Statistical Computing Final Project

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Contents

0.0.1 Package Management -> Importing the necessary packages that will be used in this project

```
suppressPackageStartupMessages({
  library(corrplot)
  library(cluster)
  library(dendextend)
  library(dplyr)
  library(factoextra)
  library(ggplot2)
  library(ggpubr)
  library(ggstatsplot)
  library(ggrepel)
  library(gtsummary)
  library(haven)
  library(huxtable)
  library(kableExtra)
  library(knitr)
  library(performance)
  library(psych)
  library(rstatix)
  library(readr)
  library(rempsyc)
  library(Rtsne)
  library(see)
  library(sjPlot)
  library(sjlabelled)
  library(sjmisc)
  library(tibble)
  library(tidyr)
  library(tidyverse)
  library(tinytex)
  library(gridExtra)
  library(flextable)
```

```
})
```

1 Date Pre-processing & Preparation

1. Import dataset (SLC_2007.sav)
2. Rename column headers to be more descriptive.
3. convert the .sav file to a .csv file

```
dataframe <- read_sav("F:/DataSpell/Statistical Computing Project/dataset/SLC_2007.sav")

# rename column names to a more descriptive column name

colnames(dataframe)[1:45] <- c("HH_Num", "Final_Weight", "Water_Bill", "HH_Size_All", "HH_Size_Mem", "Pe

# convert all the column names to lower case
colnames(dataframe) <- tolower(colnames(dataframe))

# coverting the SLC_2007.sav to csv

converted_df <- write.table(x=dataframe,file="F:/DataSpell/Statistical Computing Project/dataset/SLC_20
```

1.1 Data Wrangling

This process of the Data Science lifecycle involves cleaning, transforming and restructuring the raw data to make it suitable for analysis.

```
# Set the seed and take 90% of the random sample

set.seed(710)

# import dataset
SLC_2007.Data <- read.csv("F:/DataSpell/Statistical Computing Project/dataset/SLC_2007.csv")


# random sample
n <- nrow(SLC_2007.Data)
sample_size <- round(0.9 * n) # calculate the desired sample size as 90% of the total number of rows

SLC_2007.Sample <- SLC_2007.Data[sample(seq_len(n), size = sample_size, replace = FALSE),] # take a ran
```

```
# create a sub dataset with the demographic variables
SLC_2007.Subset <- select(SLC_2007.Sample,
                           area_code,type_dwelling,
                           type_toilet,toilet_shared,kitchen_shared,own_dwelling,
                           water_source,hh_size_all,hh_size_mem,
                           per_cap_con_all,water_bill,water_source, water_bill_latest, water_source_shar
                           water_meter
```

```
)
```

```r
# rename all the elements of the rows in our subset to labels.

SLC_2007.Subset <- SLC_2007.Subset %>%
  rename(
    area_code = area_code,
    type_dwelling = type_dwelling,
    type_toilet = type_toilet,
    toilet_shared = toilet_shared,
    kitchen_shared = kitchen_shared,
    own_dwelling = own_dwelling,
    water_source = water_source,
    water_source_shared = water_source_shared,
    water_meter = water_meter,

  ) %>%
  mutate(
    area_code = case_when(
      area_code == 1 ~ "KMA",
      area_code == 2 ~ "Other Town",
      area_code == 3 ~ "Rural",
      TRUE ~ as.character(area_code) # keep original value if not matched
    ),
    type_dwelling = case_when(
      type_dwelling == 1 ~ "SEPARATE HOUSE DETACHED",
      type_dwelling == 2 ~ "SEMI-DETACHED HOUSE",
      type_dwelling == 3 ~ "PARTS OF A HOUSE",
      type_dwelling == 4 ~ "APARTMENT BUILDING",
      type_dwelling == 5 ~ "TOWNHOUSE",
      type_dwelling == 6 ~ "IMPROVISED HOUSING UNIT",
      type_dwelling == 7 ~ "PARTS OF COMMERCIAL BUILDING",
      type_dwelling == 8 ~ "OTHER (SPECIFY)",
      TRUE ~ as.character(type_dwelling) # keep original value if not matched
    ),

    type_toilet = case_when(
      type_toilet == 1 ~ "W.C. LINKED TO SEWER",
      type_toilet == 2 ~ "W.C. NOT LINKED",
      type_toilet == 3 ~ "PIT",
      type_toilet == 4 ~ "OTHER",
      type_toilet == 5 ~ "NONE",
      TRUE ~ as.character(type_toilet) # keep original value if not matched
    ),
    toilet_shared = case_when(
      toilet_shared == 1 ~ "EXCLUSIVE USE",
      toilet_shared == 2 ~ "SHARED",
      TRUE ~ as.character(toilet_shared) # keep original value if not matched
    ),
    kitchen_shared = case_when(
      kitchen_shared == 1 ~ "EXCLUSIVE USE",
      kitchen_shared == 2 ~ "SHARED",
      kitchen_shared == 3 ~ "NONE",
```

```r
      TRUE ~ as.character(kitchen_shared) # keep original value if not matched
    ),
    own_dwelling = case_when(
      own_dwelling == 1 ~ "YES",
      own_dwelling == 2 ~ "NO",
      TRUE ~ as.character(own_dwelling) # keep original value if not matched
    ),
    water_source = case_when(
      water_source == 1 ~ "Indoor tap/pipe",
      water_source == 2 ~ "Outside private",
      water_source == 3 ~ "Public standpipe",
      water_source == 4 ~ "Well",
      water_source == 5 ~ "River, Lake, Spring, Pond",
      water_source == 6 ~ "Rainwater (Tank)",
      water_source == 7 ~ "Trucked water (NWC)",
      water_source == 8 ~ "Bottled Water",
      water_source == 9 ~ "Other (Specify)",

      TRUE ~ as.character(water_source) # keep original value if not matched
    ),
    water_source_shared = case_when(
      water_source_shared == 1 ~ "YES",
      water_source_shared == 2 ~ "NO",
      TRUE ~ as.character(water_source_shared) # keep original value if not matched
    ),
    water_meter = case_when(
      water_meter == 1 ~ "Group",
      water_meter == 2 ~ "Individual",
      water_meter == 3 ~ "No Meter",
      TRUE ~ as.character(water_meter) # keep original value if not matched
    ),


  )
```

2 Demographic Analysis

2.1

```r
SLC_2007.Subset2 <- SLC_2007.Subset %>%
        rename("Area Code" = area_code)

table1 <- SLC_2007.Subset2 %>%
        select("Area Code") %>%
        filter(!(`Area Code` %in% c(4, 5))) %>% # exclude Area Codes 4 and 5
        tbl_summary(
                missing = "no"
        ) %>%
        add_n() %>%
        modify_header(label = "**Characteristic**") %>%
        bold_labels()%>%
```

```
        as_kable_extra() %>% # Convert to kableExtra table
        kable_styling(latex_options = "hold_position", position = "center") # Center the table in the P



table1
```

Characteristic	**N**	**N = 5,863**
Area Code	5,863	
KMA		919 (16%)
Other Town		1,208 (21%)
Rural		3,736 (64%)

[1] n (%)

```
SLC_2007.Subset2 <- SLC_2007.Subset %>%
        rename("Type of Toilet" = type_toilet)
table2 <- SLC_2007.Subset2 %>%
        select("Type of Toilet") %>%
        tbl_summary(
                missing = "no"
        ) %>%
        add_n() %>% # add column with total number of non-missing observations
        modify_header(label = "**Characteristic**") %>% # update the column header
        bold_labels()%>%
        as_kable_extra() %>% # Convert to kableExtra table
        kable_styling(latex_options = "hold_position", position = "center") # Center the table in the P



table2
```

Characteristic	**N**	**N = 6,278**
Type of Toilet	6,255	
NONE		110 (1.8%)
OTHER		7 (0.1%)
PIT		2,931 (47%)
W.C. LINKED TO SEWER		957 (15%)
W.C. NOT LINKED		2,250 (36%)

[1] n (%)

```
# Load necessary libraries

# Create a sub dataset with the demographic variables
SLC_2007.Subset_demographics <- select(SLC_2007.Subset,
                                       water_source_shared,
                                       kitchen_shared, toilet_shared, area_code)

# Prepare the dataset
SLC_2007.Demographics <- select(SLC_2007.Subset_demographics,
```

```r
                                    water_source_shared,
                                    kitchen_shared, toilet_shared, area_code)


# Filter out area codes 4 and 5
SLC_2007.Demographics_filtered <- SLC_2007.Demographics %>%
  filter(area_code != 4 & area_code != 5)

# Create summary statistics table
summary_table <- SLC_2007.Demographics_filtered %>%
  tbl_summary(
    by = area_code,
    type = list(
      water_source_shared = "categorical",
      kitchen_shared = "categorical",
      toilet_shared = "categorical"
    ),
    statistic = list(
      water_source_shared ~ "{n} ({p}%)",
      kitchen_shared ~ "{n} ({p}%)",
      toilet_shared ~ "{n} ({p}%)"
    ),
    missing = "no",
    label = list(
      area_code ~ "Area Code",
      water_source_shared ~ "Water Source Shared",
      kitchen_shared ~ "Kitchen Shared",
      toilet_shared ~ "Toilet Shared"
    )
  )%>%
  add_n() %>% # add column with total number of non-missing observations
  modify_header(label = "**Characteristic**") %>% # update the column header
  bold_labels()%>%
  as_kable_extra() %>% # Convert to kableExtra table
  kable_styling(latex_options = "hold_position", position = "center") # Center the table in the PDF out

summary_table
```

Characteristic	**N**	**KMA**, N = 919	**Other Town**, N = 1,208	**Rural**, N = 3,736
Water Source Shared	1,431			
NO		45 (73%)	160 (86%)	1,076 (91%)
YES		17 (27%)	27 (14%)	106 (9.0%)
Kitchen Shared	5,839			
EXCLUSIVE USE		641 (70%)	980 (81%)	3,141 (84%)
NONE		88 (9.6%)	113 (9.4%)	367 (9.9%)
SHARED		187 (20%)	110 (9.1%)	212 (5.7%)
Toilet Shared	5,709			
EXCLUSIVE USE		586 (64%)	912 (77%)	3,017 (83%)
SHARED		324 (36%)	266 (23%)	604 (17%)

[1] n (%)

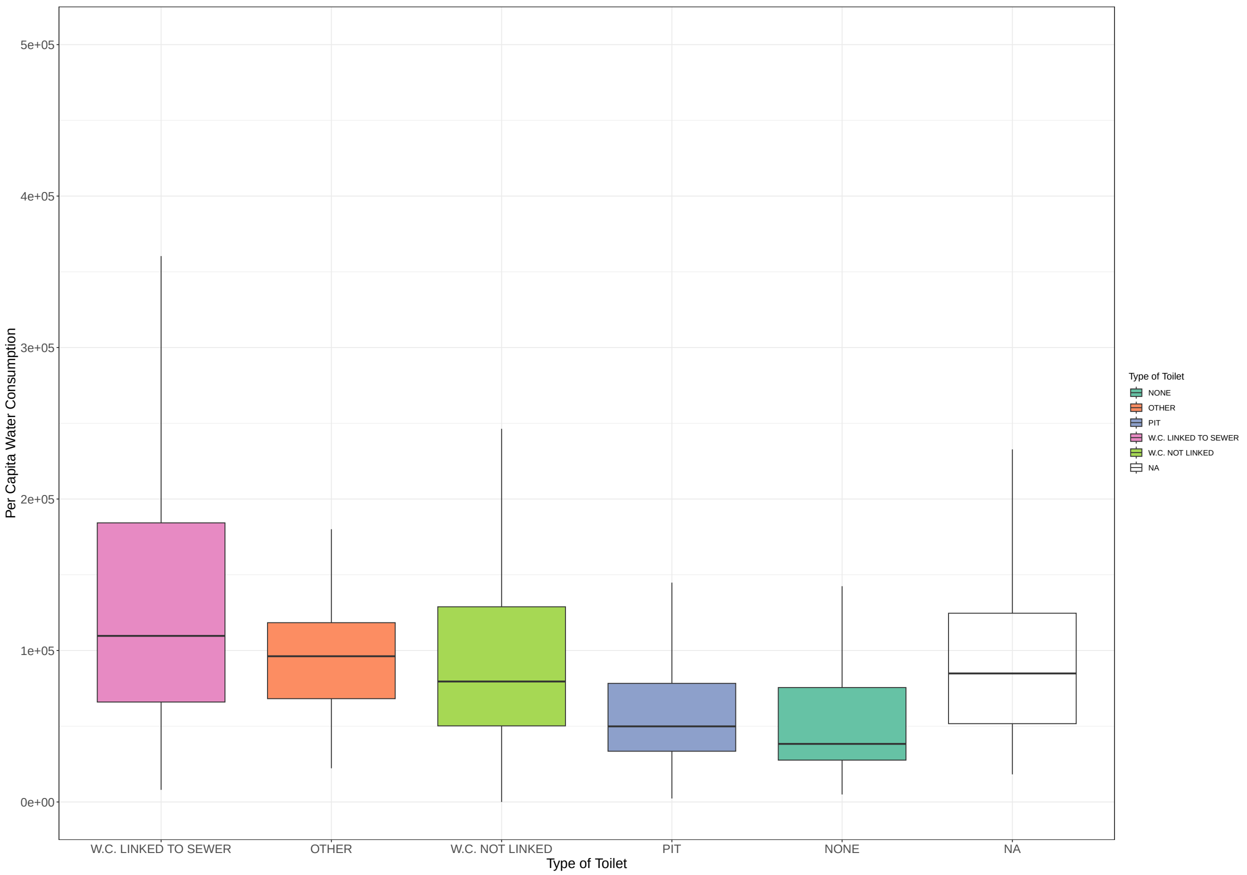
Characteristic	N	**KMA**, N = 919	**Other Town**, N = 1,208	**Rural**, N = 3,736
per_cap_con_all	5,863			
Mean		131,854.05	105,834.19	76,277.71
SD		137,062.67	110,473.95	91,693.03

```
SLC_2007.Subset2 <- SLC_2007.Subset %>%
  rename("Area Code" = area_code)

table3 <- SLC_2007.Subset2 %>%
  select("Area Code", per_cap_con_all) %>%
  filter(!(`Area Code` %in% c(4, 5))) %>% # exclude Area Codes 4 and 5
  group_by(`Area Code`) %>%
  tbl_summary(
    by = `Area Code`,
    type = all_continuous() ~ "continuous2",
    statistic = list(all_continuous() ~ c("{mean}", "{sd}")),
    digits = all_continuous() ~ c(2, 2),
    missing = "no"
  ) %>%
  add_n() %>%
  modify_header(label = "**Characteristic**") %>%
  bold_labels()%>%
  as_kable_extra() %>% # Convert to kableExtra table
  kable_styling( position = "center") # Center the table in the PDF output


table3
```

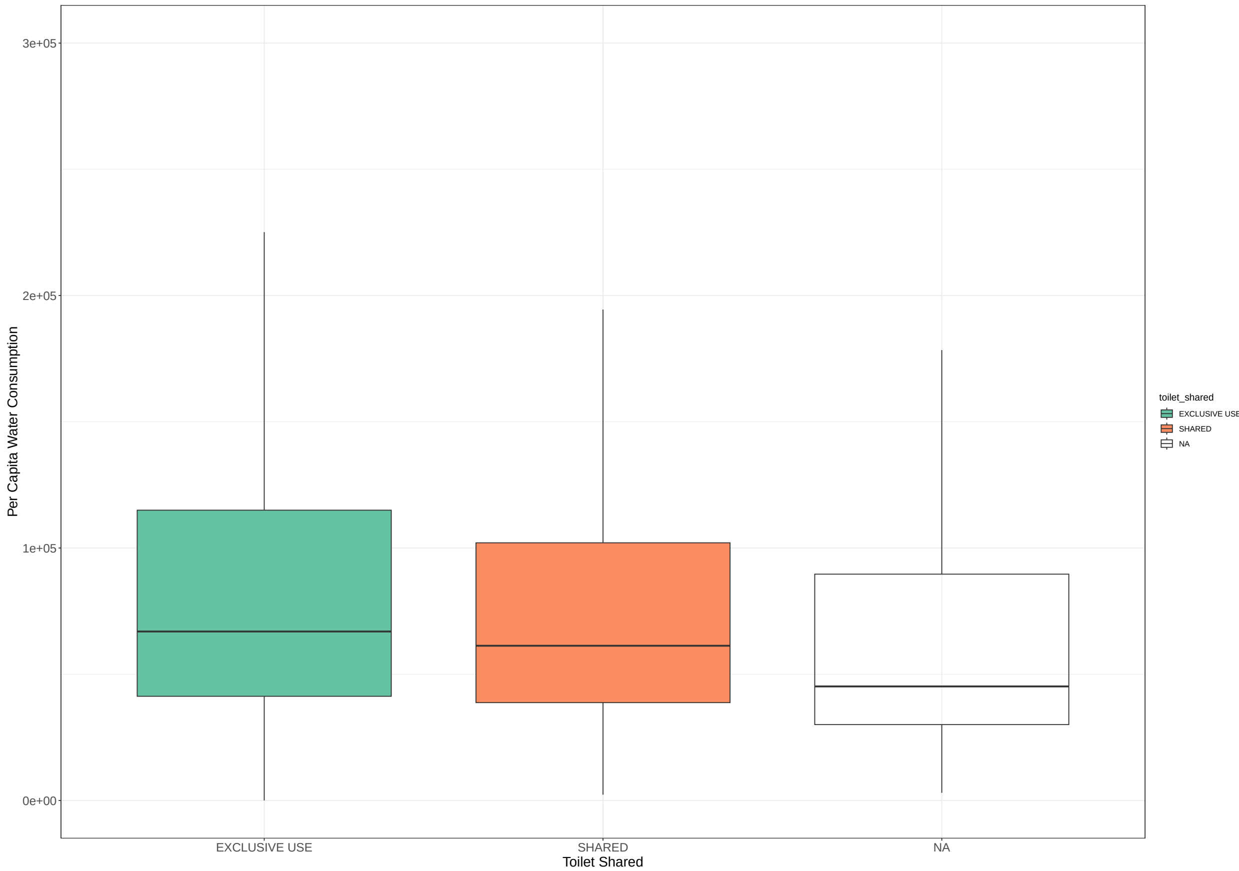
3 Key Variable Analysis

```
SLC_2007.Subset2 <- SLC_2007.Subset %>%
  rename("Type of Toilet" = type_toilet)

# Calculate median per capita water consumption for each Type of Toilet
medians <- SLC_2007.Subset2 %>%
  group_by(`Type of Toilet`) %>%
  summarise(Median = median(per_cap_con_all, na.rm = TRUE))

# Merge calculated medians back into the main data frame
SLC_2007.Subset2 <- SLC_2007.Subset2 %>%
  left_join(medians, by = "Type of Toilet")

# Create a boxplot with reordered Type of Toilet on the x-axis
boxplot_colored_labeled_sorted <- ggplot(SLC_2007.Subset2, aes(x = reorder(`Type of Toilet`, -Median), y
  geom_boxplot(outlier.shape = NA, coef = 1.5) + # Remove outliers by setting outlier.shape to NA and c
  coord_cartesian(ylim = c(0, 5e+05)) + # Set y-axis limits to 0 and 5e+05
  scale_fill_brewer(palette = "Set2") + # Apply a color theme from the ColorBrewer palette
  theme_bw() + # Use a black and white theme for the plot
  labs(
```

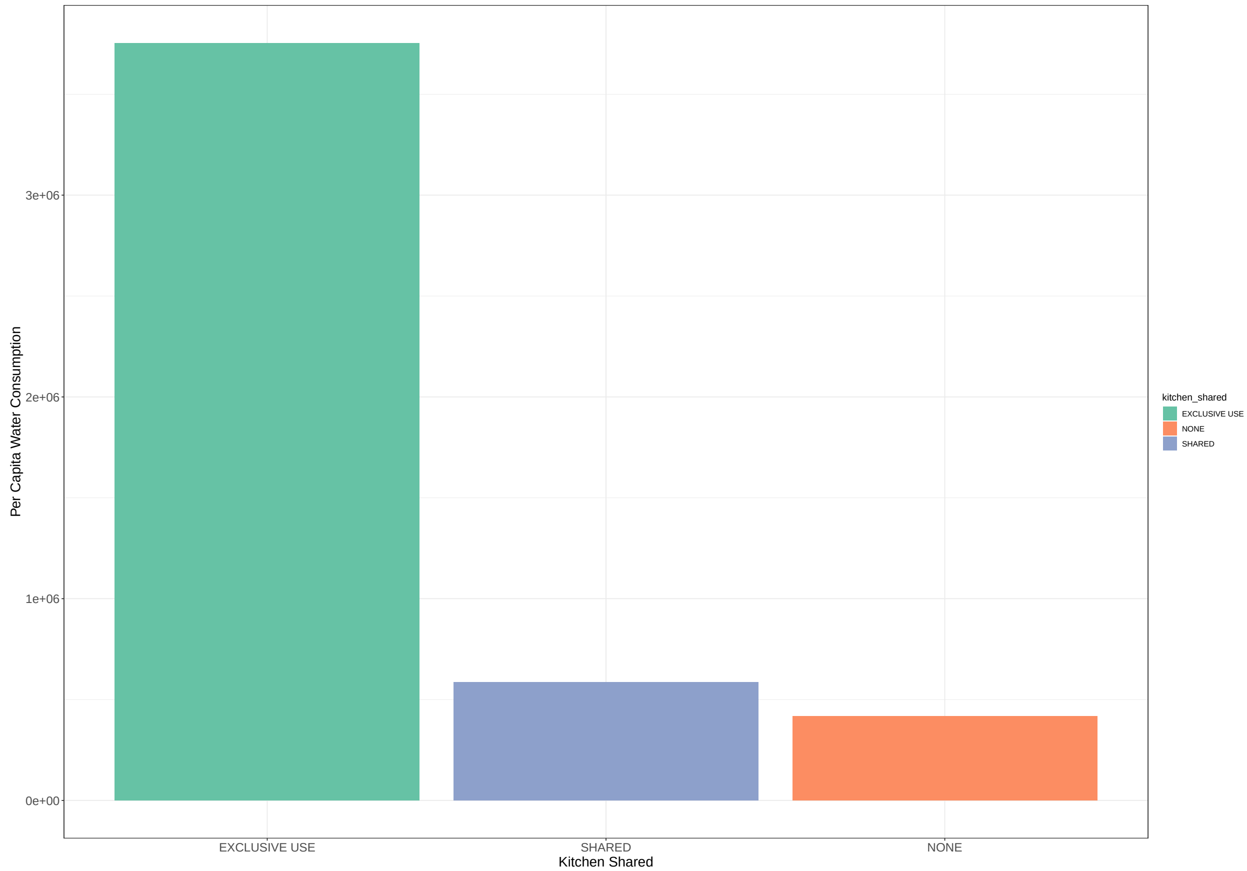
```r
    x = "Type of Toilet",
    y = "Per Capita Water Consumption") +
  theme(axis.text = element_text(size = 14), # Increase the font size of the axis text to 14
        axis.title = element_text(size = 16)) # Increase the font size of the axis titles to 16

# Print the sorted boxplot
boxplot_colored_labeled_sorted
```



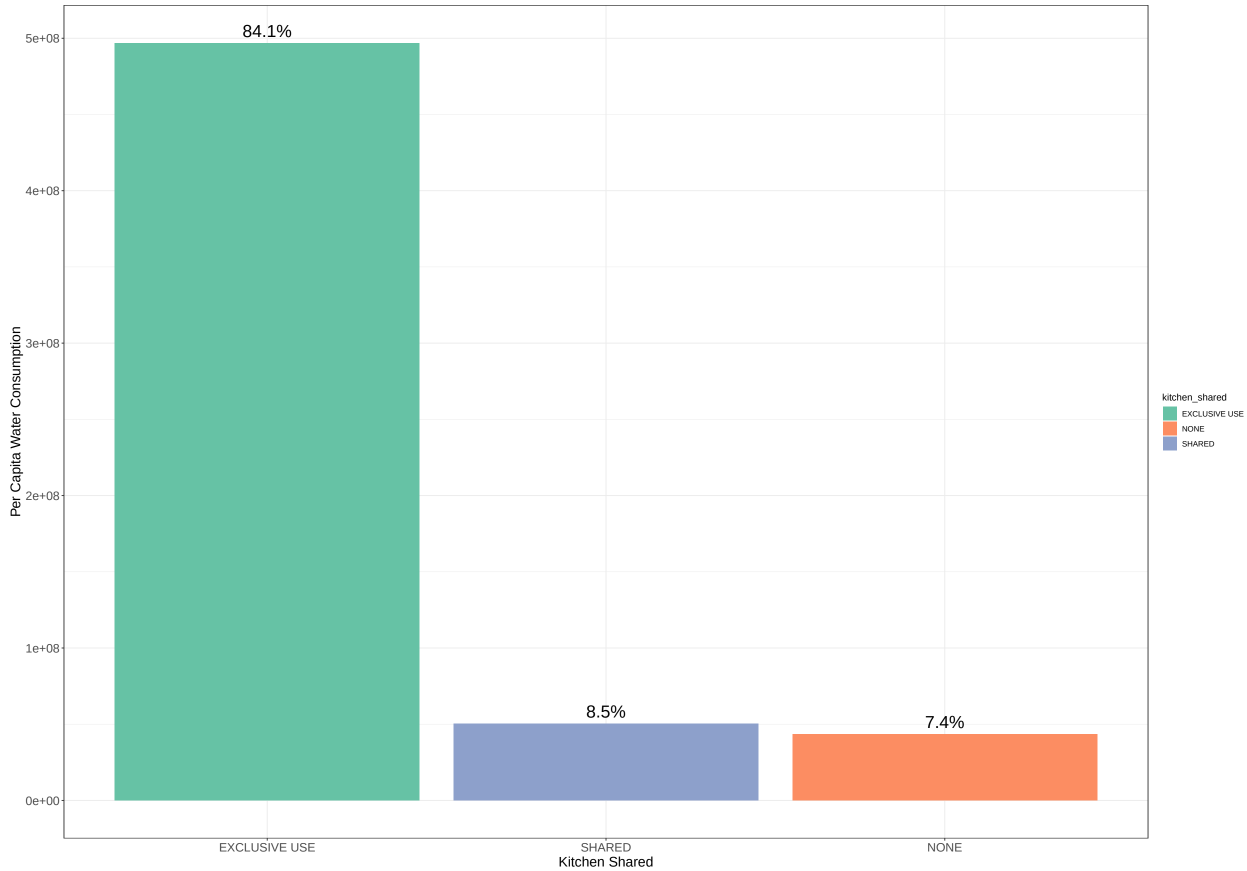

```r
# Create a boxplot of toilet_shared and per_cap_con_all
boxplot_colored <- ggplot(SLC_2007.Subset, aes(x = toilet_shared, y = per_cap_con_all, fill = toilet_sha
  geom_boxplot(outlier.shape = NA, coef = 1.5) + # Remove outliers by setting outlier.shape to NA and c
  coord_cartesian(ylim = c(0, 3e+05)) + # Set y-axis limits to 0 and 5e+05
  scale_fill_brewer(palette = "Set2") + # Apply a color theme from the ColorBrewer palette
  theme_bw() + # Use a black and white theme for the plot
  labs(
    x = "Toilet Shared",
    y = "Per Capita Water Consumption") +
  theme(axis.text = element_text(size = 14), # Increase the font size of the axis text to 14
        axis.title = element_text(size = 16)) # Increase the font size of the axis titles to 16

# Print the boxplot
boxplot_colored
```




```
# Calculate the percentages for each kitchen_shared category, removing NA values
SLC_2007.Subset4 <- SLC_2007.Subset %>%
  filter(!is.na(kitchen_shared)) %>%
  select(kitchen_shared, per_cap_con_all) %>% # Include 'per_cap_con_all' in the dataframe
  count(kitchen_shared, per_cap_con_all) %>% # Add 'per_cap_con_all' in the count function
  mutate(percentage = n / sum(n) * 100) %>%
  arrange(desc(percentage))

# Create a bar chart of kitchen_shared and per_cap_con_all, with percentage labels
bar_chart_colored <- ggplot(SLC_2007.Subset4, aes(x = reorder(kitchen_shared, -per_cap_con_all), y = pe
  geom_bar(stat = "identity", position = position_dodge(width = 0.9)) + # Use the identity statistic to
  scale_fill_brewer(palette = "Set2") + # Apply a color theme from the ColorBrewer palette
  theme_bw() + # Use a black and white theme for the plot
  labs(
    x = "Kitchen Shared",
    y = "Per Capita Water Consumption") +
  theme(axis.text = element_text(size = 14), # Increase the font size of the axis text to 14
        axis.title = element_text(size = 16)) # Increase the font size of the axis titles to 16

# Print the bar chart
bar_chart_colored
```




```r
# Calculate the total per capita water consumption for each kitchen_shared category, removing NA values
SLC_2007.Subset4 <- SLC_2007.Subset %>%
  filter(!is.na(kitchen_shared)) %>%
  select(kitchen_shared, per_cap_con_all) %>%
  group_by(kitchen_shared) %>%
  summarise(total_per_cap_con_all = sum(per_cap_con_all, na.rm = TRUE))

# Calculate the percentage of per capita water consumption for each kitchen_shared category
SLC_2007.Subset4 <- SLC_2007.Subset4 %>%
  mutate(percentage = total_per_cap_con_all / sum(total_per_cap_con_all))

# Create a bar chart of kitchen_shared and per_cap_con_all, with percentage labels
bar_chart_colored <- ggplot(SLC_2007.Subset4, aes(x = reorder(kitchen_shared, -total_per_cap_con_all), y
  geom_bar(stat = "identity", position = position_dodge(width = 0.9)) +
  geom_text(aes(label = paste0(round(percentage * 100, 1), "%")), position = position_dodge(width = 0.9)
  scale_fill_brewer(palette = "Set2") +
  theme_bw() +
  labs(
    x = "Kitchen Shared",
    y = "Per Capita Water Consumption") +
  theme(axis.text = element_text(size = 14),
        axis.title = element_text(size = 16))

# Print the bar chart
bar_chart_colored
```




```
SLC_2007.Subset4 <- select(SLC_2007.Subset, area_code,kitchen_shared, per_cap_con_all,hh_size_all, )

SLC_2007.Subset4  <- SLC_2007.Subset4 %>%
  mutate(
    hh_size_all = case_when(
      hh_size_all == 1 ~ "1 person",
      hh_size_all == 2 ~ "2 person",
      hh_size_all == 3 ~ "3 person",
      hh_size_all >= 4 ~ "4 or more"
    )
  )


SLC_2007.Subset4  <- SLC_2007.Subset4 %>%
  filter(area_code != "Unknown")
```

```
SLC_2007.Subset2 <- SLC_2007.Subset %>%
        rename("Type of Toilet" = type_toilet)

# Calculate summary statistics for each Type of Toilet
summary_table <- SLC_2007.Subset2 %>%
        group_by(toilet_shared) %>%
        summarise(
                Count = n(),
                Min = min(per_cap_con_all, na.rm = TRUE),
```

```
                Q1 = quantile(per_cap_con_all, 0.25, na.rm = TRUE),
                Median = median(per_cap_con_all, na.rm = TRUE),
                Mean = mean(per_cap_con_all, na.rm = TRUE),
                Q3 = quantile(per_cap_con_all, 0.75, na.rm = TRUE),
                Max = max(per_cap_con_all, na.rm = TRUE),
                SD = sd(per_cap_con_all, na.rm = TRUE)
        ) %>%
        as.data.frame()
```

4 Inferential Analysis

4.1 Goal 1: To determine if there is a difference in per capita water consumption based on location (area).

-

4.1.1 Test: One-way ANOVA

```
# Select the columns from your dataset
SLC_2007.Goal_1 <- select(SLC_2007.Subset, area_code, per_cap_con_all)
SLC_2007.Goal_1 <- SLC_2007.Goal_1 %>%
        mutate(area_code = recode(area_code,
                                     `1` = "KMA",
                                     `2` = "Other Town",
                                     `3` = "Rural",

        )
        ) %>%
        filter(area_code != "4", area_code != "5")
```

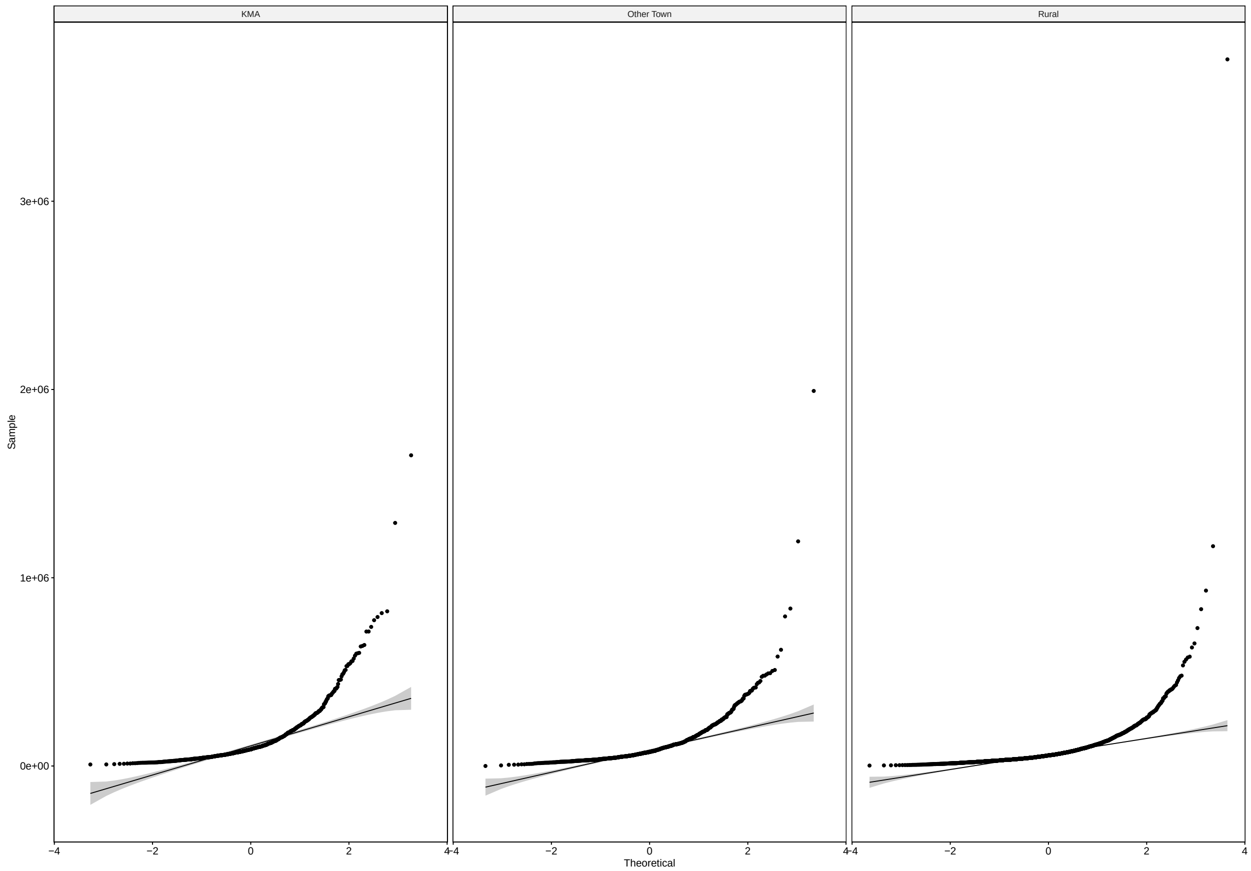
4.2 Check for Normality

Run the Linear Model

```
aov.model.test <- lm(per_cap_con_all ~ area_code, data = SLC_2007.Goal_1)
```

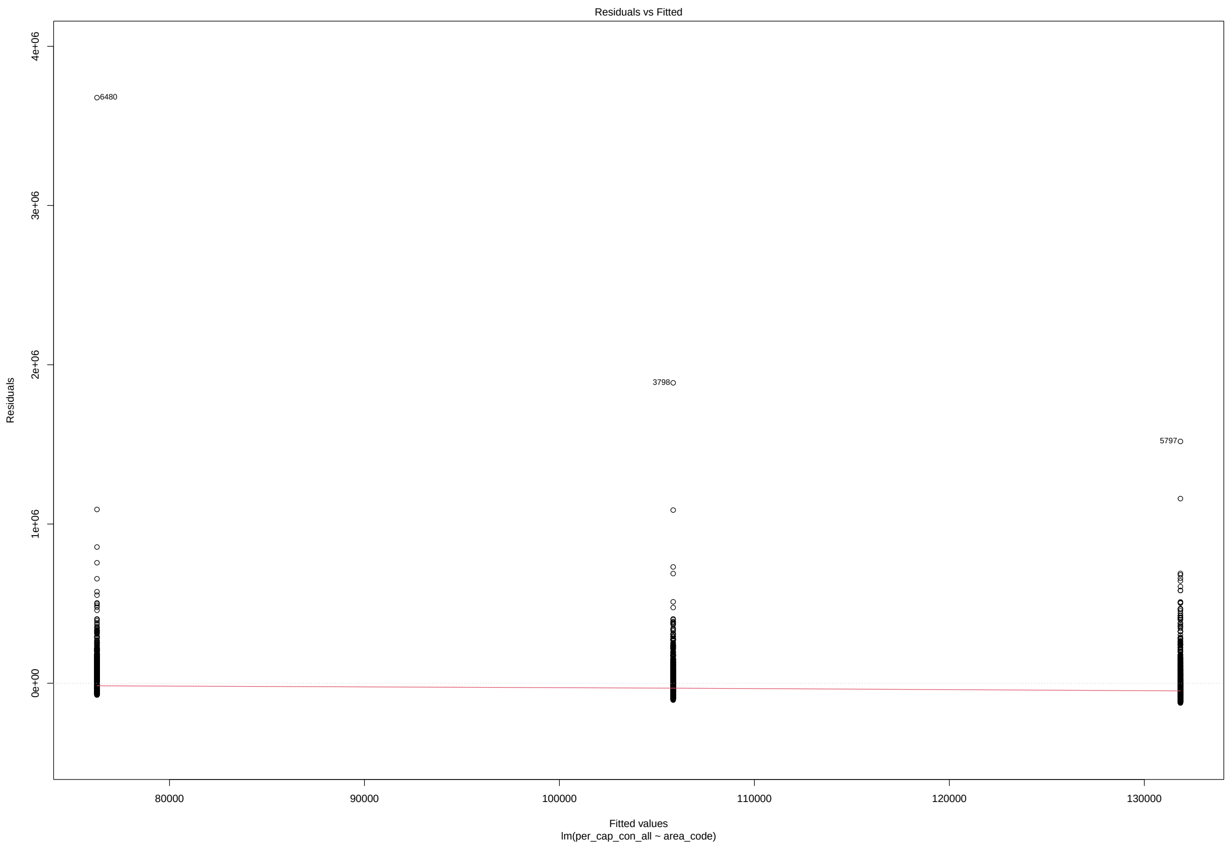
4.3 Normality by Groups

```
# Check normality by groups, ignoring NA values
ggqqplot(na.omit(SLC_2007.Goal_1 ), "per_cap_con_all", facet.by = "area_code")
```



Check for equal variance

```
plot(aov.model.test,1)
```



One-Way ANOVA Test

```
# One-Way ANOVA Test
# aov.test <- aov(per_cap_con_all ~ area_code, data = SLC_2007.Goal_1)
# summary(aov.test)
#
# # Calculate r^2
# RSq <- var(predict(aov.test)) / var(SLC_2007.Goal_1$per_cap_con_all, na.rm = TRUE)
# round(RSq, 4)
# One-Way ANOVA Test
aov.test <- aov(per_cap_con_all ~ area_code, data = SLC_2007.Goal_1)
aov.summary <- summary(aov.test)

# Calculate r^2
RSq <- var(predict(aov.test)) / var(SLC_2007.Goal_1$per_cap_con_all, na.rm = TRUE)
RSq <- round(RSq, 4)

# Extract data for the table
anova_table <- data.frame(
  Df = aov.summary[[1]][, "Df"],
  SumSq = aov.summary[[1]][, "Sum Sq"],
  MeanSq = aov.summary[[1]][, "Mean Sq"],
  FValue = aov.summary[[1]][, "F value"],
  Pr = aov.summary[[1]][, "Pr(>F)"]
)
```

```r
# Add R-squared to the table
anova_table <- rbind(anova_table,
                     data.frame(Df = NA,
                                SumSq = NA,
                                MeanSq = NA,
                                FValue = NA,
                                Pr = RSq))


# anova_table
```

4.4 multiple comparisons test

```r
# pairwise.t.test(SLC_2007.Goal_1$per_cap_con_all, SLC_2007.Goal_1$area_code, p.adjust.method = "bonfer
# Perform the pairwise t-test
pairwise_test <- pairwise.t.test(SLC_2007.Goal_1$per_cap_con_all, SLC_2007.Goal_1$area_code, p.adjust.me

# Extract data for the table
pairwise_matrix <- pairwise_test$p.value
pairwise_values <- as.data.frame(pairwise_matrix)

# Create a new data frame to store the pairwise t-test results
pairwise_table <- data.frame(
  Comparison = rownames(pairwise_values),
  KMA = pairwise_values[, "KMA"],
  Other_Town = pairwise_values[, "Other Town"]
)

# pairwise_table
```

4.5 Comparison Plot

```r
# Create the plot using ggbetweenstats()
anova_plot <- ggbetweenstats(
  data = SLC_2007.Goal_1,
  x = area_code,
  y = per_cap_con_all,
  type = "parametric",
  var.equal = TRUE,
  plot.type = "box",
  pairwise.comparisons = TRUE,
  p.adjust.method = "bonferroni",
  pairwise.display = "significant",
  centrality.plotting = FALSE,
  bf.message = FALSE
)

# Modify y-axis title
anova_plot <- anova_plot +
```

```r
  ylab("Per Capita Water Consumption") +
  xlab("Area")

# Customize the theme to enlarge elements
anova_plot <- anova_plot +
  theme(
    text = element_text(size = 16), # Increase base text size
    axis.title = element_text(size = 18), # Increase axis title size
    axis.text = element_text(size = 14), # Increase axis text size
    plot.title = element_text(size = 20, face = "bold"), # Increase plot title size
    strip.text = element_text(size = 16), # Increase facet label text size
    legend.text = element_text(size = 14), # Increase legend text size
    legend.title = element_text(size = 16), # Increase legend title size
    panel.spacing = unit(1, "lines") # Increase space between facets
  )

# Display the plot
# anova_plot
```

4.6 Goal 2: To determine if there is a difference in per capita water consumption based on whether toilet facilities are shared or not.

-

4.7 Test: Independent Sample t-test

```r
# Prepare the dataset
SLC_2007.Goal_2 <- select(SLC_2007.Subset, toilet_shared, per_cap_con_all)
SLC_2007.Goal_2 <- SLC_2007.Goal_2 %>%
        mutate(toilet_shared = recode(toilet_shared,
                                      `1` = "EXCLUSIVE USE",
                                      `2` = "SHARED",

        )
        ) %>%
  filter(toilet_shared != "NA")

# Run the independent sample t-test
t_test_result <- SLC_2007.Goal_2 %>%
        filter(toilet_shared != "Unknown") %>% # Remove rows with "Unknown" values
        tbl_summary(
                by = toilet_shared,
                type = c(per_cap_con_all = "continuous"),
                statistic = list(per_cap_con_all ~ "{mean} ({sd})"),
                missing = "no",
                label = list(
                        per_cap_con_all ~ "Per Capita Water Consumption"
                )
        ) %>%
        add_difference()
```

```
# Display the result
# t_test_result
```

4.8 Independent Sample t-test

```
# Run the independent sample t-test using Version 2
t_test_result_v2 <- nice_t_test(data = SLC_2007.Goal_2,
                                response = "per_cap_con_all",
                                group = "toilet_shared",
                                warning = FALSE) %>%
        nice_table()

# Display the result
# t_test_result_v2
```

4.9 Goal 3:To determine if there is a relationship between per capita water consumption and household size (add control – area, toilet, kitchen)

-

```
SLC_2007.Goal_3 <- select(SLC_2007.Subset, per_cap_con_all,hh_size_all,area_code,toilet_shared,kitchen_s
# recode variables.
SLC_2007.Goal_3 <- SLC_2007.Goal_3 %>%
        mutate(
                toilet_shared = recode(toilet_shared,
                                       `1` = "EXCLUSIVE USE",
                                       `2` = "SHARED"
                ),
                kitchen_shared = recode(kitchen_shared,
                                        `1` = "EXCLUSIVE USE",
                                        `2` = "SHARED",
                                        `3` = "NONE"
                ),
                area_code = recode(area_code,
                                  `1` = "KMA",
                                  `2` = "Other Town",
                                  `3` = "Rural",

                ),
                hh_size_all = case_when(
                        hh_size_all == 1 ~ "1 person",
                        hh_size_all == 2 ~ "2 person",
                        hh_size_all == 3 ~ "3 person",
                        hh_size_all >= 4 ~ "4 or more"
                )
        )%>%
        filter(area_code != "4", area_code != "5",
```

```
                kitchen_shared != "NA",
                toilet_shared != "NA",

        )
```

4.10 multiple linear regression model

```
# Convert nominal variables to factors
SLC_2007.Goal_3_recoded <- SLC_2007.Goal_3 %>%
        mutate(
                toilet_shared = as.factor(toilet_shared),
                kitchen_shared = as.factor(kitchen_shared),
                area = as.factor(area_code),
                hh_size_all = as.factor(hh_size_all)

        )

# Run the multiple linear regression model
model <- lm(per_cap_con_all ~ hh_size_all + area_code + toilet_shared + kitchen_shared, data = SLC_2007
tab_model(model)
```

per_cap_con_all

Predictors

Estimates

CI

p

(Intercept)

197755.96

189129.45 – 206382.47

<0.001

hh size all [2 person]

-35544.51

-43693.29 – -27395.73

<0.001

hh size all [3 person]

-63484.62

-71991.16 – -54978.08

<0.001

hh size all [4 or more]

-89313.20

-96073.49 – -82552.90

<0.001

area code [Other Town]

-26864.13

-35436.19 – -18292.07

<0.001

area code [Rural]

-58285.36

-65595.41 – -50975.30

<0.001

toilet shared [SHARED]

-20724.74

-28938.66 – -12510.82

<0.001

kitchen shared [NONE]

-25857.20

-35979.09 – -15735.31

<0.001

kitchen shared [SHARED]

-11615.35

-22932.87 – -297.84

0.044

Observations

5699

R2 / R2 adjusted

0.155 / 0.153

4.11 Diagnostic Plots

```
# Diagnostic Plots
check_model(model)
```

5 Advanced Data Analysis

```
SLC_2007.Subset200 <- sample_n(SLC_2007.Subset, 200)

SLC_2007.Subset200 <- SLC_2007.Subset200 %>%
  filter(area_code != 4 & area_code != 5)
```

5.1 Filter the dataset to only include Location and Per Capita water Consumption

```
SLC_2007.Subset200_filtered <- SLC_2007.Subset200 %>%
  select(area_code, per_cap_con_all,hh_size_all)

SLC_2007.Subset200_filtered  <- SLC_2007.Subset200_filtered  %>%
  mutate(
    hh_size_all = case_when(
```

```
      hh_size_all == 1 ~ "1 person",
      hh_size_all == 2 ~ "2 person",
      hh_size_all == 3 ~ "3 person",
      hh_size_all >= 4 ~ "4 or more"
    )
  )

SLC_2007.Subset200_filtered$area_code <- recode(SLC_2007.Subset200_filtered$area_code,
                                                "Rural" = 1,
                                                "KMA" = 2,
                                                "Other Town" = 3)

SLC_2007.Subset200_filtered$hh_size_all <- recode(SLC_2007.Subset200_filtered$hh_size_all,
                                                  "1 person" = 1,
                                                  "2 person" = 2,
                                                  "3 person"= 3,
                                                  "4 or more"= 4
)
```

5.2 Create the dissimilarity matrix using Gower's distance

```
DistanceMatrix <- daisy(SLC_2007.Subset200_filtered, metric = "gower")
```

5.3 Perform hierarchical clustering

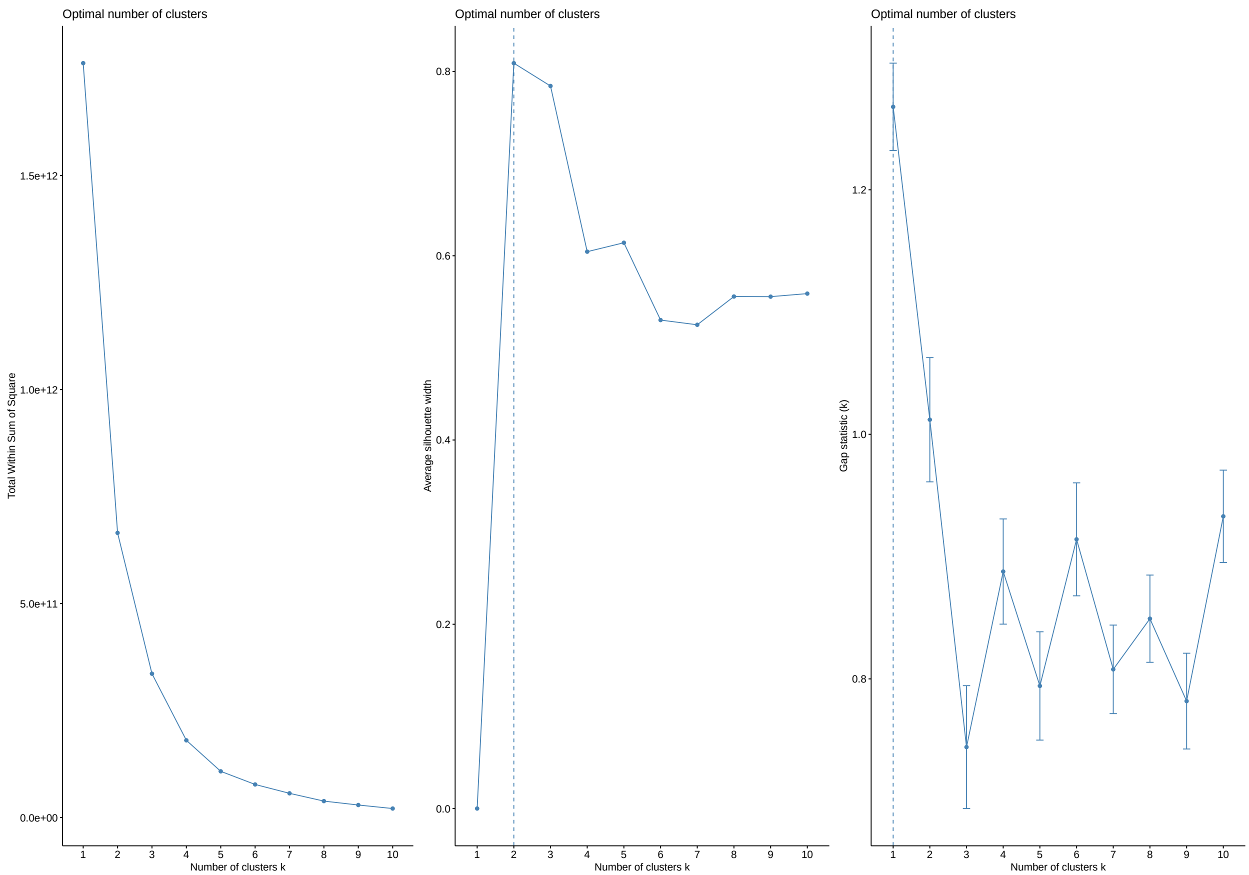
```
hc <- hclust(DistanceMatrix, method = "complete")
```

5.4 Determine the optimal number of clusters

```
library(factoextra)

plot1 <- fviz_nbclust(SLC_2007.Subset200_filtered, FUN = hcut, method = "wss")
plot2 <- fviz_nbclust(SLC_2007.Subset200_filtered, FUN = hcut, method = "silhouette")
gap_stat <- clusGap(SLC_2007.Subset200_filtered, FUN = hcut, nstart = 25, K.max = 10, B = 50)
```

```
## Clustering k = 1,2,..., K.max (= 10): .. done
## Bootstrapping, b = 1,2,..., B (= 50)  [one "." per sample]:
## .................................................. 50
```

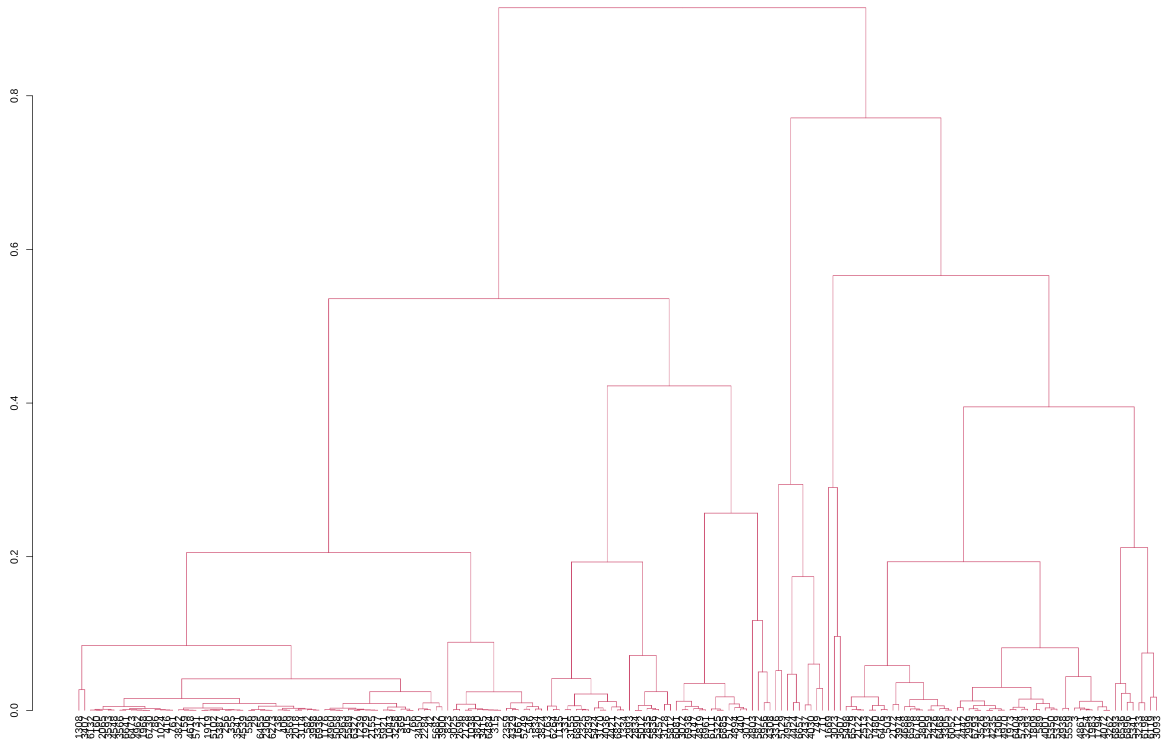
```r
plot3 <- fviz_gap_stat(gap_stat)

grid.arrange(plot1, plot2, plot3, ncol = 3)
```




```r
# 3 plots side by side
#ggarrange
```

5.5 Visualize the dendrogram

```r
dendrogram <- as.dendrogram(hc)
ColourDendrogram <- color_branches(dendrogram, h = 3)
plot(ColourDendrogram)
```



Assign cluster labels to the observations

```
clusterLabs <- cutree(hc, k = 2)  # Replace  with the optimal number of clusters found
SLC_2007.Subset200_clusters <- cbind(SLC_2007.Subset200_filtered, cluster = as.factor(clusterLabs))
```

5.6 Visualize the clusters in a 2D plot

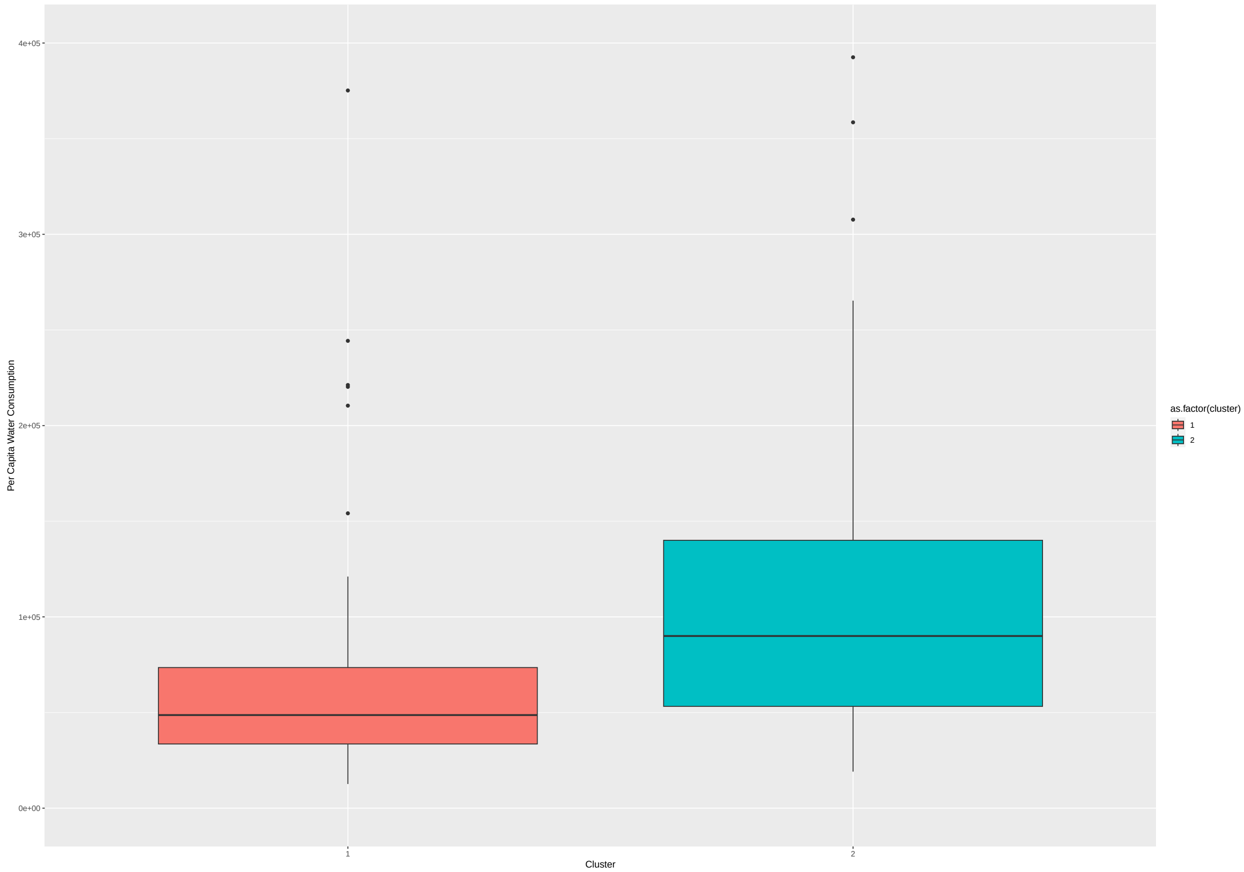
```
fviz_cluster(list(data = SLC_2007.Subset200_filtered, cluster = clusterLabs))
```

5.7 Create a cluster summary

```
cluster_summary <- SLC_2007.Subset200_clusters %>%
  group_by(cluster) %>%
  summarise(across(everything(), mean, na.rm = TRUE))
```

5.8 Visualize the cluster summary

```
ggplot(SLC_2007.Subset200_clusters, aes(x = as.factor(cluster), y = per_cap_con_all, fill = as.factor(cl
  geom_boxplot() +
  coord_cartesian(ylim = c(0, 4e+05)) +
  labs(x = "Cluster", y = "Per Capita Water Consumption")
```




```
# Create a summary table for per capita water consumption by cluster
summary_table_boxplot <- SLC_2007.Subset200_clusters %>%
  mutate(cluster = as.factor(cluster)) %>%
  select(cluster, per_cap_con_all) %>%
  gtsummary::tbl_summary(by = cluster,
                         missing = "no",
                         type = list(per_cap_con_all = "continuous"),
                         statistic = list(per_cap_con_all = "{mean} ({sd}); Median: {median}; IQR: {p25

# Display the summary table
summary_table_boxplot
```

```
## Table printed with `knitr::kable()`, not {gt}. Learn why at
```

```
## https://www.danieldsjoberg.com/gtsummary/articles/rmarkdown.html
## To suppress this message, include `message = FALSE` in code chunk header.
```

Characteristic

1, N = 119

2, N = 66

per_cap_con_all

62,731 (50,524); Median: 48,680; IQR: 33,562-73,519

129,553 (139,887); Median: 90,008; IQR: 53,234-140,047

```
# Create a summary table
summary_table <- SLC_2007.Subset200_clusters %>%
  mutate(cluster = as.factor(cluster),
         area_code = recode(area_code,
                            "1" = "Rural",
                            "2" = "KMA",
                            "3" = "Other Town"),
         hh_size_all = recode(hh_size_all,
                              "1" = "1 person",
                              "2" = "2 person",
                              "3" = "3 person",
                              "4" = "4 or more")) %>%
  group_by(cluster) %>%
  select(cluster, area_code, hh_size_all, per_cap_con_all) %>%
  gtsummary::tbl_summary(by = cluster,
                         missing = "no",
                         type = list(area_code = "categorical",
                                     hh_size_all = "categorical",
                                     per_cap_con_all = "continuous"),
                         statistic = list(area_code = "{n} ({p}%)",
                                          hh_size_all = "{n} ({p}%)",
                                          per_cap_con_all = "{mean} ({sd})"))

# Display the summary table
summary_table
```

```
## Table printed with `knitr::kable()`, not {gt}. Learn why at
## https://www.danieldsjoberg.com/gtsummary/articles/rmarkdown.html
## To suppress this message, include `message = FALSE` in code chunk header.
```

Characteristic

1, N = 119

2, N = 66

area_code

KMA

17 (14%)

8 (12%)

Other Town

22 (18%)

9 (14%)

Rural

80 (67%)

49 (74%)

hh_size_all

1 person

0 (0%)

38 (58%)

2 person

0 (0%)

28 (42%)

3 person

29 (24%)

0 (0%)

4 or more

90 (76%)

0 (0%)

per_cap_con_all

62,731 (50,524)

129,553 (139,887)

6 Composite Index

6.1 Recode the variables

```
SLC_2007.Subset_Index <- SLC_2007.Subset %>%
  select(kitchen_shared,toilet_shared,water_source_shared,water_meter,per_cap_con_all,hh_size_all,water_

# remove NAs
SLC_2007.Subset_Index <- na.omit(SLC_2007.Subset_Index)
```

```r
SLC_2007.Subset_Index <- SLC_2007.Subset_Index %>%
  mutate(
    kitchen_shared_recode = ifelse(kitchen_shared == "SHARED", 1, 0),
    toilet_shared_recode = ifelse(toilet_shared == "SHARED", 1, 0),
    water_source_shared_recode = ifelse(water_source_shared == "YES", 1, 0),
    water_meter_recode = ifelse(water_meter == "Group", 1, 0)
  )
```

6.2 Calculate the sum of the recoded variables

```r
SLC_2007.Subset_Index <- SLC_2007.Subset_Index %>%
  mutate(shared_facilities_sum = kitchen_shared_recode +
    toilet_shared_recode +
    water_meter_recode
    # water_source_shared_recode
  )

# Calculate the highest possible score
highest_possible_score <- 3

# Normalize the sum to create the index
SLC_2007.Subset_Index <- SLC_2007.Subset_Index %>%
  mutate(shared_facilities_index = shared_facilities_sum / highest_possible_score)
```

6.3 Cronbach Alpha analysis

```r
# List the names of the columns (variables) you will include in your index
Cron_Cols <- c("kitchen_shared_recode",
               "toilet_shared_recode",
               "water_meter_recode" )

# Create a subset of the data with only the selected columns
Cron_Data <- subset(SLC_2007.Subset_Index, select = Cron_Cols)


# Run the Cronbach Alpha analysis
Cron.Alpha <- psych::alpha(Cron_Data)
```

```r
alpha_table <- data.frame(
  raw_alpha = Cron.Alpha[["total"]][["raw_alpha"]],
  std_alpha = Cron.Alpha[["total"]][["std.alpha"]],
  G6_smc = Cron.Alpha[["total"]][["G6(smc)"]],
```

```r
  average_r = Cron.Alpha[["total"]][["average_r"]],
  S_N = Cron.Alpha[["total"]][["S/N"]],
  ase = Cron.Alpha[["total"]][["ase"]],
  mean = Cron.Alpha[["total"]][["mean"]],
  sd = Cron.Alpha[["total"]][["sd"]],
  median_r = Cron.Alpha[["total"]][["median_r"]]
)


kable(alpha_table, digits = 2, caption = "Cronbach Alpha Table") %>%
  kable_styling(position = "center")
```

Cronbach Alpha Table

raw_alpha

std_alpha

G6_smc

average_r

S_N

ase

mean

sd

median_r

0.65

0.66

0.61

0.39

1.95

0.05

0.21

0.31

0.33

```r


# Extract relevant information from the Cron.Alpha object
alpha_stats <- data.frame(
        items = rownames(Cron.Alpha$alpha.drop),
        raw_alpha = Cron.Alpha$alpha.drop[, "raw_alpha"],
        std_alpha = Cron.Alpha$alpha.drop[, "std.alpha"],
        G6_smc = Cron.Alpha$alpha.drop[, "G6(smc)"],
        mean = Cron.Alpha$item.stats[, "mean"],
        sd = Cron.Alpha$item.stats[, "sd"]
)

# Print overall alpha values
cat("Overall alpha values:\n")
```

```
## Overall alpha values:
```

```r
cat("Raw alpha:", Cron.Alpha$total$raw_alpha, "\n")
```

```
## Raw alpha: 0.6485423
```

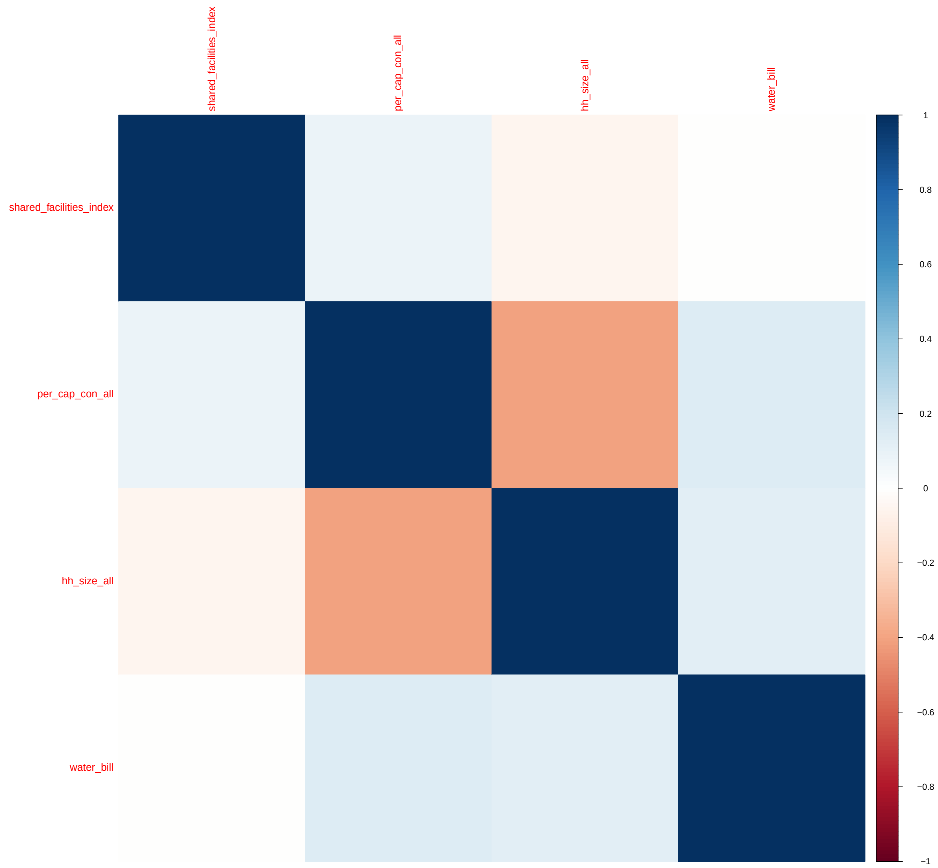
```r
cat("Standardized alpha:", Cron.Alpha$total$std.alpha, "\n")
```

```
## Standardized alpha: 0.661318
```

```r
cat("\n")
```

```r
# Formatting and printing the alpha_stats table
formatted_alpha_stats <- alpha_stats %>%
        kable(col.names = c("Items", "Raw Alpha", "Standardized Alpha", "G6 (smc)", "Mean", "SD"),
              caption = "Cronbach's Alpha Analysis", align = 'c', digits = 2)  %>%
        kable_styling(latex_options = "hold_position", position = "center") # Center the table in the P

# formatted_alpha_stats
```

```r
# Check for missing values and handle them
correlation_data <- SLC_2007.Subset_Index %>%
  select(shared_facilities_index, per_cap_con_all, hh_size_all,water_bill) %>%
  na.omit()

# Ensure data types are numeric
correlation_data$hh_size_all <- as.numeric(correlation_data$hh_size_all)
correlation_data$per_cap_con_all <- as.numeric(correlation_data$per_cap_con_all)
correlation_data$water_bill <- as.numeric(correlation_data$water_bill)
# Calculate the correlation matrix
correlation_matrix <- cor(correlation_data)

# Create the correlation plot
corrplot(correlation_matrix, method = "color")
```




```r
# Convert the correlation matrix to a table
correlation_table <- kable(correlation_matrix, digits = 3, caption = "Correlation Matrix") %>%
  kable_styling(position = "center")

# Print the correlation table
# correlation_table
```

7 Inferential Analysis of Composite Index

7.1 Goal 5 Is there a relationship between shared facilities index and per capita water consumption?

- Test: Simple Linear Regression

```r
indexModel <- lm(per_cap_con_all ~ shared_facilities_index, data = SLC_2007.Subset_Index)
tab_model(indexModel)
```

per_cap_con_all

Predictors

Estimates

CI

p

(Intercept)

122261.32

99008.29 – 145514.34

<0.001

shared facilities index

31123.76

-30711.05 – 92958.58

0.322

Observations

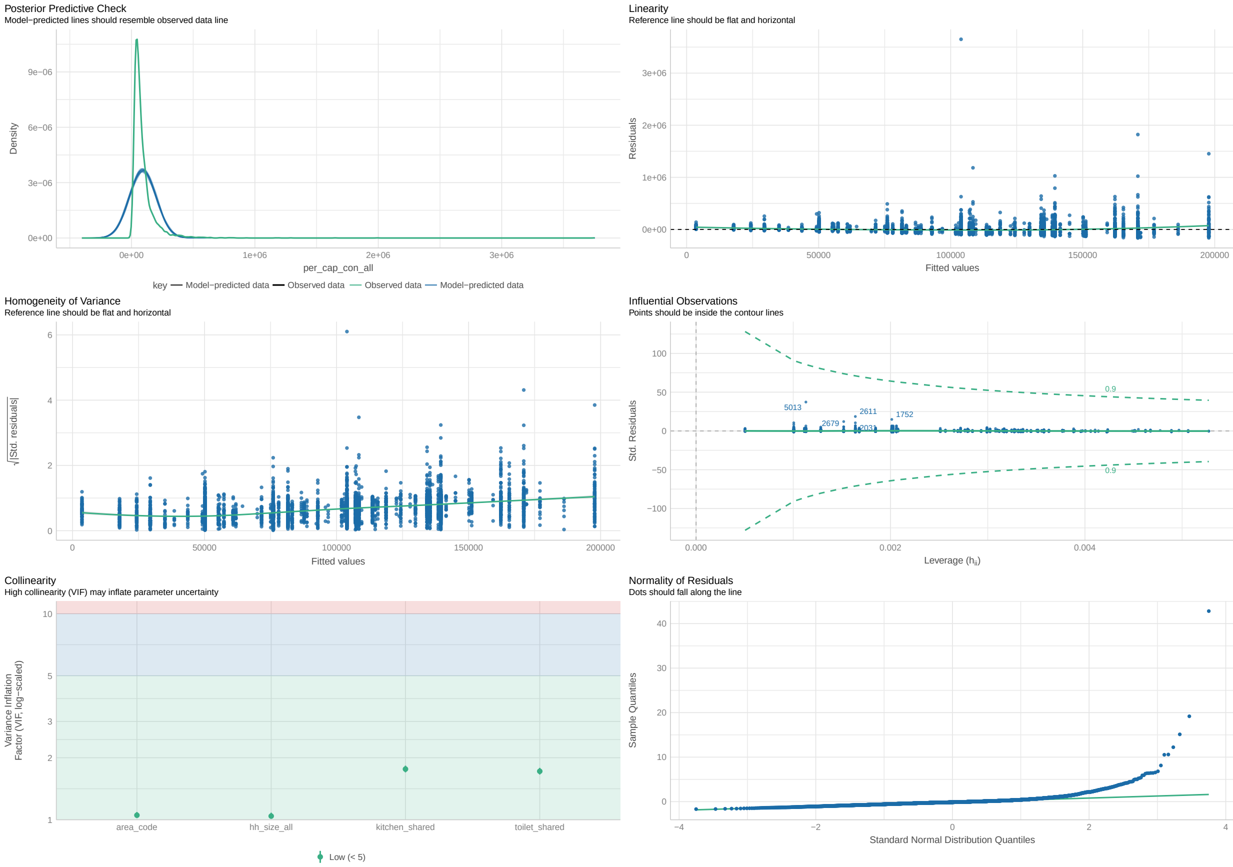
154

R2 / R2 adjusted

0.006 / -0.000

7.2 Diagnostic Plots

```
# Diagnostic Plots
check_model(model)
```


Posterior Predictive Check
Model−predicted lines should resemble observed data line
Density
per_cap_con_all
key — Model−predicted data — Observed data — Observed data — Model−predicted data
Linearity
Reference line should be flat and horizontal
Residuals
Fitted values
Homogeneity of Variance
Reference line should be flat and horizontal
√|Std. residuals|
Fitted values
Influential Observations
Points should be inside the contour lines
Std. Residuals
Leverage (hii)
Collinearity
High collinearity (VIF) may inflate parameter uncertainty
Variance Inflation Factor (VIF, log−scaled)
area_code
hh_size_all
kitchen_shared
toilet_shared
Low (< 5)
Normality of Residuals
Dots should fall along the line
Sample Quantiles
Standard Normal Distribution Quantiles