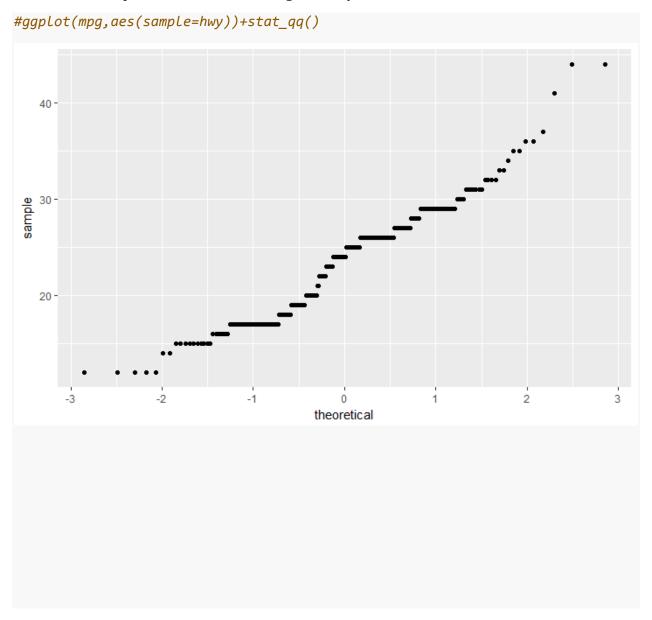
## **EDA ASSignment-1**

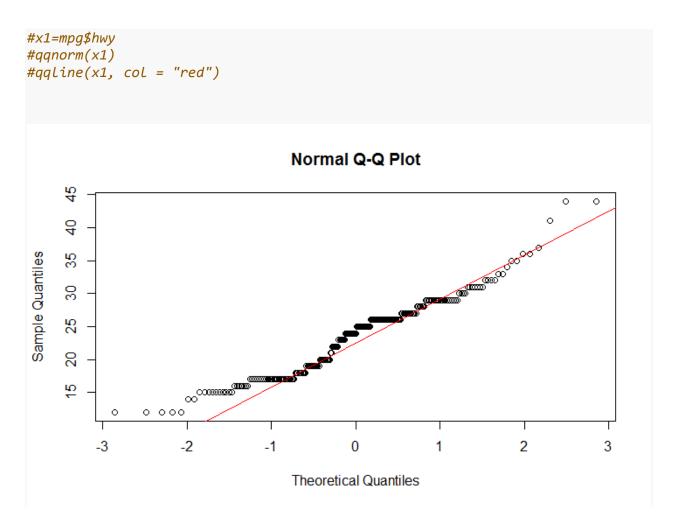
vinoth

August 31, 2017

Q1. Does highway miles per gallon follow a normal distribution? If not, how does the data differ from a normal distribution?

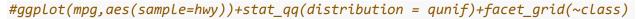
Here is the first plot which whether the given hwy is normal distribution

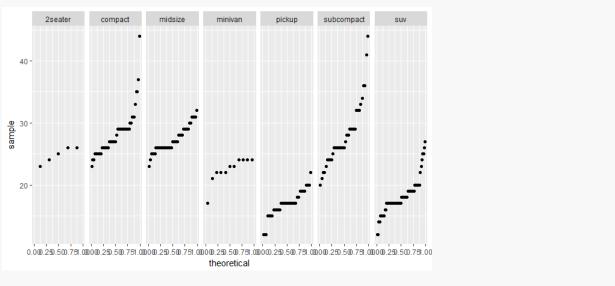




By seeing the above given graph the data "hwy" does not follow the normal distribution because curve which formed by given data does not look like a straight line.

## Q2. How does the distribution of "hwy" change with "class"?

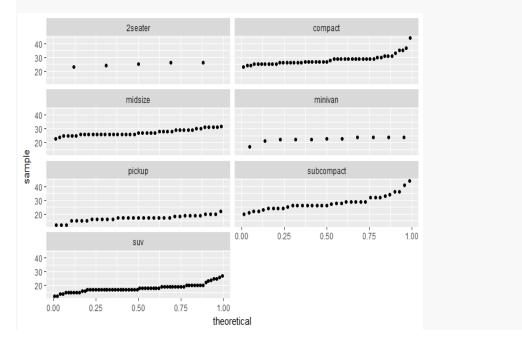




For more clarification I am using other step

here we have seven different class of car models the graph is cramped.the picture will be more efficient when used 4 by 2 graphs.

#ggplot(mpg,aes(sample=hwy))+stat\_qq(distribution=qunif)+facet\_wrap(~class,nc ol=2)

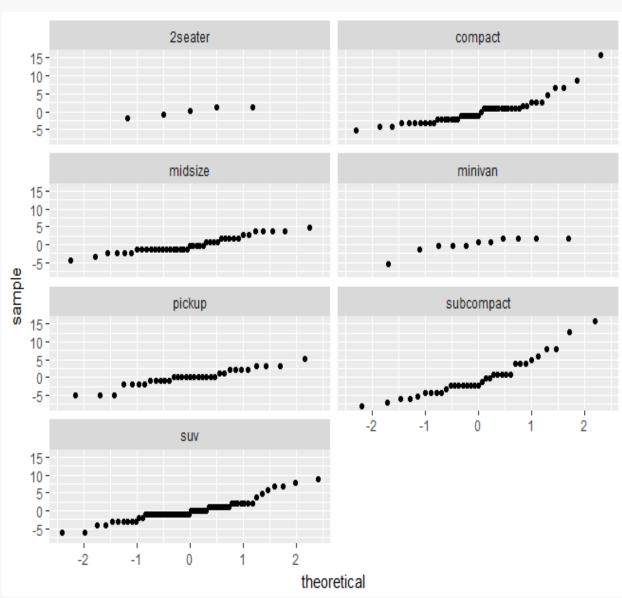


In this two sample distribution its clear that midsize class only form normal distribution.other class car type does not form normal distribution.

problem 3 Using lm(), fit a simple linear model for highway miles per gallon:

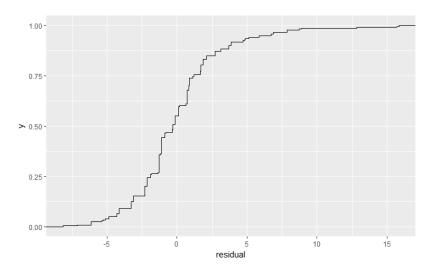
To check the given data Does it look like we can pool the residuals

```
mpg.lm=lm(hwy~class,data = mpg)
mpg.res=data. Frame(class=mpg$class,residual=residuals(mpg.lm))
ggplot(mpg.res,aes(sample=residual))+stat_qq()+facet_wrap(~class,ncol=2)
```



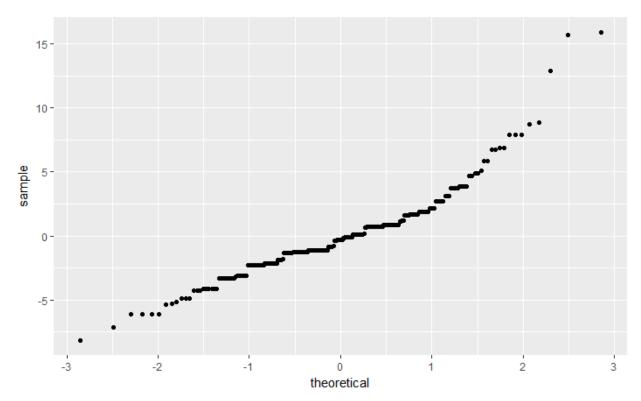
The above given data does not look a reasonably straight and the scales does not look similar for all seven class. To check more normality distribution

ggplot(mpg.res,aes(x=residual))+stat\_ecdf()



Other step check with normality by using following commend

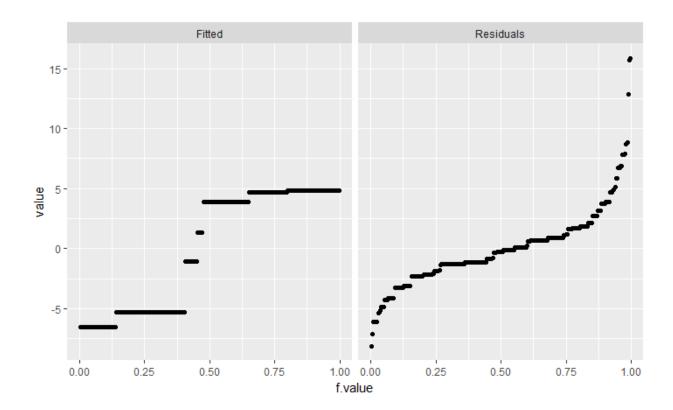
ggplot(mpg.res,aes(sample=residual))+stat\_qq()



If we look at the above graph its clear that its does not form a straight line so we cannot pool the residuals.

```
mpg.fitted=sort(fitted.values(mpg.lm))-mean(fitted.values(mpg.lm))
mpg.residuals=sort(residuals(mpg.lm))
```

```
n=length(mpg.residuals) f.value=(0.5:(n-0.5))/n mpg.fit=data.frame(f.value,Fitted=mpg.fitted,Residuals=mpg.residuals) mpg.fit.long=mpg.fit \%>\% \ gather(type, value, Fitted:Residuals) ggplot(mpg.fit.long, aes(x = f.value, y = value)) + geom_point() + facet_wrap(~type)
```



If we see above given its clear that fitted values not closer to residuals. So its clear that which residual values are greater than the fitted values.