Cancer Mortality Exploration

Andrew Carlson, Brandon Cummings, Tako Hisada

Research Question

Our team was hired by a health government agency that would like to understand factors that predict cancer mortality rates. Their ultimate goal is to identify communities for social interventions and of understanding which interventions are likely to have the most impact. Our main objective is to perform an exploratory analysis to understand how county-level characteristics are related to cancer mortality.

Dataset Analysis

```r
Cancer = read.csv('cancer.csv')
```

This dataset consists of 29 variables (not including the index column), all pertaining to county level information. Overall there were about 3047 observations per variable.

The types of variables present in the dataset can be categorized into 8 groups:

1) Region

2) Population

3) Birthrate

4) Race

5) Marital Status

6) Insurance coverage

7) Income status

8) Education

All variables in dataset:

```r
colnames(Cancer)
```

```
##  [1] "X"                     "avgAnnCount"          "medIncome"
##  [4] "popEst2015"            "povertyPercent"       "binnedInc"
##  [7] "MedianAge"             "MedianAgeMale"        "MedianAgeFemale"
## [10] "Geography"             "AvgHouseholdSize"     "PercentMarried"
## [13] "PctNoHS18_24"          "PctHS18_24"           "PctSomeCol18_24"
## [16] "PctBachDeg18_24"       "PctHS25_Over"         "PctBachDeg25_Over"
## [19] "PctEmployed16_Over"    "PctUnemployed16_Over" "PctPrivateCoverage"
## [22] "PctEmpPrivCoverage"    "PctPublicCoverage"    "PctWhite"
## [25] "PctBlack"              "PctAsian"             "PctOtherRace"
## [28] "PctMarriedHouseholds"  "BirthRate"            "deathRate"
```

Data Quality

Overall the data quality was reasonable and usable. There were some observations in different decimal states, many NAs, and some variables that didn't seem relevant to cancer mortality at all. Other than that we found the data to be easy to analyze. Below are some data observations and assumptions:

"deathRate" - This is the column that we have assumed is the number of average yearly deaths per county.

"MedianAge" - This variable is the median age for a county, the dataset column had a range of 22-624, when analyzing this correlation we trimmed all numbers above 65 due to the numbers after 65 started in the 300s.

"PctSomeCol18_2"4 - This is the percent of some college attended between the age of 18-24. This column only had 762 of 3047 observations that were not NA. We still used this column when analyzing correlation, but it is worth noting that we removed all NAs.

"Race" - When it came to the percentage of race for each county, we noticed that a mojority of the counties surveyed were "white". This may or may not be a significant datapoint, but it may lead to assumptions about populations that are incorrect.

"avgAnnCount" - This was clarified as "2009-2013 mean incidences per county", we did not know what "incidences" this was referring to, we ended up not finding a direct correlation with other important variables, so we did not make any further assumptions and left it out of our analysis.

"AvgHouseholdSize" - This had 61 entries with less than 1, meaning that there are observations of 0 or negative household sizes, we removed these when analyzing houshold size with other key variables.

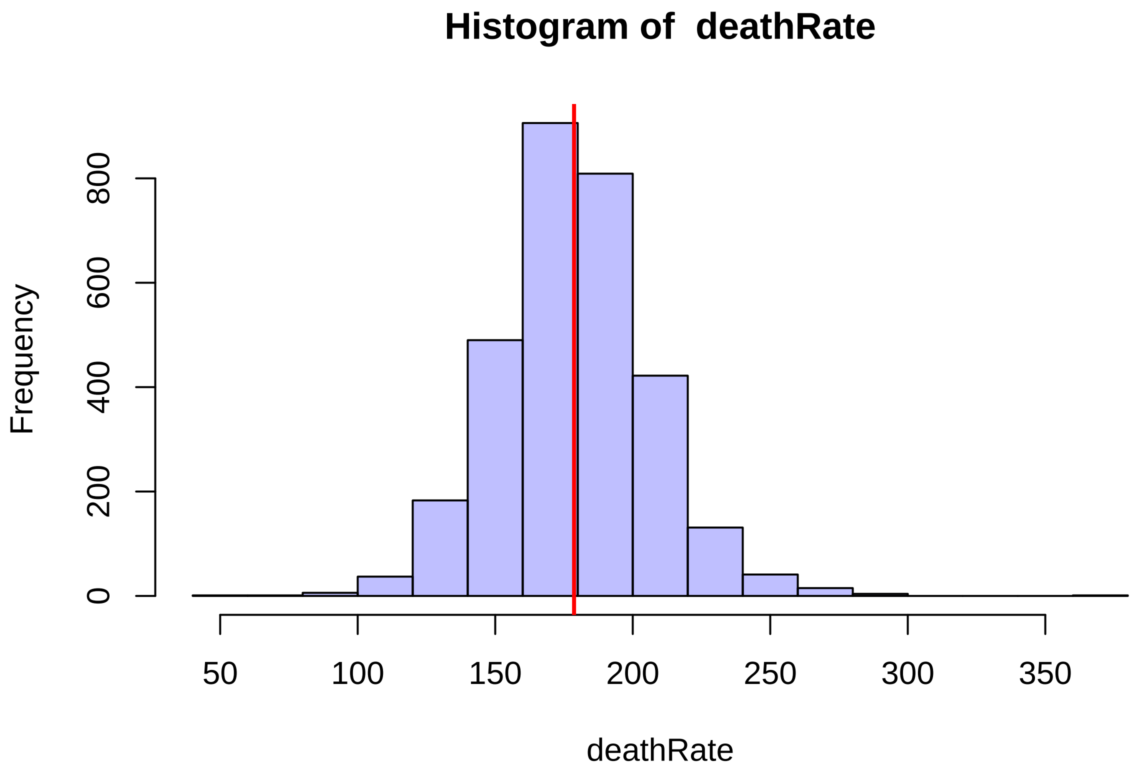
"PctEmployed16_Over" - There were 152 missing observations in this column, we removed these NAs from our dataset when analyzing this column with other key variables.

Analysis of Key Variables and Relationships

```r
# convenient wrapper function for a prettier histogram
histWithMean <- function(vec, name) {
  hist(vec, col=rgb(0,0,1,1/4), main=paste("Histogram of ", name), xlab=name)
  # add a red line down the mean
  abline(v = mean(vec, na.rm=TRUE), col="red", lwd=2)
}
```

The dependant variable for this analysis is `deathRate`, which is assumed to be the death rate from cancer.

```r
histWithMean(deathRate, "deathRate")
```



Unclean Data

```
# function that counts the number of elements in a vector that satisfy the predicate
# convenient for checking certain sanity bounds and counting how many are out of the bounds
count.by <- function(vec, predicate) {
  yes <- 0
  no <- 0
  for (n in vec) {
    if (predicate(n)) {
      yes <- yes + 1
    } else {
      no <- no + 1
    }
  }
  return(c(yes, no))
}
```

61 of the AvgHouseholdSize entries are less than 1. This is probably a coding error. A mean less than 1 for a set of integers is only possible if some values are 0 or negative. These values are nonsensical for a household size.

```
count.by(AvgHouseholdSize, function(num) num < 1)
```

```
## [1]   61 2986
```

30 of the MedianAge entries are greater than 200. This seems flagrantly improbable.

```
count.by(MedianAge, function(num) num > 200)
```

```
## [1]   30 3017
```

152 of the PctEmployed16_Over entries are NA.

```
count.by(PctEmployed16_Over, is.na)
```

```
## [1]  152 2895
```

2285 of the PctSomeCol18_24 entries are NA.

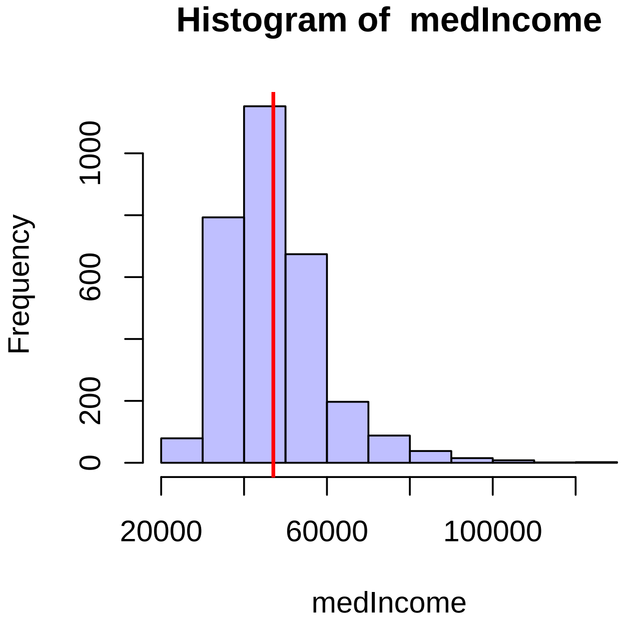
```
count.by(PctSomeCol18_24, is.na)
```

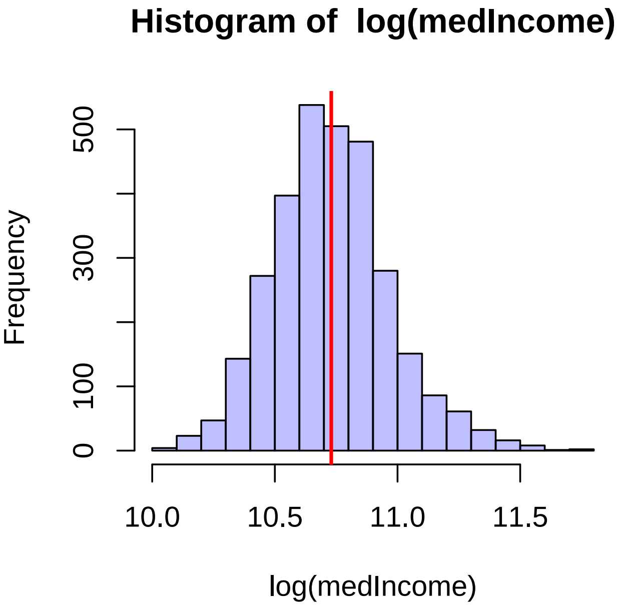
```
## [1] 2285  762
```

Correlated Variables

Here are some histograms of the variables that turned out to be related to `deathRate`.

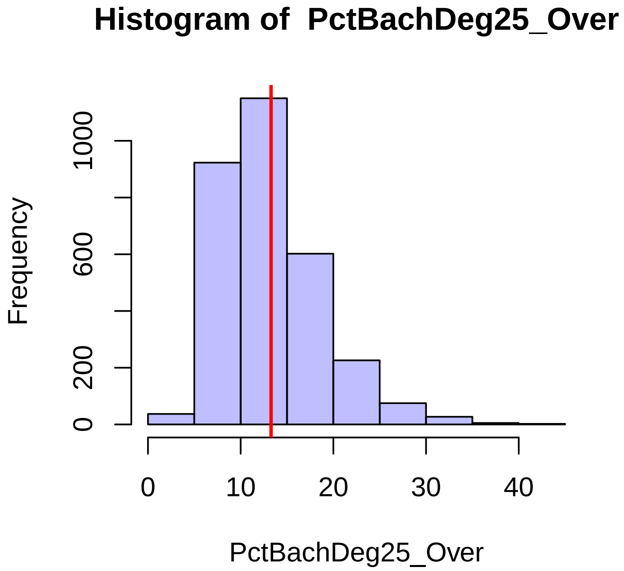
`medIncome` looks like a positively skewed distribution. In fact, in some populations it may look more like a power law distribution than a normal [link]. If we plot `log(medIncome)`, it *looks* closer to a normal distribution. We can check this transformation for correlation with `deathRate` in addition to the plain `medIncome` variable.

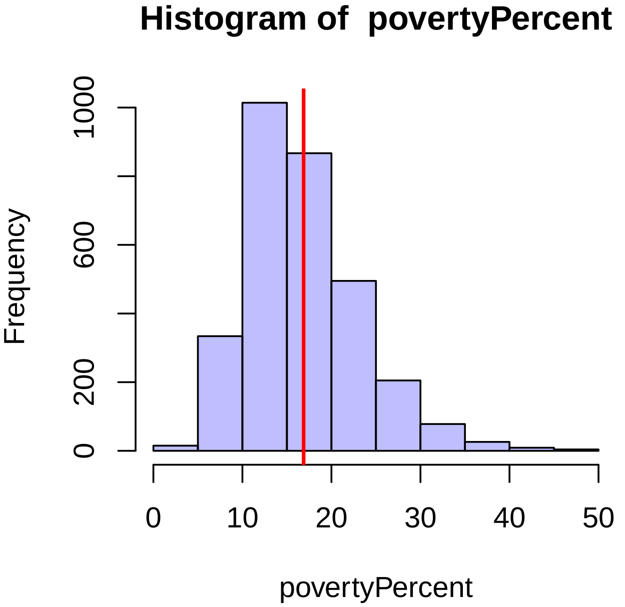


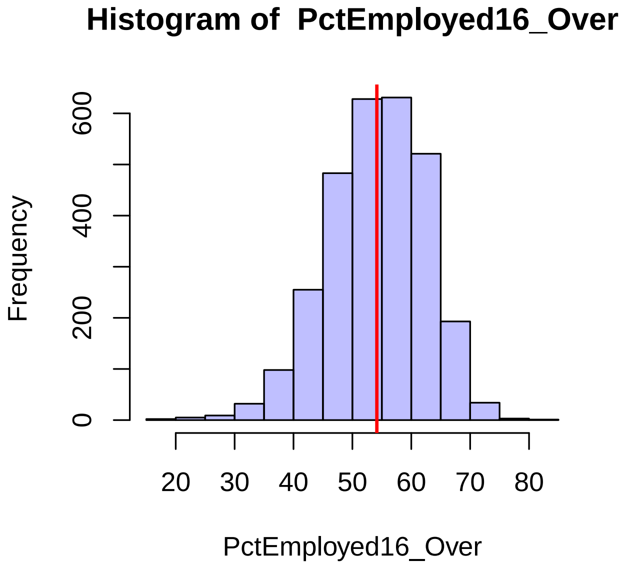


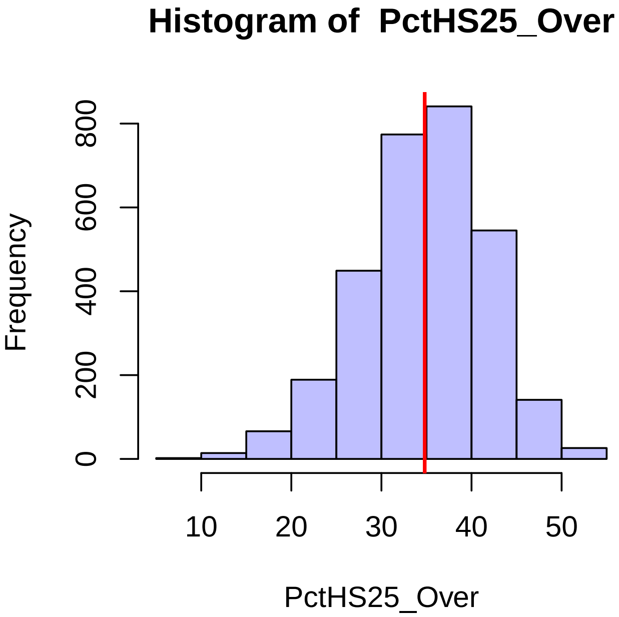
```r
Cancer$logMedIncome <- log(medIncome)
```

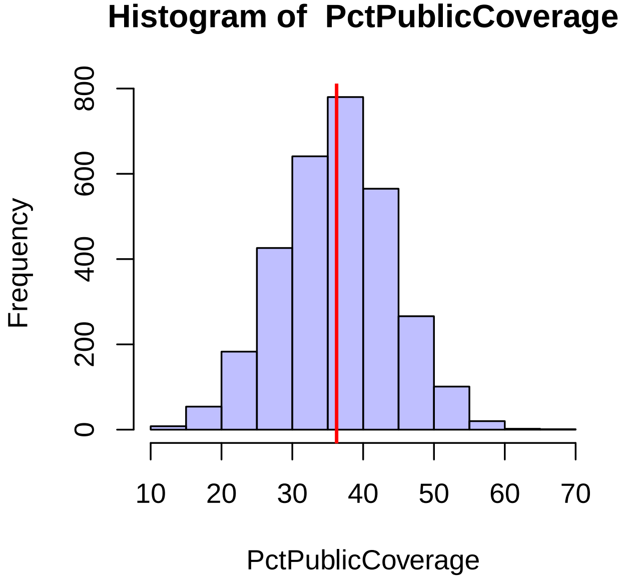
The rest look like clean, valid data. There are no obvious transformations to apply.

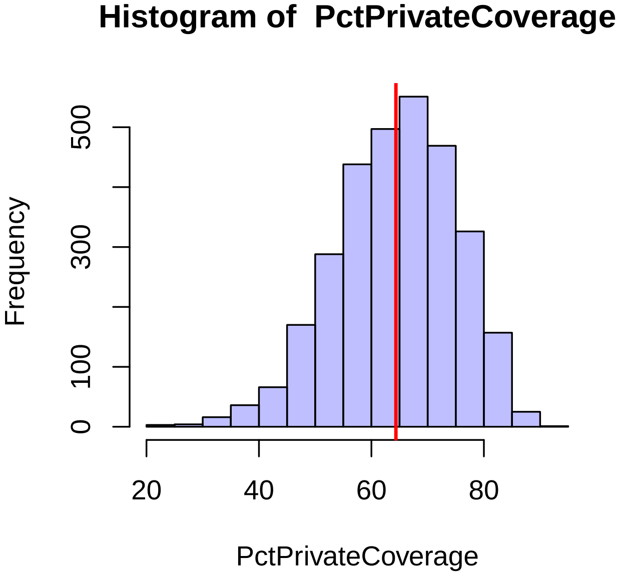


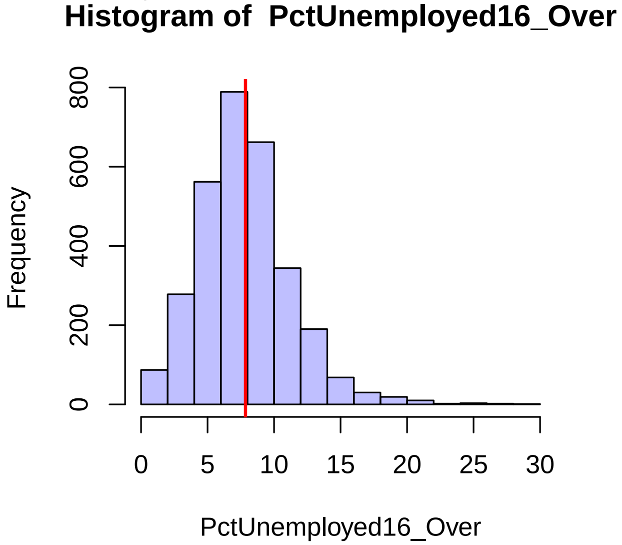



Histogram of PctEmployed16_Over
Frequency
0
200
400
600
20
30
40
50
60
70
80
PctEmployed16_Over


Histogram of PctHS25_Over
Frequency
0
200
400
600
800
10
20
30
40
50
PctHS25_Over


Histogram of PctPublicCoverage
Frequency
0
200
400
600
800
10
20
30
40
50
60
70
PctPublicCoverage


Histogram of PctPrivateCoverage
Frequency
0
100
300
500
20
40
60
80
PctPrivateCoverage


Histogram of PctUnemployed16_Over
Frequency
0
200
400
600
800
0
5
10
15
20
25
30
PctUnemployed16_Over

Finding strongest correlations

The numeric variables were taken. The correlation with each numeric variable was calculated and sorted by descending absolute value.

```r
# get just the numeric columns
numericColumns <- sapply(Cancer, is.numeric)
NumericCancer <- Cancer[, numericColumns]
# get each correlations with each column
correlations <- apply(NumericCancer, 2, function(col) cor(col, deathRate))
correlations <- correlations[!is.na(correlations)]
```

Now we have a vector of all the correlations. We just filtered out the `NA`s, which includes `PctEmployed16_Over` because some of the entries were `NA`. We'll have to add it back manually after dealing with the `NA`s.

```r
# clean the NAs out of PctEmployed16_Over and calculate correlation
cleanPctEmployed16_Over <- !is.na(PctEmployed16_Over)
corPctEmployed16_Over <- cor(PctEmployed16_Over[cleanPctEmployed16_Over], deathRate[cleanPctEmployed16_
# append it to the vector of correlations and name the entry
correlations <- c(correlations, corPctEmployed16_Over)
names(correlations)[length(correlations)] <- "PctEmployed16_Over"
```

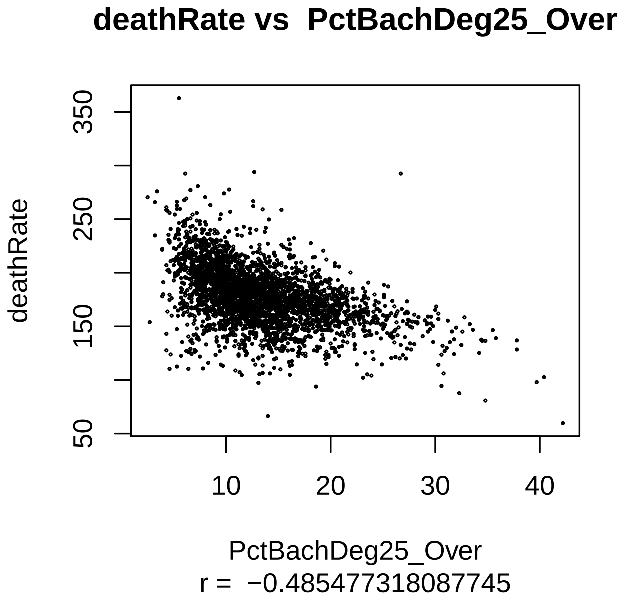
Now we can focus on the correlations that are significant.

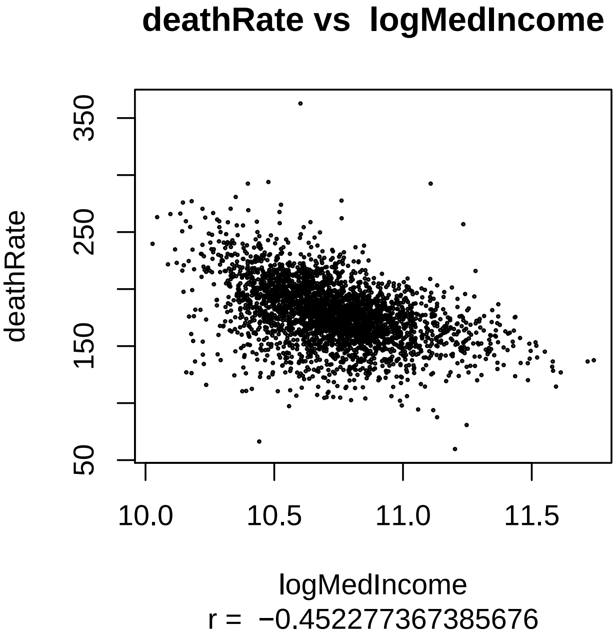
```r
# sort them
correlations <- correlations[order(abs(correlations), decreasing=TRUE)]
correlations <- correlations[2:length(correlations)]
correlations <- correlations[abs(correlations) >= 0.3]
correlations
```

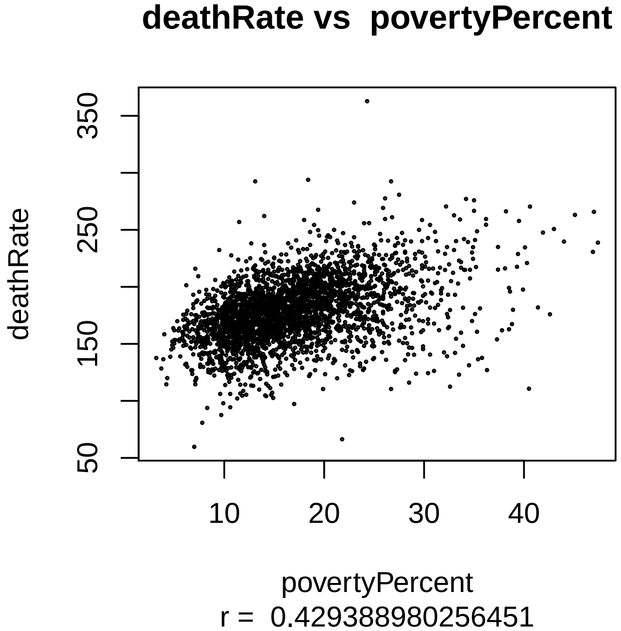
```
##    PctBachDeg25_Over         logMedIncome       povertyPercent
##           -0.4854773           -0.4522774            0.4293890
##            medIncome   PctEmployed16_Over          PctHS25_Over
##           -0.4286149           -0.4120458            0.4045891
##    PctPublicCoverage   PctPrivateCoverage PctUnemployed16_Over
##            0.4045717           -0.3860655            0.3784124
```

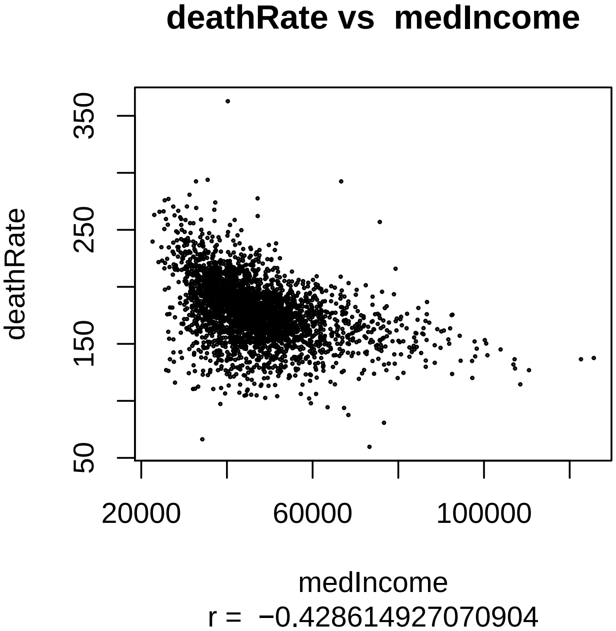
We will consider correlations of `0.3` or greater a significant association. This includes 9 of the variables, one of which is our transformed log(medianIncome). This actually had stronger correlation with `deathRate` than `medIncome`.

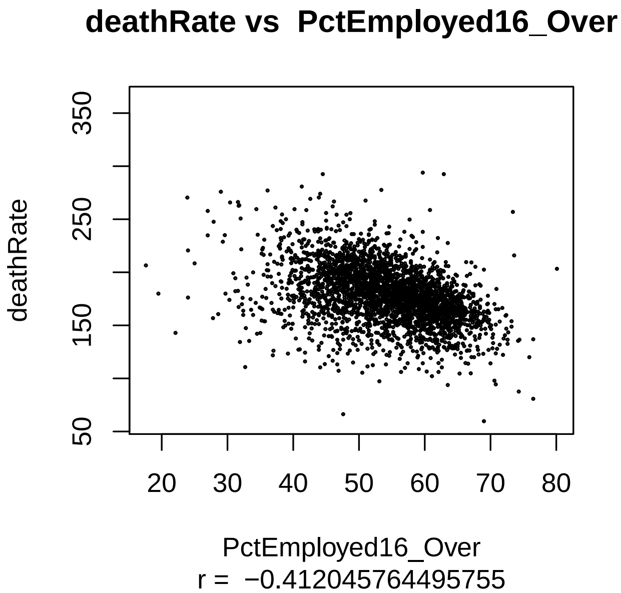
Plot deathRate with all variables with at least a weak correlation

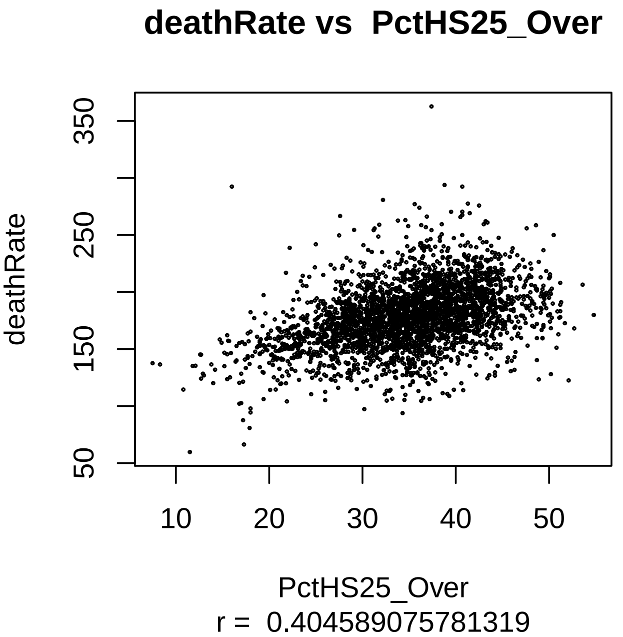


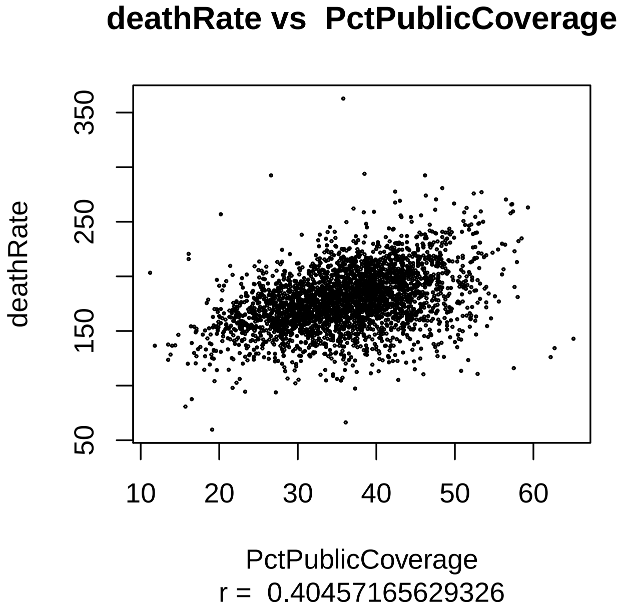


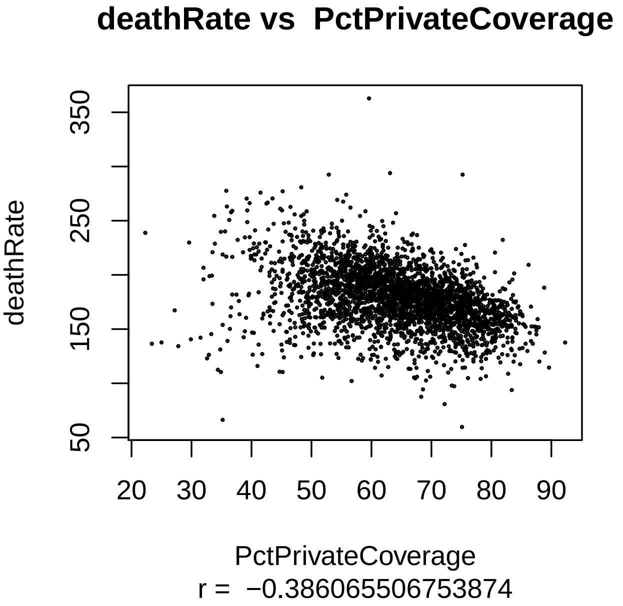


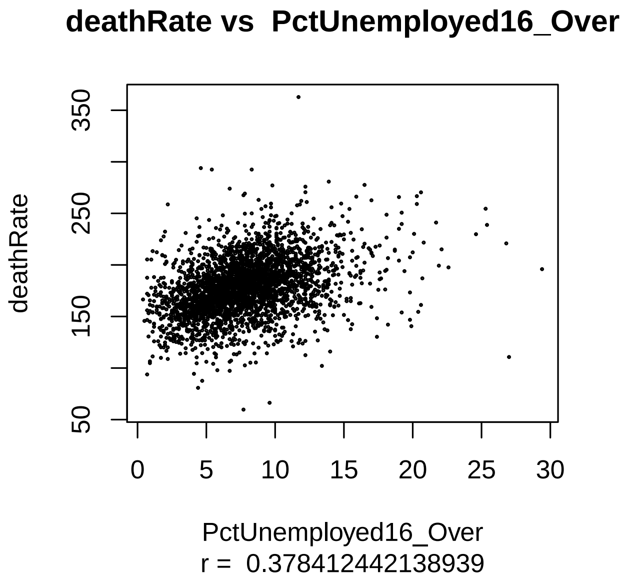



deathRate vs PctEmployed16_Over
deathRate
50
150
250
350
20
30
40
50
60
70
80
PctEmployed16_Over
r = −0.412045764495755


deathRate vs PctHS25_Over
deathRate
50
150
250
350
10
20
30
40
50
PctHS25_Over
r = 0.404589075781319


deathRate vs PctPublicCoverage
deathRate
50
150
250
350
10
20
30
40
50
60
PctPublicCoverage
r = 0.40457165629326


deathRate vs PctPrivateCoverage
deathRate
50
150
250
350
20
30
40
50
60
70
80
90
PctPrivateCoverage
r = −0.386065506753874



Analysis of Secondary Effects