Cancer Mortality Exploration

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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

```
Cancer = read.csv('cancer.csv')
par(mar = rep(2, 4))
```

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:

```
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, but rather pointed stronger to secondary effects. 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 due to cancer.

"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_24" - 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.

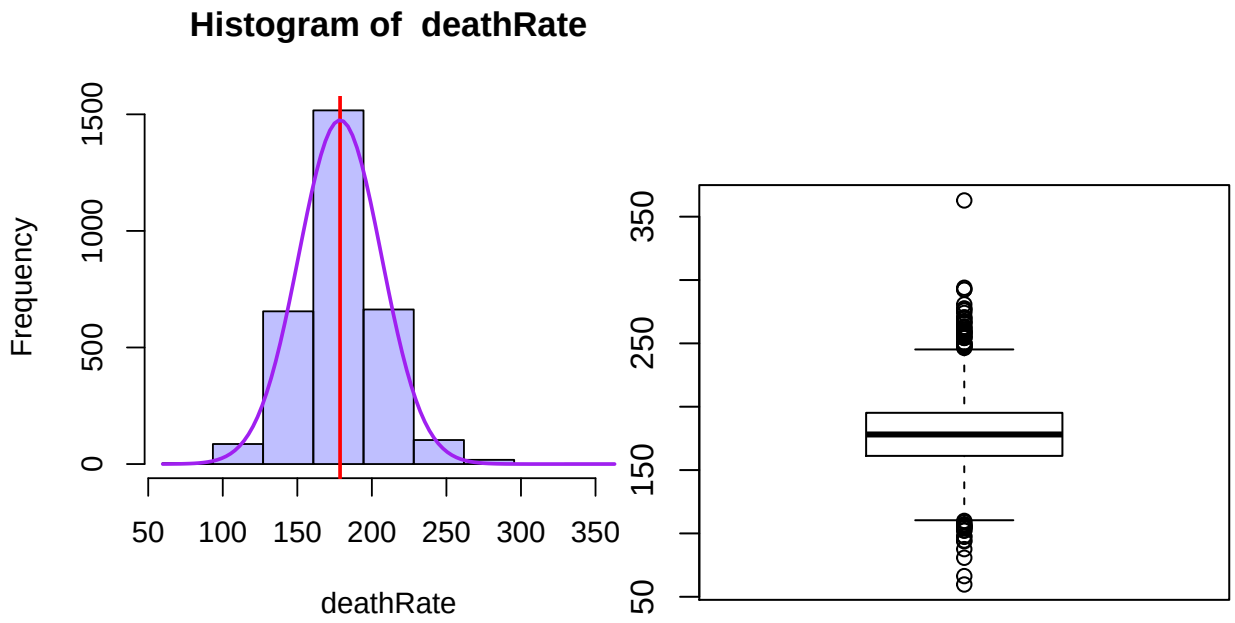
Analysis of Key Variables and Relationships

```
# convenient wrapper function for a prettier histogram
histWithNorm <- function(vec, name) {
  # calculate the breaks for the histogram
  vecMin <- min(vec, na.rm=TRUE)
  vecMax <- max(vec, na.rm=TRUE)
  breaks <- seq(vecMin, vecMax, length.out=10)
  vecHist <- hist(
    vec, col=rgb(0,0,1,1/4),
    breaks=breaks,
    main=paste("Histogram of ",name),
    xlab=name
  )

  # add a red line down the mean
  vecMean <- mean(vec, na.rm=TRUE)
  abline(v = vecMean, col="red", lwd=2)

  # plot a normal distribution over the histogram to visually compare the distributions
  vecSd <- sd(vec, na.rm=TRUE)
  # create the domain. span 6 sd's centered at the mean
  x <- seq(vecMean - 3 * vecSd, vecMean + 3 * vecSd, length.out=100)
  # get the width between each break
  histWidth <- breaks[2] - breaks[1]
  # calculate the area of the histogram and use it as the scale factor
  scaleFactor <- sum(histWidth * vecHist$counts)
  curve(dnorm(x, mean=vecMean, sd=vecSd) * scaleFactor, add=TRUE, col="purple", lwd=2)
}
```

The dependent variable for this analysis is `deathRate`, which is assumed to be the death rate from cancer. The histogram appears normally distributed.



Anomalous Data

We'll count the number of vector elements that violate some constraints to check for anomalies. If entries are missing or clearly erroneous, we can remove them from the data set before calculating the correlation.

```
# 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
```

```
cleanAvgHouseholdSize <- AvgHouseholdSize >= 1
```

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

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

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

```
cleanMedianAge <- MedianAge < 200
```

152 of the `PctEmployed16_Over` entries are `NA`.

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

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

```
cleanPctEmployed16_Over <- !is.na(PctEmployed16_Over)
```

2285 of the `PctSomeCol18_24` entries are `NA`. This is most of the rows, but there are still enough for a meaningful association.

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

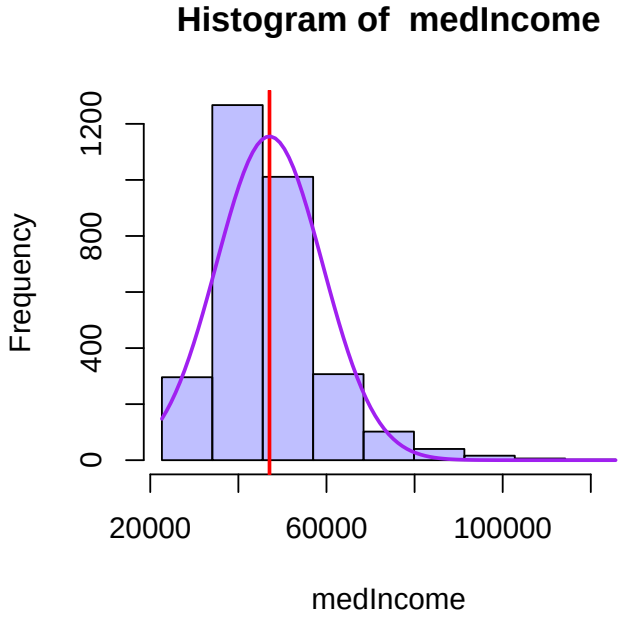
```
## [1] 2285  762
```

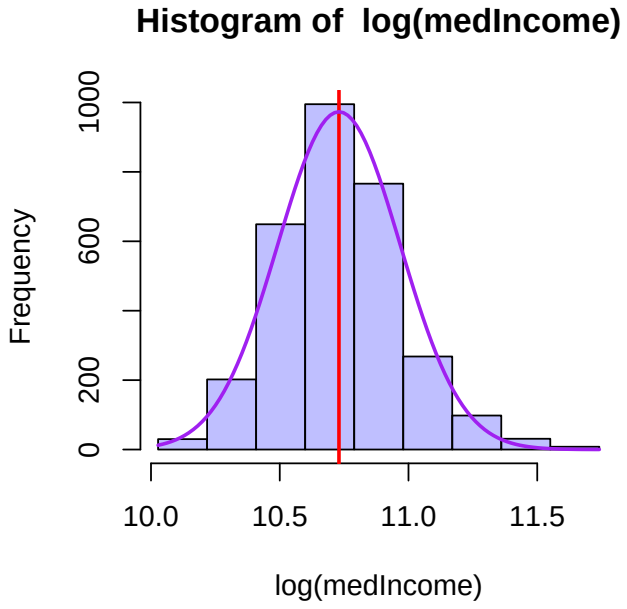
```
cleanPctSomeCol18_24 <- !is.na(PctSomeCol18_24)
```

Key Variables

Here are some histograms of the variables that turned out to be related to `deathRate`. How we determined this in the **correlated variables** section.

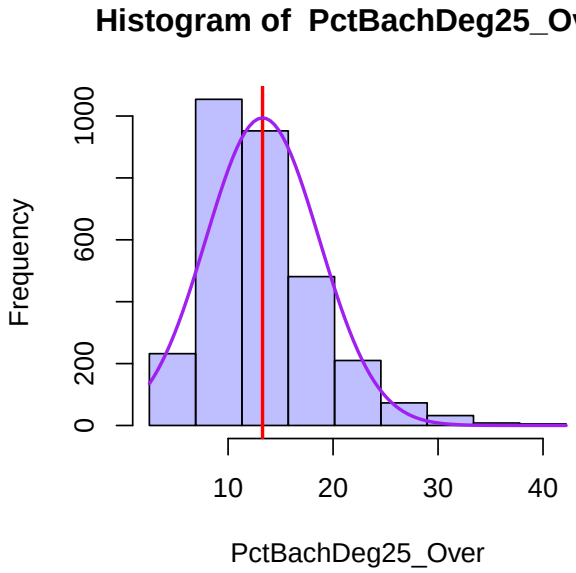
`medIncome` looks like a positively skewed distribution. In fact, in some populations it may look more like a power law distribution than a normal [link]. If we plot `log(medIncome)`, it *looks* closer to a normal distribution. We can check this transformation for correlation with `deathRate` in addition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

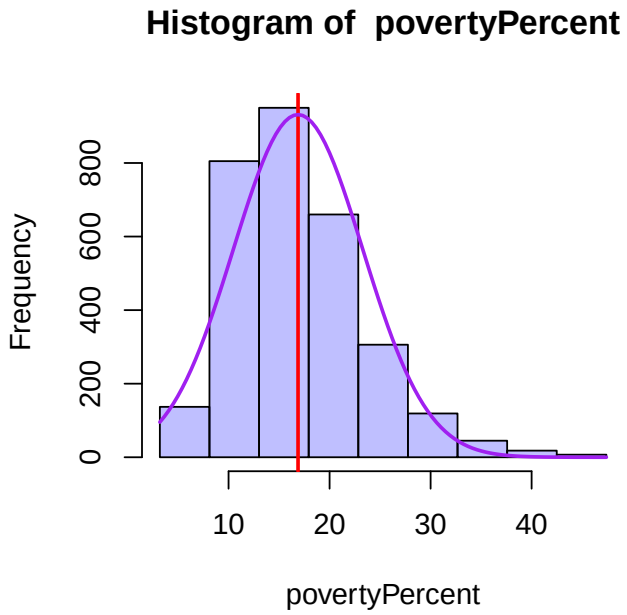


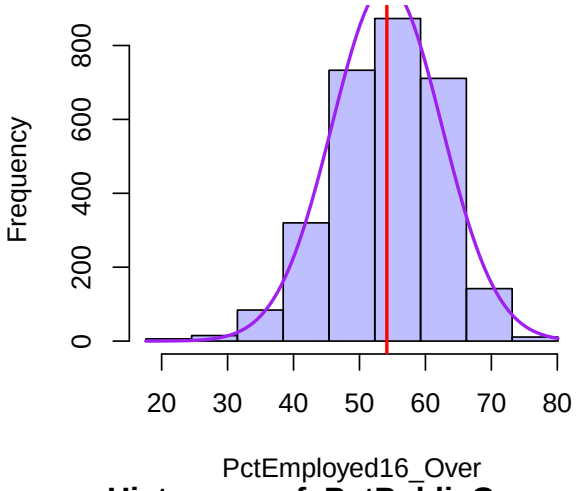


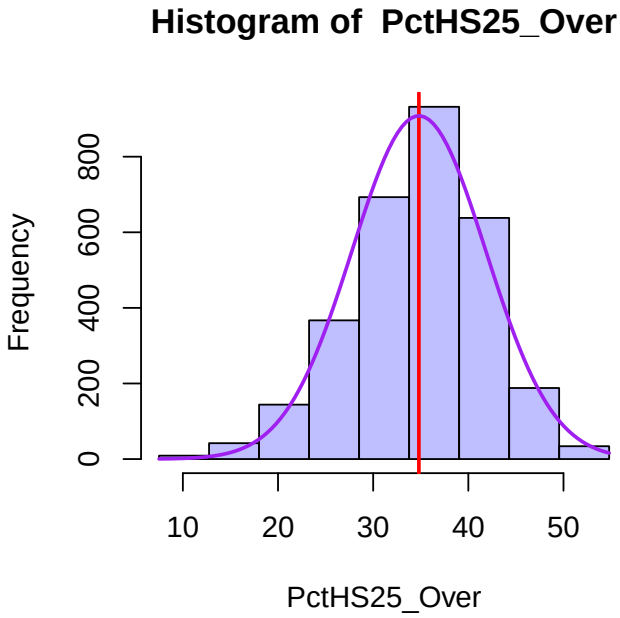

```
Cancer$logMedIncome <- log(medIncome)
```

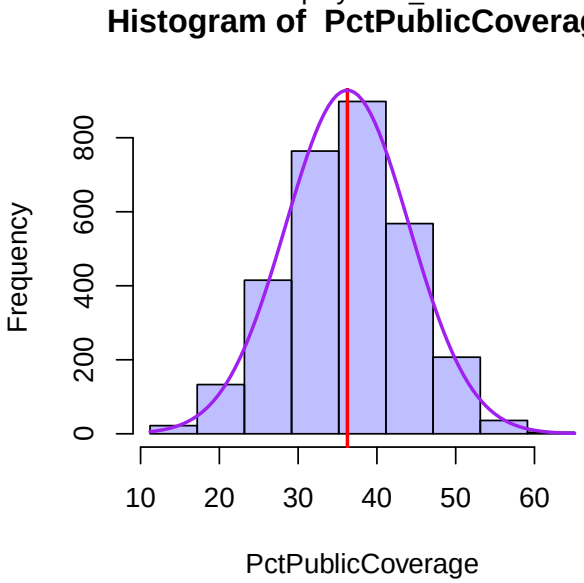
The rest look like clean, valid, approximately normally-distributed variables. There are no obvious transformations to apply.

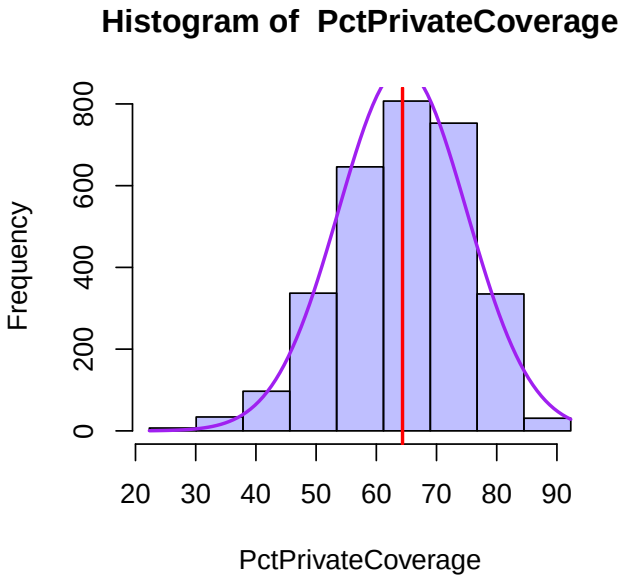


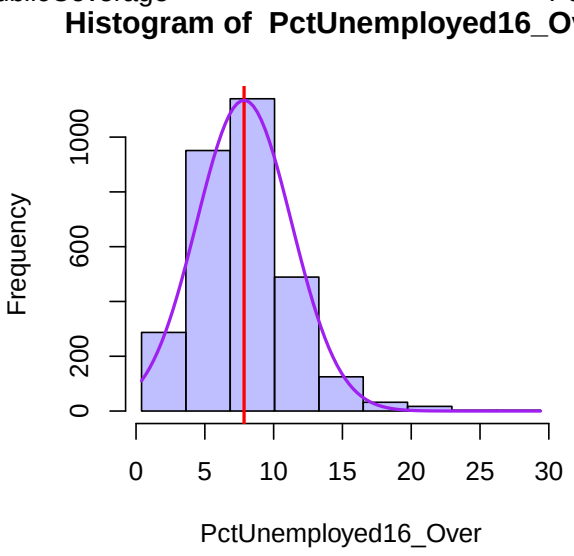



Histogram of PctEmployed16_Over
Frequency
0
200
400
600
800
20
30
40
50
60
70
80
PctEmployed16_Over


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
PctPublicCoverage


Histogram of PctPrivateCoverage
Frequency
0
200
400
600
800
20
30
40
50
60
70
80
90
PctPrivateCoverage


Histogram of PctUnemployed16_Over
Frequency
0
200
600
1000
0
5
10
15
20
25
30
PctUnemployed16_Over

Correlated Variables

The numeric variables were taken. The correlation with each numeric variable was calculated. Some of these variables had `NA`s, so those will get removed.

```
# 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 anomalous data, 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.

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

# add the rest of the cleaned variables
corPctSomeCol18_24 <- cor(PctSomeCol18_24[cleanPctSomeCol18_24],
                          deathRate[cleanPctSomeCol18_24])
correlations <- c(correlations, corPctSomeCol18_24)
names(correlations)[length(correlations)] <- "PctSomeCol18_24"

corAvgHouseholdSize <- cor(AvgHouseholdSize[cleanAvgHouseholdSize],
                           deathRate[cleanAvgHouseholdSize])
correlations <- c(correlations, corAvgHouseholdSize)
names(correlations)[length(correlations)] <- "cleanAvgHouseholdSize"

corMedianAge <- cor(MedianAge[cleanMedianAge],
                    deathRate[cleanMedianAge])
correlations <- c(correlations, corMedianAge)
names(correlations)[length(correlations)] <- "cleanMedianAge"
```

```
correlations
```

```
##                     X           avgAnnCount             medIncome
##           0.051913500          -0.143531620          -0.428614927
##             popEst2015        povertyPercent             MedianAge
##          -0.120073096           0.429388980           0.004375077
##         MedianAgeMale       MedianAgeFemale      AvgHouseholdSize
##          -0.021929429           0.012048386          -0.036905314
##        PercentMarried          PctNoHS18_24            PctHS18_24
##          -0.266820464           0.088462610           0.261975940
##       PctBachDeg18_24          PctHS25_Over     PctBachDeg25_Over
##          -0.287817410           0.404589076          -0.485477318
##  PctUnemployed16_Over    PctPrivateCoverage    PctEmpPrivCoverage
##           0.378412442          -0.386065507          -0.267399428
##     PctPublicCoverage              PctWhite              PctBlack
##           0.404571656          -0.177399980           0.257023560
##              PctAsian          PctOtherRace  PctMarriedHouseholds
##          -0.186331105          -0.189893571          -0.293325341
##            BirthRate             deathRate          logMedIncome
##          -0.087406970           1.000000000          -0.452277367
##    PctEmployed16_Over       PctSomeCol18_24 cleanAvgHouseholdSize
##          -0.412045764          -0.188687667          -0.034641021
##        cleanMedianAge
##          -0.004288054
```

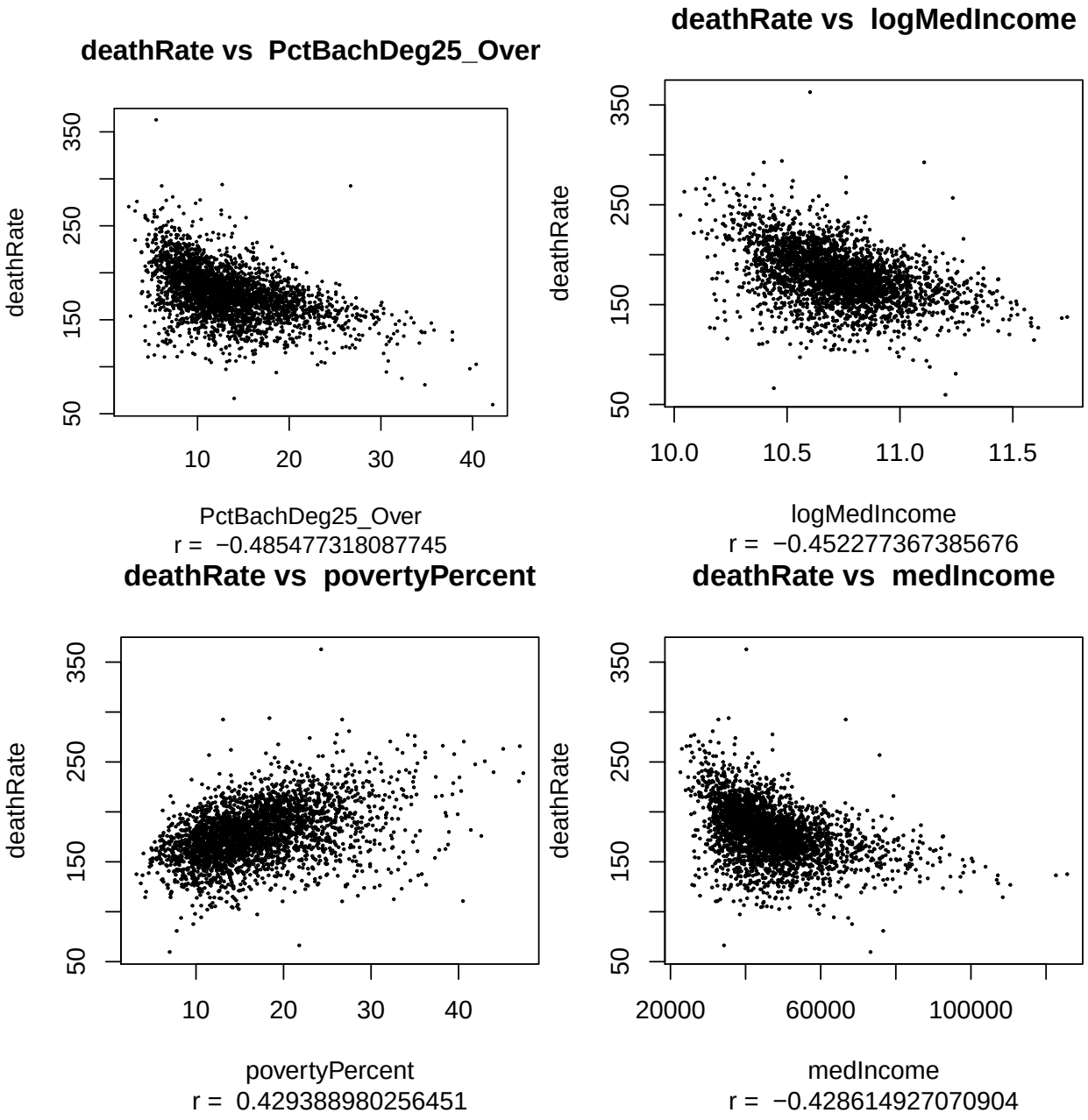
Now we can determine the correlations that are significant. We'll sort these by descending order of absolute value.

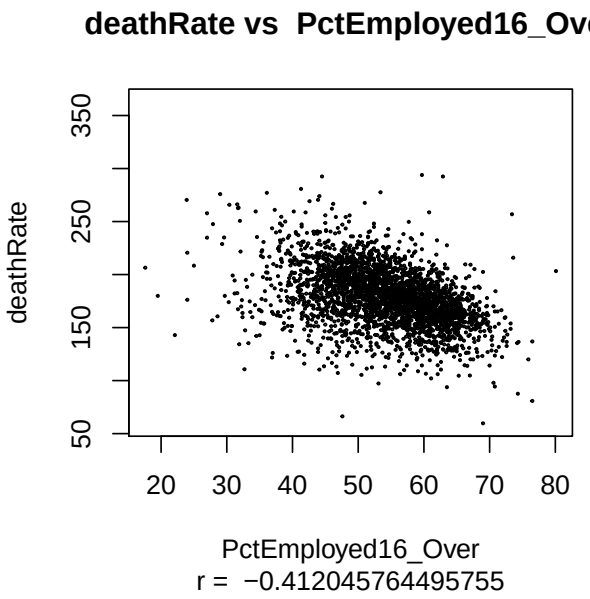
```
# sort them
correlations <- correlations[order(abs(correlations), decreasing=TRUE)]
# remove the cor of deathRate with itself, which is 1, and always the first element after sorting
correlations <- correlations[2:length(correlations)]
correlations <- correlations[abs(correlations) >= 0.3]
correlations
```

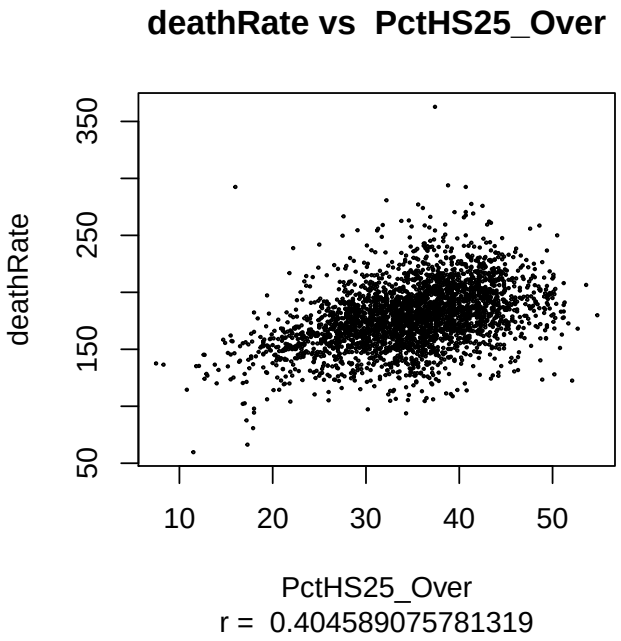
```
##    PctBachDeg25_Over         logMedIncome       povertyPercent
##           -0.4854773           -0.4522774            0.4293890
##            medIncome   PctEmployed16_Over         PctHS25_Over
##           -0.4286149           -0.4120458            0.4045891
##    PctPublicCoverage   PctPrivateCoverage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

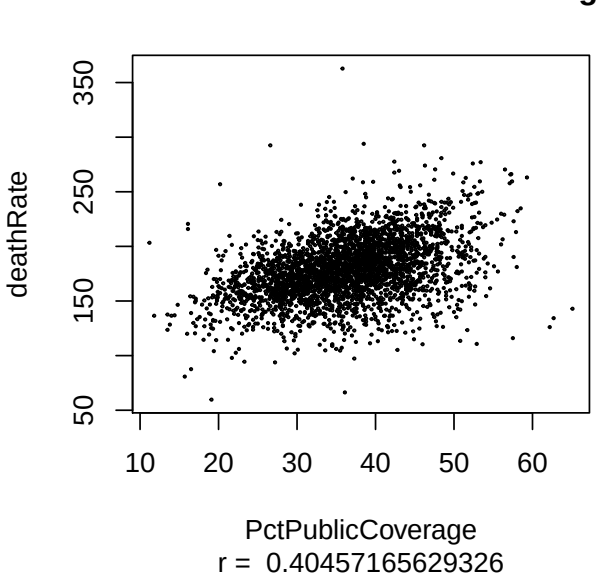
We will consider correlations of `0.3` or stronger a significant association. This includes 9 of the variables, one of which is our transformed log(medianIncome). This actually had stronger correlation with `deathRate` than `medIncome`.

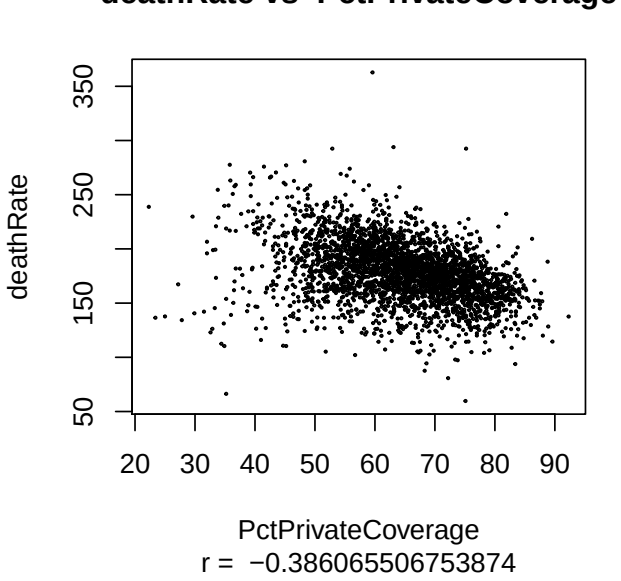
Plot Bivariate Associations

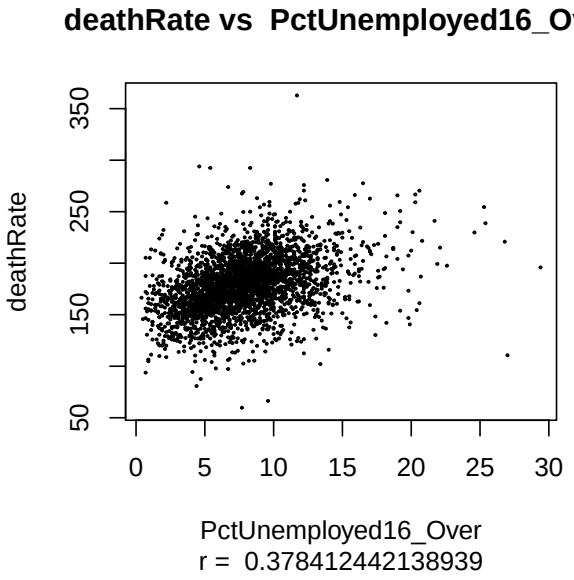



deathRate vs PctEmployed16_Over
deathRate
50
150
250
350
20
30
40
50
60
70
80
PctEmployed16_Over
r = −0.412045764495755


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



These variables have a positive correlation, meaning counties in this set which have higher values are more likely to have a higher `deathRate`: `povertyPercent`, `PctHS25_Over`, `PctPublicCoverage`, `PctUnemployed16_Over`. The rest of the variables are associated with lower `deathRate`: `PctBachDeg25_Over`, `logMedIncome`, `medIncome`, `PctEmployed16_Over`, `PctPrivateCoverage`.

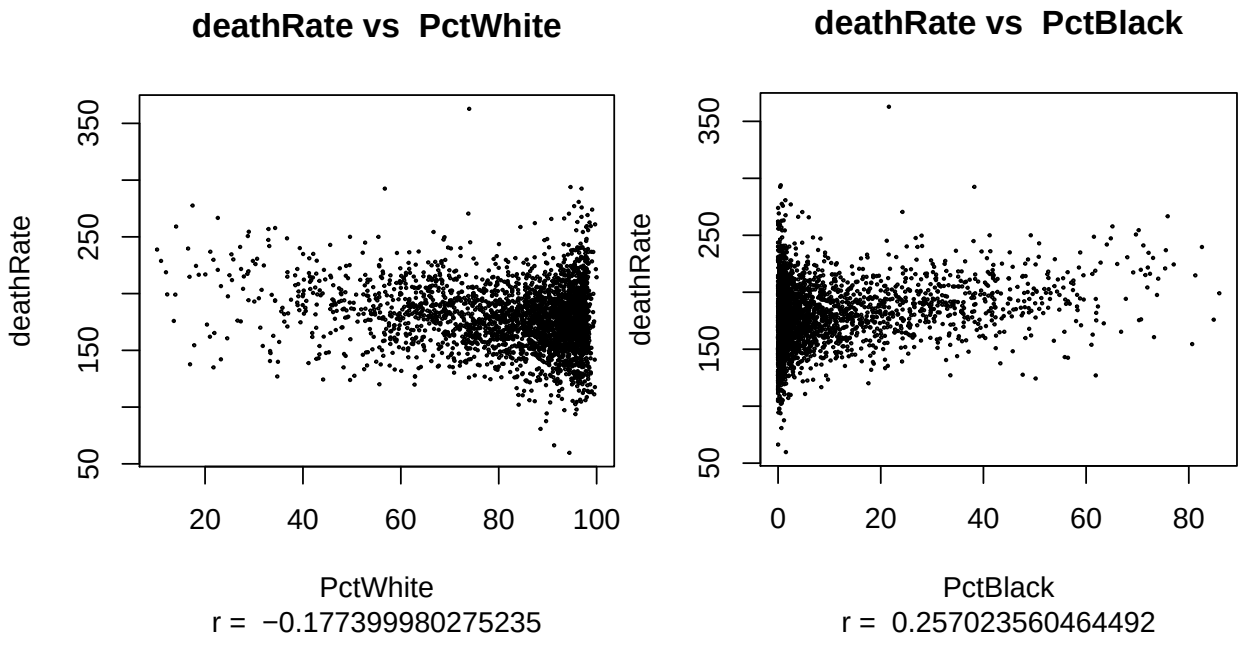
Analysis of Secondary Effects

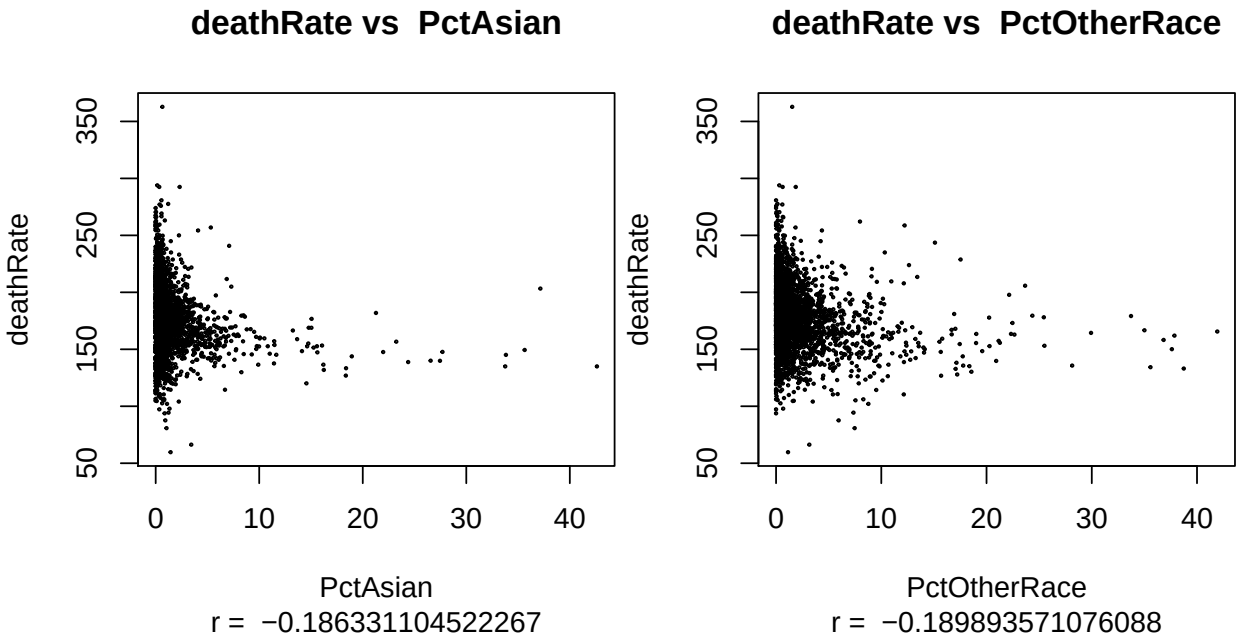
Confounding Variables

As we analyzed the dataset, we observed some interesting correlations between some of the variables. At first glance, these correlations suggest that there are potentially causal relationships which are not in alignment with our general understanding of how cancer operates and its effects it has on us. Deeper analysis into the dataset however revealed these relationship are results of confounding associations these variables have with other variables that are more directly contributing to the correlations with `deathRate` we are observing.

Racial Groups

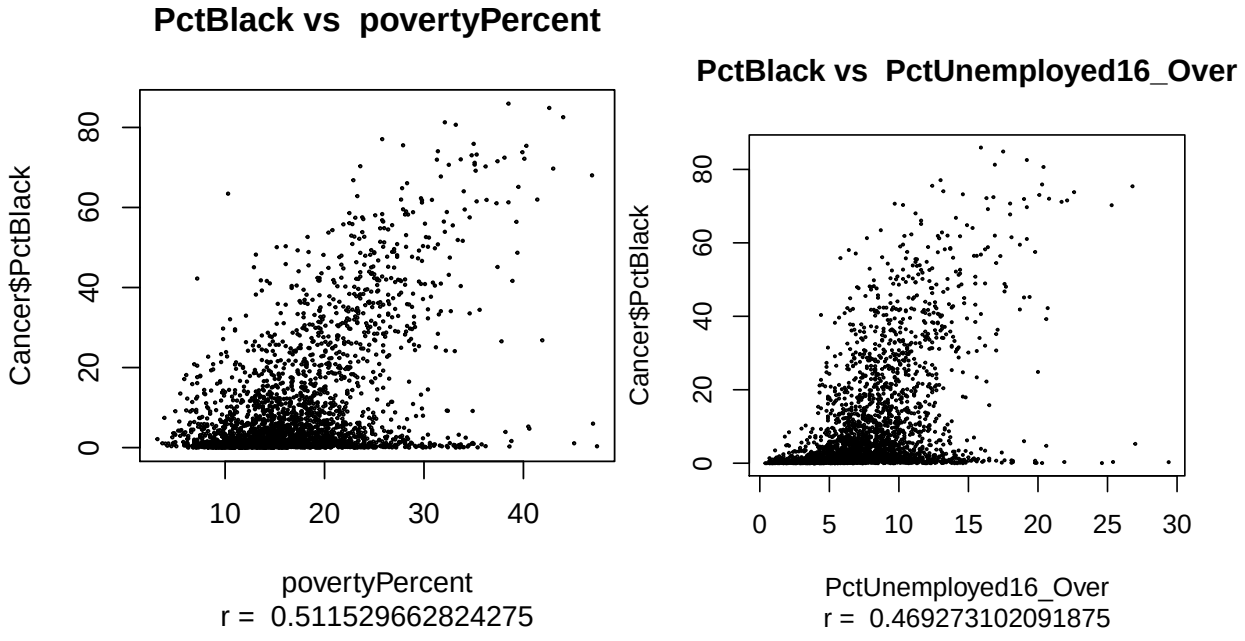
We identified certain racial groups are exhibiting higher cancer death rate than others, namely black people (`PctBlack`).



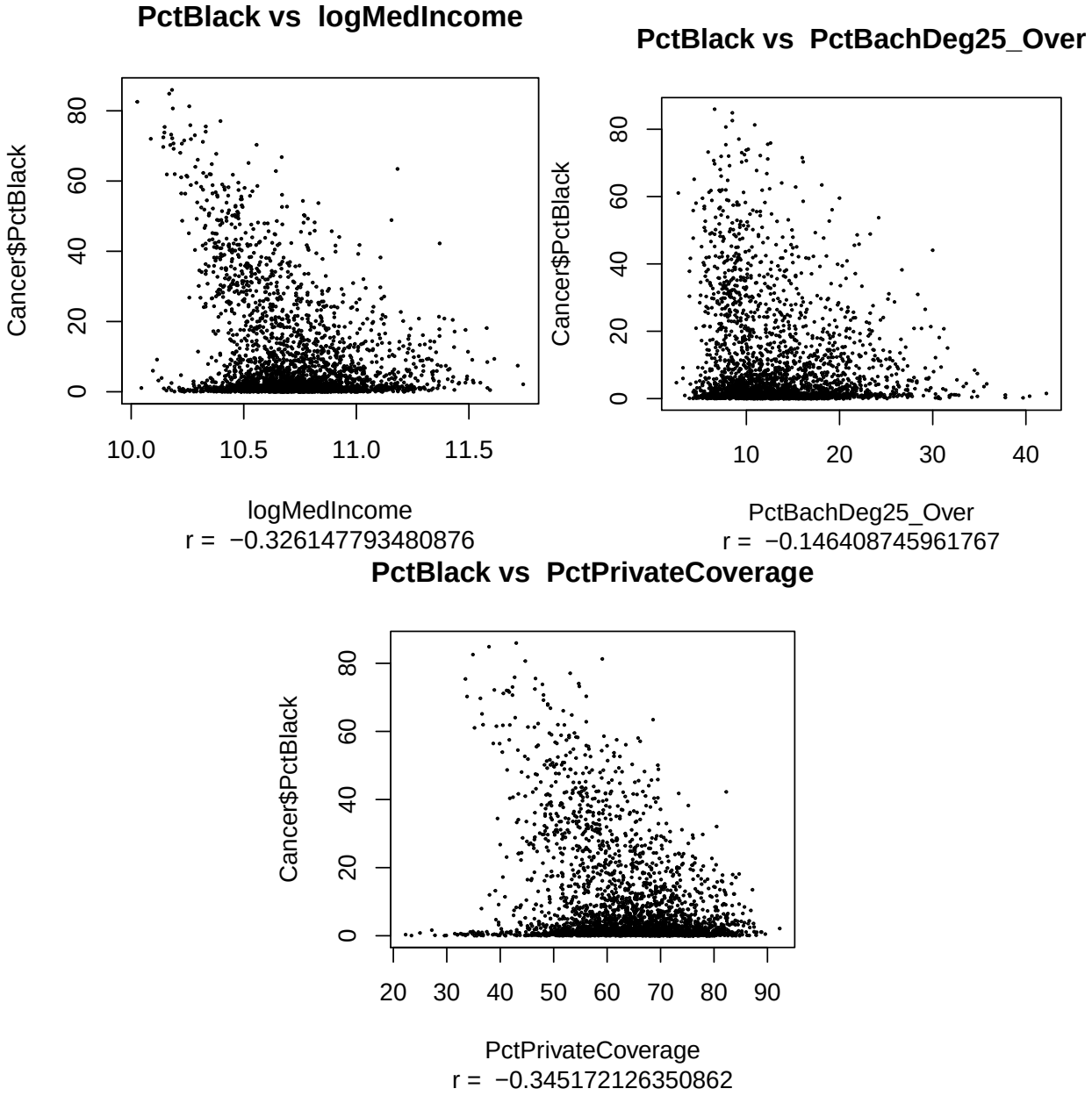


While the other groups are showing negative correlations with the death rate, `PctBlack` is showing a positive correlation of 0.257. This makes it seem as though black people are somehow more susceptible to cancer.

Looking further, we find `PctBlack` has strong positive correlations with `povertyPercent` and `PctUnemployed16_Over`, which are among the variables we have identified to have the strongest positive correlations with `deathRate`.



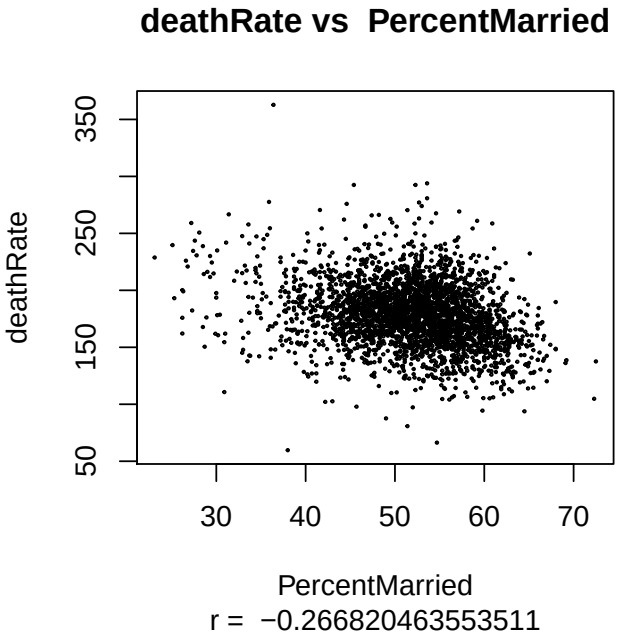
We also see negative correlations between `PctBlack` and the variables we have identified to have strong negative correlations with `deathRate` such as `logMedIncome`, `PctBachDeg25_Over` and `PctPrivateCoverage`.

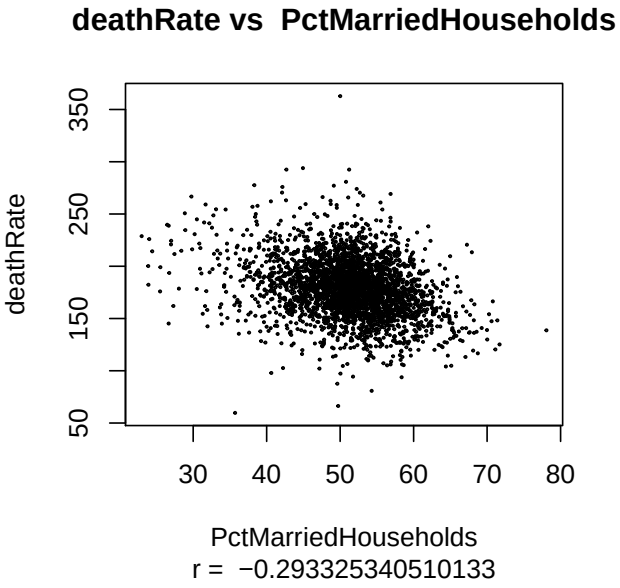


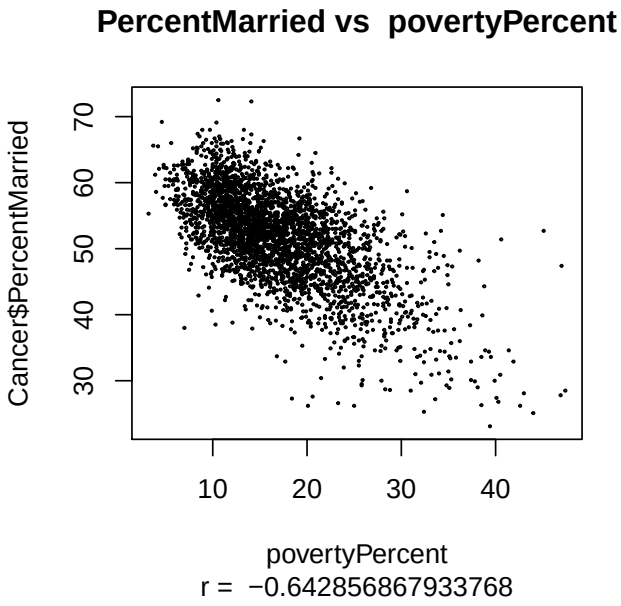
Therefore we believe it is not their race that is increasing the cancer death rate for black people but rather the group's relatively poor economic standing that is contributing to the elevated `deathRate`.

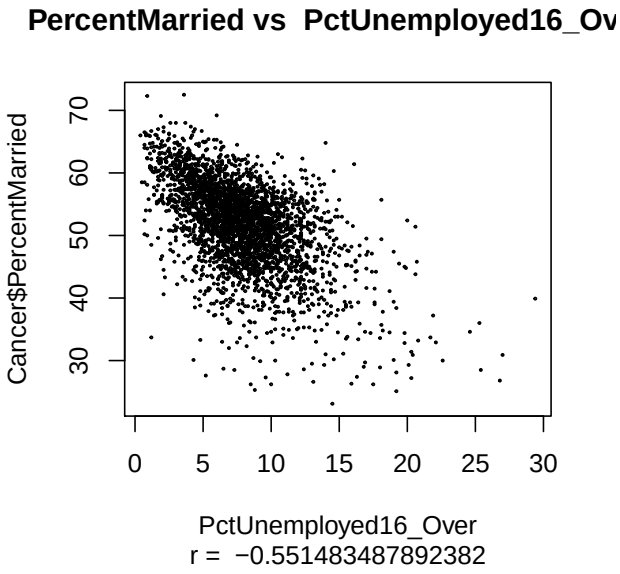
Marital-Status

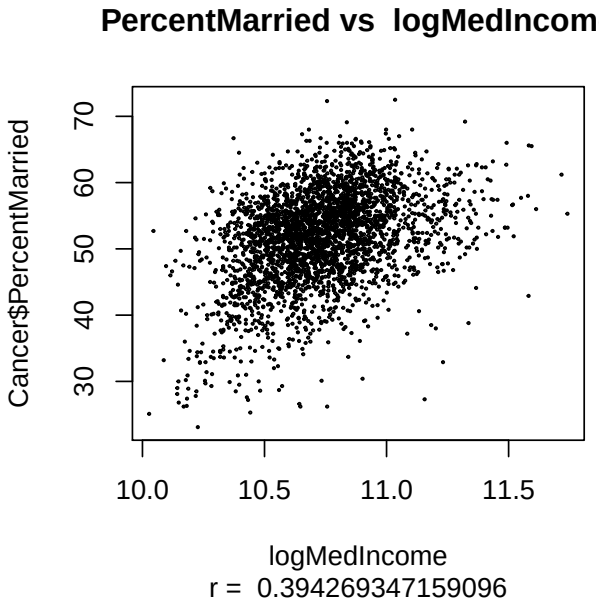
We are also seeing negative correlations between marital status-related variables `PercentMarried` and `PctMarriedHouseholds` and `deathRate`. Marriage somehow decreases the chance of dying from cancer. Similarly to racial groups, however, after looking at the correlations between the marital-status variables and the same set of variables strongly correlated with `deathRate`, we see married people are considerably less likely to be in poverty. This explains the negative correlation observed between the marital status-related variables and `deathRate` rather than people's marital statuses themselves somehow magically reducing the cancer death rate.

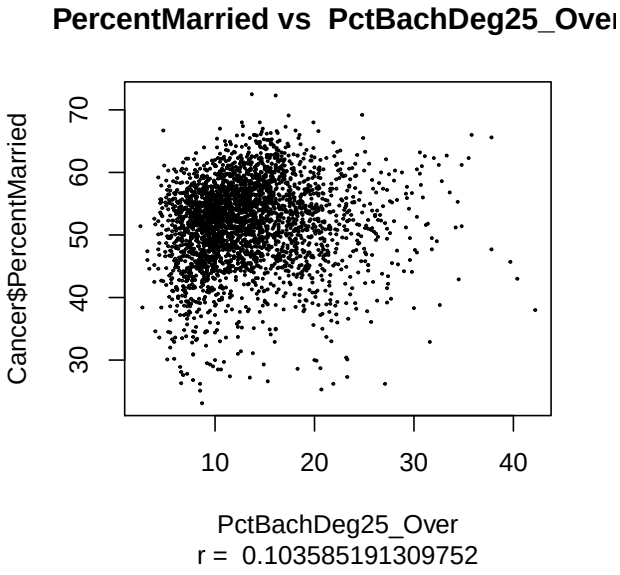

deathRate vs PercentMarried
deathRate
50
150
250
350
30
40
50
60
70
PercentMarried
r = −0.266820463553511

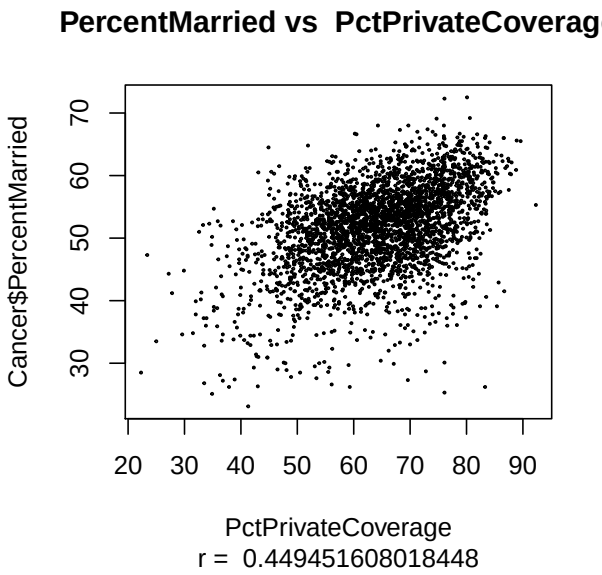

deathRate vs PctMarriedHouseholds
deathRate
50
150
250
350
30
40
50
60
70
80
PctMarriedHouseholds
r = −0.293325340510133

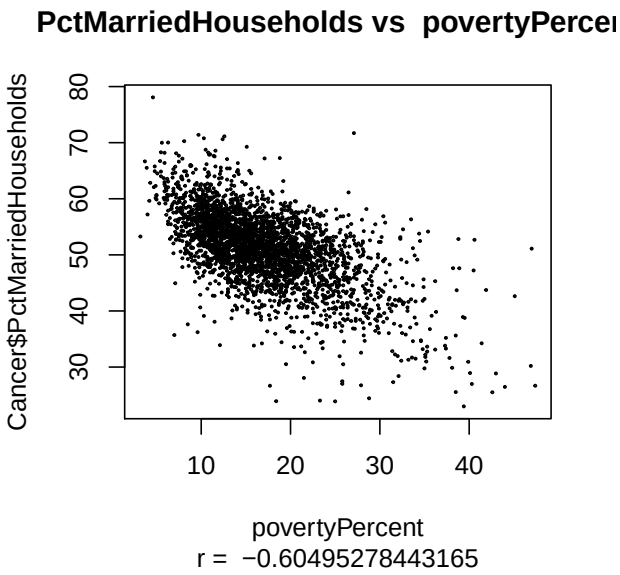

PercentMarried vs povertyPercent
Cancer$PercentMarried
30
40
50
60
70
10
20
30
40
povertyPercent
r = −0.642856867933768

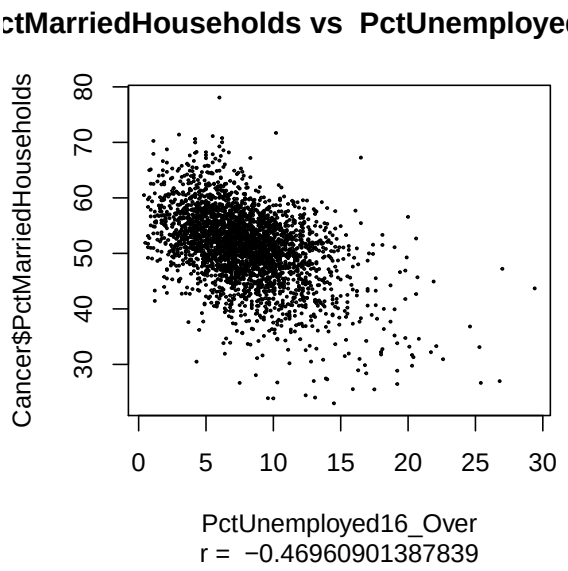

PercentMarried vs PctUnemployed16_Ov
Cancer$PercentMarried
30
40
50
60
70
0
5
10
15
20
25
30
PctUnemployed16_Over
r = −0.551483487892382

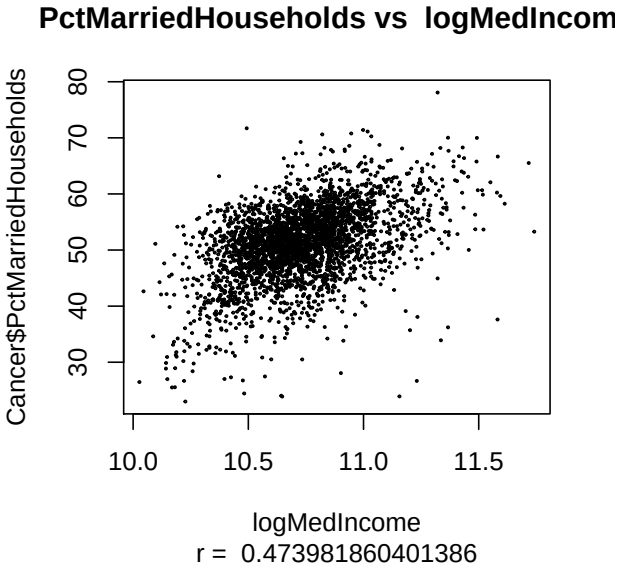

PercentMarried vs logMedIncome
Cancer$PercentMarried
30
40
50
60
70
10.0
10.5
11.0
11.5
logMedIncome
r = 0.394269347159096

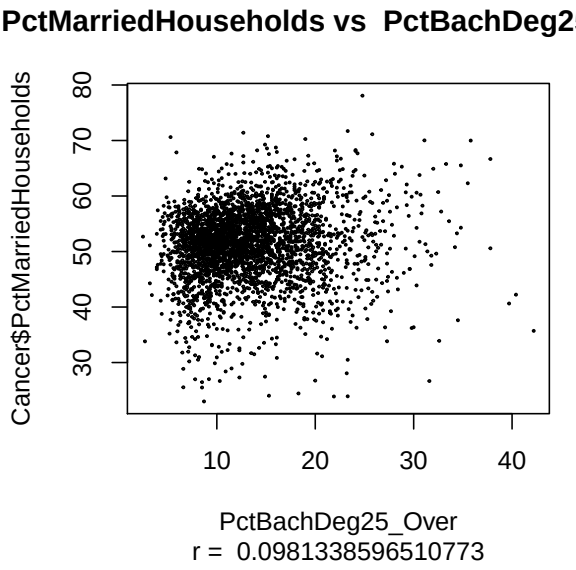

PercentMarried vs PctBachDeg25_Over
Cancer$PercentMarried
30
40
50
60
70
10
20
30
40
PctBachDeg25_Over
r = 0.103585191309752

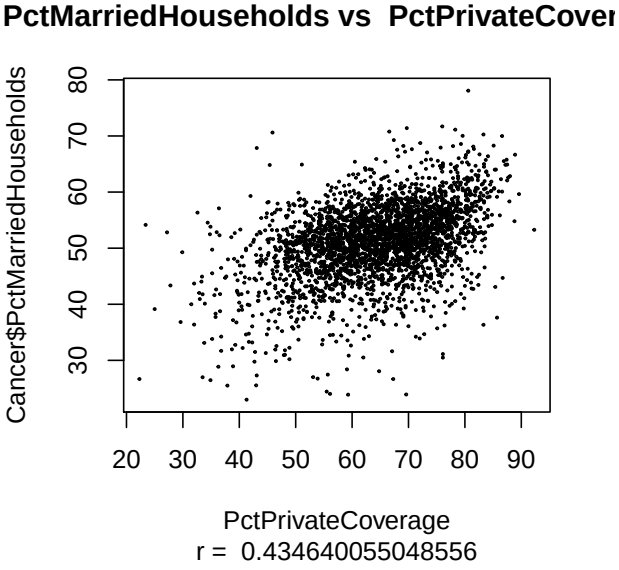

PercentMarried vs PctPrivateCoverage
Cancer$PercentMarried
30
40
50
60
70
20
30
40
50
60
70
80
90
PctPrivateCoverage
r = 0.449451608018448


PctMarriedHouseholds vs povertyPercen
Cancer$PctMarriedHouseholds
30
40
50
60
70
80
10
20
30
40
povertyPercent
r = −0.60495278443165


ctMarriedHouseholds vs PctUnemployed16
Cancer$PctMarriedHouseholds
PctUnemployed16_Over
r = −0.46960901387839


PctMarriedHouseholds vs logMedIncom
Cancer$PctMarriedHouseholds
logMedIncome
r = 0.473981860401386


PctMarriedHouseholds vs PctBachDeg25_(
Cancer$PctMarriedHouseholds
PctBachDeg25_Over
r = 0.0981338596510773


PctMarriedHouseholds vs PctPrivateCover
Cancer$PctMarriedHouseholds
PctPrivateCoverage
r = 0.434640055048556

Employment, Education and Wealth

The correlations can be summarized as such: employment, education, and wealth are linked to lower cancer mortality. We can speculate about the underlying causality between some of the variables. For example, suppose the correlation with `PctBachDeg25_Over` is because educated people are aware of cancer causes and choose to avoid those causes. Education also enables people to make more money. `PctBachDeg25_Over` would therefore confound the association between `medIncome` and `deathRate`. However, suppose it's actually income that lowers cancer mortality because people can afford better treatment. In that case, its `medIncome` that confounds the association of `PctBachDeg25_Over` with `deathRate` because the wealthy are more likely to afford tuition for school. A similar statement can be made about the insurance variables.

Conclusion

Of the 30 variables included in the Cancer Mortality dataset, we are observing strongest correlations between `deathRate` and the below 9 variables:

```
## [1] "PctBachDeg25_Over"    "logMedIncome"         "povertyPercent"
## [4] "medIncome"            "PctEmployed16_Over"   "PctHS25_Over"
## [7] "PctPublicCoverage"    "PctPrivateCoverage"   "PctUnemployed16_Over"
```

These variables fall under the categories Insurance coverage, Income Status and Education while variables that are categorized under Region, Population, Birthrate, Race and Marital Status are not showing as strong of relationships with `deathRate`.

The following variables have a positive correlation, meaning counties in this set which have higher values are more likely to have a higher `deathRate`: `povertyPercent, PctHS25_Over, PctPublicCoverage, PctUnemployed16_Over`. The rest of the variables are associated with lower `deathRate`: `PctBachDeg25_Over, logMedIncome, medIncome, PctEmployed16_Over, PctPrivateCoverage`.

From this, we are able to conclude that for the US counties included in the dataset, people's economic standing is the deciding factor for their cancer mortality rate rather than geographical factors such as region and population. Other factors such as race and marital status also appear to be directly correlated with `deathRate`. However, we found that these variables have strong correlations with Income Status and Insurance Coverage variables which lead us to suspect it is not the racial demographics or marital statuses of the residents that are directly influencing `deathRate` but rather their economic implications that are affecting the cancer death rate in these counties.