Strawberry Data EDA

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R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
datacen <- read.csv("straw_cen_cleaned2.csv")
datasur <- read.csv("straw_sur_cleaned2.csv")
str(datasur)
```

```
## 'data.frame':    1432 obs. of  16 variables:
##  $ Program          : chr  "SURVEY" "SURVEY" "SURVEY" "SURVEY" ...
##  $ Year             : int  2024 2024 2023 2023 2023 2023 2023 2023 2023 2023 ...
##  $ Period           : chr  "YEAR" "YEAR" "MARKETING YEAR" "MARKETING YEAR" ...
##  $ Geo.Level        : chr  "NATIONAL" "NATIONAL" "NATIONAL" "NATIONAL" ...
##  $ State            : chr  "US TOTAL" "US TOTAL" "US TOTAL" "US TOTAL" ...
##  $ State.ANSI       : int  -1 -1 -1 -1 -1 6 12 -1 -1 -1 ...
##  $ Commodity        : chr  "STRAWBERRIES" "STRAWBERRIES" "STRAWBERRIES" "STRAWBERRIES" ...
##  $ Market_Type      : chr  "FRESH MARKET" "PROCESSING" "OTHER" "FRESH MARKET" ...
##  $ Measure_Operation: chr  "PRICE RECEIVED, ADJUSTED BASE" "PRICE RECEIVED, ADJUSTED BASE" "PRICE REC
##  $ Unit_of_Measure  : chr  "$ / CWT" "$ / TON" "$ / CWT" "$ / CWT" ...
##  $ Domain           : chr  "TOTAL" "TOTAL" "TOTAL" "TOTAL" ...
##  $ Chemical_Use     : chr  "NOT SPECIFIED" "NOT SPECIFIED" "NOT SPECIFIED" "NOT SPECIFIED" ...
##  $ Chemical_Name    : chr  "NOT SPECIFIED" "NOT SPECIFIED" "NOT SPECIFIED" "NOT SPECIFIED" ...
##  $ Chemical_Code    : logi  NA NA NA NA NA NA ...
##  $ Value            : num  10.9 4.04 123 142 43.8 121 147 142 43.8 485 ...
##  $ CV....           : logi  NA NA NA NA NA NA ...
```

```
unique1<- unique(datasur$Chemical_Name)
unique2<- unique(datasur$Chemical_Code)
ca_chemical <- subset(datasur, State != "California")
ca_chemical1 <- subset(ca_chemical, !(Chemical_Name %in% c("NOT SPECIFIED", "TOTAL")))
head(ca_chemical1)
```

```
##    Program Year Period Geo.Level      State State.ANSI    Commodity Market_Type
## 19  SURVEY 2023   YEAR     STATE CALIFORNIA          6 STRAWBERRIES     BEARING
## 20  SURVEY 2023   YEAR     STATE CALIFORNIA          6 STRAWBERRIES     BEARING
## 21  SURVEY 2023   YEAR     STATE CALIFORNIA          6 STRAWBERRIES     BEARING
## 22  SURVEY 2023   YEAR     STATE CALIFORNIA          6 STRAWBERRIES     BEARING
## 23  SURVEY 2023   YEAR     STATE CALIFORNIA          6 STRAWBERRIES     BEARING
## 24  SURVEY 2023   YEAR     STATE CALIFORNIA          6 STRAWBERRIES     BEARING
##    Measure_Operation              Unit_of_Measure                Domain
## 19      APPLICATIONS                           LB CHEMICAL, INSECTICIDE
## 20      APPLICATIONS LB / ACRE / APPLICATION, AVG   CHEMICAL, FUNGICIDE
## 21      APPLICATIONS LB / ACRE / APPLICATION, AVG   CHEMICAL, FUNGICIDE
## 22      APPLICATIONS LB / ACRE / APPLICATION, AVG   CHEMICAL, FUNGICIDE
## 23      APPLICATIONS LB / ACRE / APPLICATION, AVG   CHEMICAL, FUNGICIDE
## 24      APPLICATIONS LB / ACRE / APPLICATION, AVG   CHEMICAL, FUNGICIDE
##    Chemical_Use      Chemical_Name Chemical_Code   Value CV....
## 19  INSECTICIDE         (ABAMECTIN            NA 300.000     NA
## 20    FUNGICIDE      (AZOXYSTROBIN            NA   0.234     NA
## 21    FUNGICIDE (BORAX DECAHYDRATE            NA   0.042     NA
## 22    FUNGICIDE          (BOSCALID            NA   0.354     NA
## 23    FUNGICIDE            (CAPTAN            NA   1.693     NA
## 24    FUNGICIDE        (CYPRODINIL            NA   0.316     NA
```

```r
ca_chemical2 <- ca_chemical1[ca_chemical1$Year %in% 2018:2023, ]
```

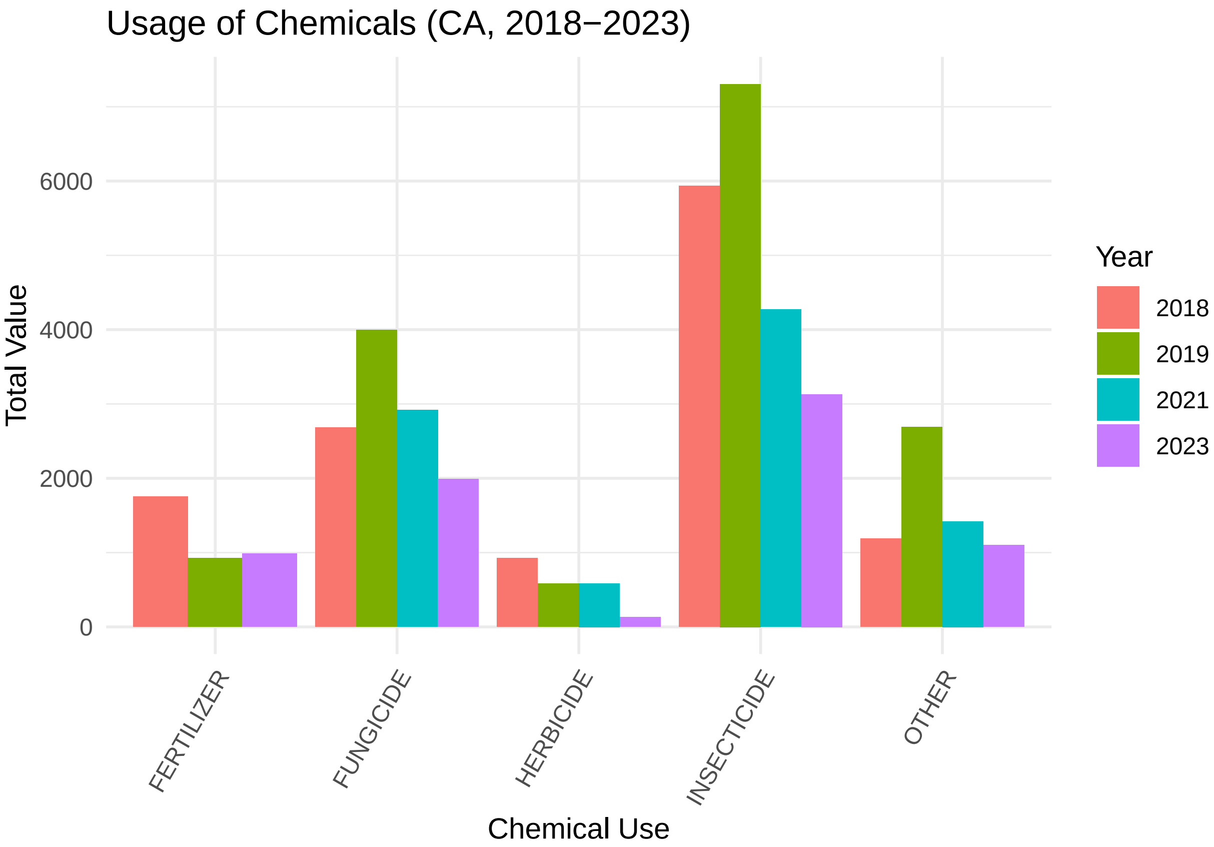
```r
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.1     v tibble    3.2.1
## v lubridate 1.9.3     v tidyr     1.3.1
## v purrr     1.0.2
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```r
ca_chemical3 <- ca_chemical2 %>%
  group_by(Chemical_Use, Year) %>%
  summarise(Total_Value = sum(Value, na.rm = TRUE)) %>%
  ungroup()
```

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

```r
ggplot(ca_chemical3, aes(x = Chemical_Use, y = Total_Value, fill = as.factor(Year))) +
  geom_col(position = "dodge") +  #   geom_col   geom_bar(stat = "identity")
  labs(title = "Usage of Chemicals (CA, 2018-2023)",
       x = "Chemical Use",
       y = "Total Value",
       fill = "Year") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 60, hjust = 1))
```



```
library(dplyr)
library(ggplot2)
ca_chemical_agg <- ca_chemical2 %>%
  group_by(Chemical_Name, Year) %>%
  summarise(Total_Value = sum(Value, na.rm = TRUE)) %>%
  ungroup()
```

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

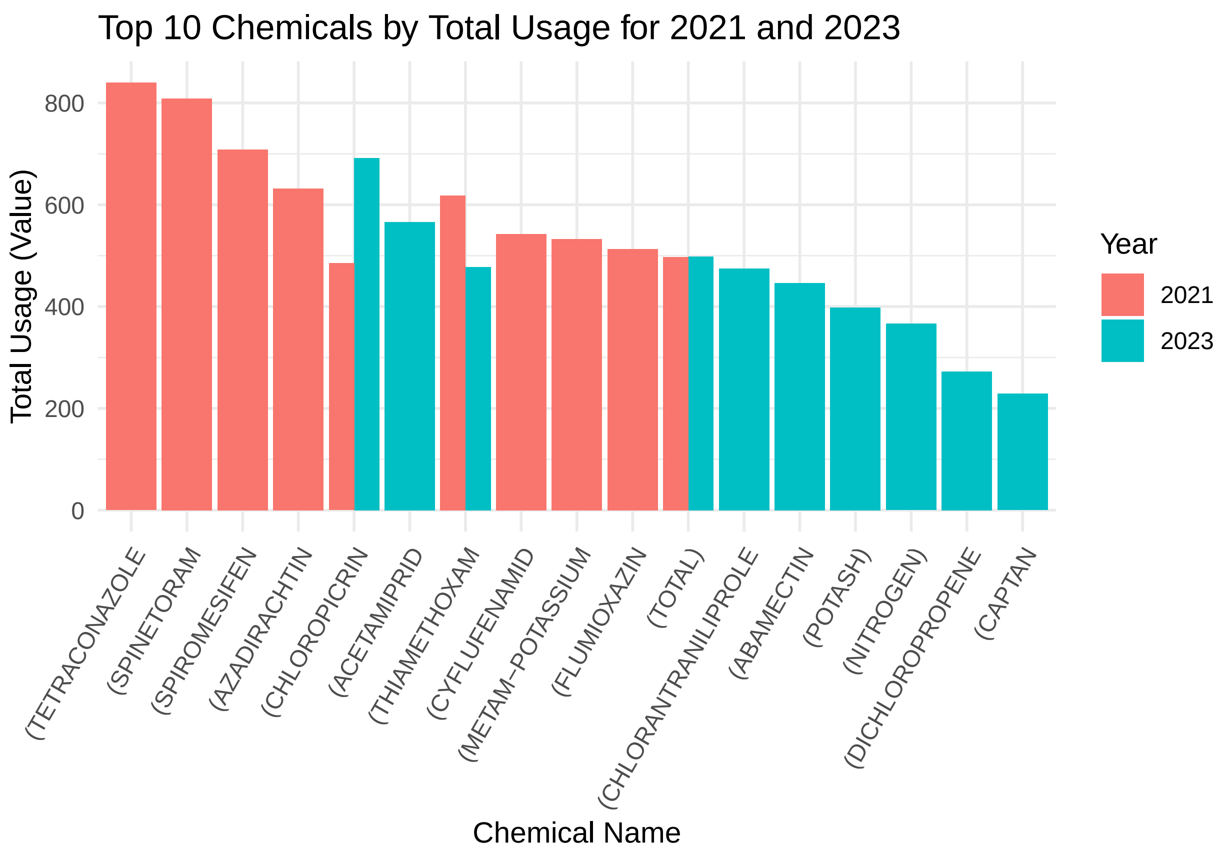
```
tenchemicals <- function(data, year) {
  data %>%
    filter(Year == year) %>%
    arrange(desc(Total_Value)) %>%
    slice_head(n = 10)
}

top_10_2023 <- tenchemicals(ca_chemical_agg, 2023)
top_10_2021 <- tenchemicals(ca_chemical_agg, 2021)

print(top_10_2023)
```

```
## # A tibble: 10 x 3
##    Chemical_Name          Year Total_Value
##    <chr>                 <int>       <dbl>
##  1 (CHLOROPICRIN          2023        692.
##  2 (ACETAMIPRID           2023        566.
##  3 (TOTAL)                2023        498
##  4 (THIAMETHOXAM         2023        478.
##  5 (CHLORANTRANILIPROLE  2023        475.
##  6 (ABAMECTIN            2023        447.
##  7 (POTASH)              2023        398.
##  8 (NITROGEN)            2023        366.
##  9 (DICHLOROPROPENE      2023        273.
## 10 (CAPTAN               2023        229.
```

```r
print(top_10_2021)
```

```
## # A tibble: 10 x 3
##    Chemical_Name     Year Total_Value
##    <chr>            <int>       <dbl>
##  1 (TETRACONAZOLE    2021        840.
##  2 (SPINETORAM       2021        809.
##  3 (SPIROMESIFEN     2021        709.
##  4 (AZADIRACHTIN     2021        632.
##  5 (THIAMETHOXAM     2021        619.
##  6 (CYFLUFENAMID     2021        542.
##  7 (METAM-POTASSIUM  2021        533.
##  8 (FLUMIOXAZIN      2021        513.
##  9 (TOTAL)           2021        497
## 10 (CHLOROPICRIN     2021        485.
```

```r
top_10_all <- bind_rows(
  top_10_2023 %>% mutate(Year = 2023),
  top_10_2021 %>% mutate(Year = 2021)
)

ggplot(top_10_all, aes(x = reorder(Chemical_Name, -Total_Value), y = Total_Value, fill = as.factor(Year
  geom_col(position = "dodge") +
  labs(title = "Top 10 Chemicals by Total Usage for 2021 and 2023",
       x = "Chemical Name",
       y = "Total Usage (Value)",
       fill = "Year") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 60, hjust = 1))
```



```
library(dplyr)
library(ggplot2)

ca_chemical2_filtered <- ca_chemical2 %>%
  filter(Chemical_Use == "INSECTICIDE")

ca_chemical_agg1 <- ca_chemical2_filtered %>%
  group_by(Chemical_Name, Year) %>%
  summarise(Total_Value = sum(Value, na.rm = TRUE)) %>%
  ungroup()
```

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

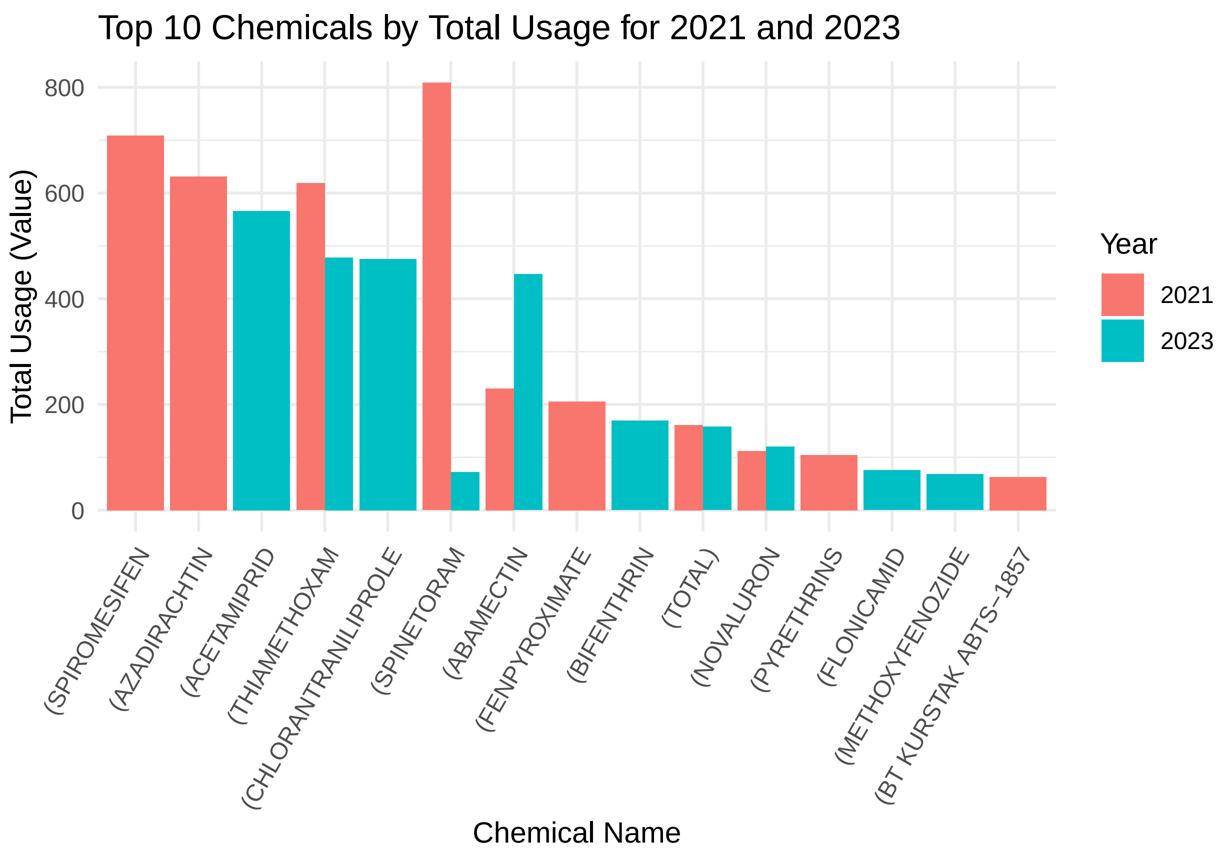
```
get_top_10 <- function(data, year) {
  data %>%
    filter(Year == year) %>%
    arrange(desc(Total_Value)) %>%
    slice_head(n = 10)
}

top_10_2023_new <- get_top_10(ca_chemical_agg1, 2023)
top_10_2021_new <- get_top_10(ca_chemical_agg1, 2021)

print(top_10_2023_new)
```

```
## # A tibble: 10 x 3
##    Chemical_Name         Year Total_Value
##    <chr>                <int>       <dbl>
##  1 (ACETAMIPRID          2023       566.
##  2 (THIAMETHOXAM         2023       478.
##  3 (CHLORANTRANILIPROLE  2023       475.
##  4 (ABAMECTIN            2023       447.
##  5 (BIFENTHRIN           2023       169.
##  6 (TOTAL)               2023       158
##  7 (NOVALURON            2023       121.
##  8 (FLONICAMID           2023        75.6
##  9 (SPINETORAM           2023        72.0
## 10 (METHOXYFENOZIDE      2023        68.0
```

```
print(top_10_2021_new)
```

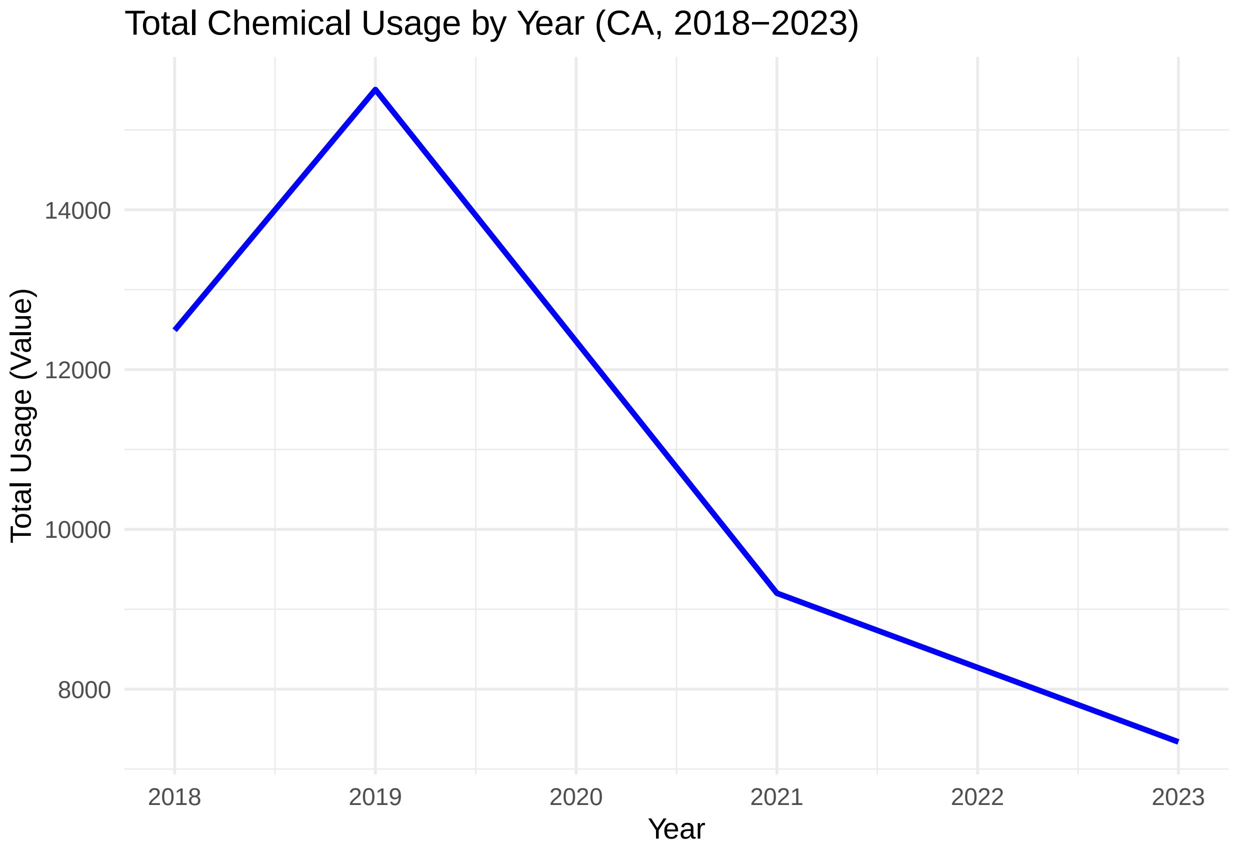
```
## # A tibble: 10 x 3
##    Chemical_Name          Year Total_Value
##    <chr>                 <int>       <dbl>
##  1 (SPINETORAM            2021       809.
##  2 (SPIROMESIFEN          2021       709.
##  3 (AZADIRACHTIN          2021       632.
##  4 (THIAMETHOXAM          2021       619.
##  5 (ABAMECTIN             2021       231.
##  6 (FENPYROXIMATE         2021       205.
##  7 (TOTAL)                2021       161
##  8 (NOVALURON             2021       112.
##  9 (PYRETHRINS            2021       105.
## 10 (BT KURSTAK ABTS-1857  2021        62.5
```

```
top_10_all_new <- bind_rows(
  top_10_2023_new %>% mutate(Year = 2023),
  top_10_2021_new %>% mutate(Year = 2021)
)

ggplot(top_10_all_new, aes(x = reorder(Chemical_Name, -Total_Value), y = Total_Value, fill = as.factor(
  geom_col(position = "dodge") +
  labs(title = "Top 10 Chemicals by Total Usage for 2021 and 2023",
       x = "Chemical Name",
       y = "Total Usage (Value)",
       fill = "Year") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 60, hjust = 1))
```



```r
ca_chemical_total <- ca_chemical2 %>%
  group_by(Year) %>%
  summarise(Total_Value = sum(Value, na.rm = TRUE))

ggplot(ca_chemical_total, aes(x = Year, y = Total_Value)) +
  geom_line(color = "blue", size = 1) +
  labs(title = "Total Chemical Usage by Year (CA, 2018-2023)",
       x = "Year",
       y = "Total Usage (Value)") +
  theme_minimal()
```

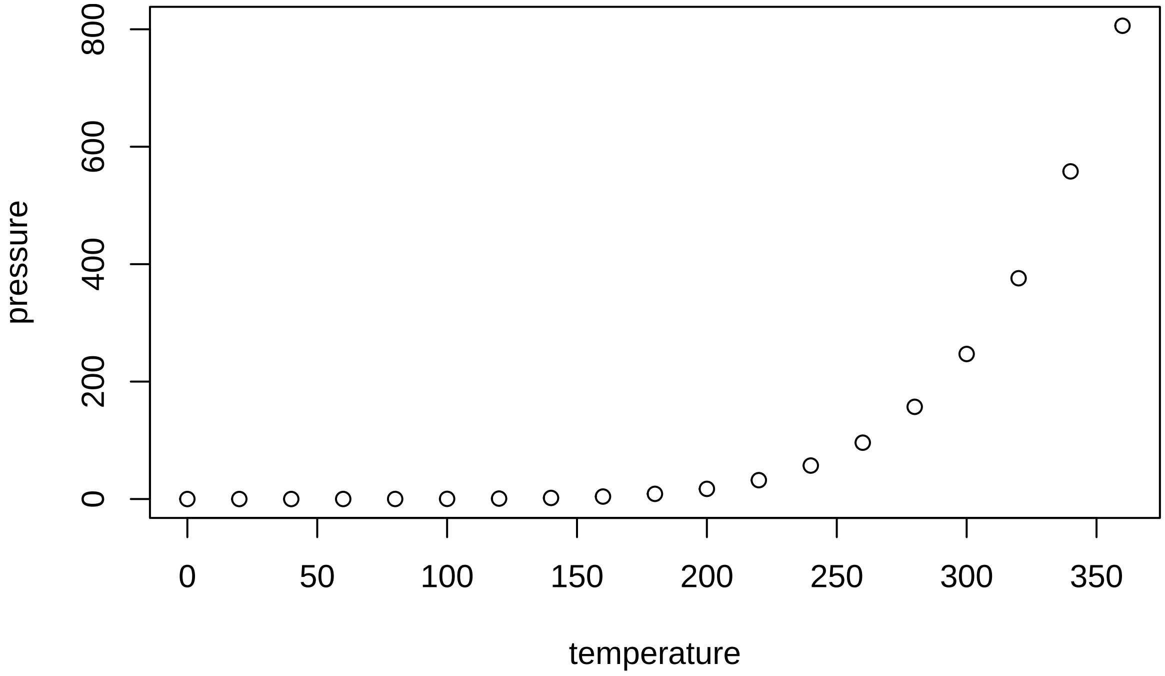
```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



"'

Including Plots

You can also embed plots, for example:



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.