Manuscript

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```
# Load packages
library(tidyverse)
library(NatParksPalettes)
library(here)
library(gtsummary)
library(naniar)

# Set ggplot2 theme for whole script
ggplot2::theme_set(ggplot2::theme_linedraw())

# Set paths
here::here()
```

```
## [1] "/Users/savannahhammerton/Desktop/GitHub/EPID7500_Final_Project"
```

Data

The data used for this project is the "Bee Colonies" TidyTuesday data. The GitHub repository with the data itself, instructions on how to load the data into R, and explanations of the data can be found at https://github.com/rfordatascience/tidytuesday/tree/master/data/2022/2022-01-11. In order to preserve the data files I used for this project, I have downloaded the data via GitHub in another script and saved them as .rds files in this project.

The data originally comes from the USDA, and contains information on the number of bee colonies in various states during specific quarters (specified three month periods during a specified year). The data is split into two files: a `colony.csv` file (containing basic colony information) and a `stressor.csv` file (containing information on the specific stressors colonies experienced). In the `colony.csv` file, there is data on the total number of colonies, the maximum number of colonies, the number of colonies lost, the percent of total colonies lost, the number of colonies added, the number of colonies renovated, and the percent of colonies renovated. In the `stressor.csv` file, there is information of the types of stress experienced by colonies, and the percent of colonies affected by that stressor during that quarter (this allows for multiple stressors in the same quarter). Both files have three identifying variables: year, months (or, quarter), and state. Since both files have these three variables, they can be used to join the two data sets into one for easier exploration and analysis.

Data import and basic info

```
# Load data
colony <- readr::read_rds(here::here("data/colony.rds"))
stressor <- readr::read_rds(here::here("data/stressor.rds"))

# Check out the data
dplyr::glimpse(colony)
```

```
## Rows: 1,222
## Columns: 10
## $ year            <dbl> 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, ~
## $ months          <chr> "January-March", "January-March", "January-March", "Ja~
## $ state           <chr> "Alabama", "Arizona", "Arkansas", "California", "Color~
## $ colony_n        <dbl> 7000, 35000, 13000, 1440000, 3500, 3900, 305000, 10400~
## $ colony_max      <dbl> 7000, 35000, 14000, 1690000, 12500, 3900, 315000, 1050~
## $ colony_lost     <dbl> 1800, 4600, 1500, 255000, 1500, 870, 42000, 14500, 380~
## $ colony_lost_pct <dbl> 26, 13, 11, 15, 12, 22, 13, 14, 4, 4, 40, 22, 18, 23, ~
## $ colony_added    <dbl> 2800, 3400, 1200, 250000, 200, 290, 54000, 47000, 3400~
## $ colony_reno     <dbl> 250, 2100, 90, 124000, 140, NA, 25000, 9500, 760, 8000~
## $ colony_reno_pct <dbl> 4, 6, 1, 7, 1, NA, 8, 9, 7, 9, 4, 1, 2, 1, NA, 13, NA,~
```

```
dplyr::glimpse(stressor)
```

```
## Rows: 7,332
## Columns: 5
## $ year       <dbl> 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015,~
## $ months     <chr> "January-March", "January-March", "January-March", "January~
## $ state      <chr> "Alabama", "Alabama", "Alabama", "Alabama", "Alabama", "Ala~
## $ stressor   <chr> "Varroa mites", "Other pests/parasites", "Disesases", "Pest~
## $ stress_pct <dbl> 10.0, 5.4, NA, 2.2, 9.1, 9.4, 26.9, 20.5, 0.1, NA, 1.8, 3.1~
```

The `colony.rds` data set has 10 variables and 1,222 observations/records, while the `stressor.rds` data set has 5 variables and 7,332 observations/records. Both data sets have both character and numeric variables. All numeric variables are integers excepting the `stress_pct` variable in the `stressor.rds` data set. This matches the information in the data dictionary supplied on the GitHub page linked above.

Data processing

I'm going to join the colony and stressor data sets into one, matching on `year`, `months`, and `state`. now so I have one final data set to work with. I don't really want any data about stressors without any colony data, so I'm going to keep all the rows in the colony dataset, using `dplyr::left_join()`.

```
# Join data sets on year, months, and state, keeping all the rows in colony
savethebees <-
  dplyr::left_join(colony, stressor,
                   by = c("year", "months", "state"))
# Check out the new data set
dplyr::glimpse(savethebees)
```

```
## Rows: 7,332
## Columns: 12
## $ year            <dbl> 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, ~
## $ months          <chr> "January-March", "January-March", "January-March", "Ja~
## $ state           <chr> "Alabama", "Alabama", "Alabama", "Alabama", "Alabama",~
## $ colony_n        <dbl> 7000, 7000, 7000, 7000, 7000, 7000, 35000, 35000, 3500~
## $ colony_max      <dbl> 7000, 7000, 7000, 7000, 7000, 7000, 35000, 35000, 3500~
## $ colony_lost     <dbl> 1800, 1800, 1800, 1800, 1800, 1800, 4600, 4600, 4600, ~
## $ colony_lost_pct <dbl> 26, 26, 26, 26, 26, 26, 13, 13, 13, 13, 13, 13, 11, 11~
## $ colony_added    <dbl> 2800, 2800, 2800, 2800, 2800, 2800, 3400, 3400, 3400, ~
## $ colony_reno     <dbl> 250, 250, 250, 250, 250, 250, 2100, 2100, 2100, 2100, ~
## $ colony_reno_pct <dbl> 4, 4, 4, 4, 4, 4, 6, 6, 6, 6, 6, 6, 1, 1, 1, 1, 1, 1, ~
## $ stressor        <chr> "Varroa mites", "Other pests/parasites", "Disesases", ~
## $ stress_pct      <dbl> 10.0, 5.4, NA, 2.2, 9.1, 9.4, 26.9, 20.5, 0.1, NA, 1.8~
```

Since I now have the same number of rows in my final dataset that I did in the stressor dataset (which had

exactly six times the number of rows in the colony data set), I can conclude that there are six stressors observed, and the data collectors included all of the six stressors for each year/location combination. I want to break those stressors into indicator/dummy variables so I can explore them a little more in depth. I will use `tidyr::pivot_wider()`, pulling names from the stressors themselves, and values from the percentage of colonies affected by the stressors during that time period in that location. When I do that, I will also rename the two stressors that have spaces in the names, and use `janitor::clean_names()` to make sure every variable is lower case.

```
# Pivot stressor data wider and rename variables with spaces
savethebees_wide <-
  savethebees |>
  dplyr::mutate(stressor = ifelse(stressor == "Disesases", "Diseases", stressor)) |>
  tidyr::pivot_wider(names_from = stressor, values_from = stress_pct) |>
  dplyr::rename(varroa_mites = `Varroa mites`,
                other_pests_parasites = `Other pests/parasites`) |>
  janitor::clean_names()

# Check out new data
dplyr::glimpse(savethebees_wide)
```

```
## Rows: 1,222
## Columns: 16
## $ year                  <dbl> 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, ~
## $ months                <chr> "January-March", "January-March", "January-March~
## $ state                 <chr> "Alabama", "Arizona", "Arkansas", "California", ~
## $ colony_n              <dbl> 7000, 35000, 13000, 1440000, 3500, 3900, 305000,~
## $ colony_max            <dbl> 7000, 35000, 14000, 1690000, 12500, 3900, 315000~
## $ colony_lost           <dbl> 1800, 4600, 1500, 255000, 1500, 870, 42000, 1450~
## $ colony_lost_pct       <dbl> 26, 13, 11, 15, 12, 22, 13, 14, 4, 4, 40, 22, 18~
## $ colony_added          <dbl> 2800, 3400, 1200, 250000, 200, 290, 54000, 47000~
## $ colony_reno           <dbl> 250, 2100, 90, 124000, 140, NA, 25000, 9500, 760~
## $ colony_reno_pct       <dbl> 4, 6, 1, 7, 1, NA, 8, 9, 7, 9, 4, 1, 2, 1, NA, 1~
## $ varroa_mites          <dbl> 10.0, 26.9, 17.6, 24.7, 14.6, 2.5, 22.3, 6.2, 38~
## $ other_pests_parasites <dbl> 5.4, 20.5, 11.4, 7.2, 0.9, 1.4, 13.5, 4.9, 37.7,~
## $ diseases              <dbl> NA, 0.1, 1.5, 3.0, 1.8, NA, 0.8, 3.3, 1.6, 12.5,~
## $ pesticides            <dbl> 2.2, NA, 3.4, 7.5, 0.6, NA, 8.9, 2.6, NA, 4.8, 0~
## $ other                 <dbl> 9.1, 1.8, 1.0, 6.5, 2.6, 21.2, 5.1, 4.8, 2.0, 8.~
## $ unknown               <dbl> 9.4, 3.1, 1.0, 2.8, 5.9, 2.4, 4.4, 10.5, NA, 4.9~
```

The data set is now back to the number of rows in the initial colony data set, which makes sense as the stressor variables were what were making the dataset longer. I'm now going to check for missingness using `naniar::gg_miss_var()`, which will show me the number of data points missing for each variable.

```
# Create function to rename variables in long (initial) dataset
rename_long <- function(data) {
  data |>
    dplyr::rename(Year = year,
                  Quarter = months,
                  State = state,
                  `Number of colonies` = colony_n,
                  `Maximum colonies` = colony_max,
                  `Colonies lost` = colony_lost,
                  `Percentage of total colonies lost` = colony_lost_pct,
                  `Colonies added` = colony_added,
                  `Colonies renovated` = colony_reno,
                  `Percent of colonies renoavated` = colony_reno_pct,
```

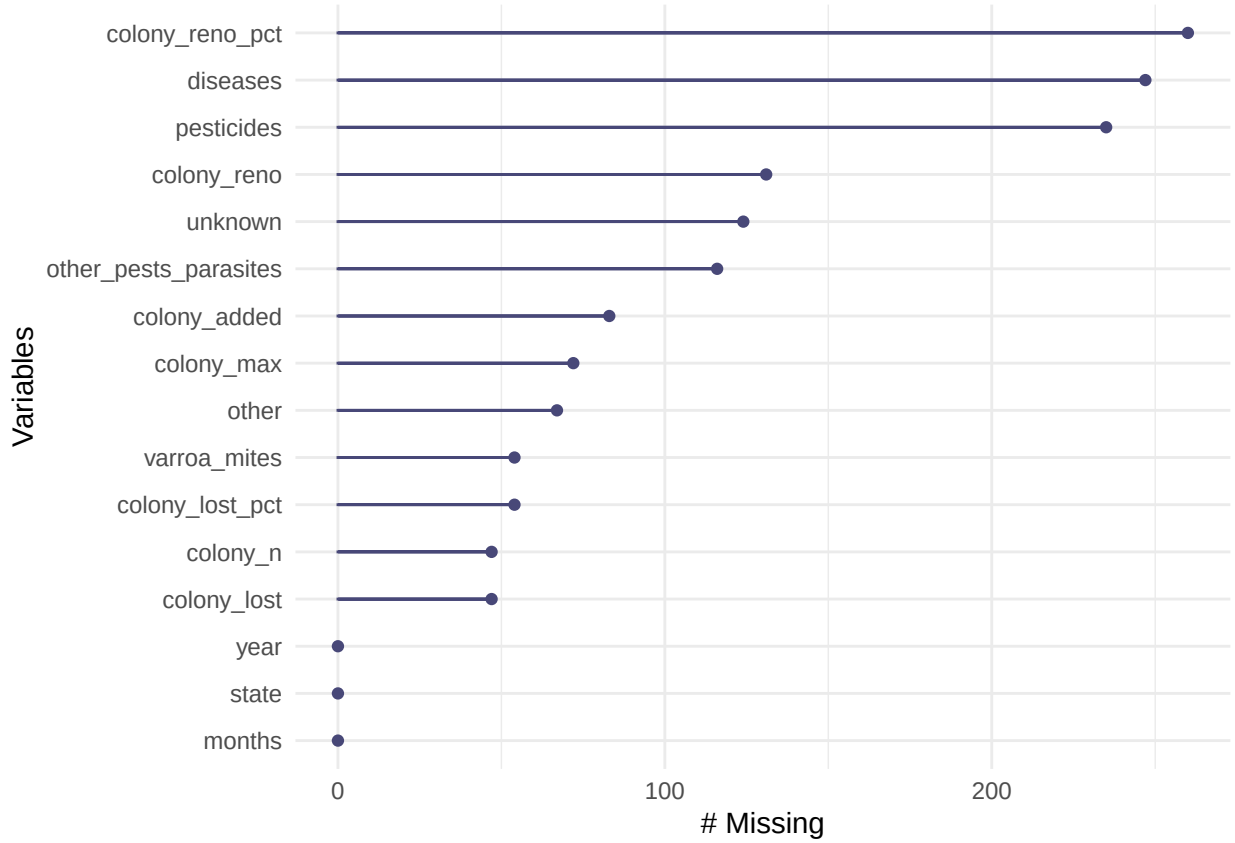
```
                  `Stress type` = stressor,
                  `Percent of colonies affected by stressor in quarter` =
                    stress_pct)
}

# Create function to rename variables in qide dataset
rename_wide <- function(data) {
    data |>
    dplyr::rename(Year = year,
                  Quarter = months,
                  State = state,
                  `Number of colonies` = colony_n,
                  `Maximum colonies` = colony_max,
                  `Colonies lost` = colony_lost,
                  `Percentage of total colonies lost` = colony_lost_pct,
                  `Colonies added` = colony_added,
                  `Colonies renovated` = colony_reno,
                  `Percent of colonies renoavated` = colony_reno_pct,
                  `Varroa mites` = varroa_mites,
                  `Other pests and parasites` = other_pests_parasites,
                  `Diseases` = diseases,
                  `Pesticides` = pesticides,
                  `Other` = other,
                  `Unknown` = unknown)

}
```

```
# Check for missingness
naniar::gg_miss_var(savethebees_wide)
```

```
## Warning: It is deprecated to specify ‘guide = FALSE‘ to remove a guide. Please
## use ‘guide = "none"‘ instead.
```



The variable with the most missing data points is `colony_reno_pct`, which is the percentage of colonies renovated. I'm going to check what the range is of that variable, and see if it's possible that the NA's actually just mean it should be zero. While I'm at it, I'm going to do this for all the variables since all but the identifier variables have some missing values.

```
# savethebees_wide |>
#   rename_wide() |>
#   dplyr::select(!c(Year, Quarter, State)) |>
#   dplyr::summarise(dplyr::across(.cols = everything(),
#                                  .fns = min, na.rm = TRUE)) |>
#   t() |>
#   as.data.frame() |>
#   gt::gt()
```