

Chapter4

4.7 Summarizing data

An important part of exploratory data analysis is summarizing data. The average and standard deviation are two examples of widely used summary statistics. More informative summaries can often be achieved by first splitting data into groups. In this section, we cover two new dplyr verbs that make these computations easier: `summarize` and `group_by`. We learn to access resulting values using the `pull` function.

4.7.1 summarize

The `summarize` function in dplyr provides a way to compute summary statistics with intuitive and readable code. We start with a simple example based on heights. The heights dataset includes heights and sex reported by students in an in-class survey.

```
library(dplyr)

##
##           : 'dplyr'

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

library(dslabs)
data(heights)
```

The following code computes the average and standard deviation for females:

```
s <- heights %>%
  filter(sex == "Female") %>%
  summarize(average = mean(height), standart_deviation =(sd(height)))
s

##   average standart_deviation
## 1 64.93942          3.760656
```

This takes our original data table as input, filters it to keep only females, and then produces a new summarized table with just the average and the standard deviation of heights. We get to choose the names of the columns of the resulting table. For example, above we decided to use `average` and `standart_deviation`, but we could have used other names just the same.

Because the resulting table stored in `s` is a data frame, we can access the components with the accessor `$`:

```
s$average
```

```
## [1] 64.93942
```

```
s$standart_deviation
```

```
## [1] 3.760656
```

As with most other dplyr functions, summarize is aware of the variable names and we can use them directly. So when inside the call to the summarize function we write `mean(height)`, the function is accessing the column with the name “height” and then computing the average of the resulting numeric vector. We can compute any other summary that operates on vectors and returns a single value.

For another example of how we can use the summarize function, let’s compute the average murder rate for the United States. Remember our data table includes total murders and population size for each state and we have already used dplyr to add a murder rate column:

```
murders <- murders %>% mutate(rate = total/population*100000)
```

Remember that the US murder rate is not the average of the state murder rates:

```
summarize(murders, mean(rate))
```

```
##    mean(rate)
## 1    2.779125
```

This is because in the computation above the small states are given the same weight as the large ones. The US murder rate is the total number of murders in the US divided by the total US population. So the correct computation is:

```
us_murder_rate <- murders %>%
  summarize(rate = sum(total)/sum(population)*100000)
us_murder_rate
```

```
##      rate
## 1 3.034555
```

This computation counts larger states proportionally to their size which results in a larger value.

4.7.2 Multiple summaries

Suppose we want three summaries from the same variable such as the median, minimum, and maximum heights. We can use summarize like this:

But we can obtain these three values with just one line using the quantile function: `quantile(x, c(0.5, 0, 1))` returns the median (50th percentile), the min (0th percentile), and max (100th percentile) of the vector x. We can use it with summarize like this:

```
heights %>%
  filter(sex == "Female") %>%
  summarize(median_min_max = quantile(height, c(0.5, 0, 1)))
```

```
##   median_min_max
## 1      64.98031
## 2      51.00000
## 3      79.00000
```

However, notice that the summaries are returned in a row each. To obtain the results in different columns, we have to define a function that returns a data frame like this:

```
median_min_max <- function(x){
  qs <- quantile(x, c(0.5, 0, 1))
  data.frame(median = qs[1], minimum = qs[2], maximum = qs[3])
}
heights %>%
  filter(sex == "Female") %>%
  summarize(median_min_max(height))
```

```
##      median minimum maximum
## 1 64.98031      51      79
```

4.7.3 Group then summarize with group_by

A common operation in data exploration is to first split data into groups and then compute summaries for each group. For example, we may want to compute the average and standard deviation for men's and women's heights separately. The `group_by` function helps us do this.

If we type this:

```
heights %>% group_by(sex)
```

```
## # A tibble: 1,050 x 2
## # Groups:   sex [2]
##   sex    height
##   <fct>   <dbl>
## 1 Male     75
## 2 Male     70
## 3 Male     68
## 4 Male     74
## 5 Male     61
## 6 Female   65
## 7 Female   66
## 8 Female   62
## 9 Female   66
## 10 Male    67
## # ... with 1,040 more rows
```

The result does not look very different from `heights`, except we see `Groups: sex [2]` when we print the object. Although not immediately obvious from its appearance, this is now a special data frame called a grouped

data frame, and dplyr functions, in particular summarize, will behave differently when acting on this object. Conceptually, you can think of this table as many tables, with the same columns but not necessarily the same number of rows, stacked together in one object. When we summarize the data after grouping, this is what happens:

```
heights %>%
  group_by(sex) %>%
  summarize(average = mean(height), standard_deviation = sd(height))
```

```
## # A tibble: 2 x 3
##   sex      average standard_deviation
##   <fct>    <dbl>          <dbl>
## 1 Female    64.9            3.76
## 2 Male     69.3            3.61
```

The summarize function applies the summarization to each group separately.

For another example, let's compute the median, minimum, and maximum murder rate in the four regions of the country using the median_min_max defined above:

```
murders %>%
  group_by(region) %>%
  summarize(median_min_max(rate))

## # A tibble: 4 x 4
##   region      median minimum maximum
##   <fct>    <dbl>    <dbl>   <dbl>
## 1 Northeast    1.80    0.320    3.60
## 2 South        3.40    1.46    16.5
## 3 North Central 1.97    0.595    5.36
## 4 West         1.29    0.515    3.63
```

4.8 pull

The us_murder_rate object defined above represents just one number. Yet we are storing it in a data frame:

```
class(us_murder_rate)
```

```
## [1] "data.frame"
```

since, as most dplyr functions, summarize always returns a data frame.

This might be problematic if we want to use this result with functions that require a numeric value. Here we show a useful trick for accessing values stored in data when using pipes: when a data object is piped that object and its columns can be accessed using the pull function. To understand what we mean take a look at this line of code:

```
us_murder_rate %>% pull(rate)
```

```
## [1] 3.034555
```

This returns the value in the rate column of `us_murder_rate` making it equivalent to `us_murder_rate$rate`.

To get a number from the original data table with one line of code we can type:

```
us_murder_rate <- murders %>%
  summarize(rate = sum(total) / sum(population) * 100000) %>%
  pull(rate)
```

which is now a numeric:

```
class(us_murder_rate)
```

```
## [1] "numeric"
```

4.9 Sorting data frames

When examining a dataset, it is often convenient to sort the table by the different columns. We know about the `order` and `sort` function, but for ordering entire tables, the dplyr function `arrange` is useful. For example, here we order the states by population size:

```
murders %>%
  arrange(population) %>%
  head()
```

##	state	abb	region	population	total	rate
## 1	Wyoming	WY	West	563626	5	0.8871131
## 2	District of Columbia	DC	South	601723	99	16.4527532
## 3	Vermont	VT	Northeast	625741	2	0.3196211
## 4	North Dakota	ND	North Central	672591	4	0.5947151
## 5	Alaska	AK	West	710231	19	2.6751860
## 6	South Dakota	SD	North Central	814180	8	0.9825837

With `arrange` we get to decide which column to sort by. To see the states by murder rate, from lowest to highest, we arrange by `rate` instead:

```
murders %>%
  arrange(rate) %>%
  head()
```

##	state	abb	region	population	total	rate
## 1	Vermont	VT	Northeast	625741	2	0.3196211
## 2	New Hampshire	NH	Northeast	1316470	5	0.3798036
## 3	Hawaii	HI	West	1360301	7	0.5145920
## 4	North Dakota	ND	North Central	672591	4	0.5947151
## 5	Iowa	IA	North Central	3046355	21	0.6893484
## 6	Idaho	ID	West	1567582	12	0.7655102

Note that the default behavior is to order in ascending order. In dplyr, the function `desc` transforms a vector so that it is in descending order. To sort the table in descending order, we can type:

```
murders %>% arrange(desc(rate))
```

##		state	abb	region	population	total	rate
## 1	District of Columbia	DC	South	601723	99	16.4527532	
## 2	Louisiana	LA	South	4533372	351	7.7425810	
## 3	Missouri	MO	North Central	5988927	321	5.3598917	
## 4	Maryland	MD	South	5773552	293	5.0748655	
## 5	South Carolina	SC	South	4625364	207	4.4753235	
## 6	Delaware	DE	South	897934	38	4.2319369	
## 7	Michigan	MI	North Central	9883640	413	4.1786225	
## 8	Mississippi	MS	South	2967297	120	4.0440846	
## 9	Georgia	GA	South	9920000	376	3.7903226	
## 10	Arizona	AZ	West	6392017	232	3.6295273	
## 11	Pennsylvania	PA	Northeast	12702379	457	3.5977513	
## 12	Tennessee	TN	South	6346105	219	3.4509357	
## 13	Florida	FL	South	19687653	669	3.3980688	
## 14	California	CA	West	37253956	1257	3.3741383	
## 15	New Mexico	NM	West	2059179	67	3.2537239	
## 16	Texas	TX	South	25145561	805	3.2013603	
## 17	Arkansas	AR	South	2915918	93	3.1893901	
## 18	Virginia	VA	South	8001024	250	3.1246001	
## 19	Nevada	NV	West	2700551	84	3.1104763	
## 20	North Carolina	NC	South	9535483	286	2.9993237	
## 21	Oklahoma	OK	South	3751351	111	2.9589340	
## 22	Illinois	IL	North Central	12830632	364	2.8369608	
## 23	Alabama	AL	South	4779736	135	2.8244238	
## 24	New Jersey	NJ	Northeast	8791894	246	2.7980319	
## 25	Connecticut	CT	Northeast	3574097	97	2.7139722	
## 26	Ohio	OH	North Central	11536504	310	2.6871225	
## 27	Alaska	AK	West	710231	19	2.6751860	
## 28	Kentucky	KY	South	4339367	116	2.6732010	
## 29	New York	NY	Northeast	19378102	517	2.6679599	
## 30	Kansas	KS	North Central	2853118	63	2.2081106	
## 31	Indiana	IN	North Central	6483802	142	2.1900730	
## 32	Massachusetts	MA	Northeast	6547629	118	1.8021791	
## 33	Nebraska	NE	North Central	1826341	32	1.7521372	
## 34	Wisconsin	WI	North Central	5686986	97	1.7056487	
## 35	Rhode Island	RI	Northeast	1052567	16	1.5200933	
## 36	West Virginia	WV	South	1852994	27	1.4571013	
## 37	Washington	WA	West	6724540	93	1.3829942	
## 38	Colorado	CO	West	5029196	65	1.2924531	
## 39	Montana	MT	West	989415	12	1.2128379	
## 40	Minnesota	MN	North Central	5303925	53	0.9992600	
## 41	South Dakota	SD	North Central	814180	8	0.9825837	
## 42	Oregon	OR	West	3831074	36	0.9396843	
## 43	Wyoming	WY	West	563626	5	0.8871131	
## 44	Maine	ME	Northeast	1328361	11	0.8280881	
## 45	Utah	UT	West	2763885	22	0.7959810	
## 46	Idaho	ID	West	1567582	12	0.7655102	
## 47	Iowa	IA	North Central	3046355	21	0.6893484	
## 48	North Dakota	ND	North Central	672591	4	0.5947151	
## 49	Hawaii	HI	West	1360301	7	0.5145920	
## 50	New Hampshire	NH	Northeast	1316470	5	0.3798036	

```
## 51          Vermont VT      Northeast      625741      2 0.3196211
```

4.9.1 Nested sorting

If we are ordering by a column with ties, we can use a second column to break the tie. Similarly, a third column can be used to break ties between first and second and so on. Here we order by region, then within region we order by murder rate:

```
murders %>%
  arrange(region, rate) %>%
  head()
```

```
##           state abb   region population total      rate
## 1      Vermont  VT Northeast      625741      2 0.3196211
## 2 New Hampshire NH Northeast     1316470      5 0.3798036
## 3         Maine  ME Northeast     1328361     11 0.8280881
## 4  Rhode Island RI Northeast     1052567     16 1.5200933
## 5 Massachusetts MA Northeast     6547629    118 1.8021791
## 6      New York  NY Northeast     19378102   517 2.6679599
```

4.9.2 The top n

In the code above, we have used the function `head` to avoid having the page fill up with the entire dataset. If we want to see a larger proportion, we can use the `top_n` function. This function takes a data frame as its first argument, the number of rows to show in the second, and the variable to filter by in the third. Here is an example of how to see the top 5 rows:

```
murders %>% top_n(5, rate)
```

```
##           state abb   region population total      rate
## 1 District of Columbia DC      South      601723      99 16.452753
## 2      Louisiana  LA      South     4533372     351  7.742581
## 3      Maryland  MD      South     5773552     293  5.074866
## 4      Missouri MO North Central     5988927     321  5.359892
## 5  South Carolina SC      South     4625364     207  4.475323
```

Note that rows are not sorted by rate, only filtered. If we want to sort, we need to use `arrange`. Note that if the third argument is left blank, `top_n` filters by the last column.

4.10 Exercises

For these exercises, we will be using the data from the survey collected by the United States National Center for Health Statistics (NCHS). This center has conducted a series of health and nutrition surveys since the 1960's. Starting in 1999, about 5,000 individuals of all ages have been interviewed every year and they complete the health examination component of the survey. Part of the data is made available via the NHANES package. Once you install the NHANES package, you can load the data like this:

```
library(NHANES)
data(NHANES)
```

The NHANES data has many missing values. The mean and sd functions in R will return NA if any of the entries of the input vector is an NA. Here is an example:

```
library(dslabs)
data(na_example)
mean(na_example)
```

```
## [1] NA
```

To ignore the NAs we can use the na.rm argument:

```
mean(na_example, na.rm = TRUE)
```

```
## [1] 2.301754
```

```
sd(na_example, na.rm = TRUE)
```

```
## [1] 1.22338
```

Let's now explore the NHANES data.

1. We will provide some basic facts about blood pressure. First let's select a group to set the standard. We will use 20-to-29-year-old females. AgeDecade is a categorical variable with these ages. Note that the category is coded like " 20-29", with a space in front! What is the average and standard deviation of systolic blood pressure as saved in the BPSysAve variable? Save it to a variable called ref.

Hint: Use filter and summarize and use the na.rm = TRUE argument when computing the average and standard deviation. You can also filter the NA values using filter.

```
#filter NA values with na.rm
```

```
ref <- NHANES %>%
  filter(Gender == "female", AgeDecade == " 20-29") %>%
  summarize(average = mean(BPSysAve, na.rm = TRUE), standard_deviation = sd(BPSysAve, na.rm = TRUE))
ref
```

```
## # A tibble: 1 x 2
##   average standard_deviation
##   <dbl>         <dbl>
## 1    108.         10.1
```

or

```
#filter NA values using filter
```

```
ref2 <- NHANES %>%
  filter(Gender == "female", AgeDecade == " 20-29") %>% filter(!is.na(BPSysAve)) %>%
  summarize(average = mean(BPSysAve), standard_deviation = sd(BPSysAve))
ref2
```



```
## # A tibble: 1 x 2
##   average standard_deviation
##   <dbl>         <dbl>
## 1    108.           10.1
```

- Using a pipe, assign the average to a numeric variable `ref_avg`. Hint: Use the code similar to above and then pull.

```
ref_avg <- ref %>% pull(average)

ref_avg
```

```
## [1] 108.4224
```

```
class(ref_avg)
```

```
## [1] "numeric"
```

- Now report the min and max values for the same group.

```
NHANES %>%
  filter(Gender == "female", AgeDecade == " 20-29") %>% summarize(minimum = min(BPSysAve, na.rm = TRUE)
```

```
## # A tibble: 1 x 2
##   minimum maximum
##   <int>    <int>
## 1     84     179
```

- Compute the average and standard deviation for females, but for each age group separately rather than a selected decade as in question 1. Note that the age groups are defined by `AgeDecade`. Hint: rather than filtering by age and gender, filter by `Gender` and then use `group_by`.

```
NHANES %>%
  filter(Gender == "female") %>%
  group_by(AgeDecade) %>%
  summarize(average = mean(BPSysAve, na.rm = TRUE), standard_deviation = sd(BPSysAve, na.rm = TRUE))
```

```
## # A tibble: 9 x 3
##   AgeDecade average standard_deviation
##   <fct>         <dbl>         <dbl>
## 1 " 0-9"         100.           9.07
## 2 " 10-19"       104.           9.46
## 3 " 20-29"       108.          10.1
## 4 " 30-39"       111.          12.3
## 5 " 40-49"       115.          14.5
## 6 " 50-59"       122.          16.2
## 7 " 60-69"       127.          17.1
## 8 " 70+"         134.          19.8
## 9 <NA>          142.          22.9
```

- Repeat exercise 4 for males.

```
NHANES %>%
  filter(Gender == "male") %>%
  group_by(AgeDecade) %>%
  summarize(average = mean(BPSysAve, na.rm = TRUE), standard_deviation = sd(BPSysAve, na.rm = TRUE))
```

```
## # A tibble: 9 x 3
##   AgeDecade average standard_deviation
##   <fct>      <dbl>          <dbl>
## 1 " 0-9"      97.4            8.32
## 2 " 10-19"   110.            11.2
## 3 " 20-29"   118.            11.3
## 4 " 30-39"   119.            12.3
## 5 " 40-49"   121.            14.0
## 6 " 50-59"   126.            17.8
## 7 " 60-69"   127.            17.5
## 8 " 70+"     130.            18.7
## 9 <NA>      136.            23.5
```

6. We can actually combine both summaries for exercises 4 and 5 into one line of code. This is because `group_by` permits us to group by more than one variable. Obtain one big summary table using `group_by(AgeDecade, Gender)`.

```
NHANES %>%
  group_by(AgeDecade, Gender) %>%
  summarize(average = mean(BPSysAve, na.rm = TRUE), standard_deviation = sd(BPSysAve, na.rm = TRUE))
```

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

```
## # A tibble: 18 x 4
## # Groups:   AgeDecade [9]
##   AgeDecade Gender average standard_deviation
##   <fct>      <fct>      <dbl>          <dbl>
## 1 " 0-9"     female    100.            9.07
## 2 " 0-9"     male      97.4            8.32
## 3 " 10-19"   female    104.            9.46
## 4 " 10-19"   male     110.            11.2
## 5 " 20-29"   female    108.            10.1
## 6 " 20-29"   male     118.            11.3
## 7 " 30-39"   female    111.            12.3
## 8 " 30-39"   male     119.            12.3
## 9 " 40-49"   female    115.            14.5
## 10 " 40-49"   male     121.            14.0
## 11 " 50-59"   female    122.            16.2
## 12 " 50-59"   male     126.            17.8
## 13 " 60-69"   female    127.            17.1
## 14 " 60-69"   male     127.            17.5
## 15 " 70+"     female    134.            19.8
## 16 " 70+"     male     130.            18.7
## 17 <NA>      female    142.            22.9
## 18 <NA>      male     136.            23.5
```

7. For males between the ages of 40-49, compare systolic blood pressure across race as reported in the `Race1` variable. Order the resulting table from lowest to highest average systolic blood pressure.

```
NHANES %>%
  filter(Gender == "male", AgeDecade == " 40-49") %>% group_by(Race1) %>%
  summarize(BPSysAve_mean = mean(BPSysAve, na.rm = TRUE)) %>%
  arrange(BPSysAve_mean)
```

```
## # A tibble: 5 x 2
##   Race1      BPSysAve_mean
##   <fct>         <dbl>
## 1 White          120.
## 2 Other          120.
## 3 Hispanic       122.
## 4 Mexican        122.
## 5 Black          126.
```

4.11 Tibbles

Tidy data must be stored in data frames. We introduced the data frame in Section 2.4.1 and have been using the murders data frame throughout the book. In Section 4.7.3 we introduced the `group_by` function, which permits stratifying data before computing summary statistics. But where is the group information stored in the data frame?

```
murders %>% group_by(region)
```

```
## # A tibble: 51 x 6
## # Groups:   region [4]
##   state      abb region population total rate
##   <chr>      <chr> <fct>         <dbl> <dbl> <dbl>
## 1 Alabama    AL    South      4779736   135  2.82
## 2 Alaska     AK    West       710231    19  2.68
## 3 Arizona    AZ    West      6392017   232  3.63
## 4 Arkansas   AR    South      2915918    93  3.19
## 5 California CA    West     37253956  1257  3.37
## 6 Colorado   CO    West      5029196    65  1.29
## 7 Connecticut CT    Northeast  3574097    97  2.71
## 8 Delaware   DE    South       897934    38  4.23
## 9 District of Columbia DC    South       601723    99 16.5
## 10 Florida    FL    South     19687653   669  3.40
## # ... with 41 more rows
```

Notice that there are no columns with this information. But, if you look closely at the output above, you see the line A tibble followed by dimensions. We can learn the class of the returned object using:

```
murders %>% group_by(region) %>% class()
```

```
## [1] "grouped_df" "tbl_df"      "tbl"         "data.frame"
```

The `tbl`, pronounced tibble, is a special kind of data frame. The functions `group_by` and `summarize` always return this type of data frame. The `group_by` function returns a special kind of `tbl`, the `grouped_df`. We will say more about these later. For consistency, the dplyr manipulation verbs (`select`, `filter`, `mutate`, and `arrange`) preserve the class of the input: if they receive a regular data frame they return a regular data frame,

while if they receive a tibble they return a tibble. But tibbles are the preferred format in the tidyverse and as a result tidyverse functions that produce a data frame from scratch return a tibble. For example, in Chapter 5 we will see that tidyverse functions used to import data create tibbles.

Tibbles are very similar to data frames. In fact, you can think of them as a modern version of data frames. Nonetheless there are three important differences which we describe next.

4.11.1 Tibbles display better

The print method for tibbles is more readable than that of a data frame. To see this, compare the outputs of typing `murders` and the output of `murders` if we convert it to a tibble. We can do this using `as_tibble(murders)`. If using RStudio, output for a tibble adjusts to your window size. To see this, change the width of your R console and notice how more/less columns are shown.

`murders`

```
##           state abb      region population total      rate
## 1      Alabama  AL      South   4779736    135  2.8244238
## 2      Alaska  AK       West    710231     19  2.6751860
## 3      Arizona AZ       West   6392017    232  3.6295273
## 4      Arkansas AR      South   2915918     93  3.1893901
## 5      California CA     West  37253956   1257  3.3741383
## 6      Colorado CO      West   5029196     65  1.2924531
## 7      Connecticut CT    Northeast  3574097     97  2.7139722
## 8      Delaware DE      South    897934     38  4.2319369
## 9 District of Columbia DC     South    601723     99 16.4527532
## 10     Florida  FL      South  19687653   669  3.3980688
## 11     Georgia  GA      South   9920000   376  3.7903226
## 12     Hawaii  HI       West   1360301     7  0.5145920
## 13     Idaho   ID       West   1567582    12  0.7655102
## 14     Illinois IL North Central 12830632   364  2.8369608
## 15     Indiana IN North Central  6483802   142  2.1900730
## 16     Iowa    IA North Central  3046355    21  0.6893484
## 17     Kansas  KS North Central  2853118     63  2.2081106
## 18     Kentucky KY      South   4339367   116  2.6732010
## 19     Louisiana LA     South   4533372   351  7.7425810
## 20     Maine   ME      Northeast 1328361     11  0.8280881
## 21     Maryland MD     South   5773552   293  5.0748655
## 22     Massachusetts MA    Northeast  6547629   118  1.8021791
## 23     Michigan MI North Central  9883640   413  4.1786225
## 24     Minnesota MN North Central  5303925    53  0.9992600
## 25     Mississippi MS      South   2967297   120  4.0440846
## 26     Missouri MO North Central  5988927   321  5.3598917
## 27     Montana MT       West    989415     12  1.2128379
## 28     Nebraska NE North Central  1826341     32  1.7521372
## 29     Nevada  NV       West   2700551     84  3.1104763
## 30     New Hampshire NH    Northeast  1316470      5  0.3798036
## 31     New Jersey NJ      Northeast  8791894   246  2.7980319
## 32     New Mexico NM       West   2059179     67  3.2537239
## 33     New York NY      Northeast 19378102   517  2.6679599
## 34     North Carolina NC      South   9535483   286  2.9993237
## 35     North Dakota ND North Central   672591      4  0.5947151
## 36     Ohio    OH North Central 11536504   310  2.6871225
## 37     Oklahoma OK      South   3751351   111  2.9589340
```

```
## 38      Oregon OR      West 3831074 36 0.9396843
## 39    Pennsylvania PA    Northeast 12702379 457 3.5977513
## 40      Rhode Island RI    Northeast 1052567 16 1.5200933
## 41    South Carolina SC      South 4625364 207 4.4753235
## 42    South Dakota SD North Central 814180 8 0.9825837
## 43      Tennessee TN      South 6346105 219 3.4509357
## 44      Texas TX      South 25145561 805 3.2013603
## 45      Utah UT      West 2763885 22 0.7959810
## 46      Vermont VT    Northeast 625741 2 0.3196211
## 47      Virginia VA      South 8001024 250 3.1246001
## 48      Washington WA      West 6724540 93 1.3829942
## 49    West Virginia WV      South 1852994 27 1.4571013
## 50      Wisconsin WI North Central 5686986 97 1.7056487
## 51      Wyoming WY      West 563626 5 0.8871131
```

```
tblmurders <- as_tibble(murders)
tblmurders
```

```
## # A tibble: 51 x 6
##   state      abb region population total rate
##   <chr>    <chr> <fct>      <dbl> <dbl> <dbl>
## 1 Alabama AL    South 4779736 135 2.82
## 2 Alaska AK    West 710231 19 2.68
## 3 Arizona AZ    West 6392017 232 3.63
## 4 Arkansas AR    South 2915918 93 3.19
## 5 California CA    West 37253956 1257 3.37
## 6 Colorado CO    West 5029196 65 1.29
## 7 Connecticut CT    Northeast 3574097 97 2.71
## 8 Delaware DE    South 897934 38 4.23
## 9 District of Columbia DC    South 601723 99 16.5
## 10 Florida FL    South 19687653 669 3.40
## # ... with 41 more rows
```

4.11.2 Subsets of tibbles are tibbles

If you subset the columns of a data frame, you may get back an object that is not a data frame, such as a vector or scalar. For example:

```
class(murders[,4])
```

```
## [1] "numeric"
```

is not a data frame. With tibbles this does not happen:

```
class(as_tibble(murders)[,4])
```

```
## [1] "tbl_df"      "tbl"        "data.frame"
```

This is useful in the tidyverse since functions require data frames as input.

With tibbles, if you want to access the vector that defines a column, and not get back a data frame, you need to use the accessor `$`:

```
class(as_tibble(murders)$population)
```

```
## [1] "numeric"
```

A related feature is that tibbles will give you a warning if you try to access a column that does not exist. If we accidentally write `Population` instead of `population` this:

```
murders$Population
```

```
## NULL
```

returns a `NULL` with no warning, which can make it harder to debug. In contrast, if we try this with a tibble we get an informative warning:

```
as_tibble(murders)$Population
```

```
## Warning: Unknown or uninitialised column: `Population`.
```

```
## NULL
```

4.11.3 Tibbles can have complex entries

While data frame columns need to be vectors of numbers, strings, or logical values, tibbles can have more complex objects, such as lists or functions. Also, we can create tibbles with functions:

```
tibble(id = c(1, 2, 3), func = c(mean, median, sd))
```

```
## # A tibble: 3 x 2
##       id func
##   <dbl> <list>
## 1     1 <fn>
## 2     2 <fn>
## 3     3 <fn>
```

4.11.4 Tibbles can be grouped

The function `group_by` returns a special kind of tibble: a grouped tibble. This class stores information that lets you know which rows are in which groups. The tidyverse functions, in particular the `summarize` function, are aware of the group information.

4.11.5 Create a tibble using `tibble` instead of `data.frame`

It is sometimes useful for us to create our own data frames. To create a data frame in the tibble format, you can do this by using the `tibble` function.

```
grades <- tibble(names = c("John", "Juan", "Jean", "Yao"),
                  exam_1 = c(95, 80, 90, 85),
                  exam_2 = c(90, 85, 85, 90))
grades
```

```
## # A tibble: 4 x 3
##   names exam_1 exam_2
##   <chr>   <dbl> <dbl>
## 1 John     95     90
## 2 Juan     80     85
## 3 Jean     90     85
## 4 Yao      85     90
```

Note that base R (without packages loaded) has a function with a very similar name, `data.frame`, that can be used to create a regular data frame rather than a tibble.

```
grades <- data.frame(names = c("John", "Juan", "Jean", "Yao"),
                     exam_1 = c(95, 80, 90, 85),
                     exam_2 = c(90, 85, 85, 90))
grades
```

```
##   names exam_1 exam_2
## 1  John     95     90
## 2  Juan     80     85
## 3  Jean     90     85
## 4   Yao     85     90
```

To convert a regular data frame to a tibble, you can use the `as_tibble` function.

```
as_tibble(grades) %>% class()
```

```
## [1] "tbl_df"      "tbl"        "data.frame"
```

4.12 The dot operator

One of the advantages of using the pipe `%>%` is that we do not have to keep naming new objects as we manipulate the data frame. As a quick reminder, if we want to compute the median murder rate for states in the southern states, instead of typing:

```
tab_1 <- filter(murders, region == "South")
tab_2 <- mutate(tab_1, rate = total / population * 10^5)
rates <- tab_2$rate
median(rates)
```

```
## [1] 3.398069
```

We can avoid defining any new intermediate objects by instead typing:

```
filter(murders, region == "South") %>%
  mutate(rate = total / population * 10^5) %>%
  summarize(median = median(rate)) %>%
  pull(median)
```

```
## [1] 3.398069
```

We can do this because each of these functions takes a data frame as the first argument. But what if we want to access a component of the data frame. For example, what if the pull function was not available and we wanted to access `tab_2$rate`? What data frame name would we use? The answer is the dot operator.

For example to access the rate vector without the pull function we could use

```
rates <- filter(murders, region == "South") %>%
  mutate(rate = total / population * 10^5) %>%
  .$rate
median(rates)
```

```
## [1] 3.398069
```

4.13 The purrr package

In Section 3.5 we learned about the `sapply` function, which permitted us to apply the same function to each element of a vector. We constructed a function and used `sapply` to compute the sum of the first `n` integers for several values of `n` like this:

```
compute_s_n <- function(n){
  x <- 1:n
  sum(x)
}
n <- 1:25
s_n <- sapply(n, compute_s_n)
s_n
```

```
## [1] 1 3 6 10 15 21 28 36 45 55 66 78 91 105 120 136 153 171 190
## [20] 210 231 253 276 300 325
```

This type of operation, applying the same function or procedure to elements of an object, is quite common in data analysis. The `purrr` package includes functions similar to `sapply` but that better interact with other tidyverse functions. The main advantage is that we can better control the output type of functions. In contrast, `sapply` can return several different object types; for example, we might expect a numeric result from a line of code, but `sapply` might convert our result to character under some circumstances. `purrr` functions will never do this: they will return objects of a specified type or return an error if this is not possible.

The first `purrr` function we will learn is `map`, which works very similar to `sapply` but always, without exception, returns a list:

```
library(purrr)
s_n <- map(n, compute_s_n)
class(s_n)
```

```
## [1] "list"
```

If we want a numeric vector, we can instead use `map_dbl` which always returns a vector of numeric values.

```
s_n <- map_dbl(n, compute_s_n)
class(s_n)
```



```
## [1] "numeric"
```

This produces the same results as the `sapply` call shown above.

A particularly useful `purrr` function for interacting with the rest of the tidyverse is `map_df`, which always returns a tibble data frame. However, the function being called needs to return a vector or a list with names. For this reason, the following code would result in a `Argument 1 must have names` error:

```
#s_n <- map_df(n, compute_s_n)
```

Error: Argument 1 must have names.

We need to change the function to make this work:

```
compute_s_n <- function(n){  
  x <- 1:n  
  tibble(sum = sum(x))  
}  
s_n <- map_df(n, compute_s_n)  
s_n
```

```
## # A tibble: 25 x 1  
##       sum  
##   <int>  
## 1     1  
## 2     3  
## 3     6  
## 4    10  
## 5    15  
## 6    21  
## 7    28  
## 8    36  
## 9    45  
## 10   55  
## # ... with 15 more rows
```

The `purrr` package provides much more functionality not covered here. For more details you can consult this [online resource](#).

4.14 Tidyverse conditionals

A typical data analysis will often involve one or more conditional operations. In Section 3.1 we described the `ifelse` function, which we will use extensively in this book. In this section we present two `dplyr` functions that provide further functionality for performing conditional operations.

4.14.1 `case_when`

The `case_when` function is useful for vectorizing conditional statements. It is similar to `ifelse` but can output any number of values, as opposed to just `TRUE` or `FALSE`. Here is an example splitting numbers into negative, positive, and 0:

```
x <- c(-2, -1, 0, 1, 2)
case_when(x<0 ~ "Negative",
          x>0 ~ "Positive",
          TRUE ~ "Zero")
```

```
## [1] "Negative" "Negative" "Zero"      "Positive" "Positive"
```

A common use for this function is to define categorical variables based on existing variables. For example, suppose we want to compare the murder rates in four groups of states: New England, West Coast, South, and other. For each state, we need to ask if it is in New England, if it is not we ask if it is in the West Coast, if not we ask if it is in the South, and if not we assign other. Here is how we use `case_when` to do this:

```
murders %>%
  mutate(group = case_when(
    abb %in% c("ME", "NH", "VT", "MA", "RI", "CT") ~ "New England",
    abb %in% c("WA", "OR", "CA") ~ "West Coast",
    region == "South" ~ "South",
    TRUE ~ "Other")) %>%
  group_by(group) %>%
  summarize(rate = sum(total) / sum(population) * 105)
```

```
## # A tibble: 4 x 2
##   group      rate
##   <chr>    <dbl>
## 1 New England 1.72
## 2 Other      2.71
## 3 South      3.63
## 4 West Coast 2.90
```

4.14.2 between

A common operation in data analysis is to determine if a value falls inside an interval. We can check this using conditionals. For example, to check if the elements of a vector `x` are between `a` and `b` we can type

```
#x >= a % x<= b
```

However, this can become cumbersome, especially within the tidyverse approach. The `between` function performs the same operation.

```
#between(x, a, b)
```

4.15 Exercises

1. Load the `murders` dataset. Which of the following is true?

```
head(murders)
```

```
##      state abb region population total    rate
## 1  Alabama AL  South   4779736   135 2.824424
```

```
## 2     Alaska AK    West    710231    19 2.675186
## 3     Arizona AZ    West    6392017   232 3.629527
## 4     Arkansas AR   South    2915918    93 3.189390
## 5 California CA    West    37253956  1257 3.374138
## 6     Colorado CO    West    5029196    65 1.292453
```

- murders is in tidy format and is stored in a tibble.
- murders is in tidy format and is stored in a data frame.
- murders is not in tidy format and is stored in a tibble.
- murders is not in tidy format and is stored in a data frame.

-> answer: b

- Use `as_tibble` to convert the murders data table into a tibble and save it in an object called `murders_tibble`.

```
murders_tibble <- as_tibble(murders)
```

- Use the `group_by` function to convert murders into a tibble that is grouped by region.

```
murders_tibble %>%
  group_by(region)
```

```
## # A tibble: 51 x 6
## # Groups:   region [4]
##   state      abb region population total rate
##   <chr>      <chr> <fct>      <dbl> <dbl> <dbl>
## 1 Alabama    AL    South    4779736   135 2.82
## 2 Alaska     AK    West     710231    19 2.68
## 3 Arizona    AZ    West    6392017   232 3.63
## 4 Arkansas   AR    South    2915918    93 3.19
## 5 California CA    West    37253956  1257 3.37
## 6 Colorado   CO    West    5029196    65 1.29
## 7 Connecticut CT    Northeast 3574097    97 2.71
## 8 Delaware   DE    South     897934    38 4.23
## 9 District of Columbia DC    South     601723    99 16.5
## 10 Florida   FL    South    19687653  669 3.40
## # ... with 41 more rows
```

- Write tidyverse code that is equivalent to this code:

```
exp(mean(log(murders$population)))
```

```
## [1] 3675209
```

Write it using the pipe so that each function is called without arguments. Use the dot operator to access the population. Hint: The code should start with `murders %>%`.

```

murders$population %>%
  log() %>%
  mean() %>%
  exp()

```

```
## [1] 3675209
```

5. Use the `map_df` to create a data frame with three columns named `n`, `s_n`, and `s_n_2`. The first column should contain the numbers 1 through 100. The second and third columns should each contain the sum of 1 through n with n the row number.

```

n <- 1:100
compute_s_n <- function(n){
  x <- 1:n
  tibble(n = n,
         s_n = sum(x),
         s_n2 = sum(x))
}
Sn <- map_df(n, compute_s_n)
Sn

```

```

## # A tibble: 100 x 3
##       n    s_n s_n2
##   <int> <int> <int>
## 1     1     1     1
## 2     2     3     3
## 3     3     6     6
## 4     4    10    10
## 5     5    15    15
## 6     6    21    21
## 7     7    28    28
## 8     8    36    36
## 9     9    45    45
## 10    10    55    55
## # ... with 90 more rows

```