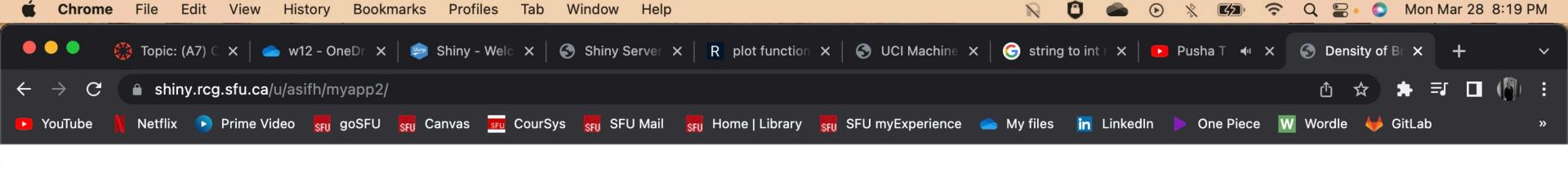
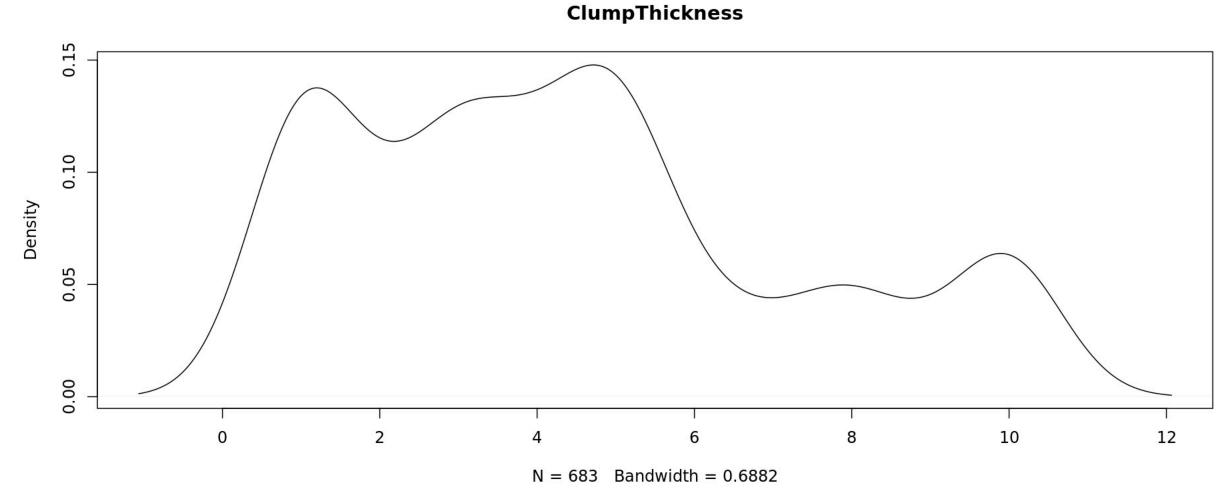


```
Go to file/function
                                                - Addins →
                                                                                                                                                                                         Project: (None)
asn07.R × ui.R × server.R × breast-cancer-wisconsin.data × breast-cancer-wisconsin.names × ui.R × server.R ×
1 library(stringr)
  2
      dat <- read.table("breast-cancer-wisconsin.data")</pre>
     ClumpThickness <- vector(mode="numeric")</pre>
      UniformityOfCellSize <- vector(mode="numeric")</pre>
      UniformityOfCellShape <- vector(mode="numeric")</pre>
      MarginalAdhesion <- vector(mode="numeric")</pre>
      SingleEpithelialCellSize <- vector(mode="numeric")</pre>
 10
 11 * for(i in 1:length(dat[[1]])) {
  12
        vec <- strtoi(str_extract_all(dat[[1]][i], "\\d+\\b")[[1]])</pre>
 13
        # dupm rows that contain missing values
       if(length(vec) == 11) {
 14 -
 15
          # use 5 variables
  16
          ClumpThickness[length(ClumpThickness)+1] <- vec[2]</pre>
 17
          UniformityOfCellSize[length(UniformityOfCellSize)+1] <- vec[3]</pre>
 18
          UniformityOfCellShape[length(UniformityOfCellShape)+1] <- vec[4]</pre>
 19
          MarginalAdhesion [length (MarginalAdhesion)+1] <- vec [5]
  20
          SingleEpithelialCellSize[length(SingleEpithelialCellSize)+1] <- vec[6]</pre>
  21 -
 22 - }
  23
  24
      df <- data.frame("ClumpThickness"=ClumpThickness,</pre>
                       "UniformityOfCellSize"=UniformityOfCellSize,
 25
                       "UniformityOfCellShape"=UniformityOfCellShape,
  26
                       "Marginal Adhesion" = Marginal Adhesion,
  27
  28
                        "SingleEpithelialCellSize"=SingleEpithelialCellSize)
  29
  30 - server <- function(input, output, session) {
        # Combine the selected variables into a new data frame
  31
 32 -
        selectedData <- reactive({</pre>
  33
          df[, input$xcol]
  34 -
        3)
  35
  36 -
        output$plot1 <- renderPlot({</pre>
 37
          palette(c("#E41A1C", "#377EB8", "#4DAF4A", "#984EA3",
  38
            "#FF7F00", "#FFFF33", "#A65628", "#F781BF", "#999999"))
  39
  40
          par(mar = c(5.1, 4.1, 4.1, 1))
  41
  42
          plot(density(selectedData()),
  43
               main=input$xcol)
 44 -
       })
  45 ^ }
 45:2
      (Top Level) $
                                                                                                                                                                                               R Script $
                                                                                                                                                                                                 Console
```









































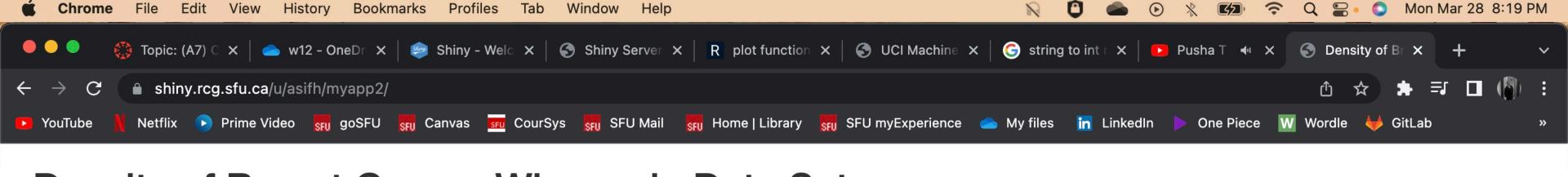














UniformityOfCellSize 0.15 0.05 2 10 6 12 N = 683 Bandwidth = 0.7283

































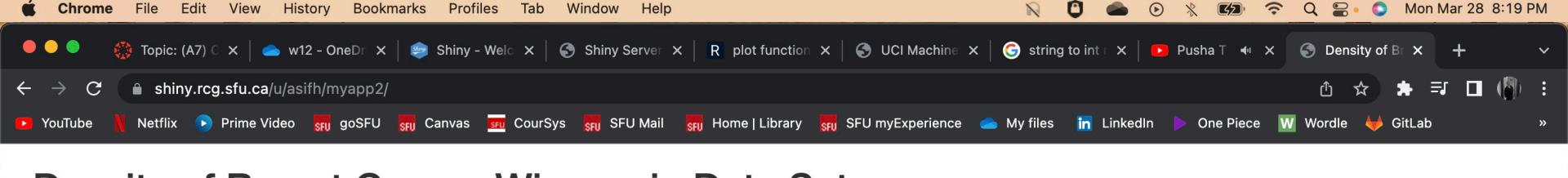














UniformityOfCellShape Density 0.15 0.05 0.00 2 10 6 12 N = 683 Bandwidth = 0.7283



































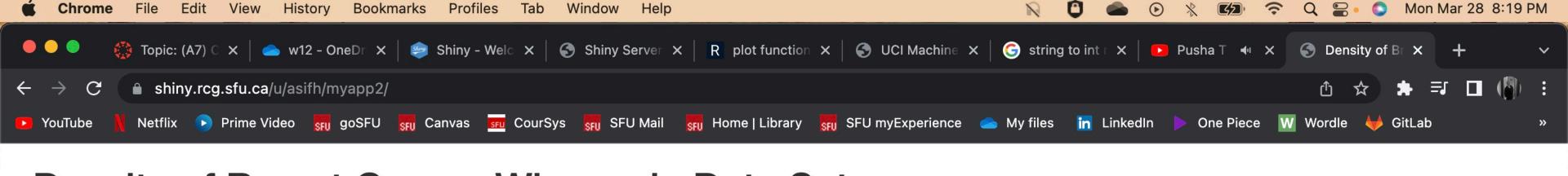


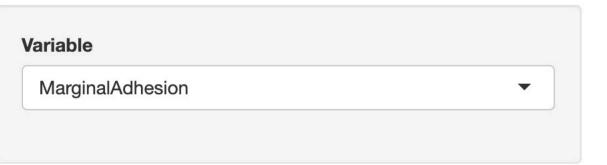












Density 0.1 0.0 2 10 12 6 N = 683 Bandwidth = 0.5462

MarginalAdhesion



































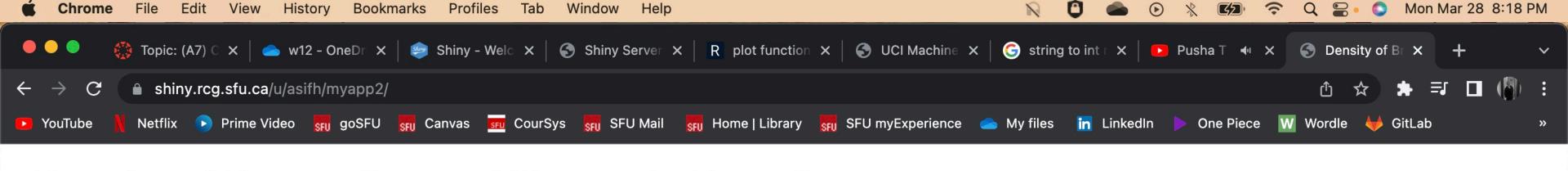














SingleEpithelialCellSize Density 0.0 2 10 N = 683 Bandwidth = 0.3642

