Cancer_reg_EDA

PCA group

2022-07-14

```
# load packages
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

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

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

```
library(ggplot2)
library(readr)
library(haven)
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --
```

```
## v tibble  3.1.7     v stringr 1.4.0
## v tidyr   1.2.0     v forcats 0.5.1
## v purrr   0.3.4
```

```
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(sandwich)
library(lmtest)
```

```
## Loading required package: zoo
```

```
##
## Attaching package: 'zoo'
```

```
## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
```

```
library(stargazer)
```

```
##
## Please cite as:
```

```
##  Hlavac, Marek (2022). stargazer: Well-Formatted Regression and Summary Statistics Tables.
```

```
##  R package version 5.2.3. https://CRAN.R-project.org/package=stargazer
```

```
library(Hmisc)
```

```
## Loading required package: lattice
```

```
## Loading required package: survival
```

```
## Loading required package: Formula
```

```
##
## Attaching package: 'Hmisc'
```

```
## The following objects are masked from 'package:dplyr':
##
##     src, summarize
```

```
## The following objects are masked from 'package:base':
##
##     format.pval, units
```

```
library(funModeling)
```

```
## funModeling v.1.9.4 :)
## Examples and tutorials at livebook.datascienceheroes.com
##  / Now in Spanish: librovivodecienciadedatos.ai
```

```
library(olsrr)
```

```
##
## Attaching package: 'olsrr'
```

```
## The following object is masked from 'package:datasets':
##
##     rivers
```

```
cancer <- read_csv("cancer_reg.csv")
```

```
## Rows: 3047 Columns: 33
```

```
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr  (2): binnedinc, geography
## dbl (31): avganncount, avgdeathsperyear, target_deathrate, incidencerate, me...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

Correlation table:

```
correlation_table(data = cancer, target = "target_deathrate")
```

```
##                   Variable target_deathrate
## 1         target_deathrate            1.00
## 2   pctpubliccoveragealone            0.39
## 3            incidencerate            0.38
## 4             pcths25_over            0.38
## 5           povertypercent            0.37
## 6        pctpubliccoverage            0.35
## 7     pctunemployed16_over            0.32
## 8                 pctblack            0.26
```

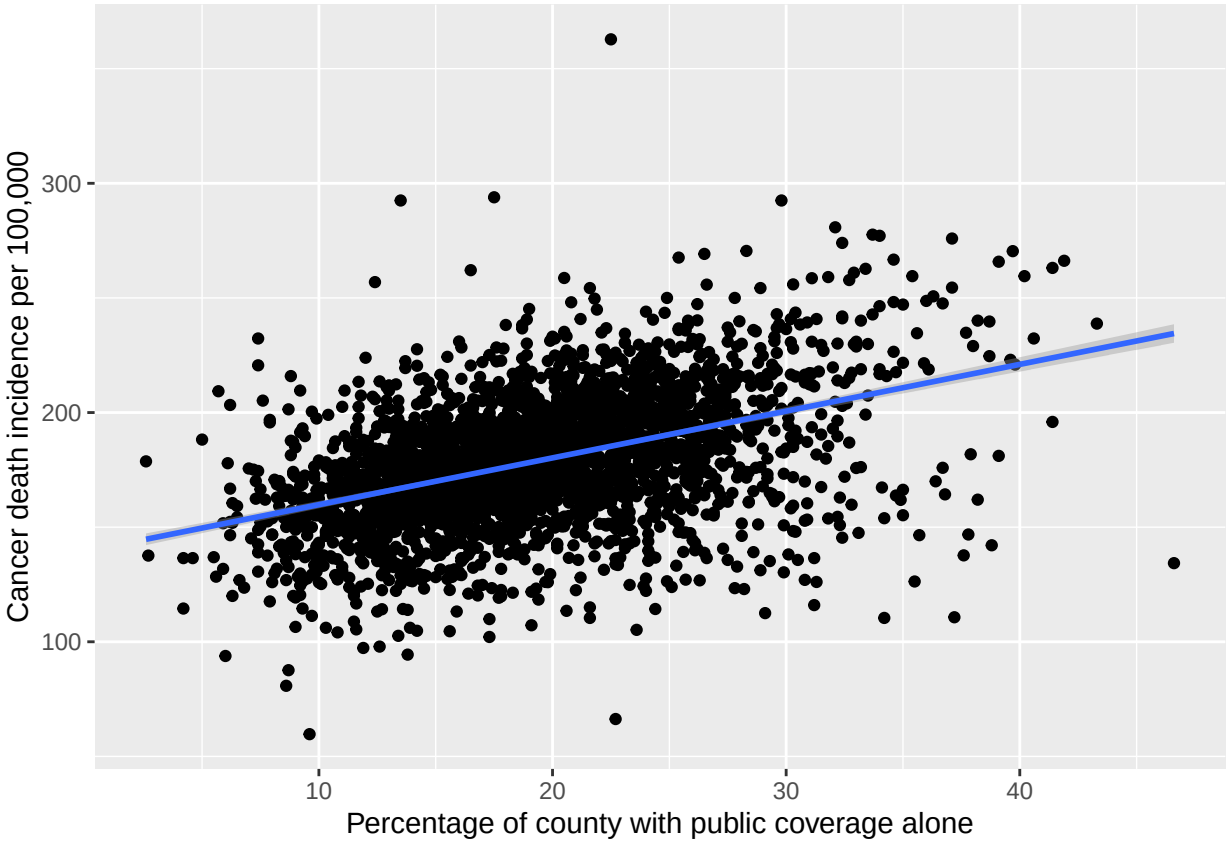
```
## 9               pcths18_24            0.25
## 10            pctnohs18_24            0.08
## 11         medianagefemale            0.02
## 12                medianage           -0.01
## 13             studypercap           -0.03
## 14           medianagemale           -0.03
## 15                birthrate           -0.05
## 16        avgdeathsperyear           -0.10
## 17              popest2015           -0.11
## 18             avganncount           -0.13
## 19         pctsomecol18_24           -0.16
## 20                pctwhite           -0.16
## 21                pctasian           -0.20
## 22            pctotherrace           -0.21
## 23          percentmarried           -0.23
## 24      pctempprivcoverage           -0.23
## 25    pctmarriedhouseholds           -0.29
## 26         pctbachdeg18_24           -0.30
## 27 pctprivatecoveragealone           -0.32
## 28      pctprivatecoverage           -0.34
## 29      pctemployed16_over           -0.37
## 30                medincome           -0.38
## 31       pctbachdeg25_over           -0.44
```

Plot positive correlations:

Positive correlations: pctpubliccoveragealone, incidencerate, pcths25_over, povertypercent, pctpubliccoverage, pctunemployed16_over

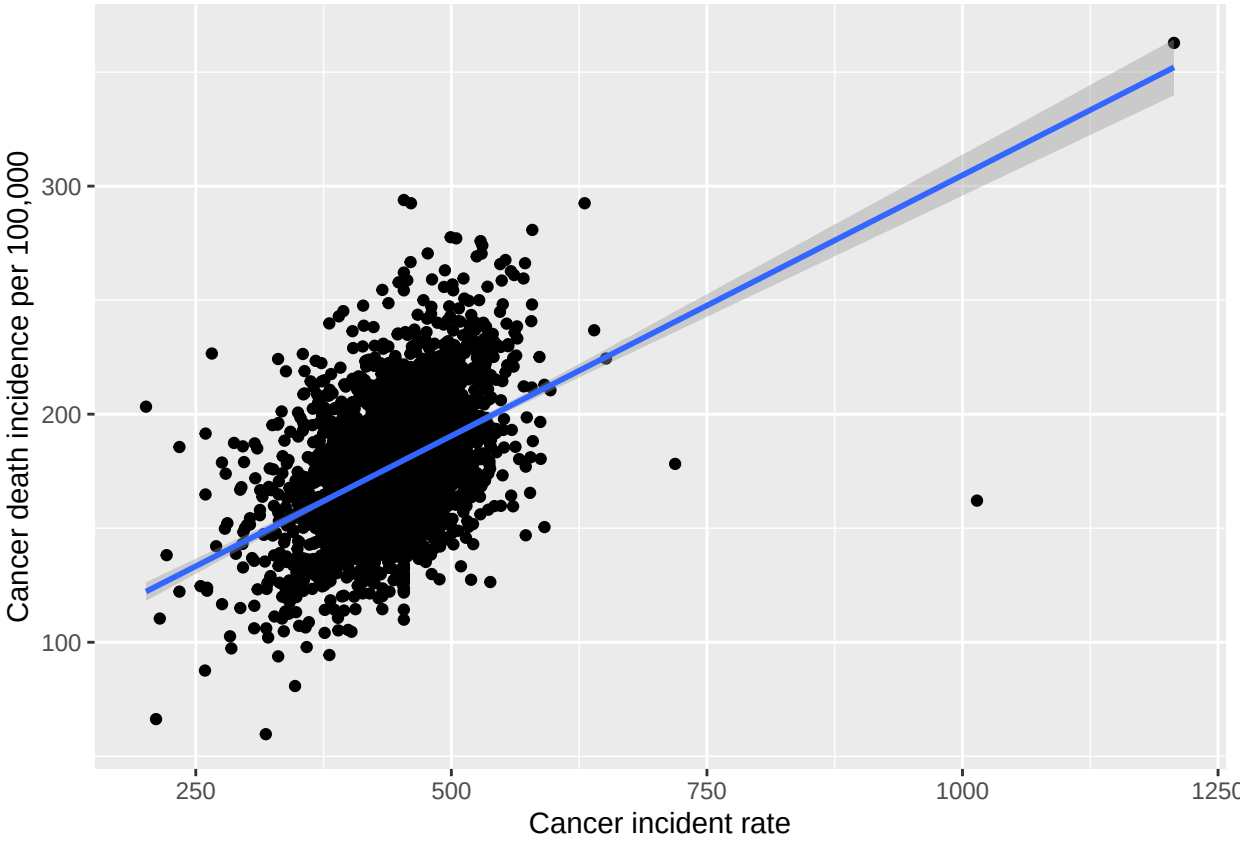
```
ggplot(data = cancer, aes(x = pctpubliccoveragealone, y = target_deathrate))+
  geom_point()+
  geom_smooth(method = lm)+labs(x = "Percentage of county with public coverage alone", y = "Cancer deatl
```

```
## `geom_smooth()` using formula 'y ~ x'
```



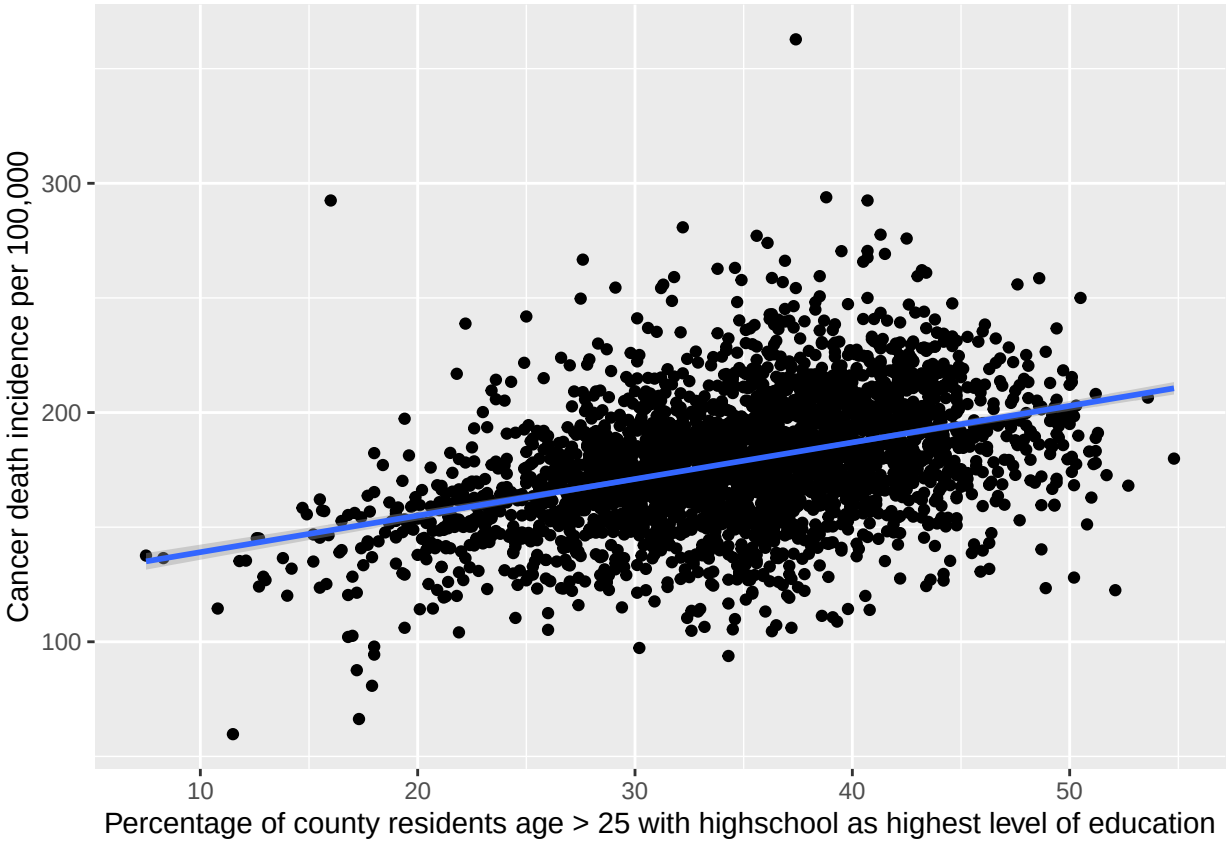

```
ggplot(data = cancer, aes(x = incidencerate, y = target_deathrate))+
  geom_point()+
  geom_smooth(method = lm)+labs(x = "Cancer incident rate", y = "Cancer death incidence per 100,000")
```

```
## `geom_smooth()` using formula 'y ~ x'
```



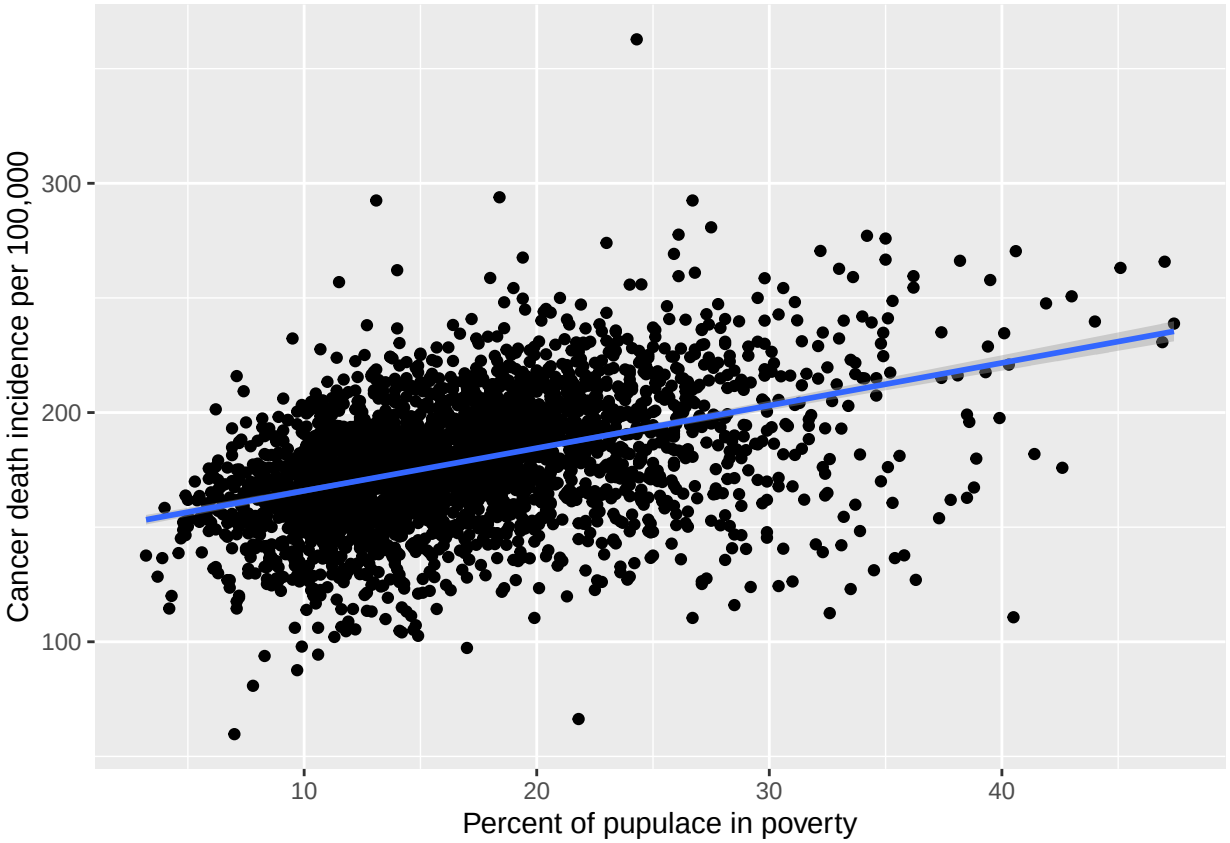

```
ggplot(data = cancer, aes(x = pcths25_over, y = target_deathrate))+
  geom_point()+
  geom_smooth(method = lm)+labs(x="Percentage of county residents age > 25 with highschool as highest l
```

```
## `geom_smooth()` using formula 'y ~ x'
```



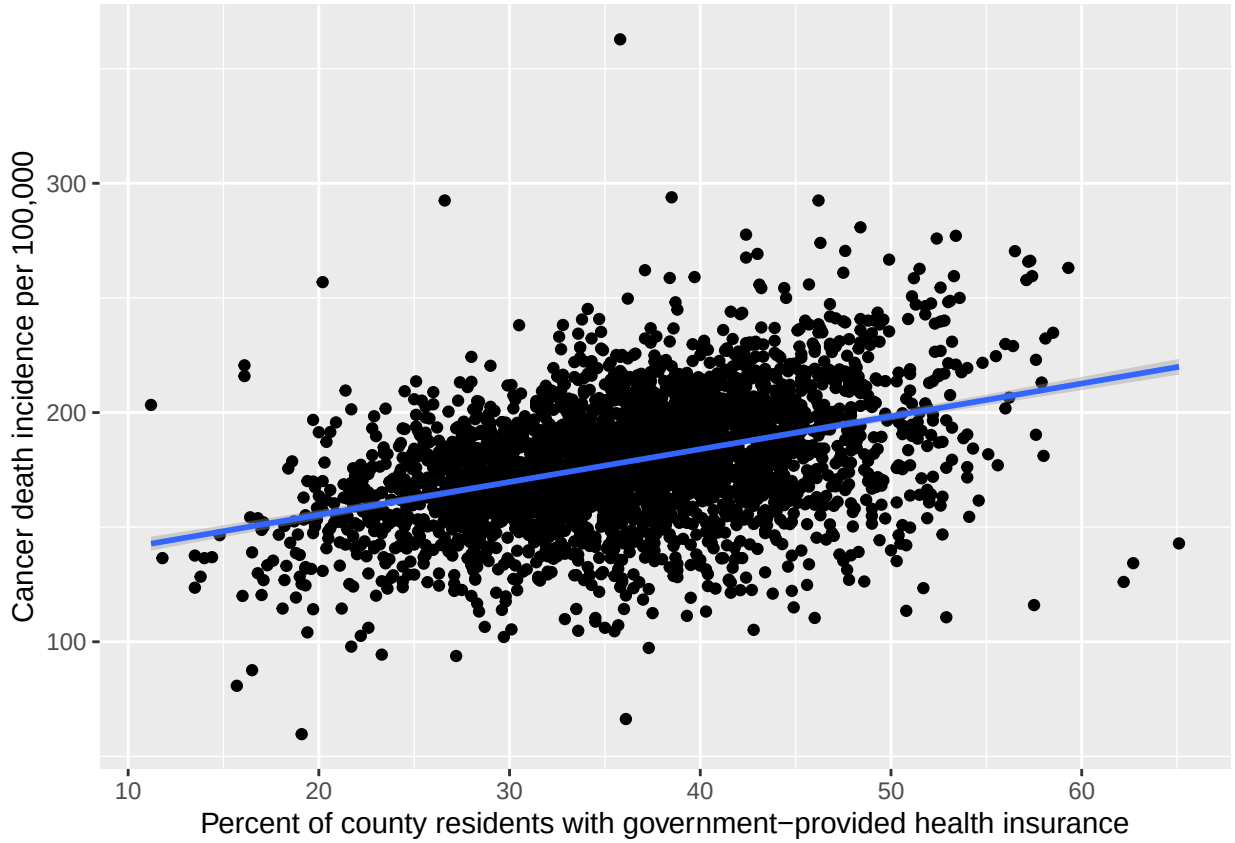

```
ggplot(data = cancer, aes(x = povertypercent, y = target_deathrate))+
  geom_point()+
  geom_smooth(method = lm)+
  labs(x="Percent of pupulace in poverty", y= "Cancer death incidence per 100,000")
```

```
## `geom_smooth()` using formula 'y ~ x'
```



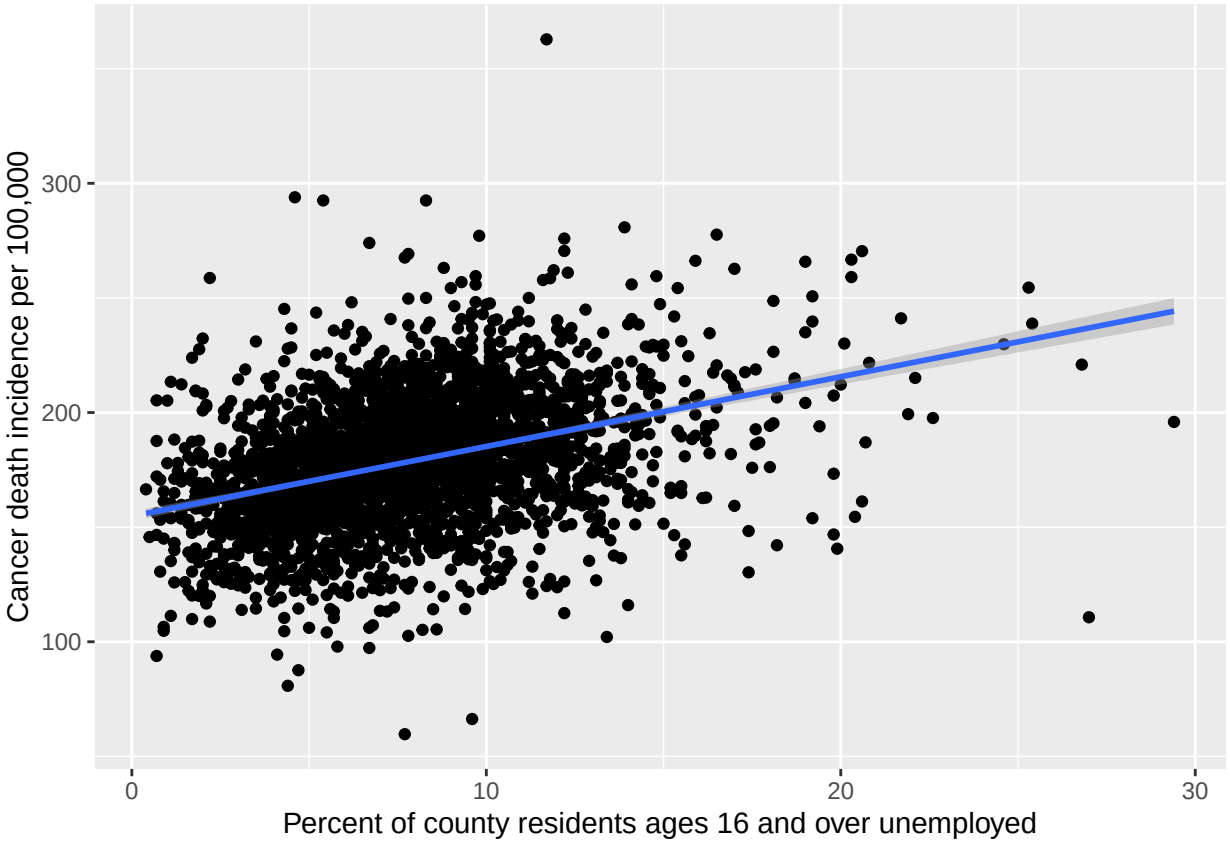

```
ggplot(data = cancer, aes(x = pctpubliccoverage, y = target_deathrate))+
  geom_point()+
  geom_smooth(method = lm)+
  labs(x="Percent of county residents with government-provided health insurance", y= "Cancer death inci
```

```
## `geom_smooth()` using formula 'y ~ x'
```




```
ggplot(data = cancer, aes(x = pctunemployed16_over, y = target_deathrate))+
  geom_point()+
  geom_smooth(method = lm)+
  labs(x="Percent of county residents ages 16 and over unemployed", y= "Cancer death incidence per 100,
```

```
## `geom_smooth()` using formula 'y ~ x'
```

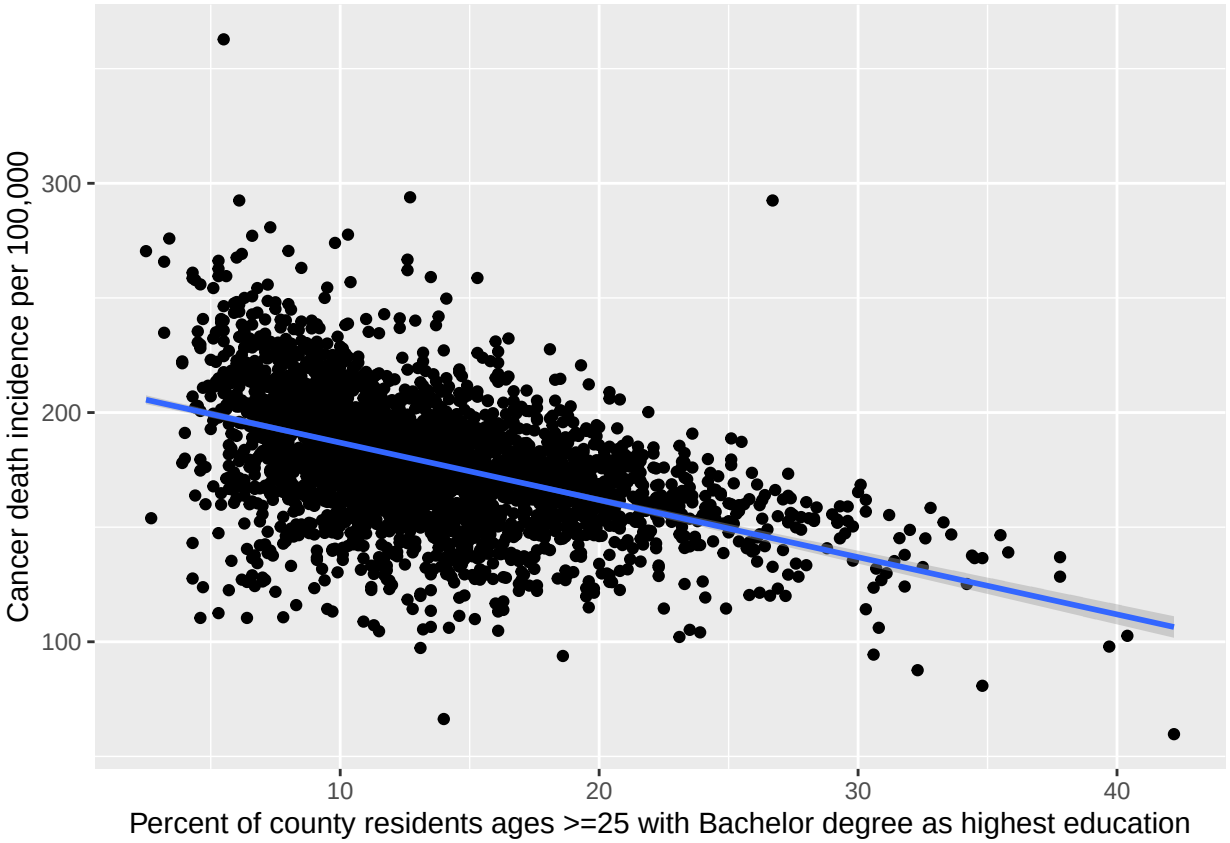


Plot negative correlations:

pctbachdeg25_over -.44 medincome -0.38 pctemployed16_over -0.37 pctprivatecoverage -0.34 pctprivatecoveragealone -0.32

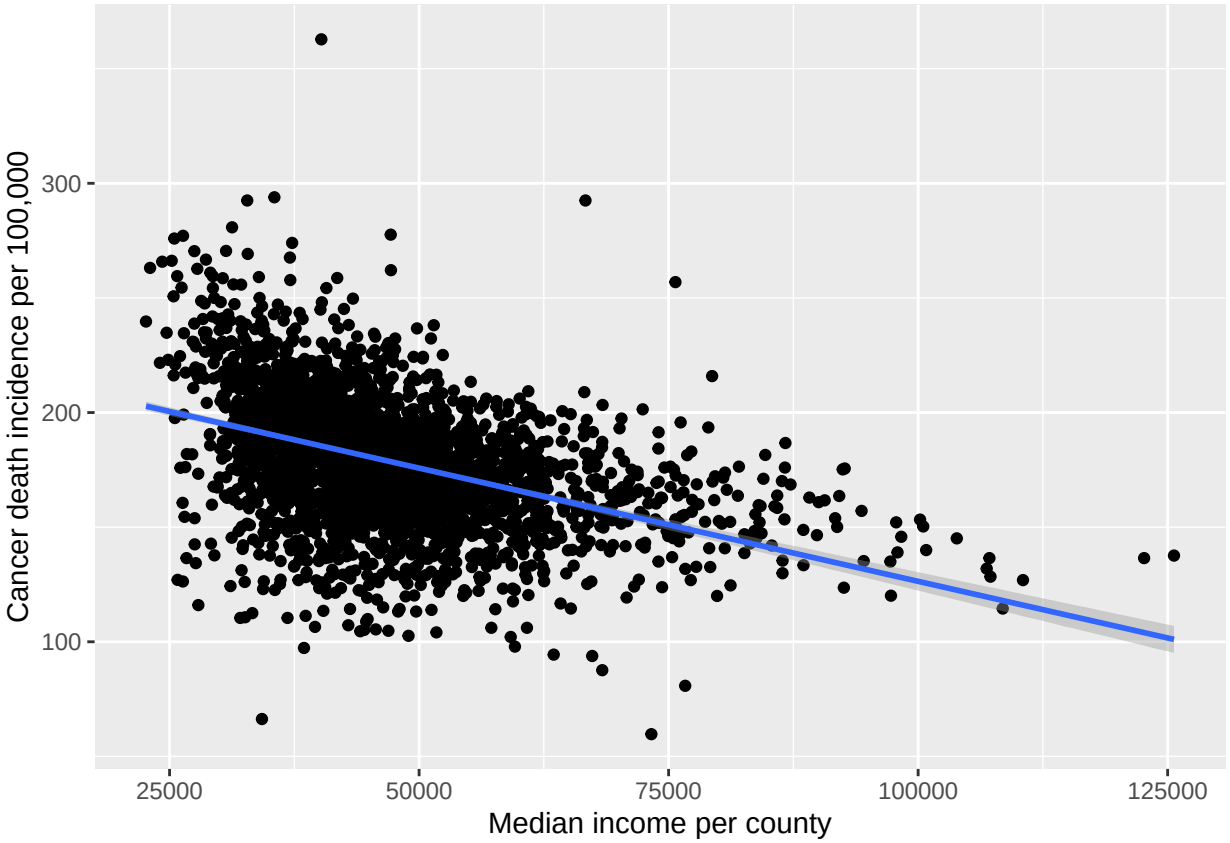
```
ggplot(data = cancer, aes(x = pctbachdeg25_over, y = target_deathrate))+
  geom_point()+
  geom_smooth(method = lm)+
  labs(x="Percent of county residents ages >=25 with Bachelor degree as highest education", y= "Cancer
```

```
## `geom_smooth()` using formula 'y ~ x'
```




```
ggplot(data = cancer, aes(x = medincome, y = target_deathrate))+
  geom_point()+
  geom_smooth(method = lm)+
  labs(x="Median income per county", y= "Cancer death incidence per 100,000")
```

```
## `geom_smooth()` using formula 'y ~ x'
```

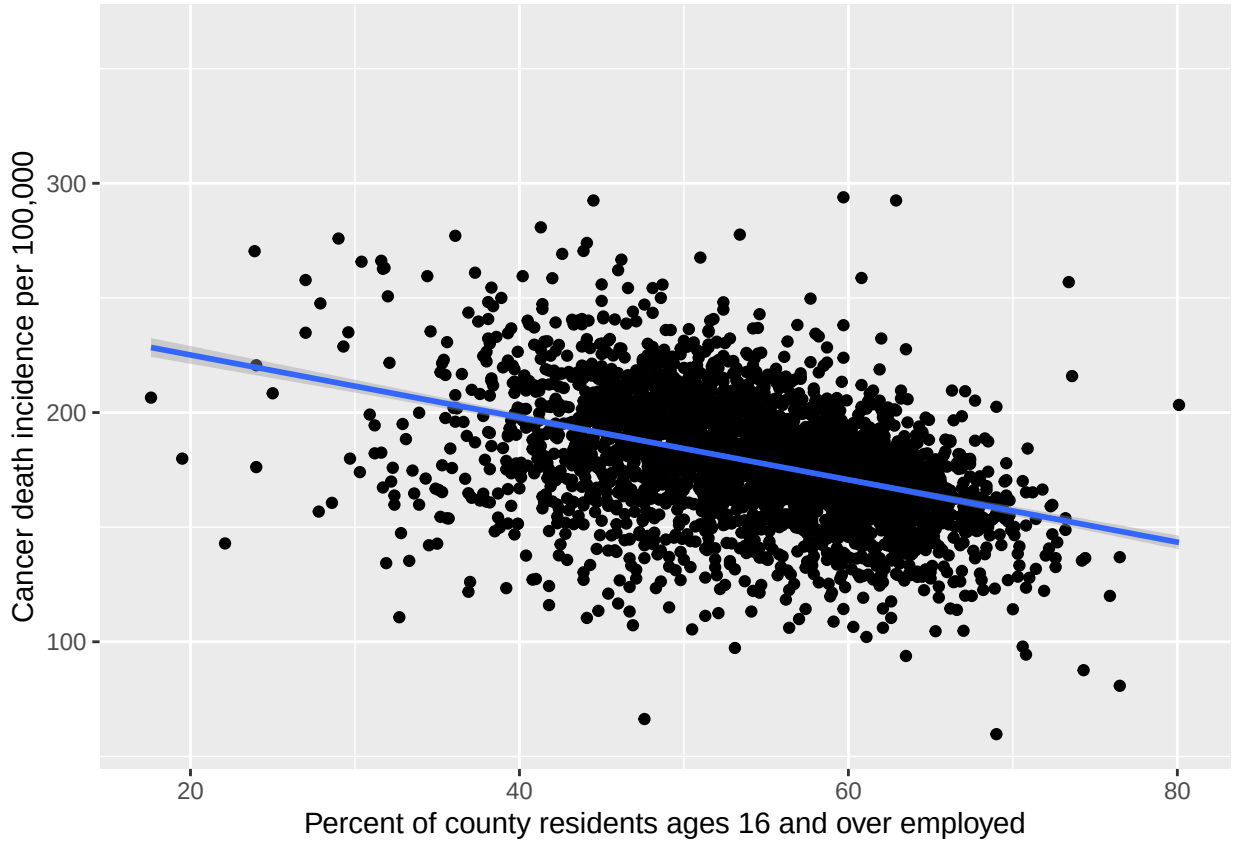



```
ggplot(data = cancer, aes(x = pctemployed16_over, y = target_deathrate))+
  geom_point()+
  geom_smooth(method = lm)+
  labs(x="Percent of county residents ages 16 and over employed", y= "Cancer death incidence per 100,000
```

```
## `geom_smooth()` using formula 'y ~ x'
```

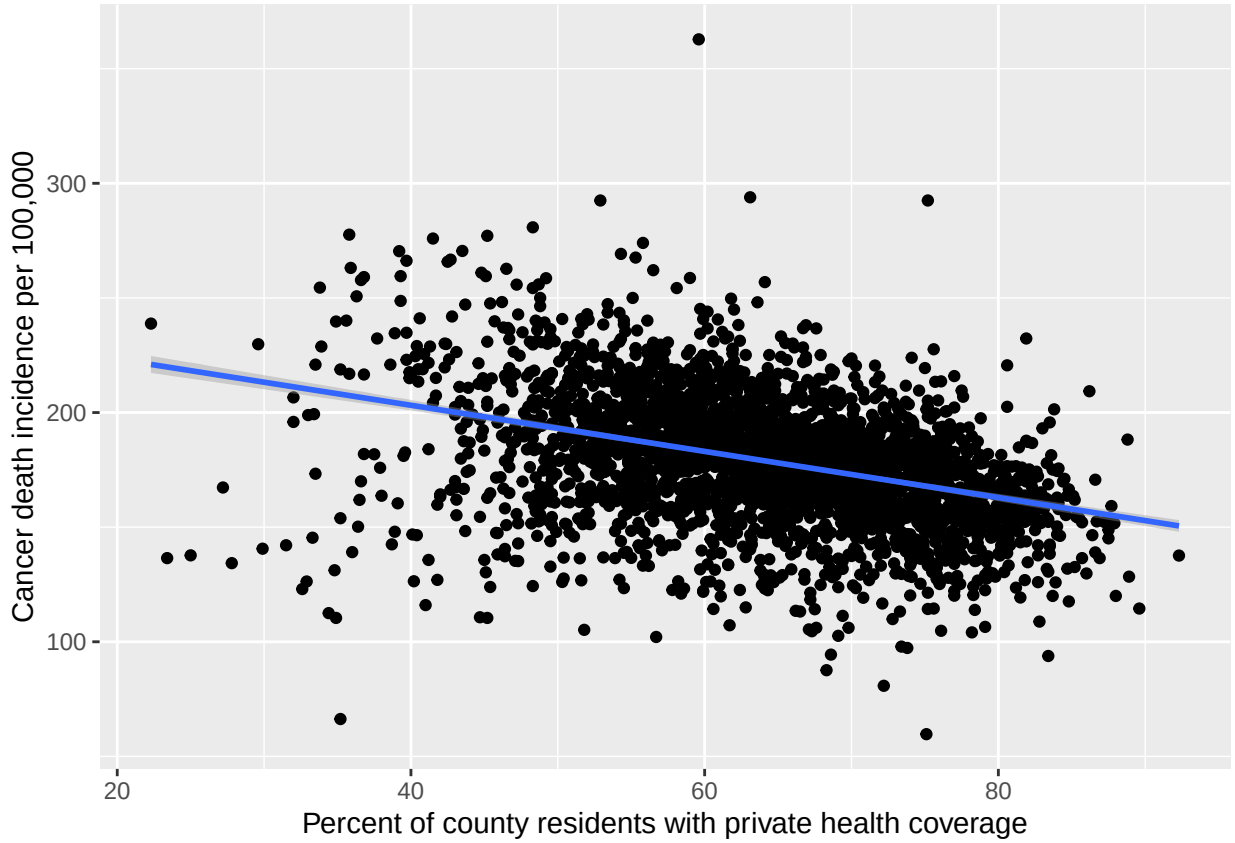
```
## Warning: Removed 152 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 152 rows containing missing values (geom_point).
```




```
ggplot(data = cancer, aes(x = pctprivatecoverage, y = target_deathrate))+
  geom_point()+
  geom_smooth(method = lm)+
  labs(x="Percent of county residents with private health coverage", y= "Cancer death incidence per 100
```

```
## `geom_smooth()` using formula 'y ~ x'
```

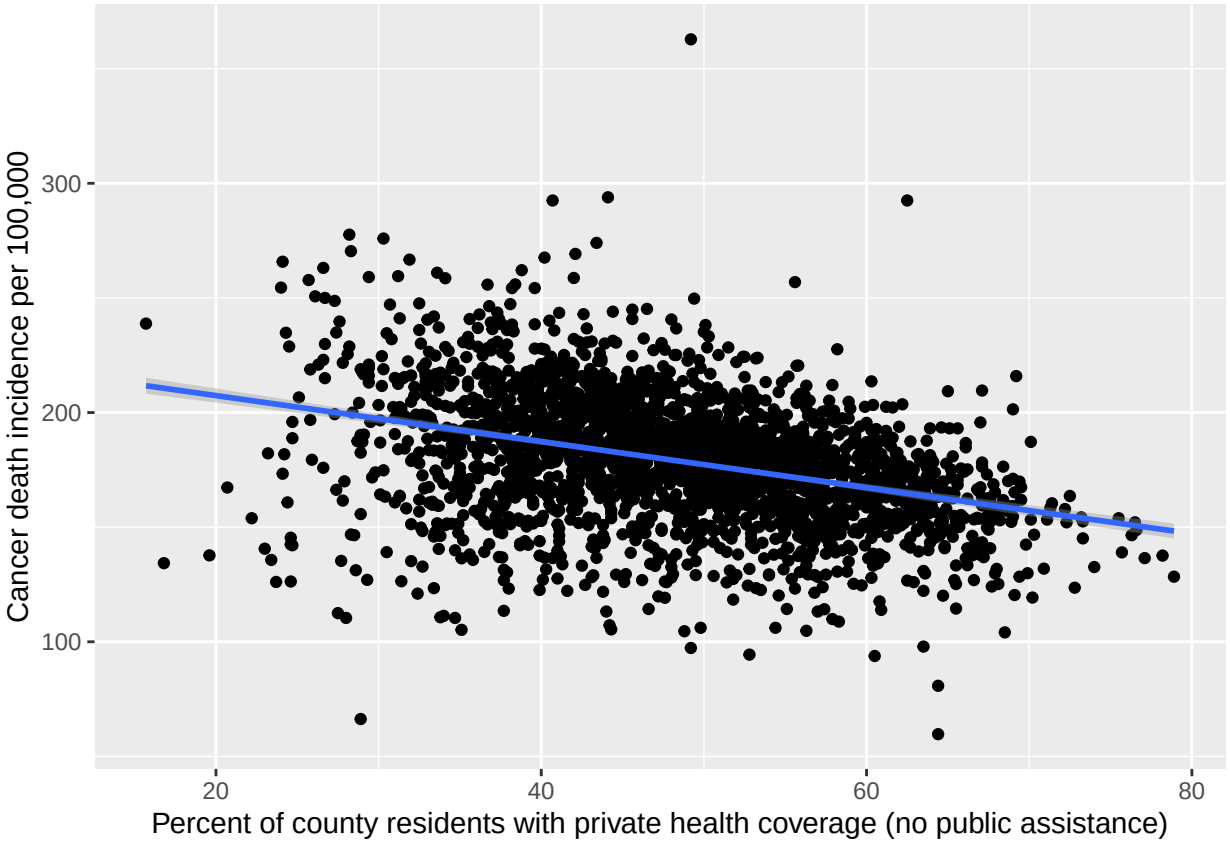



```
ggplot(data = cancer, aes(x = pctprivatecoveragealone, y = target_deathrate))+
  geom_point()+
  geom_smooth(method = lm)+
  labs(x="Percent of county residents with private health coverage (no public assistance)", y= "Cancer
```

```
## `geom_smooth()` using formula 'y ~ x'
```

```
## Warning: Removed 609 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 609 rows containing missing values (geom_point).
```




```
canc_fit_01 <- cancer %>% lm(target_deathrate ~  povertypercent + incidencerate + pctpubliccoveragealone
+ pctbachdeg25_over, data = .)
canc_fit_01_se <- canc_fit_01 %>% vcovHC(type = "HC1") %>% diag() %>% sqrt()
stargazer(canc_fit_01, type="text",se = list(canc_fit_01_se))
```

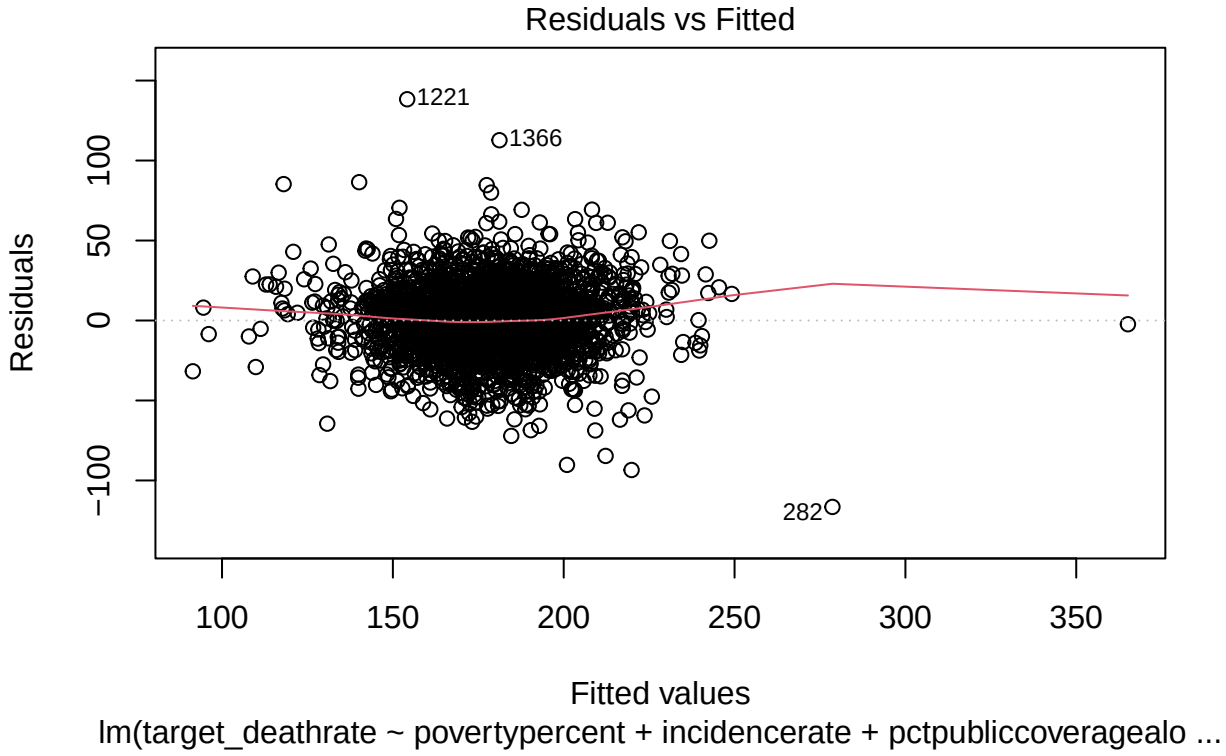
```
##
## ================================================
##                          Dependent variable:
##                      ---------------------------
##                           target_deathrate
## ------------------------------------------------
## povertypercent                0.785***
##                                (0.112)
##
## incidencerate                 0.220***
##                                (0.011)
##
## pctpubliccoveragealone        0.439***
##                                (0.125)
##
## pctbachdeg25_over             -1.615***
##                                (0.089)
##
## Constant                      79.957***
##                                (5.829)
##
```

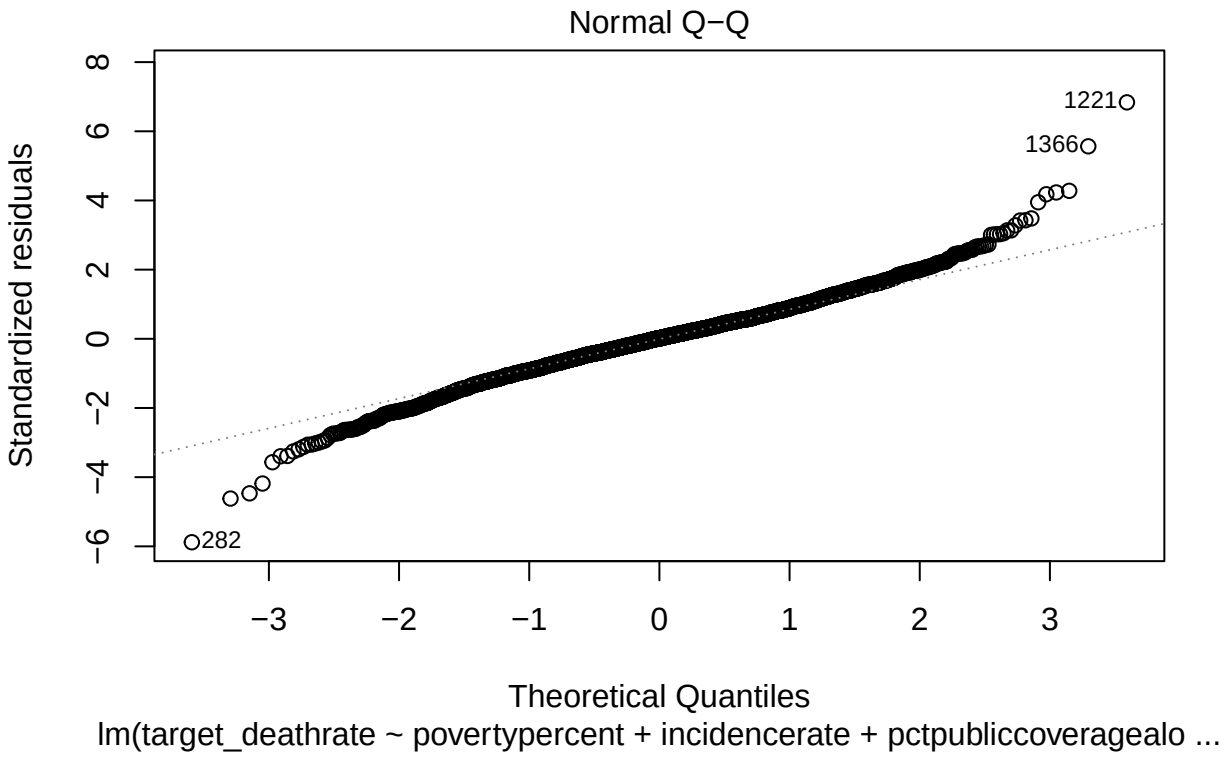
```
## ------------------------------------------------
## Observations                      3,047
## R2                                0.468
## Adjusted R2                       0.467
## Residual Std. Error        20.258 (df = 3042)
## F Statistic             668.610*** (df = 4; 3042)
## ================================================
## Note:                   *p<0.1; **p<0.05; ***p<0.01
```

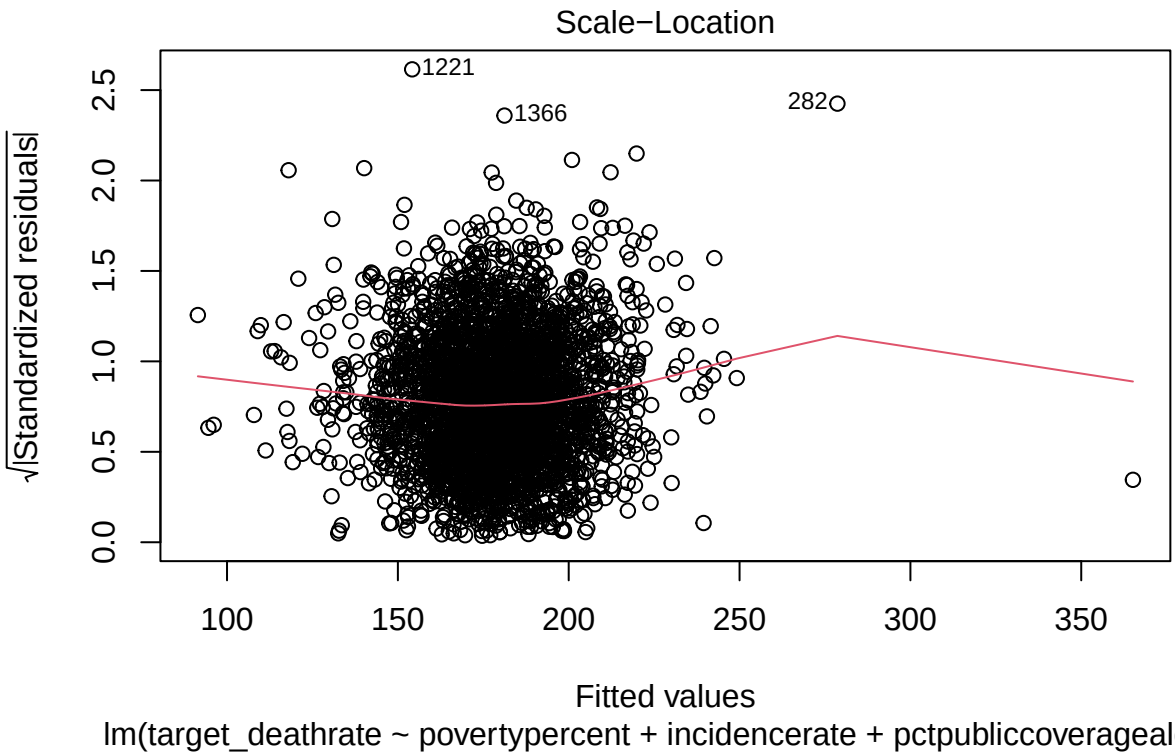
```
coeftest(canc_fit_01, vconv = vcovHC(type = "HC1"))
```

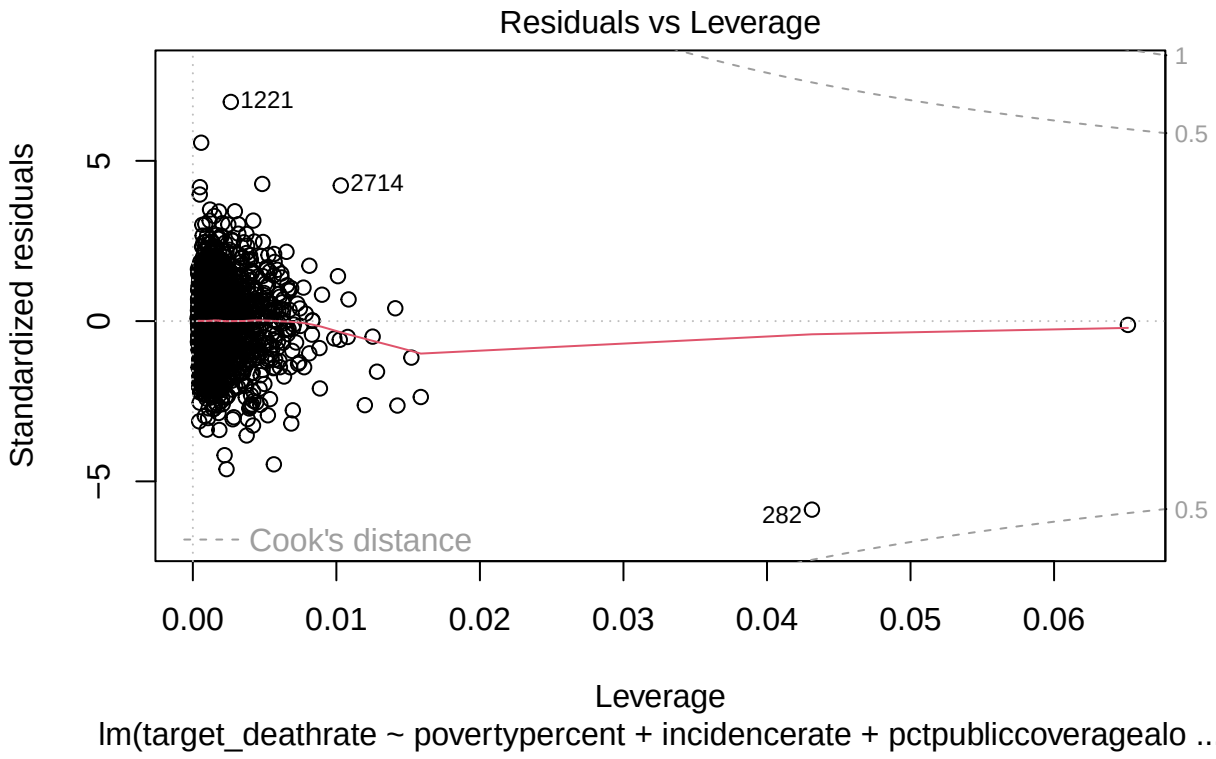
```
##
## t test of coefficients:
##
##                            Estimate Std. Error  t value  Pr(>|t|)
## (Intercept)             79.9566621  3.8371228  20.8377 < 2.2e-16 ***
## povertypercent           0.7851067  0.0957224   8.2019 3.451e-16 ***
## incidencerate            0.2196573  0.0067396  32.5920 < 2.2e-16 ***
## pctpubliccoveragealone   0.4390008  0.1068518   4.1085 4.087e-05 ***
## pctbachdeg25_over       -1.6153912  0.0859613 -18.7921 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
canc_fit_o1_vif = ols_vif_tol(canc_fit_01)
plot(canc_fit_01)
```




Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(target_deathrate ~ povertypercent + incidencerate + pctpubliccoveragealo ...
1221
1366
282
−6
−4
−2
0
2
4
6
8
−3
−2
−1
0
1
2
3


Scale−Location
√|Standardized residuals|
1221
1366
282
0.0
0.5
1.0
1.5
2.0
2.5
100
150
200
250
300
350
Fitted values
lm(target_deathrate ~ povertypercent + incidencerate + pctpubliccoveragealo ...




```
lmtest::bptest(canc_fit_01)
```

```
##
##  studentized Breusch-Pagan test
##
## data:  canc_fit_01
## BP = 59.327, df = 4, p-value = 4.017e-12
```