Homework 2

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1. *Loading and cleaning*

(a)

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

(b)

```r
dim(ca_pa)
```

```
## [1] 11275    34
```

So the data frame has 11275 rows and 34 columns.

(c)

```r
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
```

This command is used to count the number of NA (not a number) values in each column of the data frame.

- The `apply()` function loops through all the elements of the matrix `ca_pa` and applies the `is.na()` function which returns TRUE if the element is not a number and FALSE otherwise.
- The resulting matrix of TRUE and FALSE values is then given as input to `colSums()` function, which counts the number of TRUE values in each column.

(d)

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

(e)

```
nrow(ca_pa)-nrow(new_ca_pa)
```

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

The result shows that the `na.omit()` command eliminate 670 rows.

(f) My answer in (c) and (e) are compatible. We can run the following command to verify this:

```
colSums(apply(new_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                          0
##                Total_units                Vacant_units
##                          0                          0
##               Median_rooms  Mean_household_size_owners
##                          0                          0
## Mean_household_size_renters         Built_2005_or_later
##                          0                          0
##          Built_2000_to_2004                Built_1990s
##                          0                          0
```

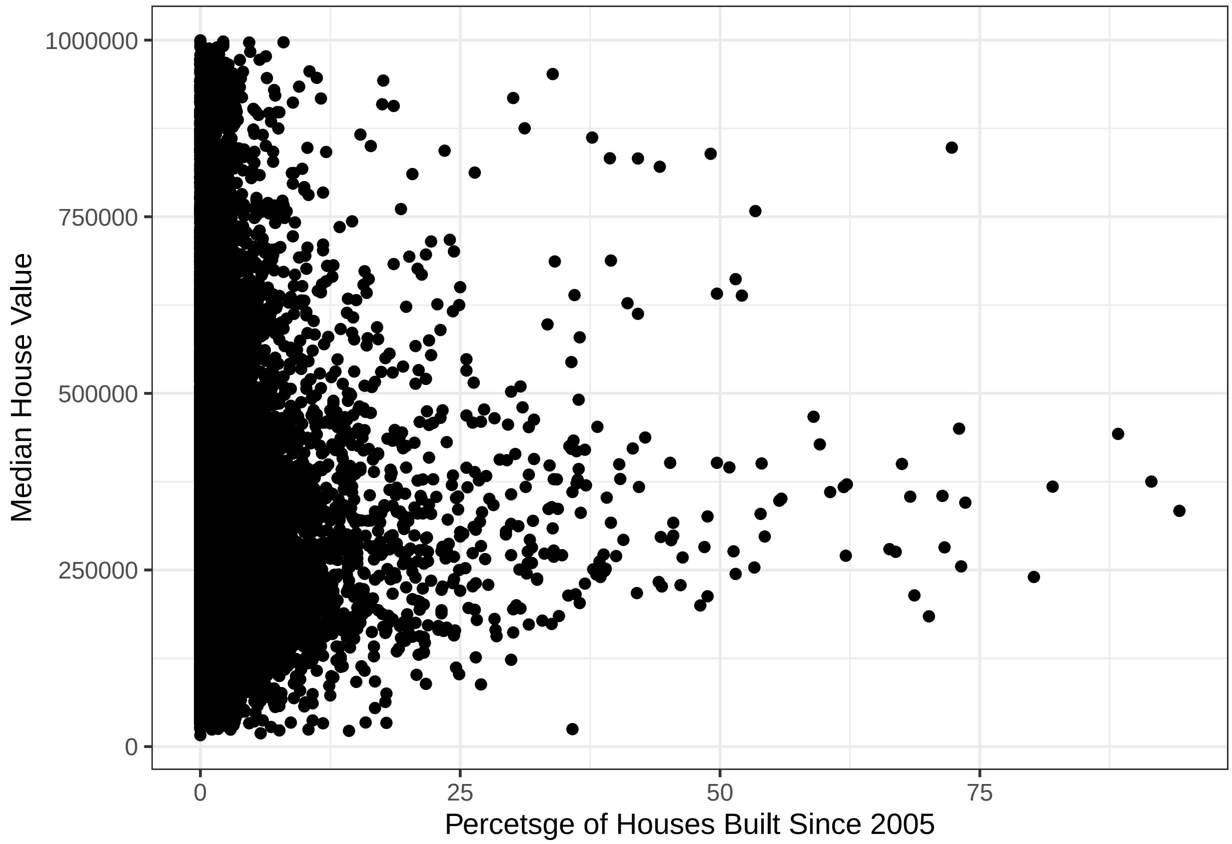
```
##                Built_1980s                Built_1970s
##                          0                          0
##                Built_1960s                Built_1950s
##                          0                          0
##                Built_1940s       Built_1939_or_earlier
##                          0                          0
##                 Bedrooms_0                 Bedrooms_1
##                          0                          0
##                 Bedrooms_2                 Bedrooms_3
##                          0                          0
##                 Bedrooms_4          Bedrooms_5_or_more
##                          0                          0
##                     Owners                    Renters
##                          0                          0
##    Median_household_income      Mean_household_income
##                          0                          0
```

The values of all columns are all 0, which means that we have successfully purged ca_pa from any row containing NA value.

2. ***This Very New House***

(a)

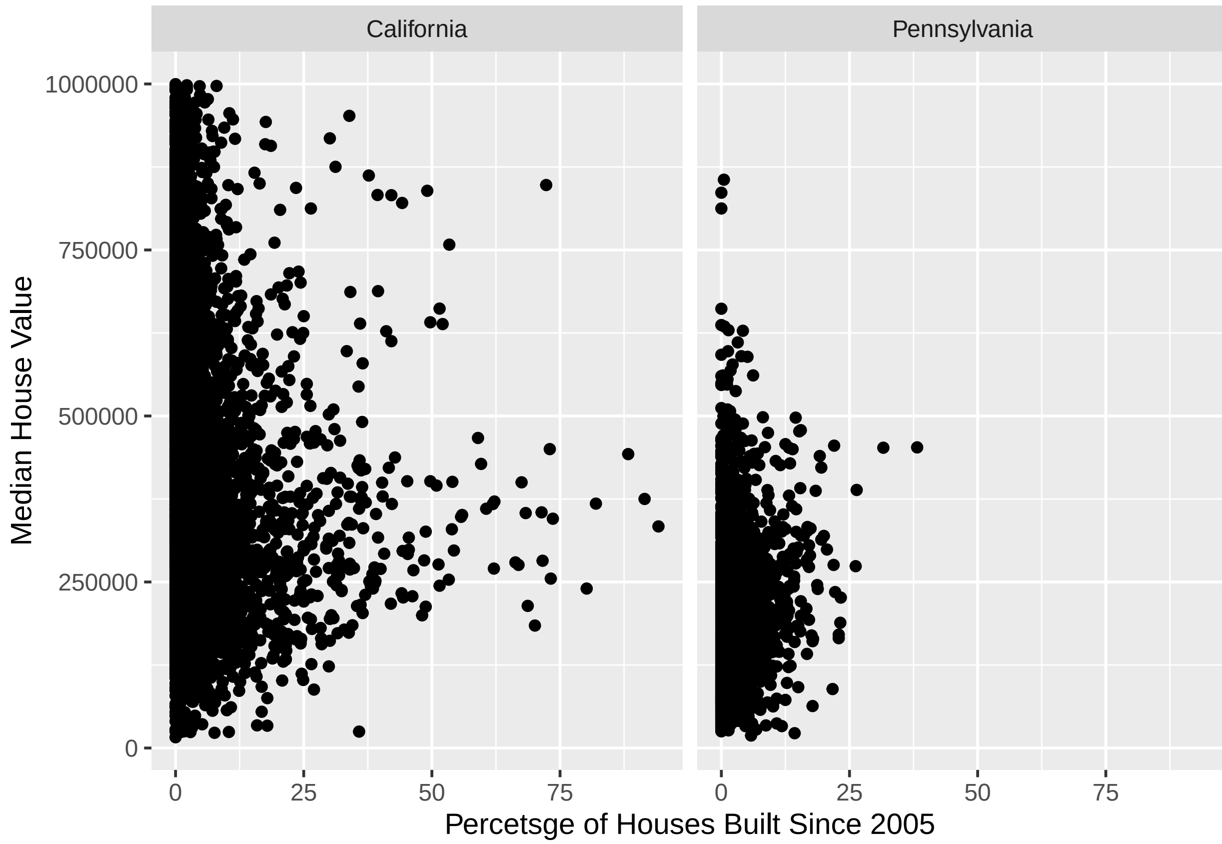
```
ggplot(data = new_ca_pa) +
geom_point(aes(x = Built_2005_or_later,
    y = Median_house_value),na.rm = TRUE) +
labs(x = "Percetsge of Houses Built Since 2005",
y = "Median House Value") +
theme_bw() +
theme(legend.title=element_blank())
```



(b) With following commands, we make a pair of plots that breaks this out by state, which shows the median house prices against `Built_2005_or_later` in California(state 6) and Pennsylvania(state 42) respectively.

```
d<-data.frame(STATEFP=c(6,42),state=c("California","Pennsylvania"))
ca_pa2<-left_join(new_ca_pa,d,by="STATEFP")
```

```
ggplot(data = ca_pa2) +
geom_point(aes(x = Built_2005_or_later,
    y = Median_house_value),na.rm = TRUE) +
labs(x = "Percetsge of Houses Built Since 2005",
y = "Median House Value") +facet_wrap(~ state)
```



3. ***Nobody Home***

(a) Add a new column to the dataframe which contains the vacancy rate.

```
ca_pa3 <- ca_pa2 %>%
  mutate(Vacant_Rate=Vacant_units/Total_units)
```

Minimum:

```
min(ca_pa3$Vacant_Rate,na.rm = TRUE)
```

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

Maximum:

```
max(ca_pa3$Vacant_Rate,na.rm = TRUE)
```

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

Mean:

```
mean(ca_pa3$Vacant_Rate,na.rm = TRUE)
```

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

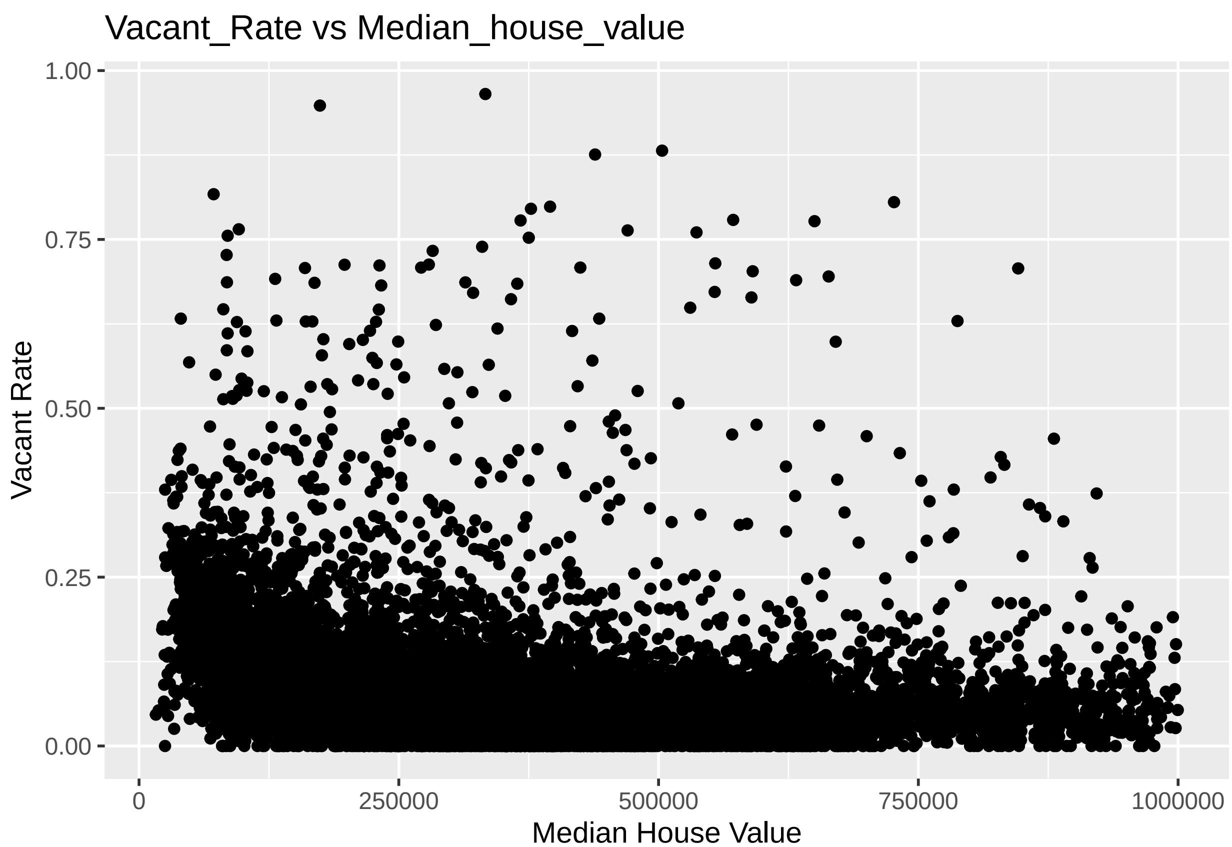
Median:

```
median(ca_pa3$Vacant_Rate,na.rm = TRUE)
```

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

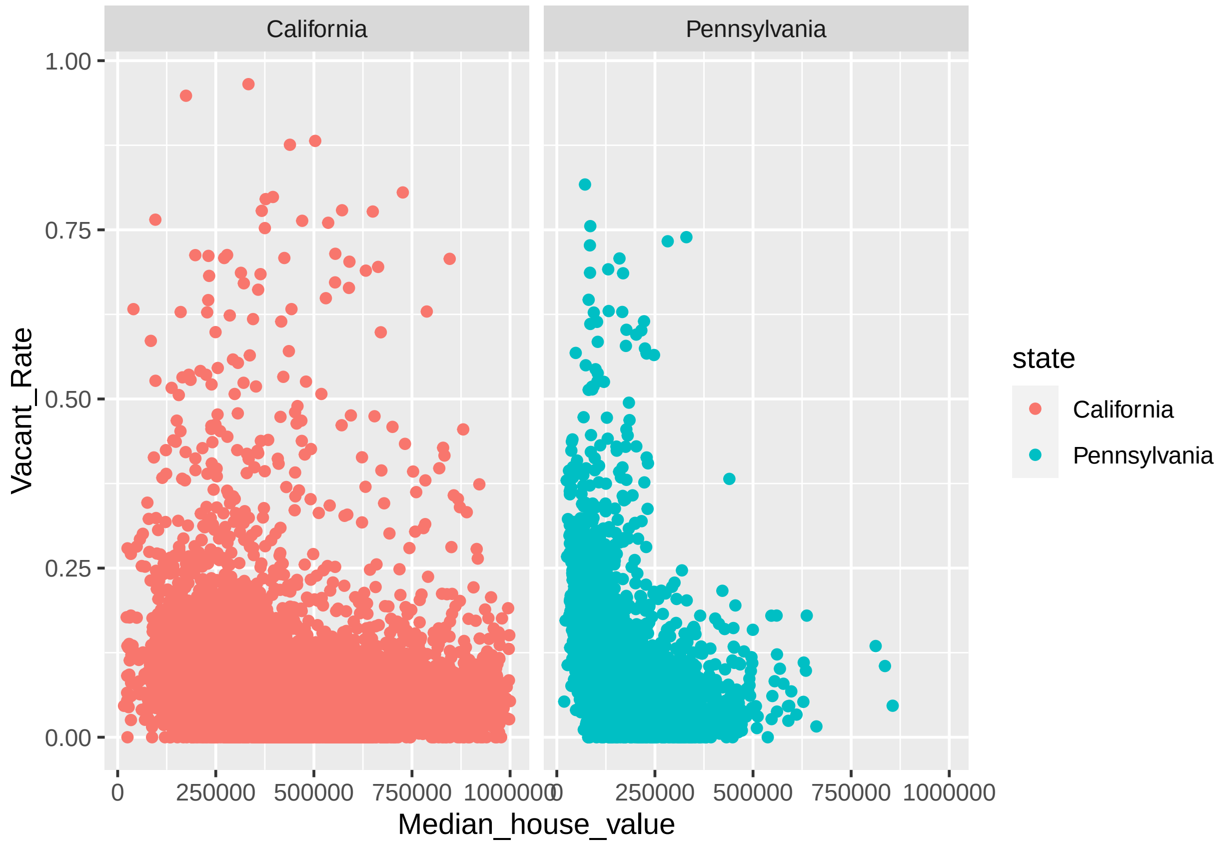
(b) Plot the vacancy rate against median house value:

```
ggplot(data = ca_pa3) +
geom_point(aes(x = Median_house_value,
    y = Vacant_Rate),na.rm = TRUE) +
labs(x = "Median House Value",
y = "Vacant Rate",title = "Vacant_Rate vs Median_house_value")
```



(c) Plot vacancy rate against median house value separately for California and for Pennsylvania:

```
ggplot(data = ca_pa3) +
geom_point(aes(x = Median_house_value,
    y = Vacant_Rate,color=state),na.rm = TRUE) +
facet_wrap(~ state)
```



4.

(a) The block of code is supposed to calculate the median house value in Alameda Country (country 1 in California). It firstly selects the rows of California, whose STATEFP=6, and then selects the rows of Alameda, whose COUNTRYFP=1 among the selected rows. Finally select median value of these rows' Median house value to get the median house value in Alameda.

(b) We can obtain the same result as the block of code with following command:

```
ca_pa3 %>% filter(STATEFP==6,COUNTYFP==1) %>% {median(.$Median_house_value,na.rm = TRUE)}
```

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

(c) We can obtain the average percentages of housing built since 2005 for Alameda, Santa Clara and Allegheny Counties with following commands: (i) For Alameda:

```
(Alameda_avg <- ca_pa3 %>% filter(STATEFP==6&COUNTYFP==1 )) %>% {mean(.$Built_2005_or_later,na.rm = TRUE
```

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

(ii) For Santa Clara:

```
(Alameda_avg <- ca_pa3 %>% filter(STATEFP==6&COUNTYFP==85 )) %>% {mean(.$Built_2005_or_later,na.rm = TRU
```

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

(ii) For Allegheny:

```
(Alameda_avg <- ca_pa3 %>% filter(STATEFP==42&COUNTYFP==3 )) %>% {mean(.$Built_2005_or_later,na.rm = TRU
```

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

(d) the correlation between median house value and the percent of housing built since 2005 (i) In the whole data:

```
cor(ca_pa3$Median_house_value,ca_pa3$Built_2005_or_later)
```

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

(ii) In all of California

```
ca_pa3 %>% filter(STATEFP==6) %>%
  {cor(.$Median_house_value,.$Built_2005_or_later)}
```

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

(iii) In all of Pennsylvania

```
ca_pa3 %>% filter(STATEFP==42) %>%
  {cor(.$Median_house_value,.$Built_2005_or_later)}
```

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

(iv) In Alameda County

```
ca_pa3 %>% filter(STATEFP==6,COUNTYFP==1) %>%
  {cor(.$Median_house_value,.$Built_2005_or_later)}
```

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

(v) In Santa Clara County

```
ca_pa3 %>% filter(STATEFP==6,COUNTYFP==85) %>%
  {cor(.$Median_house_value,.$Built_2005_or_later)}
```

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

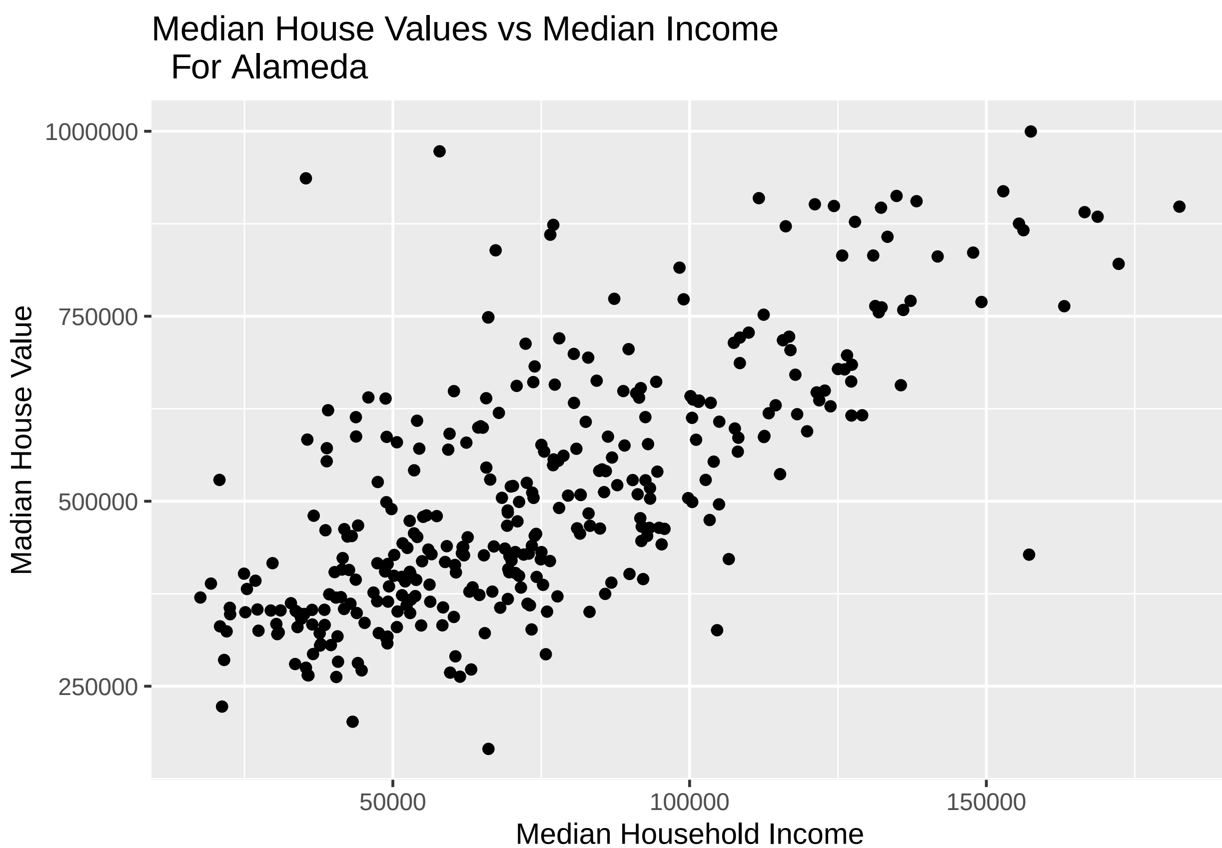
(vi) In Allegheny Count

```
ca_pa3 %>% filter(STATEFP==42,COUNTYFP==3) %>%
  {cor(.$Median_house_value,.$Built_2005_or_later)}
```

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

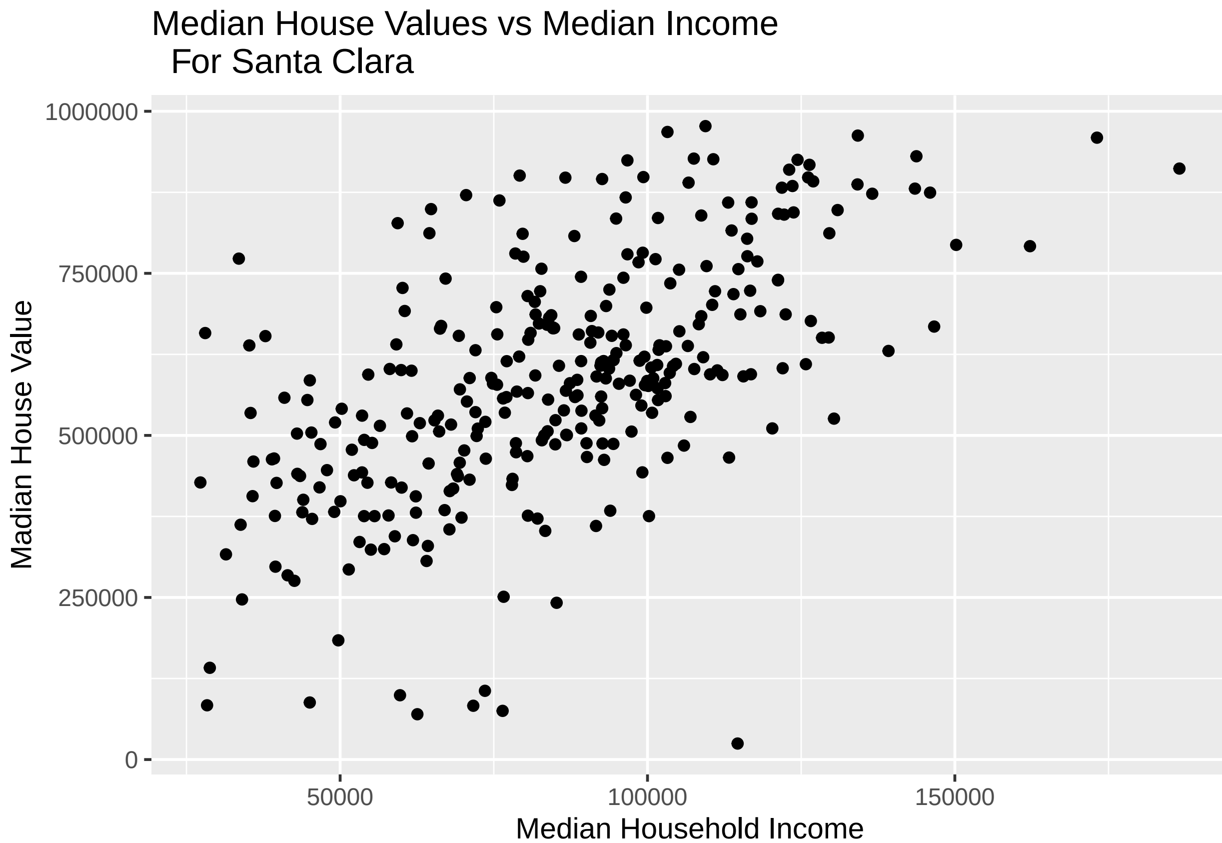
(e) Median house values against median income. (i) For Alameda:

```
ca_pa3 %>% filter(STATEFP==6,COUNTYFP==1) %>%
  ggplot() +
  geom_point(aes(x = Median_household_income,
    y = Median_house_value),na.rm = TRUE) +
  labs(x = "Median Household Income",
  y = "Madian House Value",title = "Median House Values vs Median Income
  For Alameda")
```



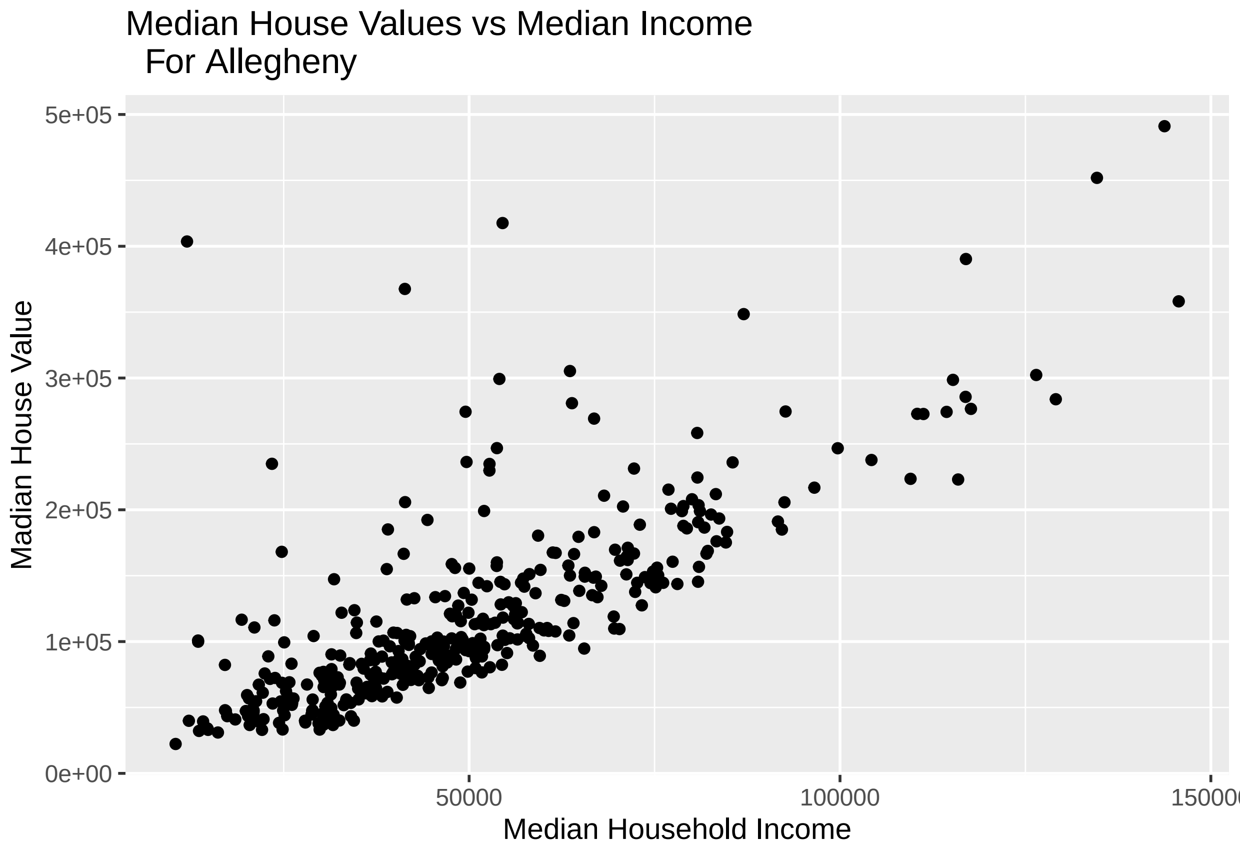
(ii) For Santa Clara:

```
ca_pa3 %>% filter(STATEFP==6,COUNTYFP==85) %>%
  ggplot() +
  geom_point(aes(x = Median_household_income,
    y = Median_house_value),na.rm = TRUE) +
  labs(x = "Median Household Income",
  y = "Madian House Value",title = "Median House Values vs Median Income
  For Santa Clara")
```



(iii) For Allegheny:

```
ca_pa3 %>% filter(STATEFP==42,COUNTYFP==3) %>%
  ggplot() +
  geom_point(aes(x = Median_household_income,
    y = Median_house_value),na.rm = TRUE) +
  labs(x = "Median Household Income",
  y = "Madian House Value",title = "Median House Values vs Median Income
  For Allegheny")
```



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
```

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

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

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

Explain: `table` uses the cross-classifying factors to build a contingency table of the counts at each combination of factor levels. That is, it is used to calculate frequency.

i) In the first command, `factor` turns a vector into a factor data type. And then `gender` has 91 'female's and 92 'male's, with levels ("female","male").

ii) In the second command, attribute `levels=()` is used to returns the value of the levels of its argument , which select values that fits levels in the data as valid levels. Then we use table to count frequency of the levels ("male", "female"), in order.

iii) In the third command, attribute `levels=()` is used to set the attribute, which makes "Male" that is not in gender a level, and the number of its value is 0, and all "male"s in gender is discarded as invalid values.

iv) In the fourth command, we use `exclude=NULL` in `table()` to count all the invalid values. So previous discarded "male"s are counted and was outputted as :92

MB.Ch1.12.

```r
k<-0
Func <- function(x,cutoff_value){
  for(i in x){
    if (i>cutoff_value){
      k<-k+1
    }
  }
  prop <- k/length(x)
  return(prop)
}
```

(a) For the sequence of numbers 1, 2, . . . , 100, we set the value cutoff 35,67.3 and 89, then the expected proportion result is 0.65, 0.33 and 0.11 correspondingly. And following codes check this.

```r
x<-1:100
vc<-35
Func(x,vc)
```

```
## [1] 0.65
```

```r
vc<-67.3
Func(x,vc)
```

```
## [1] 0.33
```

```r
vc<-89
Func(x,vc)
```

```
## [1] 0.11
```

MB.Ch1.18. Using following commands, we can convert Rabbit to the required form.

```r
Dose <- unstack(Rabbit, Dose ~ Animal)[,1]
Treatment <- unstack(Rabbit, Treatment ~ Animal)[,1]
BPchange <- unstack(Rabbit, BPchange ~ Animal)
Rabbit.df <- data.frame(Treatment, Dose, BPchange)
Rabbit.df
```

```
##    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
```