

# **DeCAV Tool: A Dengue Case Analysis and Visualization Tool**

A System Presented to the  
Faculty of College of Arts and Sciences  
Rizal Technological University

In Partial Fulfillment of the Requirements for the Degree of  
Bachelor of Science in Statistics

by

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**RIZAL TECHNOLOGICAL UNIVERSITY**  
 Cities of Mandaluyong and Pasig  
**COLLEGE OF ARTS AND SCIENCES**



This is to certify that the research result and innovation consist of improvements/modifications made to existing design, process, or product,

### **DeCAV Tool: A Dengue Case Analysis and Visualization Tool**

of the project developed by the following developers:

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was adopted and utilized at Mandaluyong City Epidemiology and Surveillance Unit.

Issued on the 21st day of May 2024, Mandaluyong City, Philippines

  
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## Description of the System

Endemic is the term used by medical professionals to describe a disease that regularly occurs in a specific place. Dengue fever is considered endemic in the Philippines. As of February 2024, there are already thousands of dengue cases, and a total of 67 deaths have been reported for this year. According to the Department of Health, these numbers already represent a downtrend compared to previous years.

Given the ongoing challenge posed by dengue fever, it is essential and practical to have a tool that can help analyze and understand large quantities of data related to dengue cases. Such a tool where it is capable of easily and rapidly providing visual interpretations of the data. Since dengue fever is a regular occurrence in the Philippines, local government units (LGUs) routinely report these cases in their respective cities.

As a result, we introduce an innovative system, Dengue Case Analysis and Visualization Tool (DeCAV Tool), designed to provide visual presentations of the data and is capable of downloading those images for various purposes. It also generates simple interpretations of the data for easier understanding of the graphs and aims to give assistance to the user in any way they choose to use the graphs. Visual presentations such as a threshold histogram that visualizes the frequency and intensity of dengue cases based on the date of acquisition and age Group Bar Graph that illustrates differences in dengue incidence among various age groups, highlighting which age groups are most likely to contract

dengue fever, Gender Pie Chart that determines the gender distribution of dengue cases, showing which gender is more frequently affected, Age Group By Gender Stack Bar Graph that illustrates the differences on the age group and gender of those who acquired dengue fever, and lastly it also provides a presentation showing the number of dengue cases in all barangays in the city.

This innovative system aims to provide aid to the local government unit with a tool needed to monitor dengue cases in a city, this tool ensures reactive data processing that helps to utilize and maximize the time of those who will use this system.

## Purpose

DeCAV Tool: A Dengue Case Analysis and Visualization Tool is vital for the public. Regular monitoring makes it easier to identify crucial thresholds, identify outbreaks early, and allocate resources effectively. Health officials can minimize dengue incidence and protect at-risk groups by looking at past data to find patterns and implement timely preventive interventions, like mosquito control and public awareness programs.

Long-term dengue monitoring improves resource distribution considerably. Health officials can allocate resources to the most afflicted areas in a prioritized manner if they have knowledge about the times and locations of dengue case increases. By ensuring that interventions such as mosquito control, public

awareness campaigns, and increased medical support are implemented properly, this tailored method maximizes their effectiveness and lowers the burden of disease on communities.

Using R to perform thorough monitoring and analysis of dengue cases over a five-year period enhances the ability to contain and stop outbreaks. By ensuring prompt, targeted, and efficient public health responses, this strategy safeguards communities against this enduring and potentially fatal illness. Health officials and academics can create effective ways to control and eventually eradicate dengue by methodically collecting and evaluating data on the disease, which will improve the health outcomes for impacted communities.

### **Scope and Limitation of the System**

The scope of the DeCAV Tool: A Dengue Case Analysis and Visualization Tool includes allowing users to upload Excel files with dengue case data and perform two main types of analysis: threshold computation and case analysis. For threshold computation, the tool calculates weekly averages from historical data to set alert and epidemic thresholds. It then compares the current data to these thresholds to identify potential outbreaks. The case analysis feature offers various visualizations, such as incidence rates, age group distributions, gender comparisons, and the number of cases per barangay. These features provide detailed insights into the spread and demographics of dengue cases.

However, there are some limitations to this system. The accuracy of the analysis depends heavily on the quality and completeness of the uploaded data; any errors or missing data can lead to inaccurate results. The tool is best suited for users who have a basic understanding of epidemiological data and statistical concepts, which might limit its use for those without such knowledge. Additionally, the performance of the tool may slow down with very large datasets, affecting its responsiveness. Lastly, while the tool provides useful visualizations and basic statistical analysis, it does not support more advanced epidemiological modeling or predictive analytics.

## Definition of Terms

**Dengue Case Analysis and Visualization Tool** - the name of the system being used.

**Dengue Fever** - it is a viral infection spread through people by mosquitoes, and is considered endemic in the Philippines.

**Incidence Rate** - the rate of dengue cases that occurred at a specific time or date.

**Morbidity Week** - refers to a specific week during which the prevalence, incidence, and other metrics of a particular disease like dengue are monitored, recorded, or analyzed.

**Population Size** - the total number of individuals presented in the data, the number of people that acquired dengue fever.

**Threshold** - it is a specific point or level at which something starts to happen or change like an outbreak of a disease.

## Systems Available in the Global Market

In the global market, there are numerous dengue monitoring cases; identifying threshold using r. Such as the Philippine integrated disease surveillance and response. "PIDSR" Vaccine preventable disease (VPD) surveillance under the umbrella of the Philippine Integrated Disease Surveillance and Response (PIDSR) that was established in 2007 has an objective of improving the quality of disease surveillance nationwide, thus, assisting in disease prevention and control programs of the Department of Health. The goal is to improve the capacity of the health system through timely detection and appropriate response to diseases and conditions with high levels of morbidity, disability, and mortality.

Disease Surveillance is recognized as the cornerstone of public health decision-making and practice. Surveillance data provide information that can be used for priority setting, policy decisions, planning, implementation, resource mobilization and allocation, prediction, and early detection of epidemics. A surveillance system can also be used for monitoring, evaluation, and improvement of disease prevention and control programs.

Unlike Philippine Integrated Disease Surveillance and Response (PIDSR) the DeCAV Tool is designed so that users can upload excel files with specified columns, like Case\_Date, Age, Gender, and Barangay. After the material is uploaded, the system uses the user-provided population size as a basis for processing the data to determine monthly incidence rates. In addition, the system

summarizes gender statistics, ages, and cases per barangay. Textual statistics regarding age groups, gender distribution, and the number of instances within a given time frame are available for users to view. In addition, the system provides four distinct kinds of visualizations: a gender pie chart, an age group by gender stack bar graph, a threshold histogram, and an age group bar graph. You can save these plots as PNG files to use offline.

## **Enhancement**

DeCAV Tool: A Dengue Case Analysis and Visualization Tool is an evolving system with the means for future enhancement and development. Here are a few conceivable improvements:

First and foremost, our current system only accepts excel files which means an end-user cannot upload files in other formats. So for future development, we would like to offer other uploading file options like CSV and plain text.

Secondly, our system can only download the graphs individually. So, for future enhancement, we want to download them all at once instead of one by one.

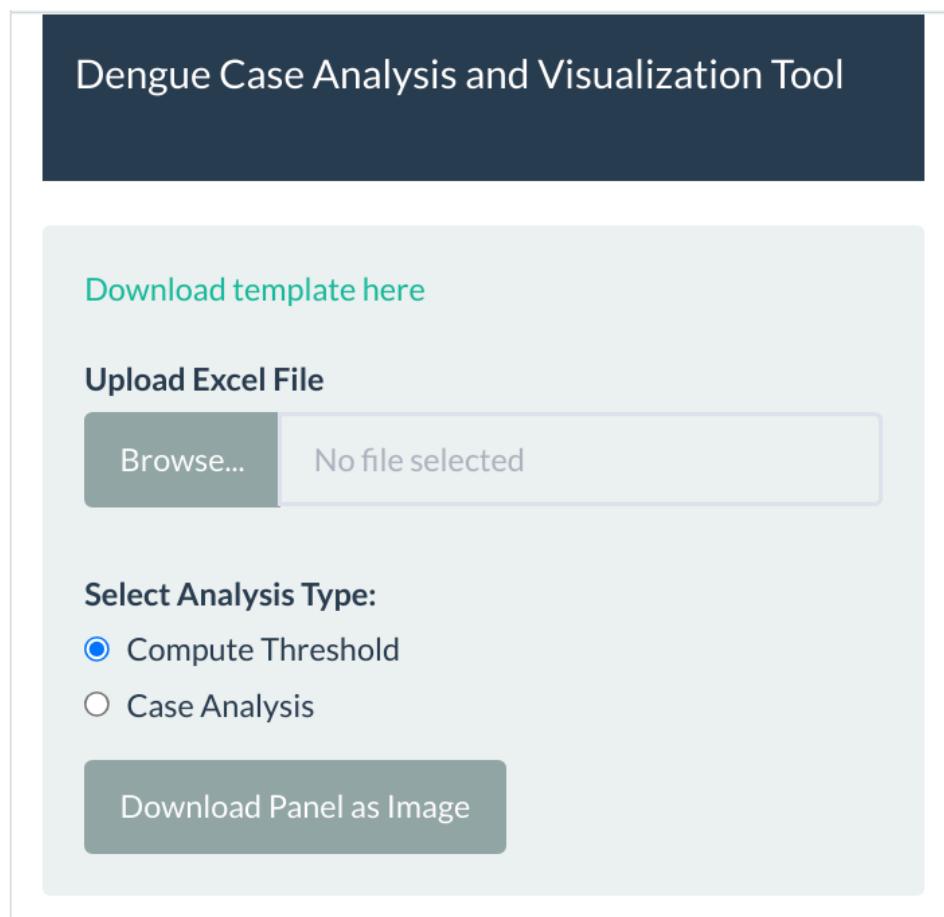
Furthermore, our system cannot send an automatic email containing the end product to the user, So for future development, we want it to be modified for the convenience of the user.

Lastly, the system might be expanded to provide accessible data reports. The user could customize their data based on the name, age, gender, and time

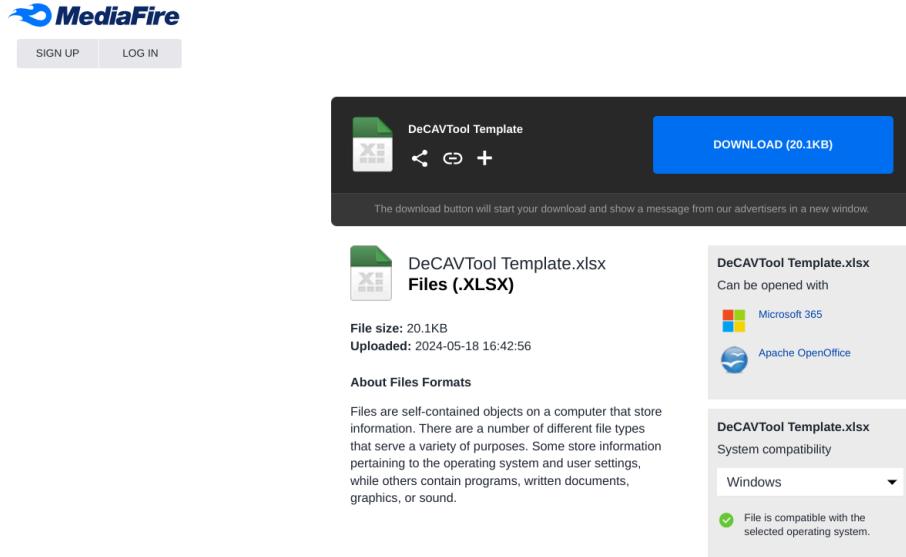
frames and generate those in a variety of formats, such as plots. This would increase the system's flexibility and give the user access to the precise data they require for their analysis.

## User Manual

The DeCAV Tool's main panel will feature a download button for the template, an option to upload an Excel file, and a selection for the analysis type. This panel will also include a download option for graphs along with their interpretations.



To use the DeCAV Tool, the user should start by clicking the ‘Download template here’ button. This will open a new window, where the user needs to click the ‘DOWNLOAD’ button to complete the file download.



After downloading the template, the user needs to fill in all the necessary information required for the analysis. On the ‘data’ sheet, the user should input the ‘Case\_Date’, ‘Age’, ‘Gender’, and ‘Barangay’. While on the ‘MW’ sheet, the user should enter the cases per year by morbidity week. Once all the data is entered, save the file.

**DeCAVTool Template**

File Edit View Insert Format Data Tools Extensions Help

100% 123 Arial J K L M N O

J14 A Case\_Date Age Gender Barangay E F G H I J K L M N O

14

Morbidity\_Week 2017 2018 2020 2021 2022 2023 H I J K L M N O P Q R S T U

A1

+ data MW

The user should go to the main panel and then upload the Excel file by clicking the ‘Browse’ button. If the selected analysis type is ‘Compute Threshold’, it will display the table containing the Mean, SD, 2SD, Alert, Epidemic, and Status.

Dengue Case Analysis and Visualization Tool													
Morbidity_Week	2017	2018	2020	2021	2022	2023	Mean	SD	2SD	Alert	Epidemic	Status	
1.00	12.00	17.00	39.00	16.00	5.00	6.00	17.80	12.76	20.92	33.67	51.47	Below Threshold	
2.00	12.00	19.00	48.00	19.00	4.00	4.00	20.40	16.62	27.26	43.88	64.28	Below Threshold	
3.00	11.00	17.00	26.00	11.00	8.00	27.00	14.60	7.16	11.75	18.91	33.51	Below Threshold	
4.00	4.00	11.00	13.00	13.00	3.00	16.00	8.80	4.92	8.07	12.99	21.79	Below Threshold	
5.00	7.00	19.00	5.00	15.00	3.00	10.00	9.80	6.87	11.27	18.14	27.94	Below Threshold	
6.00	5.00	10.00	4.00	10.00	4.00	9.00	6.60	3.13	5.13	8.26	14.86	Below Threshold	
7.00	7.00	10.00	1.00	4.00	4.00	8.00	5.20	3.42	5.61	9.03	14.23	Below Threshold	
8.00	5.00	14.00	4.00	5.00	1.00	10.00	5.80	4.87	7.98	12.85	18.65	Below Threshold	
9.00	7.00	7.00	4.00	5.00	3.00	8.00	5.20	1.79	2.93	4.72	9.92	Below Threshold	
10.00	2.00	8.00	2.00	3.00	2.00	10.00	3.40	2.61	4.28	6.88	10.28	Below Threshold	
11.00	7.00	10.00	3.00	6.00	2.00	5.00	5.60	3.21	5.26	8.47	14.07	Below Threshold	
12.00	5.00	6.00	3.00	4.00	1.00	6.00	3.80	1.92	3.15	5.08	8.88	Below Threshold	
13.00	5.00	4.00	1.00	3.00	2.00	4.00	3.00	1.58	2.59	4.17	7.17	Below Threshold	
14.00	1.00	3.00	0.00	2.00	2.00	4.00	1.60	1.14	1.87	3.01	4.61	Below Threshold	
15.00	3.00	6.00	0.00	2.00	5.00	4.00	3.20	2.39	3.92	6.30	9.50	Below Threshold	
16.00	2.00	6.00	0.00	2.00	3.00	4.00	2.60	2.19	3.59	5.78	8.38	Below Threshold	
17.00	3.00	2.00	0.00	0.00	10.00	6.00	3.00	4.12	6.76	10.88	13.88	Below Threshold	
18.00	2.00	0.00	0.00	0.00	4.00	1.00	1.20	1.79	2.93	4.72	5.92	Below Threshold	
19.00	1.00	1.00	3.00	1.00	4.00	2.00	2.00	1.41	2.32	3.73	5.73	Below Threshold	
20.00	4.00	2.00	0.00	0.00	3.00	1.00	1.80	1.79	2.93	4.72	6.52	Below Threshold	

Selecting ‘Case Analysis’ will ask the user to input the Population Size and the Plot Type. It includes the Incident Rate, Age Group Bar Graph, Gender Pie Chart, Age Group by Gender Stack Bar Graph, and Total Cases per Barangay.



Incident Rate (Monthly Incident Rate of Dengue Cases)

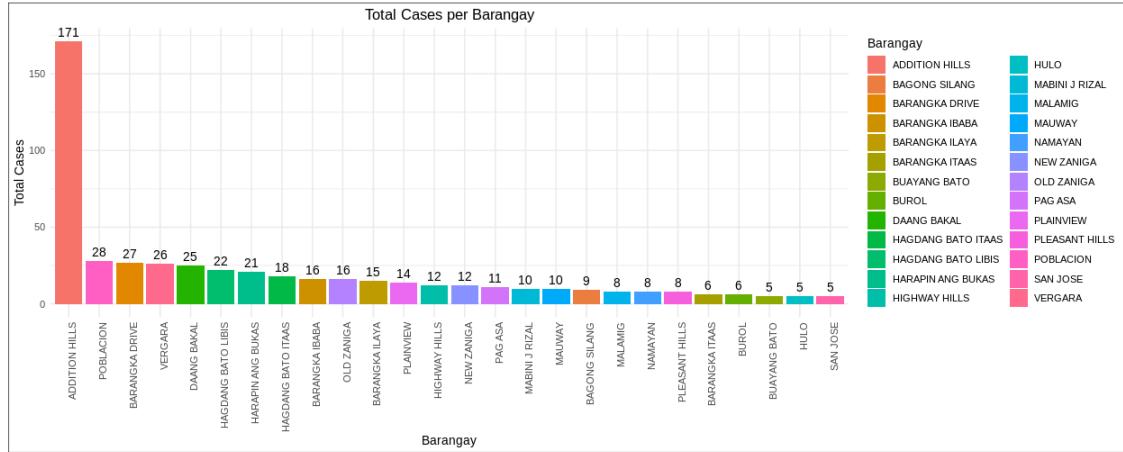


Gender Pie Chart



Age Group by Gender Stack Bar Graph

The barangay with the highest number of cases is ADDITION HILLS with 171 cases, accounting for 33.27 % of the total cases. The second is POBLACION with 28 cases, accounting for 5.45 % of the total cases. The third, fourth, and fifth barangays are BARANGKA DRIVE , VERGARA , and DAANG BAKAL respectively. Finally, SAN JOSE has the fewest cases, with 5 cases, accounting for 0.97 % of the total cases.



Barangay	Total_Cases		
ADDITION HILLS	171	NEW ZANIGA	12
POBLACION	28	PAG ASA	11
BARANGKA DRIVE	27	MABINI J RIZAL	10
VERGARA	26	MAUWAY	10
DAANG BAKAL	25	BAGONG SILANG	9
HAGDANG BATOLIBIS	22	MALAMIG	8
HARAPIN ANG BUKAS	21	NAMAYAN	8
HAGDANG BATITOAS	18	PLEASANT HILLS	8
BARANGKA IBABA	16	BARANGKA ITAAS	6
OLD ZANIGA	16	BUROL	6
BARANGKA ILAYA	15	BUAYANG BATOLIBIS	5
PLAINVIEW	14	HULO	5
HIGHWAY HILLS	12	SAN JOSE	5

### Total Cases per Barangay

There is also an option to download the plot. The user can download the plot itself by selecting the ‘Download Plot as Image’ button and selecting the ‘Download Panel as Image’ button can download the plot together with the interpretation.

## Developer Organization

<b>Personnel</b>	<b>Roles</b>
Aquino, Aien Mariel N.	Systems Available in the Global Market Enhancements
Fajardo, Crisanta Rae M.	Source Code User Manual Definition of Terms
Lumbre, Risshi Mae B.	Description of the System Definition of Terms
Melendres, Erica Jeanne M.	Purpose
Rodriguez, Joshua B.	Source Code User Manual
Sunga, Cheedel Mae J.	Scope and Limitation of the System
Viñalon, Ma. Ellaine S.	User Manual Source Code Bibliography Developer Organization

## Source Code

```
#Install packages  
  
install.packages("shiny")  
  
install.packages("readxl")  
  
install.packages("dplyr")  
  
install.packages("lubridate")  
  
install.packages("ggplot2")  
  
install.packages("shinythemes")  
  
library(shiny)  
  
library(readxl)  
  
library(dplyr)  
  
library(lubridate)  
  
library(ggplot2)  
  
library(shinythemes)  
  
# UI  
  
ui <- fluidPage(theme = shinytheme("flatly"),  
  
  navbarPage("Dengue Case Analysis and Visualization Tool"),  
  
  sidebarLayout(  
  
    sidebarPanel(  
  
      HTML('<a href="https://tinyurl.com/DeCAVTemp" target="_blank">Download  
template here</a><br><br>'),  
  
      fileInput("file", "Upload Excel File"),  
  
      radioButtons("analysis_type", "Select Analysis Type:",
```

```

choices = list("Compute Threshold" = "threshold", "Case Analysis" =
"case_analysis")),

uiOutput("additional_inputs"),actionButton("download_image", "Download
Panel as Image"),

mainPanel(
  id = "main_panel",
  style = "background-color: white;",
  uiOutput("main_output"),
  uiOutput("show_graphs_button"))),
tags$head(tags$script(src =
"https://cdnjs.cloudflare.com/ajax/libs/html2canvas/0.4.1/html2canvas.min.js"),
tags$script(HTML("

Shiny.addCustomMessageHandler('captureContent', function(message) {

  var element = document.getElementById('main_panel');

  html2canvas(element, {
    backgroundColor: 'white',
    onrendered: function(canvas) {
      var img = canvas.toDataURL('image/png');
      var link = document.createElement('a');
      link.href = img;
      link.download = 'dengue_analysis.png';
      document.body.appendChild(link);
      link.click();
    }
  });
}))
```

```

document.body.removeChild(link);});});}); ")))))

# Server

server <- function(input, output, session) {

  observeEvent(input$analysis_type, {

    output$additional_inputs <- renderUI({

      if (input$analysis_type == "case_analysis") {

        tagList(

          numericInput("population", "Population Size:", value = 400000, min = 1),
          selectInput("plot_type", "Select Plot Type:",
                     choices = c("Incidence Rate", "Age Group Bar Graph", "Gender Pie
Chart", "Age Group by Gender Stack Bar Graph", "Total Cases per Barangay")),
          downloadButton("downloadPlot", "Download Plot as Image")))}}

    data <- reactive({

      req(input$file)

      if (input$analysis_type == "case_analysis") {

        read_excel(input$file$datapath, sheet = "data")

      } else {

        read_excel(input$file$datapath, sheet = "MW")})

      #Formula for threshold analysis

      threshold_analysis <- reactive({

        req(input$analysis_type == "threshold", data())

        mw_data <- data())
    })
  })
}

```

```

mw_data <- mw_data %>%
  mutate(
    Mean = rowMeans(select(mw_data, `2017`, `2018`, `2020`, `2021`, `2022`),
    na.rm = TRUE),
    SD = apply(select(mw_data, `2017`, `2018`, `2020`, `2021`, `2022`), 1, sd,
    na.rm = TRUE),
    `2SD` = SD * 1.64,
    Alert = SD + `2SD`,
    Epidemic = Alert + Mean,
    Status = ifelse(`2023` > Epidemic, "Above Threshold", "Below Threshold")
  )
mw_data
})

output$main_output <- renderUI({
  if (input$analysis_type == "threshold") {
    tagList(
      tableOutput("threshold_table"),
      plotOutput("threshold_plot")
    )
  } else {
    tagList(
      plotOutput("plot"),
      fluidRow(

```

```
column(12, align = "center",
       textOutput("age_statistics"),
       textOutput("gender_statistics"),
       textOutput("incidence_statistics"),
       textOutput("brgy_statistics")
     )
  ),
  plotOutput("brgy_bargraph"),
  tableOutput("brgy_cases")
)
}

output$threshold_table <- renderTable({
  req(threshold_analysis())
  threshold_analysis()
})

output$threshold_plot <- renderPlot({
  req(threshold_analysis())
  mw_data <- threshold_analysis()
  ggplot(mw_data, aes(x = Morbidity_Week)) +
    geom_col(aes(y = `2023`), fill = ifelse(mw_data>Status == "Above
Threshold", "red", "green")) +
    geom_line(aes(y = Epidemic), color = "blue", size = 1) +
})
```

```
  labs(x = "Morbidity Week", y = "Cases", title = "Threshold Analysis with
Epidemic Line") +
  theme_minimal() +
  scale_y_continuous(sec.axis = sec_axis(~ ., name = "Epidemic Threshold"))
}

observeEvent(input$show_graphs, {
  showModal(modalDialog(
    title = "Threshold Analysis",
    plotOutput("threshold_plot"),
    easyClose = TRUE,
    footer = modalButton("Close")
  ))
}

MIR <- reactive({
  req(data())
  data.frame <- data()
  data.frame <- data.frame %>%
    mutate(Case_Date = dmy(Case_Date)) %>%
    filter(!is.na(Case_Date))
  incidence_df <- data.frame %>%
    group_by(month = floor_date(Case_Date, "month")) %>%
    summarise(Incidence_Rate = n() / input$population * 1000)
  return(incidence_df)
})
```

```
})

brgy_cases <- reactive({  
  req(data())  
  
  data.frame <- data()  
  
  brgy_case_summary <- data.frame %>%  
    group_by(Barangay) %>%  
    summarise(Total_Cases = n()) %>%  
    arrange(desc(Total_Cases))  
  
  return(brgy_case_summary)  
})  
  
output$brgy_cases <- renderTable({  
  req(input$plot_type == "Total Cases per Barangay")  
  brgy_cases()  
})  
  
output$brgy_bargraph <- renderPlot({  
  req(input$plot_type == "Total Cases per Barangay")  
  brgy_bargraph(brgy_cases())  
})  
  
output$age_statistics <- renderText({  
  req(input$plot_type)  
  
  if (input$plot_type == "Age Group Bar Graph") {  
    age_stats <- table(cut(data()$Age, breaks = c(0, 5, 18, 30, 50, Inf), labels =  
      c("Babies", "Children", "Young Adults", "Middle Age Adults", "Seniors")))
```

```

max_age_group <- names(sort(age_stats, decreasing = TRUE)[1])

second_max_age_group <- names(sort(age_stats, decreasing = TRUE)[2])

third_max_age_group <- names(sort(age_stats, decreasing = TRUE)[3])

min_age_group <- names(sort(age_stats)[1])

paste("In age group:",

      "Individuals aged", max_age_group, "were mostly affected, followed by",

      second_max_age_group, "next were", third_max_age_group,

      "and", min_age_group, "were the rarely affected by dengue.")

} else {""
}

output$gender_statistics <- renderText({

req(input$plot_type)

if (input$plot_type == "Gender Pie Chart") {

  gender_stats <- table(data()$Gender)

  total_cases <- nrow(data())

  female_percentage <- round((gender_stats["female"] / total_cases) * 100, 2)

  male_percentage <- round((gender_stats["male"] / total_cases) * 100, 2)

  paste("In Gender:",

        "A total of", total_cases, "cases,",

        female_percentage, "% of them are Female and",

        male_percentage, "% are Male.")

} else {""
}

})

```

```
output$incidence_statistics <- renderText({  
  req(input$plot_type)  
  if (input$plot_type == "Incidence Rate") {  
    num_cases <- nrow(data())  
    paste("There were", num_cases, "cases of dengue cases")  
  } else {""}  
})  
  
output$brgy_statistics <- renderText({  
  req(input$plot_type)  
  if (input$plot_type == "Total Cases per Barangay") {  
    brgy_data <- brgy_cases()  
    if (nrow(brgy_data) >= 5) {  
      highest_cases_brgy <- brgy_data$Barangay[1]  
      highest_cases <- brgy_data$Total_Cases[1]  
      highest_percentage <- round((highest_cases /  
        sum(brgy_data$Total_Cases)) * 100, 2)  
      second_highest_cases_brgy <- brgy_data$Barangay[2]  
      second_highest_cases <- brgy_data$Total_Cases[2]  
      second_highest_percentage <- round((second_highest_cases /  
        sum(brgy_data$Total_Cases)) * 100, 2)  
      third_highest_cases_brgy <- brgy_data$Barangay[3]  
      third_highest_cases <- brgy_data$Total_Cases[3]  
      fourth_highest_cases_brgy <- brgy_data$Barangay[4]  
    }  
  }  
})
```

```

fourth_highest_cases <- brgy_data$Total_Cases[4]

fifth_highest_cases_brgy <- brgy_data$Barangay[5]

least_cases_brgy <- brgy_data$Barangay[nrow(brgy_data)]

least_cases <- brgy_data$Total_Cases[nrow(brgy_data)]

least_percentage <- round((least_cases / sum(brgy_data$Total_Cases)) *
100, 2)

paste("The barangay with the highest number of cases is",
highest_cases_brgy, "with", highest_cases,

"cases, accounting for", highest_percentage, "% of the total cases. The
second is", second_highest_cases_brgy,
"with", second_highest_cases, "cases, accounting for",
second_highest_percentage, "% of the total cases. The third, fourth, and fifth
barangays are",

third_highest_cases_brgy, ",",
fourth_highest_cases_brgy, ", and",
fifth_highest_cases_brgy, "respectively. Finally,", least_cases_brgy,
"has the fewest cases, with", least_cases, "cases, accounting for",
least_percentage, "% of the total cases.")

} else {

"Not enough data to display barangay statistics."
}

} else {""
})

output$plot <- renderPlot({

```

```
req(input$plot_type)

if (input$plot_type == "Incidence Rate") {

  incidence_rate_plot(MIR())

} else if (input$plot_type == "Age Group Bar Graph") {

  abargraph(data())

} else if (input$plot_type == "Gender Pie Chart") {

  gpiechart(data())

} else if (input$plot_type == "Age Group by Gender Stack Bar Graph") {

  aggraph(data())

}

})

observeEvent(input$download_image, {

  session$sendCustomMessage("captureContent", list())

})

output$downloadPlot <- downloadHandler(
  filename = function() {

    paste("plot", input$plot_type, ".png", sep = "")

  },
  content = function(file) {

    plot <- switch(input$plot_type,
      "Incidence Rate" = incidence_rate_plot(MIR()),
      "Age Group Bar Graph" = abargraph(data()),
      "Gender Pie Chart" = gpiechart(data()),
```

```

"Age Group by Gender Stack Bar Graph" = aggraph(data()),

"Total Cases per Barangay" = brgy_bargraph(brgy_cases()))

ggsave(file, plot = plot, bg = "white")

}}}

# Incidence Rate Plot

incidence_rate_plot <- function(MIR) {

  ggplot(MIR, aes(x = month, y = Incidence_Rate)) +
    geom_line(color = "blue") +
    geom_point(color = "red") +
    labs(x = "Month", y = "Incidence Rate per 1000 People", title = "Monthly
Incidence Rate of Dengue Cases") +
    theme_minimal() +
    theme(plot.title = element_text(hjust = 0.5), plot.background = element_rect(fill
= "white"))}

# Bar Graph

abargraph <- function(data) {

  data <- data %>%
    mutate(Age_Group = cut(Age, breaks = c(0, 5, 18, 30, 50, Inf), labels =
c("Babies", "Children", "Young Adults", "Middle Age Adults", "Old Adults")))

  ggplot(data, aes(x = Age_Group, fill = Age_Group)) +
    geom_bar() +
    labs(x = "Age Group", y = "Count", title = "Age Group Bar Graph") +
    theme_minimal()
}

```

```

theme(plot.title = element_text(hjust = 0.5), plot.background = element_rect(fill
= "white")) +
  geom_text(stat = "count", aes(label = ..count..), vjust = -0.5) }

# Pie Chart gender

gpiechart <- function(data) {

  gender_counts <- table(data$Gender)

  gender_counts_df <- data.frame(Gender = names(gender_counts), Count =
  as.numeric(gender_counts))

  gender_counts_df <- gender_counts_df[order(gender_counts_df$Count,
decreasing = TRUE), ]

  pie_chart <- ggplot(gender_counts_df, aes(x = "", y = Count, fill = Gender)) +
    geom_bar(stat = "identity") +
    coord_polar("y", start = 0) +
    labs(title = "Gender Pie Chart") +
    theme_void() +
    geom_text(aes(label = paste0(Gender, ": ", round(Count/sum(Count) * 100, 1),
"%")), position = position_stack(vjust = 0.5)) +
    scale_fill_manual(values = c("skyblue", "pink")) +
    theme(plot.background = element_rect(fill = "white"))

  return(pie_chart)}

# Stack Bar Graph age at gender

aggraph <- function(data) {

  data <- data %>%

```

```

    mutate(Age_Group = cut(Age, breaks = c(0, 5, 18, 30, 50, Inf), labels =
c("Babies", "Children", "Young Adults", "Middle Age Adults", "Old Adults")))

stacked_bar <- ggplot(data, aes(x = Age_Group, fill = Gender)) +
  geom_bar(position = "stack") +
  labs(x = "Age Group", y = "Count", title = "Age Group by Gender Stack Bar
Graph") +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5), plot.background = element_rect(fill
= "white")) +
  geom_text(stat = "count", aes(label = ..count..), position = position_stack(vjust
= 0.5))

return(stacked_bar)
}

# Barangay Bar Graph

brgy_bargraph <- function(brgy_cases) {

  ggplot(brgy_cases, aes(x = reorder(Barangay, -Total_Cases), y = Total_Cases,
fill = Barangay)) +
  geom_bar(stat = "identity") +
  labs(x = "Barangay", y = "Total Cases", title = "Total Cases per Barangay") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 90, hjust = 1),
plot.title = element_text(hjust = 0.5),
plot.background = element_rect(fill = "white")) +
  geom_text(aes(label = Total_Cases), vjust = -0.5)}

```

```
shinyApp(ui = ui, server = server)
```

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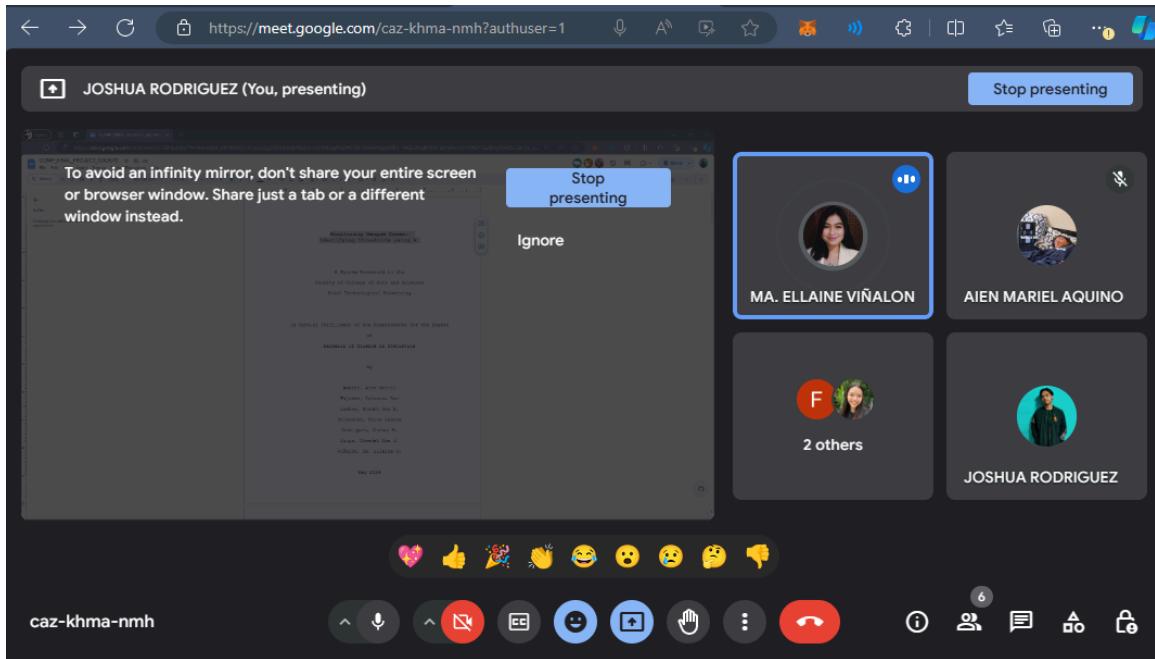
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## APPENDIX

### DOCUMENTATION



## APPENDIX

### EVALUATION

#### **The System Usability Scale (SUS): Post-Test Assessment of Usability**

Please rate your experience using the system by putting a check from 1= Strongly Disagree (SD), 2=Disagree (D), 3= Moderately Agree (MA), 4=Agree (A), and 4=Strongly Agree (SA).

STATEMENTS	1	2	3	4	5
1. I think that I would like to use this system frequently.				√	
2. I found the system unnecessarily complex.			√		
3. I thought the system was easy to use.				√	
4. I think that I would need the support of a technical person to be able to use this system.					√
5. I found the various functions in this system were well integrated.					√
6. I thought there was too much inconsistency in this system.		√			
7. I would imagine that most people would learn to use this system very quickly.					√
8. I found the system very cumbersome to use.		√			
9. I felt very confident using the system.					√
10. I needed to learn a lot of things before I could get going with this system.	√				

End User: May C Villariña, MD



### Rubrics

<b>Criteria</b>	<b>Points</b>	<b>Score</b>
Functionality: Does the system meet all requirements and accurately perform statistical analyses and computations?	25	
Code Quality: Is the code well-written, readable, well-structured, and efficient?	20	
User Experience: Is the system easy to use and navigate for users with a basic understanding of statistics? Does it provide helpful messages and error handling?	30	
Documentation: Is the code and system documentation complete and clear, including explanations of statistical concepts and procedures used?	15	
Presentation: Is the presentation clear, concise, and visually appealing, including charts and graphs where applicable?	10	
<b>TOTAL</b>	<b>100</b>	