Homework 2 - Report

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2020/7/8

The data set calif_penn_2011.csv contains information about the housing stock of California and Pennsylvania, as of 2011. Information as aggregated into "Census tracts", geographic regions of a few thousand people which are supposed to be fairly homogeneous economically and socially.

1. *Loading and cleaning*

a. Load the data into a dataframe called `ca_pa`.

```
ca_pa <- read.csv("../data/calif_penn_2011.csv", header = TRUE, sep = ",")
```

b. How many rows and columns does the dataframe have?

```
rows <- dim(ca_pa)[1]
columns <- dim(ca_pa)[2]
```

c. Run this command, and explain, in words, what this does:

Ans: this command can figure out the number of missing values in every column.

```
colSums(apply(ca_pa,c(1,2),is.na))
```

```
##                            X                      GEO.id2
##                            0                            0
##                      STATEFP                     COUNTYFP
##                            0                            0
##                      TRACTCE                   POPULATION
##                            0                            0
##                     LATITUDE                    LONGITUDE
##                            0                            0
##            GEO.display.label           Median_house_value
##                            0                          599
##                  Total_units                 Vacant_units
##                            0                            0
##                 Median_rooms  Mean_household_size_owners
##                          157                          215
## Mean_household_size_renters          Built_2005_or_later
##                          152                           98
##            Built_2000_to_2004                  Built_1990s
##                           98                           98
##                  Built_1980s                  Built_1970s
##                           98                           98
##                  Built_1960s                  Built_1950s
##                           98                           98
##                  Built_1940s          Built_1939_or_earlier
##                           98                           98
##                   Bedrooms_0                   Bedrooms_1
```

```
##                        98                       98
##                Bedrooms_2               Bedrooms_3
##                        98                       98
##                Bedrooms_4       Bedrooms_5_or_more
##                        98                       98
##                    Owners                  Renters
##                       100                      100
##   Median_household_income    Mean_household_income
##                       115                      126
```

d. The function `na.omit()` takes a dataframe and returns a new dataframe, omitting any row containing an NA value. Use it to purge the data set of rows with incomplete data.

```
ca_pa <- na.omit(ca_pa)
```

e. How many rows did this eliminate?

```
rows - dim(ca_pa)[1]
```

```
## [1] 670
```

f. Are your answers in (c) and (e) compatible? Explain.

Ans: They are compatible. The command in (c) check the number of missing values in every column, and the command in (e) check the number of rows with incomplete data. We can infer that after purging, the number of missing values in every column will be zero. And we can use the command below to check out the truth.

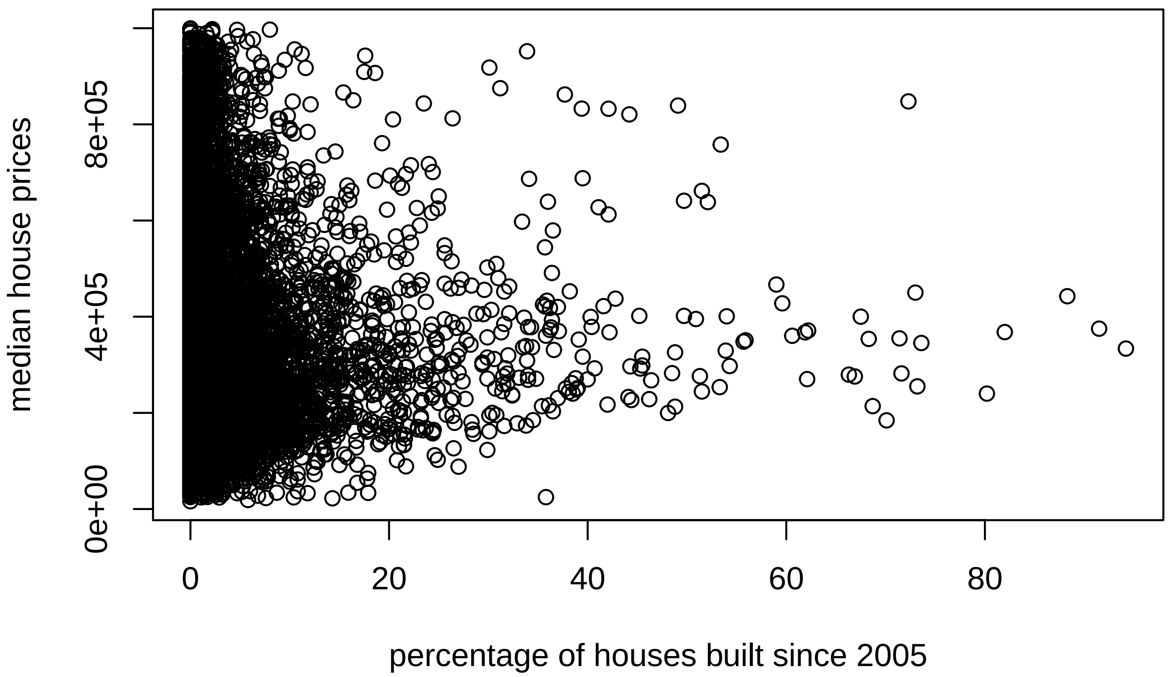
```
sum(colSums(apply(ca_pa,c(1,2),is.na)))
```

```
## [1] 0
```

2. *This Very New House*

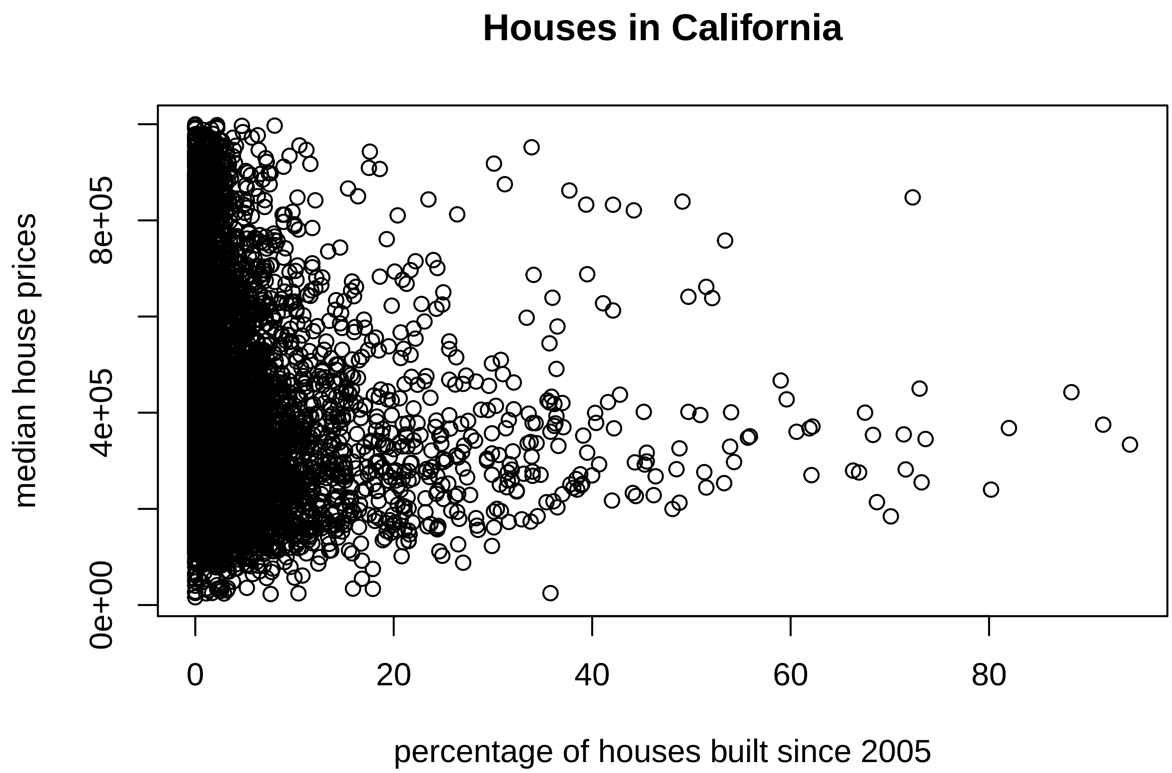
a. The variable `Built_2005_or_later` indicates the percentage of houses in each Census tract built since 2005. Plot median house prices against this variable.

```
plot(ca_pa$Median_house_value ~ ca_pa$Built_2005_or_later,
     xlab = "percentage of houses built since 2005",
     ylab = "median house prices")
```

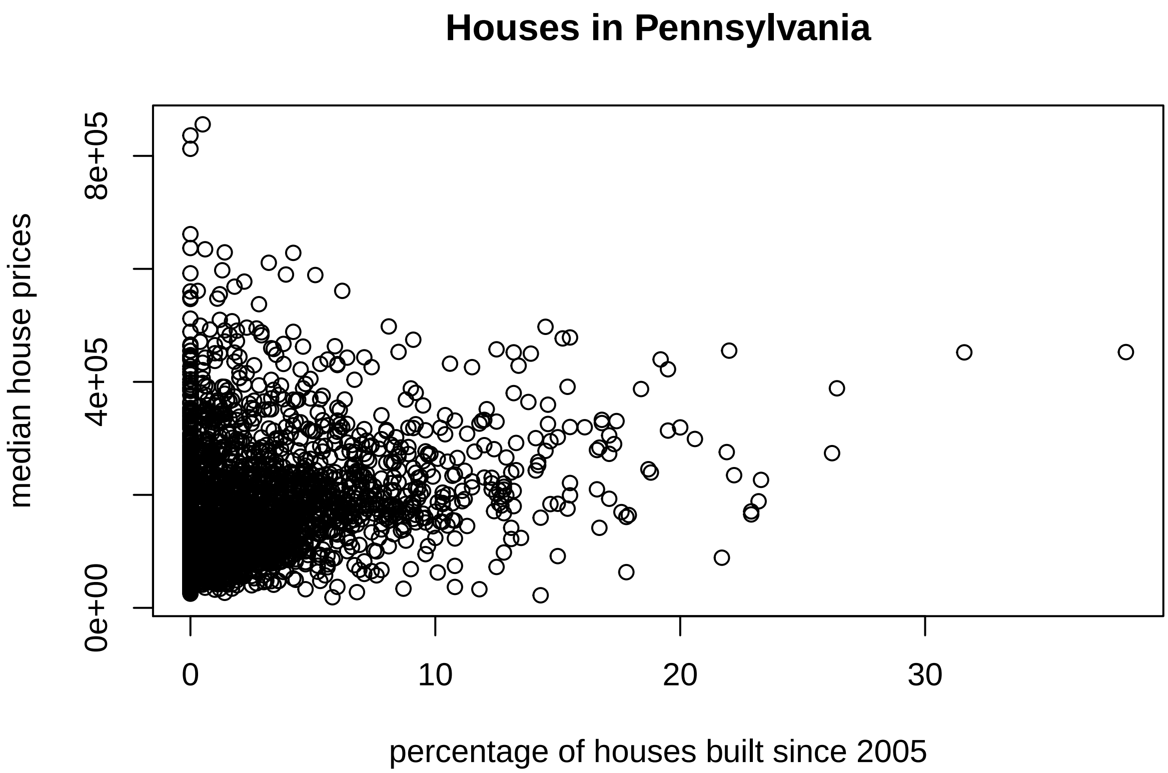


b. Make a new plot, or pair of plots, which breaks this out by state. Note that the state is recorded in the `STATEFP` variable, with California being state 6 and Pennsylvania state 42.

```
plot(ca_pa$Built_2005_or_later[ca_pa$STATEFP == 6],
     ca_pa$Median_house_value[ca_pa$STATEFP == 6],
     xlab = "percentage of houses built since 2005",
     ylab = "median house prices",
     main = "Houses in California")
```




```r
plot(ca_pa$Built_2005_or_later[ca_pa$STATEFP == 42],
     ca_pa$Median_house_value[ca_pa$STATEFP == 42],
     xlab = "percentage of houses built since 2005",
     ylab = "median house prices",
     main = "Houses in Pennsylvania")
```



3. *Nobody Home*

The vacancy rate is the fraction of housing units which are not occupied. The dataframe contains columns giving the total number of housing units for each Census tract, and the number of vacant housing units.

a. Add a new column to the dataframe which contains the vacancy rate. What are the minimum, maximum, mean, and median vacancy rates?

```
Vacancy_rate <- ca_pa$Vacant_units / ca_pa$Total_units
ca_pa <- data.frame(ca_pa, Vacancy_rate)
max(Vacancy_rate)
```

```
## [1] 0.965311
```

```
min(Vacancy_rate)
```

```
## [1] 0
```

```
mean(Vacancy_rate)
```

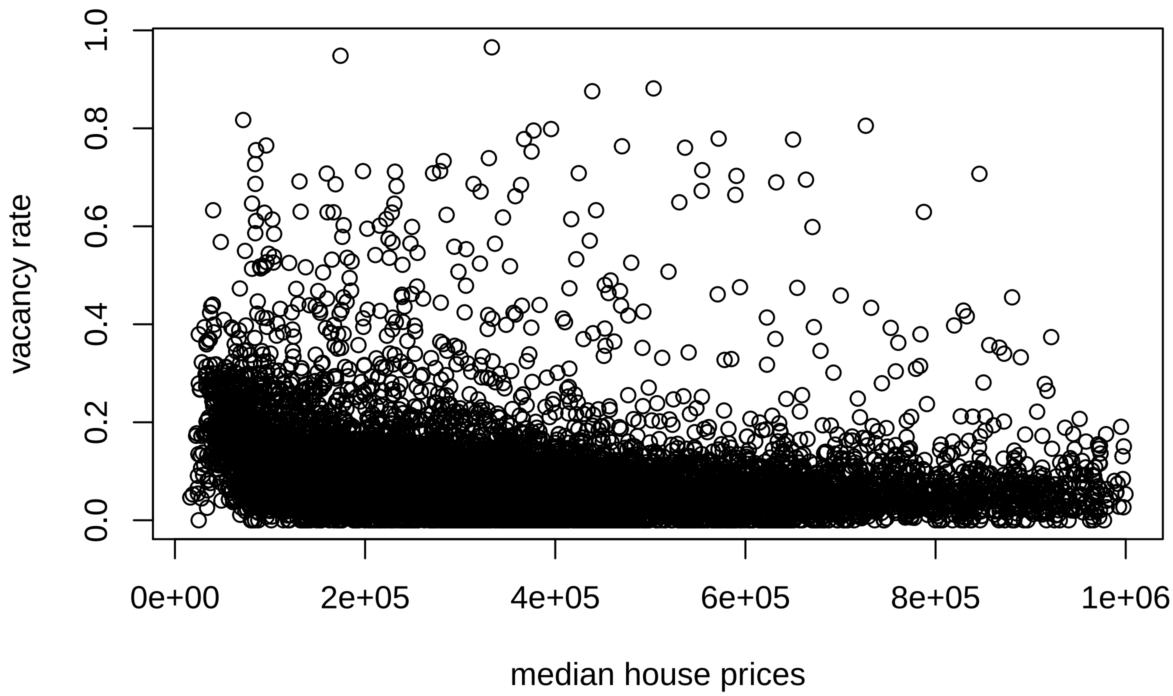
```
## [1] 0.08888789
```

```
median(Vacancy_rate)
```

```
## [1] 0.06767283
```

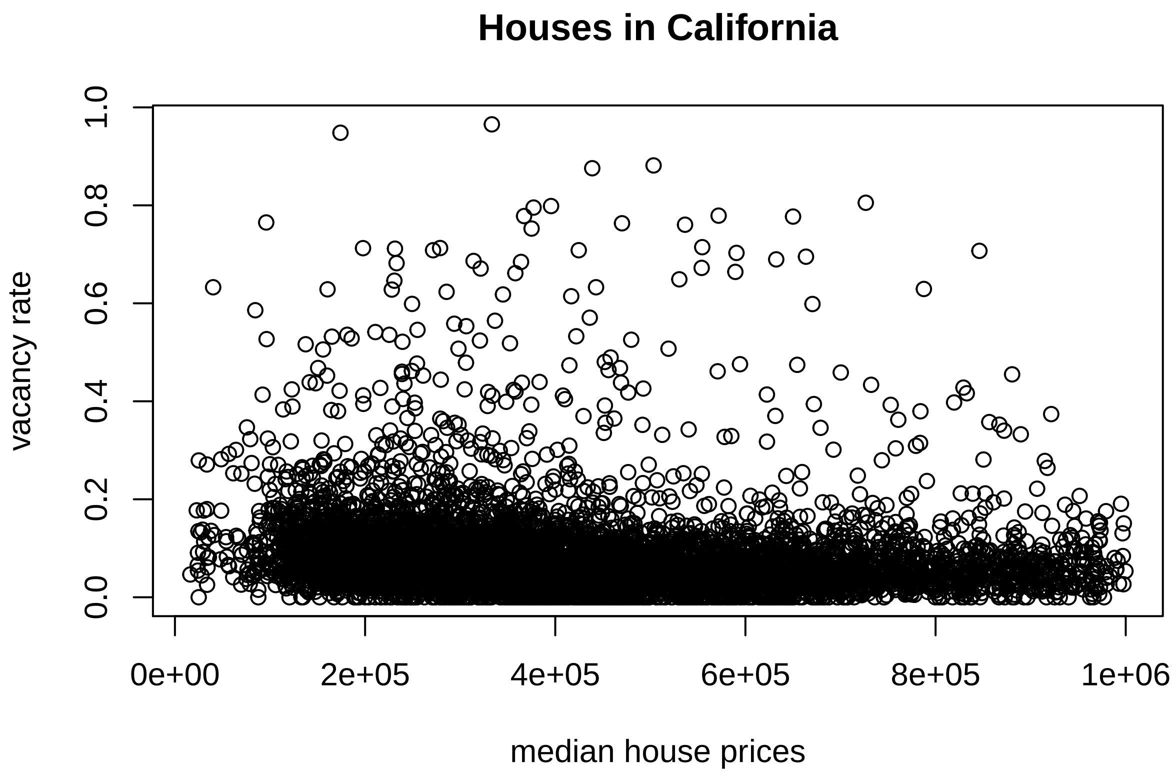
b. Plot the vacancy rate against median house value.

```
plot(ca_pa$Median_house_value, ca_pa$Vacancy_rate,
     xlab = "median house prices", ylab = "vacancy rate")
```

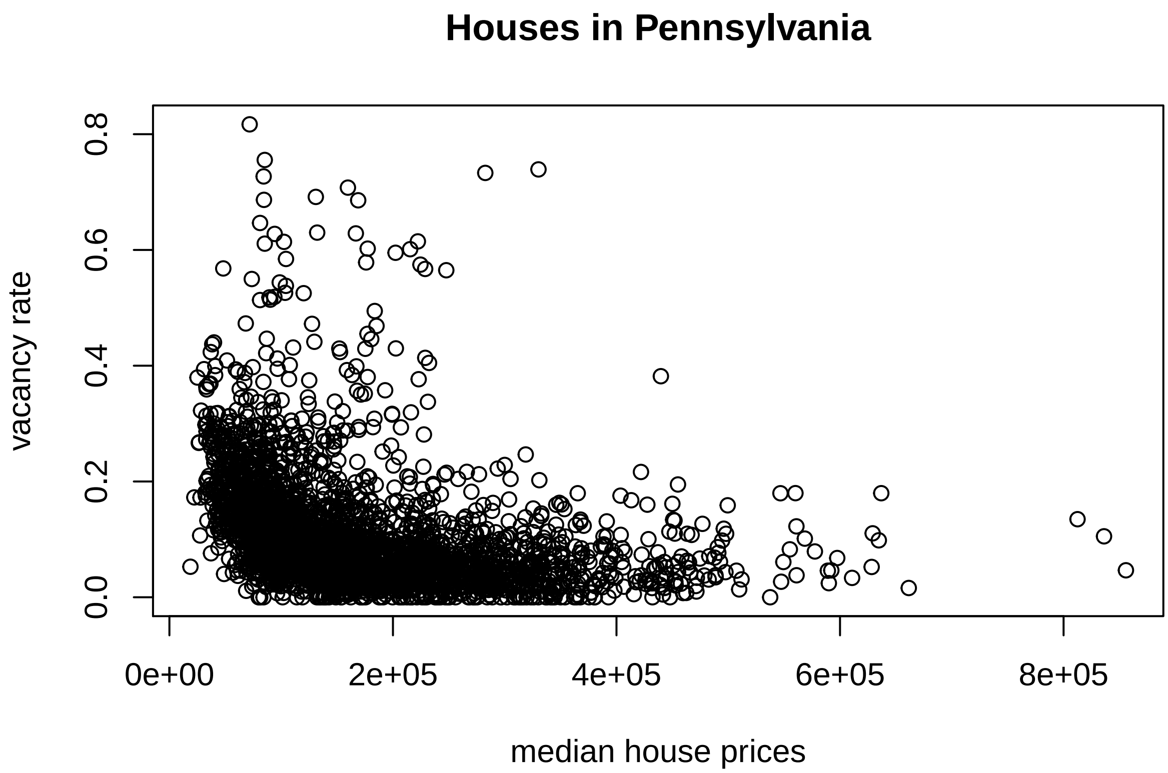


c. Plot vacancy rate against median house value separately for California and for Pennsylvania. Is there a difference?

```
plot(ca_pa$Median_house_value[ca_pa$STATEFP == 6],
     ca_pa$Vacancy_rate[ca_pa$STATEFP == 6],
     xlab = "median house prices", ylab = "vacancy rate",
     main = "Houses in California")
```




```r
plot(ca_pa$Median_house_value[ca_pa$STATEFP == 42],
     ca_pa$Vacancy_rate[ca_pa$STATEFP == 42],
     xlab = "median house prices", ylab = "vacancy rate",
     main = "Houses in Pennsylvania")
```



The houses in California have higher median house value, and houses with different median house value all have some samples whose vacancy rate is high. The houses in Pennsylvania have lower median house value, and only houses with low median house value have samples whose vacancy rate is high.

4. The column `COUNTYFP` contains a numerical code for counties within each state. We are interested in Alameda County (county 1 in California), Santa Clara (county 85 in California), and Allegheny County (county 3 in Pennsylvania).

a. Explain what the block of code at the end of this question is supposed to accomplish, and how it does it.

Ans: This block of code is supposed to pick up the tracts in Alameda County and compute the median of the median house values of those tracts. The code firstly traverse all the tracts in `ca_pa`, and if a tract matches condition, it will be stored in a new vector `acca`. Then the code traverse again to store the median house values of the tracts in `acca` into `accamhv`. Finally the code call `median` function to compute the median of `accamhv`.

b. Give a single line of R which gives the same final answer as the block of code. Note: there are at least two ways to do this; you just have to find one.

```
median(ca_pa$Median_house_value[ca_pa$STATEFP == 6 & ca_pa$COUNTYFP == 1])
```

```
## [1] 474050
```

c. For Alameda, Santa Clara and Allegheny Counties, what were the average percentages of housing built since 2005?

```
# Alameda
mean(ca_pa$Built_2005_or_later[ca_pa$STATEFP == 6 & ca_pa$COUNTYFP == 1])
```

```
## [1] 2.820468
```

```r
# Santa Clara
mean(ca_pa$Built_2005_or_later[ca_pa$STATEFP == 6 & ca_pa$COUNTYFP == 85])
```

```
## [1] 3.200319
```

```r
# Allegheny
mean(ca_pa$Built_2005_or_later[ca_pa$STATEFP == 42 & ca_pa$COUNTYFP == 3])
```

```
## [1] 1.474219
```

d. The `cor` function calculates the correlation coefficient between two variables. What is the correlation between median house value and the percent of housing built since 2005 in (i) the whole data, (ii) all of California, (iii) all of Pennsylvania, (iv) Alameda County, (v) Santa Clara County and (vi) Allegheny County?

```r
# (i) the whole data
cor(ca_pa$Median_house_value, ca_pa$Built_2005_or_later)
```

```
## [1] -0.01893186
```

```r
# (ii) all of California
cor(ca_pa$Median_house_value[ca_pa$STATEFP == 6],
    ca_pa$Built_2005_or_later[ca_pa$STATEFP == 6])
```

```
## [1] -0.1153604
```

```r
# (iii) all of Pennsylvania
cor(ca_pa$Median_house_value[ca_pa$STATEFP == 42],
    ca_pa$Built_2005_or_later[ca_pa$STATEFP == 42])
```

```
## [1] 0.2681654
```

```r
# (iv) Alameda
cor(ca_pa$Median_house_value[ca_pa$STATEFP == 6 & ca_pa$COUNTYFP == 1],
    ca_pa$Built_2005_or_later[ca_pa$STATEFP == 6 & ca_pa$COUNTYFP == 1])
```

```
## [1] 0.01303543
```

```r
# (v) Santa Clara
cor(ca_pa$Median_house_value[ca_pa$STATEFP == 6 & ca_pa$COUNTYFP == 85],
    ca_pa$Built_2005_or_later[ca_pa$STATEFP == 6 & ca_pa$COUNTYFP == 85])
```

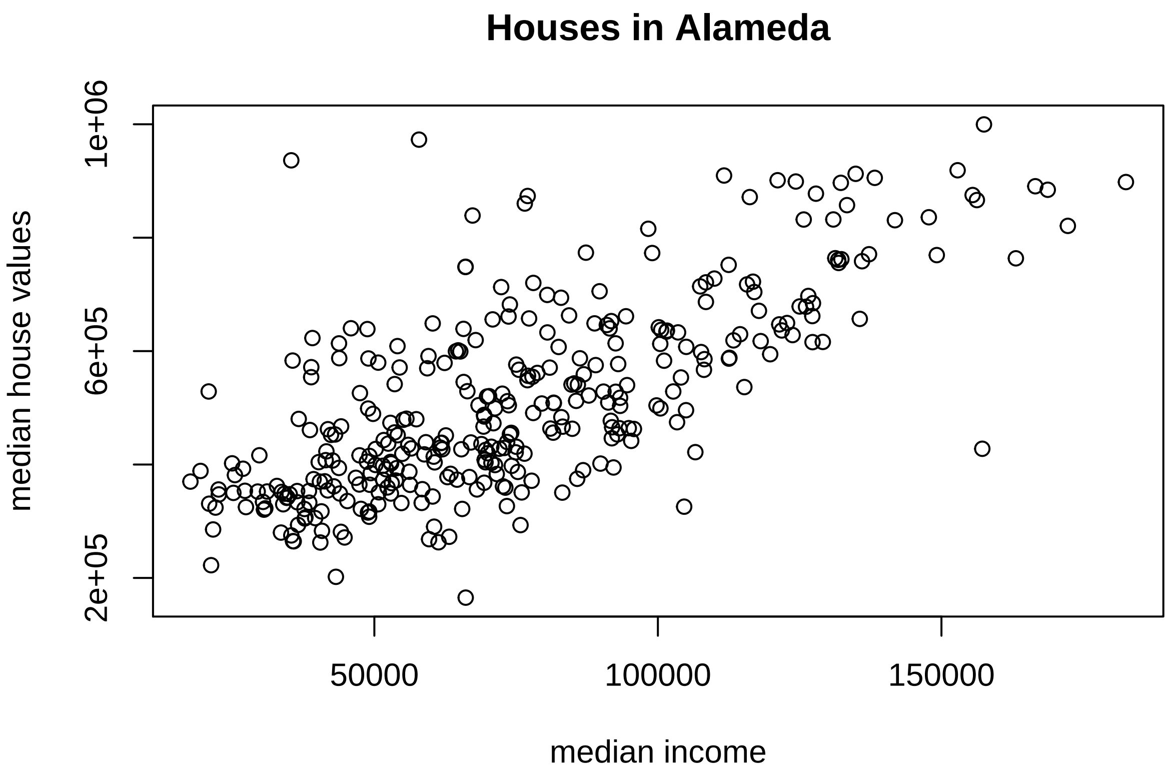
```
## [1] -0.1726203
```

```r
# (vi) Allegheny
cor(ca_pa$Median_house_value[ca_pa$STATEFP == 42 & ca_pa$COUNTYFP == 3],
    ca_pa$Built_2005_or_later[ca_pa$STATEFP == 42 & ca_pa$COUNTYFP == 3])
```

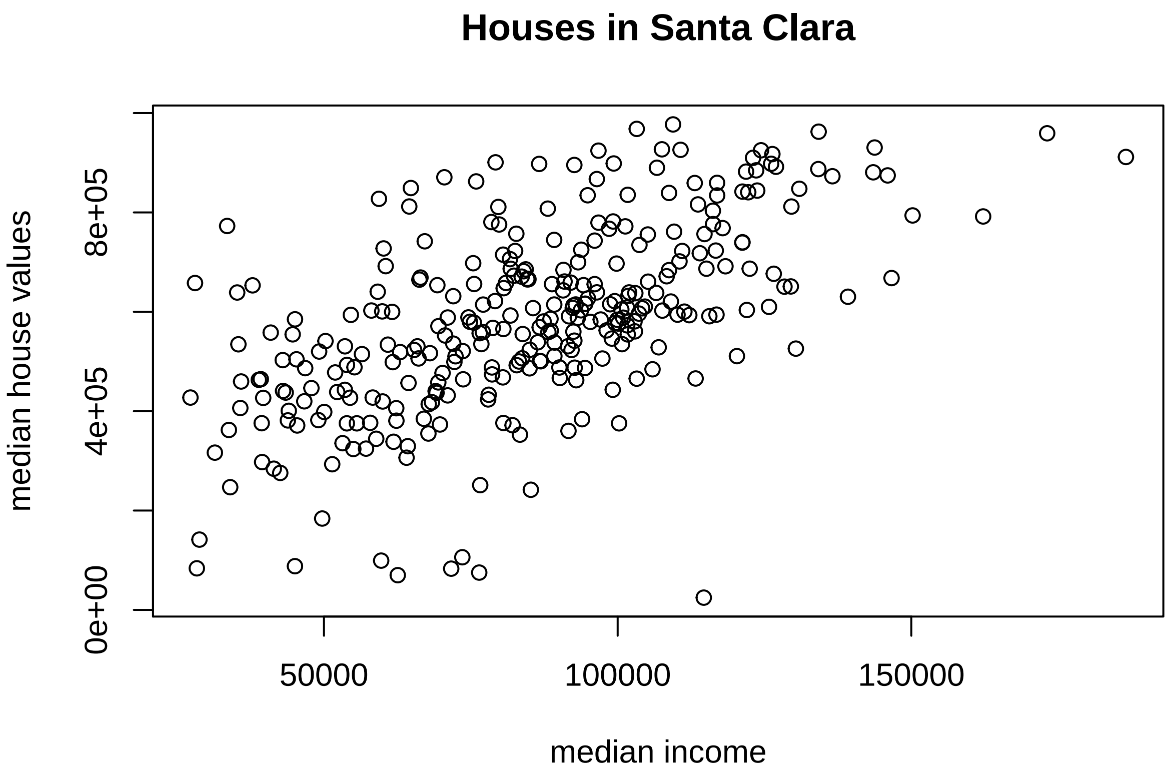
```
## [1] 0.1939652
```

e. Make three plots, showing median house values against median income, for Alameda, Santa Clara, and Allegheny Counties. (If you can fit the information into one plot, clearly distinguishing the three counties, that's OK too.)

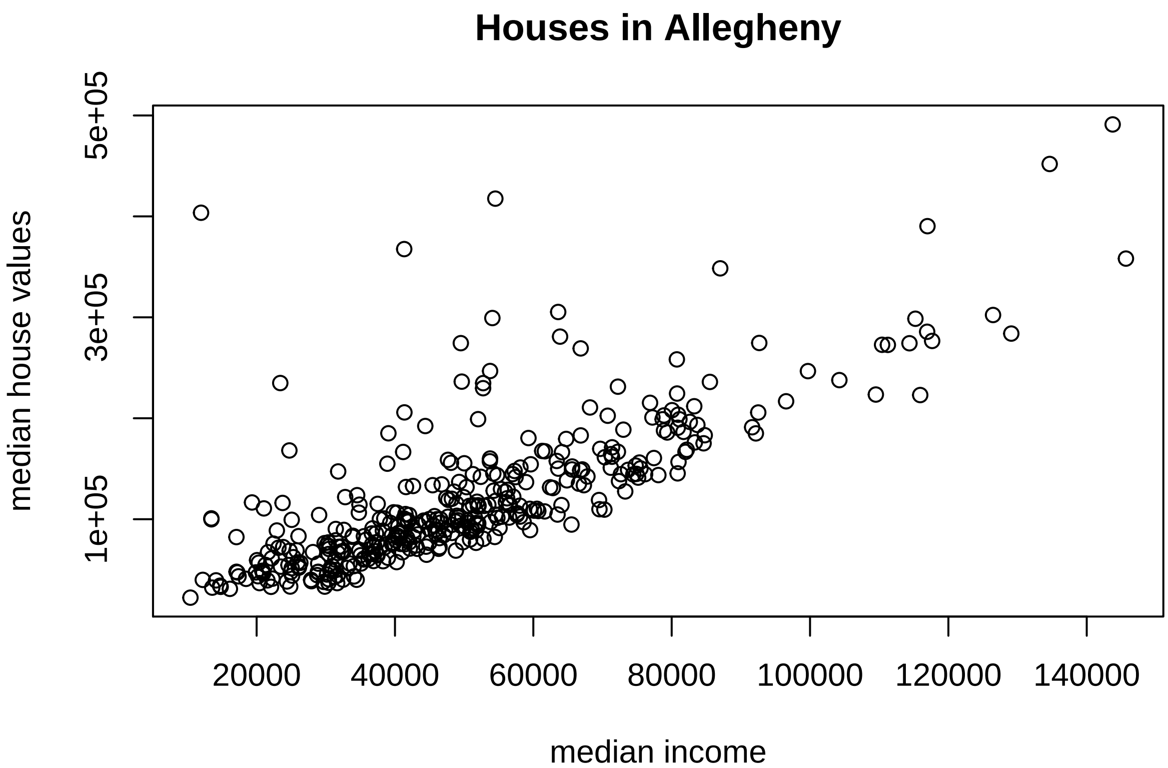
```r
#Alameda
plot(ca_pa$Median_household_income[ca_pa$STATEFP == 6 & ca_pa$COUNTYFP == 1],
     ca_pa$Median_house_value[ca_pa$STATEFP == 6 & ca_pa$COUNTYFP == 1],
     xlab = "median income", ylab = "median house values",
     main = "Houses in Alameda")
```




```r
# Santa Clara
plot(ca_pa$Median_household_income[ca_pa$STATEFP == 6 & ca_pa$COUNTYFP == 85],
     ca_pa$Median_house_value[ca_pa$STATEFP == 6 & ca_pa$COUNTYFP == 85],
     xlab = "median income", ylab = "median house values",
     main = "Houses in Santa Clara")
```




```
# Allegheny
plot(ca_pa$Median_household_income[ca_pa$STATEFP == 42 & ca_pa$COUNTYFP == 3],
     ca_pa$Median_house_value[ca_pa$STATEFP == 42 & ca_pa$COUNTYFP == 3],
     xlab = "median income", ylab = "median house values",
     main = "Houses in Allegheny")
```




```
acca <- c()
for (tract in 1:nrow(ca_pa)) {
  if (ca_pa$STATEFP[tract] == 6) {
    if (ca_pa$COUNTYFP[tract] == 1) {
      acca <- c(acca, tract)
    }
  }
}
accamhv <- c()
for (tract in acca) {
  accamhv <- c(accamhv, ca_pa[tract,10])
}
median(accamhv)
```

MB.Ch1.11. Run the following code:

```
gender <- factor(c(rep("female", 91), rep("male", 92)))
table(gender)
```

```
## gender
## female   male
##     91     92
```

```
gender <- factor(gender, levels=c("male", "female"))
table(gender)
```

```
## gender
##   male female
```

```
##     92     91
```

```
gender <- factor(gender, levels=c("Male", "female"))
# Note the mistake: "Male" should be "male"
table(gender)
```

```
## gender
##   Male female
##      0     91
```

```
table(gender, exclude=NULL)
```

```
## gender
##   Male female   <NA>
##      0     91     92
```

```
rm(gender)  # Remove gender
```

Explain the output from the successive uses of table().

Ans:

- We can use `table()` function to display the number of labels in a factor.
- Firstly, `gender` is initialized to be a factor with 91 females and 92 males, so `table(gender)` will display the number of females and the number of males.
- Secondly the code changes the levels of `gender`, exchanges the order of the two labels. So `table(gender)` will display the number of males and the number of females.
- Thirdly, the code sets the levels of `gender` with a wrong case. Because the number of Males is zero, `table(gender)` will display the number of Males, which is zero, and the number of females.
- Finally, the code uses `table(gender, exlude=NULL)` to display all the data, and the data without levels will be showed, too.

MB.Ch1.12. Write a function that calculates the proportion of values in a vector x that exceed some value cutoff.

```
cutoff_proportion <- function(x, cutoff) {
  return(sum(x > cutoff) / length(x))
}
```

(a) Use the sequence of numbers 1, 2, . . . , 100 to check that this function gives the result that is expected.

Ans: We can use the code below to check the correctness. The code will return 0.5 if the code is correct.

```
cutoff_proportion(seq(1, 100), 50)
```

```
## [1] 0.5
```

(b) Obtain the vector ex01.36 from the Devore6 (or Devore7) package. These data give the times required for individuals to escape from an oil platform during a drill. Use dotplot() to show the distribution of times. Calculate the proportion of escape times that exceed 7 minutes.

```
# This problem is deleted
```

MB.Ch1.18. The Rabbit data frame in the MASS library contains blood pressure change measurements on five rabbits (labeled as R1, R2, . . . ,R5) under various control and treatment conditions. Read the help file for more information. Use the unstack() function (three times) to convert Rabbit to the following form:

Treatment Dose R1 R2 R3 R4 R5

1 Control 6.25 0.50 1.00 0.75 1.25 1.5

2 Control 12.50 4.50 1.25 3.00 1.50 1.5

….

```
rabbit <- MASS::Rabbit
treatment <- unstack(rabbit, Treatment ~ Animal)
dose <- unstack(rabbit, Dose ~ Animal)
bpc <- unstack(rabbit, BPchange ~ Animal)
rabbit <- data.frame(treatment[, 1], dose[, 1], bpc)
name <- c("Treatment", "Dose", "R1", "R2", "R3", "R4", "R5")
names(rabbit) <- name
rabbit
```

```
##    Treatment   Dose    R1    R2    R3    R4   R5
## 1    Control   6.25  0.50  1.00  0.75  1.25  1.5
## 2    Control  12.50  4.50  1.25  3.00  1.50  1.5
## 3    Control  25.00 10.00  4.00  3.00  6.00  5.0
## 4    Control  50.00 26.00 12.00 14.00 19.00 16.0
## 5    Control 100.00 37.00 27.00 22.00 33.00 20.0
## 6    Control 200.00 32.00 29.00 24.00 33.00 18.0
## 7        MDL   6.25  1.25  1.40  0.75  2.60  2.4
## 8        MDL  12.50  0.75  1.70  2.30  1.20  2.5
## 9        MDL  25.00  4.00  1.00  3.00  2.00  1.5
## 10       MDL  50.00  9.00  2.00  5.00  3.00  2.0
## 11       MDL 100.00 25.00 15.00 26.00 11.00  9.0
## 12       MDL 200.00 37.00 28.00 25.00 22.00 19.0
```