EDA

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Previous data preperation: Tidy the chemical data.

```
library (tidyr)
library (dplyr)
##
## 载入程序包: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
       filter, lag
## The following objects are masked from 'package:base':
##
##
       intersect, setdiff, setequal, union
library (stringr)
## Tidy'Domain.Category' column.
strawberry2<-read.csv("cleaned_strawberry_data.csv")
strawberry3 <- strawberry2 %>%
  extract(`Domain.Category`,
          into = c("Chemical_Type", "Specific_Chemical", "Chemical_Name", "Quantity"),
          regex = "([\hat{},]+),?\\\s*([\hat{}:]+)?:?\\\s*\\\(([\hat{}=]+)?\\\s*=\\\s*([0-9]+)?\\\)",
  mutate (Chemical Type = ifelse (Chemical Type == "NOT SPECIFIED", NA, Chemical Type),
         Specific_Chemical = ifelse(is.na(Specific_Chemical) | Specific_Chemical == "", NA, Spe
cific Chemical),
         Chemical Name = ifelse(is.na(Chemical Name) | Chemical Name == "", NA, Chemical Name),
         Quantity = ifelse(is.na(Quantity) | Quantity == "", NA, Quantity),
         Specific_Chemical = ifelse(grep1("FERTILIZER", Chemical_Type) & is.na(Specific_Chemica
1), "FERTILIZER", Specific Chemical),
    Chemical Name = ifelse(grep1("FERTILIZER", Chemical Type) & is.na(Chemical Name),
                           str_extract(Chemical_Type, "(?<=FERTILIZER: \().+?(?=\))"),
                           Chemical_Name)
  )
```

```
strawberry_update <- strawberry_update %>%
mutate(
    Quantity = ifelse(
        Quantity == "TOTAL",
        Quantity,
        str_extract(Quantity, "\\d+")
    )
)
```

Seprate Census data and Survey data

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

```
##
## 载入程序包: 'kableExtra'
```

```
## The following object is masked from 'package:dplyr':
##
group_rows
```

```
library(tidyverse)
```

```
## — Attaching core tidyverse packages — tidy verse 2.0.0 — ## ✓ forcats 1.0.0 ✓ purrr 1.0.2 ## ✓ ggplot2 3.5.1 ✓ readr 2.1.5 ## ✓ lubridate 1.9.3 ✓ tibble 3.2.1
```

```
library (magrittr)
```

```
##
## 载入程序包: 'magrittr'
##
## The following object is masked from 'package:purrr':
##
## set_names
##
## The following object is masked from 'package:tidyr':
##
## extract
```

```
straw_cen <- strawberry_update|> filter(Program=="CENSUS")
straw_sur <- strawberry_update |> filter(Program=="SURVEY")
```

Analysis for chemical in survey data.

WHO list six deadly carcinogens, this report will look for the use of these chemicals between different growing regions.

6 Deadly carcinogens:

CAPTAFOL, ethylene dibromide, GLYPHOSATE, MALATHION, DIAZINON, Dichlorodiphenyltrichloroethane(DDT).

Searching each chemical in the data 'straw_sur', there are three carcinogens could be found. Therefore, I will analysis these three carcinogens: 'GLYPHOSATE ISO. SALT', 'MALATHION', 'DIAZINON'.

diazinon: an organophosphorus insecticide

glyphosate: herbicide

malathion: a man-made organophosphate insecticide

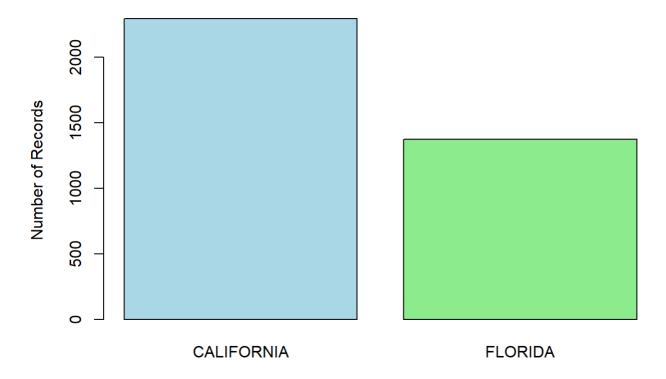
Step 1: Select rows containing three chemicals, list the names of different regions where the data come from.

It shows that strawberries which used any kind of these three chemicals come from California and Florida.

Compare the difference of survey data volume between the two regions.

```
state_counts <- table(straw_sur$State[straw_sur$State %in% c("CALIFORNIA", "FLORIDA")])
barplot(state_counts,
    main = "Comparison of CALIFORNIA and FLORIDA Counts",
    ylab = "Number of Records",
    col = c("lightblue", "lightgreen"),
    names.arg = c("CALIFORNIA", "FLORIDA"))</pre>
```

Comparison of CALIFORNIA and FLORIDA Counts



The bar plot shows that California has more survey data records than Florida.

Step 2: Sepreat the two regions' data.

```
# Tidy the 'Quantity' cloumn
filtered_data$Quantity <- as.numeric(gsub("[^0-9]", "", filtered_data$Quantity))

# I find that there is a mistake on variable's name. 'Quantity' column should be the code of chemical, not the quantity. Thus change the column name.
names(filtered_data)[names(filtered_data) == "Quantity"] <- "Code"

# Split into two separate data boxes by the State column
library(dplyr)
cali <- filtered_data %>% filter(State == "CALIFORNIA")
flor <- filtered_data %>% filter(State == "FLORIDA")
```

Q1: What about the use of these three chemicals in California?

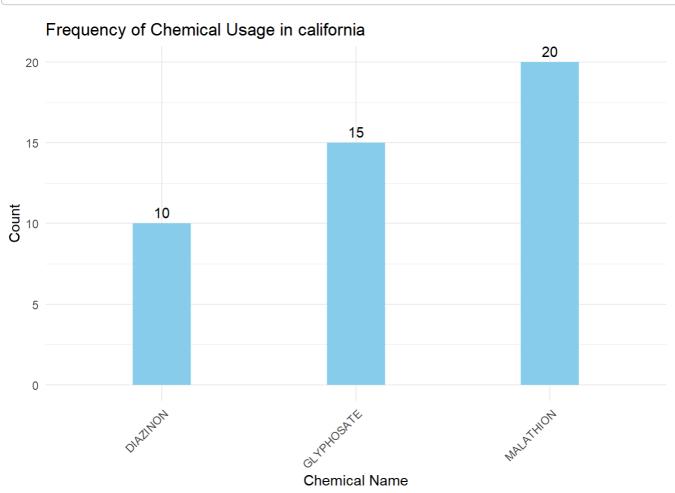
```
# Check out the column unique(cali$Chemical_Name)
```

```
## [1] "MALATHION" "GLYPHOSATE ISO. SALT" "DIAZINON"
```

```
diazinon_count <- sum(grep1("DIAZINON", cali$Chemical_Name))
malathion_count <- sum(grep1("MALATHION", cali$Chemical_Name))
glyphosate_count <- sum(grep1("GLYPHOSATE", cali$Chemical_Name))

chemical_data <- data.frame(
   Chemical = c("DIAZINON", "MALATHION", "GLYPHOSATE"),
   Count = c(diazinon_count, malathion_count, glyphosate_count)
)

library(ggplot2)
ggplot(chemical_data, aes(x = Chemical, y = Count)) +
   geom_bar(stat = "identity", fill = "skyblue", width = 0.3) +
   geom_text(aes(label = Count), vjust = -0.5) +
   theme_minimal() +
   labs(title = "Frequency of Chemical Usage in california",
        x = "Chemical Name",
        y = "Count") +
   theme(axis.text.x = element_text(angle = 45, hjust = 1))</pre>
```

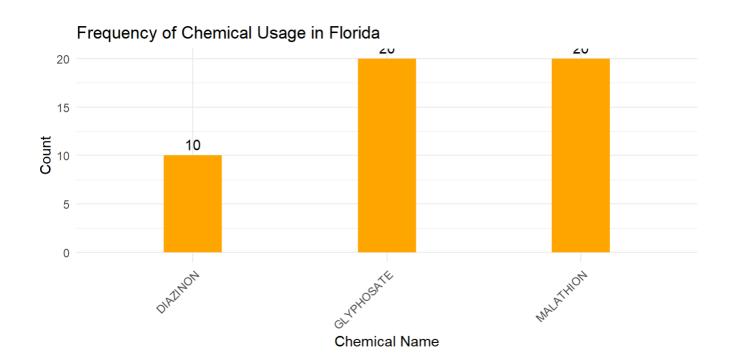


As the bar plot shows, California uses 'MALATHION' the most.

Q2: What about the use of these three chemicals in

florida?

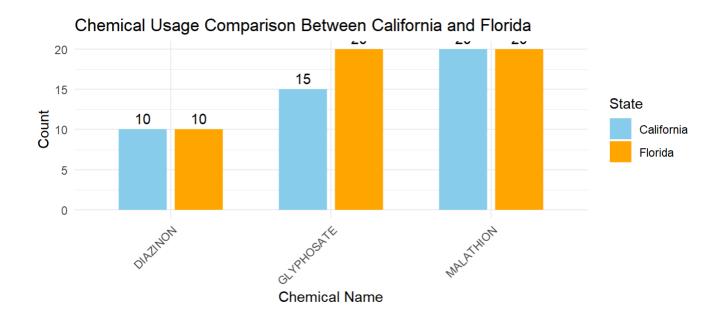
```
diazinon count <- sum(grep1("DIAZINON", flor$Chemical Name))</pre>
malathion_count <- sum(grep1("MALATHION", flor$Chemical_Name))</pre>
glyphosate_count <- sum(grep1("GLYPHOSATE", flor$Chemical_Name))</pre>
chemical_data_flor <- data.frame(</pre>
Chemical = c("DIAZINON", "MALATHION", "GLYPHOSATE"),
Count = c(diazinon_count, malathion_count, glyphosate_count)
ggplot(chemical\_data\_flor, aes(x = Chemical, y = Count)) +
geom_bar(stat = "identity",
          fill = "orange",
          width = 0.3) +
geom_text(aes(label = Count),
           v.just = -0.5) +
theme minimal() +
 labs(title = "Frequency of Chemical Usage in Florida",
      x = "Chemical Name",
      v = "Count") +
 theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
coord fixed (ratio = 0.05)
```



Q3: What are the similarities and differences in the

use of chemical substances in the two places?

```
# California data
cali_diazinon <- sum(grep1("DIAZINON", cali$Chemical_Name))</pre>
cali_malathion <- sum(grep1("MALATHION", cali$Chemical_Name))</pre>
cali_glyphosate <- sum(grep1("GLYPHOSATE", cali$Chemical_Name))</pre>
# Florida data
flor_diazinon <- sum(grep1("DIAZINON", flor$Chemical_Name))</pre>
flor_malathion <- sum(grep1("MALATHION", flor$Chemical_Name))</pre>
flor_glyphosate <- sum(grep1("GLYPHOSATE", flor$Chemical_Name))</pre>
# combined data
combined_data <- data.frame(</pre>
  Chemical = rep(c("DIAZINON", "MALATHION", "GLYPHOSATE"), each = 2),
  Count = c(cali_diazinon, flor_diazinon,
            cali_malathion, flor_malathion,
            cali_glyphosate, flor_glyphosate),
  State = rep(c("California", "Florida"), 3)
ggplot(combined_data, aes(x = Chemical, y = Count, fill = State)) +
  geom_bar(stat = "identity",
           position = position dodge(width = 0.7),
           width = 0.6) +
  geom_text(aes(label = Count),
            position = position_dodge(width = 0.7),
            vjust = -0.5) +
  theme_minimal() +
  labs(title = "Chemical Usage Comparison Between California and Florida",
       x = "Chemical Name",
       y = "Count") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
  scale_fill_manual(values = c("skyblue", "orange")) +
  coord fixed(ratio = 0.05)
```



As the figure shows, two region have same level of diazinon and malathion usage. The usage of malathion is twice as much as the usage of diaziono. For glyphosate, a widely used herbicide, florida use it more than california.

Some possible inference:

As diazinon and malathion are both insecticide, two pesticides were used very closely in both states, which may mean that the two pesticides are common pest control methods in agriculture in these areas.

California uses more herbicide, thus it may be a higher demand for herbicides for strawberry growing in california rather than floridia.

^{*}Acknowledgement: Use chatgpt to resolve code errors, chart exceptions, etc.