 2)

#Q. Generate a publication figure

g <- ggplot(genes) + aes(x=Condition1, y=Condition2, col=State) + geom\_point()

g

#Add more custom layers

g + theme\_bw() + scale\_color\_manual(values=c(“blue”, “gray”, “red”)) + labs(x=“Control(no drug)”, y=“Drug treated”, title=“Gene expression changes example plot”)