

Analysis of Data for the Agency for Healthcare Research and Quality Inpatient Mortality Indicators for California Hospitals, over the period 2012-2015

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```
library(rvest)
```

```
## Loading required package: xml2
```

```
library(tidyr)
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)
install.packages('ggmap', repos="http://ftp.iitm.ac.in/cran")
```

```
##
## The downloaded binary packages are in
##   /var/folders/_q/5wf9q71n3gj3n1srx3hh68qc0000gn/T//Rtmpa3CvUT/downloaded_packages
```

```
library(ggmap)
```

Frame

What was year-wise death toll. Is there any trend (ascending) or (descending) in year-wise death count

Which county recorded maximum death

Which hospital recorded maximum contribution to death toll.

Which procedure are proved to be least successful in the hospital contributed to maximum death toll.

Acquire

Getting data from following link:

<https://data.chhs.ca.gov/dataset/05fee607-cea9-4bf1-8b53-20ca584748a3/resource/5012b03a-fc44-4709-a060-1fb448947377/download/california-hospital-inpatient-mortality-rates-and-quality-ratings.csv>
(<https://data.chhs.ca.gov/dataset/05fee607-cea9-4bf1-8b53-20ca584748a3/resource/5012b03a-fc44-4709-a060-1fb448947377/download/california-hospital-inpatient-mortality-rates-and-quality-ratings.csv>)

Dataset was downloaded as a CSV file prior to the analysis.

```
getwd()
```

```
## [1] "/Volumes/MYDISK/GreatLake/Day3_Assignments/Oct_8_2017"
```

```
mydata1=read.csv("calHosInpMortality.csv", header =TRUE)
```

```
names(mydata1)
```

```
## [1] "Year" "County"
## [3] "Hospital" "OSHPDID"
## [5] "Procedure.Condition" "Risk.Adjusted.Mortality.Rate"
## [7] "X..of.Deaths" "X..of.Cases"
## [9] "Hospital.Ratings" "Longitude"
## [11] "Latitude"
```

```
attach(mydata1)
str(mydata1)
```

```
## 'data.frame': 22270 obs. of 11 variables:
## $ Year : int 2012 2012 2012 2012 2012 2012 2012 2012 2012 2012
2012 ...
## $ County : Factor w/ 56 levels "AAAA","Alameda",...: 1 1 1 1
1 1 1 1 1 1 ...
## $ Hospital : Factor w/ 465 levels "Adventist Medical Center",.
.: 414 414 414 414 414 414 414 414 414 414 ...
## $ OSHPDID : int NA NA NA NA NA NA NA NA NA NA ...
## $ Procedure.Condition : Factor w/ 18 levels "AAA Repair","AAA Repair Unru
ptured",...: 17 18 11 15 7 10 5 4 13 16 ...
## $ Risk.Adjusted.Mortality.Rate: Factor w/ 501 levels "", ".", "0", "0.2",...: 132 1 1
28 135 422 391 387 167 1 131 ...
## $ X..of.Deaths : Factor w/ 133 levels "", ".", "0", "1",...: 9 1 10 40
57 40 38 47 1 74 ...
## $ X..of.Cases : Factor w/ 761 levels "", ".", "1", "10",...: 398 1 48
6 705 468 374 401 17 1 118 ...
## $ Hospital.Ratings : Factor w/ 3 levels "As Expected",...: 1 1 1 1 1 1
1 1 1 1 ...
## $ Longitude : Factor w/ 342 levels "", "-114.5956",...: 1 1 1 1 1
1 1 1 1 1 ...
## $ Latitude : Factor w/ 342 levels "", ".", "32.61909",...: 1 1 1
1 1 1 1 1 1 ...
```

Refine

```
## Modify column names for easier operation.
column_names <- c('year','county','hospitalName','hospitalId','procedureName','riskRa
te','numDeath','numCases','hospRating','long','lat')
colnames(mydata1) <- column_names
tail(mydata1,1)
```

```
##          year county          hospitalName hospitalId
## 22270 2015    Yuba Rideout Memorial Hospital 106580996
##          procedureName riskRate numDeath numCases  hospRating
## 22270 AAA Repair Unruptured          0          0          10 As Expected
##          long          lat
## 22270 -121.594363 39.138222
```

```
unique(mydata1$county)
```

```
## [1] AAAA          Alameda          Amador          Butte
## [5] Calaveras       Colusa           Contra Costa    Del Norte
## [9] El Dorado       Fresno          Glenn           Humboldt
## [13] Imperial       Inyo            Kern            Kings
## [17] Lake           Lassen          Los Angeles     Madera
## [21] Marin          Mariposa        Mendocino       Merced
## [25] Modoc          Mono            Monterey        Napa
## [29] Nevada         Orange          Placer          Plumas
## [33] Riverside      Sacramento      San Benito      San Bernardino
## [37] San Diego      San Francisco   San Joaquin     San Luis Obispo
## [41] San Mateo      Santa Barbara   Santa Clara     Solano
## [45] Sonoma         Santa Cruz      Shasta          Siskiyou
## [49] Stanislaus     Trinity         Tehama          Tulare
## [53] Tuolumne       Ventura         Yolo            Yuba
## 56 Levels: AAAA Alameda Amador Butte Calaveras Colusa ... Yuba
```

```
str(mydata1)
```

```
## 'data.frame':    22270 obs. of  11 variables:
## $ year          : int  2012 2012 2012 2012 2012 2012 2012 2012 2012 2012 2012 ...
## $ county        : Factor w/ 56 levels "AAAA","Alameda",...: 1 1 1 1 1 1 1 1 1 1 1 ...
## $ hospitalName  : Factor w/ 465 levels "Adventist Medical Center",...: 414 414 414
414 414 414 414 414 414 414 ...
## $ hospitalId    : int  NA NA NA NA NA NA NA NA NA NA NA ...
## $ procedureName: Factor w/ 18 levels "AAA Repair","AAA Repair Unruptured",...: 17
18 11 15 7 10 5 4 13 16 ...
## $ riskRate      : Factor w/ 501 levels "", ".", "0", "0.2",...: 132 1 128 135 422 391
387 167 1 131 ...
## $ numDeath      : Factor w/ 133 levels "", ".", "0", "1",...: 9 1 10 40 57 40 38 47 1
74 ...
## $ numCases      : Factor w/ 761 levels "", ".", "1", "10",...: 398 1 486 705 468 374 4
01 17 1 118 ...
## $ hospRating    : Factor w/ 3 levels "As Expected",...: 1 1 1 1 1 1 1 1 1 1 1 ...
## $ long          : Factor w/ 342 levels "", "-114.5956",...: 1 1 1 1 1 1 1 1 1 1 1 ...
## $ lat           : Factor w/ 342 levels "", ".", "32.61909",...: 1 1 1 1 1 1 1 1 1 1 1 .
..
```

```
dim(mydata1)
```

```
## [1] 22270 11
```

```
dim(mydata1 %>% filter(is.na(county)))
```

```
## [1] 0 11
```

```
mydata1$county <- as.character(mydata1$county)
mydata1$hospitalName <- as.character(mydata1$hospitalName)
mydata1$hospitalId <- as.character(mydata1$hospitalId)
mydata1$procedureName <- as.character(mydata1$procedureName)
mydata1$riskRate <- as.numeric(mydata1$riskRate)
mydata1$numDeath <- as.numeric(mydata1$numDeath)
mydata1$numCases <- as.numeric(mydata1$numCases)
mydata1$hospRating <- as.character(mydata1$hospRating)
mydata1$long <- as.numeric(mydata1$long)
mydata1$lat <- as.numeric(mydata1$lat)
```

```
str(mydata1)
```

```
## 'data.frame': 22270 obs. of 11 variables:
## $ year : int 2012 2012 2012 2012 2012 2012 2012 2012 2012 2012 ...
## $ county : chr "AAAA" "AAAA" "AAAA" "AAAA" ...
## $ hospitalName : chr "STATEWIDE" "STATEWIDE" "STATEWIDE" "STATEWIDE" ...
## $ hospitalId : chr NA NA NA NA ...
## $ procedureName: chr "PCI" "Pneumonia" "GI Hemorrhage" "Pancreatic Other" ...
## $ riskRate : num 132 1 128 135 422 391 387 167 1 131 ...
## $ numDeath : num 9 1 10 40 57 40 38 47 1 74 ...
## $ numCases : num 398 1 486 705 468 374 401 17 1 118 ...
## $ hospRating : chr "As Expected" "As Expected" "As Expected" "As Expected" ...
## $ long : num 1 1 1 1 1 1 1 1 1 1 ...
## $ lat : num 1 1 1 1 1 1 1 1 1 1 ...
```

```
unique(mydata1$hospRating)
```

```
## [1] "As Expected" "Better" "Worse"
```

```
## Let's perform NA analysis
dim(mydata1 %>% filter(is.na(county)))
```

```
## [1] 0 11
```

```
dim(mydata1 %>% filter(is.na(hospitalName)))
```

```
## [1] 0 11
```

```
dim(mydata1 %>% filter(is.na(hospitalId)))
```

```
## [1] 68 11
```

```
dim(mydata1 %>% filter(is.na(procedureName)))
```

```
## [1] 0 11
```

```
dim(mydata1 %>% filter(is.na(riskRate)))
```

```
## [1] 0 11
```

```
dim(mydata1 %>% filter(is.na(numDeath)))
```

```
## [1] 0 11
```

```
dim(mydata1 %>% filter(is.na(numCases)))
```

```
## [1] 0 11
```

```
dim(mydata1 %>% filter(is.na(hospRating)))
```

```
## [1] 0 11
```

```
dim(mydata1 %>% filter(is.na(long)))
```

```
## [1] 0 11
```

```
dim(mydata1 %>% filter(is.na(lat)))
```

```
## [1] 0 11
```

```
## It is evident from the above excersise that there are 68 records for which hospita  
l id is NULL.
```

```
## Let's find out the details about those record where hospital ID is NULL.
```

```
dNullID <- mydata1 %>% filter(is.na(hospitalId))
```

```
## it is observed all 68 records belongs to hospital "STATEWIDE", It is also observed  
that this hospital
```

```
## belongs to AAAA county. Let's assign a hospitalID (OSPDID)
```

```
## retrieve county code from all the OSPDID, to find the pattern of county code. As p  
er the data dictionary, "OSPDID" is a unique number established by the Office of Stat  
ewide Health Planning and Development (OSHDP) for identifying facilities and used in  
the Licensed Facility Information System (LFIS). The first 3 numbers identify the typ  
e of facility, the next two represent the county number, and the last five are random  
ly assigned wihin each county.
```

```
unique(substr(mydata1$hospitalId,4,5))
```

```
## [1] NA "01" "03" "04" "05" "06" "07" "08" "09" "10" "11" "12" "13" "14"  
## [15] "15" "16" "17" "18" "19" "20" "21" "22" "23" "24" "25" "26" "27" "28"  
## [29] "29" "30" "31" "32" "33" "34" "35" "36" "37" "38" "39" "40" "41" "42"  
## [43] "43" "48" "49" "44" "45" "47" "50" "53" "52" "54" "55" "56" "57" "58"
```

```
## it is clear that range of county code starts from 01, ends at 58. So, we can assign  
n country code as 00 to this county. Also We noticed that first 3 digit is always 106  
. Hence our derived hospital id for this particular hospital "STATEWIDE" is 106001234  
5.
```

```
##
```

TRANSFORM

```
mydata1 <- mydata1 %>%  
  mutate (hospitalId = ifelse(hospitalName == "STATEWIDE", "1060012345", hospitalId))  
  
str(mydata1)
```

```
## 'data.frame':    22270 obs. of  11 variables:
##  $ year          : int  2012 2012 2012 2012 2012 2012 2012 2012 2012 2012 ...
##  $ county        : chr  "AAAA" "AAAA" "AAAA" "AAAA" ...
##  $ hospitalName  : chr  "STATEWIDE" "STATEWIDE" "STATEWIDE" "STATEWIDE" ...
##  $ hospitalId    : chr  "1060012345" "1060012345" "1060012345" "1060012345" ...
##  $ procedureName: chr  "PCI" "Pneumonia" "GI Hemorrhage" "Pancreatic Other" ...
##  $ riskRate      : num  132 1 128 135 422 391 387 167 1 131 ...
##  $ numDeath      : num  9 1 10 40 57 40 38 47 1 74 ...
##  $ numCases      : num  398 1 486 705 468 374 401 17 1 118 ...
##  $ hospRating    : chr  "As Expected" "As Expected" "As Expected" "As Expected" ...
##  $ long          : num  1 1 1 1 1 1 1 1 1 1 ...
##  $ lat           : num  1 1 1 1 1 1 1 1 1 1 ...
```

```
## We can see now county code is added for "AAAA" county as well.
unique(substr(mydata1$hospitalId,4,5))
```

```
##  [1] "00" "01" "03" "04" "05" "06" "07" "08" "09" "10" "11" "12" "13" "14"
## [15] "15" "16" "17" "18" "19" "20" "21" "22" "23" "24" "25" "26" "27" "28"
## [29] "29" "30" "31" "32" "33" "34" "35" "36" "37" "38" "39" "40" "41" "42"
## [43] "43" "48" "49" "44" "45" "47" "50" "53" "52" "54" "55" "56" "57" "58"
```

```
## Year-wise number of death
```

```
dfYearDeath <- mydata1 %>%
  select(year,numDeath) %>%
  group_by(year) %>%
  dplyr::summarise(TotalYearDeath = sum(numDeath)) %>%
  arrange(desc(TotalYearDeath))
```

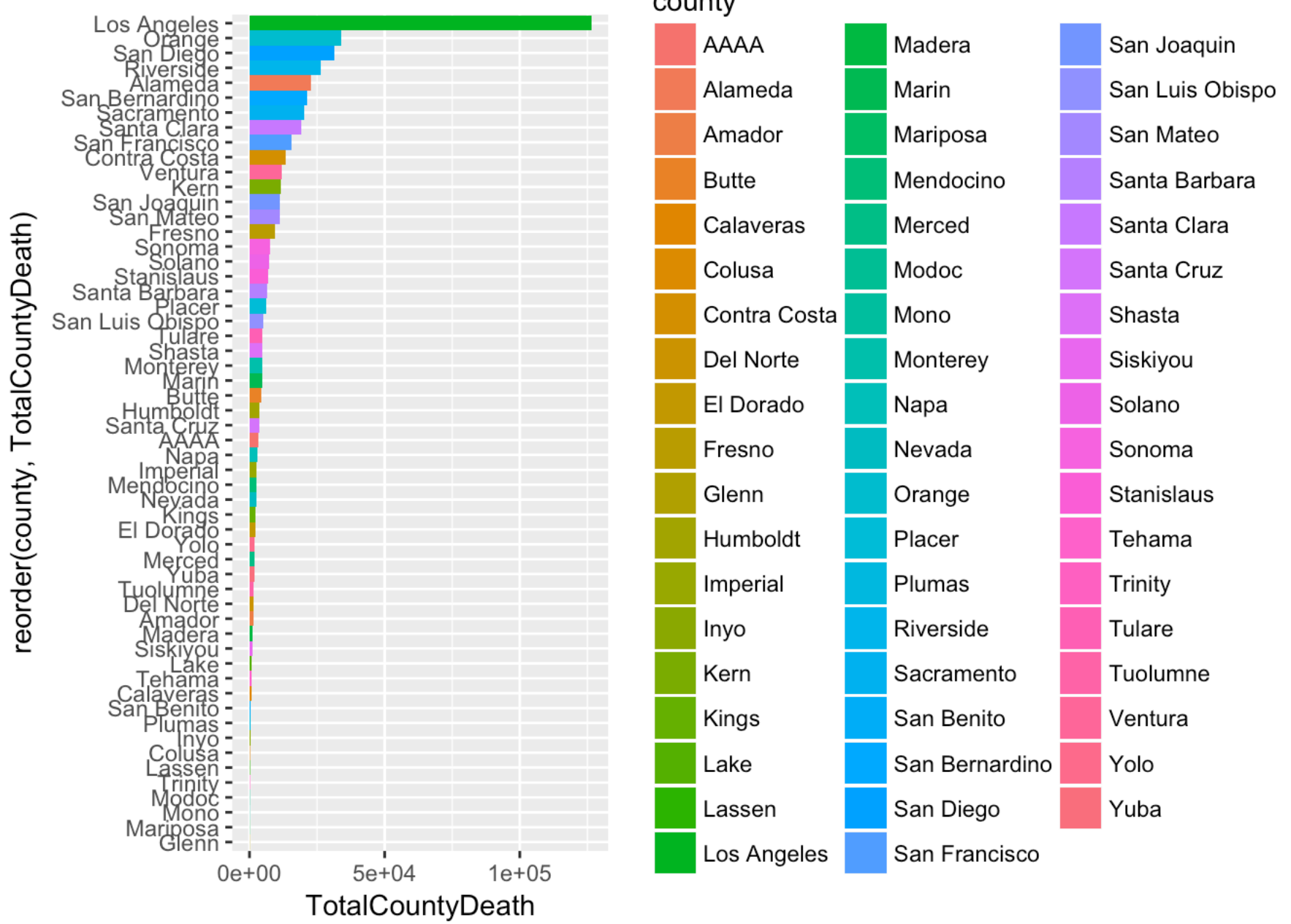
```
## Show countywise death.
```

```
dfCounty <- mydata1 %>%
  select(county,numDeath) %>%
  group_by(county) %>%
  dplyr::summarise(TotalCountyDeath = sum(numDeath)) %>%
  arrange(desc(TotalCountyDeath))
```

EXPLORE

```
## plot county-wise death.
```

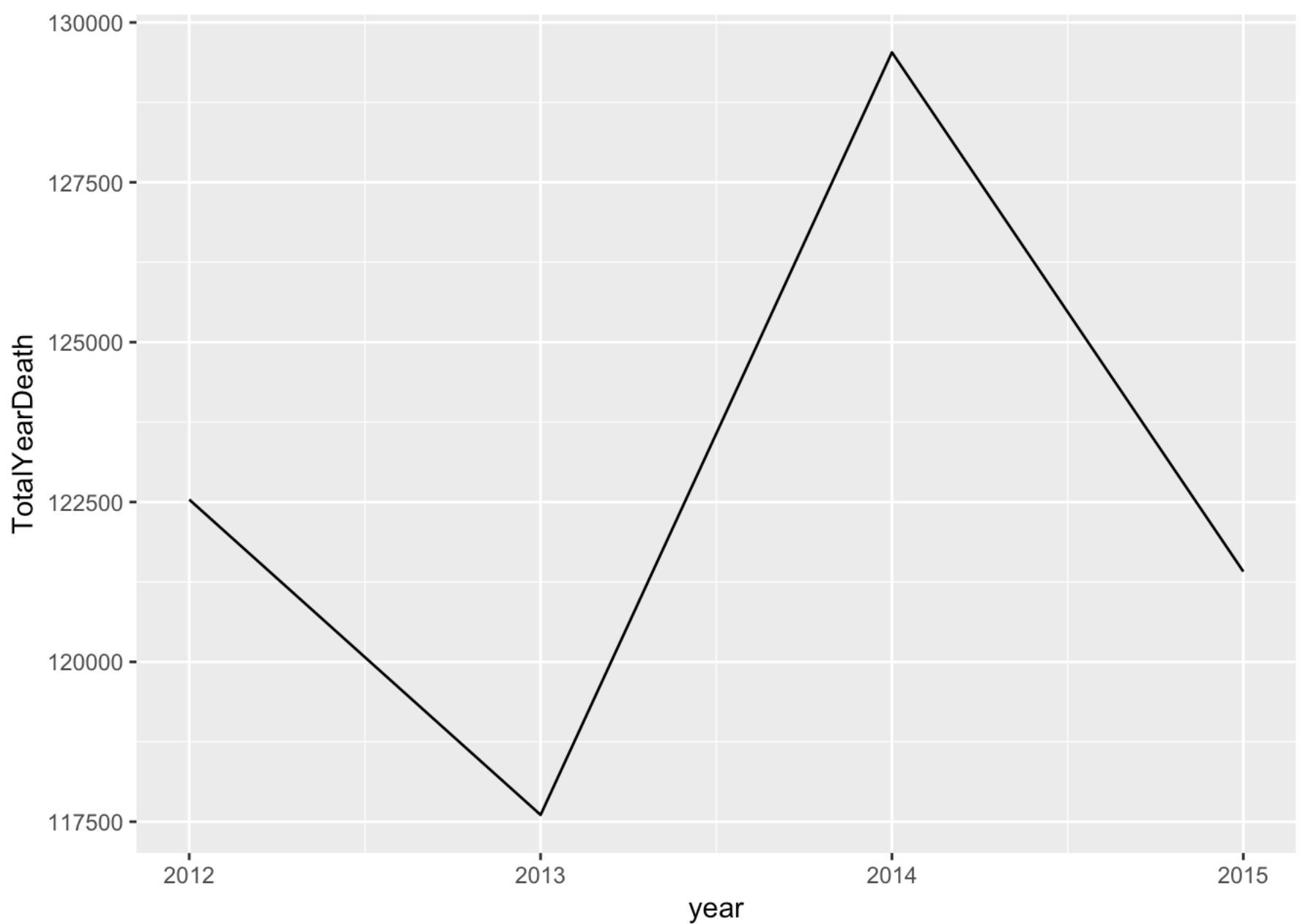
```
ggplot(dfCounty)+ aes(reorder(county>TotalCountyDeath), TotalCountyDeath, fill = coun
ty )+
  geom_col(width = 1) +
  coord_flip()
```

It is evident that, overall, "Los Angeles" county is maximum contributor to the death toll.

plot year-wise death.

```
ggplot(dfYearDeath) + aes(year, TotalYearDeath) + geom_line()
```



```
## from the plot, it is evident that , maximum number of death occurred in year 2014
```

```
## Show county wise death toll for the year 2014
```

```
df2014 <- mydata1 %>% filter(year==2014)
```

```
dfCountyDeath <- df2014 %>%
```

```
  select(county,numDeath) %>%
```

```
  group_by(county) %>%
```

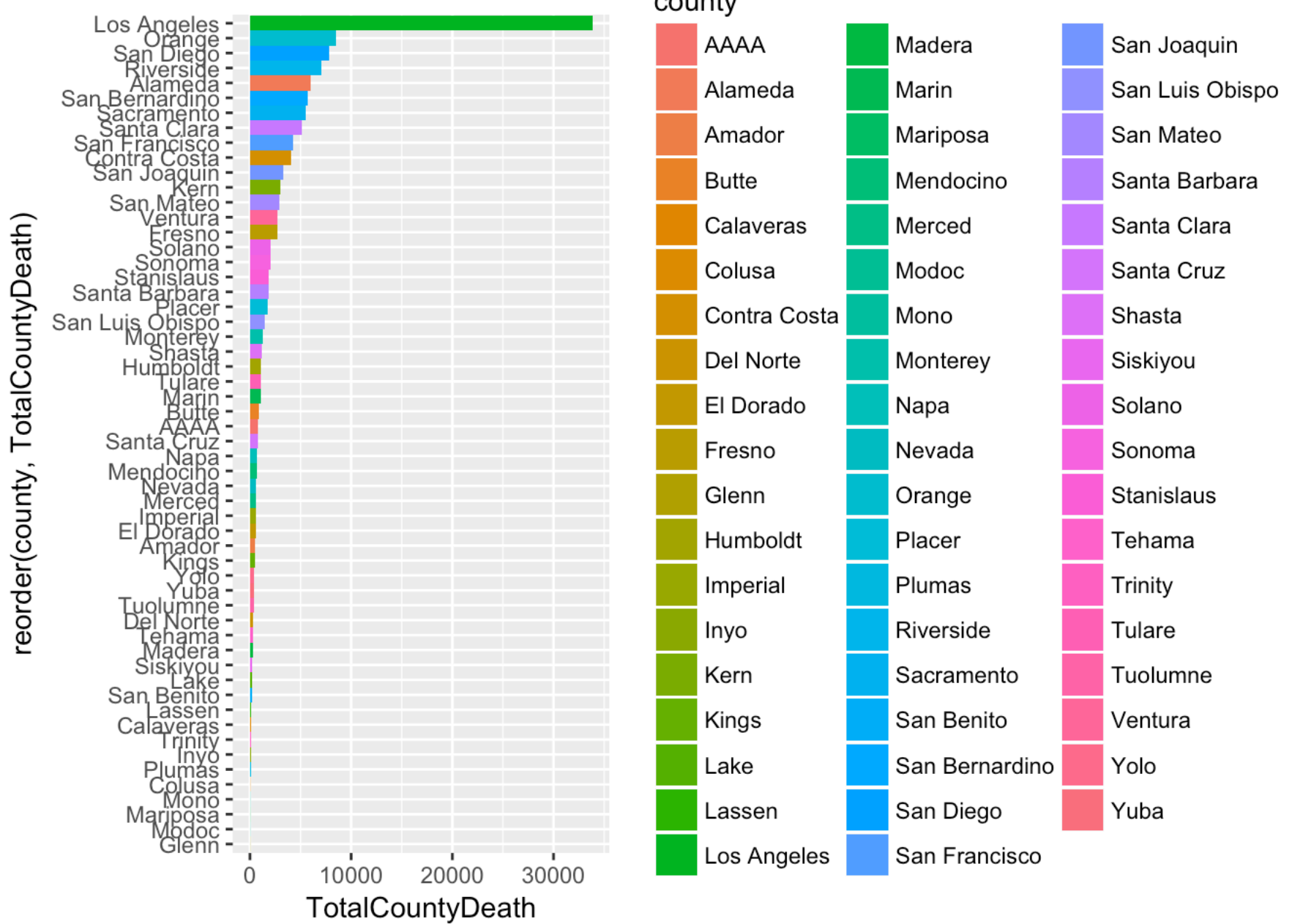
```
  dplyr::summarise(TotalCountyDeath = sum(numDeath)) %>%
```

```
  arrange(desc(TotalCountyDeath))
```

```
## plot county-wise death for 2014.
```

```
ggplot(dfCountyDeath)+ aes(reorder(county,TotalCountyDeath), TotalCountyDeath, fill =  
county )+
```

```
  geom_col(width = 1) +  
  coord_flip()
```

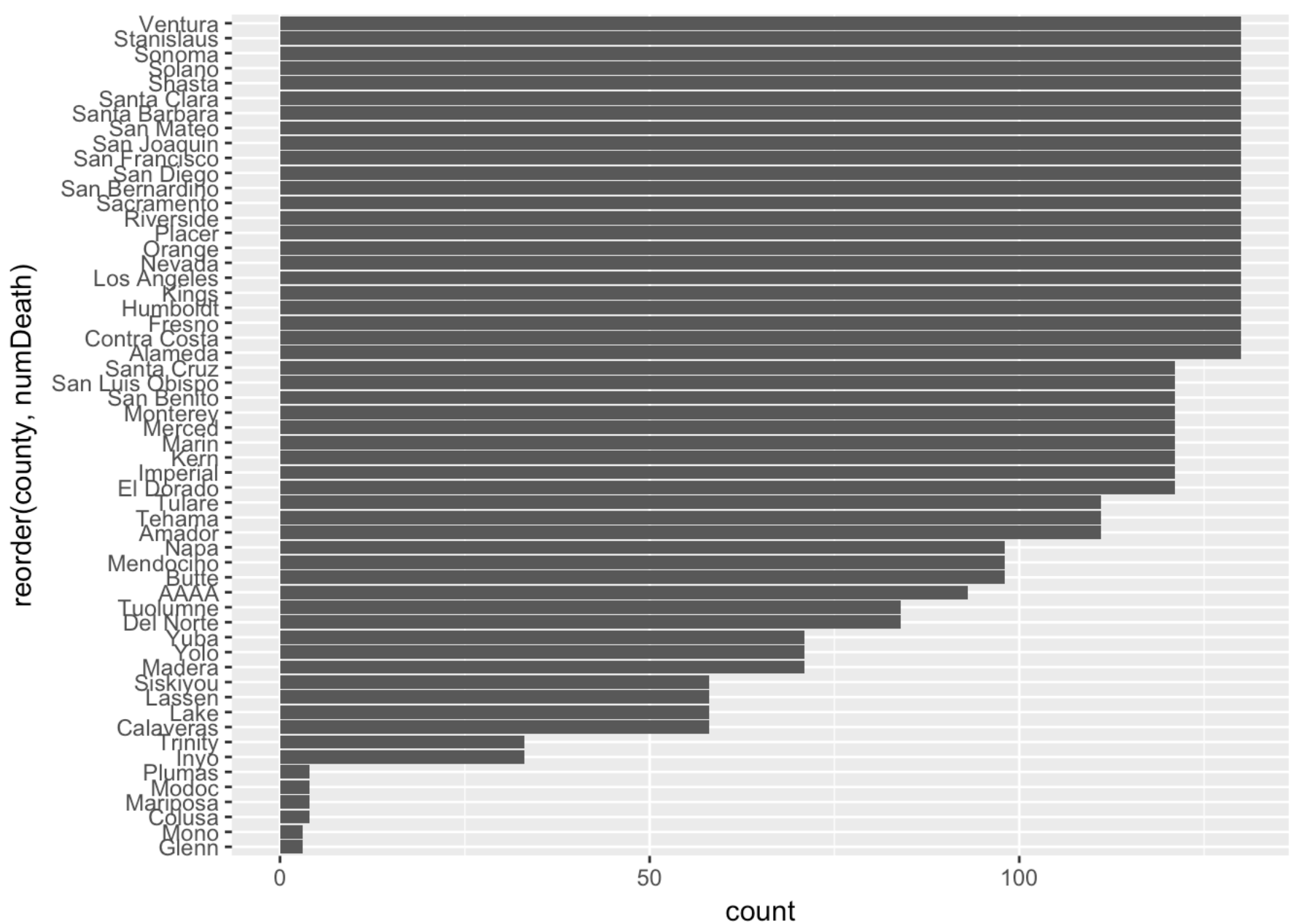


It is evident that for year 2014 also, "Los Angeles" county is maximum contributor to the death toll.

Show the county wise highest death toll

```
df2014_deathTollMax <- df2014 %>% group_by(county) %>% dplyr::summarise(numDeath=max(
numDeath))
```

```
ggplot(df2014_deathTollMax)+
aes(reorder(county,numDeath),weight=numDeath)+
geom_bar() +
coord_flip()
```



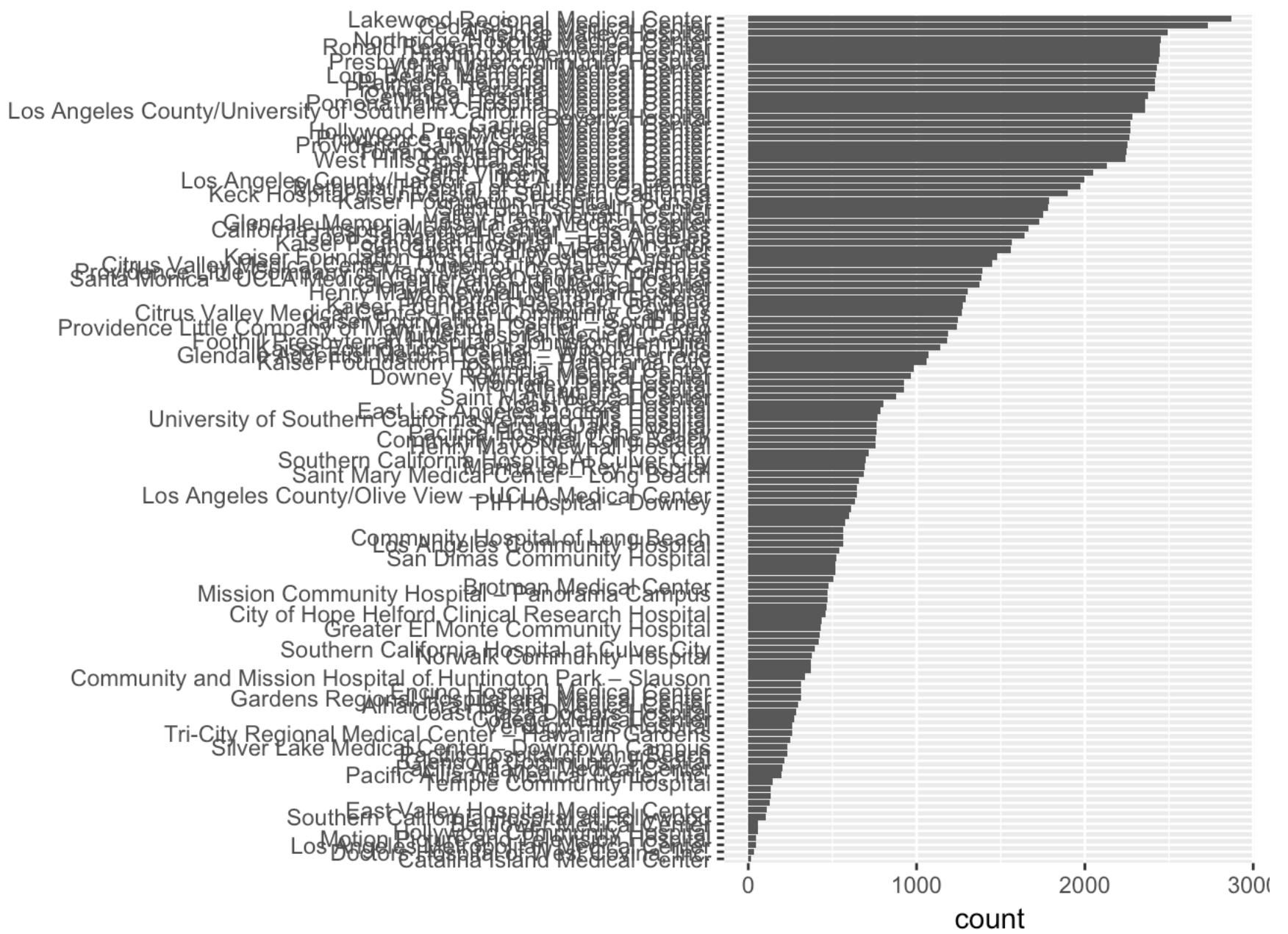
```
## Hospital-wise number of death for Los Angeles county
```

```
dfHospDeath <- mydata1 %>%
  filter(county=="Los Angeles") %>%
  select(hospitalName,numDeath) %>%
  group_by(hospitalName) %>%
  dplyr::summarise(TotalHospDeath = sum(numDeath)) %>%
  arrange(desc(TotalHospDeath))
```

```
## Plot the graph
```

```
ggplot(dfHospDeath)+
  aes(reorder(hospitalName,TotalHospDeath),weight=TotalHospDeath)+
  geom_bar() +
  coord_flip()
```

reorder(hospitalName, TotalHospDeath)



Lakewood Regional Medical Center, which belongs to Los Angeles county, is leading the list of death toll.

find out the procedure impacting maximum.

```
dfLR <- mydata1 %>%  
  filter(hospitalName == "Lakewood Regional Medical Center")%>%  
  select(procedureName,numCases,numDeath) %>%  
  group_by(procedureName) %>%  
  dplyr::summarise(procCases = sum(numCases),procDeath=sum(numDeath))
```

How many patients are alive against each of the procedure

```
dfLR$alive <- (dfLR$procCases - dfLR$procDeath)
```

Remove negative entries, number of cases cannot be less than number of death, hence those are bad data hence removed.

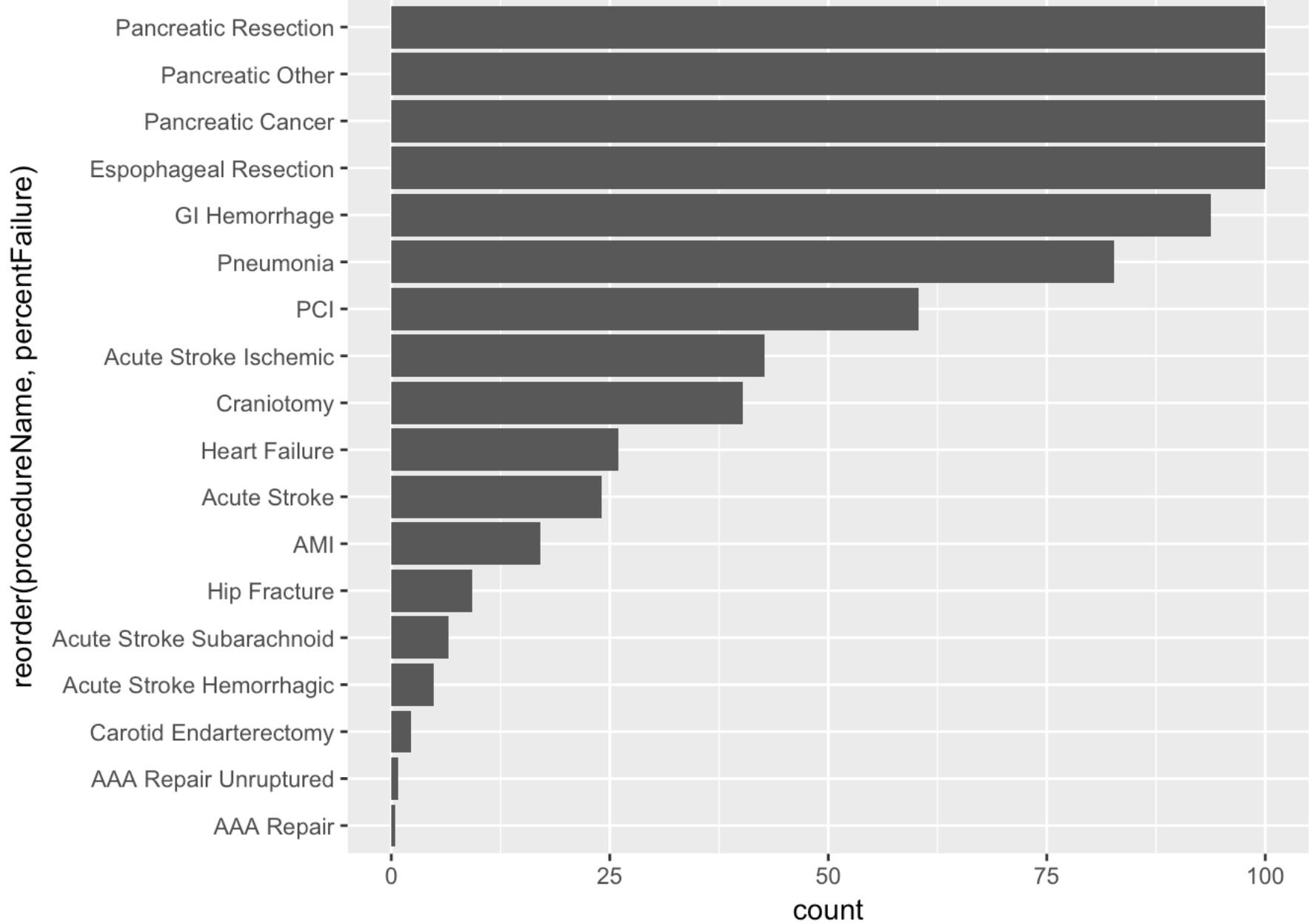
```
dfLR <- dfLR %>%  
  filter(alive >= 0)
```

find success rate against each procedure

```
dfLR$percentSuccess <- round((dfLR$alive/dfLR$procCases)*100,digits=2)  
dfLR$percentFailure <- round(100.00-dfLR$percentSuccess,digits=2)
```

Plot the procedures showing least successful in this hospital

```
ggplot(dfLR)+  
aes(reorder(procedureName,percentFailure),weight=percentFailure)+  
geom_bar() +  
coord_flip()
```

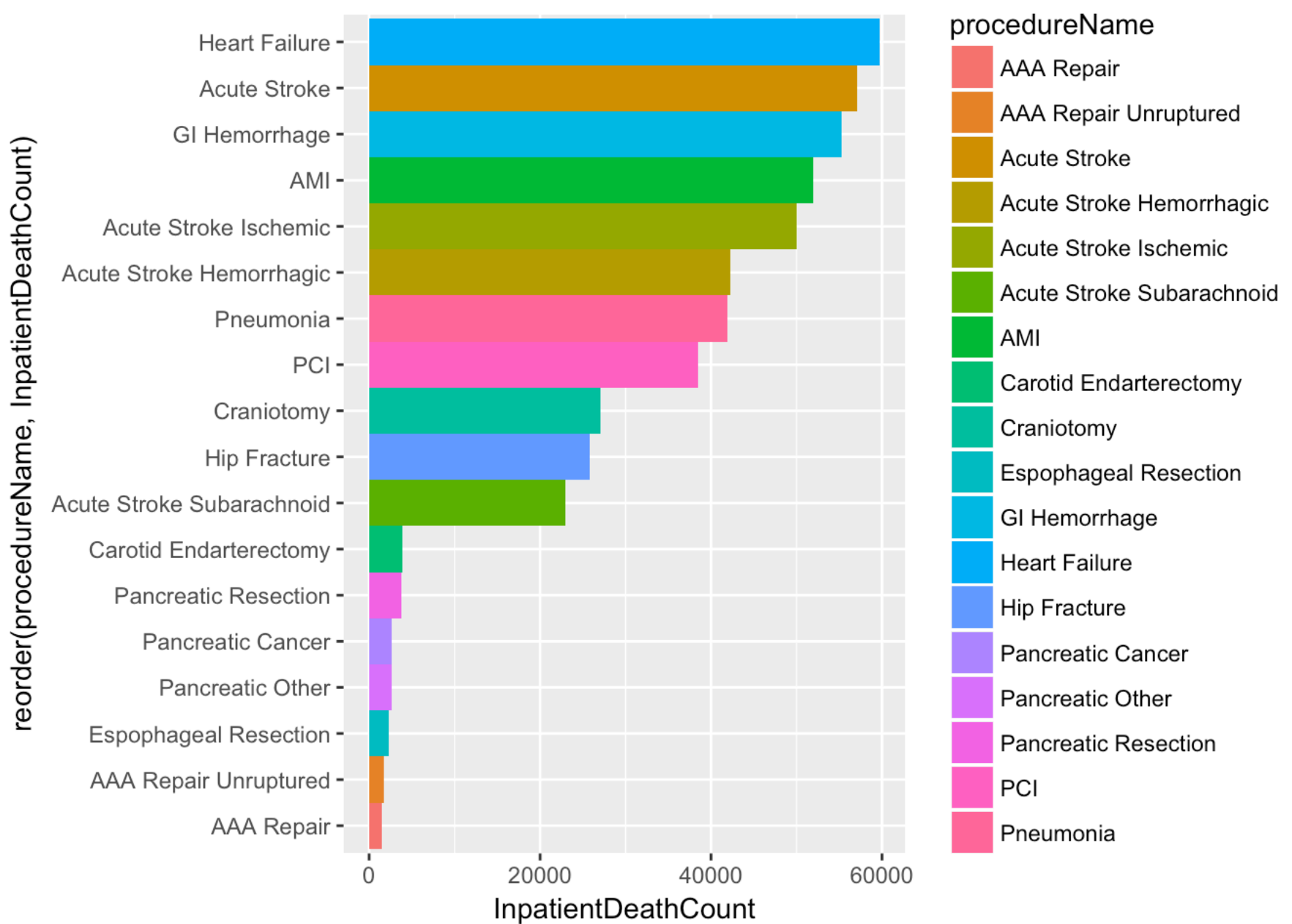


The diagram shows that this hospital has least success rate against Pancreatic Resection, Pancreatic Cancer, Esophageal Resection and other Pancreatic procedures.

Plot the procedure causing maximum inpatient death over the whole period 2012-2015

```
dfprocWise <- mydata1 %>%
  # filter(year == 2014) %>%
  group_by(procedureName) %>%
  dplyr::summarise(InpatientDeathCount = sum(numDeath)) %>%
  arrange(desc(InpatientDeathCount))

ggplot(dfprocWise)+ aes(reorder(procedureName,InpatientDeathCount), InpatientDeath
Count, fill = procedureName )+
  geom_col(width = 1) +
  coord_flip()
```

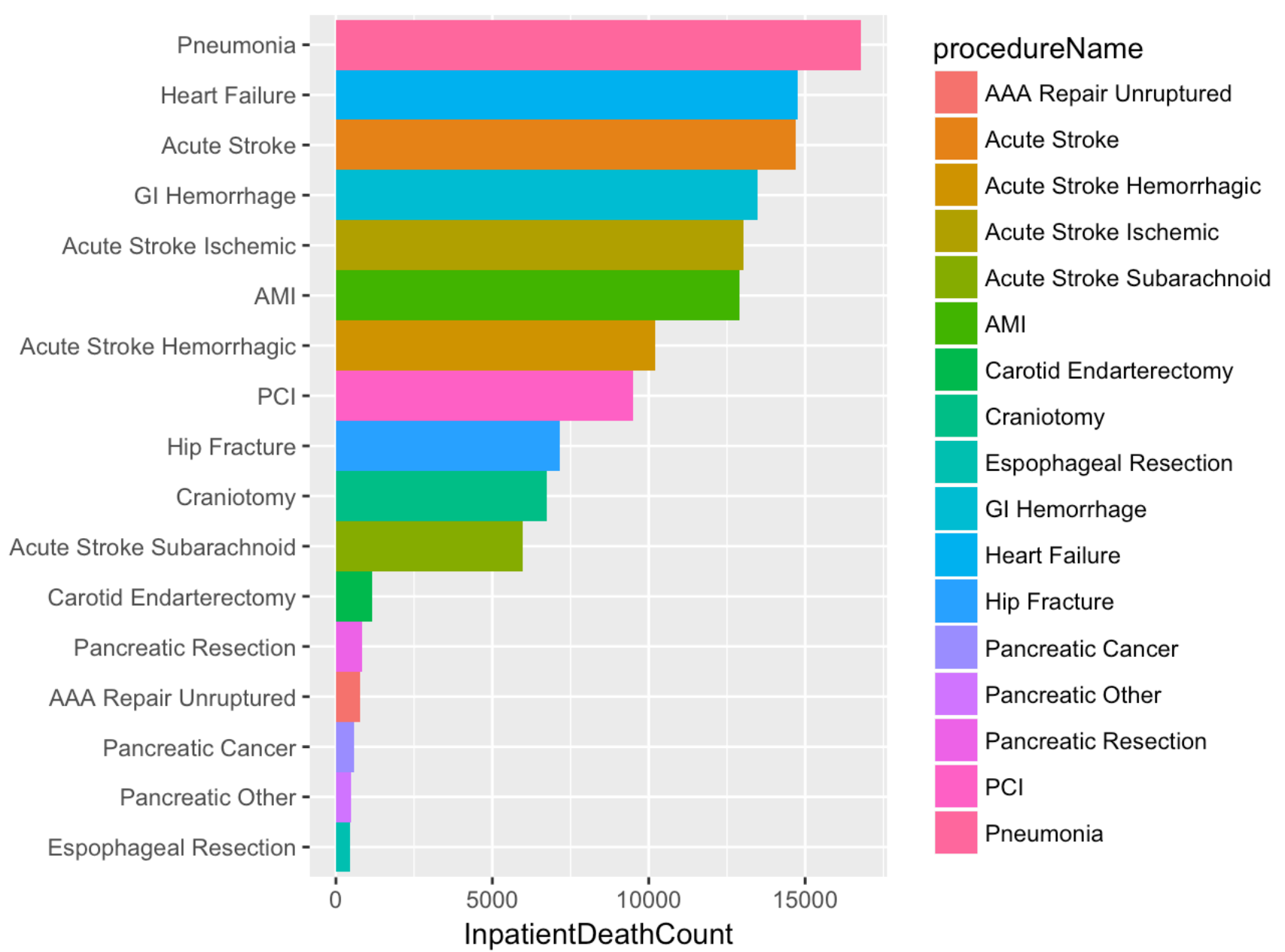


```
## Plot the procedure causing maximum inpatient death in 2014
```

```
dfprocWise2014 <- mydata1 %>%
  filter(year == 2014) %>%
  group_by(procedureName) %>%
  dplyr::summarise(InpatientDeathCount = sum(numDeath)) %>%
  arrange(desc(InpatientDeathCount))
```

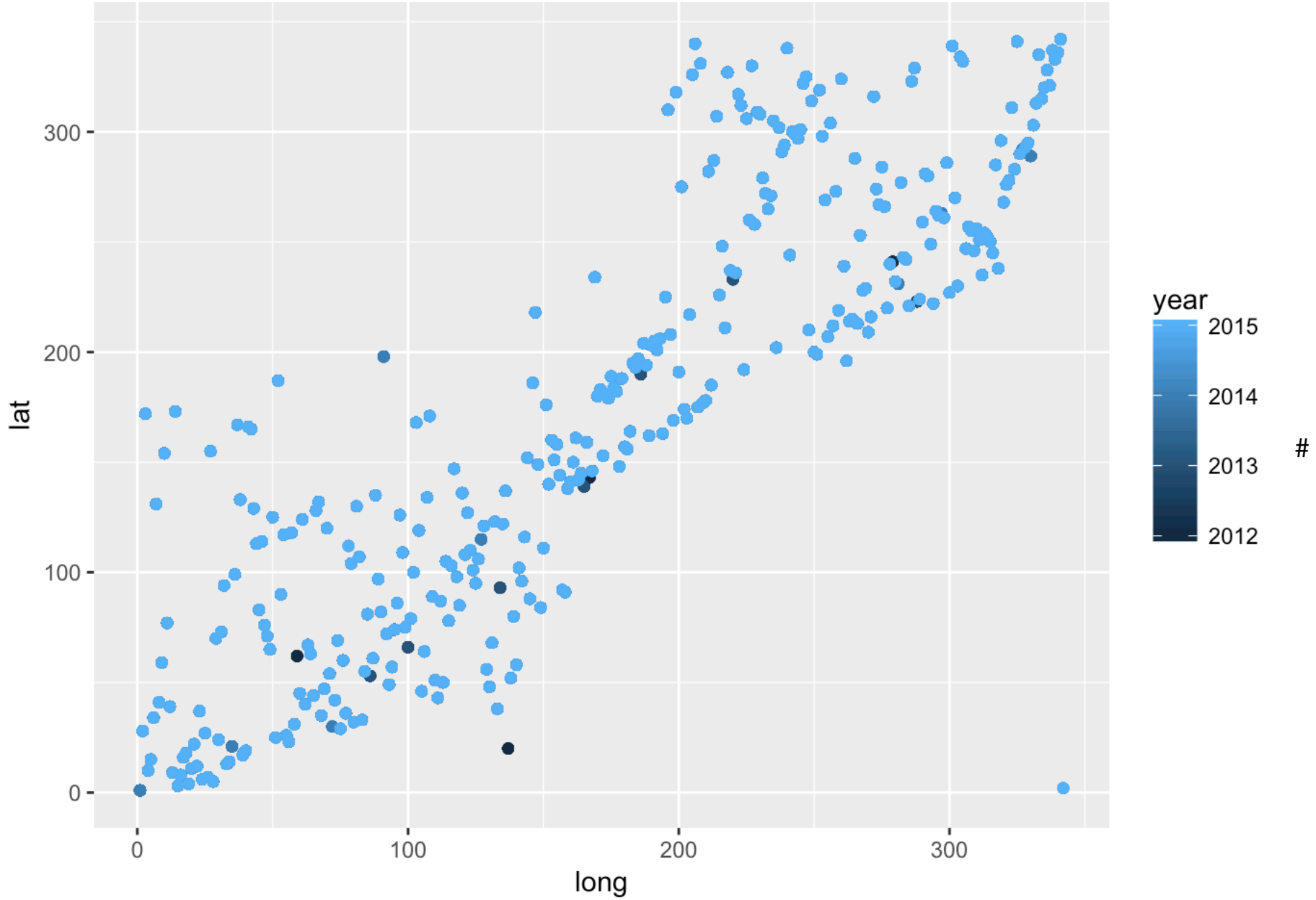
```
ggplot(dfprocWise2014)+ aes(reorder(procedureName, InpatientDeathCount), InpatientDeathCount, fill = procedureName )+
  geom_col(width = 1) +
  coord_flip()
```


reorder(procedureName, InpatientDeathCount)



#Let's plot the hospitals as per their coordinates, yearwise. It shows a good overlap with very few outliers on 2012.

```
ggplot() + geom_point(data=mydata1,aes(x=long,y=lat,color=year))
```



MODEL

Preprocessing to get the tidy dataframe

```
options(repr.plot.width=10, repr.plot.height=6)

str(mydata1)

## 'data.frame':    22270 obs. of  11 variables:
##  $ year          : int   2012 2012 2012 2012 2012 2012 2012 2012 2012 2012 ...
##  $ county        : chr   "AAAA" "AAAA" "AAAA" "AAAA" ...
##  $ hospitalName  : chr   "STATEWIDE" "STATEWIDE" "STATEWIDE" "STATEWIDE" ...
##  $ hospitalId    : chr   "1060012345" "1060012345" "1060012345" "1060012345" ...
##  $ procedureName : chr   "PCI" "Pneumonia" "GI Hemorrhage" "Pancreatic Other" ...
##  $ riskRate      : num   132 1 128 135 422 391 387 167 1 131 ...
##  $ numDeath      : num    9 1 10 40 57 40 38 47 1 74 ...
##  $ numCases      : num   398 1 486 705 468 374 401 17 1 118 ...
##  $ hospRating    : chr   "As Expected" "As Expected" "As Expected" "As Expected" ...
##  $ long          : num    1 1 1 1 1 1 1 1 1 1 ...
##  $ lat           : num    1 1 1 1 1 1 1 1 1 1 ...
```

How the risk rate and percentage failure to avoid death are related to each other.

```
unique(mydata1$procedureName)
```

```
## [1] "PCI" "Pneumonia"
## [3] "GI Hemorrhage" "Pancreatic Other"
## [5] "AMI" "Esophageal Resection"
## [7] "Acute Stroke Ischemic" "Acute Stroke Hemorrhagic"
## [9] "Hip Fracture" "Pancreatic Resection"
## [11] "Acute Stroke" "Acute Stroke Subarachnoid"
## [13] "Heart Failure" "Carotid Endarterectomy"
## [15] "Craniotomy" "AAA Repair"
## [17] "Pancreatic Cancer" "AAA Repair Unruptured"
```

```
mydata <- mydata1
mydata1$procedureName <- as.factor(mydata1$procedureName)
```

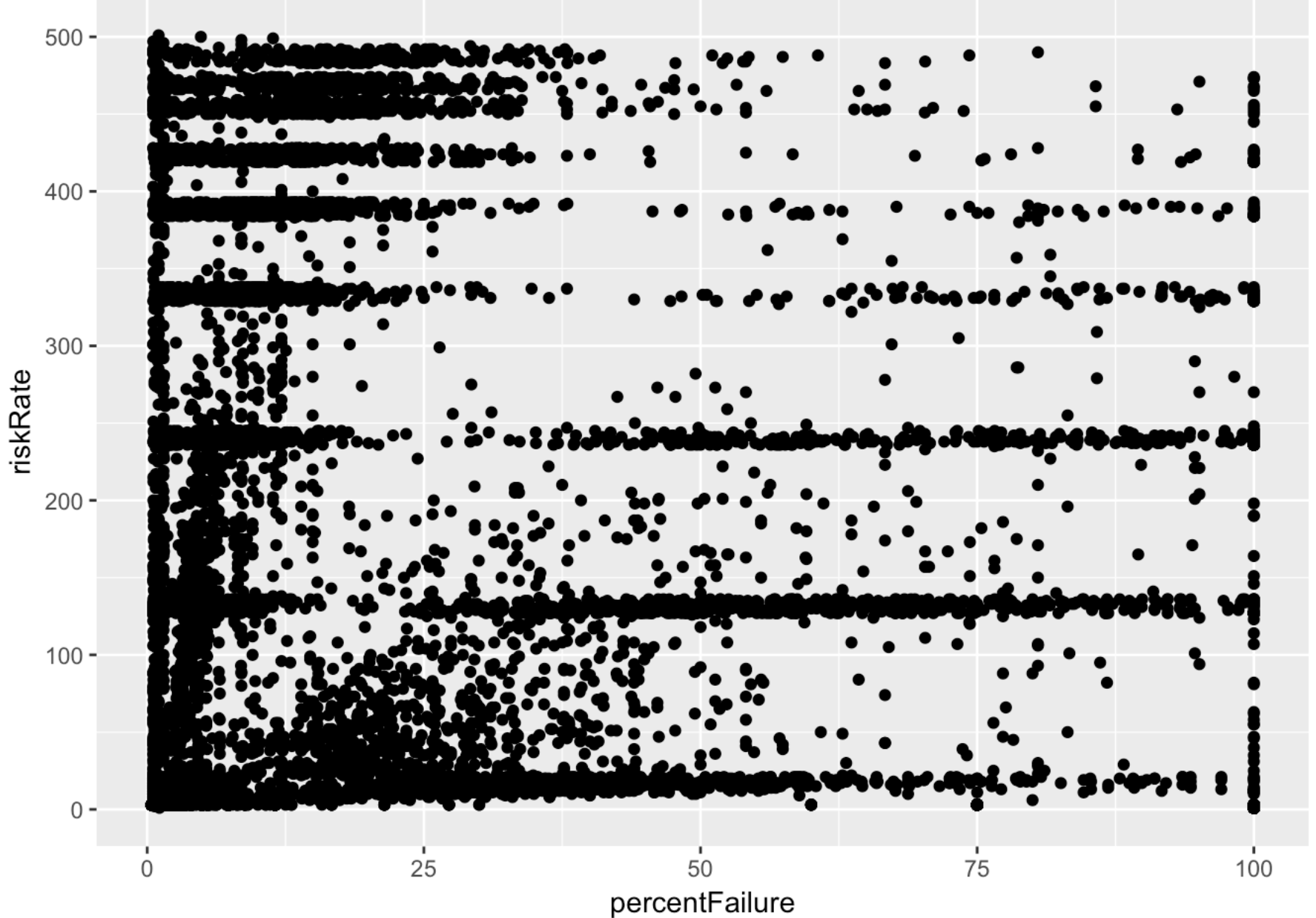
```
mydata1$alive <- (mydata1$numCases - mydata1$numDeath)
```

Remove negative entires, number of cases cannot be less than number of death, hence those are bad data hence removed.

```
mydata1 <- mydata1 %>%
  filter(alive >= 0)
```

```
mydata1$percentSuccess <- round((mydata1$alive/mydata1$numCases)*100,digits=2)
mydata1$percentFailure <- round(100.00-mydata1$percentSuccess,digits=2)
```

```
ggplot(mydata1) + aes(percentFailure,riskRate) + geom_point()
```



```
cor(mydata1$percentFailure, mydata1$riskRate)
```

```
## [1] -0.4396215
```

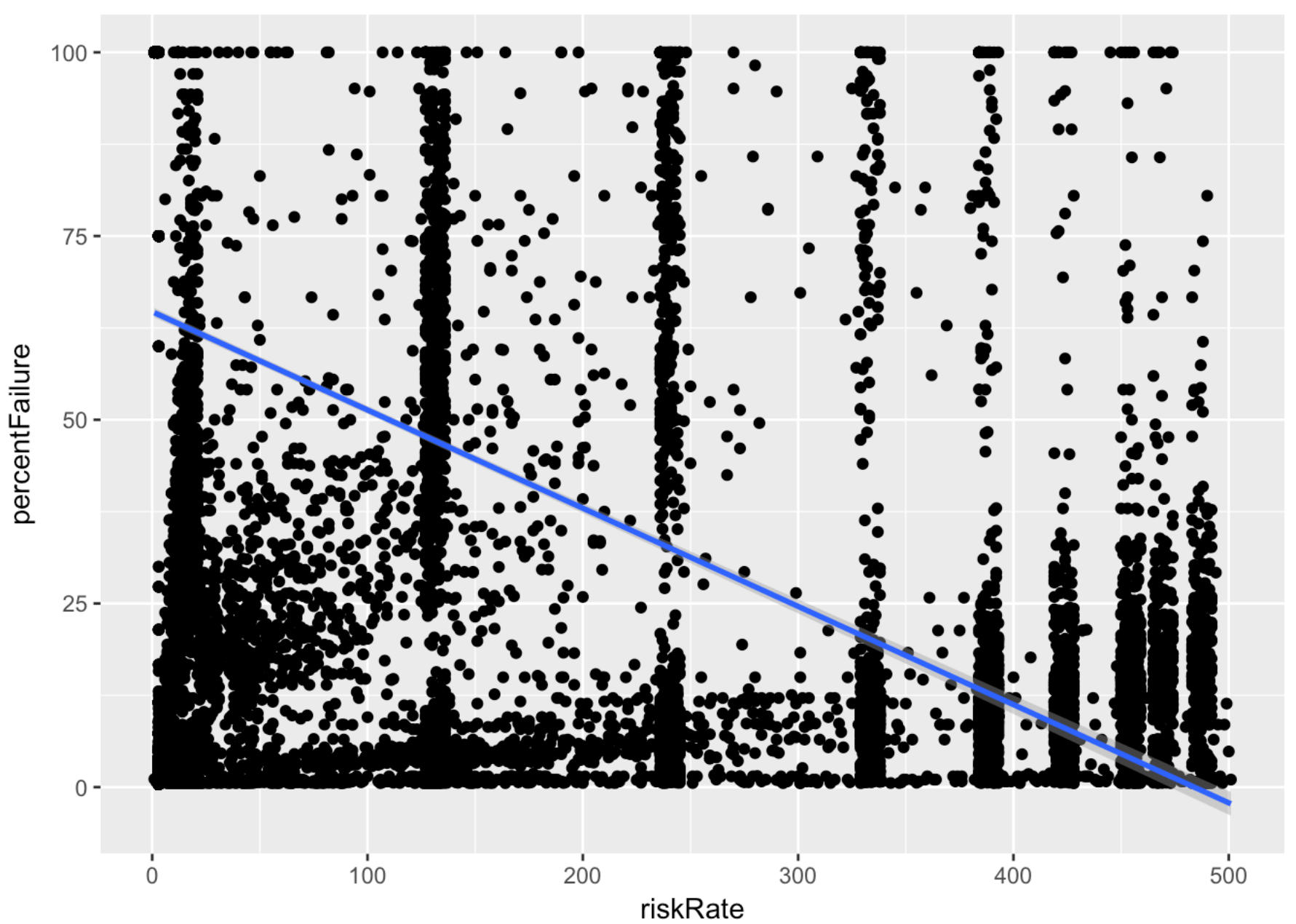
```
cor(log(mydata1$percentFailure), log(mydata1$riskRate))
```

```
## [1] -0.36639
```

```
## PRINCIPLE: Visualizing linear relationships
```

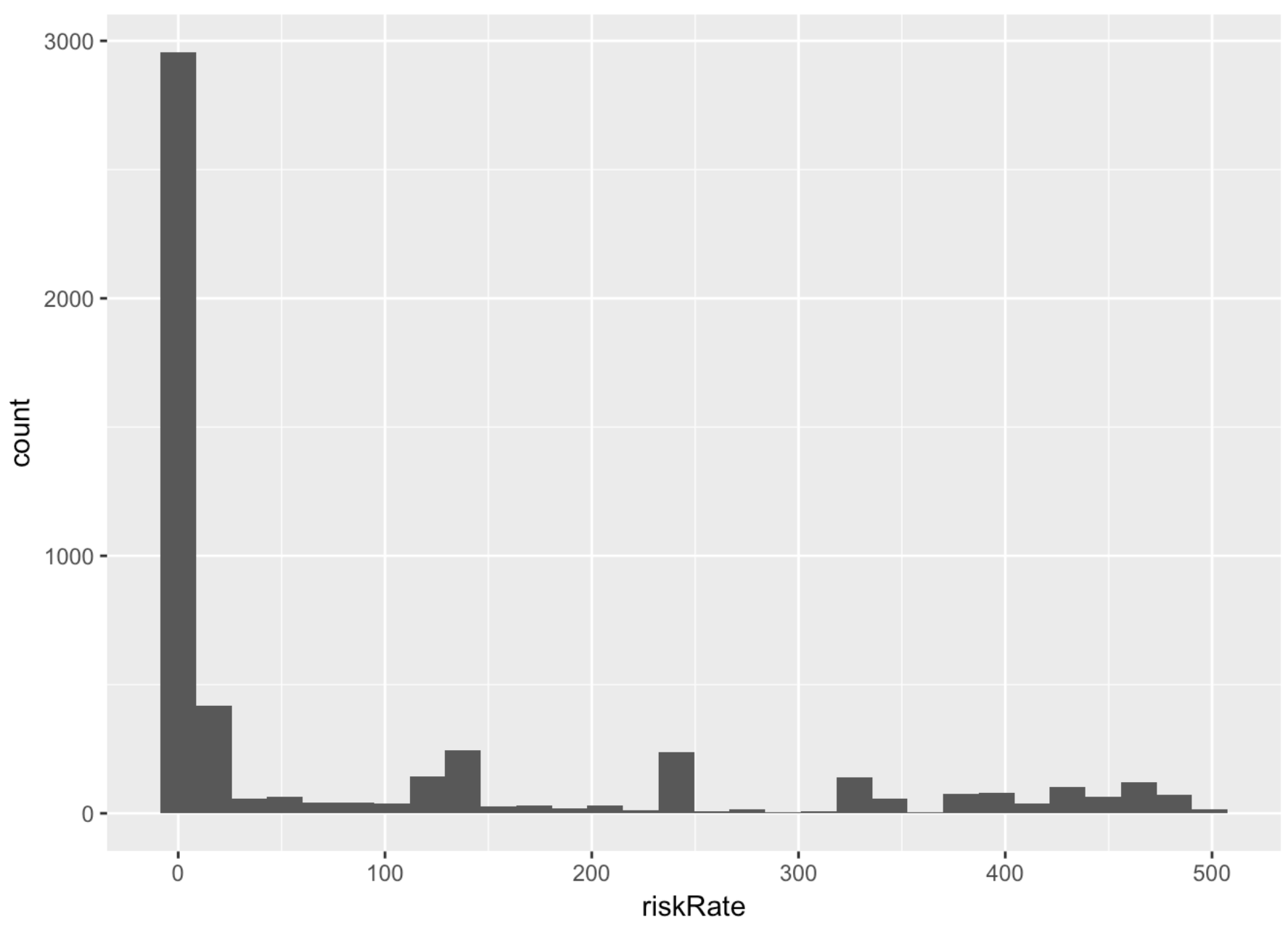
```
#We can try and fit a linear line to the data to see if there is a relationship
```

```
ggplot(mydata1) + aes( riskRate ,percentFailure)+ geom_point() + stat_smooth(method =  
'lm')
```

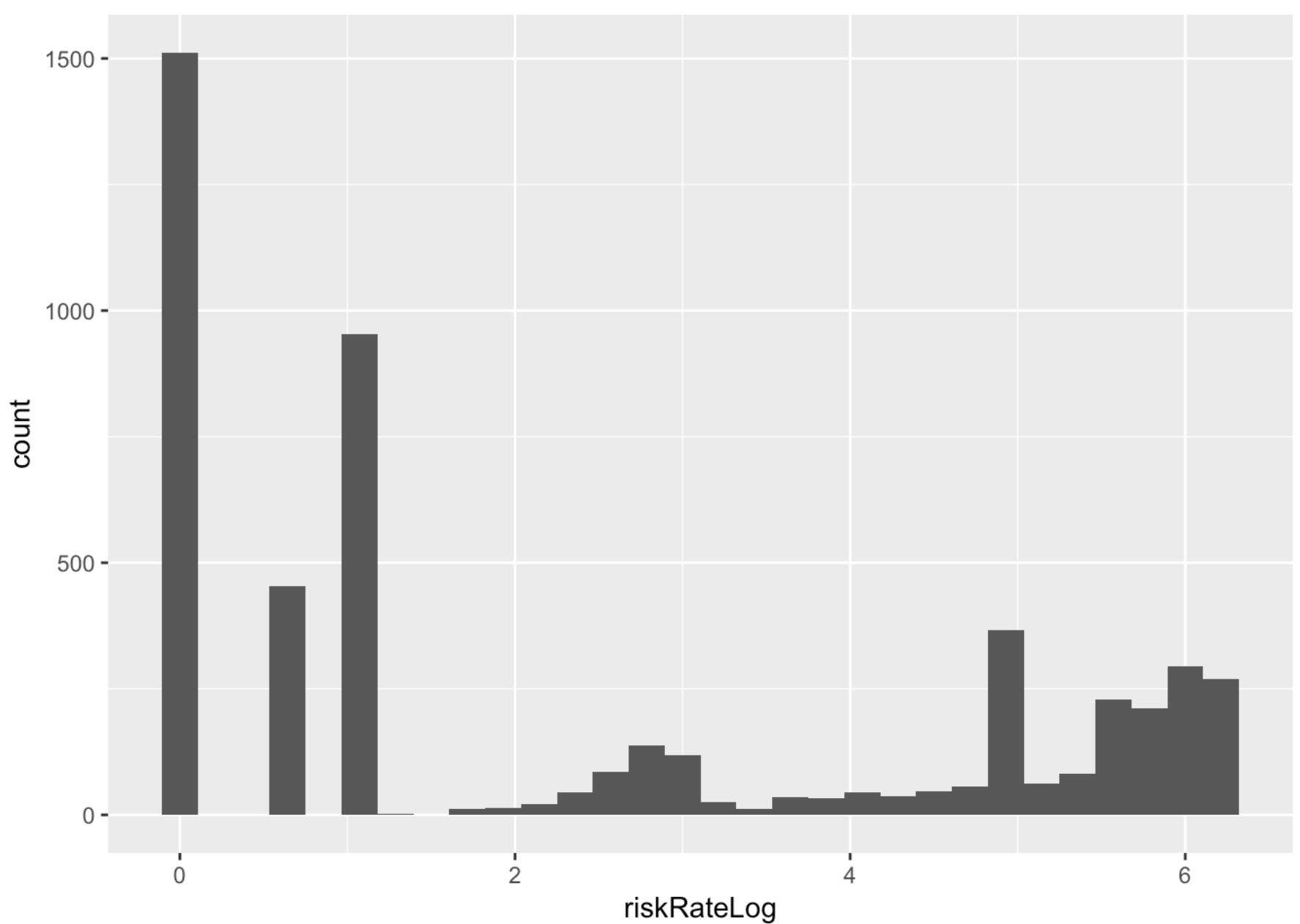


```
# Get the value for Los Angeles, as LA is the highest contributor to death number.
```

```
dfLA <- mydata1 %>%  
  filter( county == "Los Angeles")  
  #filter( year == 2014) %>%  
  #arrange(year)  
  
dfLAMutate <- dfLA %>%  
  mutate(riskRateLog = log(riskRate))  
  
ggplot(dfLAMutate) + aes(riskRate) + geom_histogram(bins = 30)
```



```
ggplot(dfLAMutate) + aes(riskRateLog) + geom_histogram(bins = 30)
```

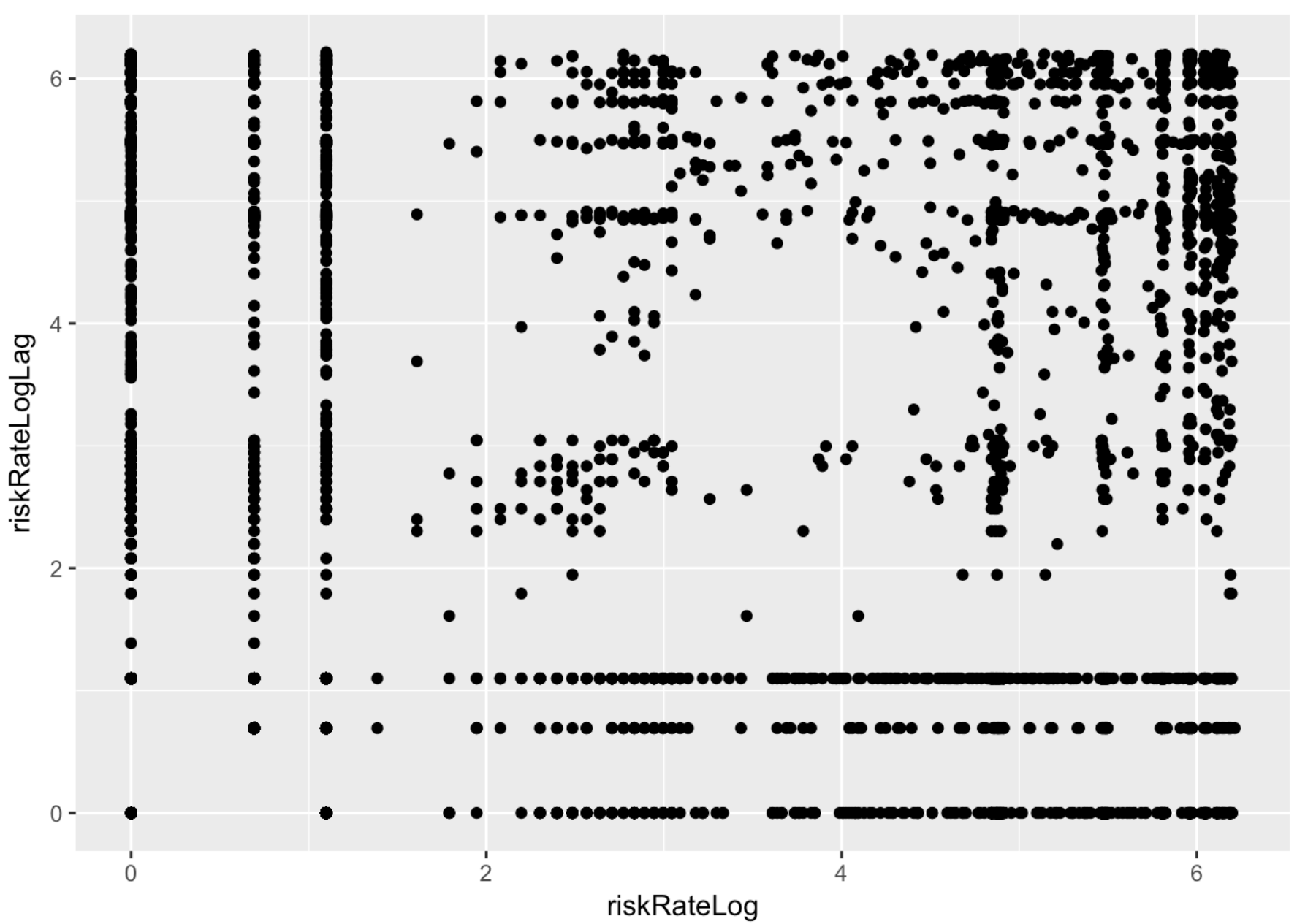


```
dfLAMutate <- dfLAMutate %>%  
  mutate(riskRateLogLag = lag(riskRateLog)) %>%  
  mutate(riskRateLogDiff = riskRateLog - lag(riskRateLogLag) )  
  
# We can see that they are slightly correlated  
cor(dfLAMutate$riskRateLog, dfLAMutate$riskRateLogLag, use = 'complete')
```

```
## [1] 0.1828183
```

```
ggplot(dfLAMutate) + aes(riskRateLog, riskRateLogLag) + geom_point()
```

```
## Warning: Removed 1 rows containing missing values (geom_point).
```



```
summary(dfLA$riskRate)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      1.00   1.00    3.00   93.07  133.00   500.00
```

```
summary(dfLA$percentSuccess)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      0.00   0.00   68.13   50.96   95.90   99.60
```

```
cor(dfLA$riskRate, dfLA$percentSuccess)
```

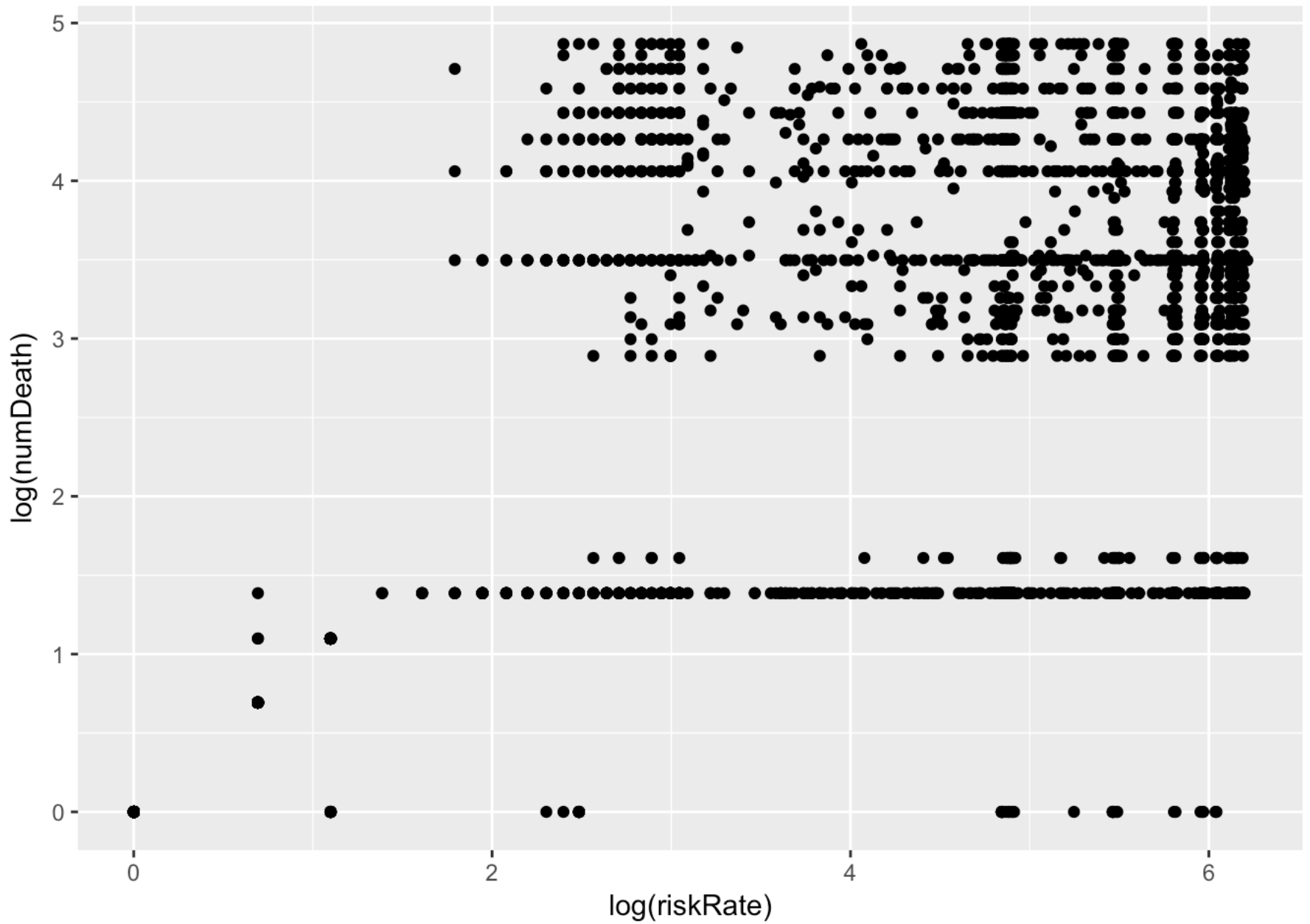
```
## [1] 0.3967339
```

```
cor(log(dfLA$riskRate), log(dfLA$numDeath))
```

```
## [1] 0.8177901
```

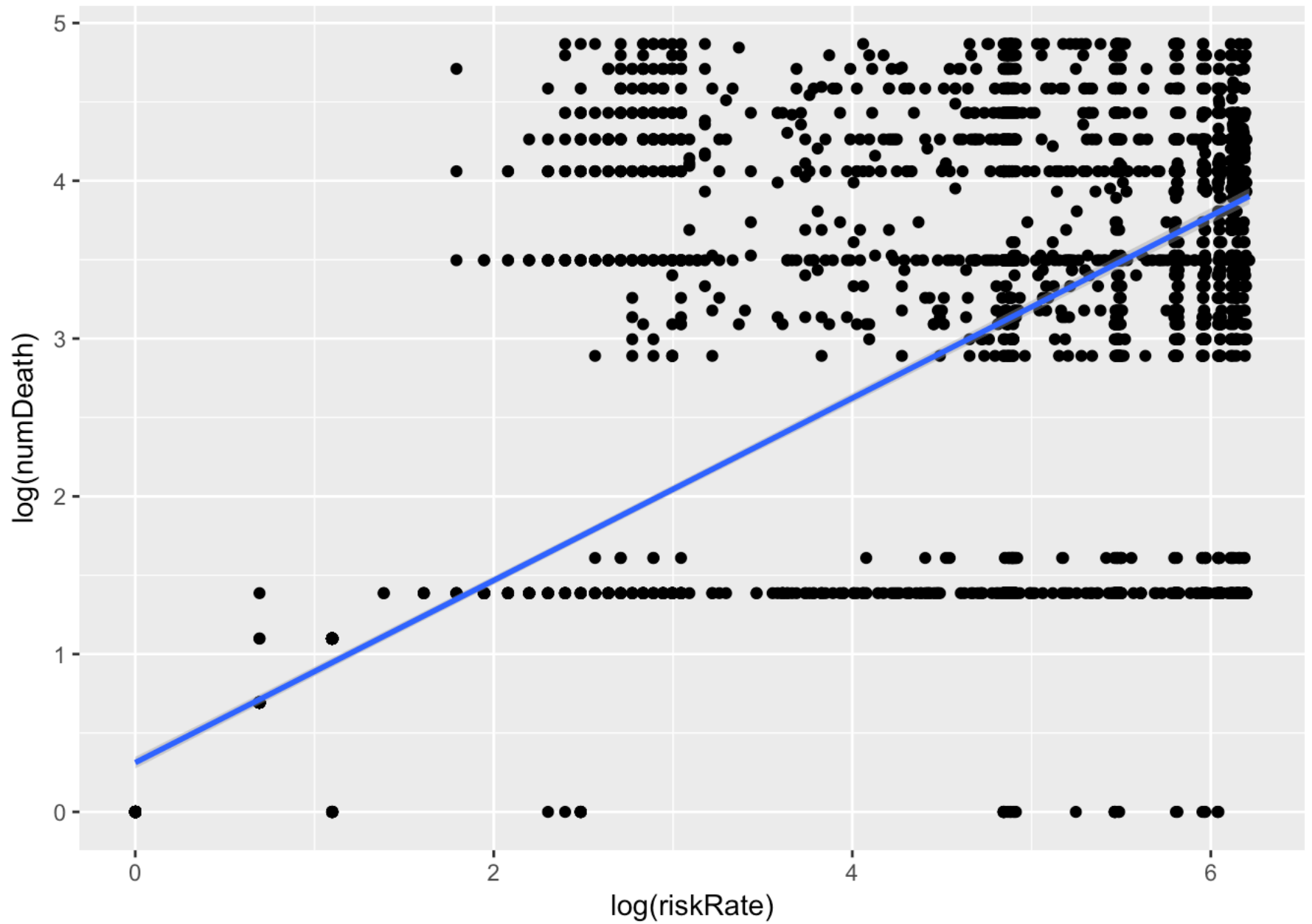

It is observed that RiskRate and number of Death at Los Angeles county are well corelated.

```
ggplot(dfLA) + aes(log(riskRate), log(numDeath)) + geom_point()
```



It is observed that log of number of death increases with log of Risrate of the procedure.

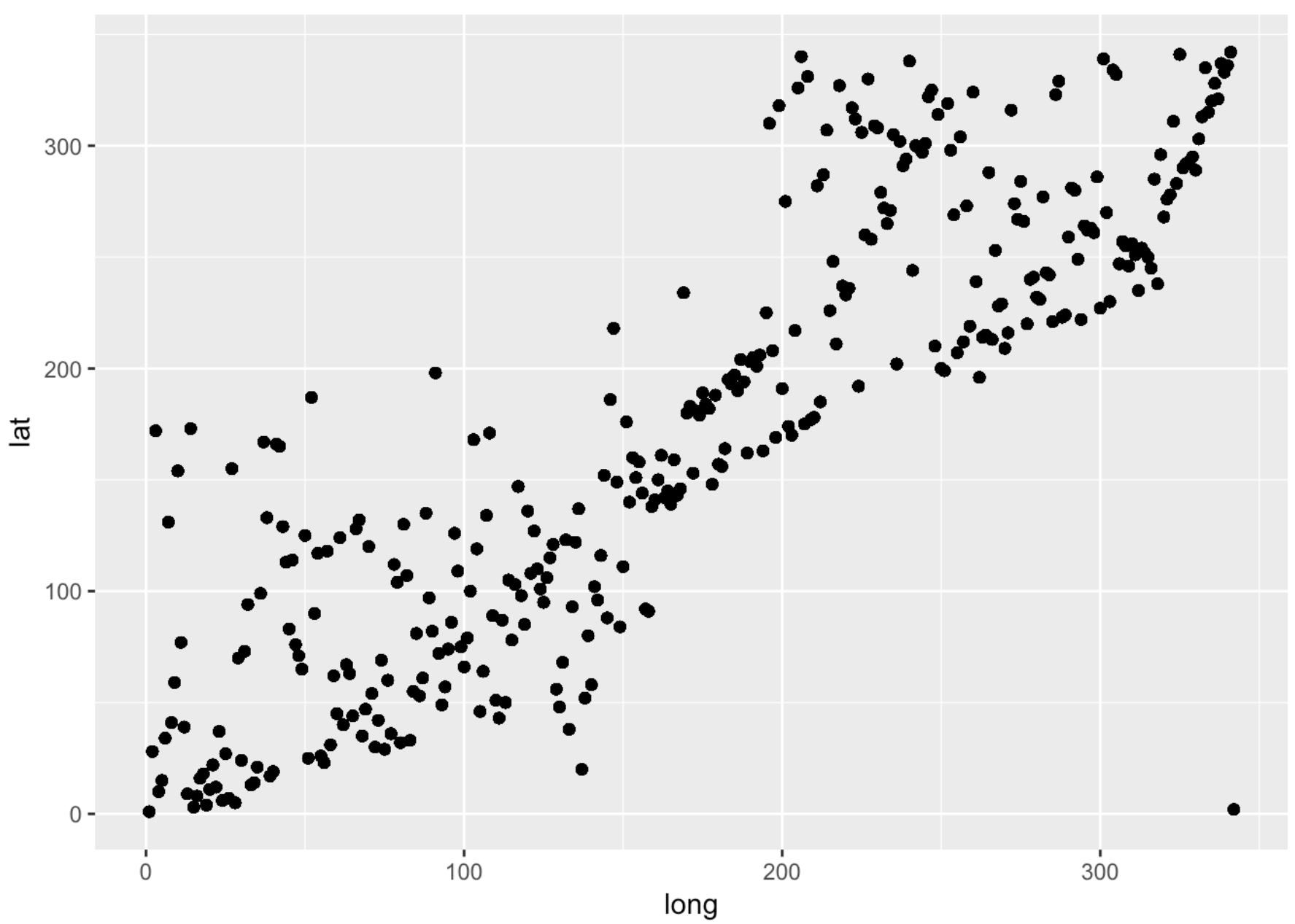
```
ggplot(dfLA) + aes(log(riskRate), log(numDeath)) + geom_point()+ stat_smooth(metho  
d = 'lm')
```



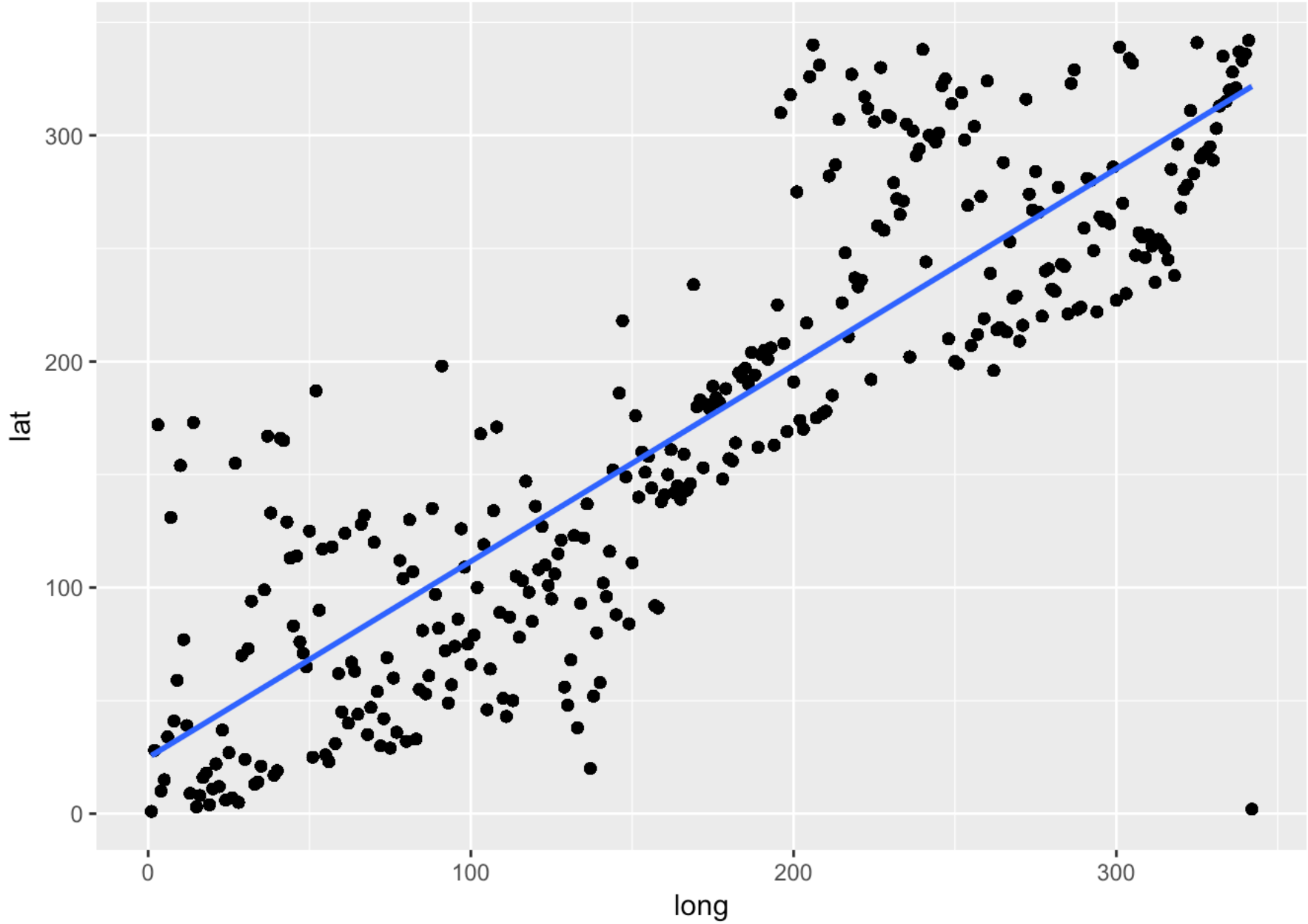
```
## Try to find relation between hospital coordinates  
cor(mydata1$long,mydata1$lat)
```

```
## [1] 0.8663495
```

```
## Seems to be very well co-related. Plot them as geom points  
ggplot(mydata1) + aes(long, lat) + geom_point()
```



```
## Try to find linear regression and fit a line among points  
ggplot(mydata1) + aes( long ,lat)+ geom_point() + stat_smooth(method = 'lm')
```



COMMUNICATE

#It is observed that Year 2014 recorded highest number of death. Also, Los Angeles county recorded maximum number of inpatient deaths. At the same time it is observed that with increased rate of risk, number of deaths increased.