732A98: Visualization - Cheatbook

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```
# Loading required R packages
library(ggplot2)
library(plotly)
```

```
##
## Attaching package: 'plotly'
```

```
## The following object is masked from 'package:ggplot2':
##
##     last_plot
```

```
## The following object is masked from 'package:stats':
##
##     filter
```

```
## The following object is masked from 'package:graphics':
##
##     layout
```

```
library(shiny)
library(gridExtra)
library(xlsx)
library(MASS)
```

```
##
## Attaching package: 'MASS'
```

```
## The following object is masked from 'package:plotly':
##
##     select
```

Reading Data

Data Mugging

Quantile Computation

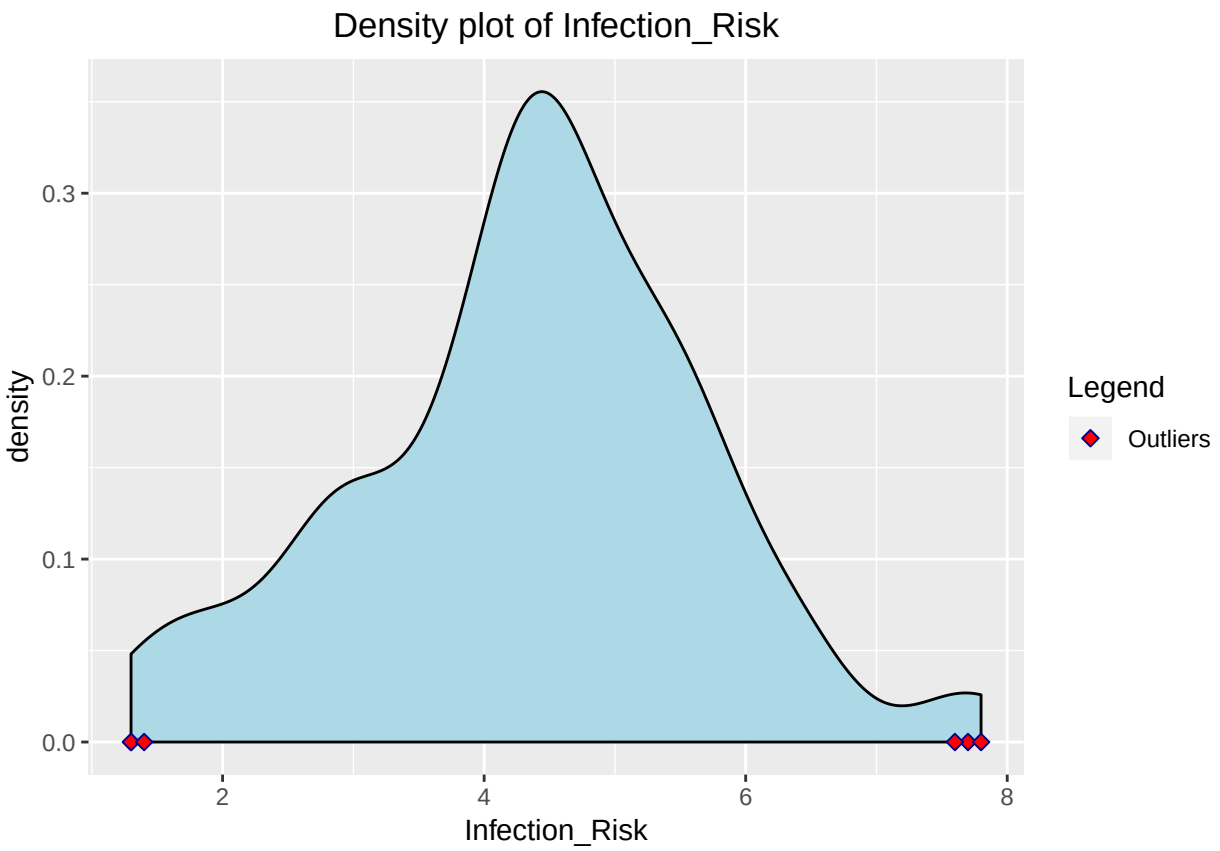
```
get_outliers <- function(x){
  quantile_values = quantile(x, probs = c(0.25, 0.75))
  q1 = quantile_values["25%"]
  q3 = quantile_values["75%"]

  return(c(which((x > (q3+1.5*(q3-q1)))), which(x < (q1-1.5*(q3-q1)))))
}
```

Single Plots

Density Plot

Density Plot with Outlier Highlight using GGplot2

```
density_plot_infection_risk = ggplot(senic_data) +
  ggtitle("Density plot of Infection_Risk")  +
  geom_density(aes(x=Infection_Risk), fill = "lightblue") +
  geom_point(data=senic_data[get_outliers(senic_data$Infection_Risk),],
             aes(x=Infection_Risk, y=0, colour="Outliers"),
             shape=23, size=2, fill="red") +
  scale_color_manual(values = c("darkblue","black")) +
  labs(colour="Legend") +
  theme(plot.title = element_text(hjust = 0.5), legend.position = "right")

density_plot_infection_risk
```



Density Plot with Outlier Highlight using Plotly (converting from ggplot2)

```
x <- ggplotly(p=density_plot_infection_risk)

x
```

Histogram Plot

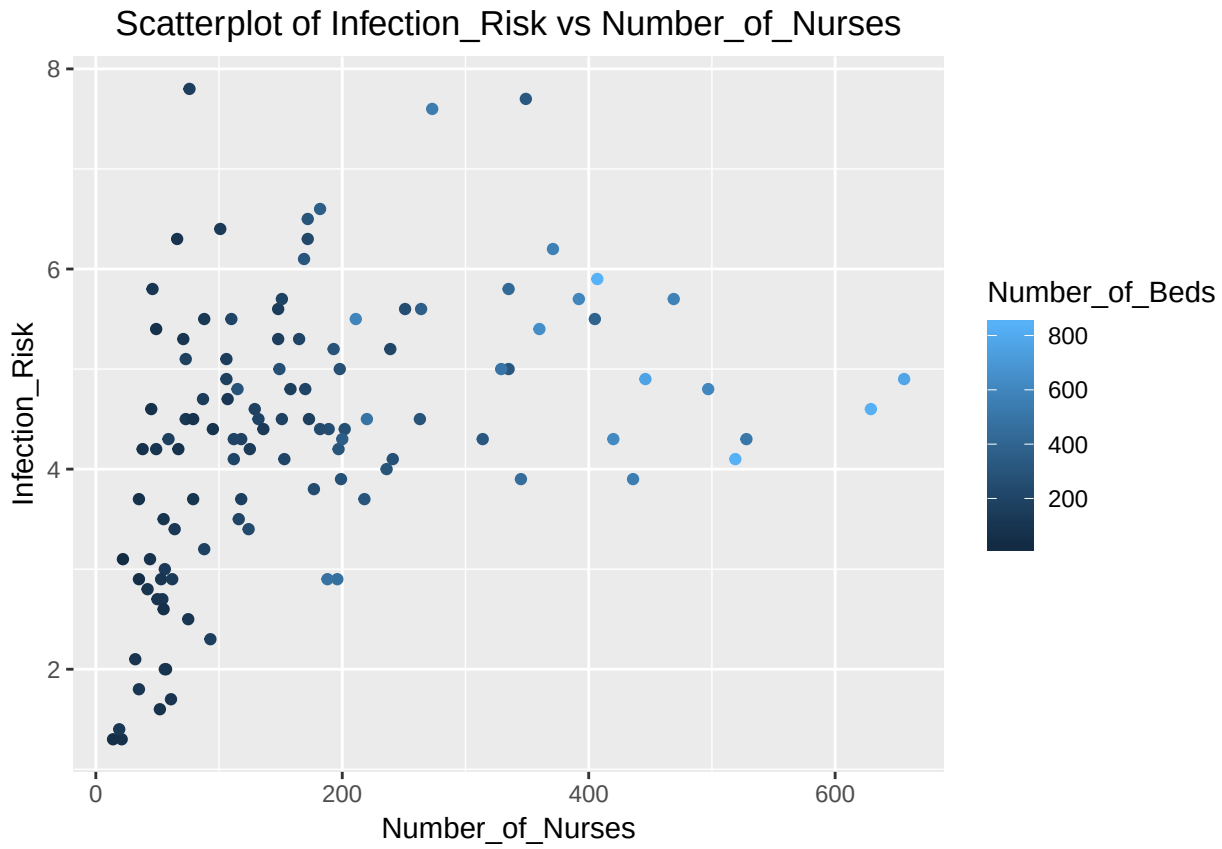
Histogram plot with Outlier Highlight using Plotly

```
outliers = senic_data[get_outliers(senic_data$Infection_Risk),c("Infection_Risk")]
senic_data$zero = 0

p <- plot_ly(senic_data, x=~Infection_Risk) %>%
  add_histogram(name="Histogram count") %>%
  filter(is.element(Infection_Risk, outliers)) %>%
  add_markers(x=~Infection_Risk,y=~zero, name="Outliers",
              marker=list(symbol="diamond", size=10, line = list(color="black", width=1))) %>%
  layout(title="Histogram of Infection_Risk", yaxis=list(title="Count"))

p
```

Scatter Plot

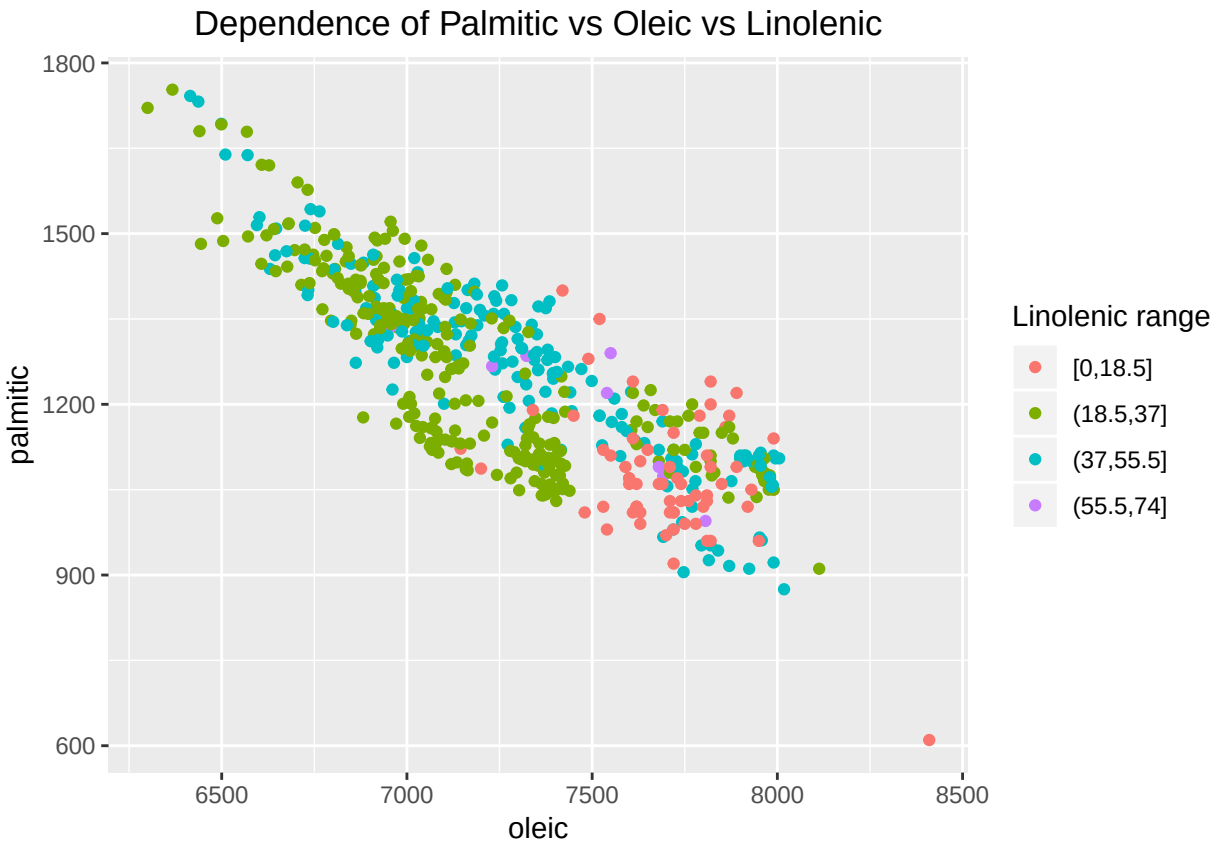
Simple scatter plot with colour

```
ggplot(senic_data) + geom_point(aes(x=Number_of_Nurses, y=Infection_Risk, color=Number_of_Beds)) +
  ggtitle("Scatterplot of Infection_Risk vs Number_of_Nurses") +
  theme(plot.title = element_text(hjust = 0.5))
```



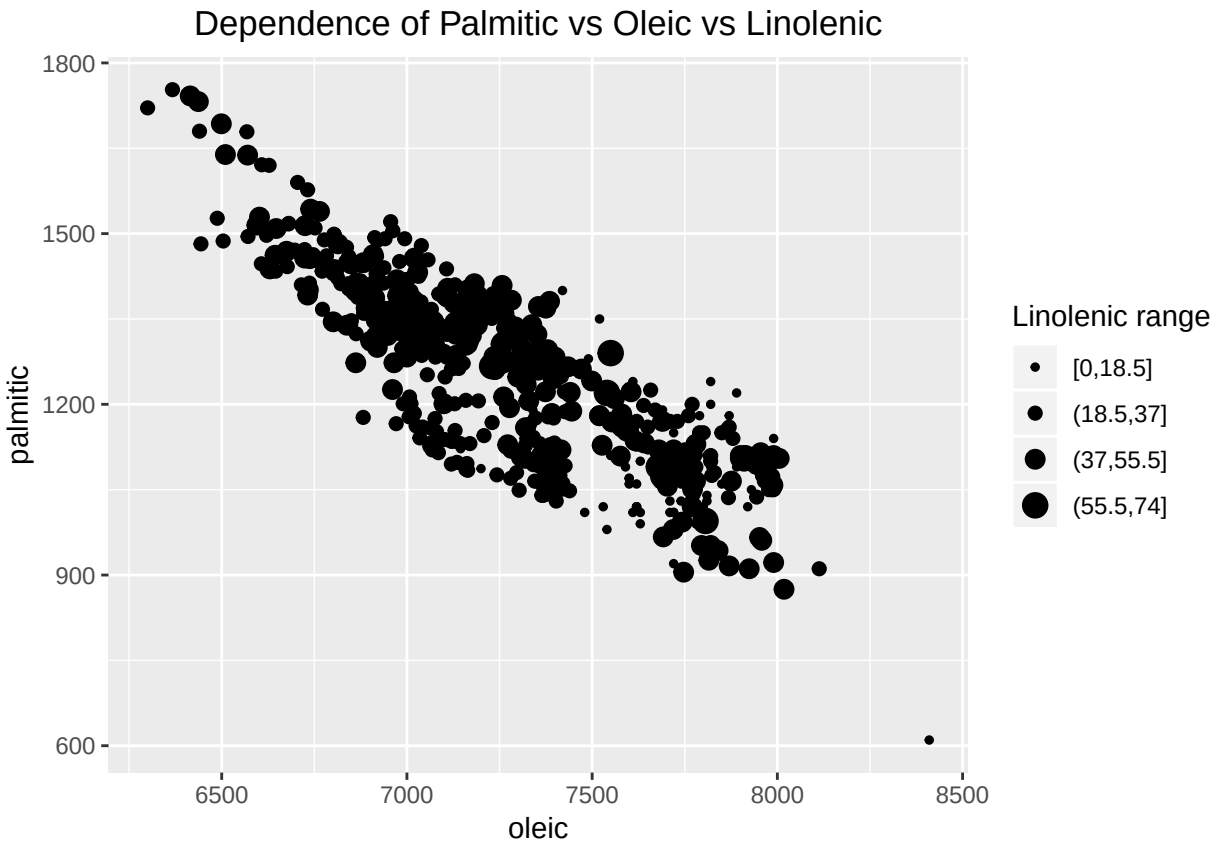
Scatter Plot with Discreetization (split a variable into classes)

```
ggplot(olive_data) +
  geom_point(aes(x = oleic, y = palmitic,
                 color=cut_interval(olive_data$linolenic, n = 4))) +
  ggtitle("Dependence of Palmitic vs Oleic vs Linolenic") +
  theme(plot.title = element_text(hjust = 0.5)) +
  labs(color = 'Linolenic range')
```



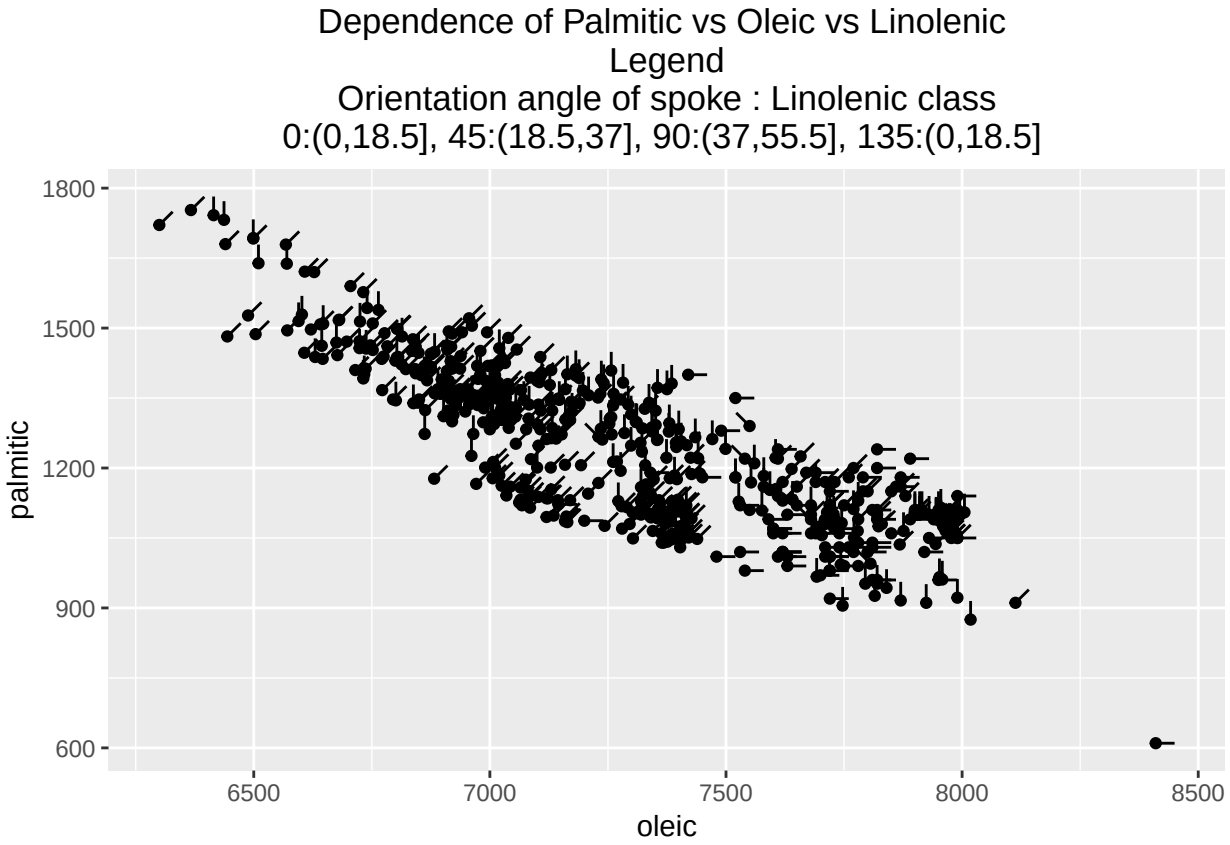
Scatter plot size varied

```
ggplot(olive_data) + geom_point(aes(x = oleic, y = palmitic, size = cut_interval(linolenic, n = 4))) +
  ggtitle("Dependence of Palmitic vs Oleic vs Linolenic") +
  theme(plot.title = element_text(hjust = 0.5)) +
  scale_size_manual(name = "Linolenic range", values = c(1, 2, 3, 4))
```



Scatter plot angle varied

```
# Pre-processing - Setting angle values based on category
olive_data$linolenic_class <- cut_interval(olive_data$linolenic, n = 4)
levels(olive_data$linolenic_class) <- (0:3) * (pi/4)
olive_data$linolenic_class <- as.numeric(as.character(olive_data$linolenic_class))

ggplot(olive_data, aes(x=oleic, y=palmitic)) + geom_point() +
  geom_spoke(aes(angle = olive_data$linolenic_class), radius=40) +
  ggtitle("Dependence of Palmitic vs Oleic vs Linolenic
Legend
Orientation angle of spoke : Linolenic class
0:(0,18.5], 45:(18.5,37], 90:(37,55.5], 135:(0,18.5] ") +
  theme(plot.title = element_text(hjust = 0.5))
```



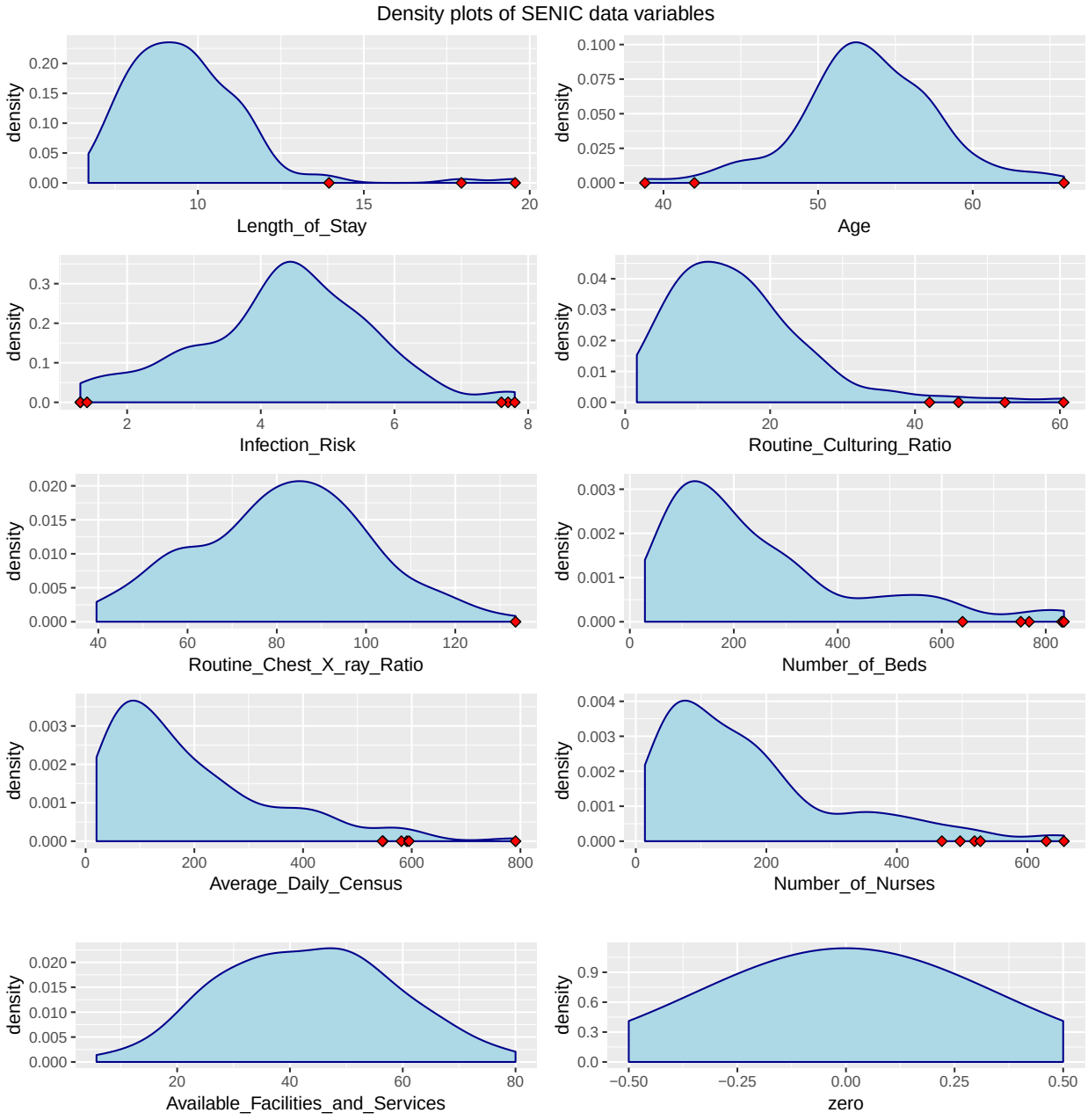
Multiple Plots

Density Plots

Density Plot with Outlier Highlight

```
plot_density_with_outliers <- function(var_data, col_name){
  p <- NULL
  df_data = setNames(data.frame(var_data),col_name)
  if(length(get_outliers(df_data[[col_name]])) > 0){
    p <- ggplot(df_data) +
      geom_density(aes_string(x=col_name), fill = "lightblue", color = "darkblue") +
      geom_point(data=df_data[get_outliers(df_data[[col_name]]),,drop=FALSE],
                 aes_string(x=col_name), y=0, shape=23, size=2, colour="black", fill="red")
  }
  else{
    p <- ggplot(df_data) +
      ggtitle(paste("")) +
      theme(plot.title = element_text(hjust = 0.5)) +
      geom_density(aes_string(x=col_name), fill = "lightblue", color = "darkblue")
  }

  return(p)
```

```
}

categorical_columns = c("Medical_School_Affiliation", "Region")
ID_columns = c("Identification_Number")
quantitative_columns = setdiff(colnames(senic_data), c(categorical_columns, ID_columns))

plot_list = mapply(plot_density_with_outliers, senic_data[, quantitative_columns],
                   colnames(senic_data[, quantitative_columns]), SIMPLIFY = FALSE)
plot_matrix <- arrangeGrob(grobs = plot_list, ncol = 2)
grid.arrange(plot_matrix, respect=TRUE, top="Density plots of SENIC data variables")
```



Shiny

```
#UI component
ui <- fluidPage(
  sliderInput(inputId="bw_value", label="Choose bandwidth size", value=4.5, min=0.1, max=80),
  checkboxGroupInput("selected_variables", "Variables to show: ", quantitative_columns, inline=TRUE),
  plotOutput("densPlot", height = "650px")
```

```
)

plot_density_with_outliers_shiny <- function(df_data, col_name, bw){
  p <- NULL
  if(length(get_outliers(senic_data[[col_name]])) > 0){
    p <- ggplot(df_data) +
      ggtitle(paste("Density plot of ", col_name)) +
      theme(plot.title = element_text(hjust = 0.5)) +
      geom_density(aes_string(x=col_name), fill = "lightblue", color = "darkblue", bw=bw) +
      geom_point(data=df_data[get_outliers(df_data[[col_name]]),],
                 aes_string(x=col_name, y=0), shape=23, size=2, colour="black", fill="red")
  }
  else{
    p <- ggplot(df_data) +
      ggtitle(paste("Density plot of ", col_name)) +
      theme(plot.title = element_text(hjust = 0.5)) +
      geom_density(aes_string(x=col_name), fill = "lightblue", color = "darkblue", bw=bw)
  }

  return(p)
}


server <- function(input, output) {

  output$densPlot <- renderPlot({

    selected_columns = input$selected_variables
    plot_list = vector("list", length(selected_columns))

    if(length(selected_columns) > 0){
      for(i in 1:length(selected_columns)){
        plot_list[[i]] = plot_density_with_outliers_shiny(senic_data, selected_columns[i],
                                                          bw = input$bw_value)
      }
      plot_matrix <- arrangeGrob(grobs = plot_list, ncol = 2)
      grid.arrange(plot_matrix)
    }

  })
}

shinyApp(ui = ui, server = server, options = list(width="800px", height="900px"))
```

Shiny applications not supported in static R Markdown documents