

Hatch SFAL Results

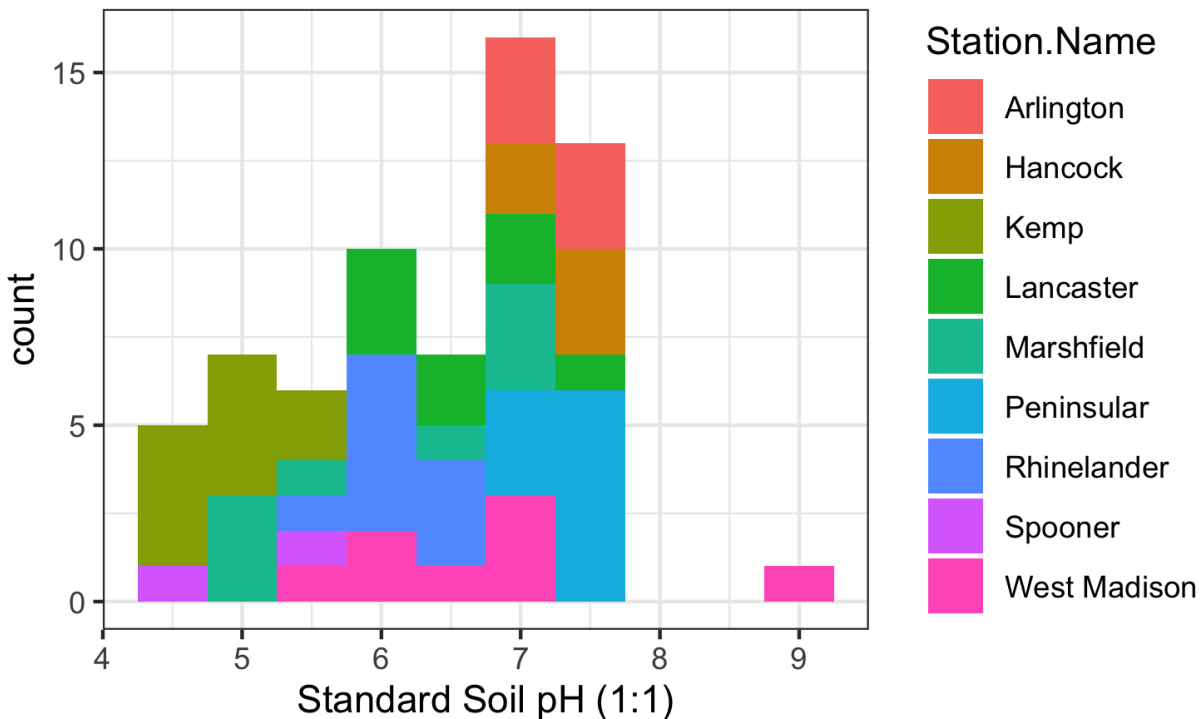
Michael J. Braus

2020-03-13

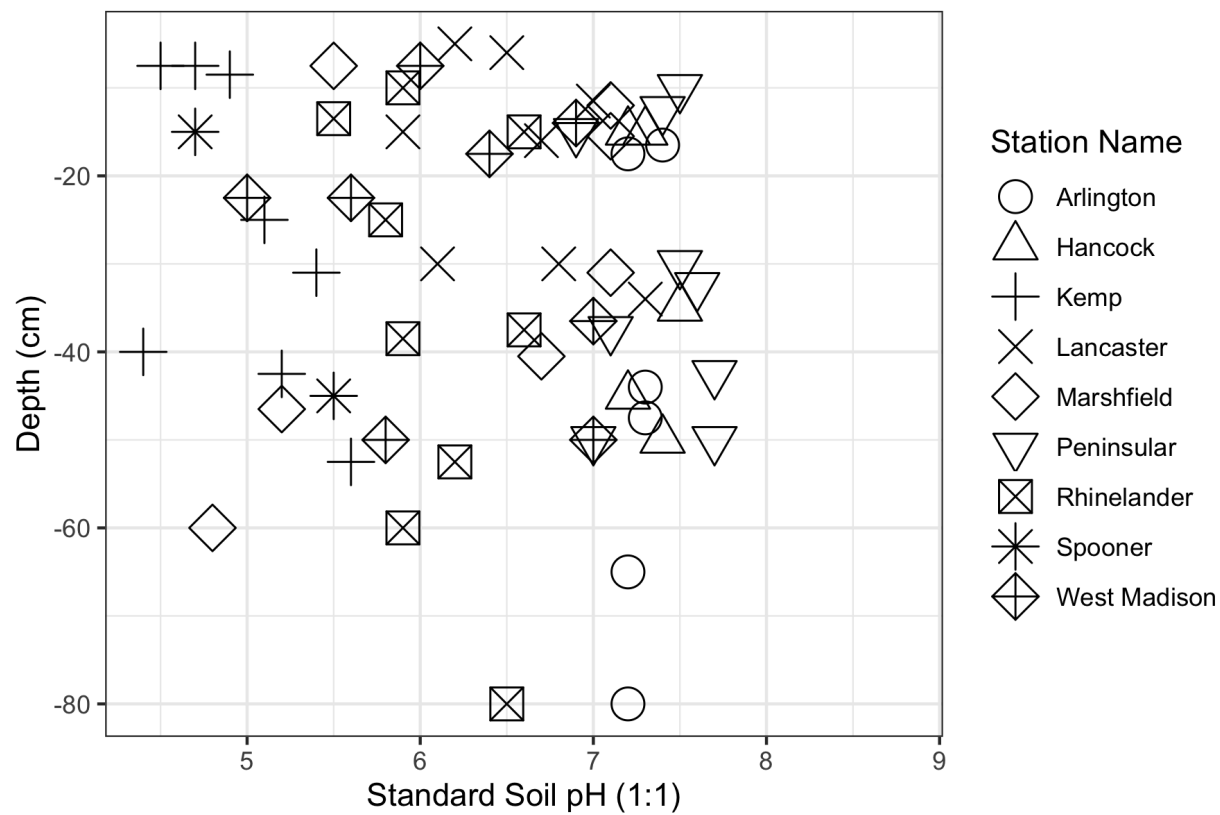
```
library(ggplot2)
```

These are the standard soil pH values we have to work with, now.

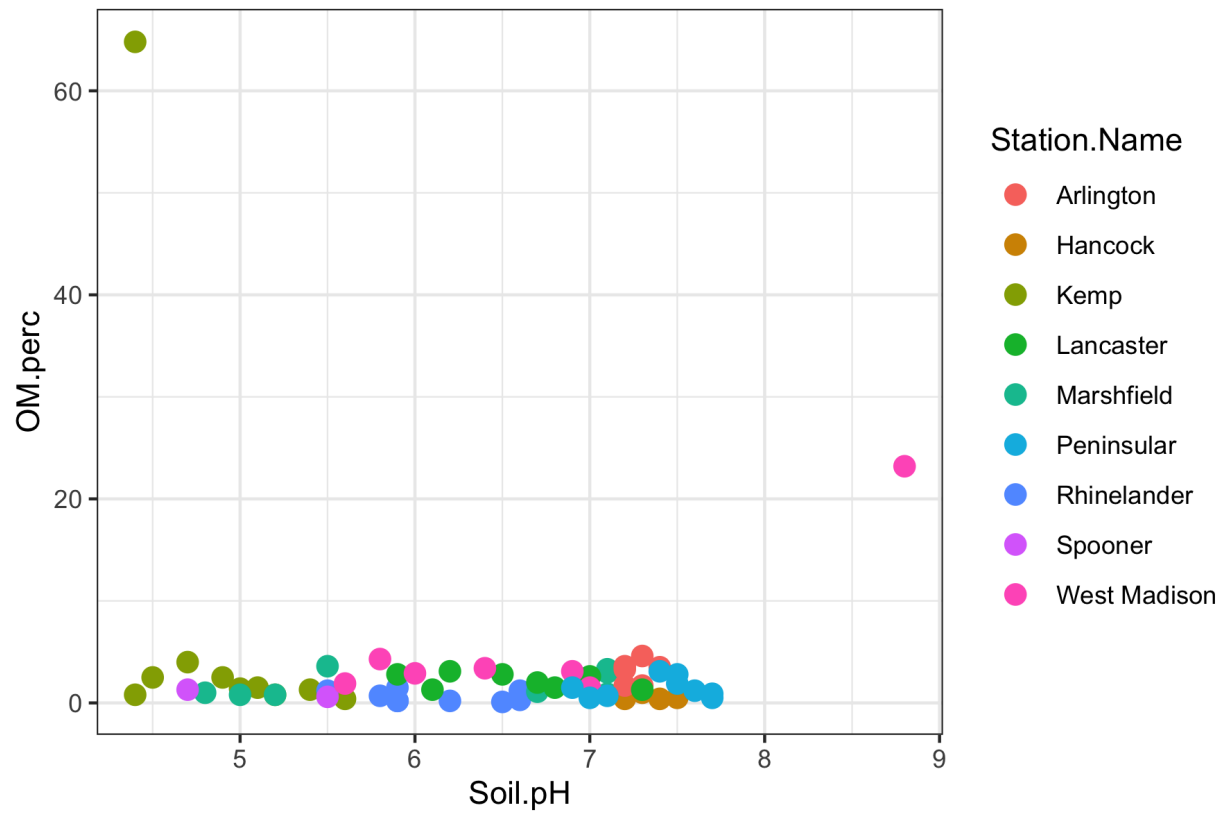
```
soil.dat <- read.csv(file = "2018-10-05-soil-analysis-report-5118-5119/5118-5119-braus-w  
header = TRUE)  
ggplot(soil.dat, aes(Soil.pH, fill = Station.Name)) +  
  geom_histogram(binwidth=0.5) + theme_bw() + labs(x = "Standard Soil pH (1:1)")
```



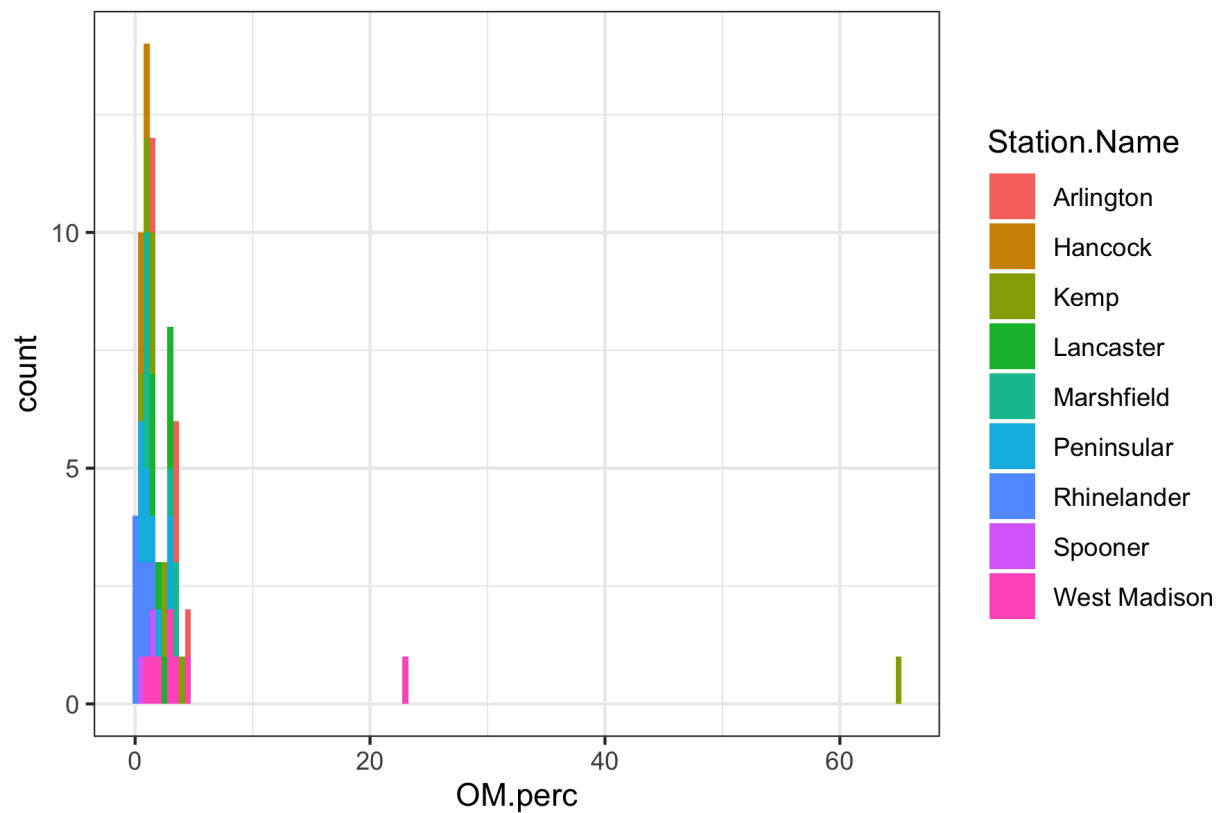
```
soil.dat$Station.Name <- as.factor(soil.dat$Station.Name)  
p <- ggplot(soil.dat, aes(Soil.pH, -(Upper.Depth.cm+Lower.Depth.cm)/2, shape=Station.Name))  
p + geom_point(size = 5) + theme_bw() + labs(x = "Standard Soil pH (1:1)", y = "Depth (cm)")  
  scale_shape_manual(values=1:nlevels(soil.dat$Station.Name)) + labs(shape='Station Name')
```



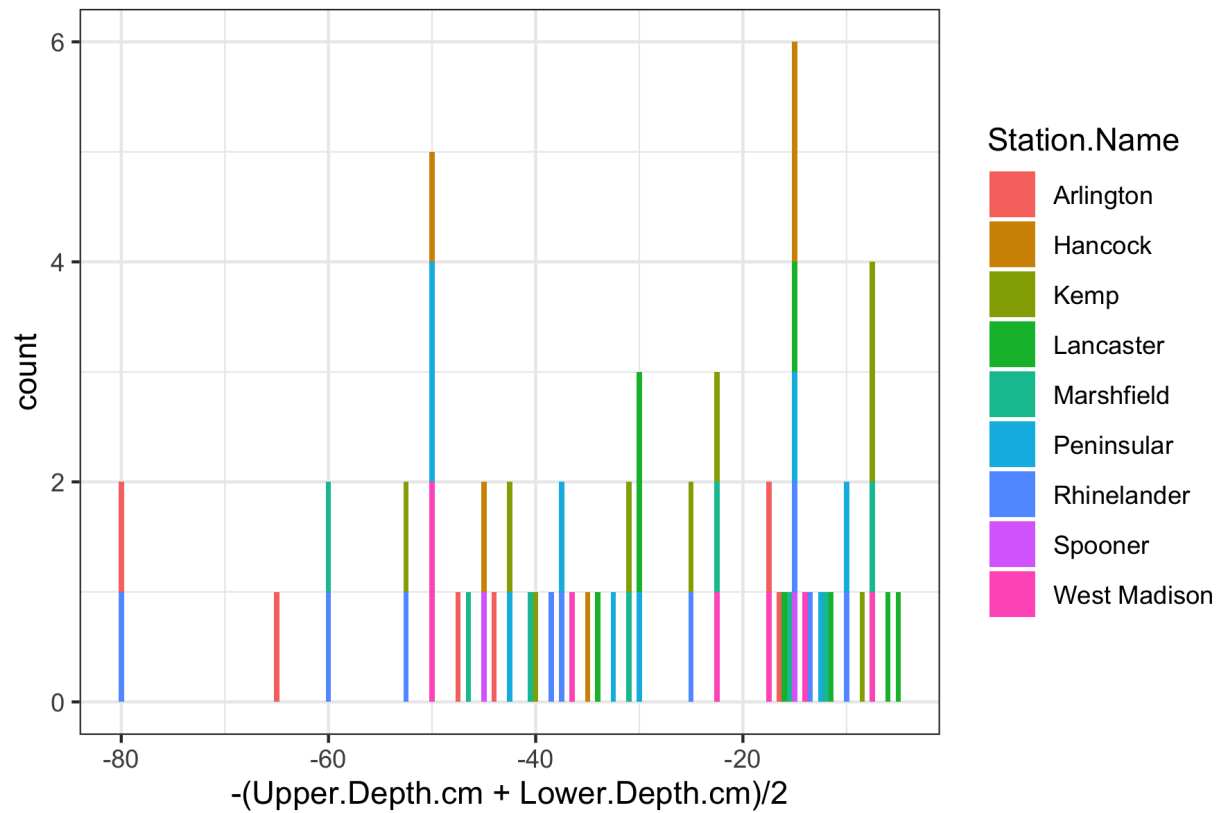
```
p <- ggplot(soil.dat, aes(Soil.pH, OM.perc, color=Station.Name))
p + geom_point(size = 3) + theme_bw()
```



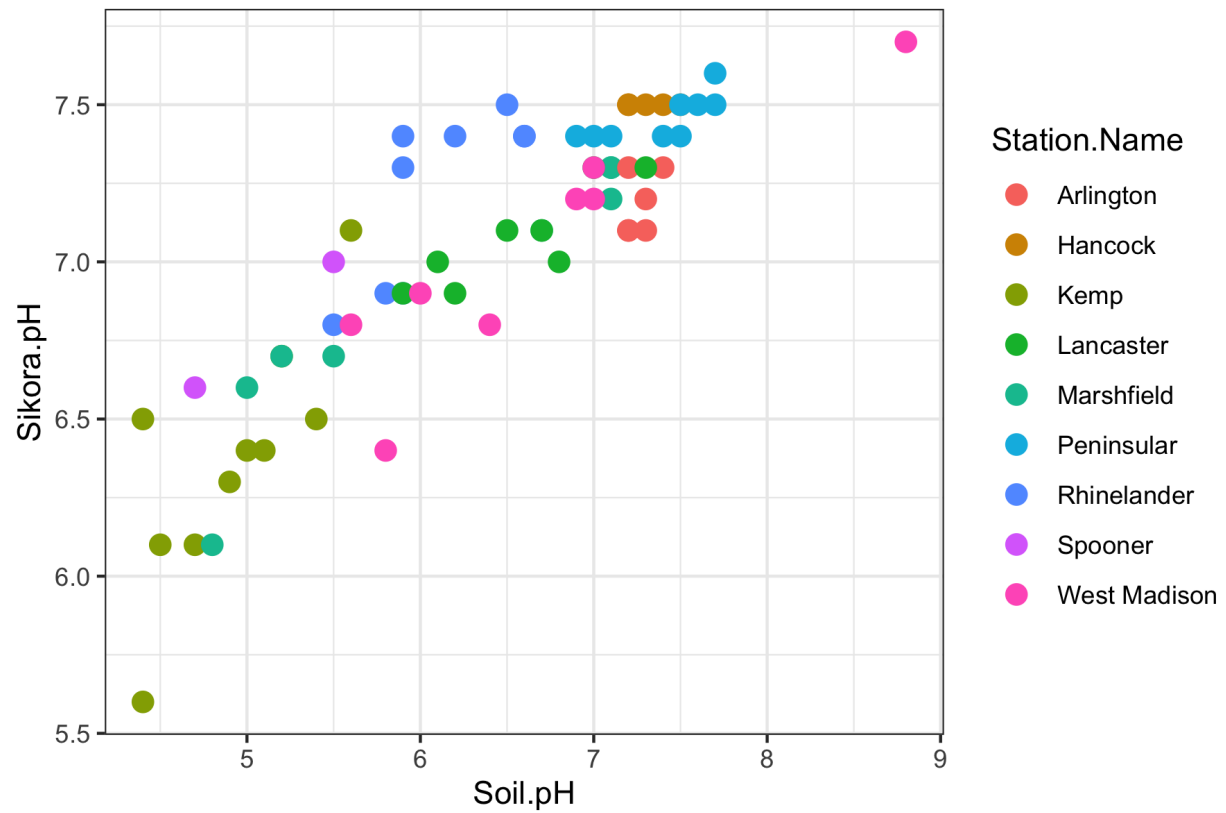
```
ggplot(soil.dat, aes(OM.perc, fill = Station.Name)) +  
  geom_histogram(binwidth=0.5) + theme_bw()
```



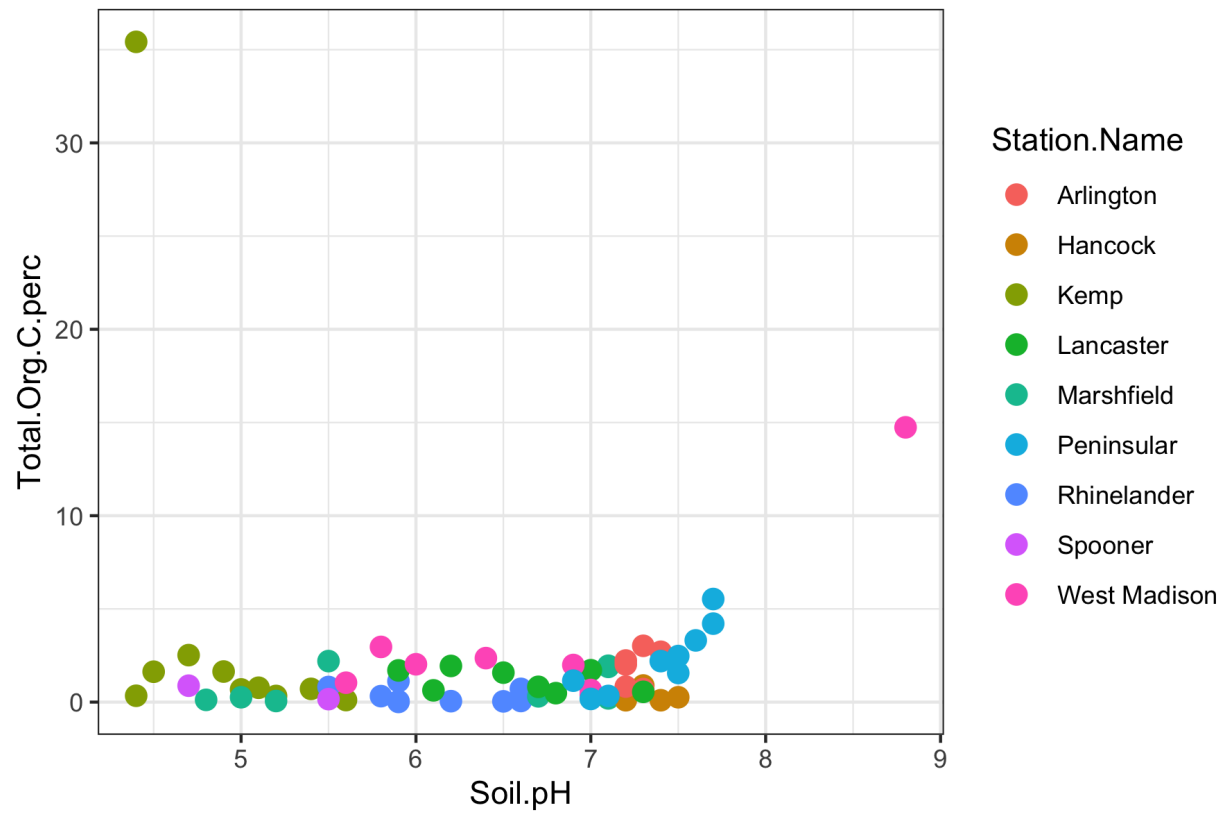
```
ggplot(soil.dat, aes(-(Upper.Depth.cm+Lower.Depth.cm)/2, fill = Station.Name)) +  
  geom_histogram(binwidth=0.5) + theme_bw()
```



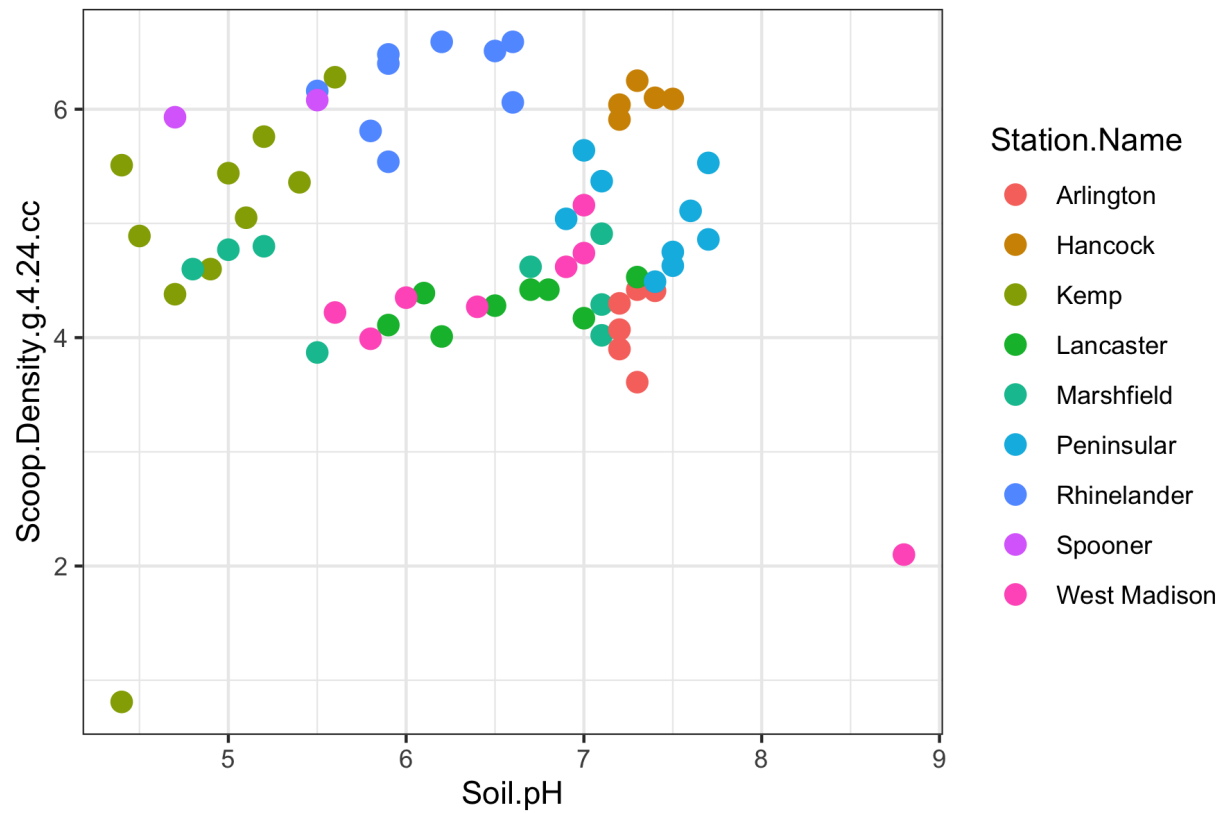
```
p <- ggplot(soil.dat, aes(Soil.pH, Sikora.pH, color=Station.Name))
p + geom_point(size = 3) + theme_bw()
```



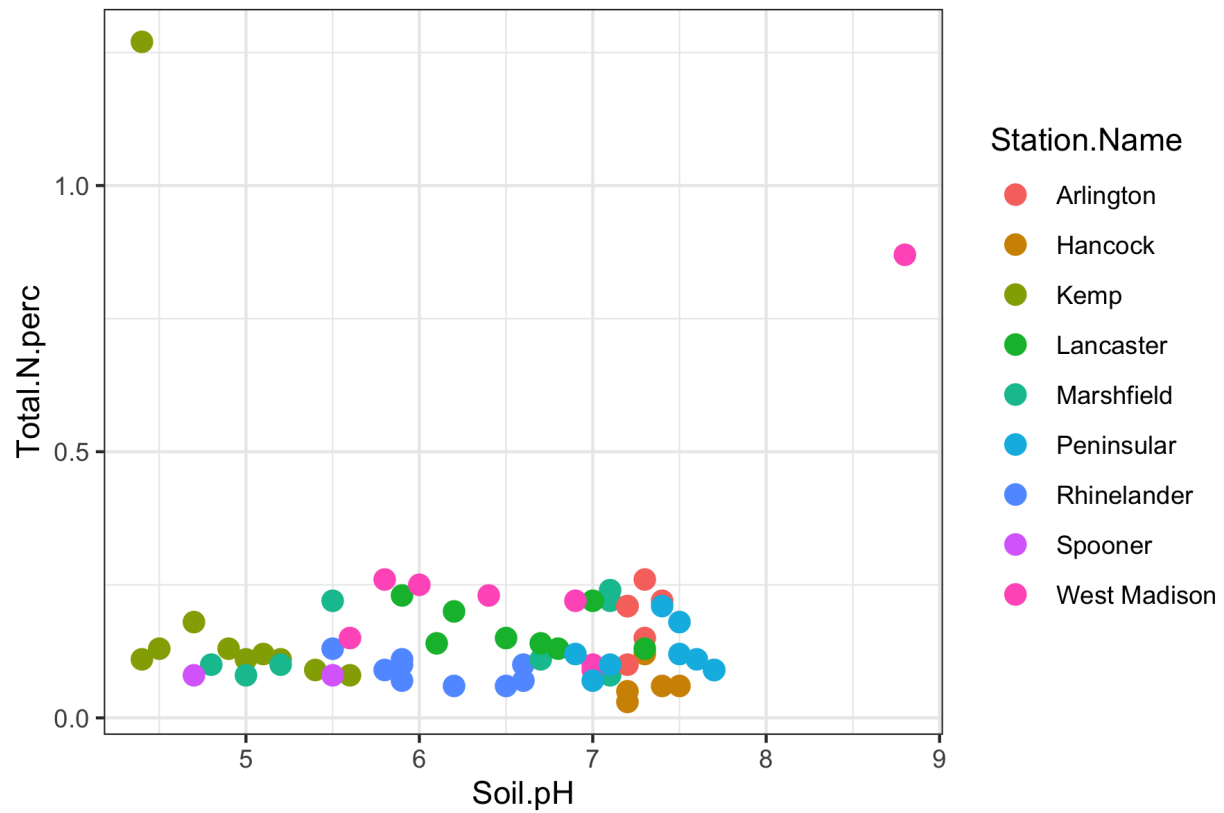
```
p <- ggplot(soil.dat, aes(Soil.pH, Total.Org.C.perc, color=Station.Name))
p + geom_point(size = 3) + theme_bw()
```



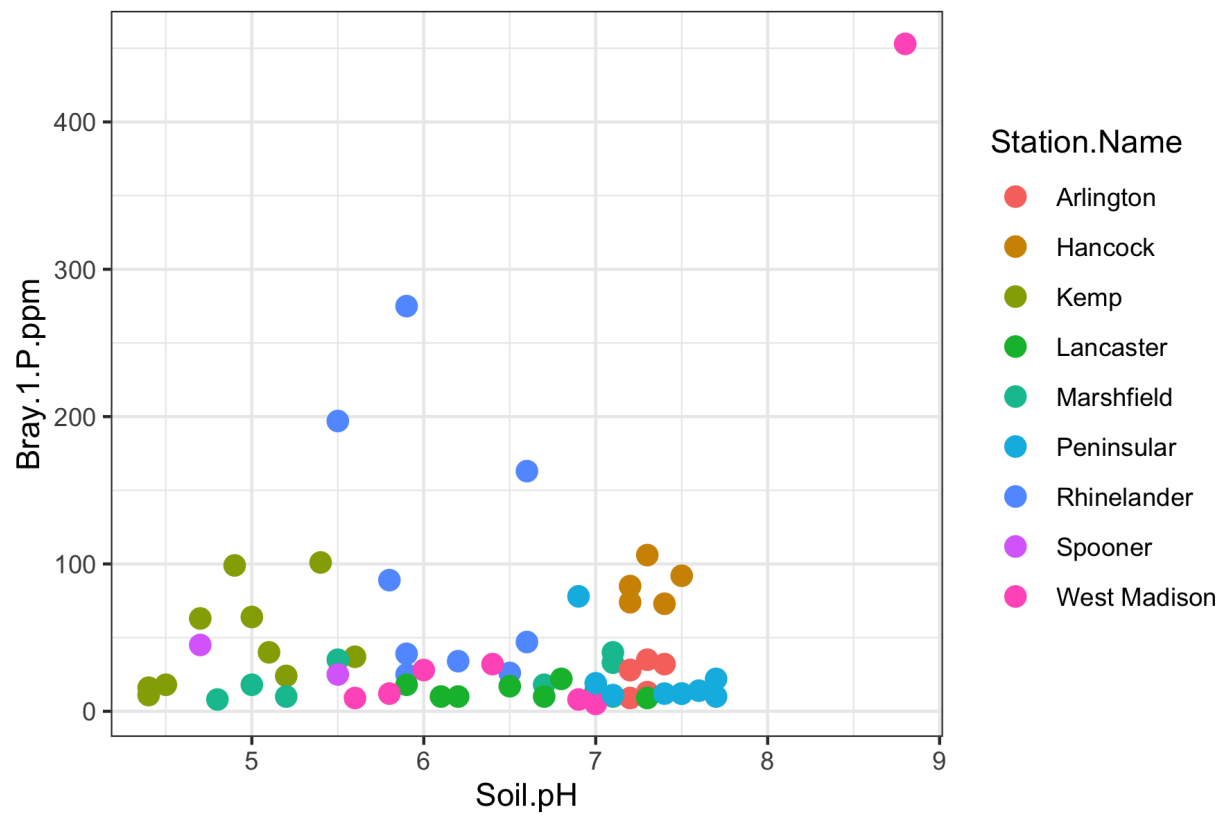
```
p <- ggplot(soil.dat, aes(Soil.pH, Scoop.Density.g.4.24.cc, color=Station.Name))
p + geom_point(size = 3) + theme_bw()
```



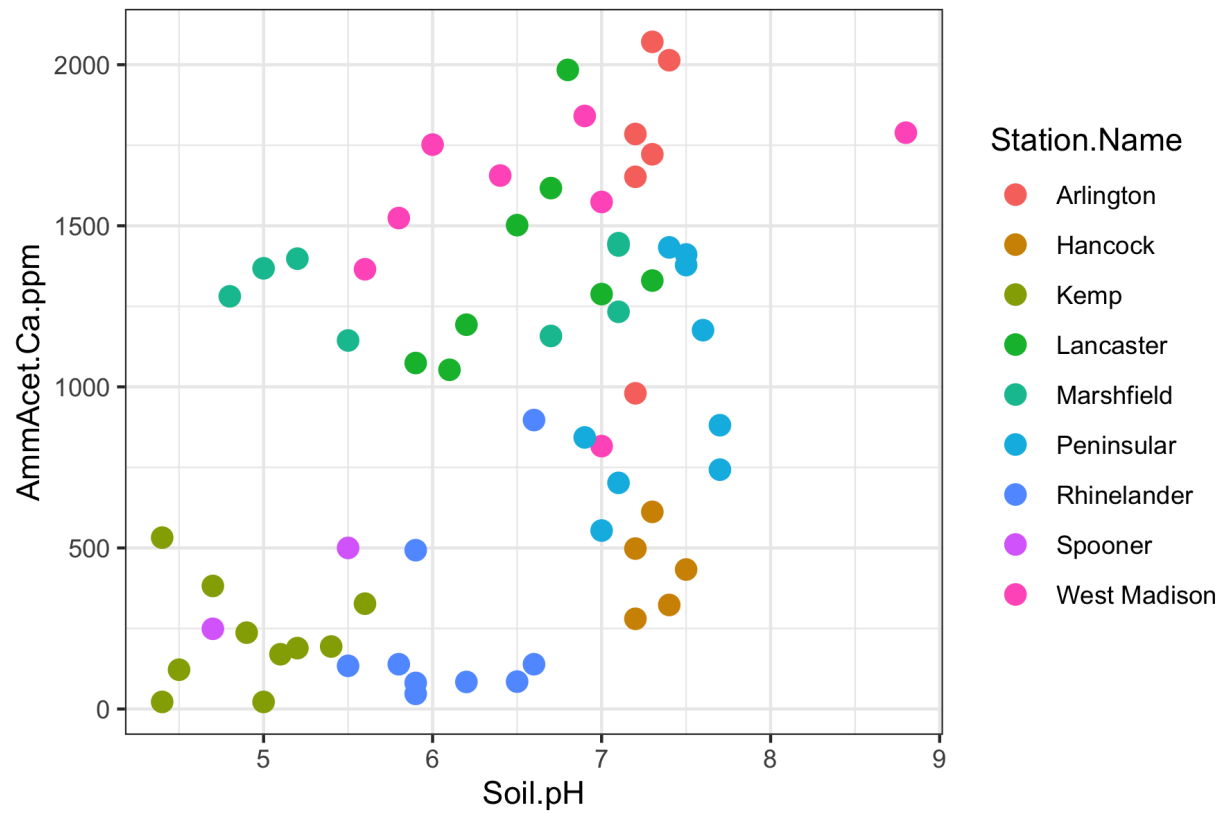
```
# str(soil.dat)
p <- ggplot(soil.dat, aes(Soil.pH, Total.N.perc, color=Station.Name))
p + geom_point(size = 3) + theme_bw()
```

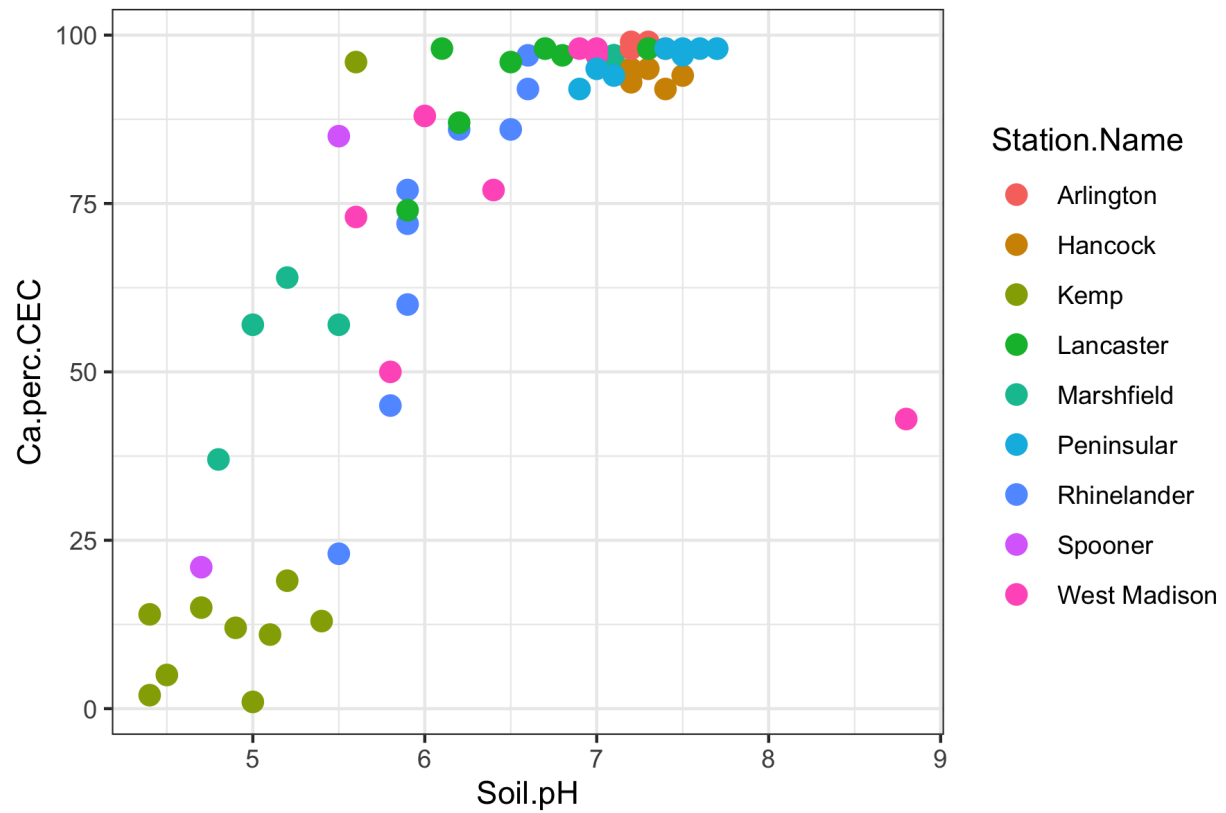
```
# str(soil.dat)
p <- ggplot(soil.dat, aes(Soil.pH, Bray.1.P.ppm, color=Station.Name))
p + geom_point(size = 3) + theme_bw()
```



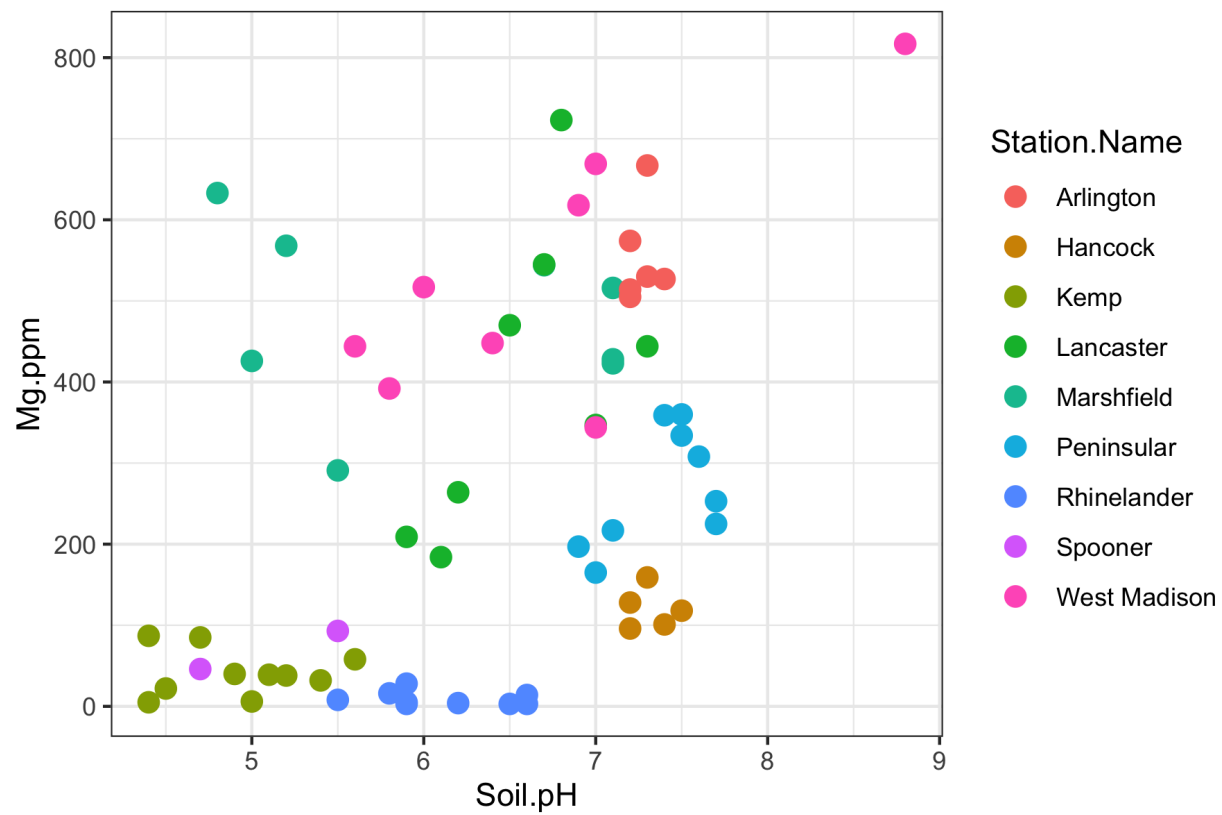
```
p <- ggplot(soil.dat, aes(Soil.pH, AmmAcet.Ca.ppm, color=Station.Name))
p + geom_point(size = 3) + theme_bw()
```



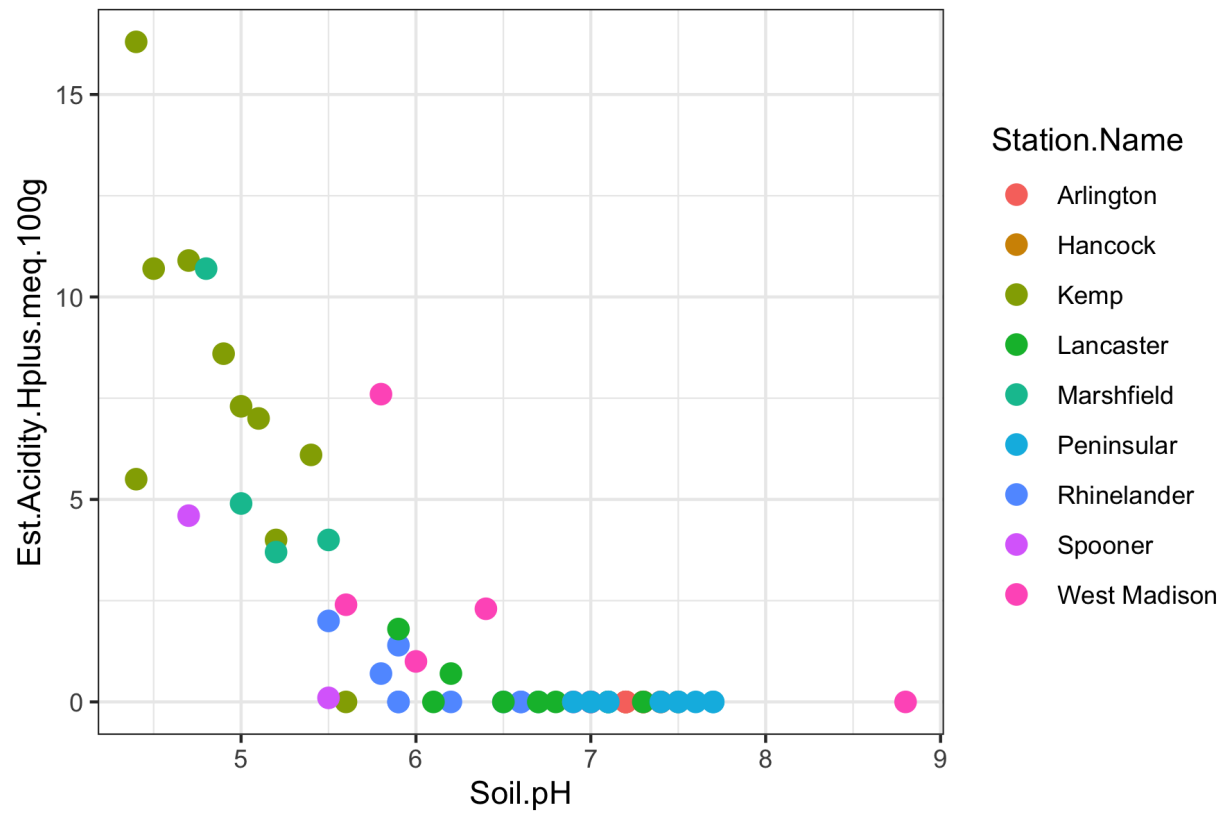
```
p <- ggplot(soil.dat, aes(Soil.pH, Ca.perc.CEC, color=Station.Name))
p + geom_point(size = 3) + theme_bw()
```



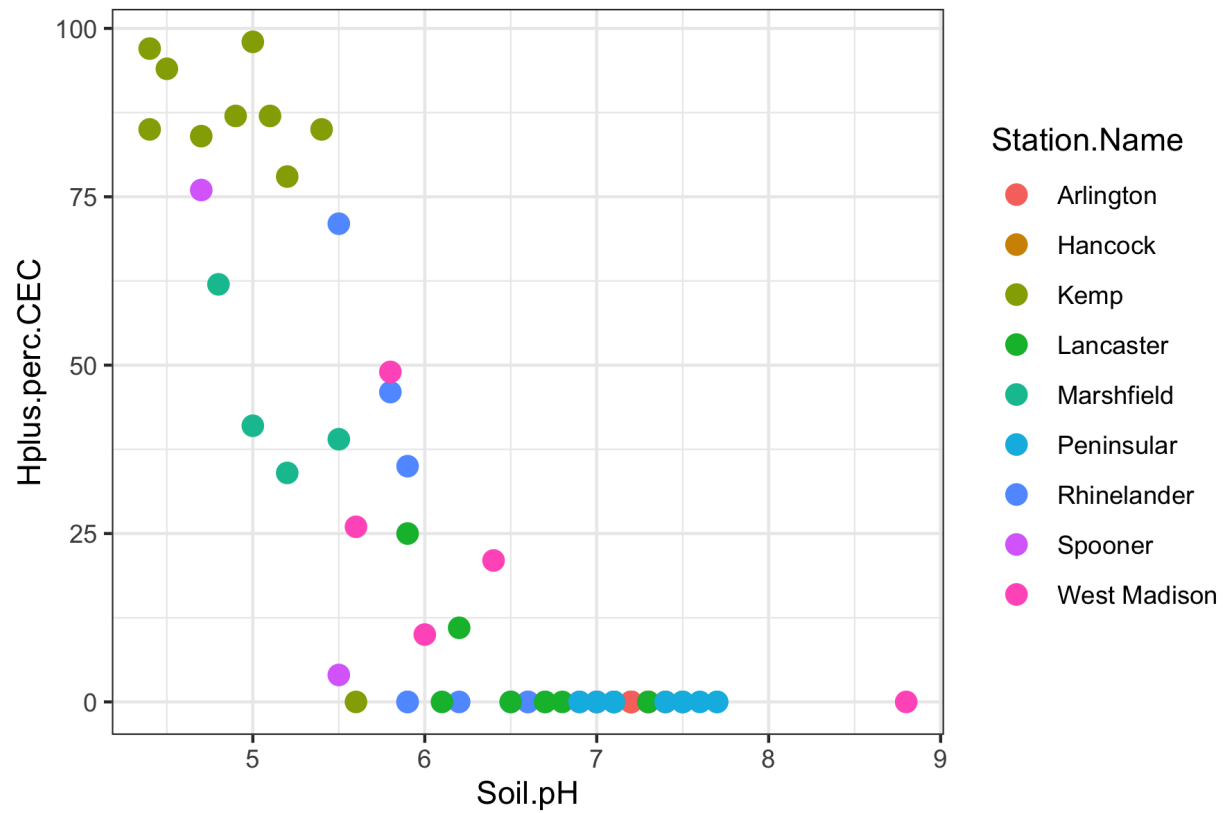
```
p <- ggplot(soil.dat, aes(Soil.pH, Mg.ppm, color=Station.Name))
p + geom_point(size = 3) + theme_bw()
```



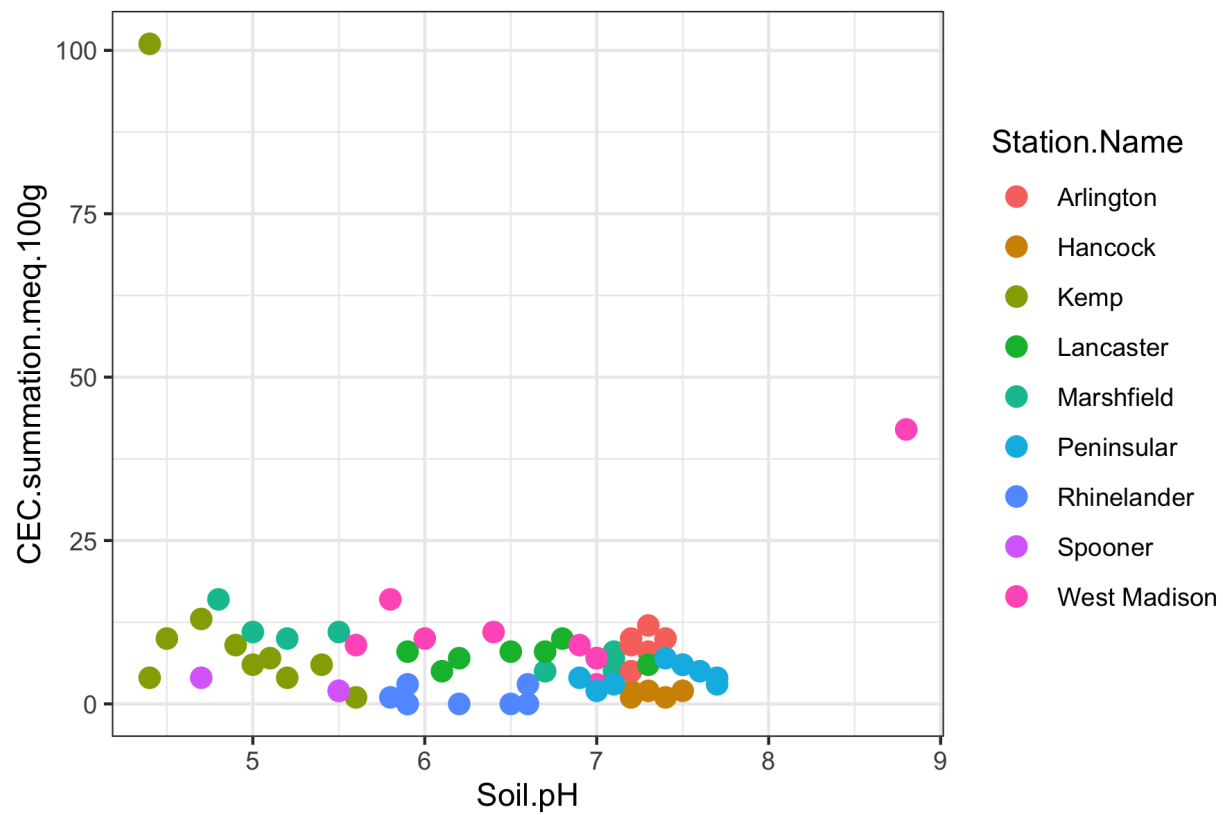
```
p <- ggplot(soil.dat, aes(Soil.pH, Est.Acidity.Hplus.meq.100g, color=Station.Name))
p + geom_point(size = 3) + theme_bw()
```



```
p <- ggplot(soil.dat, aes(Soil.pH, Hplus.perc.CEC, color=Station.Name))
p + geom_point(size = 3) + theme_bw()
```



```
p <- ggplot(soil.dat, aes(Soil.pH, CEC.summation.meq.100g, color=Station.Name))
p + geom_point(size = 3) + theme_bw()
```



See Rmd for R code.