Stawberries: exploratory data analysis

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2023-10-11

```
library(knitr)
library(kableExtra)
library(tidyverse)
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.1     v readr     2.1.4
v forcats   1.0.0     v stringr   1.5.0
v ggplot2   3.4.2     v tibble    3.2.1
v lubridate 1.9.2     v tidyr     1.3.0
v purrr     1.0.2
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter()     masks stats::filter()
x dplyr::group_rows() masks kableExtra::group_rows()
x dplyr::lag()        masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to beco
```

```
library(stringr)
```

Read the file

```
strawberry <- read_csv("strawberry_oct4.csv", col_names = TRUE)
```

Data cleaning

```
drop_one_value_col <- function(df){
  drop <- NULL
  for (i in 1:ncol(df)){
    unique_count <- n_distinct(df[, i])
    if (unique_count == 1){
      drop <- c(drop, i)
    }
  }

  if (length(drop) == 0) {
    print("No columns to drop.")
    return(df)
  } else {
    cat("Columns dropped:", colnames(df)[drop], "\n")
    strawberry <- df[, -drop]
    return(strawberry)
  }
}
str <- drop_one_value_col(strawberry)
```

```
[1] "No columns to drop."
```

```
str <- str$col_name
```

```
Warning: Unknown or uninitialised column: `col_name`.
```

```
strawberry <- strawberry |> select(!all_of(str))


vals=strawberry$Value
vals=sub(",","",vals)
vals=sub('"',"",vals)
vals=as.numeric(vals)
```

```
Warning: NAs introduced by coercion
```

```
strawberry["Value"]=vals

state_all <- strawberry |> group_by(State) |> count()

strawberry_census <- strawberry |> filter((Program=="CENSUS"))
 strawberry_census <- strawberry_census |>
  separate_wider_delim(  cols = `Data Item`,
                         delim = ",",
                         names = c("Fruit",
                                 "temp1",
                                 "temp2",
                                 "temp3"),
                         too_many = "error",
                         too_few = "align_start"
                       )

strawberry_census <- strawberry_census |>
  separate_wider_delim(  cols = temp1,
                         delim = " - ",
                         names = c("crop_type",
                                 "prop_acct"),
                         too_many = "error",
                         too_few = "align_start"
                       )



strawberry_census$crop_type <- str_trim(strawberry_census$crop_type, side = "both")

strawberry_census$temp2 <- str_trim(strawberry_census$temp2, side = "both")

strawberry_census$temp3 <- str_trim(strawberry_census$temp3, side = "both")
strawberry_census <- strawberry_census |> mutate(`Fresh Market` = temp2, .after = temp2)
strawberry_census$`Fresh Market` <- strawberry_census$`Fresh Market` |> str_replace( "^MEA
strawberry_census$`Fresh Market` <- strawberry_census$`Fresh Market` |> str_replace( "^P.*
strawberry_census$`Fresh Market`[is.na(strawberry_census$`Fresh Market`)] <- ""
 strawberry_census$temp2 <- strawberry_census$temp2 |> str_replace("^F.*", "")
strawberry_census$`Fresh Market` <- strawberry_census$`Fresh Market` |> str_replace("^FRES
strawberry_census <- strawberry_census |> mutate(`Process Market` = temp2, .after = temp2)
strawberry_census$`Process Market` <-  strawberry_census$`Process Market` |> str_replace("
strawberry_census$`Process Market`[is.na(strawberry_census$`Process Market`)] <- ""
```

```
strawberry_census$temp2 <- strawberry_census$temp2 |> str_replace("^P.*", "")
strawberry_census$`Process Market` <-  strawberry_census$`Process Market` |> str_replace("
strawberry_census$prop_acct[is.na(strawberry_census$prop_acct)] <- ""
strawberry_census$temp2[is.na(strawberry_census$temp2)] <- ""
strawberry_census$temp3[is.na(strawberry_census$temp3)] <- ""
strawberry_census <- strawberry_census |> unite(temp2, temp3, col = "Metric", sep = "")
strawberry_census$Metric <- strawberry_census$Metric |> str_replace("MEASURED IN ", "")
strawberry_census <- strawberry_census |> relocate(Metric, .before = Domain)

strawberry_census <- strawberry_census |> relocate(`Process Market`, .before = Metric)

strawberry_census <- strawberry_census |> rename(Totals = prop_acct)
```

```
strawberry_census_dollar <- strawberry_census %>%
  filter(!is.na(Value) & (Metric == "$"))

top_10_states_dollar <- strawberry_census_dollar %>%
  group_by(State) %>%
  summarise(avg_value = mean(Value, na.rm = TRUE)) %>%
  arrange(desc(avg_value)) %>%
  top_n(10)
```

```
Selecting by avg_value
```

```
strawberry_census_CWT <- strawberry_census %>%
  filter(!is.na(Value) & (Metric == "CWT"))

top_10_states_CWT <- strawberry_census_CWT %>%
  group_by(State) %>%
  summarise(avg_value = mean(Value, na.rm = TRUE)) %>%
  arrange(desc(avg_value)) %>%
  top_n(10)
```

```
Selecting by avg_value
```

```
strawberry_census_OWS <- strawberry_census %>%
  filter(!is.na(Value) & (Totals == "OPERATIONS WITH SALES" | 'Fresh Market' == "OPERATION

top_10_states_OWS <- strawberry_census_OWS %>%
```

```
  group_by(State) %>%
  summarise(avg_value = mean(Value, na.rm = TRUE)) %>%
  arrange(desc(avg_value)) %>%
  top_n(10)
```

```
Selecting by avg_value
```

```
df_ows <- data.frame(State = top_10_states_OWS$State, Metric = "OWS", avg_value = top_10_s
df_cwt <- data.frame(State = top_10_states_CWT$State, Metric = "CWT", avg_value = top_10_s
df_dollar <- data.frame(State = top_10_states_dollar$State, Metric = "Dollar", avg_value =
common_states_data <- rbind(df_ows, df_cwt, df_dollar)
common_states <- intersect(top_10_states_OWS$State, intersect(top_10_states_dollar$State,
common_states_data <- common_states_data %>%
  filter(State %in% common_states)
```

```
strwb_survey<- strawberry |> filter((Program=="SURVEY"))
stb_survey <- strwb_survey %>%
  filter(str_detect(`Data Item`, "MEASURED IN")) %>%
  mutate(`Data Item` = str_extract(`Data Item`, "(?<=MEASURED IN ).*"))
stb_survey <- stb_survey %>%
  mutate(
    Chemical = if_else(str_detect(`Domain Category`, "\\(.*=.*\\)"),
                       str_extract(`Domain Category`, "(?<=\\().*?(?=\\=)"),
                       NA_character_),
    Chemical_Code = if_else(str_detect(`Domain Category`, "\\(.*=.*\\)"),
                            str_extract(`Domain Category`, "(?<=\\=).*?(?=\\))"),
                            NA_character_)
  )


stb_survey <- subset(stb_survey, select = -Program)
stb_survey <- subset(stb_survey, select = -`Domain Category`)
```

Dealing with Missing Values, Outliers, and Duplicates

```
stb_survey <- stb_survey[, !sapply(stb_survey, function(col) all(is.na(col)))]


stb_survey <- stb_survey[!is.na(stb_survey$Value), ]
```

```r
stb_survey <- stb_survey[stb_survey$State != "OTHER STATES", ]

strawberry_survey_chemical <- stb_survey  |>
  filter(!is.na(Chemical_Code))
```

EDA

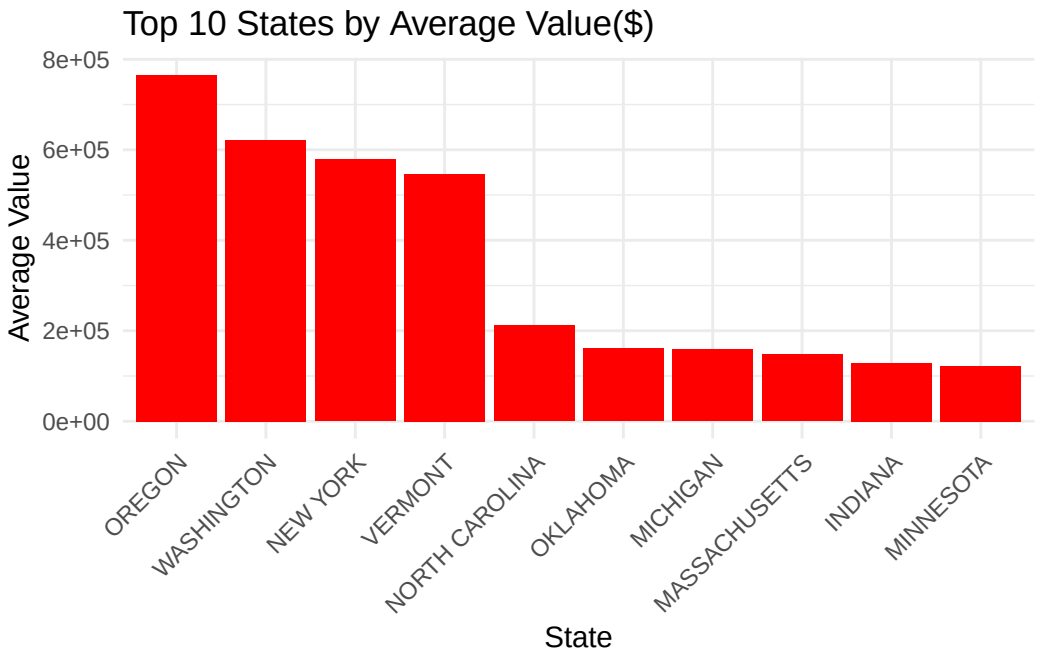
Once the data has been cleaned and organized, you must conduct your own EDA. Be sure to include a discussion of your analysis of the chemical information, including citations for data and other information you have used. Visualizations should play a key role in your analysis. Plots should be labeled and captioned.

EDA for census

data analysis

1. Top 10 States by Average Value ($)

```r
gg_dollar <- ggplot(top_10_states_dollar, aes(x = reorder(State, -avg_value), y = avg_valu
  geom_bar(stat = "identity", fill = "red") +
  labs(title = "Top 10 States by Average Value($)",
       x = "State",
       y = "Average Value") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
print(gg_dollar)
```

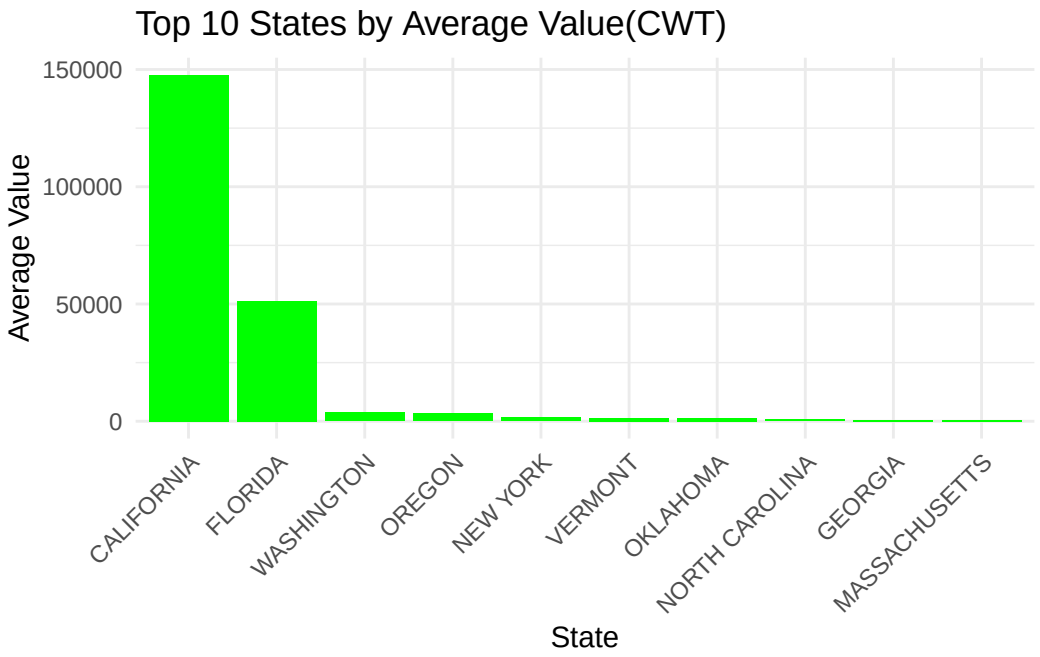



```
cat("The cities with the top 10 ave_sales are($):", top_10_states_dollar$State, "\n")
```

```
The cities with the top 10 ave_sales are($): OREGON WASHINGTON NEW YORK VERMONT NORTH CAROLI
```

2. Top 10 States by Average Value (CWT)

```
gg_cwt <- ggplot(top_10_states_CWT, aes(x = reorder(State, -avg_value), y = avg_value)) +
  geom_bar(stat = "identity", fill = "green") +
  labs(title = "Top 10 States by Average Value(CWT)",
       x = "State",
       y = "Average Value") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
print(gg_cwt)
```

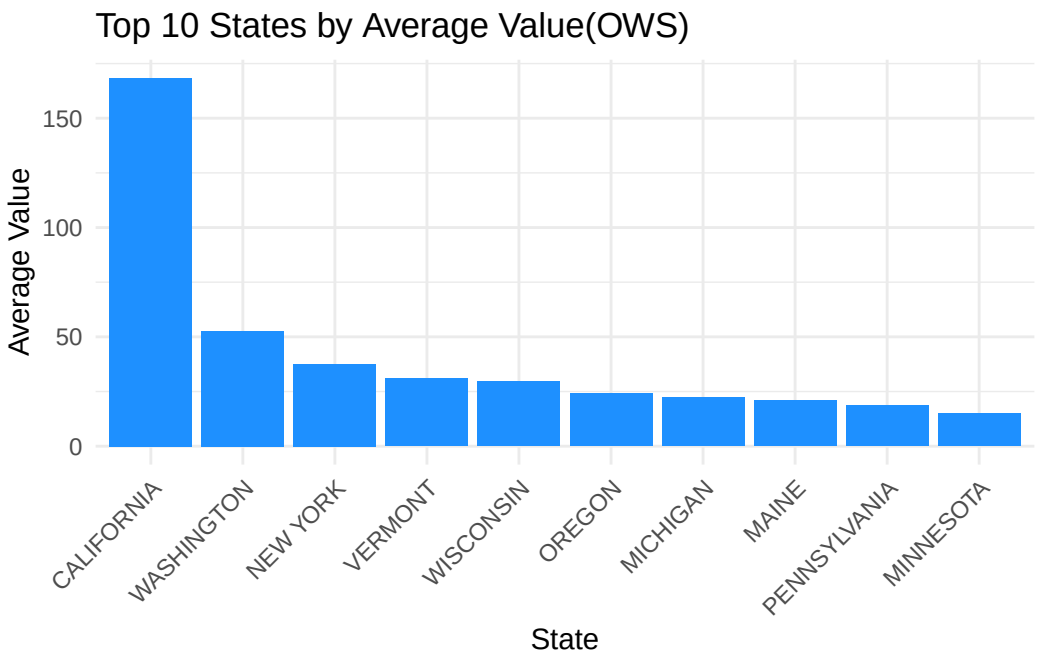



```
cat("The cities with the top 10 ave_sales are(CWT):", top_10_states_CWT$State, "\n")
```

```
The cities with the top 10 ave_sales are(CWT): CALIFORNIA FLORIDA WASHINGTON OREGON NEW YORK
```

3. Top 10 States by Average Value (OWS)

```
gg_ows <- ggplot(top_10_states_OWS, aes(x = reorder(State, -avg_value), y = avg_value)) +
  geom_bar(stat = "identity", fill = "dodgerblue") +
  labs(title = "Top 10 States by Average Value(OWS)",
       x = "State",
       y = "Average Value") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
print(gg_ows)
```




```
cat("The cities with the top 10 ave_sales are(OWS):", top_10_states_OWS$State, "\n")
```

```
The cities with the top 10 ave_sales are(OWS): CALIFORNIA WASHINGTON NEW YORK VERMONT WISCONS
```

EDA for Toxic

```
# Load the required packages
library(jsonlite)
```

```
Attaching package: 'jsonlite'

The following object is masked from 'package:purrr':

    flatten
```

```
library(httr)
library(dplyr)
library(purrr)
```

```r
# Function to translate PC to CAS
get_cas <- function(PC) {
  PC <- sprintf("%06d", as.numeric(PC))
  path <- paste0("https://ordspub.epa.gov/ords/pesticides/apprilapi/?q=%7b%22ais%22:%7b%22
  r <- GET(url = path)
  r_text <- content(r, as = "text", encoding = "UTF-8")
  df <- fromJSON(r_text, flatten = TRUE)
  df_strwb <- df$items[grepl("Strawberries", df$items$sites, fixed = TRUE), ]
  ais <- df_strwb$ais[1]
  pattern <- "\\(([^A-Za-z]+)\\/([0-9-]+)\\)"
  matches <- regmatches(ais, gregexpr(pattern, ais))
  cas <- sapply(matches, function(x) gsub(".*\\/([0-9-]+)\\)", "\\1", x))
  if (is.character(cas)) {
    return(cas[1])
  } else {
    return(NA)
  }
}

# Create a PC to CAS dataframe for the survey data
PCs <- unique(strawberry_survey_chemical$Chemical_Code)[-1]
CAS <- map_chr(PCs, get_cas)

PC_form <- data.frame(PC = PCs, CAS = CAS)

# Merge data with CAS
merged_data_cas <- left_join(strawberry_survey_chemical, PC_form, by = c("Chemical_Code" =

# Merge with toxic data
toxic <- read_csv("CAS.csv")
```

```
Rows: 1044 Columns: 2

-- Column specification --------------------------------------------------------
Delimiter: ","
chr (2): chemical, Toxic

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```r
merged_data_toxic <- toxic %>%
  filter(!is.na(Toxic))

merged_data_toxic <- merge(merged_data_cas, toxic, by.x = "CAS", by.y = "chemical", all.x

# If you're trying to filter based on the 'cas' column:
merged_data_toxic_nonna <- merged_data_toxic %>%
  filter(!is.na(Toxic))

# Check the length
length(merged_data_toxic_nonna$Toxic)
```

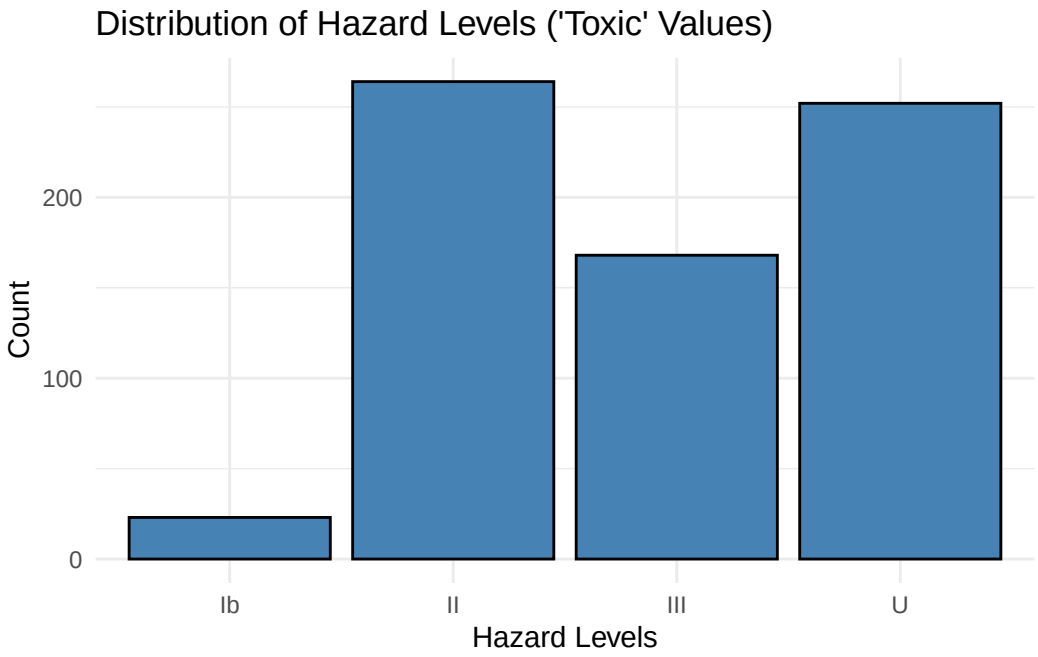
```
[1] 707
```

4.count toxic based on merged_data_toxic_nonna

```r
library(ggplot2)



ggplot(merged_data_toxic_nonna, aes(x=Toxic)) +
  geom_bar(fill="steelblue", color="black") +
  labs(title="Distribution of Hazard Levels ('Toxic' Values)", x="Hazard Levels", y="Count
  theme_minimal()
```


Distribution of Hazard Levels ('Toxic' Values)
Count
200
100
0
Ib
II
III
U
Hazard Levels