Exploratory Data Analysis

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Introduction

Before fitting a model, it is good practice to explore and summarize the data. Exploratory data analysis (EDA) serves several purposes:

- understanding the distribution of each variable individually;
- detecting unusual values, outliers, and missing data;
- identifying patterns and relationships among variables;
- motivating choices of model structure, such as transformations;
- providing context for interpreting model results.

This page is adapted from (Vittinghoff et al. 2012, chap. 2).

The WCGS data

This page illustrates exploratory data analysis using data from the Western Collaborative Group Study (WCGS) (Rosenman et al. 1975). Vittinghoff et al. (2012, 9) describe the study this way:

> The Western Collaborative Group Study (WCGS) was a large epidemiological study designed to investigate the association between the "type A" behavior pattern and coronary heart disease (CHD).

Exercise 0.1 (Type A behavior)**.** What is "type A" behavior?

Solution

Solution 0.1. From Wikipedia's article "Type A and Type B personality theory":

> The hypothesis describes Type A individuals as outgoing, ambitious, rigidly organized, highly status-conscious, impatient, anxious, proactive, and concerned

> with time management….
>
> The hypothesis describes Type B individuals as a contrast to those of Type A. Type B personalities, by definition, are noted to live at lower stress levels. They typically work steadily and may enjoy achievement, although they have a greater tendency to disregard physical or mental stress when they do not achieve.

Study design

The WCGS began in 1960 with 3,524 male volunteers employed by 11 California companies. Participants were 39 to 59 years old and free of heart disease, as determined by electrocardiogram. After the initial screening, various exclusions reduced the study population to 3,154 men and the number of companies to 10. The cohort comprised both blue- and white-collar employees. Average follow-up was 8.5 years, with repeat examinations.

This description paraphrases the help page for the `wcgs` dataset in the `faraway` R package.

At baseline, the study collected:

- socio-demographic characteristics: age, education, marital status, income, and occupation;
- physical and physiological measurements: height, weight, blood pressure, electrocardiogram, and corneal arcus;
- biochemical measurements: cholesterol and lipoprotein fractions;
- medical and family history, and use of medications;
- behavioral data: the Type A interview, smoking, exercise, and alcohol use.

Later surveys added anthropometry, triglycerides, the Jenkins Activity Survey, and caffeine use.

Loading the data

The WCGS data are distributed with Vittinghoff et al. (2012) on the book's companion website, as a Stata file that R can read directly:

```
# one unbroken string, so that link checkers test the whole URL:
url <- "https://regression.ucsf.edu/sites/g/files/tkssra16191/files/wysiwyg/home/data/wcgs.d
wcgs <- haven::read_dta(url)
```

The `rmb` R package includes the same file, which these notes use so that rendering does not depend on the website. `haven::as_factor()` converts the Stata value labels to factors:

```r
wcgs <- rmb::wcgs |> haven::as_factor()
```

```r
# attach a descriptive label to each variable;
# gtsummary tables print these labels instead of the column names:
wcgs_labels <- c(
  age = "Age (years)",
  chol = "Cholesterol (mg/dL)",
  sbp = "Systolic BP (mmHg)",
  dbp = "Diastolic BP (mmHg)",
  bmi = "BMI (kg/m^2)",
  weight = "Weight (lbs)",
  ncigs = "Cigarettes per day",
  chd69 = "CHD event by 1969",
  smoke = "Current smoker",
  arcus = "Arcus senilis",
  dibpat = "Behavioral pattern (A/B)",
  behpat = "Behavioral pattern (A1/A2/B3/B4)",
  wghtcat = "Weight category",
  agec = "Age group"
)
for (var in names(wcgs_labels)) {
  attr(wcgs[[var]], "label") <- wcgs_labels[[var]]
}
```

The dataset has one row per participant:

```r
dplyr::glimpse(wcgs)
#> Rows: 3,154
#> Columns: 22
#> $ age      <dbl> 50, 51, 59, 51, 44, 47, 40, 41, 50, 43, 59, 54, 48, 39, 49, 5~
#> $ arcus    <dbl> 1, 0, 1, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1~
#> $ behpat   <fct> A1, A1, A1, A1, A1, A1, A1, A1, A1, A1, A1, A1, A1, A1, A1, A~
#> $ bmi      <dbl> 31.3210, 25.3286, 28.6939, 22.1487, 22.3130, 27.1177, 23.2420~
#> $ chd69    <fct> No, No, No, No, No, No, No, No, No, No, No, No, No, Yes, No, ~
#> $ chol     <dbl> 249, 194, 258, 173, 214, 206, 190, 212, 130, 233, 181, 214, 2~
#> $ dbp      <dbl> 90, 74, 94, 80, 80, 76, 78, 84, 70, 80, 86, 76, 78, 74, 80, 7~
#> $ dibpat   <fct> Type A, Type A, Type A, Type A, Type A, Type A, Type A, Type ~
#> $ height   <dbl> 67, 73, 70, 69, 71, 64, 70, 70, 71, 68, 72, 67, 71, 70, 73, 7~
#> $ id       <dbl> 2343, 3656, 3526, 22057, 12927, 16029, 3894, 11389, 12681, 10~
#> $ lnsbp    <dbl> 4.88280, 4.78749, 5.06259, 4.83628, 4.83628, 4.75359, 4.80402~
#> $ lnwght   <dbl> 5.29832, 5.25750, 5.29832, 5.01064, 5.07517, 5.06259, 5.08760~
#> $ ncigs    <dbl> 25, 25, 0, 0, 0, 80, 0, 25, 0, 25, 10, 0, 20, 0, 4, 0, 0, 20,~
```

```
#> $ sbp      <dbl> 132, 120, 158, 126, 126, 116, 122, 130, 112, 120, 130, 118, 1~
#> $ smoke    <fct> Yes, Yes, No, No, No, Yes, No, Yes, No, Yes, Yes, No, Yes, No~
#> $ t1       <dbl> -1.633353, -4.063366, 0.639729, 1.121768, 2.425011, -0.787520~
#> $ time169  <dbl> 1367, 2991, 2960, 3069, 3081, 2114, 2929, 3010, 3104, 2861, 2~
#> $ typchd69 <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0~
#> $ uni      <dbl> 0.4860738, 0.1859543, 0.7277991, 0.6244636, 0.3789776, 0.7355~
#> $ weight   <dbl> 200, 192, 200, 150, 160, 158, 162, 160, 195, 187, 206, 152, 1~
#> $ wghtcat  <fct> 170-200, 170-200, 170-200, 140-170, 140-170, 140-170, 140-170~
#> $ agec     <fct> 46-50, 51-55, 56-60, 51-55, 41-45, 46-50, 35-40, 41-45, 46-50~
```

Summarizing a single variable

Measures of center

Definition 0.1 (Sample mean)**.** The **sample mean** of n observations $x_1, \ldots, x_n$ is:

$$\bar{x} \stackrel{\text{def}}{=} \frac{1}{n} \sum_{i=1}^{n} x_i$$

Example 0.1 (Mean cholesterol in the WCGS)**.** Total cholesterol (`chol`) is missing for 12 of the 3154 WCGS participants. The sample mean of the remaining 3142 values is:

```
mean(wcgs$chol, na.rm = TRUE)
#> [1] 226.372
```

Definition 0.2 (Sample median)**.** The **sample median** is the middle value when the observations are sorted in increasing order. In terms of the order statistics $x_{(1)} \leq \cdots \leq x_{(n)}$:

- if n is odd, the median is $x_{((n+1)/2)}$;
- if n is even, the median is $\frac{1}{2}\left(x_{(n/2)} + x_{(n/2+1)}\right)$.

Example 0.2 (Median cholesterol in the WCGS)**.**

```
median(wcgs$chol, na.rm = TRUE)
#> [1] 223
```

The median cholesterol is a little lower than the mean (Example 0.1). Cholesterol has a longer right tail than left tail (the maximum is 645 mg/dL), and the large values in that

tail pull the mean upward but barely change which value is in the middle. A median is less sensitive to extreme values than a mean.

Measures of spread

Definition 0.3 (Sample variance)**.** The **sample variance** of $n \geq 2$ observations is:

$$s^2 \stackrel{\text{def}}{=} \frac{1}{n-1} \sum_{i=1}^{n} (x_i - \bar{x})^2$$

Definition 0.4 (Sample standard deviation)**.** The **sample standard deviation** is the square root of the sample variance:

$$s \stackrel{\text{def}}{=} \sqrt{s^2}$$

The standard deviation has the same units as the observations, which makes it easier to interpret than the variance, whose units are squared.

Example 0.3 (Variance and standard deviation of cholesterol in the WCGS)**.**

```
var(wcgs$chol, na.rm = TRUE)
#> [1] 1885.33
sd(wcgs$chol, na.rm = TRUE)
#> [1] 43.4204
```

The sample variance is in $(\text{mg/dL})^2$, and the sample standard deviation is in mg/dL, like the cholesterol values themselves.

Definition 0.5 (Quartiles)**.** The **first quartile** Q_1 and the **third quartile** Q_3 are the sample 0.25 and 0.75 quantiles (sample quantile), also called the 25th and 75th percentiles.

With an odd number of observations, the sample 0.5 quantile equals the sample median; with an even number they can differ, because the median averages the two middle order statistics. Software packages compute quartiles with different quantile definitions, so they can disagree slightly for the same data (quantile conventions); R's `quantile(type = 1)` matches these notes' definition, and R's default, `type = 7`, interpolates.

Definition 0.6 (Interquartile range)**.** The **interquartile range** (IQR) is the difference between the third and first quartiles:

$$\text{IQR} \stackrel{\text{def}}{=} Q_3 - Q_1$$

Example 0.4 (Quartiles and IQR of cholesterol in the WCGS)**.**

```
quantile(wcgs$chol, probs = c(0.25, 0.75), na.rm = TRUE, type = 1)
#> 25% 75%
#> 197 253
IQR(wcgs$chol, na.rm = TRUE, type = 1)
#> [1] 56
```

The middle half of the cholesterol values span 56 mg/dL. Like the median, the IQR does not depend on the most extreme values, so it is less sensitive to outliers than the standard deviation.

Summary statistics in R

The `summary()` function reports the minimum, quartiles, mean, maximum, and number of missing values in one call; its quartiles use R's default interpolating quantile rule (`type = 7`), so they can differ slightly from Definition 0.5:

```
summary(wcgs$chol)
#>    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.     NAs
#>     103     197     223     226     253     645      12
```

For a formatted table of several variables at once, `gtsummary::tbl_summary()` is useful (Table 1).

Binary and categorical variables

Definition 0.7 (Sample proportion)**.** For a binary variable with values coded 1 ("success") and 0, the **sample proportion** of successes is:

$$\hat{p} \stackrel{\text{def}}{=} \frac{k}{n}$$

where k is the number of successes and n is the number of observations.

Example 0.5 (Proportion of WCGS participants with a CHD event)**.**

Table 1: WCGS: descriptive statistics for continuous variables

```
wcgs |>
  dplyr::select(age, chol, sbp, dbp, bmi, weight) |>
  gtsummary::tbl_summary(
    statistic = list(
      gtsummary::all_continuous() ~
        "{mean} ({sd}); {median} [{p25}, {p75}]"
    ),
    digits = gtsummary::all_continuous() ~ 1
  )
```

Characteristic	**N = 3,154**[1]
Age (years)	46.3 (5.5); 45.0 [42.0, 50.0]
Cholesterol (mg/dL)	226.4 (43.4); 223.0 [197.0, 253.0]
Unknown	12
Systolic BP (mmHg)	128.6 (15.1); 126.0 [120.0, 136.0]
Diastolic BP (mmHg)	82.0 (9.7); 80.0 [76.0, 86.0]
BMI (kg/m^2)	24.5 (2.6); 24.4 [23.0, 25.8]
Weight (lbs)	170.0 (21.1); 170.0 [155.0, 182.0]

[1]Mean (SD); Median [Q1, Q3]

Table 2: Frequency table for categorical variables in the WCGS dataset

```
wcgs |>
  dplyr::select(chd69, smoke, dibpat, behpat, wghtcat) |>
  gtsummary::tbl_summary()
```

Characteristic	**N = 3,154**[1]
CHD event by 1969	257 (8.1%)
Current smoker	1,502 (48%)
Behavioral pattern (A/B)	
Type B	1,565 (50%)
Type A	1,589 (50%)
Behavioral pattern (A1/A2/B3/B4)	
A1	264 (8.4%)
A2	1,325 (42%)
B3	1,216 (39%)
B4	349 (11%)
Weight category	
< 140	232 (7.4%)
140-170	1,538 (49%)
170-200	1,171 (37%)
> 200	213 (6.8%)

[1] n (%)

```
table(wcgs$chd69)
#>
#>   No  Yes
#> 2897  257
mean(wcgs$chd69 == "Yes")
#> [1] 0.0814838
```

257 of the 3154 participants had a CHD event by 1969, a sample proportion of 0.081.

For categorical variables with more than two levels, the natural descriptive statistics are the count of observations in each category and the corresponding proportions (Table 2).

Graphical methods

Graphs can reveal features of a distribution that summary statistics miss, such as skewness, multiple peaks, and outliers. Different types of graph suit different types of variable.

Histograms

Definition 0.8 (Histogram)**.** A **histogram** displays the distribution of a continuous variable by dividing the variable's range into intervals and drawing a bar over each interval whose height is the number (or proportion) of observations in that interval.

The intervals are often called *bins*.

```
wcgs |>
  ggplot2::ggplot() +
  ggplot2::aes(x = chol) +
  ggplot2::geom_histogram(bins = 30, fill = "steelblue", color = "white") +
  ggplot2::labs(x = "Cholesterol (mg/dL)", y = "Count")
```

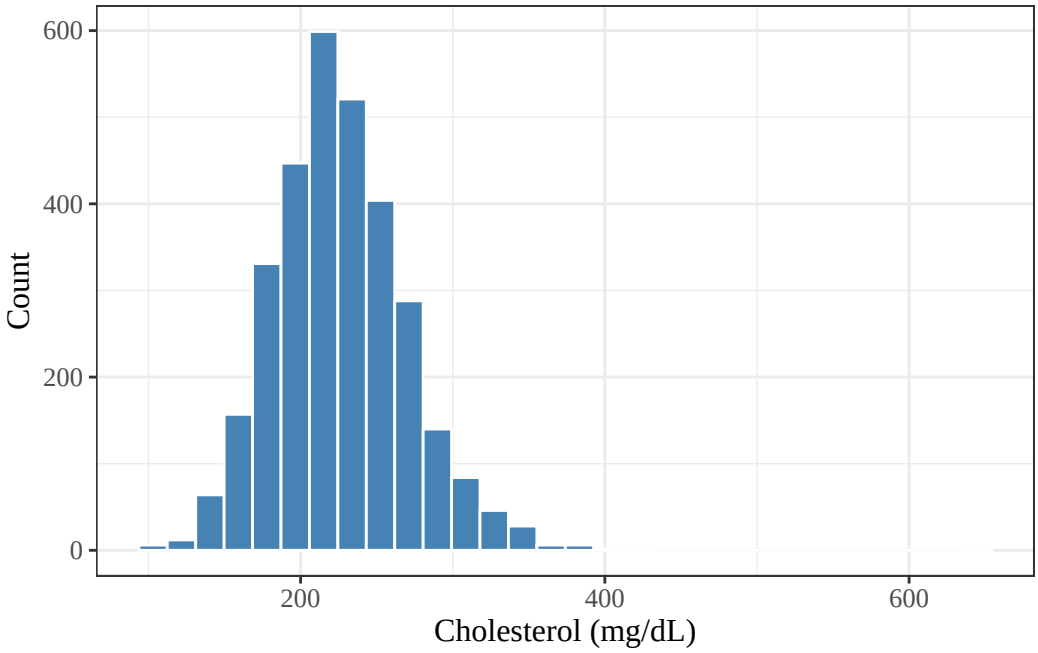


Figure 1: Histogram of total cholesterol in the WCGS dataset

Figure 1 shows a single-peaked distribution with a longer right tail than left tail: 97% of the values lie between 150 and 350 mg/dL, but the largest value is 645 mg/dL.

Density plots

Definition 0.9 (Density plot)**.** A **density plot** draws a smooth curve that estimates the probability density of a continuous variable, scaled so that the area under the curve is 1.

```
wcgs |>
  ggplot2::ggplot() +
  ggplot2::aes(x = chol) +
  ggplot2::geom_density(fill = "steelblue", alpha = 0.5) +
  ggplot2::labs(x = "Cholesterol (mg/dL)", y = "Density")
```

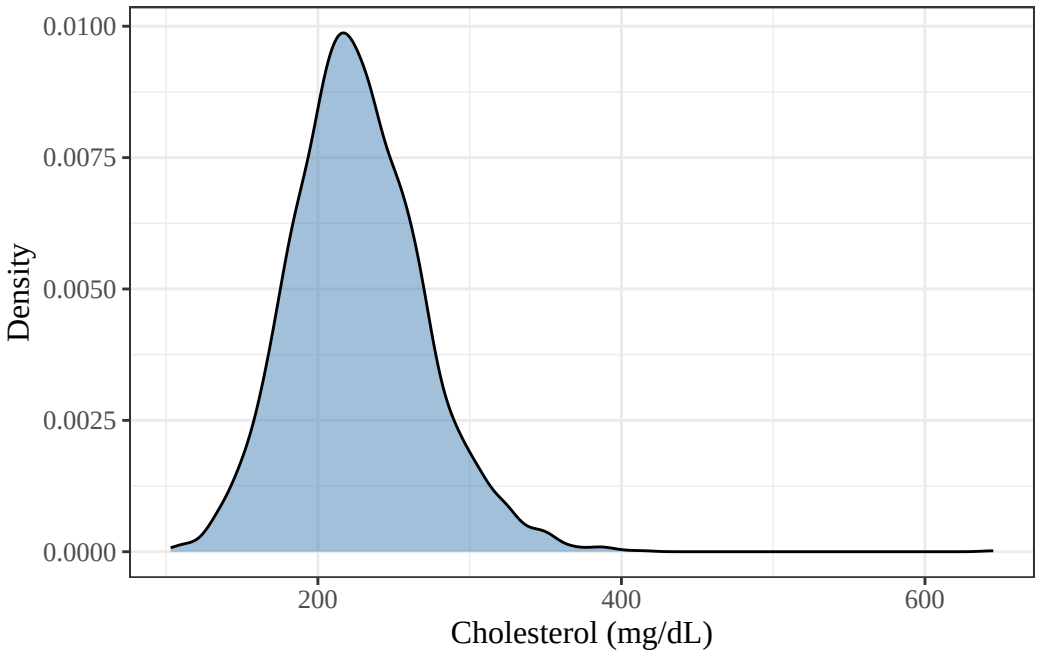


Figure 2: Density plot of total cholesterol in the WCGS dataset

Box plots

Definition 0.10 (Box plot)**.** A **box plot** (or box-and-whisker plot) summarizes the distribution of a continuous variable:

- the box spans the first to the third quartile, so its length is the IQR;
- a line inside the box marks the median;
- the whiskers extend from the box to the most extreme observations within $1.5 \times \text{IQR}$

of the box;
- observations beyond the whiskers are plotted individually, as potential outliers.

The 1.5 × IQR whisker rule is the default in R's `boxplot()` and `ggplot2::geom_boxplot()`; other software and authors use other rules, such as whiskers that run to the minimum and maximum.

```
wcgs |>
  ggplot2::ggplot() +
  ggplot2::aes(y = chol) +
  ggplot2::geom_boxplot(fill = "steelblue") +
  ggplot2::labs(y = "Cholesterol (mg/dL)") +
  ggplot2::theme(axis.text.x = ggplot2::element_blank())
```

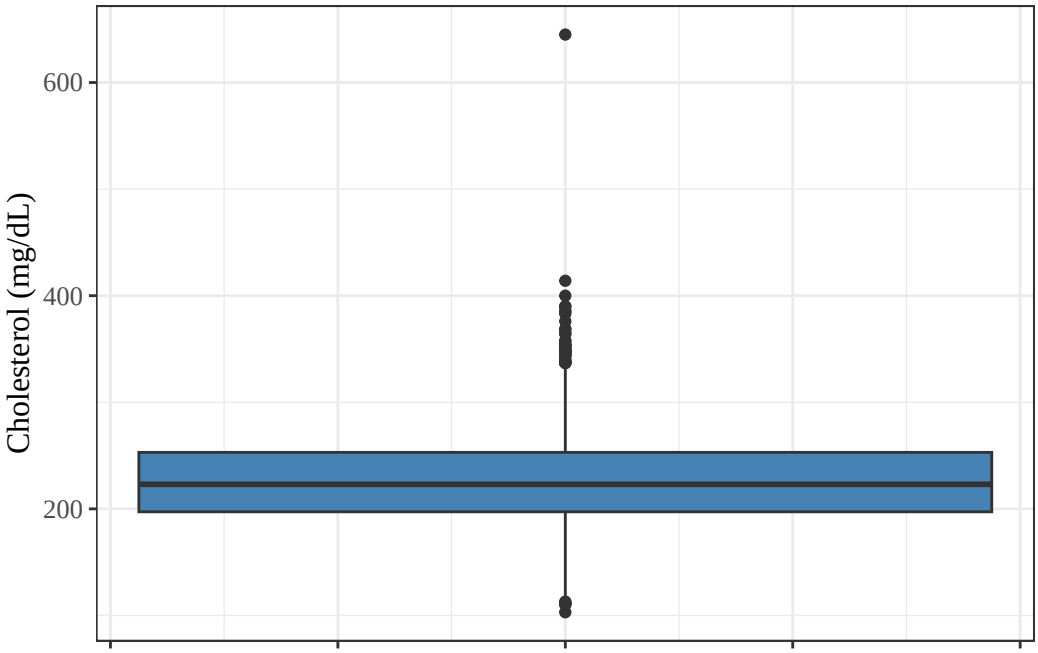


Figure 3: Box plot of total cholesterol in the WCGS dataset

Bar charts

Definition 0.11 (Bar chart)**.** A **bar chart** displays the number or proportion of observations in each category of a categorical variable, as one bar per category.

```r
wcgs |>
  ggplot2::ggplot() +
  ggplot2::aes(x = behpat) +
  ggplot2::geom_bar(fill = "steelblue") +
  ggplot2::labs(x = "Behavioral pattern", y = "Count")
```

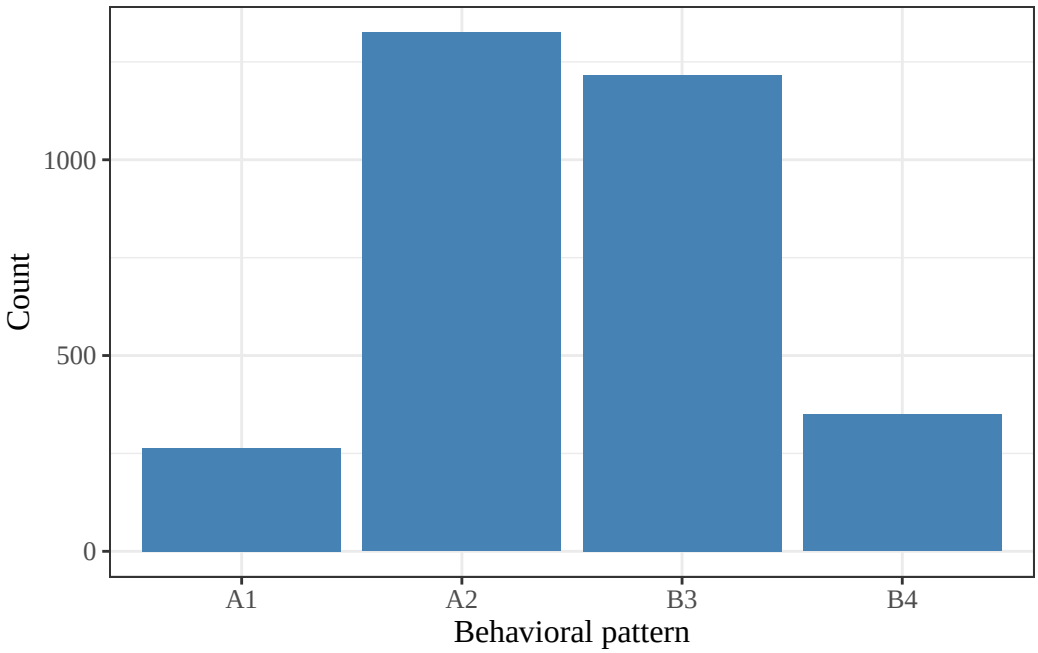


Figure 4: Bar chart of behavioral pattern in the WCGS dataset

Normal quantile-quantile plots

Definition 0.12 (Normal quantile-quantile plot)**.** A **normal quantile-quantile (Q-Q) plot** plots the sorted observations (order statistics) against the corresponding quantiles of a standard Gaussian distribution. If the variable is approximately Gaussian, the points fall close to a straight line.

```
wcgs |>
  ggplot2::ggplot() +
  ggplot2::aes(sample = chol) +
  ggplot2::stat_qq() +
  ggplot2::stat_qq_line(color = "red") +
  ggplot2::labs(x = "Standard Gaussian quantiles", y = "Cholesterol (mg/dL)")
```

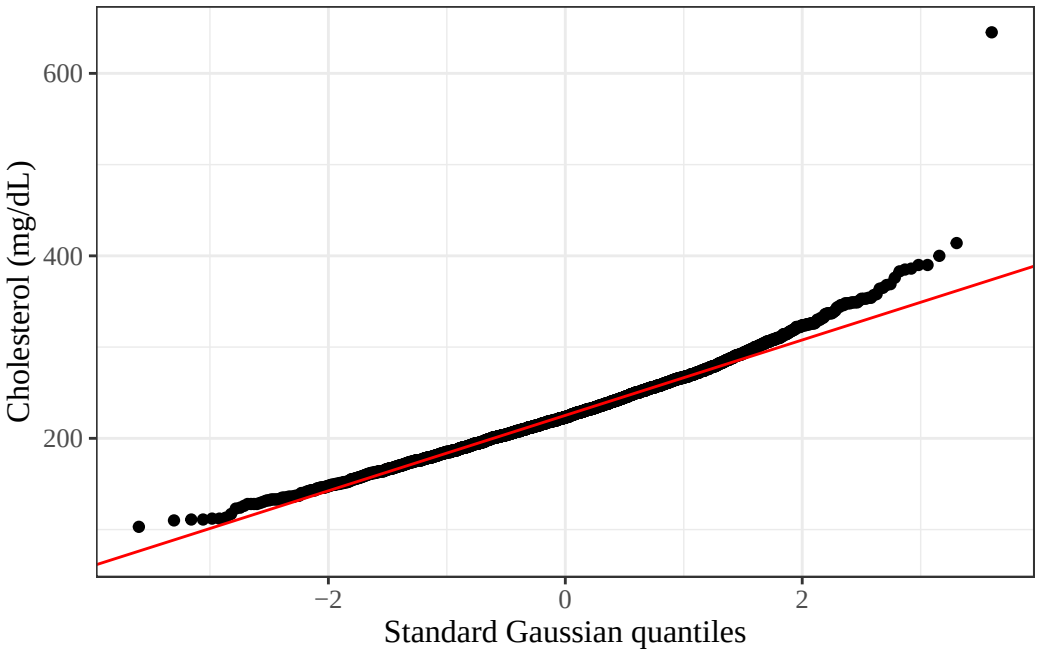


Figure 5: Normal Q-Q plot for total cholesterol in the WCGS dataset

In Figure 5, the points curve above the reference line at the right, which matches the long right tail in Figure 1.

Bivariate relationships

Two continuous variables

Definition 0.13 (Scatter plot)**.** A **scatter plot** displays the joint distribution of two continuous variables by plotting each observation as a point, with one variable on each axis.

```
wcgs |>
  ggplot2::ggplot() +
  ggplot2::aes(x = sbp, y = chol) +
  ggplot2::geom_point(alpha = 0.3) +
  ggplot2::geom_smooth(method = "lm", se = TRUE, color = "red") +
  ggplot2::labs(x = "Systolic BP (mmHg)", y = "Cholesterol (mg/dL)")
```

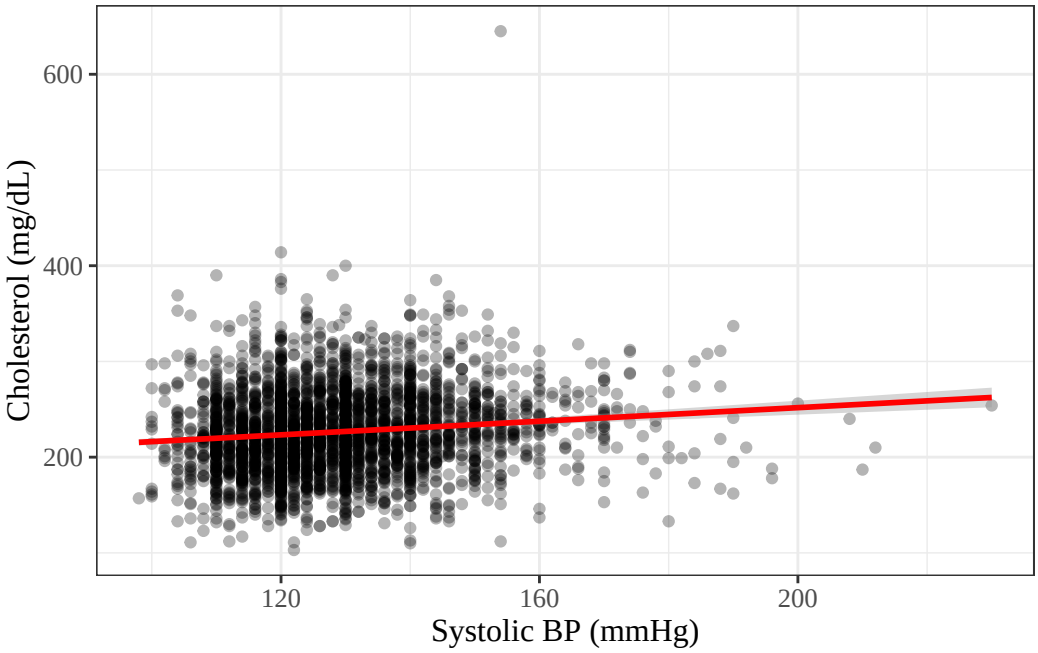


Figure 6: Cholesterol versus systolic blood pressure in the WCGS dataset, with a least-squares line

Definition 0.14 (Pearson correlation coefficient)**.** The **Pearson correlation coefficient** of n paired observations $(x_1, y_1), \ldots, (x_n, y_n)$ is:

$$r \overset{\text{def}}{=} \frac{\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^{n}(x_i - \bar{x})^2}\sqrt{\sum_{i=1}^{n}(y_i - \bar{y})^2}}$$

It is defined when neither variable is constant, so that both sums of squares are positive.

Theorem 0.1 (Range of the correlation coefficient)**.** *The Pearson correlation coefficient satisfies $-1 \le r \le 1$. Moreover, $r = 1$ if and only if the points (x_i, y_i) lie on a straight line with positive slope, and $r = -1$ if and only if they lie on a straight line with negative slope.*

Proof

Proof. Write $a_i \overset{\text{def}}{=} x_i - \bar{x}$ and $b_i \overset{\text{def}}{=} y_i - \bar{y}$, so that $r = \sum_i a_i b_i / \left(\sqrt{\sum_i a_i^2}\sqrt{\sum_i b_i^2}\right)$. The Cauchy–Schwarz inequality states that $\left|\sum_i a_i b_i\right| \le \sqrt{\sum_i a_i^2}\sqrt{\sum_i b_i^2}$, with equality if and only if one of the vectors $(a_1, \dots, a_n)$ and $(b_1, \dots, b_n)$ is a scalar multiple of the other. Dividing both sides by the (positive) right-hand side gives $|r| \le 1$.
Equality $|r| = 1$ therefore holds if and only if $b_i = c\, a_i$ for some constant $c \neq 0$ and every i, that is, $y_i = \bar{y} + c(x_i - \bar{x})$: the points lie on a line with slope c. Then $\sum_i a_i b_i = c \sum_i a_i^2$ has the sign of c, so $r = 1$ when $c > 0$ and $r = -1$ when $c < 0$. □

Example 0.6 (Correlation between cholesterol and blood pressure in the WCGS)**.**

```
cor(wcgs$chol, wcgs$sbp, use = "complete.obs")
#> [1] 0.123061
```

The correlation is positive but small: cholesterol tends to be slightly higher in participants with higher systolic blood pressure, consistent with the shallow slope and wide scatter in Figure 6.

Correlation measures linear association only

Two variables can be strongly related and still have a correlation near zero, if the relationship is not linear. For example, if $y_i = x_i^2$, the x_i are symmetric around 0, and the $|x_i|$ are not all equal, then $r = 0$, although y is a function of x. Correlation also does not imply causation.

A continuous variable by a categorical variable

Side-by-side box plots compare the distribution of a continuous variable across the groups defined by a categorical variable (Figure 7 and Figure 8).

```
wcgs |>
  ggplot2::ggplot() +
  ggplot2::aes(x = smoke, y = chol, fill = smoke) +
  ggplot2::geom_boxplot() +
  ggplot2::labs(x = "Current smoker", y = "Cholesterol (mg/dL)") +
  ggplot2::theme(legend.position = "none")
```

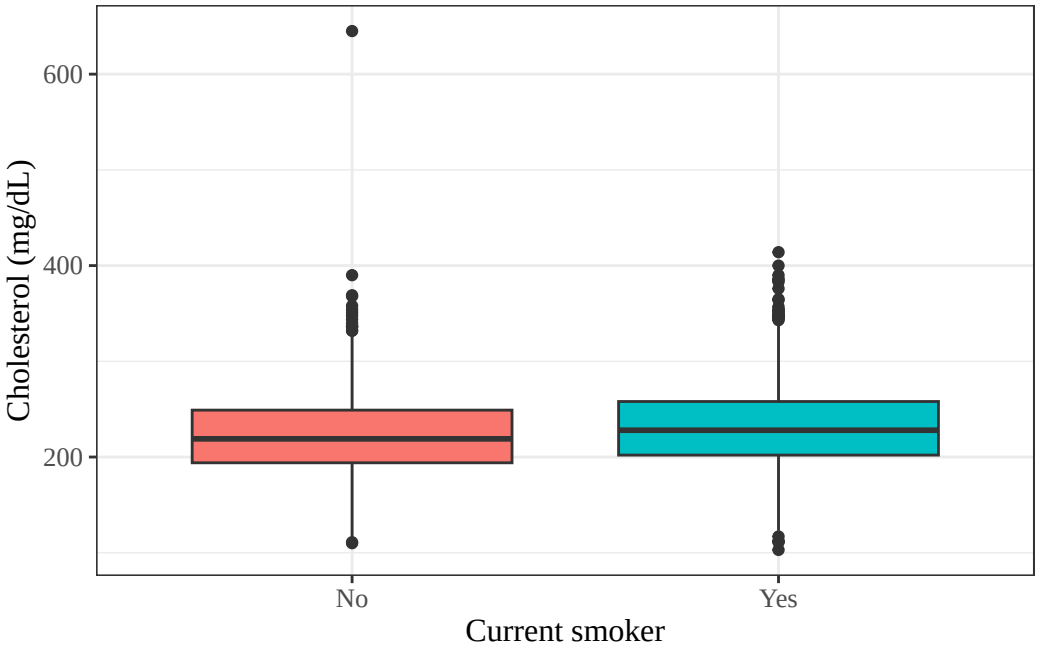


Figure 7: Box plots of cholesterol by smoking status in the WCGS dataset

Table 3 computes summary statistics separately for each group.

Two categorical variables

Definition 0.15 (Contingency table)**.** A **contingency table** (or **cross-tabulation**) displays the joint frequencies of two categorical variables: each cell counts the observations with one combination of categories. For two binary variables, the contingency table is a

```
wcgs |>
  ggplot2::ggplot() +
  ggplot2::aes(x = behpat, y = chol, fill = behpat) +
  ggplot2::geom_boxplot() +
  ggplot2::labs(x = "Behavioral pattern", y = "Cholesterol (mg/dL)") +
  ggplot2::theme(legend.position = "none")
```

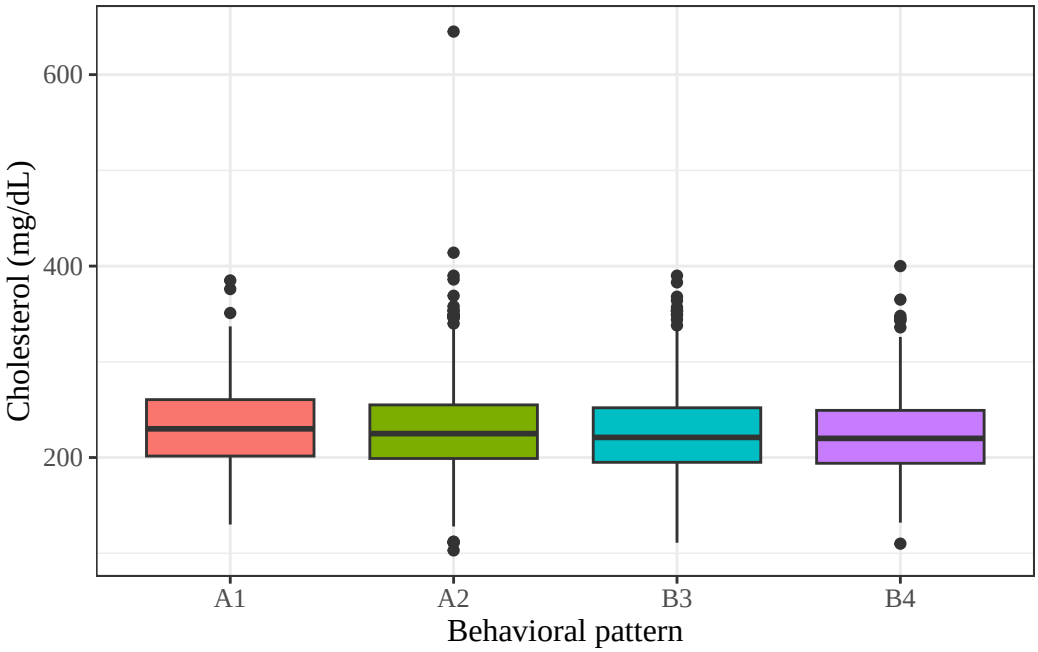


Figure 8: Box plots of cholesterol by behavioral pattern in the WCGS dataset

Table 3: Cholesterol, systolic blood pressure, and BMI by CHD status in the WCGS

```
wcgs |>
  dplyr::select(chol, sbp, bmi, chd69) |>
  gtsummary::tbl_summary(
    by = chd69,
    statistic = list(
      gtsummary::all_continuous() ~
        "{mean} ({sd})"
    ),
    digits = gtsummary::all_continuous() ~ 1
  ) |>
  gtsummary::add_overall()
```

Characteristic	**Overall** N = 3,154[1]	**No** N = 2,897[1]	**Yes** N = 257[1]
Cholesterol (mg/dL)	226.4 (43.4)	224.3 (42.2)	250.1 (49.4)
Unknown	12	12	0
Systolic BP (mmHg)	128.6 (15.1)	128.0 (14.7)	135.4 (17.5)
BMI (kg/m^2)	24.5 (2.6)	24.5 (2.6)	25.1 (2.6)

[1]Mean (SD)

2×2 table with cells a, b, c, and d:

	Outcome $= 1$	Outcome $= 0$	Total
Exposure $= 1$	a	b	$a + b$
Exposure $= 0$	c	d	$c + d$
Total	$a + c$	$b + d$	n

Example 0.7 (Smoking and CHD in the WCGS)**.**

```
table(Smoking = wcgs$smoke, CHD = wcgs$chd69)
#>         CHD
#> Smoking   No  Yes
#>     No  1554   98
#>     Yes 1343  159
```

Row proportions give the distribution of CHD status within each smoking group:

```
table(Smoking = wcgs$smoke, CHD = wcgs$chd69) |>
  prop.table(margin = 1)
#>         CHD
#> Smoking       No      Yes
#>     No  0.940678 0.059322
#>     Yes 0.894141 0.105859
```

Table 4 shows the same counts as a formatted table.

Table 4: Smoking status and CHD event in the WCGS

```
wcgs |>
  dplyr::select(smoke, chd69) |>
  gtsummary::tbl_summary(by = chd69) |>
  gtsummary::add_overall()
```

Characteristic	**Overall** N = 3,154[1]	**No** N = 2,897[1]	**Yes** N = 257[1]
Current smoker	1,502 (48%)	1,343 (46%)	159 (62%)

[1] n (%)

Data transformations

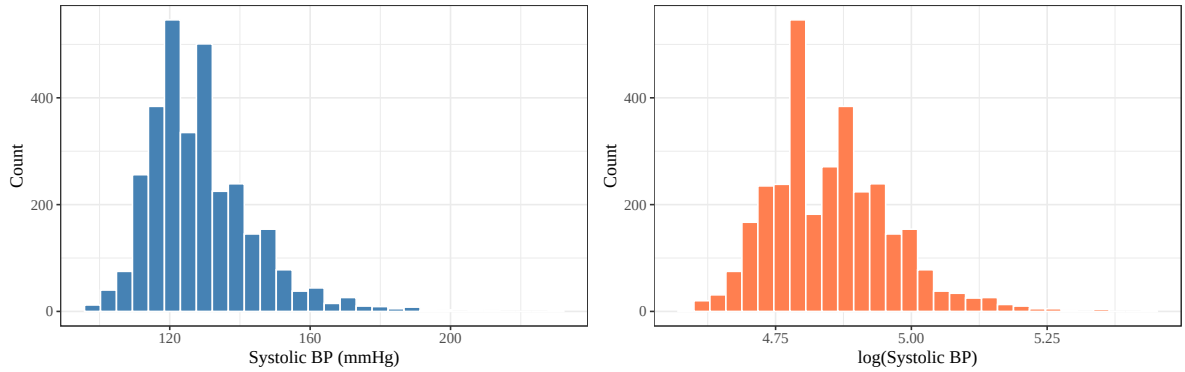
When a continuous variable has a right-skewed distribution (a longer tail to the right than to the left), a logarithmic transformation often makes the distribution more symmetric. A log-transformed variable also has a multiplicative interpretation: an increase of 1 in $\log(x)$ corresponds to multiplying x by $e \approx 2.72$, because $\log(x) + 1 = \log(e \cdot x)$.

The WCGS dataset already contains log-transformed versions of two variables:

- `lnsbp`: log(SBP);
- `lnwght`: log(weight).

```
wcgs |>
  ggplot2::ggplot() +
  ggplot2::aes(x = sbp) +
  ggplot2::geom_histogram(bins = 30, f:
  ggplot2::labs(x = "Systolic BP (mmHg)
```

```
wcgs |>
  ggplot2::ggplot() +
  ggplot2::aes(x = lnsbp) +
  ggplot2::geom_histogram(bins = 30, fill = "coral", c
  ggplot2::labs(x = "log(Systolic BP)", y = "Count")
```



(a) Raw scale

(b) Log scale

Figure 9: Distribution of systolic blood pressure in the WCGS, on two scales

```
# sample skewness: mean cubed deviation, divided by the cubed SD
skewness <- function(x) {
  x <- x[!is.na(x)]
  mean((x - mean(x))^3) / sd(x)^3
}
sbp_skew <- c(
  raw = skewness(wcgs$sbp),
  log = skewness(wcgs$lnsbp)
)
```

The log-transformed SBP is less skewed than the raw SBP (sample skewness 0.74 versus 1.2), but still not symmetric. Whether to transform a variable in a regression model depends on the assumptions of that model and on the scientific question.

An exploratory data analysis workflow

A typical exploratory data analysis proceeds as follows:

1. **Understand the dataset**: the number of observations and variables, and each variable's type.
2. **Examine each variable individually**:
    - continuous: histogram, box plot, mean, SD, median, IQR;
    - categorical: bar chart, frequency table;
    - note missing values, unusual values, and outliers.
3. **Examine relationships between variables**:
    - two continuous variables: scatter plot, correlation;
    - continuous by categorical: side-by-side box plots, group means;
    - two categorical variables: contingency table.
4. **Consider transformations** for skewed continuous variables.
5. **Summarize the findings** to guide model-building decisions.

Table 5 summarizes selected WCGS variables in one table.

References

Rosenman, Ray H, Richard J Brand, C David Jenkins, Meyer Friedman, Reuben Straus, and Moses Wurm. 1975. "Coronary Heart Disease in the Western Collaborative Group Study: Final Follow-up Experience of 8 1/2 Years." *JAMA* 233 (8): 872–77. https://doi.org/10.1001/jama.1975.03260080034016.

Vittinghoff, Eric, David V Glidden, Stephen C Shiboski, and Charles E McCulloch. 2012. *Regression Methods in Biostatistics: Linear, Logistic, Survival, and Repeated Measures Models*. 2nd ed. Springer. https://doi.org/10.1007/978-1-4614-1353-0.

Table 5: Summary of selected WCGS variables

```
wcgs |>
  dplyr::select(
    age, chol, sbp, dbp, bmi, weight, ncigs,
    chd69, smoke, dibpat, behpat
  ) |>
  gtsummary::tbl_summary()
```

Characteristic	**N = 3,154**[1]
Age (years)	45.0 (42.0, 50.0)
Cholesterol (mg/dL)	223 (197, 253)
Unknown	12
Systolic BP (mmHg)	126 (120, 136)
Diastolic BP (mmHg)	80 (76, 86)
BMI (kg/m^2)	24.39 (22.96, 25.84)
Weight (lbs)	170 (155, 182)
Cigarettes per day	0 (0, 20)
CHD event by 1969	257 (8.1%)
Current smoker	1,502 (48%)
Behavioral pattern (A/B)	
Type B	1,565 (50%)
Type A	1,589 (50%)
Behavioral pattern (A1/A2/B3/B4)	
A1	264 (8.4%)
A2	1,325 (42%)
B3	1,216 (39%)
B4	349 (11%)

[1]Median (Q1, Q3); n (%)