```
library(readr)
acs_14_1yr_s0201 <- read_csv("completed/assignment03/acs-14-1yr-s0201.csv")
table1 <- acs_14_1yr_s0201
library(ggplot2)
```

I: List the name of each field and what you believe the data type
and intent is of the data included in each field
(Example: Id - Data Type: varchar (contains text and numbers)
Intent: unique identifier for each row)

```
spec(table1)
  cols(
  Id = col_character(), -- contains numbers and characters
  Id2 = col_double(), -- includes numbers only
  Geography = col_character(), -- characters describing the observation location by county
  PopGroupID = col_double(), -- numeric (value of 1), ID denoting the population group
  `POPGROUP.display-label` = col_character(), -- character, denoting the label of the population group
  RacesReported = col_double(), -- number, a count of the reported races in the survey
  HSDegree = col_double(), -- number (float), presumably a percentage of the population with HS
Degrees
  BachDegree = col_double()) -- number (float), presumably a percentage of the population with
Bachelor's Degrees
```

II: Run the following functions and provide the results: str(); nrow(); ncol()

str(table1)

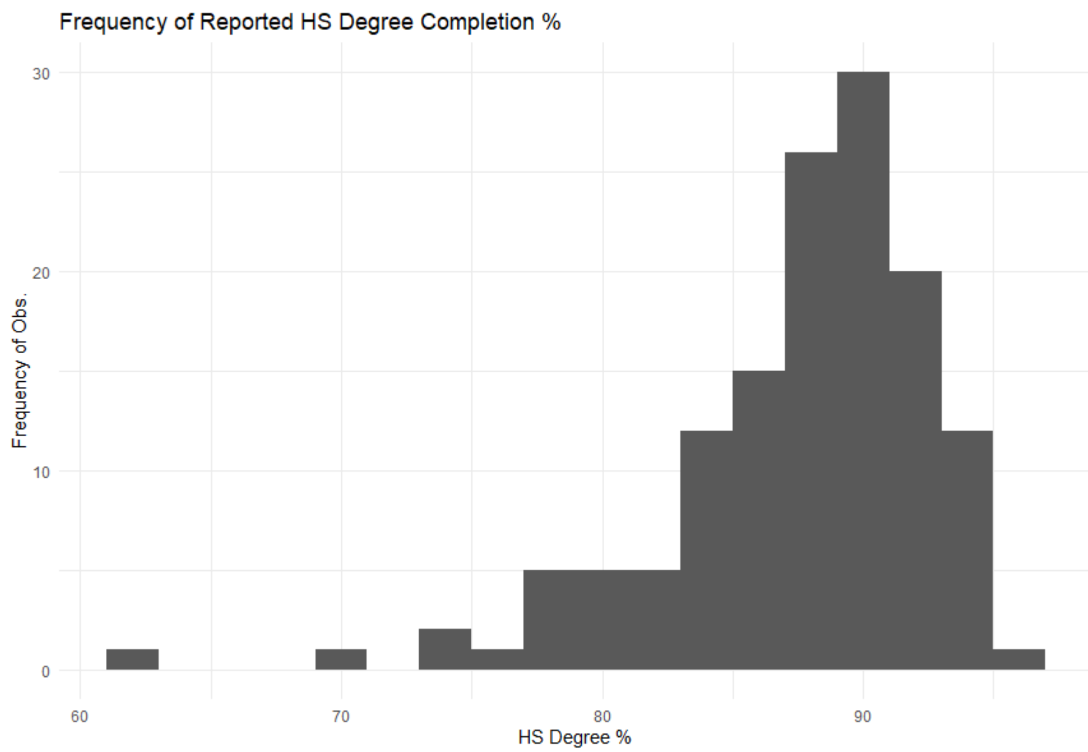
```
spc_tbl_ [136 × 8] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
 $ Id                      : chr [1:136] "0500000US01073" "0500000US04013" "050
0000US04019" "0500000US06001" ...
 $ Id2                     : num [1:136] 1073 4013 4019 6001 6013 ...
 $ Geography               : chr [1:136] "Jefferson County, Alabama" "Maricopa
County, Arizona" "Pima County, Arizona" "Alameda County, California" ...
 $ PopGroupID              : num [1:136] 1 1 1 1 1 1 1 1 1 1 ...
 $ POPGROUP.display-label: chr [1:136] "Total population" "Total population"
"Total population" "Total population" ...
 $ RacesReported           : num [1:136] 660793 4087191 1004516 1610921 1111339
...
 $ HSDegree                : num [1:136] 89.1 86.8 88 86.9 88.8 73.6 74.5 77.5
84.6 80.6 ...
 $ BachDegree              : num [1:136] 30.5 30.2 30.8 42.8 39.7 19.7 15.4 30.
3 38 20.7 ...
 - attr(*, "spec")=
  .. cols(
  ..   Id = col_character(),
  ..   Id2 = col_double(),
  ..   Geography = col_character(),
  ..   PopGroupID = col_double(),
  ..   `POPGROUP.display-label` = col_character(),
  ..   RacesReported = col_double(),
  ..   HSDegree = col_double(),
  ..   BachDegree = col_double()
  .. )
 - attr(*, "problems")=<externalptr>
```

nrow(table1) -- 136

ncol(table1) -- 8

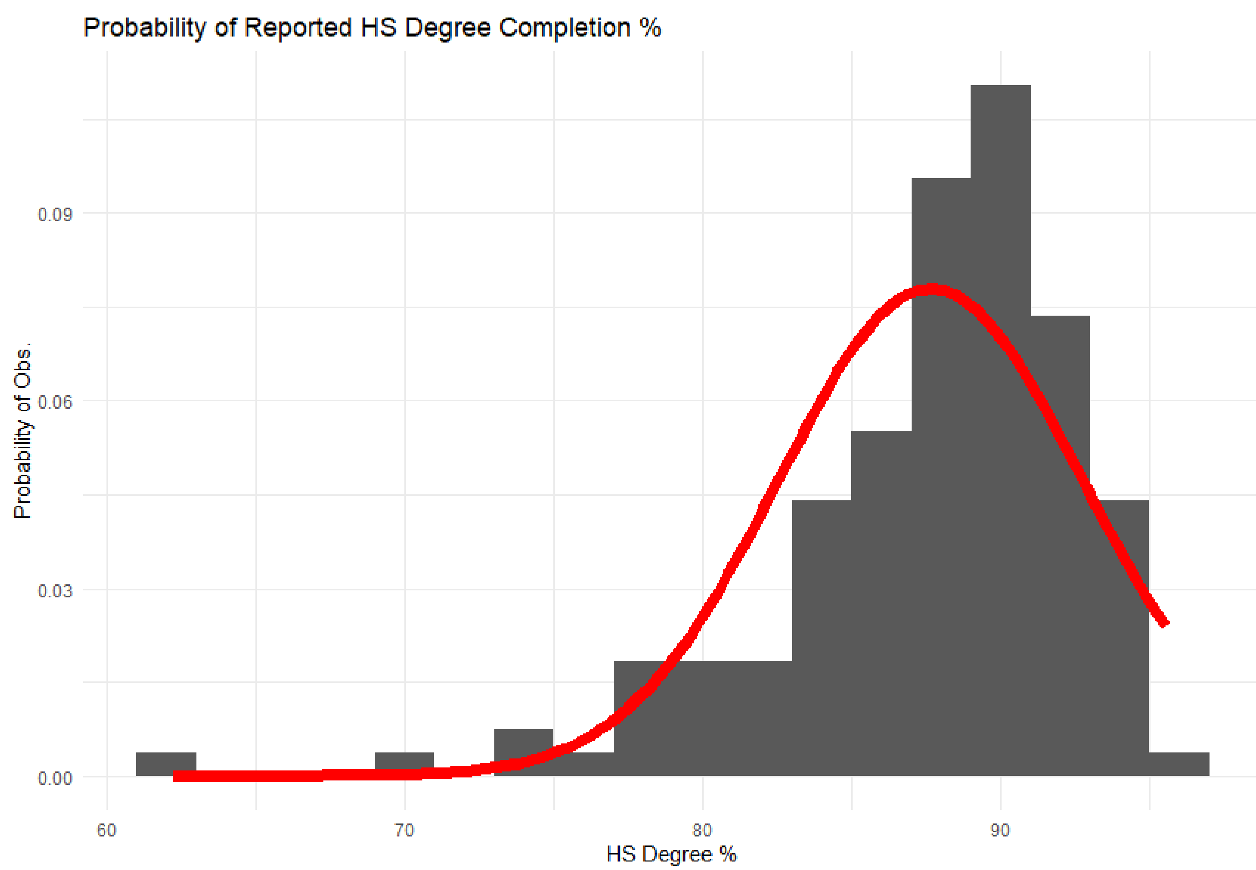
III: Create a Histogram of the HSDegree variable using the ggplot2 package.
Set a bin size for the Histogram that you think best visuals the data
(the bin size will determine how many bars display and how wide they are)
Include a Title and appropriate X/Y axis labels on your Histogram Plot.

ggplot(table1, aes(HSDegree)) + geom_histogram(binwidth = 2) + xlab("HS Degree %") + ylab("Frequency of Obs.") + ggtitle("Frequency of Reported HS Degree Completion %")



IV: Answer the following questions based on the Histogram produced:

Based on what you see in this histogram, is the data distribution unimodal? -- The data is unimodal.
Is it approximately symmetrical? -- The data is not symetrical per its left-skewdness.
Is it approximately bell-shaped? -- The data is shaped like a bell, but is not normally distributed.
Is it approximately normal? -- The data isn't normal, since the median & mode are offset right from the mean.
If not normal, is the distribution skewed? If so, in which direction? -- The distribution is left-skewed.
Include a normal curve to the Histogram that you plotted.

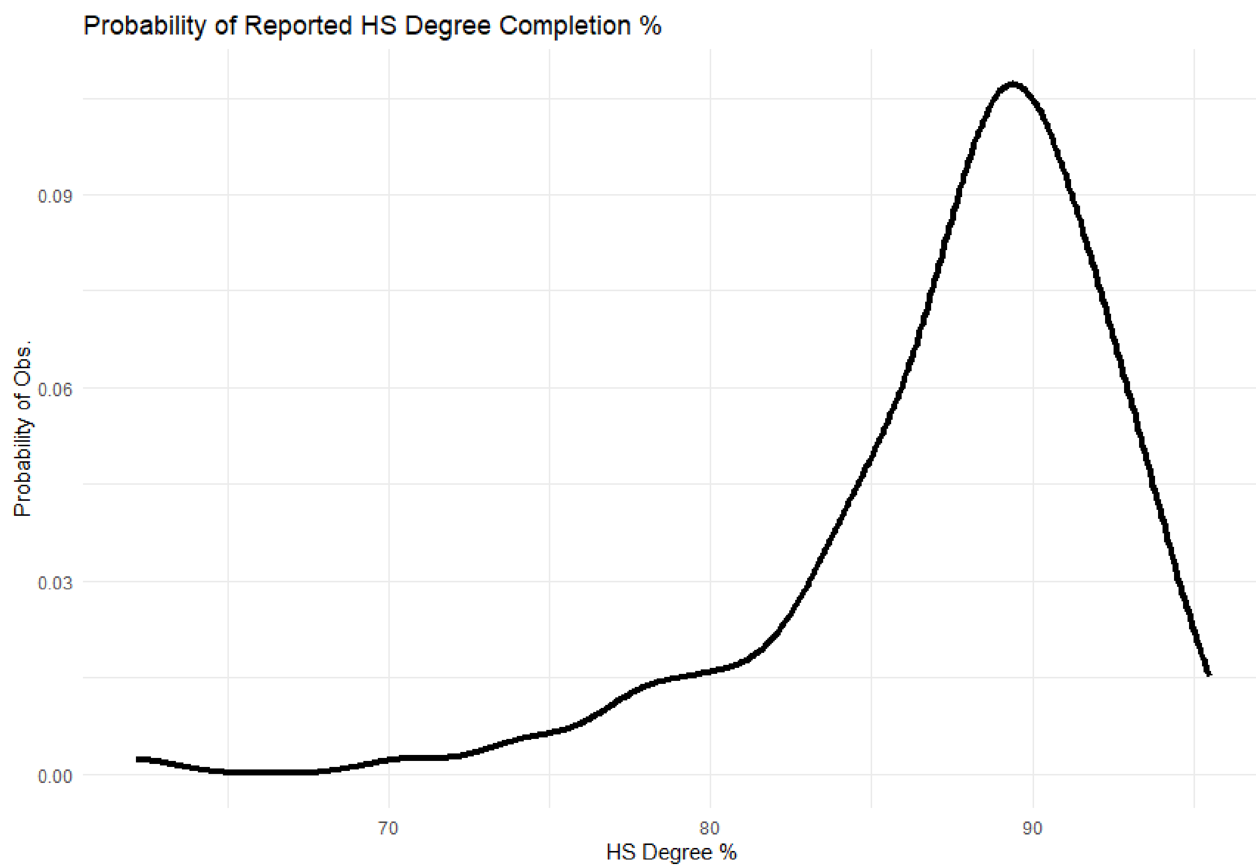



```
ggplot(table1, aes(HSDegree)) +  geom_histogram(aes(y = after_stat(density)), binwidth = 2) +
xlab("HS Degree %") + ylab("Probability of Obs.") +
ggtitle("Probability of Reported HS Degree Completion %") +
stat_function(fun = dnorm,
  args = list(mean = mean(table1$HSDegree),
  sd = sd(table1$HSDegree)),
  col = "red",
  size = 3)
```

Explain whether a normal distribution can accurately be used as a model for this data.
An offset normal distribution would be a low-accuracy predictor of the data, per the skewness and slightly positive kurtosis.
Values left of the center would be over-predicted, and the right, under-predicted.

V: Create a Probability Plot of the HSDegree variable.

```
ggplot(table1, aes(HSDegree)) + geom_density(aes(HSDegree), size = 1.5) +
xlab("HS Degree %") + ylab("Probability of Obs.") +
ggtitle("Probability of Reported HS Degree Completion %")
```



VI: Answer the following questions based on the Probability Plot:

Based on what you see in this probability plot, is the distribution approximately normal? Explain how you know.

One could argue that the distribution resembles normality, but a normal distribution would be a poor predictor of this distribution per:

the left skewdness coupled with the positive kurtosis; therefore, I would state that the distribution is not 'approximately normal'.

If not normal, is the distribution skewed? If so, in which direction? Explain how you know.

The distribution is left-skewed because: mean < median < mode.

VII: Now that you have looked at this data visually for normality, you will now quantify normality with numbers using the stat.desc() function.

Include a screen capture of the results produced.

table2 <- subset(table1, select = -c(PopGroupID))
stat.desc(table2, norm = TRUE)

```
             Id           Id2 Geography POPGROUP.display-label RacesReported
HSDegree    BachDegree
nbr.val      NA  1.360000e+02        NA                     NA  1.360000e+02  1
.360000e+02  136.00000000
nbr.null     NA  0.000000e+00        NA                     NA  0.000000e+00  0
.000000e+00    0.00000000
nbr.na       NA  0.000000e+00        NA                     NA  0.000000e+00  0
.000000e+00    0.00000000
min          NA  1.073000e+03        NA                     NA  5.002920e+05  6
.220000e+01   15.40000000
max          NA  5.507900e+04        NA                     NA  1.011671e+07  9
.550000e+01   60.30000000
range        NA  5.400600e+04        NA                     NA  9.616413e+06  3
.330000e+01   44.90000000
sum          NA  3.649306e+06        NA                     NA  1.556385e+08  1
.191800e+04 4822.70000000
median       NA  2.611200e+04        NA                     NA  8.327075e+05  8
.870000e+01   34.10000000
mean         NA  2.683313e+04        NA                     NA  1.144401e+06  8
.763235e+01   35.46102941
SE.mean      NA  1.323036e+03        NA                     NA  9.351028e+04  4
.388598e-01    0.81545273
CI.mean      NA  2.616557e+03        NA                     NA  1.849346e+05  8
.679296e-01    1.61271456
var          NA  2.380576e+08        NA                     NA  1.189207e+12  2
.619332e+01   90.43498856
std.dev      NA  1.542911e+04        NA                     NA  1.090508e+06  5
.117941e+00    9.50973126
coef.var     NA  5.750024e-01        NA                     NA  9.529072e-01  5
.840241e-02    0.26817415
skewness     NA  4.793197e-02        NA                     NA  4.976198e+00 -1
.674767e+00    0.32843046
skew.2SE     NA  1.153462e-01        NA                     NA  1.197501e+01 -4
.030254e+00    0.79035382
kurtosis     NA -1.335207e+00        NA                     NA  3.349995e+01  4
.352856e+00   -0.27742492
kurt.2SE     NA -1.617726e+00        NA                     NA  4.058826e+01  5
.273885e+00   -0.33612576
normtest.W NA  9.314546e-01        NA                     NA  5.185873e-01  8
.773635e-01    0.98316075
normtest.p NA  3.490602e-06        NA                     NA  3.040373e-19  3
.193634e-09    0.09206162
```

VIII: In several sentences provide an explanation of the result produced for skew, kurtosis, and z-scores.
In addition, explain how a change in the sample size may change your explanation?

Negative skewness is described by this relationship between summary statistics: mean < median < mode.

Positive kurtosis means the distribution is "taller" and "thinner" than a normal distribution, meaning that the data is relatively more dense around the mode, and less dense away from the mode.

The p value from the Shapiro-Wilk test is also less than 0.05, rejecting the null that the distribution is normal.

I'm not sure what is meant regarding z scores since a particular point isn't mentioned, but I'll say that a coefficient of variation of ~5 implies high variance and "instability" regarding the prediction of dependent variables using simple approximations.

A larger sample size would potentially normalize the distribution, reducing all metrics deviating from the norm in proportion to the amount of samples added.

A smaller sample size would serve to exacerbate the lack of normality in the dataset, and provide more variance.