Group2-EDA

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Clean data

import original data

```
strawb <- read_csv("data/Strawberries.csv")
pesti <- read_csv("data/Pesticides.csv")
```

data cleaning about strawb.csv

drop all NA columns

```
drop_na_info <- function(df){
  cnames = colnames(df)
  T = NULL
  for(i in 1:ncol(df)){T <- c(T, nrow(unique(df[i])))}
  drop_cols <- cnames[which(T == 1)]
  return(dplyr::select(df, !all_of(drop_cols)))
}

strawb1 <- drop_na_info(strawb)

colnames(strawb1)
```

```
##  [1] "Program"          "Year"             "Period"           "State"
##  [5] "State ANSI"       "Data Item"        "Domain"           "Domain Category"
##  [9] "Value"            "CV (%)"
```

After droping NA columns, we get strawb1 with 10 columns.

Separate ‘Data Item’ into 4 columns

```
strawb1 %<>% separate(col = 'Data Item', into = c("Strawberries", "Items", "Discription", "Units"),sep =

distinct(strawb1, Strawberries)
```

```
## # A tibble: 2 x 1
##   Strawberries
##   <chr>
## 1 STRAWBERRIES
## 2 STRAWBERRIES - YIELD
```

```
distinct(strawb1, Items)
```

```
## # A tibble: 7 x 1
##   Items
##   <chr>
## 1 " ORGANIC - OPERATIONS WITH SALES"
## 2 " ORGANIC - SALES"
## 3 " ORGANIC"
## 4 " MEASURED IN CWT / ACRE"
## 5 " MEASURED IN TONS / ACRE"
## 6 " BEARING - APPLICATIONS"
## 7 " BEARING - TREATED"
```

```
distinct(strawb1, Discription)
```

```
## # A tibble: 12 x 1
##    Discription
##    <chr>
##  1  <NA>
##  2 " MEASURED IN $"
##  3 " MEASURED IN CWT"
##  4 " FRESH MARKET - OPERATIONS WITH SALES"
##  5 " FRESH MARKET - SALES"
##  6 " PROCESSING - OPERATIONS WITH SALES"
##  7 " PROCESSING - SALES"
##  8 " MEASURED IN LB"
##  9 " MEASURED IN LB / ACRE / APPLICATION"
## 10 " MEASURED IN LB / ACRE / YEAR"
## 11 " MEASURED IN NUMBER"
## 12 " MEASURED IN PCT OF AREA BEARING"
```

```
distinct(strawb1, Units)
```

```
## # A tibble: 4 x 1
##   Units
##   <chr>
## 1  <NA>
## 2 " MEASURED IN $"
## 3 " MEASURED IN CWT"
## 4 " AVG"
```

Separate ‘Data Item’ into “Strawberries”, “Items”, “Discription”, “Units”.

Separate ‘Domain’ into 2 columns

```
strawb1 %<>% separate(col = Domain, into = c("dname", "type"), sep = ",", fill = "right")

distinct(strawb1, dname)
```

```
## # A tibble: 4 x 1
##   dname
##   <chr>
## 1 ORGANIC STATUS
## 2 TOTAL
## 3 CHEMICAL
## 4 FERTILIZER
```

```
distinct(strawb1, type)
```

```
## # A tibble: 5 x 1
##   type
##   <chr>
## 1  <NA>
## 2 " FUNGICIDE"
## 3 " HERBICIDE"
## 4 " INSECTICIDE"
## 5 " OTHER"
```

Separate ‘Domain’ into “dname”, “type”.

Separate ‘Domain Category’ into 2 columns

```
strawb1 %<>%
  mutate(Chemicals = `Domain Category`) %>%
  relocate(Chemicals, .after = `Domain Category`)

strawb1 %<>%
  separate(Chemicals, into =c('Title', 'Details'), sep = ":", fill = "right")

distinct(strawb1, Details)
```

```
## # A tibble: 159 x 1
##    Details
##    <chr>
##  1 " (NOP USDA CERTIFIED)"
##  2  <NA>
##  3 " (AZOXYSTROBIN = 128810)"
##  4 " (BACILLUS AMYLOLIQUEFACIENS MBI 600 = 129082)"
##  5 " (BACILLUS AMYLOLIQUEFACIENS STRAIN D747 = 16482)"
##  6 " (BACILLUS PUMILUS = 6485)"
##  7 " (BACILLUS SUBT. GB03 = 129068)"
##  8 " (BACILLUS SUBTILIS = 6479)"
##  9 " (BLAD = 30006)"
## 10 " (BORAX DECAHYDRATE = 11102)"
## # ... with 149 more rows
```

```
strawb1$Details <- str_replace(strawb1$Details, "\\(", "")
strawb1$Details <- str_replace(strawb1$Details, "\\)", "")

strawb1 %<>%
  separate(Details, into = c('Chemical Name', "Number"), sep = "=", fill = "right")

distinct(strawb1, `Chemical Name`)
```

```
## # A tibble: 159 x 1
##    `Chemical Name`
##    <chr>
##  1 " NOP USDA CERTIFIED"
##  2  <NA>
##  3 " AZOXYSTROBIN "
##  4 " BACILLUS AMYLOLIQUEFACIENS MBI 600 "
##  5 " BACILLUS AMYLOLIQUEFACIENS STRAIN D747 "
##  6 " BACILLUS PUMILUS "
##  7 " BACILLUS SUBT. GB03 "
##   8 " BACILLUS SUBTILIS "
##   9 " BLAD "
##  10 " BORAX DECAHYDRATE "
## # ... with 149 more rows
```

```
distinct(strawb1, Number)
```

```
## # A tibble: 153 x 1
##    Number
##    <chr>
##  1  <NA>
##  2 " 128810"
##  3 " 129082"
##  4 " 16482"
##  5 " 6485"
##  6 " 129068"
##  7 " 6479"
##  8 " 30006"
##  9 " 11102"
## 10 " 128008"
## # ... with 143 more rows
```

```
strawb1$`Chemical Name` <- str_trim(strawb1$`Chemical Name`)
```

Replicate 'Domain.Category' to new variable and separate this new variable into 'Title', 'Details'.

And then clean 'Details' and separate it into 'Chemical Name', "Number". Also captalize all words in 'Chemical Name'.

drop useless columns

```
drops <- c("Strawberries", "Domain Category")
strawb1 <- strawb1[ , !(names(strawb1) %in% drops)]
```

Drop "Strawberries", "Domain Category", because it is useless in data analysis.

data cleaning about pesti.csv

drop NA rows in pesti.csv and clean it

```
pesti1 <- pesti %>% rename('Chemical Name' = Pesticide )

pesti1 %<>% filter(!is.na(pesti1))

pesti1$`Chemical Name` <- toupper(pesti1$`Chemical Name`)
```

Drop NA rows in pesti.csv, finally we get pesti1 with 45 rows.

And then rename 'Pesticide' to 'Chemical Name' and captalize all words in 'Chemical Name'.

Define Human Toxins level

```
pesti1 <- pesti1 %>% mutate('Human Toxins' = case_when(
  pesti1$Carcinogen == "known" | pesti1$Neurotoxins== "present" | pesti1$`Developmental or Reproductive
  pesti1$Carcinogen == "possible" & pesti1$`Hormone Disruptor`=="suspected" & is.na(pesti1$Neurotoxins)
  pesti1$Carcinogen == "possible" & is.na(pesti1$`Hormone Disruptor`) & is.na(pesti1$Neurotoxins) & is.r
  pesti1$Carcinogen == "probable" & is.na(pesti1$`Hormone Disruptor`) & is.na(pesti1$Neurotoxins) & is.r
  is.na(pesti1$Carcinogen) & pesti1$`Hormone Disruptor`=="suspected" & is.na(pesti1$Neurotoxins) & is.na
))
```

Use columns ‘carcinogen’, ‘Neurotoxins’, ‘Developmental or Reproductive Toxins’ to define human toxins level.

High toxic for human: carcinogen = known or Neurotoxins = present or `Developmental or Reproductive Toxins` = present.

Moderate toxic for human: carcinogen = probable/possible and `Hormone Disruptor` = suspect.

Slight toxic for human: carcinogen= possible/possible or `Hormone Disruptor` = suspect, only one happens.

wrangling two datasets

```
strawbPesti <- inner_join(strawb1, pesti1,by="Chemical Name")

# Write the dataset into csv.
write_csv(strawbPesti, "strawbPesti.csv")
```

Combine two dataset into strawbPesti.csv by key column ‘Chemical Name’. Only keep rows with known pesticides.

Data Visualization

```
pacman::p_load('ggplot2', 'plotly',"dplyr")
```

clean strawbPesti.csv

```
distinct(strawbPesti,State)
```

```
## # A tibble: 4 x 1
##   State
##   <chr>
## 1 CALIFORNIA
## 2 FLORIDA
## 3 OREGON
## 4 WASHINGTON
```

```
strawbPesti <- arrange(strawbPesti,`Chemical Name`)
#colnames(strawbPesti)
strawbPesti1 <- strawbPesti[,-13]
strawbPesti2 <- strawbPesti1[,c(2,4,7,12,13,20)]
strawbPesti3 <- filter(strawbPesti2, Discription==" MEASURED IN LB")
strawbPesti4 <- filter(strawbPesti3, Value !="(D)")
strawbPesti4$Value <- as.numeric(sub(",", "", strawbPesti4$Value, fixed = TRUE))

strawbPestiAVG <- strawbPesti4 %>%
  group_by(State, `Chemical Name`,`Human Toxins`) %>%
  summarise(Value,Value=mean(Value))
```

Only choose columns we will use: ‘Year’, ‘State’, ‘Discription’, ‘Chemical Name’, ‘Value’, ‘Human Toxins’. Which is dataset “strawbPesti2”.

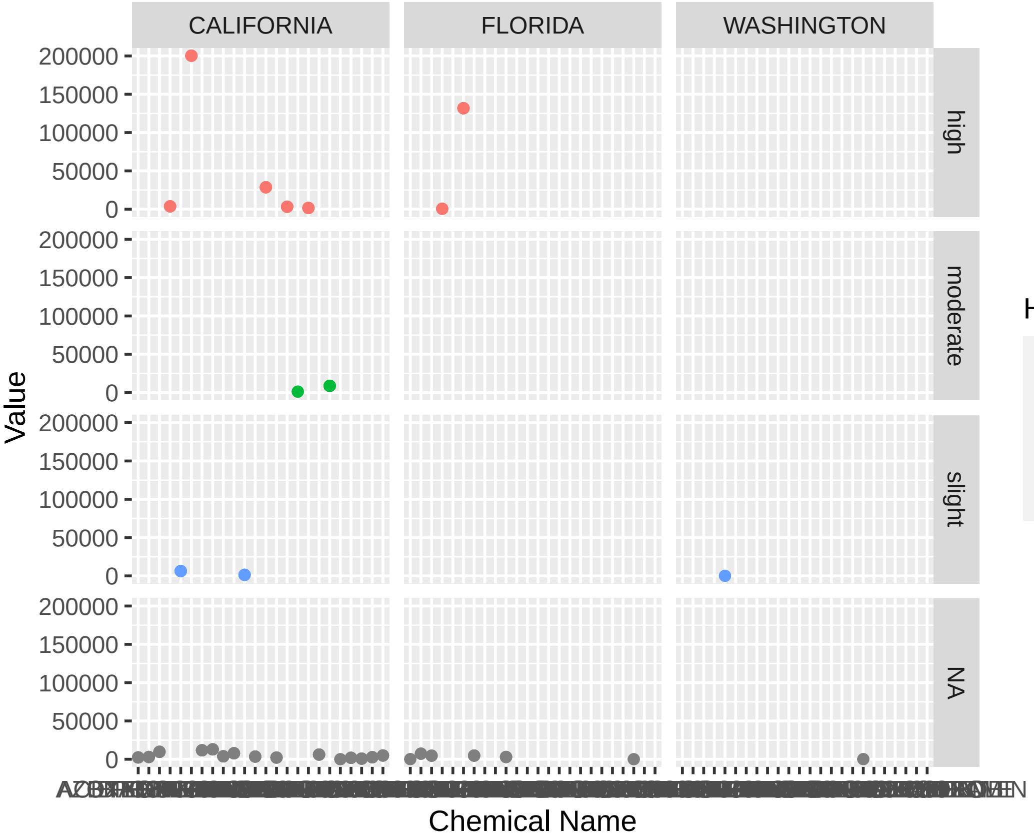
We can see from strawbPesti2, values are different depend on measured methods for each chemical type in each state, so we can choose one method to go deep, finally we chose “MEASURED IN LB”. Then we get dataset “strawbPesti3”.

Then we drop no meaning rows of value. And change value into numeric variable. Finally we get dataset “strawbPesti4”.

To compare pesticides’ toxin level, we can take average value across 2016-1019. We build dataset “strawbPestiAVG”.

show all states chemical usage value

```
ggplot(strawbPestiAVG) +
  geom_point(aes( x= `Chemical Name`, y= Value,col=`Human Toxins`)) +
  facet_grid(`Human Toxins`~State)
```

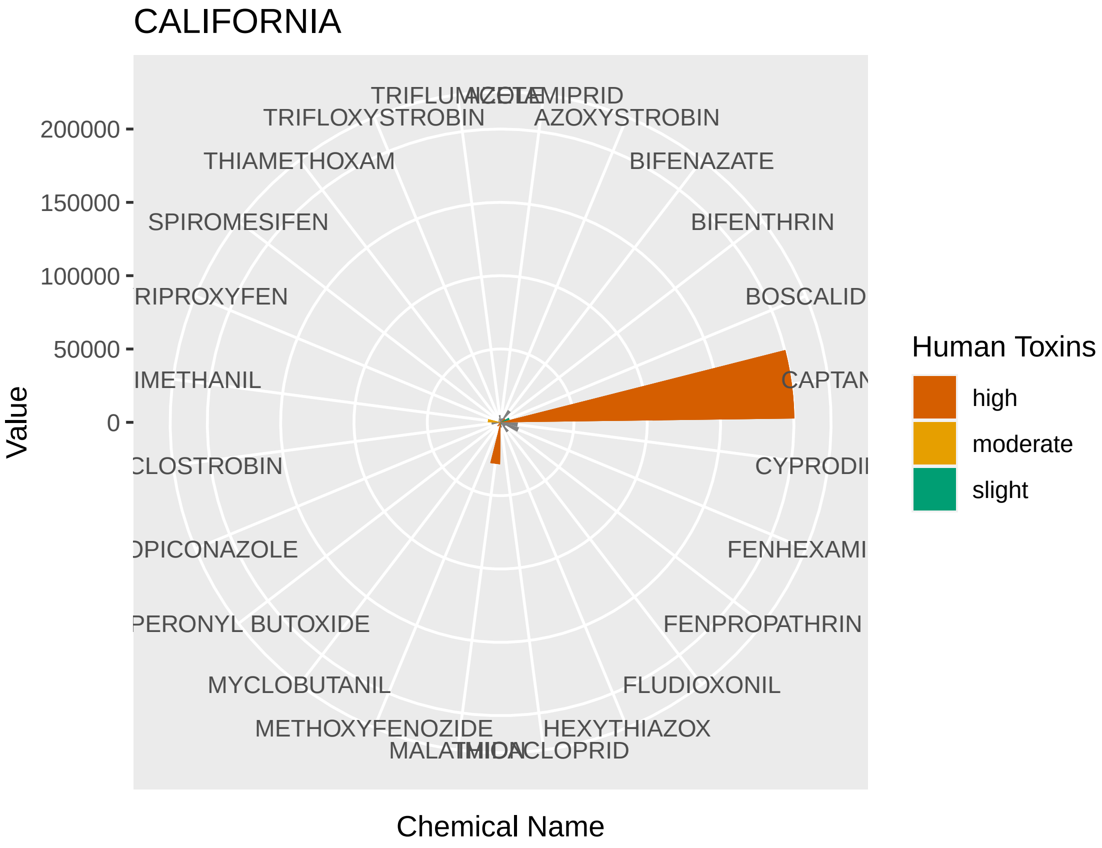


Chemical usage in different states

```
## choose input by yourself
pestiToxin <- function(state1){
  data <- filter(strawbPestiAVG,State==state1)
  bar <- ggplot(data)+
  geom_bar(mapping = aes(x=`Chemical Name`,y=Value,fill=`Human Toxins`), position = "dodge",stat = "iden
  scale_fill_manual(values = c("high" = "#D55E00", "moderate"="#E69F00", "slight"="#009E73"))+
    labs(title = state1)
  list(ggplotly(bar), bar+coord_polar())
}
```

```
pestiToxin("CALIFORNIA")
```

```
## [[1]]
##
## [[2]]
```


CALIFORNIA
Value
TRIFLUMIZOLE
ACETAMIPRID
TRIFLOXYSTROBIN
AZOXYSTROBIN
THIAMETHOXAM
BIFENAZATE
SPIROMESIFEN
BIFENTHRIN
RIPROXYFEN
BOSCALID
IMETHANIL
CAPTAN
CLOSTROBIN
CYPRODII
OPICONAZOLE
FENHEXAMI
PERONYL BUTOXIDE
FENPROPATHRIN
MYCLOBUTANIL
FLUDIOXONIL
METHOXYFENOZIDE
HEXYTHIAZOX
MALATHION
THIACLOPRID
Chemical Name
Human Toxins
high
moderate
slight