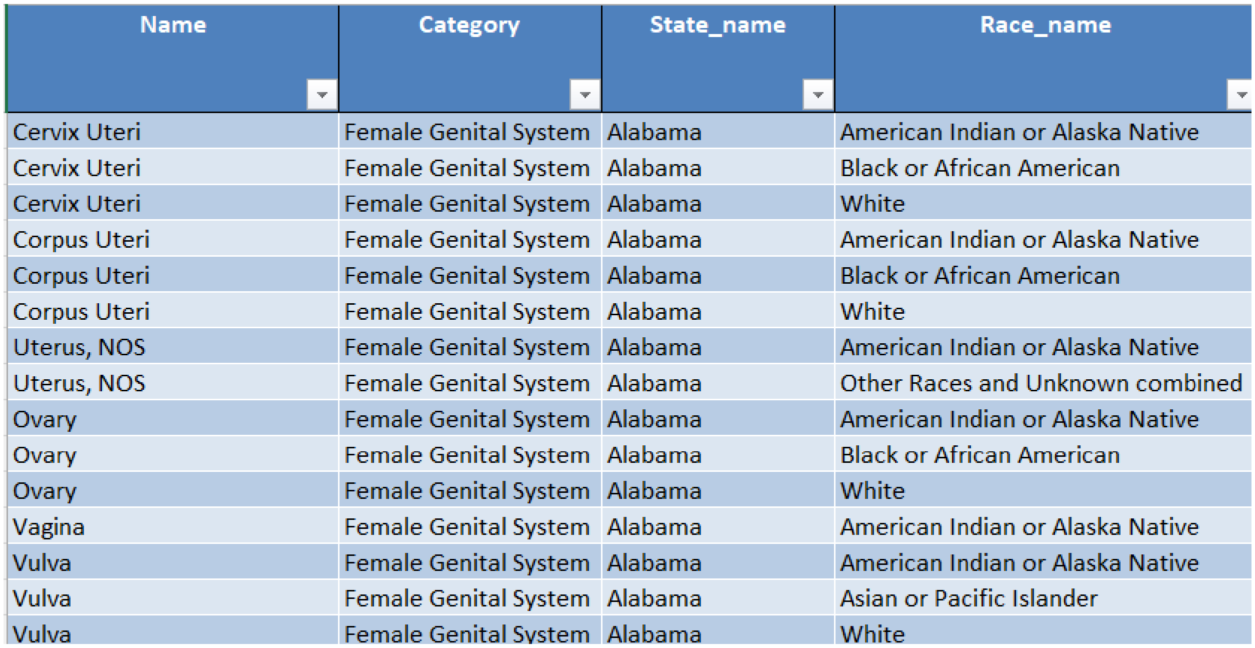
Categorical Data

- Cancer type – Nominal Data
- Race – Nominal Data
- State – Nominal Data

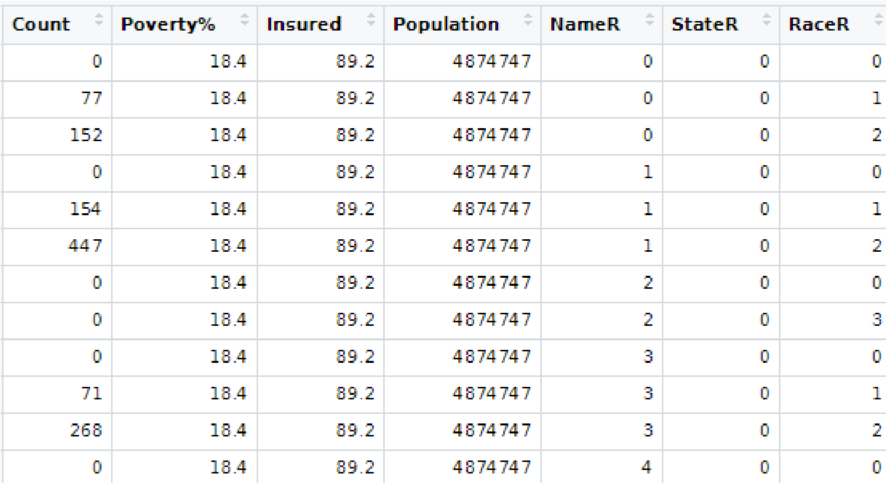
Numerical Data

- Percent of the Population below Poverty – Continuous Numerical Data
- Percent of the Population Insured – Continuous Numerical Data
- Population – Discrete Numerical Data

Encoding

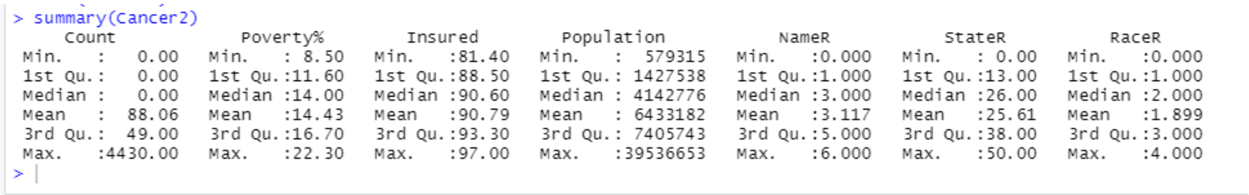


Name	Category	State_name	Race_name
Cervix Uteri	Female Genital System	Alabama	American Indian or Alaska Native
Cervix Uteri	Female Genital System	Alabama	Black or African American
Cervix Uteri	Female Genital System	Alabama	White
Corpus Uteri	Female Genital System	Alabama	American Indian or Alaska Native
Corpus Uteri	Female Genital System	Alabama	Black or African American
Corpus Uteri	Female Genital System	Alabama	White
Uterus, NOS	Female Genital System	Alabama	American Indian or Alaska Native
Uterus, NOS	Female Genital System	Alabama	Other Races and Unknown combined
Ovary	Female Genital System	Alabama	American Indian or Alaska Native
Ovary	Female Genital System	Alabama	Black or African American
Ovary	Female Genital System	Alabama	White
Vagina	Female Genital System	Alabama	American Indian or Alaska Native
Vulva	Female Genital System	Alabama	American Indian or Alaska Native
Vulva	Female Genital System	Alabama	Asian or Pacific Islander
Vulva	Female Genital System	Alabama	White



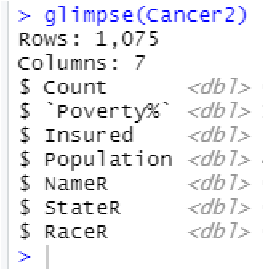
Count	Poverty%	Insured	Population	NameR	StateR	RaceR
0	18.4	89.2	4874747	0	0	0
77	18.4	89.2	4874747	0	0	1
152	18.4	89.2	4874747	0	0	2
0	18.4	89.2	4874747	1	0	0
154	18.4	89.2	4874747	1	0	1
447	18.4	89.2	4874747	1	0	2
0	18.4	89.2	4874747	2	0	0
0	18.4	89.2	4874747	2	0	3
0	18.4	89.2	4874747	3	0	0
71	18.4	89.2	4874747	3	0	1
268	18.4	89.2	4874747	3	0	2
0	18.4	89.2	4874747	4	0	0

Summary

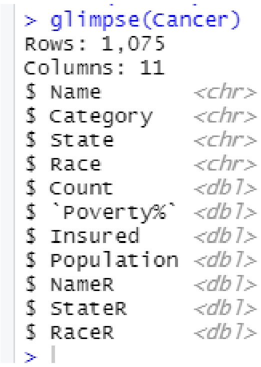


```
> summary(Cancer2)
     Count             Poverty%         Insured         Population            NameR           StateR           RaceR      
 Min.   :   0.00   Min.   : 8.50   Min.   :81.40   Min.   :  579315   Min.   :0.000   Min.   : 0.00   Min.   :0.000  
 1st Qu.:   0.00   1st Qu.:11.60   1st Qu.:88.50   1st Qu.: 1427538   1st Qu.:1.000   1st Qu.:13.00   1st Qu.:1.000  
 Median :   0.00   Median :14.00   Median :90.60   Median : 4142776   Median :3.000   Median :26.00   Median :2.000  
 Mean   :  88.06   Mean   :14.43   Mean   :90.79   Mean   : 6433182   Mean   :3.117   Mean   :25.61   Mean   :1.899  
 3rd Qu.:  49.00   3rd Qu.:16.70   3rd Qu.:93.30   3rd Qu.: 7405743   3rd Qu.:5.000   3rd Qu.:38.00   3rd Qu.:3.000  
 Max.   :4430.00   Max.   :22.30   Max.   :97.00   Max.   :39536653   Max.   :6.000   Max.   :50.00   Max.   :4.000  
> 
```

Glimpse



```
> glimpse(Cancer2)
Rows: 1,075
Columns: 7
$ Count       <dbl>
$ `Poverty%`  <dbl>
$ Insured     <dbl>
$ Population  <dbl>
$ NameR       <dbl>
$ StateR      <dbl>
$ RaceR       <dbl>
> 
```



```
> glimpse(Cancer)
Rows: 1,075
Columns: 11
$ Name        <chr>
$ Category    <chr>
$ State       <chr>
$ Race        <chr>
$ Count       <dbl>
$ `Poverty%`  <dbl>
$ Insured     <dbl>
$ Population  <dbl>
$ NameR       <dbl>
$ StateR      <dbl>
$ RaceR       <dbl>
> 
```

```
# Load package

library(tidyverse)

glimpse(CancerCombinedFile3)

# Rename works for Columns

names(CancerCombinedFile3)[names(CancerCombinedFile3) == "State_name"] <- "State"
names(CancerCombinedFile3)[names(CancerCombinedFile3) == "Race_name"] <- "Race"
names(CancerCombinedFile3)[names(CancerCombinedFile3) == "Percentage population below poverty"] <- "Poverty%"
names(CancerCombinedFile3)[names(CancerCombinedFile3) == "Percentage population insured"] <- "Insured"

glimpse(CancerCombinedFile3)

Cancer <- CancerCombinedFile3[, 2:9]
head(Cancer, n=10)

#Re-coding
library(dplyr)
library(gapminder)

Cancer$NameR <- NA

Cancer$NameR[Cancer$Name=='Cervix Uteri'] <- 0
Cancer$NameR[Cancer$Name=='Corpus Uteri'] <- 1
Cancer$NameR[Cancer$Name=='Uterus, NOS'] <- 2
```

```
Cancer$NameR[Cancer$Name=='Ovary'] <- 3

Cancer$NameR[Cancer$Name=='Vagina'] <- 4

Cancer$NameR[Cancer$Name=='Vulva'] <- 5

Cancer$NameR[Cancer$Name=='Other Female Genital Organs'] <- 6


library(plyr)

# This rename code works for data in a column


Cancer$Race[Cancer$Race == "American Indian or Alaska Native"] <- "NativeAmer"

Cancer$Race[Cancer$Race == "Black or African American"] <- "AfricanAmer"

Cancer$Race[Cancer$Race == "White"] <- "Caucasian"

Cancer$Race[Cancer$Race == "Other Races and Unknown combined"] <- "Other"

Cancer$Race[Cancer$Race == "Asian or Pacific Islander"] <- "AsianAmer"


glimpse(Cancer)


summary(Cancer)


CancerPovPerOver20 <- filter(Cancer, 'Poverty%' > 20)

CancerPovPerOver20


CancerPovPerUnder9 <- filter(Cancer, 'Poverty%' < 9)

CancerPovPerUnder9


# Box Plot


boxplot(Cancer$Race, main="Box plot", ylab="Poverty%")


# Have to make race numeric for boxplot to work
```

```
unique(Cancer$Race)
Cancer$RaceR <- NA

Cancer$RaceR[Cancer$Race=="NativeAmer"]<-0
Cancer$RaceR[Cancer$Race=="AfricanAmer"]<-1
Cancer$RaceR[Cancer$Race=="Caucasian"]<-2
Cancer$RaceR[Cancer$Race=="Other"]<-3
Cancer$RaceR[Cancer$Race=="AsianAmer"]<-4

# Basic Graphs

boxplot(Cancer$RaceR, main="Box plot", ylab="Poverty%")

hist(Cancer$RaceR)
hist(Cancer$`Poverty%`)

# Histogram with 12 Bins
hist(Cancer$`Poverty%`,
    breaks=12,
    col="red",
    xlab="Poverty Population %",
    main="Colored histogram with 12 bins")

# Histogram with Rug Plot and Density Curve
hist(Cancer$`Poverty%`,
    freq = FALSE,
    breaks = 12,
    col = "red",
    xlab = "Histogram, Rug Plot, Density Curve")
rug(jitter(Cancer$`Poverty%`))
lines(density(Cancer$`Poverty%`), col = "blue", lwd=2)

# Histogram with Normal Curve and Box
x <- Cancer$`Poverty%`
h <- hist(x,
        breaks=12,
        col="red",
        xlab="Histogram with Normal Curve and Box")
xfit <- seq(min(x), max(x), length=40)
yfit<-dnorm(xfit, mean=mean(x), sd=sd(x))
yfit <- yfit*diff(h$mids[1:2])*length(x)
lines(xfit, yfit, col="blue", lwd=2)
box()

# Boxplot

head(Cancer)

d2 <- ggplot(Cancer, aes(x = "RaceR", y = "Poverty%"))
d2 + geom_boxplot() + xlab("")

d2 <- ggplot(Cancer, aes(x = "", y = "RaceR"))
d2 + geom_boxplot() + xlab("")

# Descriptive Statistics

myvars <- c("RaceR", "Poverty%")
```

```
head(Cancer[myvars])
summary(Cancer[myvars])

mystats <- function(x, na.omit=FALSE){
  if(na.omit)
    x <- x[!is.na(x)]
  m <- mean(x)
  n <- length(x)
  s <- sd(x)
  skew <- sum((x-m)^3/s^3)/n
  kurt <- sum((x-m)^4/s^4)/n-3
  return(c(n=n, mean=m, stdev=s, skew=skew, kurtosis=kurt))
}

myvars <- c("RaceR", "Poverty%")
sapply(Cancer[myvars], mystats, na.omit=TRUE)

summary(Cancer$State)
Cancer[c("State")]
glimpse(Cancer)

unique(Cancer$State)
StateR <- as.numeric(State)
StateR

myvars <- names(Cancer) %in% c("RaceR.f", "Poverty%.f")
Cancer2 <- Cancer[!myvars]

StateR <- c("Alabama", "Alaska", "Arizona", "Arkansas", "California", "Colorado", "Connecticut",
        "District of Columbia", "Georgia", "Idaho", "Indiana", "Kansas", "Louisiana", "Maryland",
        "Michigan", "Mississippi", "Montana", "Nevada", "New Jersey", "New York", "North Dakota",
        "Oklahoma", "Pennsylvania", "South Carolina", "Tennessee", "Utah", "Virginia", "West Virginia",
        "Wyoming", "Delaware", "Florida", "Hawaii", "Illinois", "Iowa", "Kentucky", "Maine",
"Massachusetts",
        "Minnesota", "Missouri", "Nebraska", "New Hampshire", "New Mexico", "North Carolina",
"Ohio",
        "Oregon", "Rhode Island", "South Dakota", "Texas", "Vermont", "Washington", "Wisconsin"
        )
unique(Cancer$RaceR)
RaceR2 <- c(0, 1, 2, 3, 4)
unique(Cancer$`Poverty%`)


PovPerR <- c(18.4, 10.1, 17.7, 18.8, 15.8, 12.2, 10.4, 12.0, 17.9, 16.1, 17.8, 10.8, 15.2, 14.0, 15.0, 12.3,
13.3, 19.7, 13.5, 9.9, 11.4, 16.3, 22.3, 15.3, 14.9, 12.4, 8.5, 10.9, 20.9, 15.5, 16.8, 11.2, 15.4, 16.5, 15.7,
13.8, 17.2, 16.7, 11.7, 11.6, 12.7)


Cancer3 <- data.frame(RaceR2, StateR, PovPerR)


glimpse(Cancer2)


Pov_num <- as.numeric(PovPerR)
Pov_num


print(State)


Cancer$StateR <- NA


Cancer$StateR[Cancer$State=='Alabama'] <- 0
Cancer$StateR[Cancer$State=='Alaska'] <- 1
```

```
Cancer$StateR[Cancer$State=='Arizona'] <- 2

Cancer$StateR[Cancer$State=='Arkansas'] <- 3

Cancer$StateR[Cancer$State=='California'] <- 4

Cancer$StateR[Cancer$State=='Colorado'] <- 5

Cancer$StateR[Cancer$State=='Connecticut'] <- 6

Cancer$StateR[Cancer$State=='District of Columbia'] <- 7

Cancer$StateR[Cancer$State=='Georgia'] <- 8

Cancer$StateR[Cancer$State=='Idaho'] <- 9

Cancer$StateR[Cancer$State=='Indiana'] <- 10

Cancer$StateR[Cancer$State=='Kansas'] <- 11

Cancer$StateR[Cancer$State=='Louisiana'] <- 12

Cancer$StateR[Cancer$State=='Maryland'] <- 13

Cancer$StateR[Cancer$State=='Michigan'] <- 14

Cancer$StateR[Cancer$State=='Mississippi'] <- 15

Cancer$StateR[Cancer$State=='Montana'] <- 16

Cancer$StateR[Cancer$State=='Nevada'] <- 17

Cancer$StateR[Cancer$State=='New Jersey'] <- 18

Cancer$StateR[Cancer$State=='New York'] <- 19

Cancer$StateR[Cancer$State=='North Dakota'] <- 20

Cancer$StateR[Cancer$State=='Oklahoma'] <- 21

Cancer$StateR[Cancer$State=='Pennsylvania'] <- 22

Cancer$StateR[Cancer$State=='South Carolina'] <- 23

Cancer$StateR[Cancer$State=='Tennessee'] <- 24

Cancer$StateR[Cancer$State=='Utah'] <- 25

Cancer$StateR[Cancer$State=='Virginia'] <- 26

Cancer$StateR[Cancer$State=='West Virginia'] <- 27

Cancer$StateR[Cancer$State=='Wyoming'] <- 28

Cancer$StateR[Cancer$State=='Delaware'] <- 29

Cancer$StateR[Cancer$State=='Florida'] <- 30
```

```
Cancer$StateR[Cancer$State=='Hawaii'] <- 31
Cancer$StateR[Cancer$State=='Illinois'] <- 32
Cancer$StateR[Cancer$State=='Iowa'] <- 33
Cancer$StateR[Cancer$State=='Kentucky'] <- 34
Cancer$StateR[Cancer$State=='Maine'] <- 35
Cancer$StateR[Cancer$State=='Massachusetts'] <- 36
Cancer$StateR[Cancer$State=='Minnesota'] <- 37
Cancer$StateR[Cancer$State=='Missouri'] <- 38
Cancer$StateR[Cancer$State=='Nebraska'] <- 39
Cancer$StateR[Cancer$State=='New Hampshire'] <- 40
Cancer$StateR[Cancer$State=='New Mexico'] <- 41
Cancer$StateR[Cancer$State=='North Carolina'] <- 42
Cancer$StateR[Cancer$State=='Ohio'] <- 43
Cancer$StateR[Cancer$State=='Oregon'] <- 44
Cancer$StateR[Cancer$State=='Rhode Island'] <- 45
Cancer$StateR[Cancer$State=='South Dakota'] <- 46
Cancer$StateR[Cancer$State=='Texas'] <- 47
Cancer$StateR[Cancer$State=='Vermont'] <- 48
Cancer$StateR[Cancer$State=='Washington'] <- 49
Cancer$StateR[Cancer$State=='Wisconsin'] <- 50

Cancer2 <- Cancer[, 5:11]
head(Cancer2, n=10)
```