2019-08-25-hatch-ph-multifactorial-merged

Michael J. Braus 2019-08-22

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Introduction

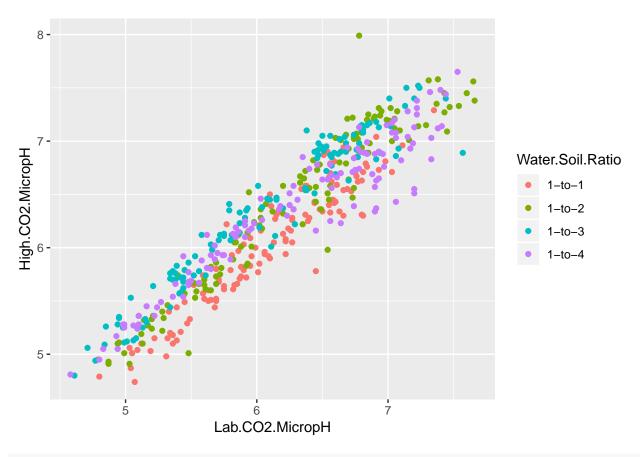
\$ Perc.Clay

 $[\dots]$

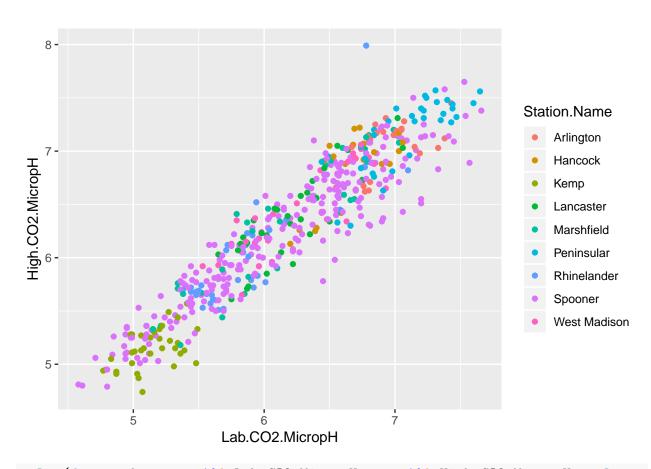
```
library(ggplot2)
dat <- read.csv(file = "2019-08-25-hatch-ph-multifactorial-merged.csv", header = T)</pre>
dat$co2.pH.diff <- dat$Lab.CO2.MicropH-dat$High.CO2.MicropH
dat$co2.exp.pH.diff <- 10^-(dat$Lab.CO2.MicropH)-10^-(dat$High.CO2.MicropH)
str(dat)
## 'data.frame':
                   500 obs. of 45 variables:
   $ Water.Soil.Ratio
                              : Factor w/ 4 levels "1-to-1", "1-to-2", ...: 1 1 1 1 1 1 1
                              : Factor w/ 125 levels "1-K1-0-17", "10-K4-30-50",...: 1 3
## $ Sample.ID
                              : int 1 2 3 5 6 7 8 9 10 11 ...
## $ Sample.Number
## $ DNA.Extr.MicropH.MoBio : logi NA NA NA NA NA NA ...
   $ Lab.CO2.MicropH
                                      5.39 5.36 5.49 5.04 5.34 5.32 5.07 5.22 5.31 5.9
                               : num
   $ High.CO2.MicropH
                               : num 5.13 5.1 5.33 4.87 5.2 5.15 4.74 5.15 4.98 5.79 .
## $ Tube.Empty.g
                                      1.06 1.07 1.06 1.07 1.05 ...
                               : num
## $ Moist.Soil.g
                                      0.756 0.785 0.813 0.807 0.826 0.76 0.795 0.859 0.
                               : num
## $ Water.Added.mL
                               : num 0.756 0.785 0.813 0.807 0.826 0.76 0.795 0.859 0.
                                      1.74 1.78 1.84 1.78 1.8 ...
## $ Tube.Dry.Soil.g
                               : num
   $ Dry.Soil.g
                               : num 0.68 0.716 0.777 0.712 0.748 0.712 0.755 0.808 0.
## $ Soil.Water.Content.mass
                             : num 0.101 0.088 0.044 0.118 0.094 0.063 0.05 0.059 0.
## $ Target.Water.Soil.ratio : num 1 1 1 1 1 1 1 1 1 1 ...
## $ Real.Water.Soil.ratio
                              : num 1.11 1.1 1.05 1.13 1.1 ...
## $ Error.Water.Soil.ratio
                               : num -0.112 -0.096 -0.046 -0.133 -0.104 -0.067 -0.053
## $ Perc.Sand
                               : num 64 68 72 64 60 70 78 74 72 82 ...
## $ Perc.Silt
                               : num 25.2 21.2 19.2 27.2 31.2 19.2 15.2 15.2 15.2 11.2
```

: num 10.8 10.8 8.8 8.8 8.8 10.8 6.8 10.8 12.8 6.8 ...

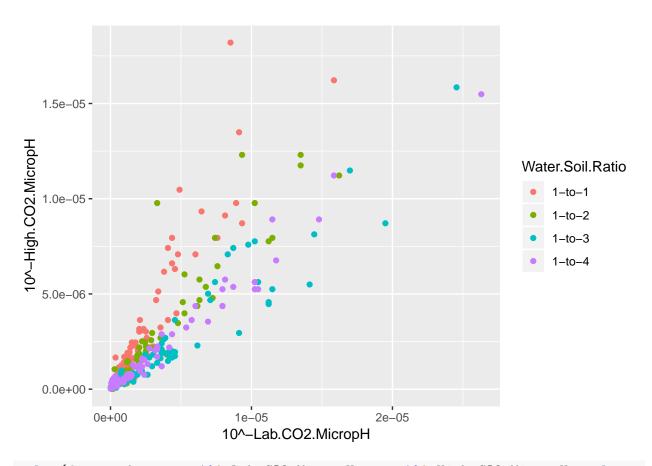
```
## $ Texture.Name
                             : Factor w/ 10 levels "", "Clay Loam", ...: 7 7 7 7 7 7 4 7
## $ OM.perc
                              : num 2.5 1.3 0.4 4 1.5 0.8 2.5 1.4 0.8 1.2 ...
## $ Scoop.Density.g.4.24.cc : num 4.6 5.36 6.28 4.38 5.05 5.76 4.89 5.44 5.51 6.16
## $ Soil.pH
                              : num 4.9 5.4 5.6 4.7 5.1 5.2 4.5 5 4.4 5.5 ...
## $ Sikora.pH
                             : num 6.3 6.5 7.1 6.1 6.4 6.7 6.1 6.4 6.5 6.8 ...
## $ Total.N.perc
                             : num 0.13 0.09 0.08 0.18 0.12 0.11 0.13 0.11 0.11 0.13
                                    1.64 0.71 0.11 2.52 0.77 0.33 1.63 0.68 0.34 0.81
## $ Total.Org.C.perc
                             : num
## $ Bray.1.P.ppm
                              : int 99 101 37 63 40 24 18 64 16 197 ...
## $ K.ppm
                              : int 44 41 26 67 57 63 42 29 23 62 ...
## $ K.perc.CEC
                             : int 1 1 4 1 2 3 1 1 1 6 ...
## $ AmmAcet.Ca.ppm
                             : int 237 194 327 382 170 189 122 22 22 134 ...
## $ Ca.perc.CEC
                              : int 12 13 96 15 11 19 5 1 2 23 ...
## $ Mg.ppm
                              : int 40 32 58 85 39 38 22 6 5 8 ...
## $ Mg.perc.CEC
                             : int 3 4 28 5 4 6 2 1 1 2 ...
## $ Na.ppm
                              : logi NA NA NA NA NA NA ...
                             : int 0000000000...
## $ Na.perc.CEC
## $ Est.Acidity.Hplus.meq.100g: num 8.6 6.1 0 10.9 7 4 10.7 7.3 5.5 2 ...
                             : int 87 85 0 84 87 78 94 98 97 71 ...
## $ Hplus.perc.CEC
                             : int 9 6 1 13 7 4 10 6 4 2 ...
## $ CEC.summation.meq.100g
                              : Factor w/ 10 levels "","11/3/2017",..: 4 4 4 4 4 4 4 4
## $ Date.of.Collection
## $ Station.Name
                             : Factor w/ 9 levels "Arlington", "Hancock", ...: 3 3 3 3
                             : num 5.4 5.4 5.4 5.4 5.4 5.4 5.4 5.4 5.5 ...
## $ St.pH.WSS
                              : int 1113334441...
## $ Site.Number
                             : int 0 17 45 0 15 35 0 15 30 0 ...
## $ Upper.Depth.cm
## $ Lower.Depth.cm
                             : int 17 45 60 15 35 50 15 30 50 27 ...
## $ co2.pH.diff
                              : num 0.26 0.26 0.16 0.17 0.14 ...
## $ co2.exp.pH.diff
                             : num -3.34e-06 -3.58e-06 -1.44e-06 -4.37e-06 -1.74e-06
qplot(data = dat, x = Lab.CO2.MicropH, y = High.CO2.MicropH, color = Water.Soil.Ratio)
```



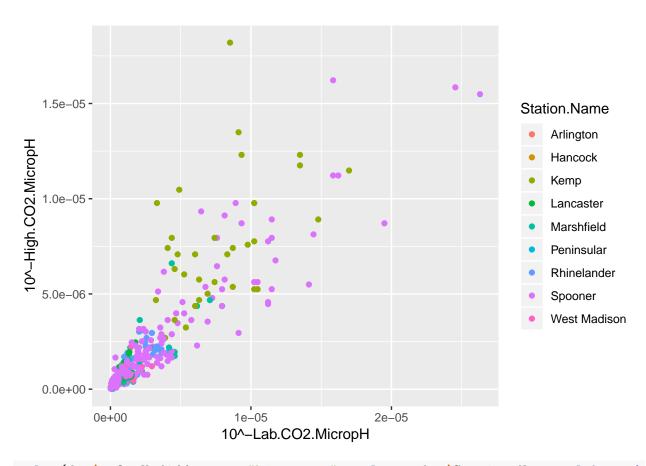
qplot(data = dat, x = Lab.CO2.MicropH, y = High.CO2.MicropH, color = Station.Name)



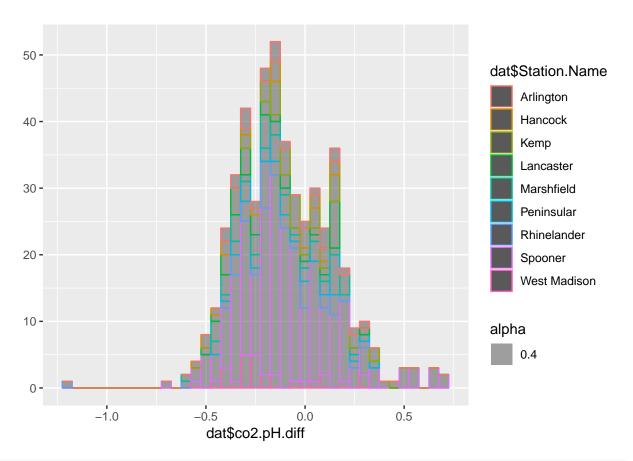
qplot(data = dat, x = 10^-Lab.CO2.MicropH, y = 10^-High.CO2.MicropH, color = Water.Soil.



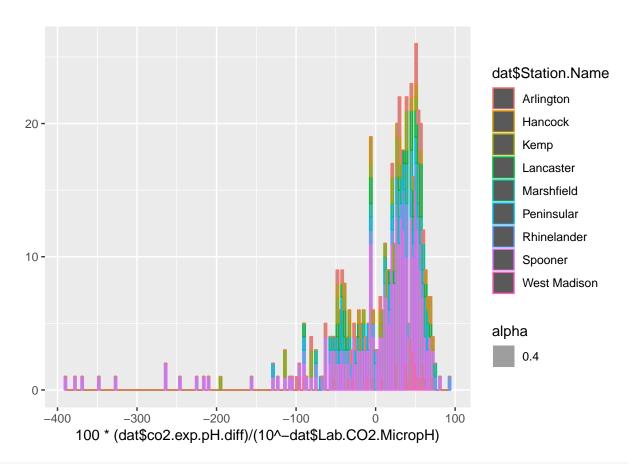
qplot(data = dat, x = 10^-Lab.CO2.MicropH, y = 10^-High.CO2.MicropH, color = Station.Nam



qplot(dat\$co2.pH.diff, geom="histogram", color = dat\$Station.Name, alpha = 0.4, binwidth



qplot(100*(dat\$co2.exp.pH.diff)/(10^-dat\$Lab.CO2.MicropH), geom="histogram", color = dat



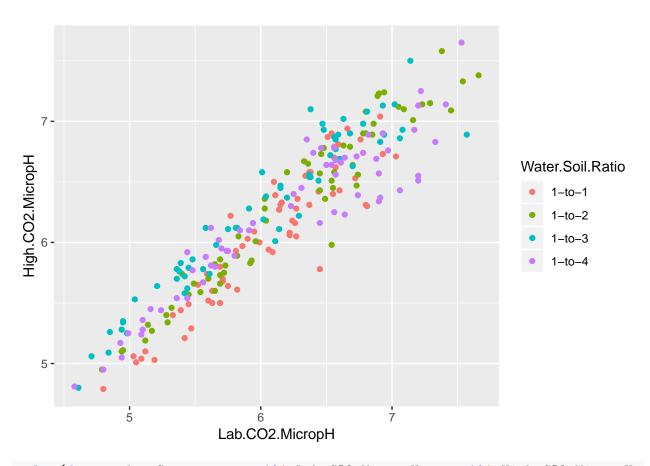
```
t.test(dat$Lab.CO2.MicropH, dat$High.CO2.MicropH, paired = TRUE, alternative = "two.side
```

```
##
## Paired t-test
##
## data: dat$Lab.C02.MicropH and dat$High.C02.MicropH
## t = -9.4651, df = 490, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.12383293 -0.08125872
## sample estimates:
## mean of the differences
## -0.1025458</pre>
```

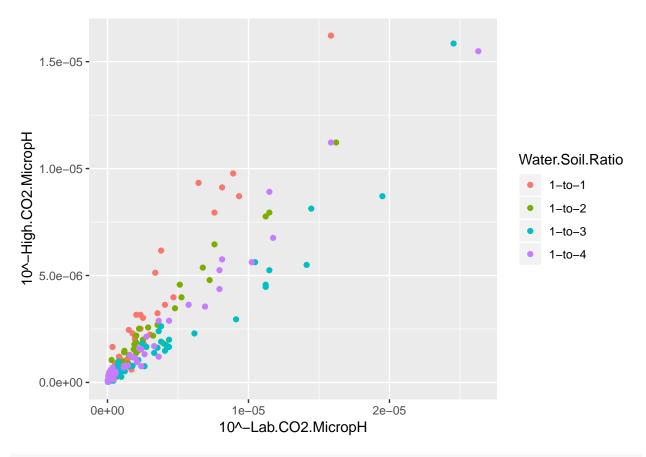
Just Spooner:

```
dat.Spooner <- subset(dat, Station.Name=="Spooner")
t.test(dat.Spooner$Lab.CO2.MicropH, dat.Spooner$High.CO2.MicropH, paired = TRUE, alterna
##
## Paired t-test</pre>
```

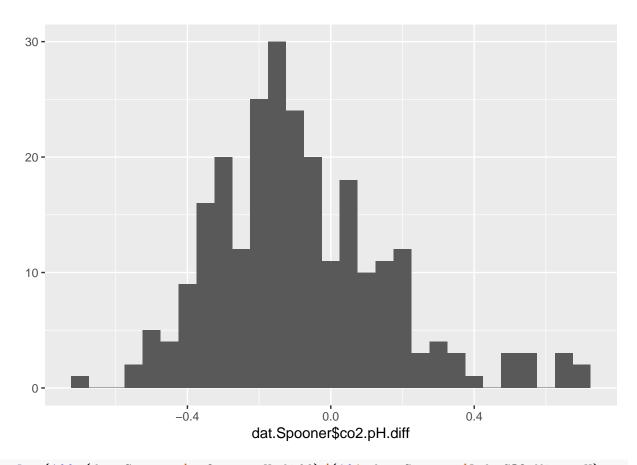
```
##
## data: dat.Spooner$Lab.CO2.MicropH and dat.Spooner$High.CO2.MicropH
## t = -5.5481, df = 251, p-value = 7.322e-08
\#\# alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.11598004 -0.05521044
## sample estimates:
## mean of the differences
               -0.08559524
t.test(10^-dat.Spooner$Lab.CO2.MicropH, 10^-dat.Spooner$High.CO2.MicropH, paired = TRUE
##
## Paired t-test
##
## data: 10^-dat.Spooner$Lab.CO2.MicropH and 10^-dat.Spooner$High.CO2.MicropH
## t = 6.2194, df = 251, p-value = 2.072e-09
\#\# alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 4.767876e-07 9.186779e-07
## sample estimates:
## mean of the differences
              6.977328e-07
qplot(data = dat.Spooner, x = Lab.CO2.MicropH, y = High.CO2.MicropH, color = Water.Soil.
```



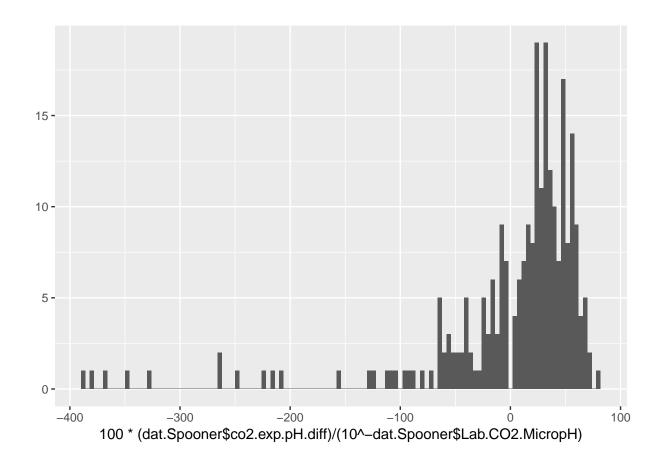
 $qplot(data = dat.Spooner, x = 10^-Lab.CO2.MicropH, y = 10^-High.CO2.MicropH, color = Water (data = dat.Spooner)$



qplot(dat.Spooner\$co2.pH.diff, geom="histogram", binwidth = 0.05)



qplot(100*(dat.Spooner\$co2.exp.pH.diff)/(10^-dat.Spooner\$Lab.CO2.MicropH), geom="histogram")

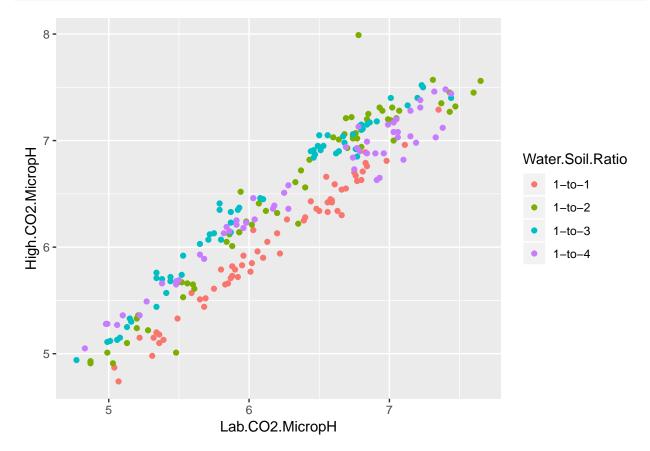


Just Wisconsin:

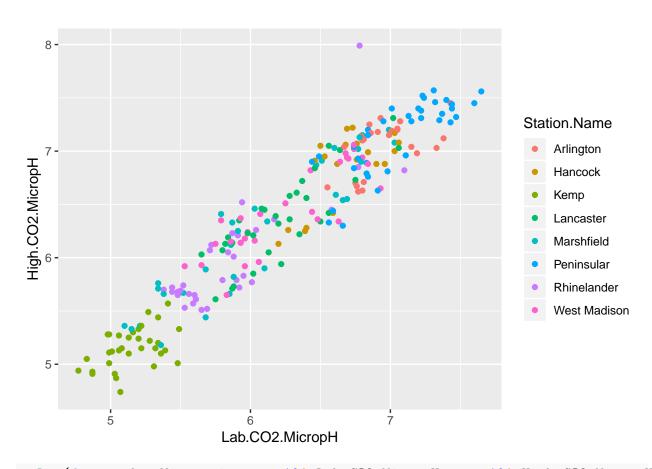
```
dat.Wisconsin <- subset(dat, Station.Name!="Spooner")</pre>
t.test(dat.Wisconsin$Lab.CO2.MicropH, dat.Wisconsin$High.CO2.MicropH, paired = TRUE, alt
##
##
   Paired t-test
## data: dat.Wisconsin$Lab.CO2.MicropH and dat.Wisconsin$High.CO2.MicropH
## t = -7.9544, df = 238, p-value = 7.276e-14
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.15024106 -0.09059576
## sample estimates:
## mean of the differences
                -0.1204184
##
t.test(10^-dat.Wisconsin$Lab.CO2.MicropH, 10^-dat.Wisconsin$High.CO2.MicropH, paired = 7
##
## Paired t-test
```

```
##
## data: 10^-dat.Wisconsin$Lab.CO2.MicropH and 10^-dat.Wisconsin$High.CO2.MicropH
## t = 2.2675, df = 238, p-value = 0.02426
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 2.742817e-08 3.906861e-07
## sample estimates:
## mean of the differences
## 2.090572e-07
```

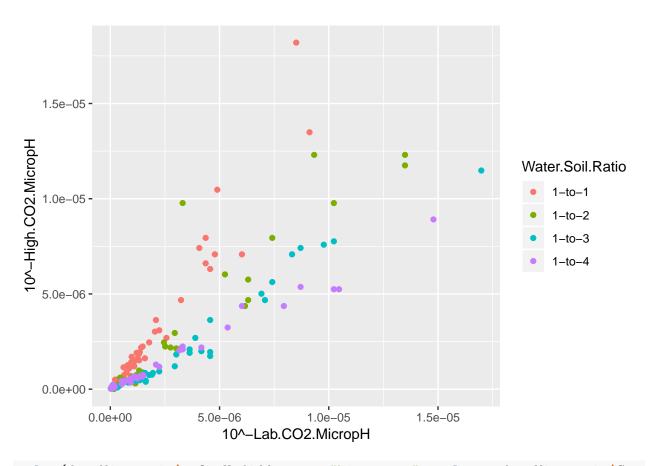
qplot(data = dat.Wisconsin, x = Lab.CO2.MicropH, y = High.CO2.MicropH, color = Water.Soi



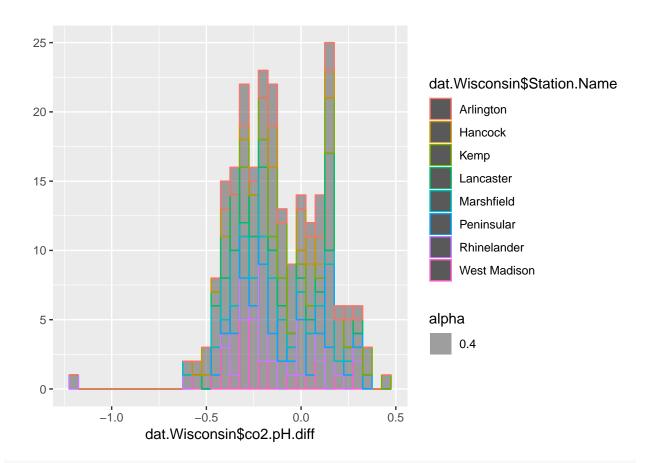
qplot(data = dat.Wisconsin, x = Lab.CO2.MicropH, y = High.CO2.MicropH, color = Station.N



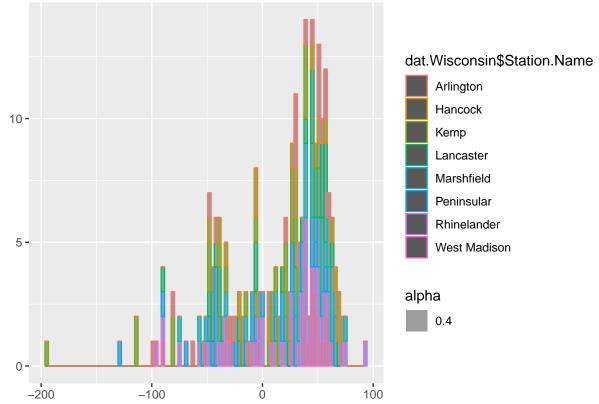
 $qplot(data = dat.Wisconsin, x = 10^-Lab.CO2.MicropH, y = 10^-High.CO2.MicropH, color = Wisconsin, x = 10^-Lab.CO2.MicropH, y = 10^-High.CO2.MicropH, color = Wisconsin, x = 10^-Lab.CO2.MicropH, y = 10^-High.CO2.MicropH, color = Wisconsin, x = 10^-Lab.CO2.MicropH, y = 10^-High.CO2.MicropH, color = Wisconsin, x = 10^-Lab.CO2.MicropH, y = 10^-High.CO2.MicropH, y = 10^-High.CO2.MicropH, color = Wisconsin, x = 10^-Lab.CO2.MicropH, y = 10^-High.CO2.MicropH, color = Wisconsin, x = 10^-Lab.CO2.MicropH, y = 10^-High.CO2.MicropH, y = 10^-Hig$



qplot(dat.Wisconsin\$co2.pH.diff, geom="histogram", color = dat.Wisconsin\$Station.Name, a



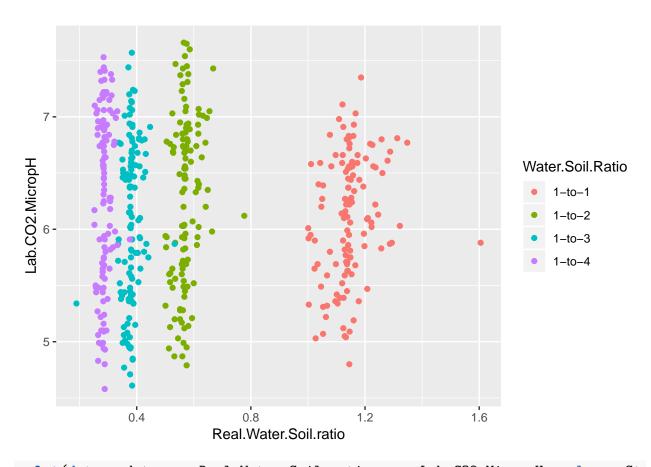
qplot(100*(dat.Wisconsin\$co2.exp.pH.diff)/(10^-dat.Wisconsin\$Lab.CO2.MicropH), geom="his



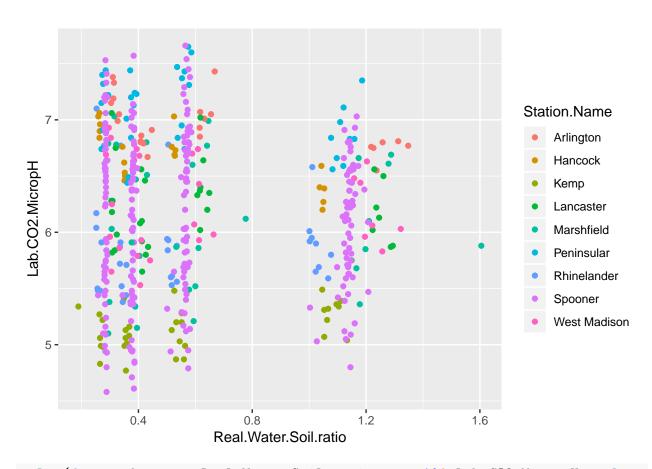
^{&#}x27; (dat.Wisconsin\$co2.exp.pH.diff)/(10^-dat.Wisconsin\$Lab.CO2.MicropH)

More Plots with All Data:

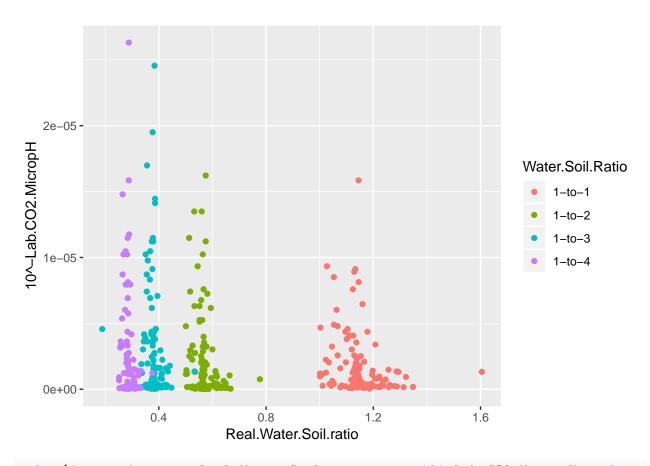
qplot(data = dat, x = Real.Water.Soil.ratio, y = Lab.CO2.MicropH, color = Water.Soil.Rat



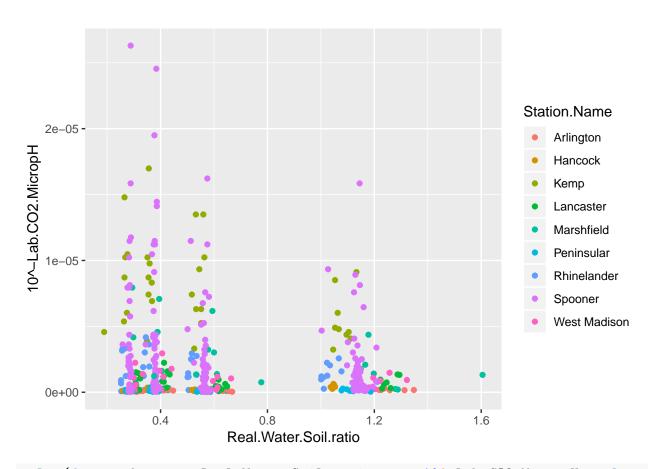
qplot(data = dat, x = Real.Water.Soil.ratio, y = Lab.CO2.MicropH, color = Station.Name)



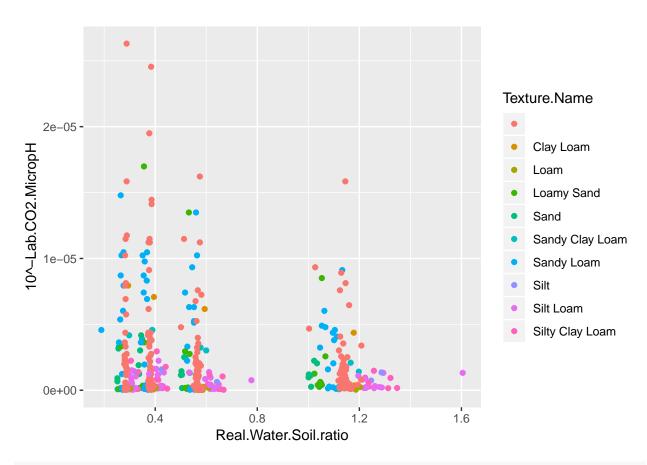
qplot(data = dat, x = Real.Water.Soil.ratio, y = 10^-Lab.CO2.MicropH, color = Water.Soil



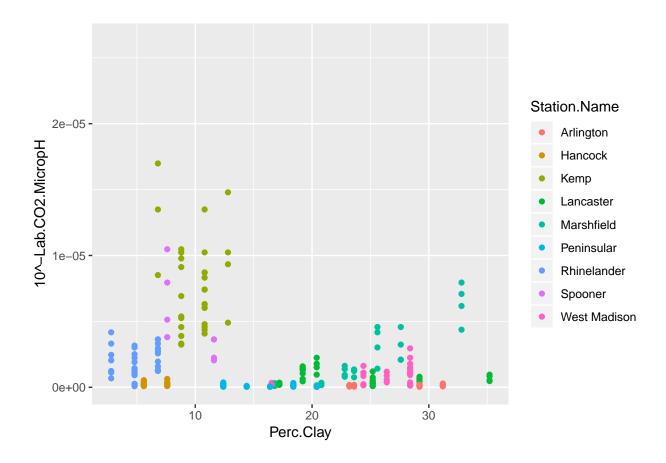
qplot(data = dat, x = Real.Water.Soil.ratio, y = 10^-Lab.CO2.MicropH, color = Station.Na



qplot(data = dat, x = Real.Water.Soil.ratio, y = 10^-Lab.CO2.MicropH, color = Texture.Na



qplot(data = dat, x = Perc.Clay, y = 10^-Lab.CO2.MicropH, color = Station.Name)



Plots with 16S Amplicon Analysis:

[...]