Data Visualization Analysis

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1 Introduction

This tutorial is designed to help you learn data visualization analysis by providing simple and useful information in a way that is easy to follow and understand.

2 Preparation

In order to draw a chart, we need to include the required packages for visualization and dataset. For example, ggplot2 package is for drawing charts and gcookbook is for using pg_mean dataset.

```
library(ggplot2)
library(gcookbook)
```

3 Datasets

Before we start with this tutorial, We will be discussing all the datasets we are going to use 1. pg_mean dataset. The dataset has two columns: group, weight.

```
pg_mean
```

This dataset compares the weight across three groups:

- ctrl: Control group (baseline, weight = 5.032).
- trt1: Treatment 1 group (weight = 4.661).
- trt2: Treatment 2 group (weight = 5.526).
- 2. BOD, The dataset has two columns: Time and demmand

BOD

This dataset compares Oxygen demand over time - Time: Time needed - demmand: Biochemical Oxygen demanded

3. iris, The dataset has 5 columns:

iris

- Sepal.Length: Length of the sepal (in cm).
- Sepal.Width: Width of the sepal (in cm).

- Petal.Length: Length of the petal (in cm).
- Petal.Width: Width of the petal (in cm).
- Species: The species of the flower (setosa, versicolor, or virginica)
- 4. birthwt, The dataset has 10 columns:

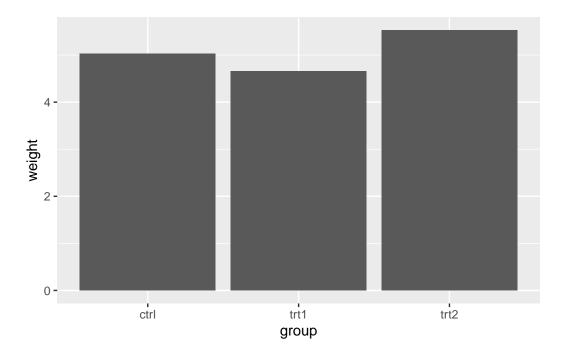
birthwt

- low: Indicator of birth weight less than 2.5 kg (0 = no, 1 = yes).
- age: Mother's age (in years).
- lwt: Mother's weight at last menstrual period (in pounds).
- race: Mother's race (1 = White, 2 = Black, 3 = Other).
- smoke: Smoking status during pregnancy (0 = no, 1 = yes).
- ptl: Number of previous premature labors.
- ht: History of hypertension (0 = no, 1 = yes).
- ui: Presence of uterine irritability (0 = no, 1 = yes).
- ftv: Number of physician visits during the first trimester (0, 1, 2, or more).
- bwt: Birth weight of the baby (in grams).

4 Bar chart

In this section, we will draw a bar chart using pg_mean dataset.

```
ggplot(pg_mean, aes(x = group, y = weight)) +
geom_col()
```



It initializes a ggplot with the dataset pg_mean.

aes(x = group, y = weight) specifies the aesthetics:

- x = group: Assign the group variable to the x-axis (categorical data, such as ctrl, trt1, trt2).
- y = weight: Assign the weight variable to the y-axis (numerical data).

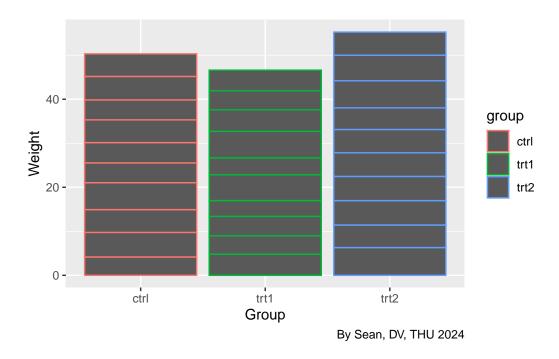
geom_col():

- Adds a column geometry to the plot.
- geom_col() creates bars where the height of each bar corresponds to the value of weight for each group.

5 Bar chart with color

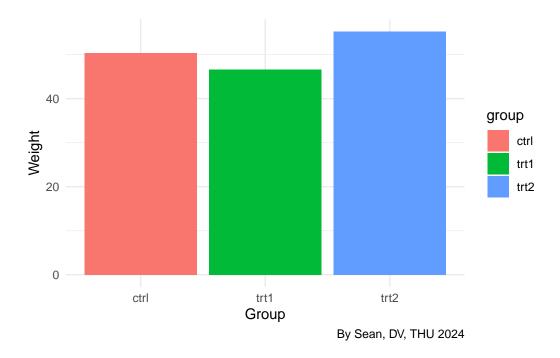
In order to give better visualization, we can use colors in order to create a more attractive appearance of your data visualization. However, it is very important that color and fill are different functions

We use color to add colors to the outline of the chart according to the group

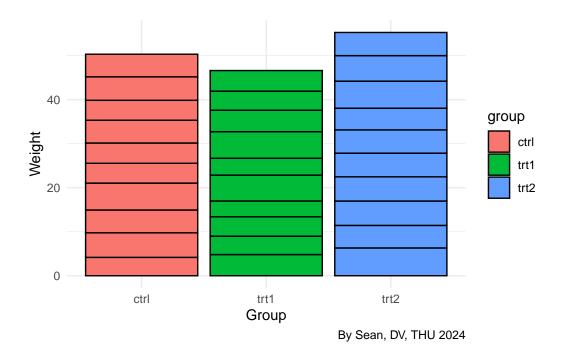


We use fill to add colors to the bars according to the group

```
ggplot(PlantGrowth, aes(x = group, y = weight, fill = group)) +
  geom_col()+
  theme_minimal()+
  labs(x= 'Group',
    y= 'Weight',
    captions= 'By Sean, DV, THU 2024')
```



When we combine the 2, it creates a better visualization



6 Line chart

In this part of the tutorial, we will also teach you how to make line chart using <code>geom_line()</code>. This is one of the many geometries or chart that are provided by the <code>ggplot2</code> package.

For this demonstration we are going to use the BOD dataset provided by the ggplot2 package

My Line Chart 20.0 17.5 15.0 10.0 2 4 6

Time

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aes(): Defines the following aesthetic:

• x = Time: Plot the Time variable to the x-axis

• y = demand: Plot the demand variable to the y-axis

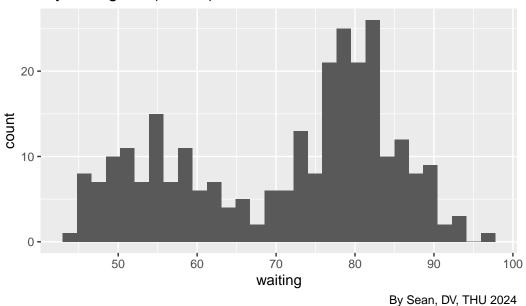
• geom_line(): Is used to draw a line chart

7 Histogram

To draw histogram we can use the <code>geom_histogram()</code> function provided by the <code>ggplot2</code> package. In this demonstration, we are going to use the <code>faithful</code> dataset provided by the <code>ggplot2</code>

`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.

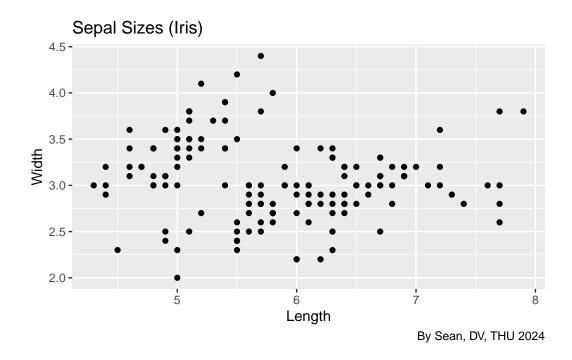




Unlike previous chart, the geom_histogram does not require the y-axis variables, this is because the histogram is a chart to show distribution, so y-axis variable is not required.

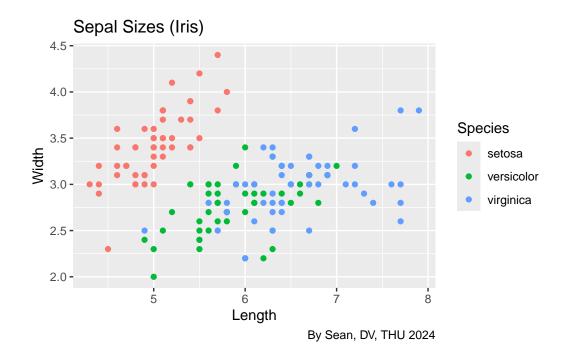
8 Correlation chart

Correlation chart or in other words scatter plot is also part of the geometrics provided by the ggplot2 package. In order to plot a scatter plot, we will be using geom_point. In this demonstration, we will be using iris dataset provided by ggplot2 package



9 Correlation chart: Color by group

When adding colors by group, similarly to the Bar chart, we can use color=species. This means that we color the Scatter plot and categorizing them by the species variable in the iris dataset



10 Multigroup histogram

library(dplyr)

A multigroup histogram is multiple histogram overlayed with each other. In this demonstration we will be using the birthwt dataset provided by the MASS. As this demonstration needed extra function and dataset, we will be loading extra packages dplyr and MASS.

```
Attaching package: 'dplyr'

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

select

The following objects are masked from 'package:stats':

filter, lag
```

The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

```
library(MASS)
```

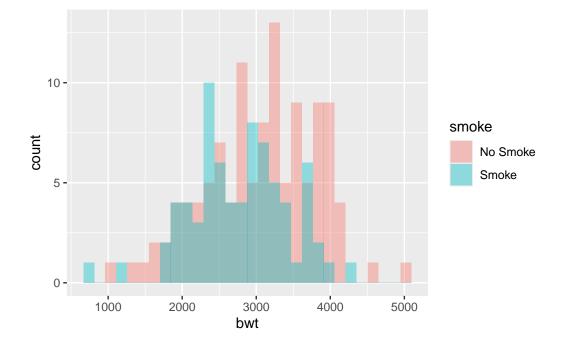
We first need to load dplyr package in order to use the recode_factor function and MASS in order to use the birthwt dataset

```
birthwt_mod <- birthwt
birthwt_mod$smoke <- recode_factor(birthwt_mod$smoke, '0' = 'No Smoke', '1' = 'Smoke')</pre>
```

Next, we will make a temporary dataset so that the original dataset will not be altered by birthwt_mod <- birthwt. The recode_factor function is used to change binary data into variables, in this case 1 and 0 is changed into Smoke and No Smoke. In order to let R know where the data is, we will need to write birthwt_mod\$smoke to indicate which dataset and column to recode

```
ggplot(birthwt_mod, aes(x = bwt, fill = smoke)) +
geom_histogram(position = "identity", alpha = 0.4)
```

`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.



Once the preparation is done, we can use geom_histogram to create the histogram. However, additional function is needed to create the multigroup histogram, which is position = identity which means that we are able to make the histogram overlay with each other, one being No smoke and the other representing smoke

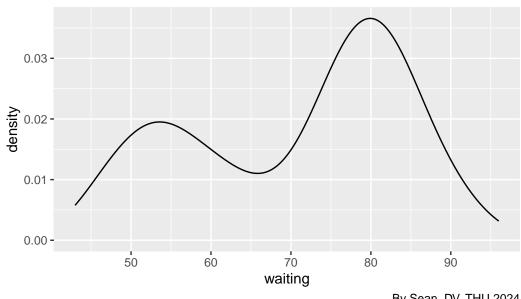
alpha is used to change the transparency of the chart and fill = smoke is the grouped variables

11 Density chart

Density chart is geometric provided by ggplot2 package that displays the distribution in a smooth line. In this demonstration, we will be using the faithful dataset provided by ggplot2 package

```
ggplot(faithful, aes(x=waiting)) +
  geom_density() +
 labs(title="My Density Curve",
       caption = 'By Sean, DV, THU 2024')
```

My Density Curve



By Sean, DV, THU 2024

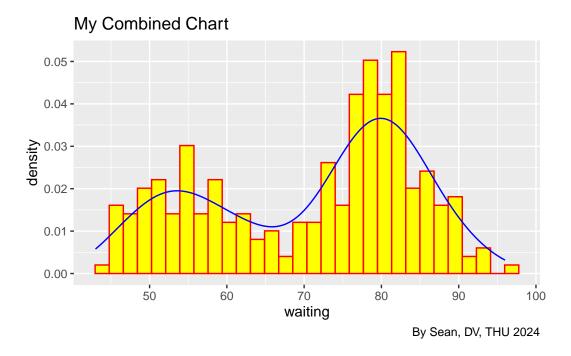
To create the Density Curve, we will be using the geom_density() function provided by ggplot2 package.

12 Histogram and Density chart

After learning the Histogram and Density Chart using the geom_histogram and geom_density. We can combine the 2 for a better visualization. The histogram will serve as a raw visualization of the data and the Density chart will visualize the smooth approximations

Warning: The dot-dot notation (`..density..`) was deprecated in ggplot2 3.4.0. i Please use `after_stat(density)` instead.

`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.



In order to create the combined chart, we must first place the appropriate aesthetics (aes()). Althought the, geom_density does not require a y-axis variable, the geom_histogram needs the y-axis variable. So in this demonstration we added y=..density.. so it ensures that it will represent the density data points

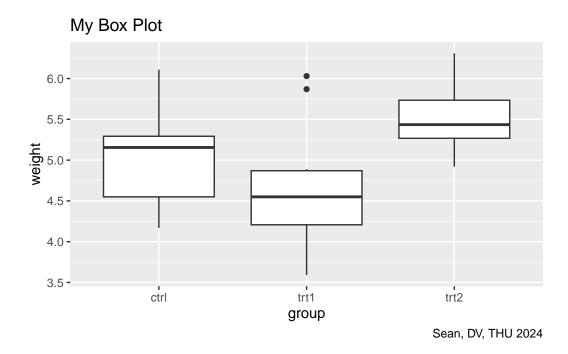
For better visualization, color and fill have been added to the appropriate geometrics

It's also very important to where to place the geom_histogram, geom_density and other geometrics when you want to display multiple chart. If you place the geom_histogram first and then geom_density, this means that the density curves will overlay the histogram.

13 Box plot

The last geometrics that will be discussed in this tutorial is Box Plot. Box plot is really useful to display mean, median, error bars and etc. In this demonstration, we will plot a simple box plot.

We will be using the PlantGrowth dataset



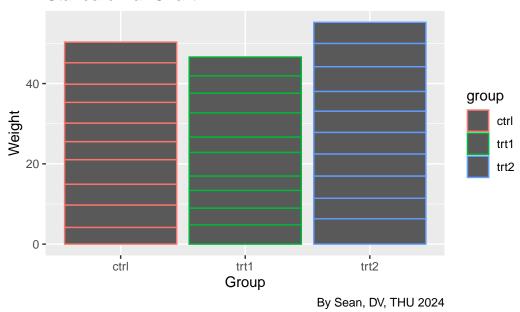
To make the box plot, we use geom_boxplot(). The following explains the plot's aesthetic

- x = group: Plot the experimental treatment.
- y = weight: Plot the weight of the plant

14 Adding Title, Captions and Axis Labels

Another important thing to do when creating our chart or visualization, is to add labels. Labels serve as a function to further enhance visualization by labeling plots which gives the reader a better understanding and direction. Moreover, it's also used to claim credits of your work.

Standard Bar Chart

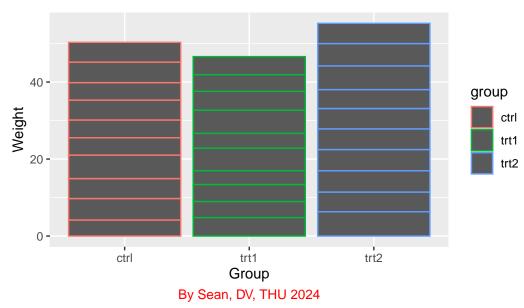


We can use labs() to change add title, axis labels and captions:

- labs(title=: Is a function to add 'text' to the title of the chart
- labs(x=: Is a function to change the x-axis label
- labs(y-: Is a function to change the y-axis label
- labs(captions=: Is a function to add 'text' on the bottom right of the chart

It is to note that whenever you are adding 'text' in R, we have to use ' ' between the text, otherwise it will be recognize as a function, instead of a 'text'

Standard Bar Chart

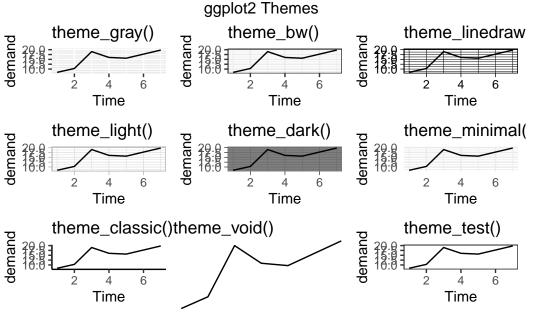


Furthermore, we can also change the appearance of the 'text' in the theme() which we will discuss in more detail in the next section

- theme(plot.title: A function to let the R know to change the title's element
- element_text: Which element to change the appearance
- size: change the font size
- hjust: changes the position of the text
- theme(plot.caption: A function to let R know to change the caption's element

15 Theme

For the last part of this tutorial, we can enhance our visualization further using theme(), it is a feature that is provided by the ggplot2 packages



By Sean, Data Visualization Lecture, Tunghai University 2024

- theme_gray() (default):
 - The signature ggplot2 theme with a grey background and white gridlines, designed to put the data forward yet make comparisons easy.
- theme_bw() (black and white):
 - The classic dark-on-light ggplot2 theme. May work better for presentations displayed with a projector.
- theme_linedraw():
 - A theme with only black lines of various widths on white backgrounds, reminiscent of a line drawing. Serves a purpose similar to theme_bw(). Note that this theme has some very thin lines (<< 1 pt) which some journals may refuse.</p>
- theme_light():
 - A theme similar to theme_linedraw() but with light grey lines and axes, to direct more attention towards the data.
- theme_dark():
 - The dark cousin of theme_light(), with similar line sizes but a dark background. Useful to make thin coloured lines pop out.
- theme minimal():
 - A minimalistic theme with no background annotations.

- theme_classic():
 - A classic-looking theme, with x and y axis lines and no gridlines.
- theme_void():
 - A completely empty theme.
- theme_test():
 - A theme for visual unit tests. It should ideally never change except for new features.

16 Adding and Removing Legend

To add Legend:

By adding fill or color options to aes(), a legend is created automatically on the right side of the plot.

- library(gridExtra): This loads the gridExtra library to use grid.arrange
- fill: Fill in the colors inside the chart
- color: Change the color of the outlines of the chart
- grid.arrange: Arrange the order of the chart
- top: Add text on the top of the chart
- bottom: Add text on the bottom of the chart

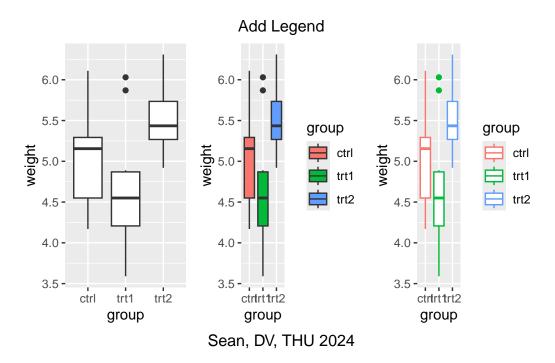
```
library(gridExtra)

p1 <- ggplot(PlantGrowth, aes(x = group, y = weight)) +
    geom_boxplot()

p2 <- ggplot(PlantGrowth, aes(x = group, y = weight, fill = group)) +
    geom_boxplot()

p3 <- ggplot(PlantGrowth, aes(x = group, y = weight, color = group)) +
    geom_boxplot()

grid.arrange(p1,p2,p3,ncol=3,top='Add Legend', bottom = 'Sean, DV, THU 2024')</pre>
```



To Remove Legend

The legend is removed by guides(fill = FALSE)

```
ggplot(PlantGrowth, aes(x = group, y = weight, fill = group)) +
  geom_boxplot() +
  guides(fill = FALSE) +
  ggtitle('Remove Legend') +
  labs(caption = 'Sean, DV, THU 2024') +
  theme(plot.title = element_text(hjust=0.5))
```

Warning: The `<scale>` argument of `guides()` cannot be `FALSE`. Use "none" instead as of ggplot2 3.3.4.

Remove Legend

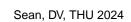
trt1 group

4.5 **-**

4.0 -

3.5 **-**

ctrl



trt2