Data Management & Descriptive Statitics SAP

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```
## Import Data
data <- read.table("C:/UHasselt/Courses/Project Learning from Data/Project Codes/final data.txt",
                   header = TRUE, sep = ";", dec = "\t")
```

```
## Percentage missing values
(colMeans(is.na(data)))*100
```

```
## Region   Crop  Lutum   Sand   Silt     pH      C Cstock  Years
##   1.25   0.00   1.25   1.25   1.25   1.25   0.00   0.00   0.00
```

```
## Data preparing
data$Lutum <- as.numeric(as.character(data$Lutum))
data$Sand <- as.numeric(as.character(data$Sand))
data$Silt <- as.numeric(as.character(data$Silt))
data$pH <- as.numeric(as.character(data$pH))
data$C <- as.numeric(as.character(data$C))
data$Cstock <- as.numeric(as.character(data$Cstock))

clean_data <- data[-c(33, 36, 66),]
summary(clean_data)
```

```
##     Region              Crop               Lutum             Sand
##  Length:397         Length:397         Min.   :0.0400   Min.   :0.1700
##  Class :character   Class :character   1st Qu.:0.1700   1st Qu.:0.2400
##  Mode  :character   Mode  :character   Median :0.2200   Median :0.2750
##                                        Mean   :0.2207   Mean   :0.3882
##                                        3rd Qu.:0.2700   3rd Qu.:0.5900
##                                        Max.   :0.4200   Max.   :0.7300
##                                        NA's   :5        NA's   :5
##       Silt              pH              C               Cstock
##  Min.   :0.1400   Min.   :4.64   Min.   :  1.550   Min.   :    73.42
##  1st Qu.:0.2300   1st Qu.:5.21   1st Qu.:  1.820   1st Qu.:    89.41
##  Median :0.4400   Median :5.83   Median :  2.010   Median :    97.38
##  Mean   :0.3909   Mean   :5.65   Mean   :  3.806   Mean   :   612.56
##  3rd Qu.:0.5100   3rd Qu.:6.04   3rd Qu.:  2.280   3rd Qu.:   104.71
##  Max.   :0.6900   Max.   :6.68   Max.   :252.000   Max.   :108650.00
##  NA's   :5        NA's   :5
##      Years
##  Min.   :10.00
##  1st Qu.:14.00
##  Median :17.00
```

```
##  Mean   :17.34
##  3rd Qu.:21.00
##  Max.   :25.00
##
```

```
clean_data <- na.omit(clean_data)
summary(clean_data)
```

```
##     Region              Crop              Lutum             Sand
##  Length:382         Length:382         Min.   :0.0400   Min.   :0.1700
##  Class :character   Class :character   1st Qu.:0.1700   1st Qu.:0.2400
##  Mode  :character   Mode  :character   Median :0.2200   Median :0.2800
##                                        Mean   :0.2204   Mean   :0.3899
##                                        3rd Qu.:0.2700   3rd Qu.:0.5900
##                                        Max.   :0.4200   Max.   :0.7300
##       Silt              pH               C               Cstock
##  Min.   :0.1400   Min.   :4.640   Min.   :  1.550   Min.   :    73.42
##  1st Qu.:0.2300   1st Qu.:5.210   1st Qu.:  1.820   1st Qu.:    88.90
##  Median :0.4400   Median :5.810   Median :  2.010   Median :    97.34
##  Mean   :0.3895   Mean   :5.644   Mean   :  3.874   Mean   :   632.57
##  3rd Qu.:0.5100   3rd Qu.:6.040   3rd Qu.:  2.250   3rd Qu.:   104.64
##  Max.   :0.6900   Max.   :6.680   Max.   :252.000   Max.   :108650.00
##      Years
##  Min.   :10.00
##  1st Qu.:14.00
##  Median :17.00
##  Mean   :17.32
##  3rd Qu.:21.00
##  Max.   :25.00
```

```
removed_indices <- which(!complete.cases(data))
removed_indices
```

```
##  [1]  93  96 145 162 166 185 242 250 251 258 270 346 354 358 385
```

```
rows_greater_than_3 <- which(clean_data$C > 3)
rows_greater_than_3
```

```
## [1]  12 128 254
```

```
clean_data <- clean_data[-c(12, 128, 254),]
clean_data <- clean_data[clean_data$C <= 3, ]
summary(clean_data)
```

```
##     Region              Crop              Lutum             Sand
##  Length:379         Length:379         Min.   :0.0400   Min.   :0.1700
##  Class :character   Class :character   1st Qu.:0.1700   1st Qu.:0.2400
##  Mode  :character   Mode  :character   Median :0.2200   Median :0.2800
##                                        Mean   :0.2198   Mean   :0.3902
##                                        3rd Qu.:0.2700   3rd Qu.:0.5900
##                                        Max.   :0.4200   Max.   :0.7300
```

```
##       Silt              pH              C             Cstock
##  Min.   :0.1400   Min.   :4.640   Min.   :1.550   Min.   :    73.42
##  1st Qu.:0.2300   1st Qu.:5.210   1st Qu.:1.820   1st Qu.:    89.03
##  Median :0.4400   Median :5.810   Median :2.010   Median :    97.31
##  Mean   :0.3898   Mean   :5.644   Mean   :2.074   Mean   :   636.72
##  3rd Qu.:0.5100   3rd Qu.:6.040   3rd Qu.:2.245   3rd Qu.:   104.48
##  Max.   :0.6900   Max.   :6.680   Max.   :2.970   Max.   :108650.00
##      Years
##  Min.   :10.00
##  1st Qu.:14.00
##  Median :17.00
##  Mean   :17.35
##  3rd Qu.:21.00
##  Max.   :25.00
```

```
rows_greater_than_130 <- which(clean_data$Cstock > 130)
rows_greater_than_130
```

```
## [1] 149 349
```

```
clean_data <- clean_data[-c(149, 349),]

summary(data)
```

```
##     Region              Crop              Lutum             Sand
##  Length:400         Length:400         Min.   :0.0400   Min.   :0.1700
##  Class :character   Class :character   1st Qu.:0.1700   1st Qu.:0.2400
##  Mode  :character   Mode  :character   Median :0.2200   Median :0.2800
##                                        Mean   :0.2202   Mean   :0.3881
##                                        3rd Qu.:0.2700   3rd Qu.:0.5900
##                                        Max.   :0.4200   Max.   :0.7300
##                                        NA's   :5        NA's   :5
##       Silt              pH              C               Cstock
##  Min.   :0.1400   Min.   :4.64   Min.   :  1.550   Min.   :    73.42
##  1st Qu.:0.2300   1st Qu.:5.21   1st Qu.:  1.820   1st Qu.:    89.38
##  Median :0.4400   Median :5.83   Median :  2.010   Median :    97.35
##  Mean   :0.3915   Mean   :5.65   Mean   :  3.792   Mean   :   608.68
##  3rd Qu.:0.5100   3rd Qu.:6.04   3rd Qu.:  2.265   3rd Qu.:   104.71
##  Max.   :0.6900   Max.   :6.68   Max.   :252.000   Max.   :108650.00
##  NA's   :5        NA's   :5
##      Years
##  Min.   :10.00
##  1st Qu.:14.00
##  Median :17.00
##  Mean   :17.32
##  3rd Qu.:21.00
##  Max.   :25.00
##
```

```
summary(clean_data)
```

```
##     Region              Crop              Lutum             Sand
```

```
##  Length:377         Length:377         Min.   :0.0400   Min.   :0.170
##  Class :character   Class :character   1st Qu.:0.1700   1st Qu.:0.240
##  Mode  :character   Mode  :character   Median :0.2200   Median :0.280
##                                        Mean   :0.2194   Mean   :0.391
##                                        3rd Qu.:0.2700   3rd Qu.:0.590
##                                        Max.   :0.4200   Max.   :0.730
##       Silt              pH              C             Cstock
##  Min.   :0.1400   Min.   :4.640   Min.   :1.550   Min.   : 73.42
##  1st Qu.:0.2300   1st Qu.:5.210   1st Qu.:1.820   1st Qu.: 88.77
##  Median :0.4400   Median :5.800   Median :2.010   Median : 97.29
##  Mean   :0.3894   Mean   :5.642   Mean   :2.075   Mean   : 97.97
##  3rd Qu.:0.5100   3rd Qu.:6.040   3rd Qu.:2.250   3rd Qu.:104.37
##  Max.   :0.6900   Max.   :6.680   Max.   :2.970   Max.   :126.85
##      Years
##  Min.   :10.00
##  1st Qu.:14.00
##  Median :17.00
##  Mean   :17.34
##  3rd Qu.:21.00
##  Max.   :25.00
```

```
clean_data$Region <- as.factor(clean_data$Region)
count(clean_data,Region)
```

```
##       Region   n
## 1    Keempen   1
## 2    Kempeen   1
## 3     Kempen 149
## 4 Leemstreek 224
## 5  Leemstrek   1
## 6  Lemstreek   1
```

```
clean_data <- clean_data %>%
  mutate(Region = case_when(
    Region == "Kempeen" ~ "Kempen",
    Region == "Keempen" ~ "Kempen",
    Region == "Leemstrek" ~ "Leemstreek",
    Region == "Lemstreek" ~ "Leemstreek",
    TRUE ~ Region
  ))

sort(clean_data$C)
```

```
##   [1] 1.55 1.58 1.60 1.63 1.64 1.64 1.64 1.64 1.65 1.66 1.66 1.67 1.67 1.67 1.68
##  [16] 1.69 1.69 1.69 1.70 1.70 1.70 1.70 1.70 1.71 1.71 1.71 1.71 1.71 1.71 1.71
##  [31] 1.72 1.72 1.72 1.72 1.72 1.72 1.73 1.73 1.73 1.73 1.73 1.73 1.73 1.74 1.74
##  [46] 1.74 1.75 1.75 1.75 1.75 1.75 1.75 1.76 1.76 1.76 1.76 1.76 1.76 1.76 1.76
##  [61] 1.76 1.76 1.76 1.76 1.77 1.77 1.77 1.77 1.77 1.77 1.77 1.77 1.77 1.78 1.78
##  [76] 1.78 1.78 1.79 1.79 1.79 1.79 1.79 1.79 1.79 1.79 1.79 1.80 1.80 1.80 1.81
##  [91] 1.81 1.81 1.81 1.82 1.82 1.82 1.82 1.82 1.82 1.82 1.82 1.82 1.83 1.83 1.83
## [106] 1.83 1.83 1.83 1.84 1.84 1.84 1.84 1.84 1.85 1.85 1.85 1.85 1.85 1.85 1.85
## [121] 1.85 1.85 1.85 1.86 1.86 1.86 1.86 1.86 1.86 1.86 1.87 1.87 1.87 1.87 1.87
## [136] 1.87 1.88 1.88 1.88 1.88 1.88 1.89 1.89 1.89 1.89 1.89 1.90 1.90 1.90 1.91
```

```
## [151] 1.91 1.91 1.91 1.91 1.92 1.93 1.93 1.93 1.94 1.94 1.94 1.95 1.95 1.95 1.95
## [166] 1.96 1.96 1.96 1.96 1.97 1.97 1.97 1.97 1.97 1.98 1.98 1.98 1.99 1.99 1.99
## [181] 1.99 2.00 2.00 2.00 2.00 2.00 2.00 2.01 2.01 2.01 2.02 2.02 2.02 2.02 2.02
## [196] 2.03 2.03 2.03 2.03 2.03 2.03 2.03 2.03 2.03 2.04 2.04 2.05 2.05 2.05 2.05
## [211] 2.06 2.06 2.06 2.06 2.07 2.07 2.07 2.07 2.08 2.08 2.08 2.08 2.09 2.09 2.09
## [226] 2.09 2.09 2.10 2.10 2.10 2.10 2.10 2.11 2.11 2.11 2.11 2.11 2.12 2.13 2.13
## [241] 2.13 2.13 2.13 2.13 2.13 2.14 2.14 2.14 2.14 2.14 2.14 2.15 2.15 2.15 2.15
## [256] 2.16 2.16 2.16 2.17 2.17 2.17 2.17 2.17 2.18 2.18 2.18 2.18 2.18 2.19 2.19
## [271] 2.19 2.19 2.19 2.19 2.20 2.20 2.20 2.20 2.21 2.21 2.21 2.24 2.25 2.25 2.25
## [286] 2.28 2.28 2.28 2.29 2.30 2.31 2.31 2.31 2.32 2.34 2.34 2.35 2.35 2.35 2.36
## [301] 2.36 2.36 2.38 2.38 2.38 2.39 2.39 2.41 2.41 2.41 2.42 2.42 2.42 2.43 2.43
## [316] 2.44 2.44 2.44 2.44 2.45 2.45 2.46 2.46 2.46 2.46 2.49 2.49 2.51 2.51 2.52
## [331] 2.52 2.53 2.54 2.54 2.54 2.55 2.55 2.56 2.57 2.57 2.57 2.57 2.58 2.58 2.58
## [346] 2.58 2.64 2.66 2.66 2.70 2.72 2.72 2.72 2.72 2.75 2.75 2.76 2.76 2.77 2.77
## [361] 2.77 2.81 2.81 2.82 2.83 2.83 2.83 2.83 2.84 2.86 2.87 2.87 2.87 2.87 2.88
## [376] 2.94 2.97
```

```
sort(clean_data$Cstock)
```

```
##   [1]  73.42  75.92  76.28  76.40  77.14  78.11  78.44  78.66  78.70  78.95
##  [11]  79.08  79.10  79.22  79.80  80.43  80.47  80.53  80.92  81.12  81.20
##  [21]  81.33  81.46  81.71  81.72  81.81  81.92  82.13  82.30  82.39  82.39
##  [31]  82.61  82.63  82.63  82.65  82.81  82.91  82.92  83.15  83.17  83.34
##  [41]  83.44  83.52  83.58  83.60  83.64  83.77  83.95  84.01  84.15  84.20
##  [51]  84.23  84.44  84.44  84.46  84.85  84.86  84.95  84.95  84.96  84.99
##  [61]  85.32  85.66  85.80  85.81  86.01  86.11  86.13  86.24  86.28  86.29
##  [71]  86.36  86.39  86.39  86.49  86.64  86.66  86.72  86.76  86.88  87.03
##  [81]  87.30  87.31  87.42  87.47  87.62  87.82  88.27  88.33  88.40  88.42
##  [91]  88.48  88.54  88.65  88.71  88.77  89.29  89.29  89.41  89.41  89.48
## [101]  89.48  89.57  89.57  89.88  89.92  90.10  90.68  90.81  90.81  90.97
## [111]  91.01  91.31  91.34  91.59  91.60  91.66  91.73  91.84  92.02  92.04
## [121]  92.06  92.43  92.58  92.58  92.77  93.04  93.11  93.27  93.36  93.54
## [131]  93.58  93.61  93.88  94.01  94.22  94.30  94.34  94.39  94.53  94.58
## [141]  94.68  94.72  94.81  94.84  94.90  94.93  94.98  95.01  95.05  95.06
## [151]  95.08  95.13  95.26  95.26  95.33  95.37  95.37  95.51  95.56  95.58
## [161]  95.64  96.05  96.06  96.08  96.10  96.13  96.16  96.16  96.20  96.24
## [171]  96.28  96.34  96.34  96.37  96.39  96.49  96.51  96.61  96.64  96.65
## [181]  96.82  97.09  97.15  97.15  97.21  97.22  97.24  97.25  97.29  97.31
## [191]  97.38  97.40  97.50  97.52  97.59  97.66  97.71  97.74  97.76  97.81
## [201]  97.85  97.86  98.01  98.05  98.06  98.07  98.07  98.24  98.31  98.45
## [211]  98.66  98.74  98.84  98.90  99.11  99.20  99.36  99.39  99.53  99.59
## [221]  99.62  99.64  99.67  99.68  99.80  99.98  99.98 100.11 100.12 100.15
## [231] 100.20 100.29 100.42 100.45 100.45 100.46 100.68 100.70 100.83 100.85
## [241] 100.96 101.02 101.14 101.27 101.31 101.38 101.46 101.52 101.65 101.65
## [251] 101.79 101.88 101.88 101.93 102.02 102.04 102.13 102.18 102.19 102.26
## [261] 102.34 102.47 102.47 102.56 102.76 102.84 102.85 103.18 103.26 103.38
## [271] 103.46 103.67 103.69 103.80 103.80 103.83 104.06 104.07 104.08 104.13
## [281] 104.18 104.28 104.37 104.46 104.50 104.68 104.71 104.80 104.83 104.97
## [291] 105.03 105.08 105.19 105.20 105.58 105.64 105.85 105.89 105.97 106.00
## [301] 106.09 106.20 106.81 106.84 106.88 106.89 106.93 107.12 107.19 107.25
## [311] 107.26 107.57 107.62 107.71 107.89 108.14 108.71 109.17 109.26 109.57
## [321] 109.63 109.82 109.99 110.38 110.66 111.06 111.75 111.91 112.14 112.85
## [331] 112.98 115.76 116.03 116.25 116.42 116.80 117.26 117.29 117.58 117.79
## [341] 117.80 118.06 118.08 118.21 118.28 118.32 118.35 118.38 118.42 118.42
```

```
## [351] 118.53 118.60 119.11 119.21 119.58 119.90 119.99 120.01 120.78 120.94
## [361] 121.01 121.06 121.08 121.28 121.58 121.58 121.66 121.78 122.01 122.46
## [371] 122.99 123.40 123.92 124.32 124.95 126.52 126.85
```

```
summary(clean_data$Cstock)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   73.42   88.77   97.29   97.97  104.37  126.85
```

```
summary(clean_data$C)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.550   1.820   2.010   2.075   2.250   2.970
```

```
clean_data$Crop <- as.factor(clean_data$Crop)
count(clean_data,Crop)
```

```
##   Crop   n
## 1   GM  98
## 2   PG  82
## 3   SM 115
## 4 SMGR  82
```

```
class(clean_data$Region)
```

```
## [1] "character"
```

```
clean_data$Region <- as.factor(clean_data$Region)
clean_data$Crop <- as.factor(clean_data$Crop)
```

```
#Export clean data

write.csv(clean_data, "C:/UHasselt/Courses/Project Learning from Data/Project Codes/Clean_data.txt",
          row.names = FALSE)
list.files("C:/UHasselt/Courses/Project Learning from Data/Project Codes/")
```

```
##  [1] "000010.png"       "000011.png"       "000012.png"       "000013.png"
##  [5] "000014.png"       "boxplot.png"      "Casual Graph.png" "Clean_data.txt"
##  [9] "final data.txt"   "Project.rmd"
```

```
# Step 4: Exploratory Data Analysis (EDA)
# Summary statistics by Region and Crop
clean_data %>%
  group_by(Region, Crop) %>%
  summarize(mean_Cstock = mean(Cstock, na.rm = TRUE),
            sd_Cstock = sd(Cstock, na.rm = TRUE),
            n = n())
```

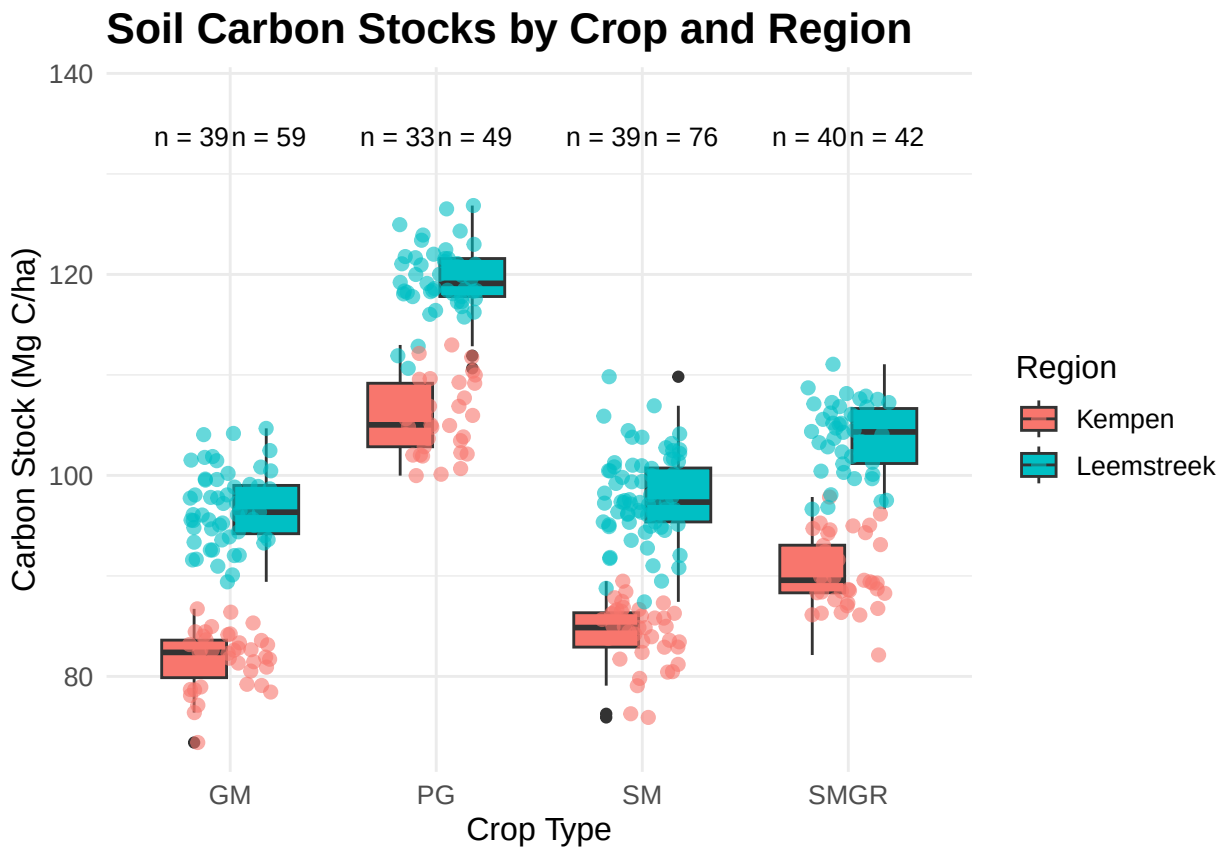
```
## `summarise()` has grouped output by 'Region'. You can override using the
## `.groups` argument.
```

```
## # A tibble: 8 x 5
## # Groups:   Region [2]
##   Region     Crop  mean_Cstock sd_Cstock     n
##   <fct>      <fct>       <dbl>     <dbl> <int>
## 1 Kempen     GM           81.8      2.84    39
## 2 Kempen     PG          106.       3.61    33
## 3 Kempen     SM           84.2      3.07    39
## 4 Kempen     SMGR         90.3      3.41    40
## 5 Leemstreek GM           96.8      3.59    59
## 6 Leemstreek PG          119.       3.29    49
## 7 Leemstreek SM           97.9      4.18    76
## 8 Leemstreek SMGR        104.       3.59    42
```

```r
# Boxplot of Soil Carbon Stocks by Crop and Region

counts <- clean_data %>%
  group_by(Crop, Region) %>%
  summarise(count = n())
```

```
## `summarise()` has grouped output by 'Crop'. You can override using the
## `.groups` argument.
```

```r
ggplot(clean_data, aes(x = Crop, y = Cstock, fill = Region)) +
  geom_boxplot(width = 0.7) +
  geom_jitter(aes(color = Region), width = 0.2, size = 2, alpha = 0.6) +
    geom_text(data = counts, aes(x = Crop, y = max(clean_data$Cstock) + 5, label = paste("n =", count)),
              position = position_dodge(width = 0.75),
              size = 3.5, # Adjusted text size
              vjust = -0.5) + # Adjust vertical position of labels, color = "black") +
  theme_minimal() +
  theme(
    plot.title = element_text(size = 16, face = "bold"),
    axis.title = element_text(size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(size = 12),
    legend.text = element_text(size = 10)
  ) +
  labs(title = "Soil Carbon Stocks by Crop and Region",
       x = "Crop Type",
       y = "Carbon Stock (Mg C/ha)") +
  # Add some padding to the top of the plot for labels
  scale_y_continuous(expand = expansion(mult = c(0.05, 0.15)))
```

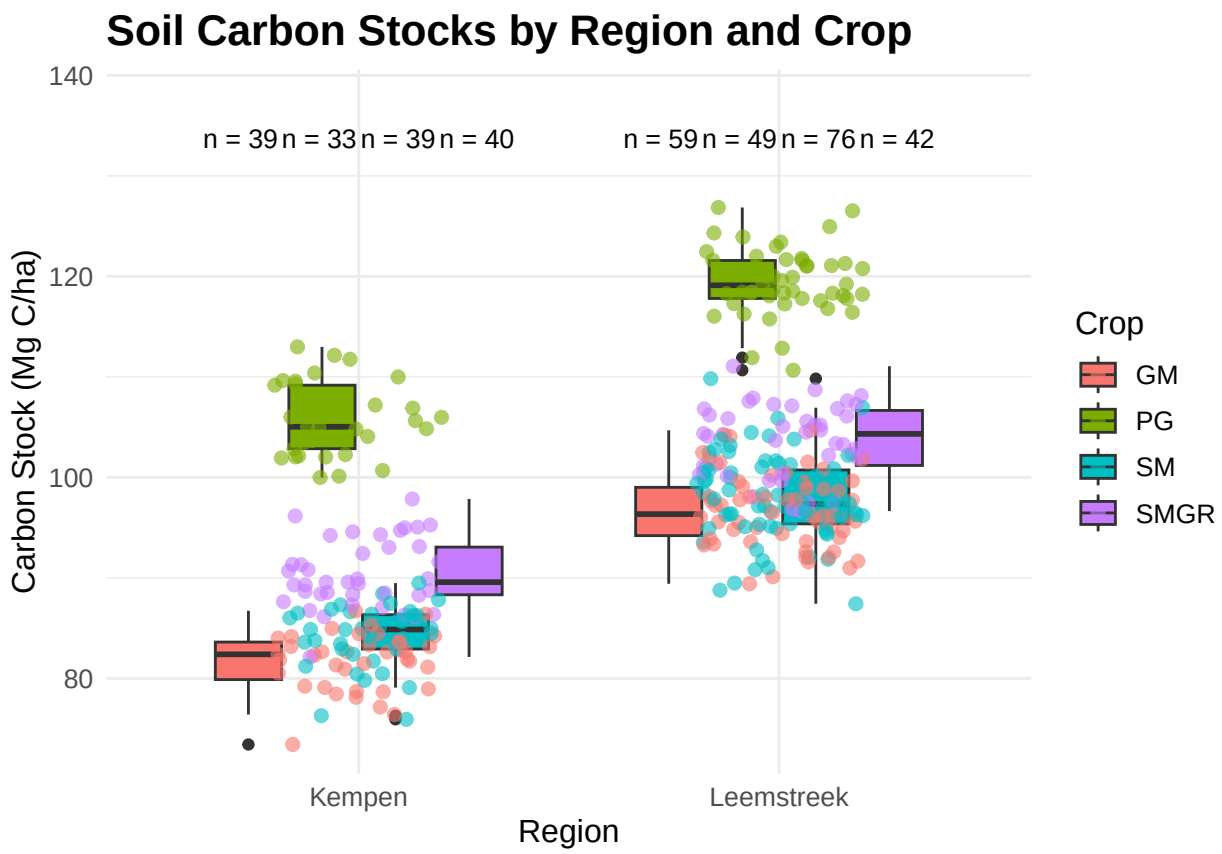



```
# Boxplot of Soil Carbon Stocks by Region and Crop
counts <- clean_data %>%
  group_by(Region, Crop) %>%
  summarise(count = n())
```

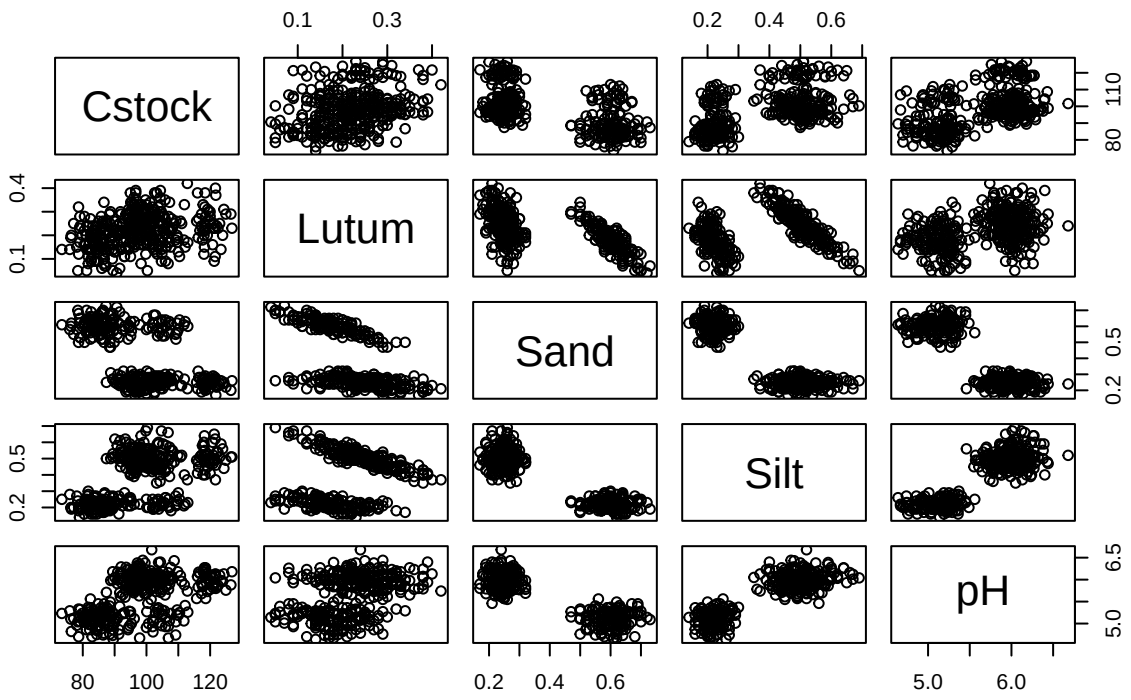
```
## `summarise()` has grouped output by 'Region'. You can override using the
## `.groups` argument.
```

```
ggplot(clean_data, aes(x = Region, y = Cstock, fill = Crop)) +
  geom_boxplot(width = 0.7) +
  geom_jitter(aes(color = Crop), width = 0.2, size = 2, alpha = 0.6) +
  geom_text(
    data = counts,
    aes(x = Region, y = max(clean_data$Cstock) + 5, label = paste("n =", count)),
    position = position_dodge(width = 0.75),
    size = 3.5, # Adjusted text size
    vjust = -0.5
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(size = 16, face = "bold"),
    axis.title = element_text(size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(size = 12),
    legend.text = element_text(size = 10)
```

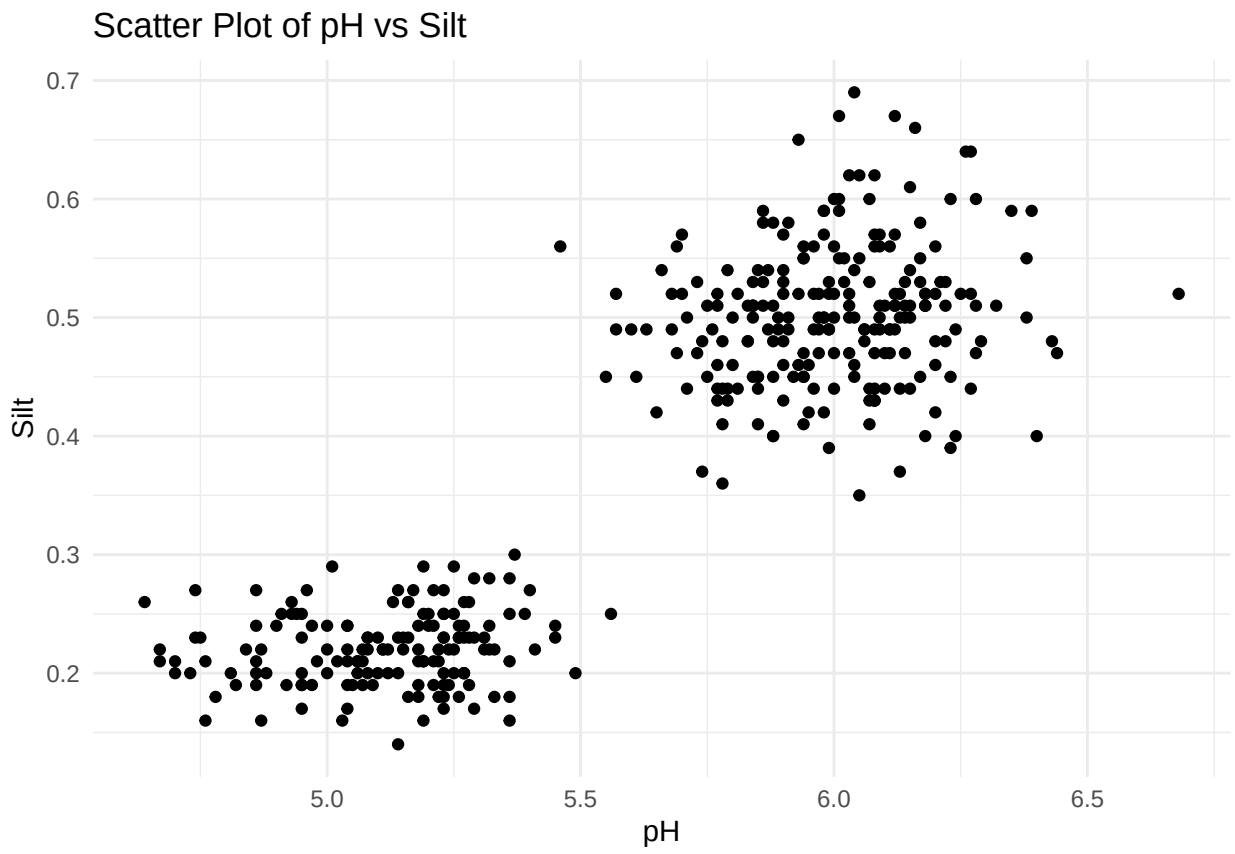
```
  ) +
  labs(
    title = "Soil Carbon Stocks by Region and Crop",
    x = "Region",
    y = "Carbon Stock (Mg C/ha)"
  ) +
  # Add some padding to the top of the plot for labels
  scale_y_continuous(expand = expansion(mult = c(0.05, 0.15)))
```



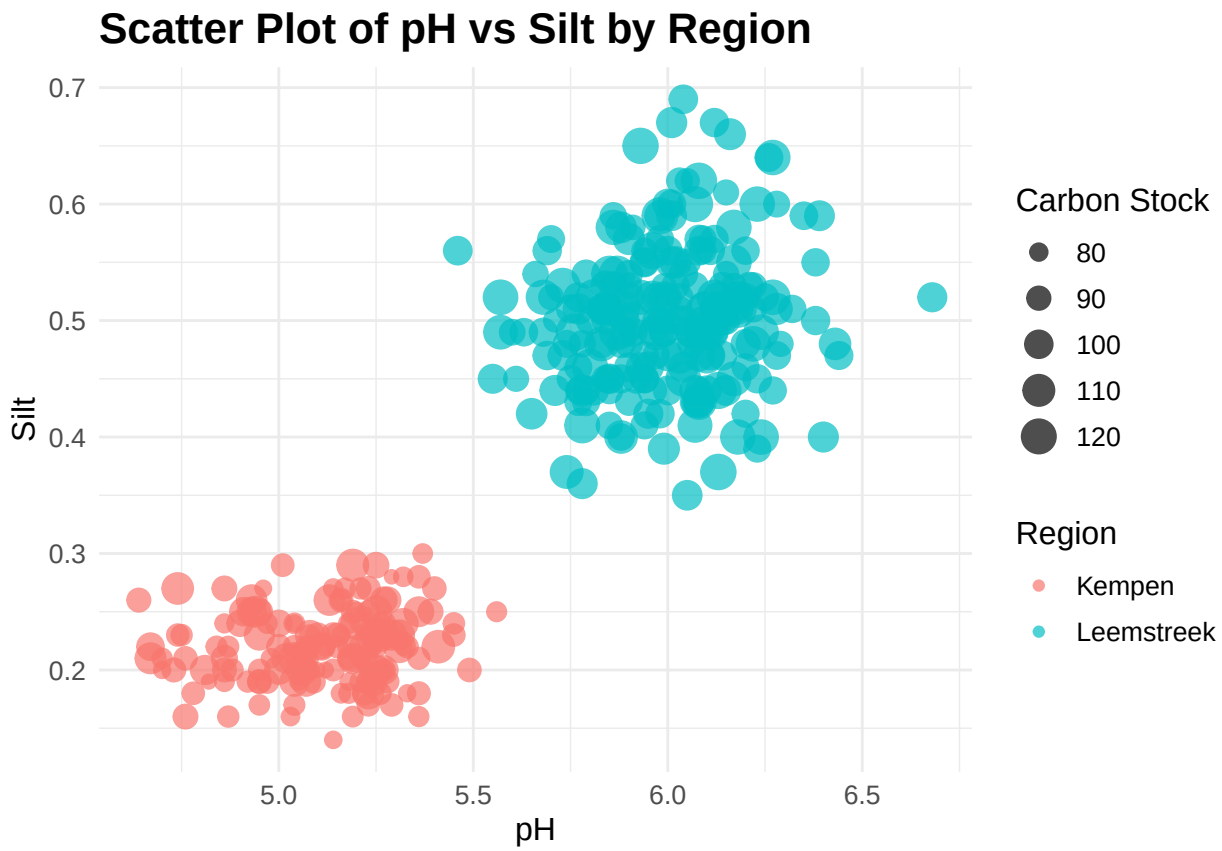

```
# Scatter plot matrix for continuous variables
pairs(clean_data[, c("Cstock", "Lutum", "Sand", "Silt", "pH")],
      main = "Scatterplot Matrix")
```




```r
ggplot(clean_data, aes(x = pH, y = Silt)) +
  geom_point() +
  labs(title = "Scatter Plot of pH vs Silt",
       x = "pH",
       y = "Silt") +
  theme_minimal()
```



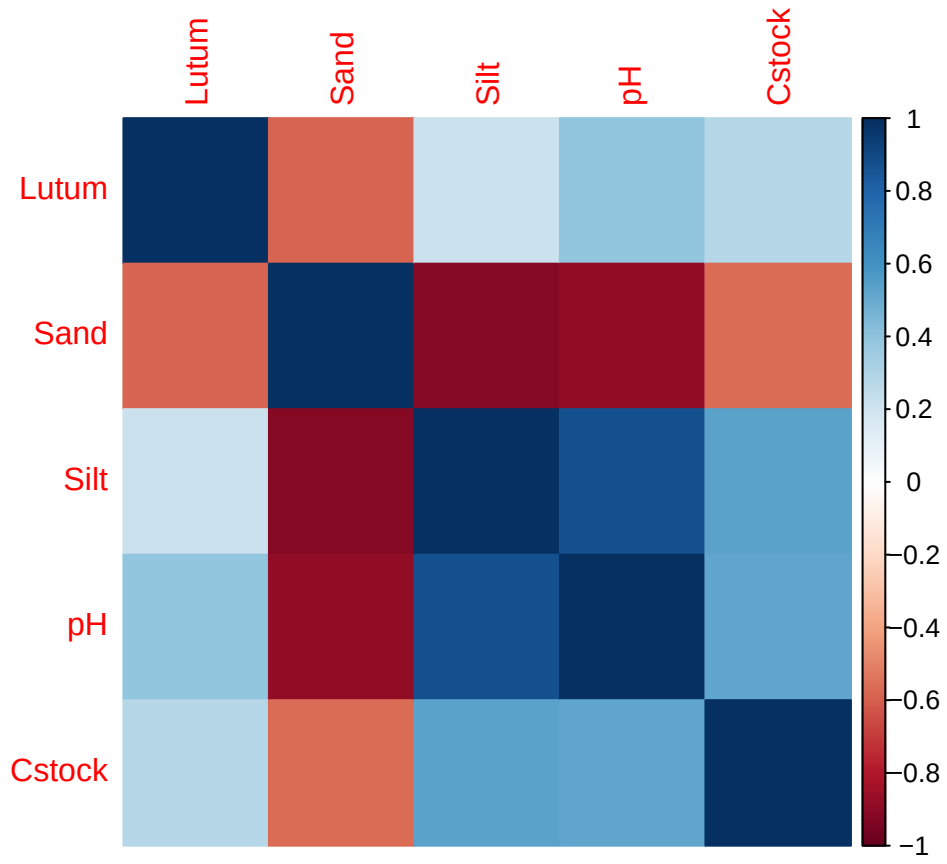

```r
library(ggplot2)

ggplot(clean_data, aes(x = pH, y = Silt, color = Region, size = Cstock)) +
  geom_point(alpha = 0.7) +  # Adjust transparency with alpha
  labs(
    title = "Scatter Plot of pH vs Silt by Region",
    x = "pH",
    y = "Silt",
    color = "Region",  # Legend title for color
    size = "Carbon Stock"  # Legend title for size
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(size = 16, face = "bold"),
    axis.title = element_text(size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(size = 12),
    legend.text = element_text(size = 10),
    legend.position = "right"  # Place legend on the right side
  )
```




```
# Correlation matrix
cor_matrix <- cor(clean_data[, c("Lutum", "Sand", "Silt", "pH", "Cstock")])
print(cor_matrix)
```

```
##             Lutum       Sand       Silt         pH     Cstock
## Lutum   1.0000000 -0.5898419  0.2188901  0.3985912  0.2812626
## Sand   -0.5898419  1.0000000 -0.9165763 -0.8888334 -0.5602512
## Silt    0.2188901 -0.9165763  1.0000000  0.8780938  0.5390980
## pH      0.3985912 -0.8888334  0.8780938  1.0000000  0.5219731
## Cstock  0.2812626 -0.5602512  0.5390980  0.5219731  1.0000000
```

```
# Visualize correlations
corrplot(cor_matrix, method = "color")
```




```
install.packages("reshape2")
```

```
## Installing package into 'C:/Users/saleh/AppData/Local/R/win-library/4.4'
## (as 'lib' is unspecified)
```

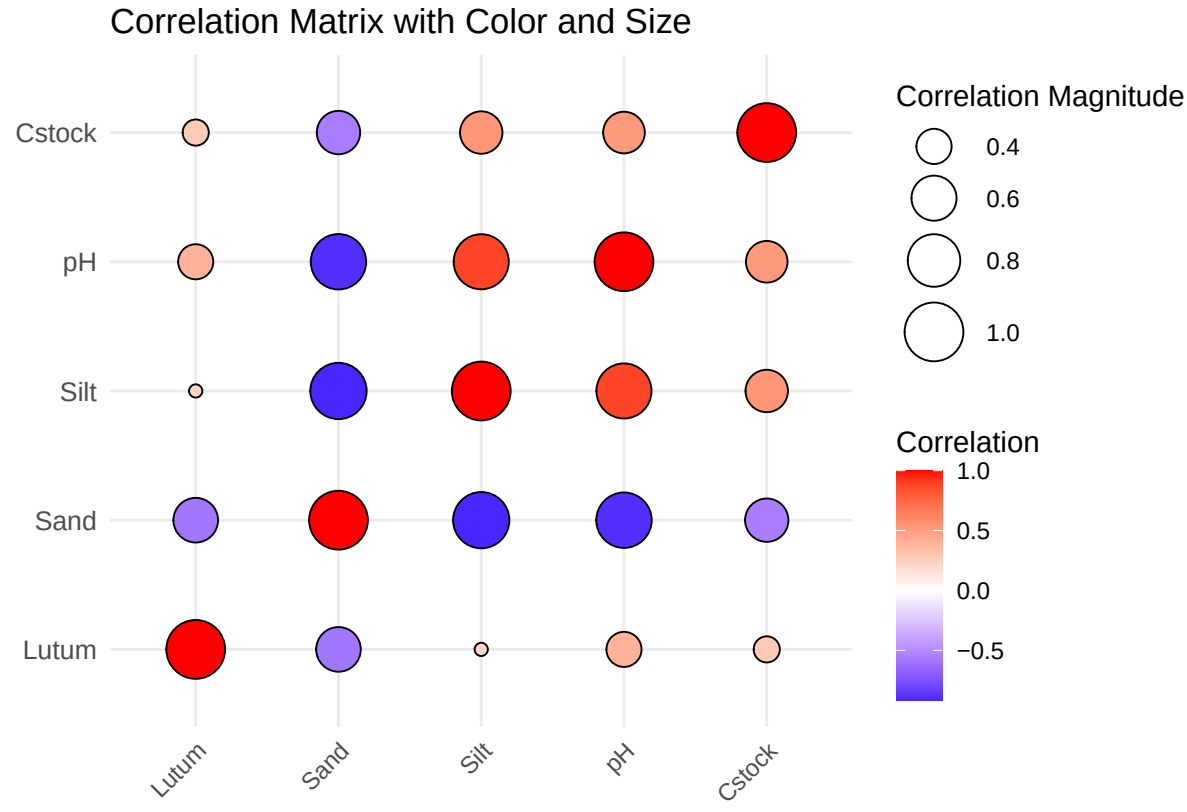
```
## package 'reshape2' successfully unpacked and MD5 sums checked
##
## The downloaded binary packages are in
##  C:\Users\saleh\AppData\Local\Temp\RtmpcXZSZw\downloaded_packages
```

```
library(ggplot2)
library(reshape2)
```

```
## Warning: package 'reshape2' was built under R version 4.4.2
```

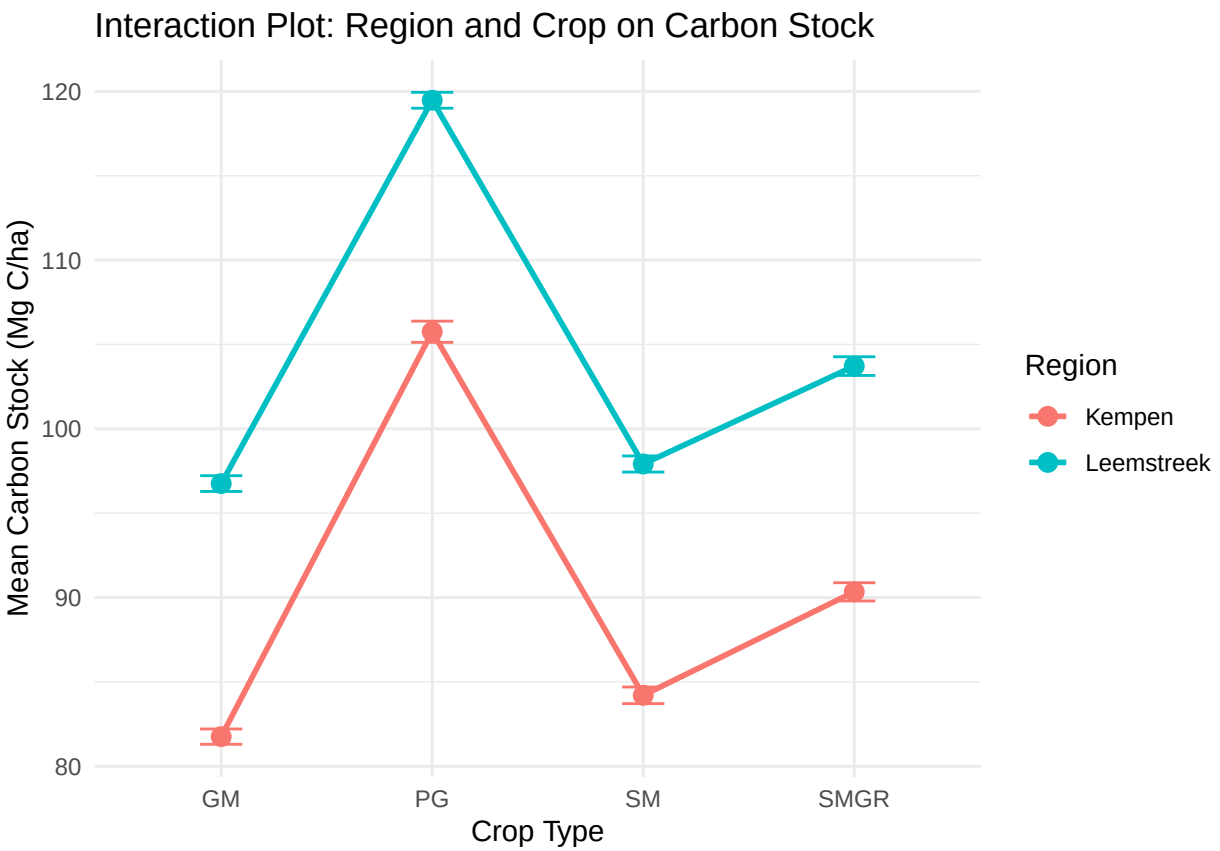
```
# Compute the correlation matrix
cor_matrix <- cor(clean_data[, c("Lutum", "Sand", "Silt", "pH", "Cstock")])

# Melt the correlation matrix into a long format
cor_melted <- melt(cor_matrix)

# Create the heatmap with size and color
ggplot(cor_melted, aes(x = Var1, y = Var2, fill = value, size = abs(value))) +
  geom_point(shape = 21, color = "black") +  # Use shape 21 for circles with borders
```

```
  scale_fill_gradient2(
    low = "blue", mid = "white", high = "red", midpoint = 0,
    name = "Correlation"
  ) +
  scale_size_continuous(range = c(2, 10), name = "Correlation Magnitude") +
  labs(
    title = "Correlation Matrix with Color and Size",
    x = "",
    y = ""
  ) +
  theme_minimal() +
  theme(
    axis.text.x = element_text(angle = 45, hjust = 1, vjust = 1),
    axis.text.y = element_text(size = 10),
    legend.position = "right"
  )
```

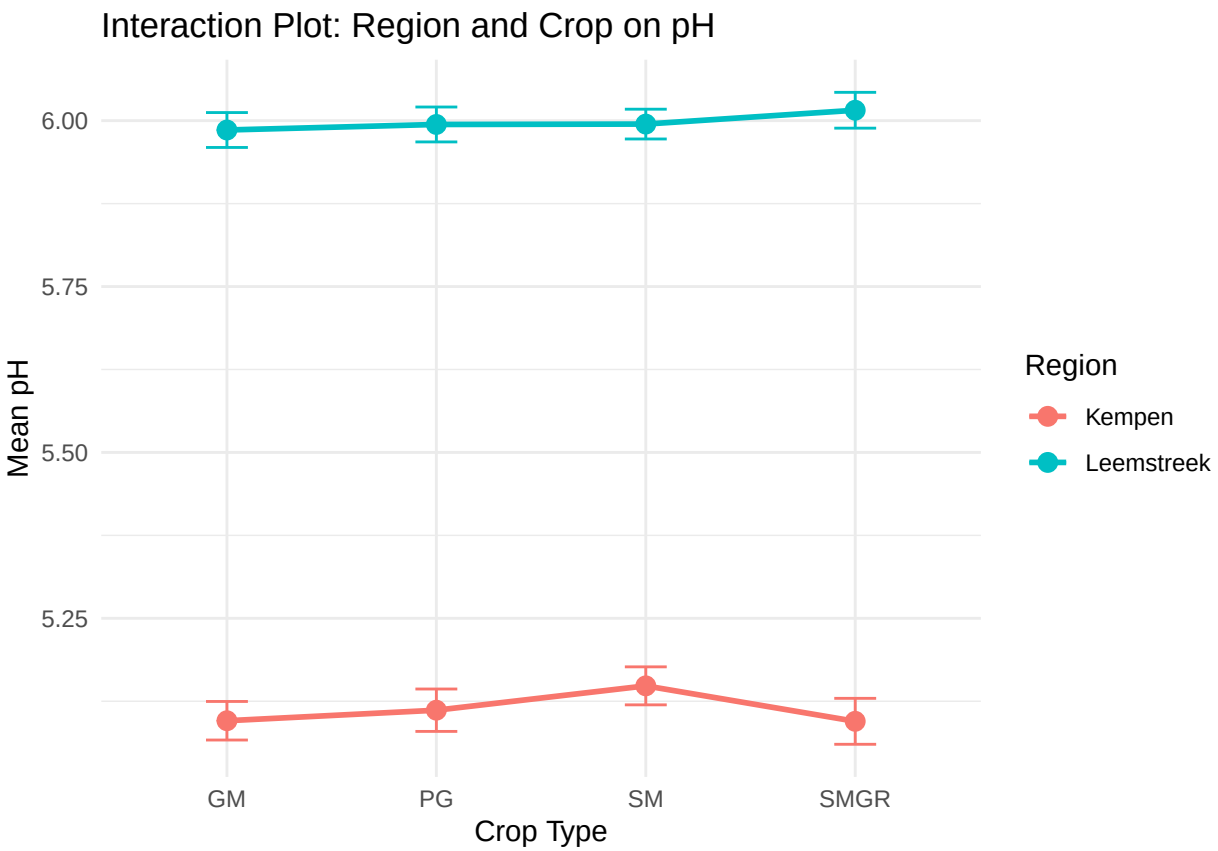



```
# Create interaction plot for Carbon Stock
ggplot_interaction_cstock <- clean_data %>%
  group_by(Region, Crop) %>%
  summarise(
    mean_Cstock = mean(Cstock, na.rm = TRUE),
    se_Cstock = sd(Cstock, na.rm = TRUE) / sqrt(n()),
    .groups = "drop"
  ) %>%
```

```
  ggplot(aes(x = Crop, y = mean_Cstock, color = Region, group = Region)) +
  geom_line(linewidth = 1) +
  geom_point(size = 3) +
  geom_errorbar(aes(ymin = mean_Cstock - se_Cstock,
                    ymax = mean_Cstock + se_Cstock),
                width = 0.2) +
  theme_minimal() +
  labs(
    title = "Interaction Plot: Region and Crop on Carbon Stock",
    x = "Crop Type",
    y = "Mean Carbon Stock (Mg C/ha)"
  )

# Create interaction plot for pH
ggplot_interaction_ph <- clean_data %>%
  group_by(Region, Crop) %>%
  summarise(
    mean_pH = mean(pH, na.rm = TRUE),
    se_pH = sd(pH, na.rm = TRUE) / sqrt(n()),
    .groups = "drop"
  ) %>%
  ggplot(aes(x = Crop, y = mean_pH, color = Region, group = Region)) +
  geom_line(linewidth = 1) +
  geom_point(size = 3) +
  geom_errorbar(aes(ymin = mean_pH - se_pH,
                    ymax = mean_pH + se_pH),
                width = 0.2) +
  theme_minimal() +
  labs(
    title = "Interaction Plot: Region and Crop on pH",
    x = "Crop Type",
    y = "Mean pH"
  )

# Print and save plots
print(ggplot_interaction_cstock)
```

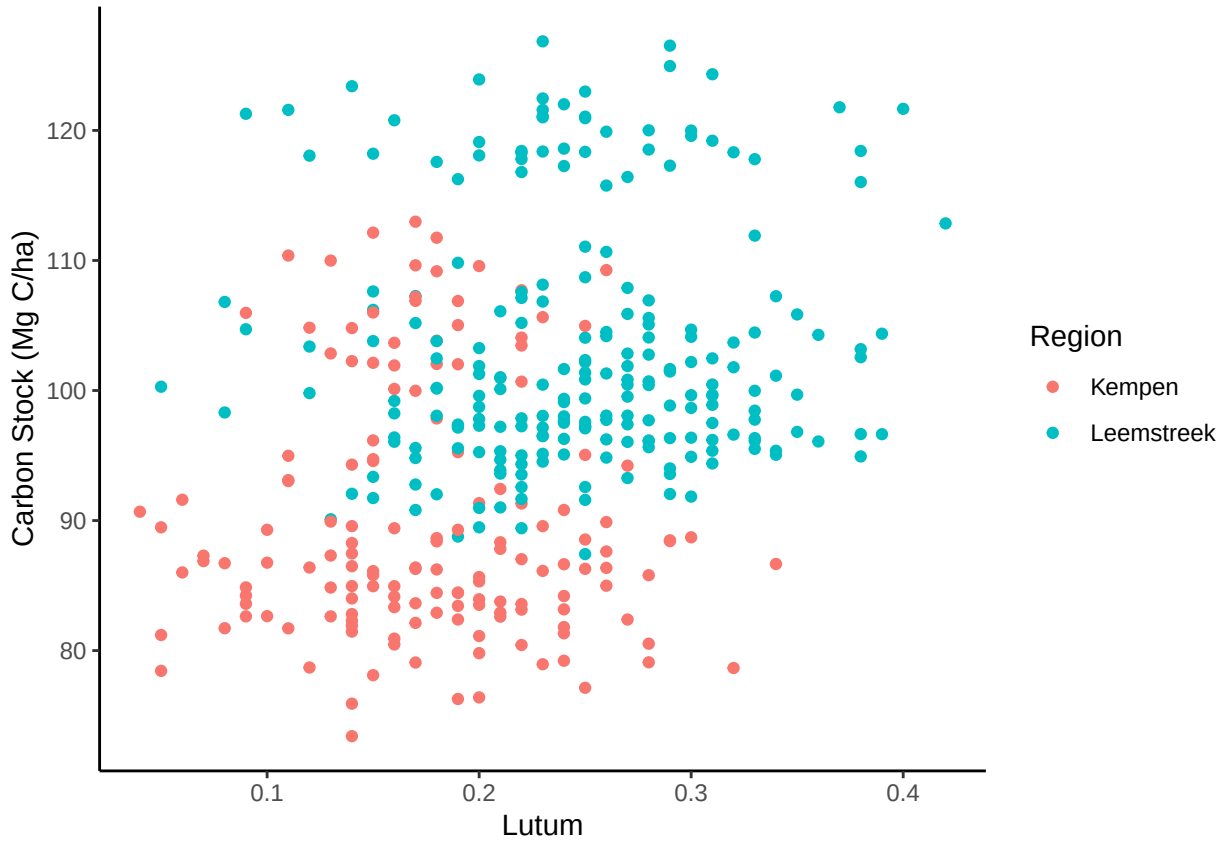



```
print(ggplot_interaction_ph)
```

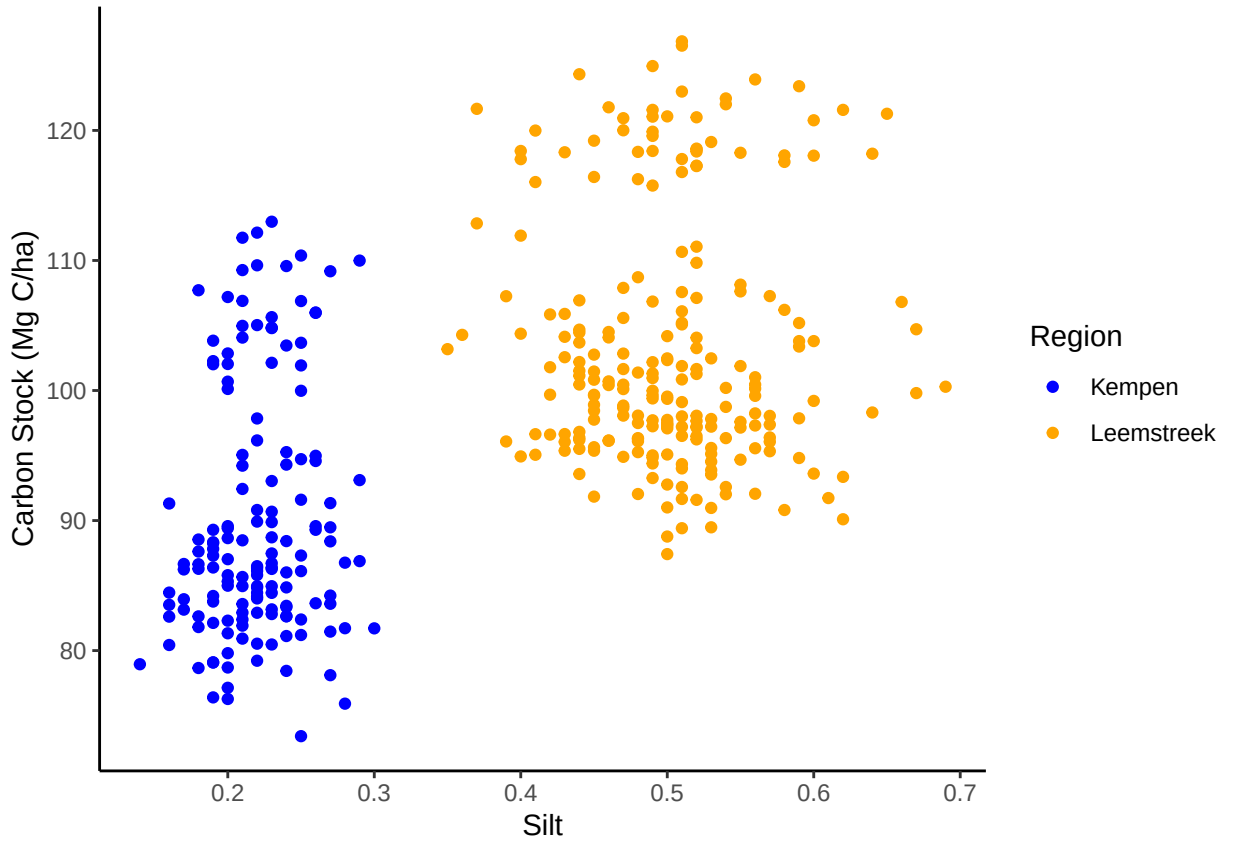



```
# Save ggplot versions
ggsave("interaction_plot_cstock.png", ggplot_interaction_cstock, width = 10, height = 6)
ggsave("interaction_plot_ph.png", ggplot_interaction_ph, width = 10, height = 6)
```

```
ggplot(clean_data, aes(x = Lutum, y = Cstock, color = Region)) +
  geom_point() +
  labs(x = "Lutum", y = "Carbon Stock (Mg C/ha)", color = "Region") +
  theme_classic()
```




```
ggplot(clean_data, aes(x = Silt, y = Cstock, color = Region)) +
  geom_point() +
  scale_color_manual(values = c("Kempen" = "blue", "Leemstreek" = "orange", "other_region" = "green")) +
  labs(x = "Silt", y = "Carbon Stock (Mg C/ha)", color = "Region") +
  theme_classic()
```

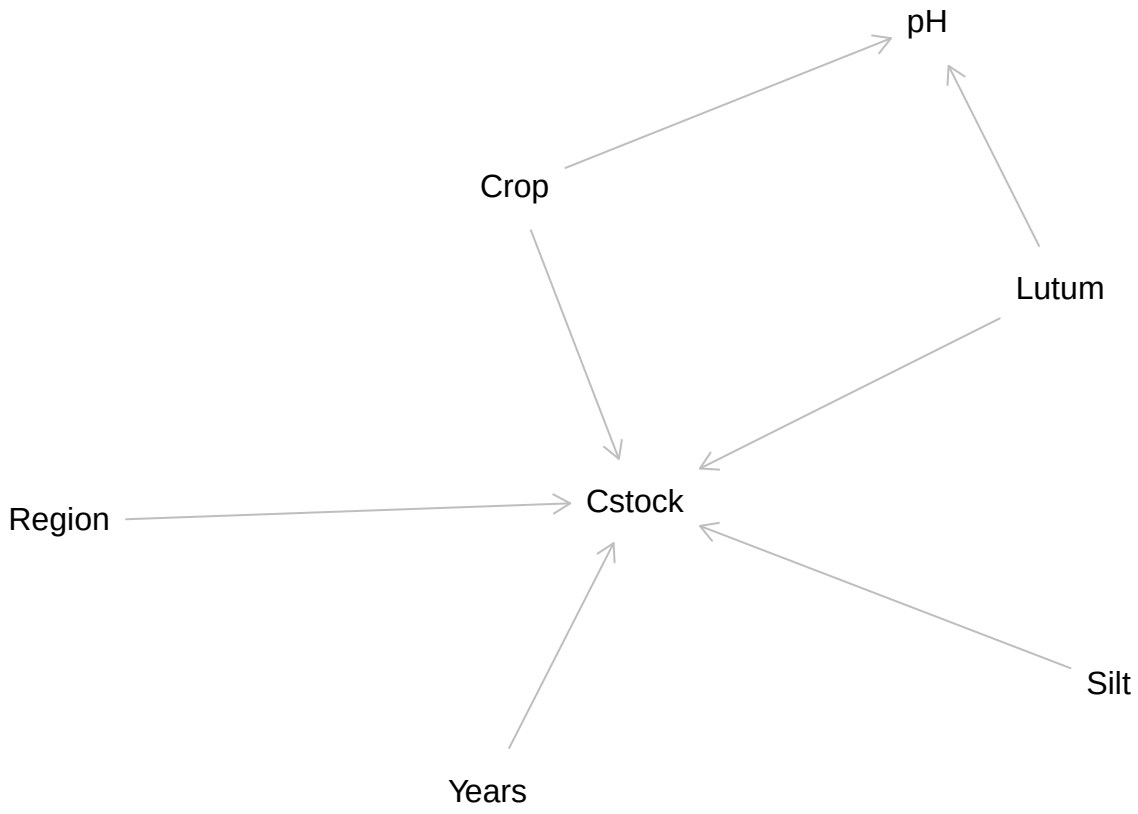



```
library(dagitty)
```

```
## Warning: package 'dagitty' was built under R version 4.4.2
```

```
# Define the causal structure
dag <- dagitty('
dag {
  "Region" -> "Cstock"
  "Years" -> "Cstock"
  "Crop" -> "Cstock"
  "Lutum" -> "Cstock"
  "Silt" -> "Cstock"
  "Crop" -> "pH"
  "Lutum" -> "pH"
}
')

# Plot the DAG
plot(dag)
```

```
## Plot coordinates for graph not supplied! Generating coordinates, see ?coordinates for how to set your
```



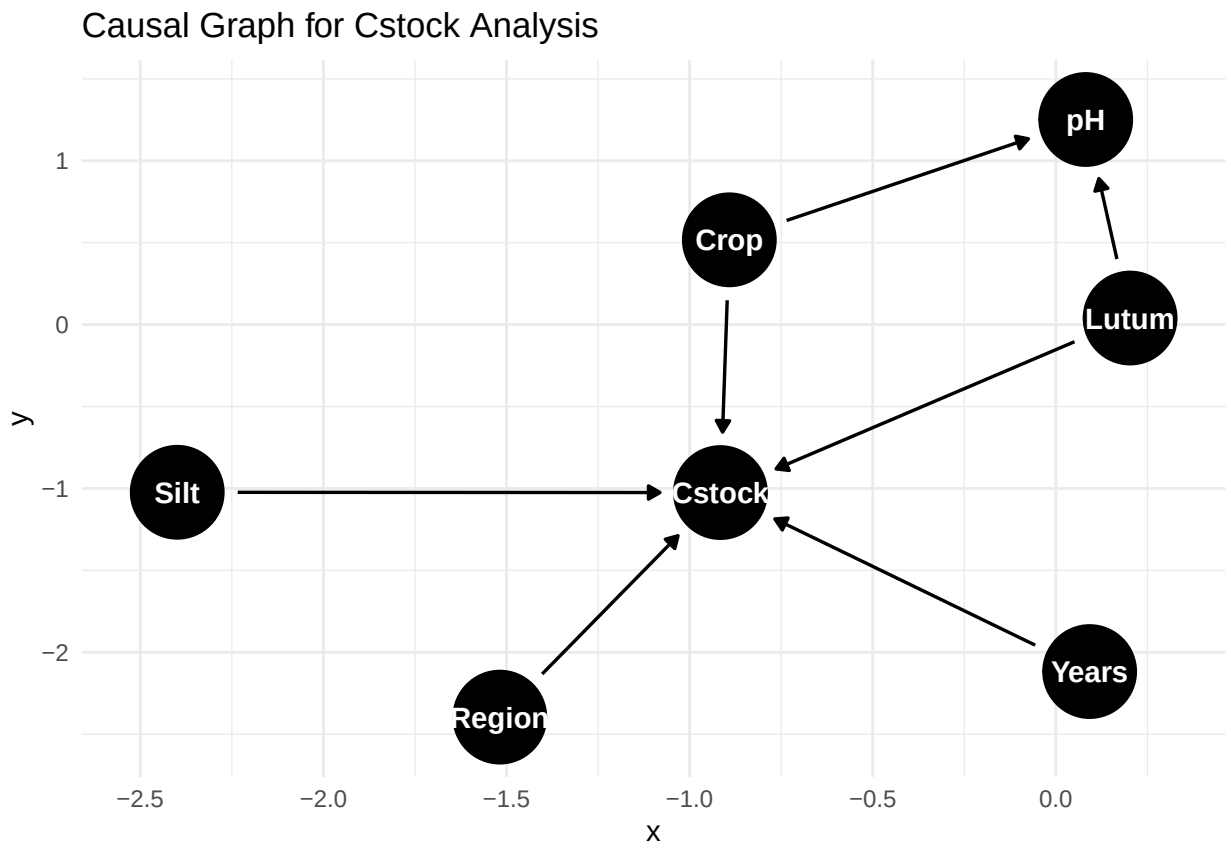

```
library(ggdag)
```

```
## Warning: package 'ggdag' was built under R version 4.4.2
```

```
##
## Attaching package: 'ggdag'
```

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

```
# Define the DAG
dag <- dagify(
  Cstock ~ Region + Years + Crop + Lutum + Silt,
  pH ~ Crop + Lutum,
  exposure = "Crop",
  outcome = "Cstock"
)

# Plot the DAG
ggdag(dag) +
  theme_minimal() +
  ggtitle("Causal Graph for Cstock Analysis")
```




```
ggsave("causal_graph.png", width = 8, height = 6)
```

```
library(DiagrammeR)
```

```
## Warning: package 'DiagrammeR' was built under R version 4.4.2
```

```
library(DiagrammeRsvg)
```

```
## Warning: package 'DiagrammeRsvg' was built under R version 4.4.2
```

```
library(rsvg)
```

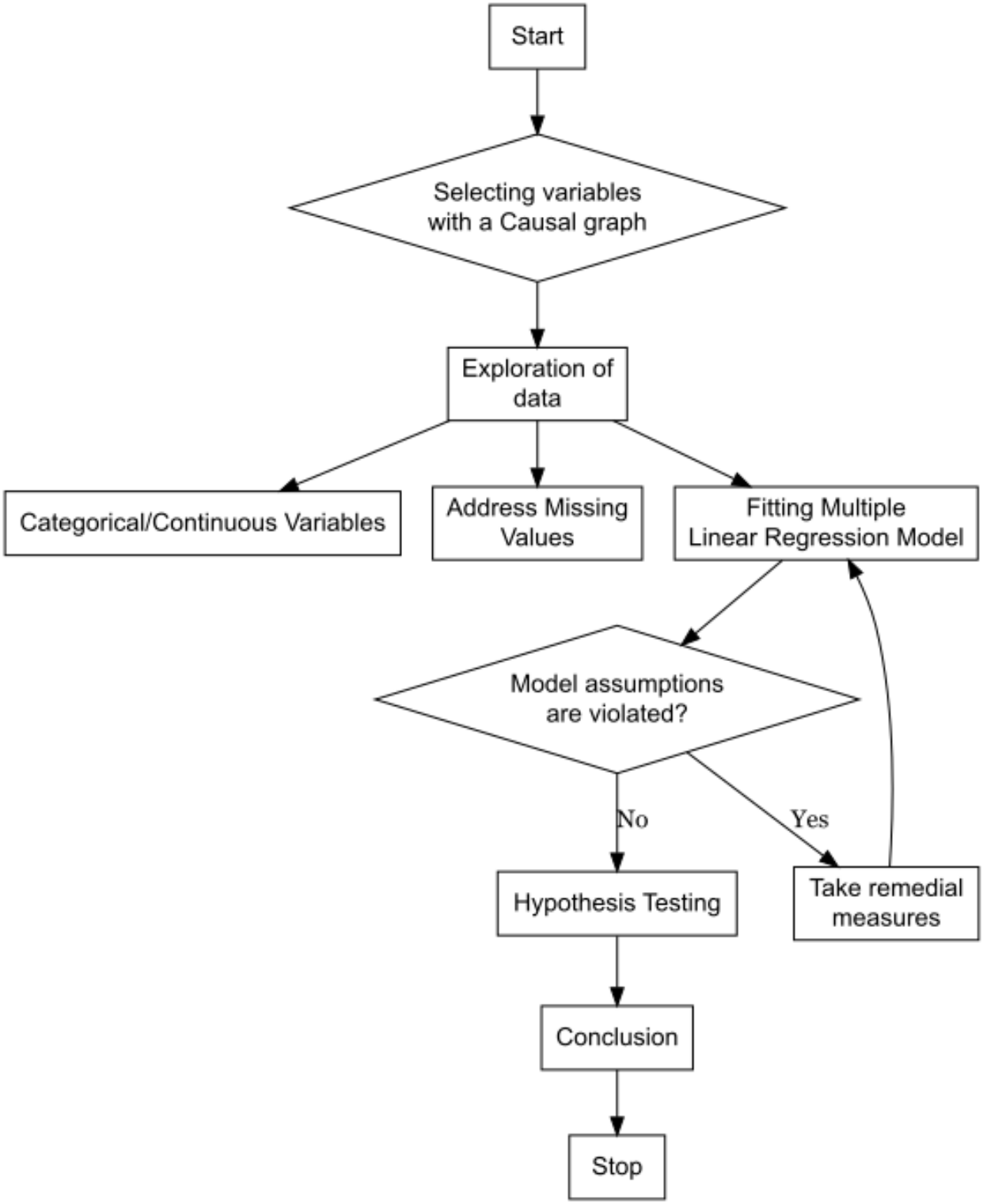
```
## Warning: package 'rsvg' was built under R version 4.4.2
```

```
## Linking to librsvg 2.57.0
```

```
# Define the flow diagram
graph <- grViz("
digraph flowchart {
  graph [layout = dot, rankdir = TB]

  node [shape = rectangle, fontname = Arial]
```

```
  # Nodes
  Start [label = 'Start']
  SelectVars [label = 'Selecting variables\nwith a Causal graph', shape = diamond]
  VarType [label = 'Categorical/Continuous Variables']
  Explore [label = 'Exploration of\ndata']
  MissingValues [label = 'Address Missing\nValues']
  FitModel [label = 'Fitting Multiple\nLinear Regression Model']
  Assumptions [label = 'Model assumptions\nare violated?', shape = diamond]
  Remedial [label = 'Take remedial\nmeasures']
  Hypothesis [label = 'Hypothesis Testing']
  Conclusion [label = 'Conclusion']
  Stop [label = 'Stop']

  # Edges
  Start -> SelectVars
  SelectVars -> Explore
  Explore -> VarType
  Explore -> FitModel
  Explore -> MissingValues
  FitModel -> Assumptions
  Assumptions -> Remedial [label = 'Yes']
  Assumptions -> Hypothesis [label = 'No']
  Remedial -> FitModel
  Hypothesis -> Conclusion
  Conclusion -> Stop

  # Subgraphs for horizontal alignment
  { rank = same; VarType; MissingValues }
}
")

# Render the flow diagram
graph
```

```
# Render the diagram
svg_code <- export_svg(graph)

# Save as PNG file
rsvg_png(charToRaw(svg_code), "flow_diagram.png")

# Display the saved PNG
knitr::include_graphics("flow_diagram.png")
```



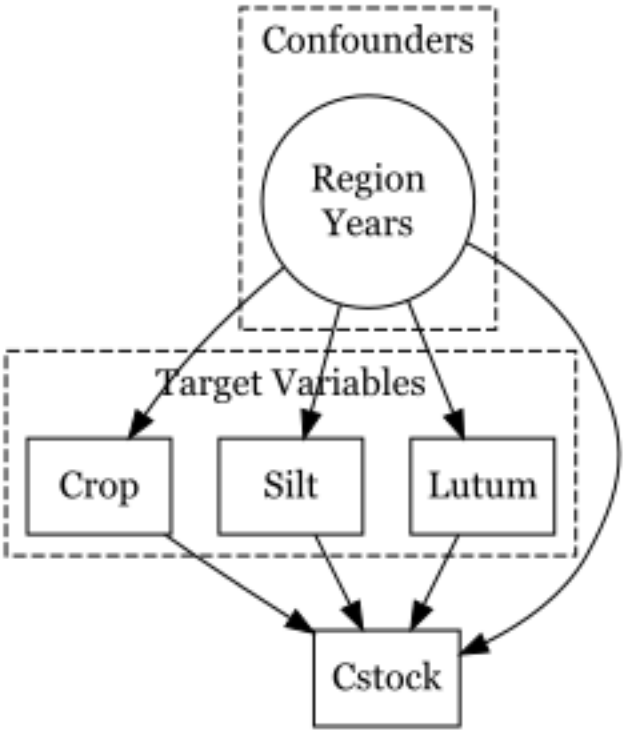

```
library(DiagrammeR)
library(DiagrammeRsvg)
library(rsvg)

# Define the causal graph
```

```
graph <- grViz("
digraph causal_graph {
  graph [layout = dot, rankdir = TB]

  # Node definitions
  subgraph cluster_confounders {
    label = 'Confounders';
    style = dashed;
    Confounders [label = 'Region\\nYears', shape = circle];
  }

  subgraph cluster_targets {
    label = 'Target Variables';
    style = dashed;
    Lutum [label = 'Lutum', shape = rectangle];
    Silt [label = 'Silt', shape = rectangle];
    Crop [label = 'Crop', shape = rectangle];
  }

  Outcome [label = 'Cstock', shape = rectangle];

  # Edges
  Confounders -> Lutum;
  Confounders -> Silt;
  Confounders -> Crop;
  Lutum -> Outcome;
  Silt -> Outcome;
  Crop -> Outcome;
  Confounders -> Outcome;
}
")

# Render the graph inline
graph
```

```
# Convert the graph to SVG
svg_code <- export_svg(graph)

# Save the SVG as a PNG file
rsvg_png(charToRaw(svg_code), "causal_graph.png")

# Output confirmation message
cat("Graph saved as 'causal_graph.png' in your working directory.\n")
```

```
## Graph saved as 'causal_graph.png' in your working directory.
```

```
# Display the saved PNG
knitr::include_graphics("causal_graph.png")
```


Confounders
Region
Years
Target Variables
Crop
Silt
Lutum
Cstock