

# Trends in Gm, rwp & cell wall chemistry

Analysis objective: To see if there is relationship between cell wall chemistry and cell wall resistance (rwp or Resistwp25) or Gm (conductance).

Problems: 1) the cell wall chemistry was taken from trunk material while Rm and rwp are calculated from leaves. 2) cell wall data were collected from various outside commongarden sites while leaf physiology was collected from greenhouse material.

```
setwd("~/GitHub/poplar_GWAS_photosyn")
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
##
## The following object is masked from 'package:stats':
##
##     filter
##
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
dat1<-read.csv("datainput_2_27_2015.csv")
head(dat1)
names(dat1)

dat1$id<-toupper(dat1$id) #all letters upper case
dat1$id<-gsub("*.CSV", "", dat1$id) # replace .csv to blank
head(dat1)
str(dat1)
```

getting counts for number of rch and rwp > 0

```
a<-dat1 %>% select(id, Resistch25, Resistwp25) %>% filter(Resistwp25 > 0)
b<-dat1 %>% select(id, Resistch25, Resistwp25) %>% filter(Resistch25 > 0)
```

Data manipulation and Gm calculation Note: can only calculate Gm for samples that have rwp > 0.

```
dat2<-dat1 %>% select(id, Duplicate, Jmax25, Rdlight25, Resistwp25, Resistch25, gamma.25, Asat_ALight) %>% filter(Duplicate == "Unique" & Resistwp25 > 0) %>% mutate(Gm = 1/Resistwp25)
```

Investigate relationships or rwp (Resistwp25) with cell wall chemistry

File names for the wall chemistry: CLA\_SG\_Input.csv CLA\_C5\_6.csv CLA\_Recalci\_Input.csv

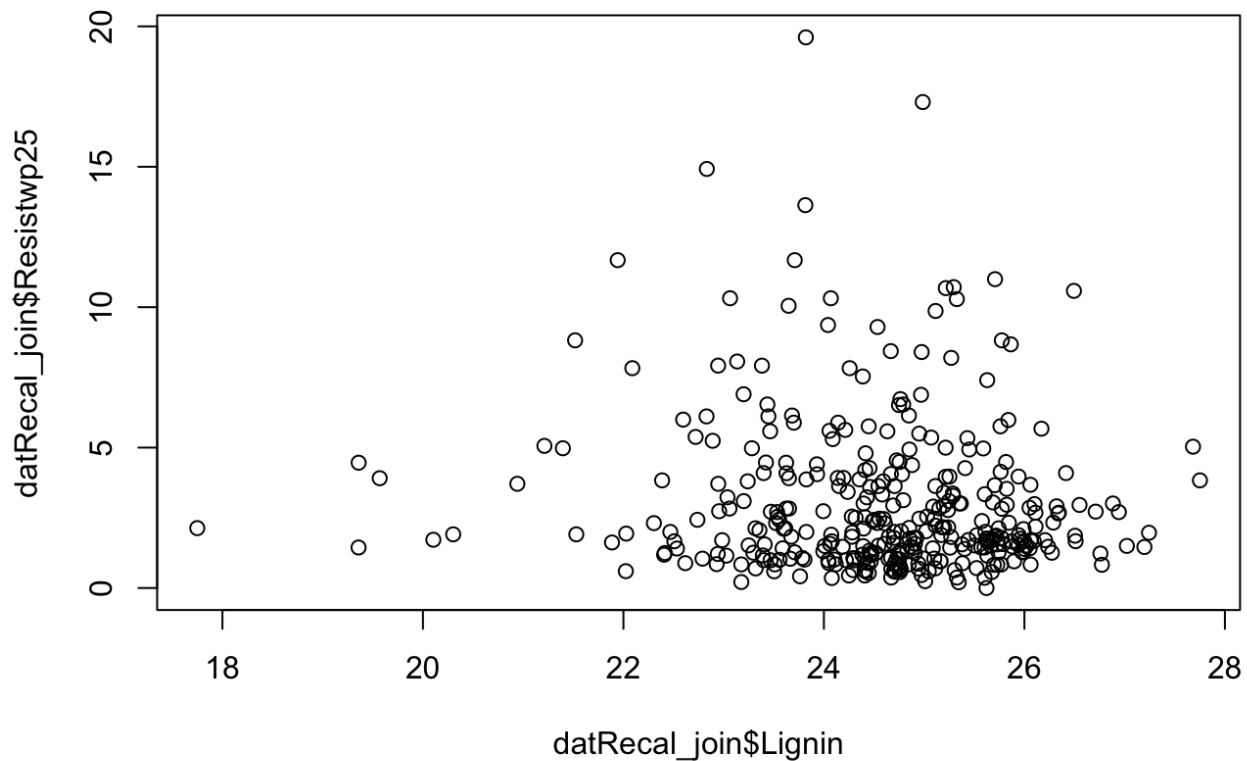
Corvallis\_2010.csv

## Plots for the Clatskine Site

```
datRecal<-read.csv("CLA_Recalci_Input.csv")  
datRecal_join<-inner_join(dat2, datRecal, by = "id")
```

```
## Warning: joining character vector and factor, coercing into character  
## vector
```

```
plot(datRecal_join$Lignin, datRecal_join$Resistwp25)
```



```
cor.test(datRecal_join$Lignin, datRecal_join$Resistwp25, method = "spearman")
```

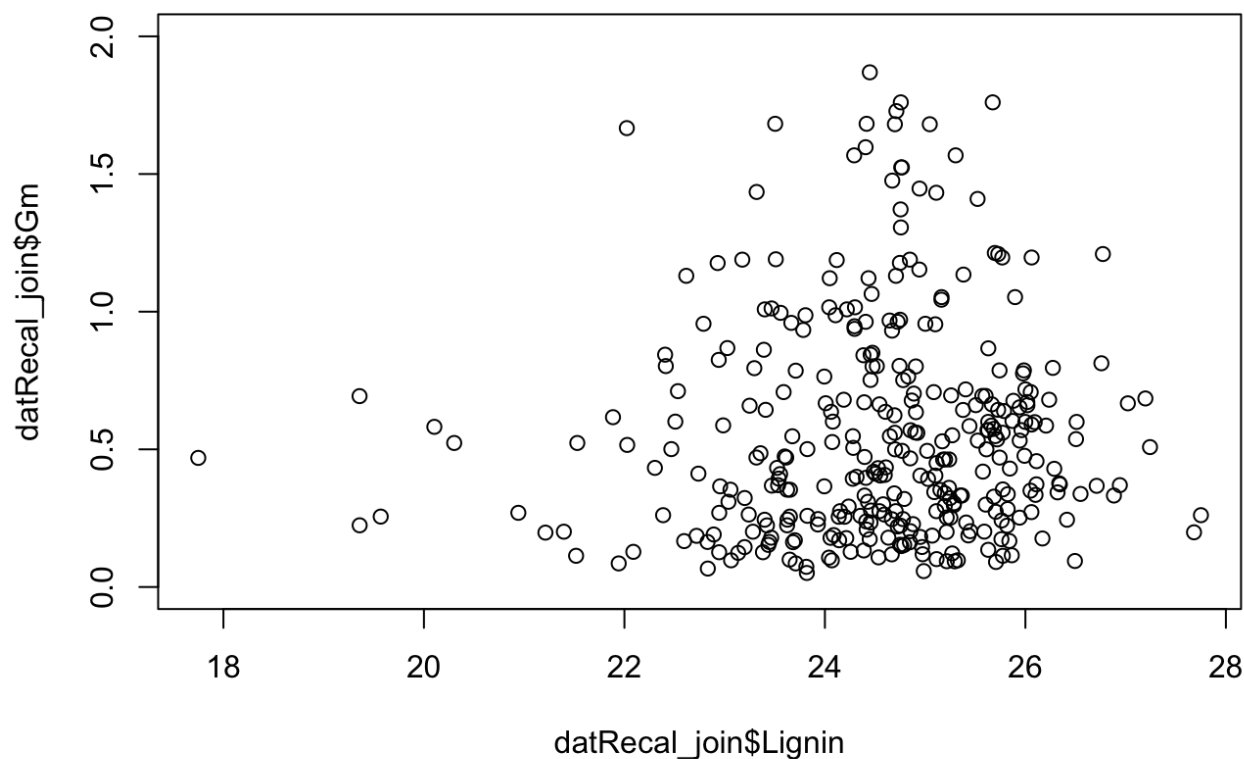
```
## Warning in cor.test.default(datRecal_join$Lignin,  
## datRecal_join$Resistwp25, : Cannot compute exact p-value with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data: datRecal_join$Lignin and datRecal_join$Resistwp25  
## S = 8100122, p-value = 0.1988  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## -0.068173
```

```
cor.test(datRecal_join$Lignin, datRecal_join$Resistwp25, method = "pearson")
```

```
##  
## Pearson's product-moment correlation  
##  
## data: datRecal_join$Lignin and datRecal_join$Resistwp25  
## t = -1.9061, df = 355, p-value = 0.05745  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.202331733 0.003179182  
## sample estimates:  
##      cor  
## -0.1006498
```

```
plot(datRecal_join$Lignin, datRecal_join$Gm, ylim=c(0,2))
```



```
cor.test(datRecal_join$Lignin, datRecal_join$Gm, method = "spearman")
```

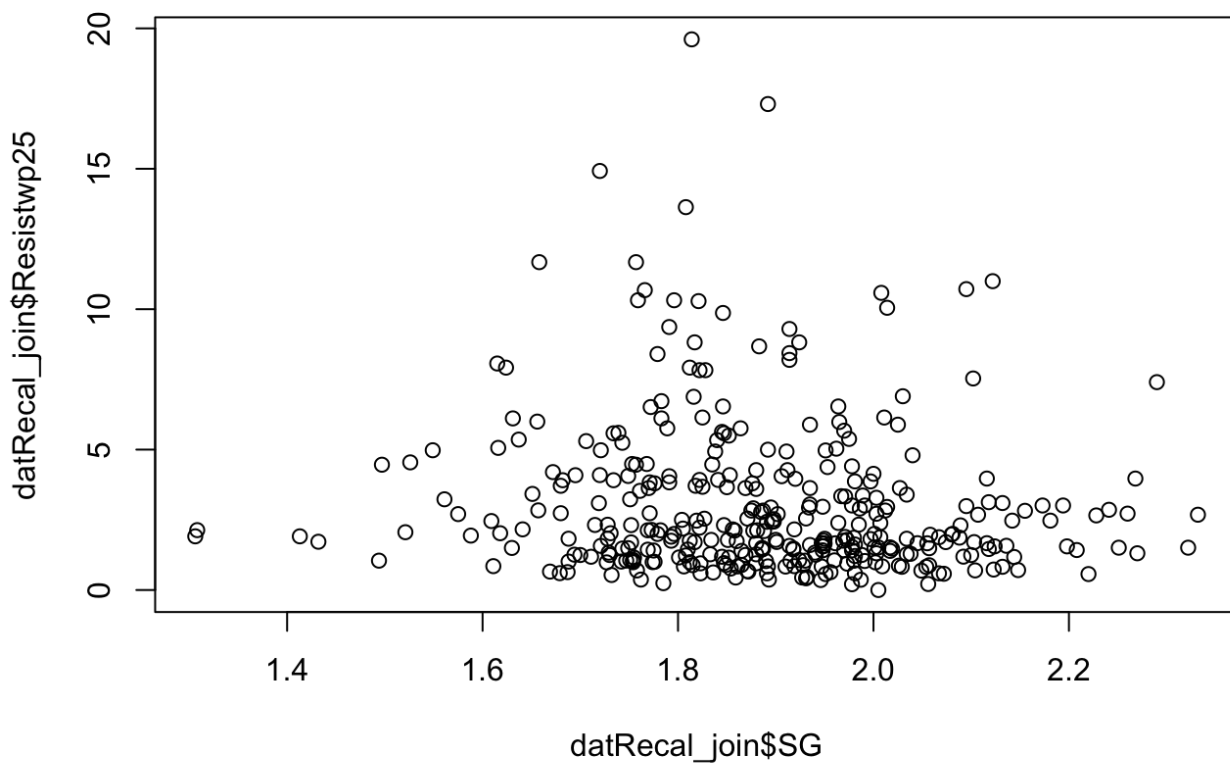
```
## Warning in cor.test.default(datRecal_join$Lignin, datRecal_join$Gm, method  
## = "spearman"): Cannot compute exact p-value with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data: datRecal_join$Lignin and datRecal_join$Gm  
## S = 7066190, p-value = 0.1988  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## 0.068173
```

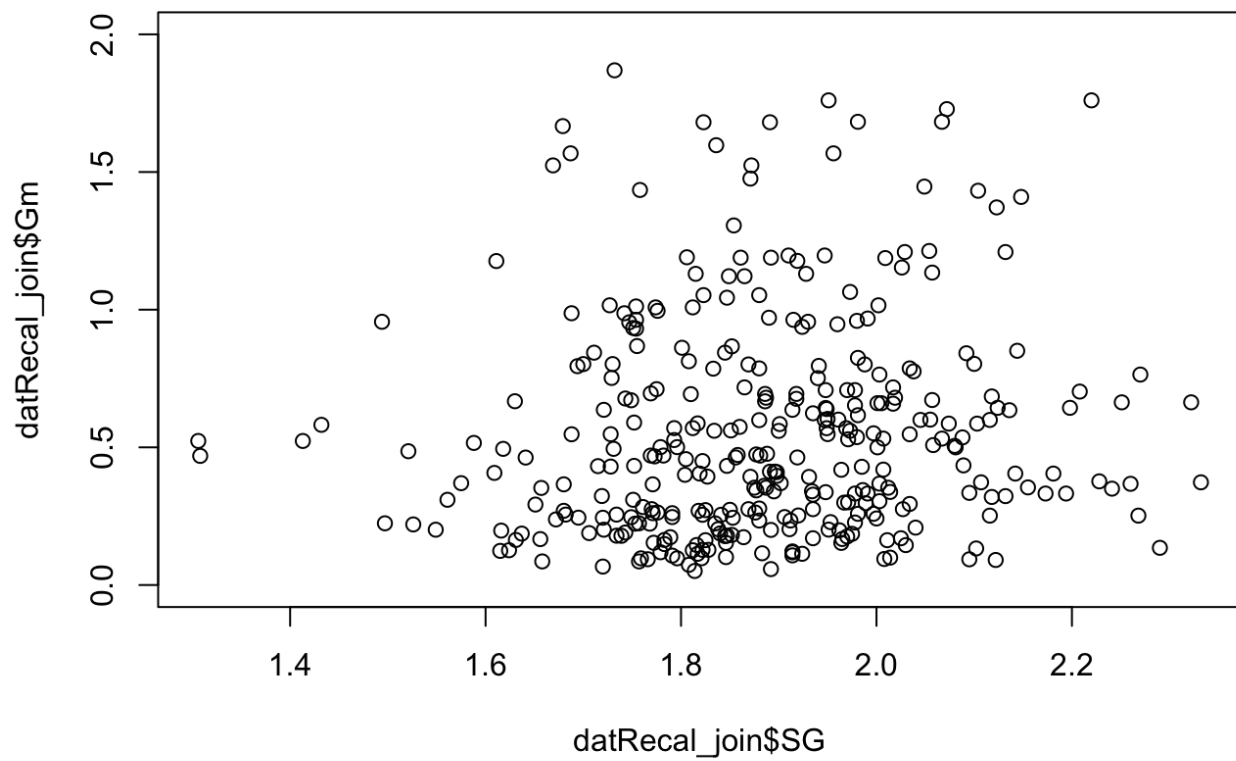
```
cor.test(datRecal_join$Lignin, datRecal_join$Gm, method = "pearson")
```

```
##  
## Pearson's product-moment correlation  
##  
## data: datRecal_join$Lignin and datRecal_join$Gm  
## t = 0.8018, df = 355, p-value = 0.4232  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.06155286 0.14566742  
## sample estimates:  
## cor  
## 0.04251449
```

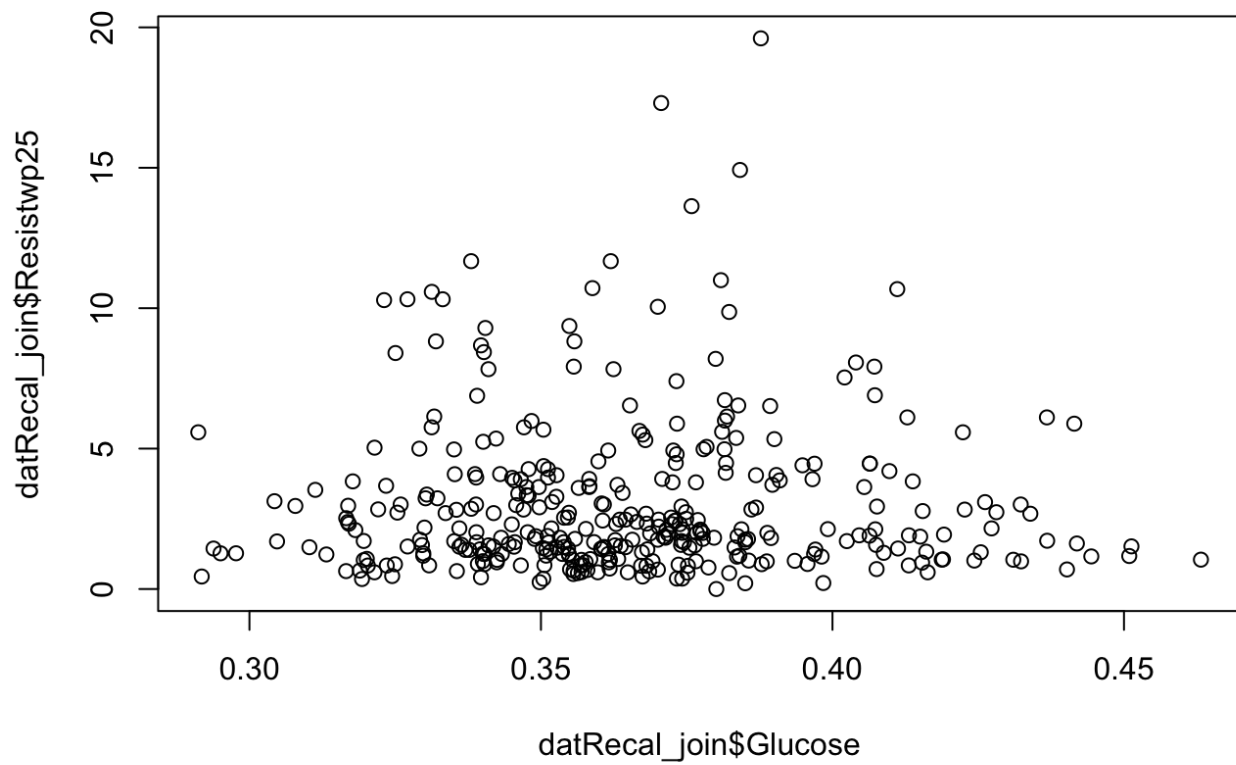
```
plot(datRecal_join$SG, datRecal_join$Resistwp25)
```



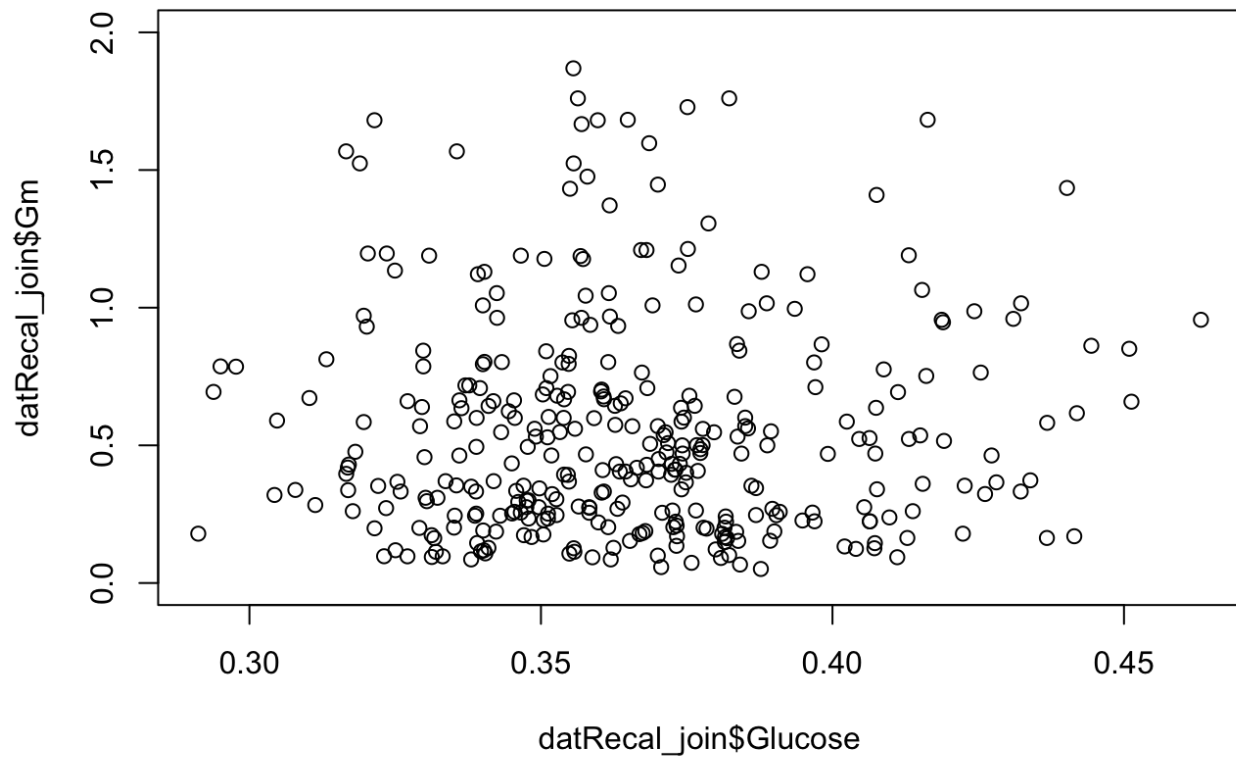
```
plot(datRecal_join$SG, datRecal_join$Gm, ylim=c(0,2))
```



```
plot(datRecal_join$Glucose, datRecal_join$Resistwp25)
```

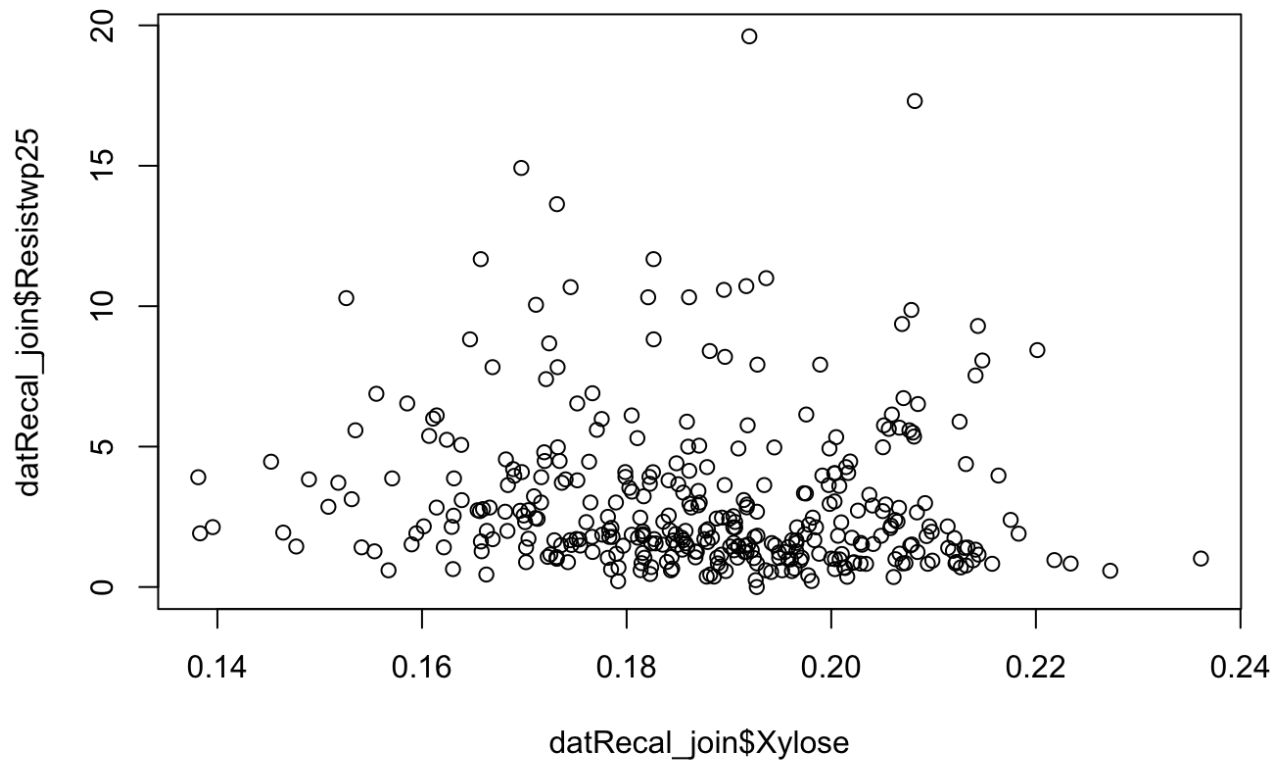


```
plot(datRecal_join$Glucose, datRecal_join$Gm, ylim=c(0,2))
```

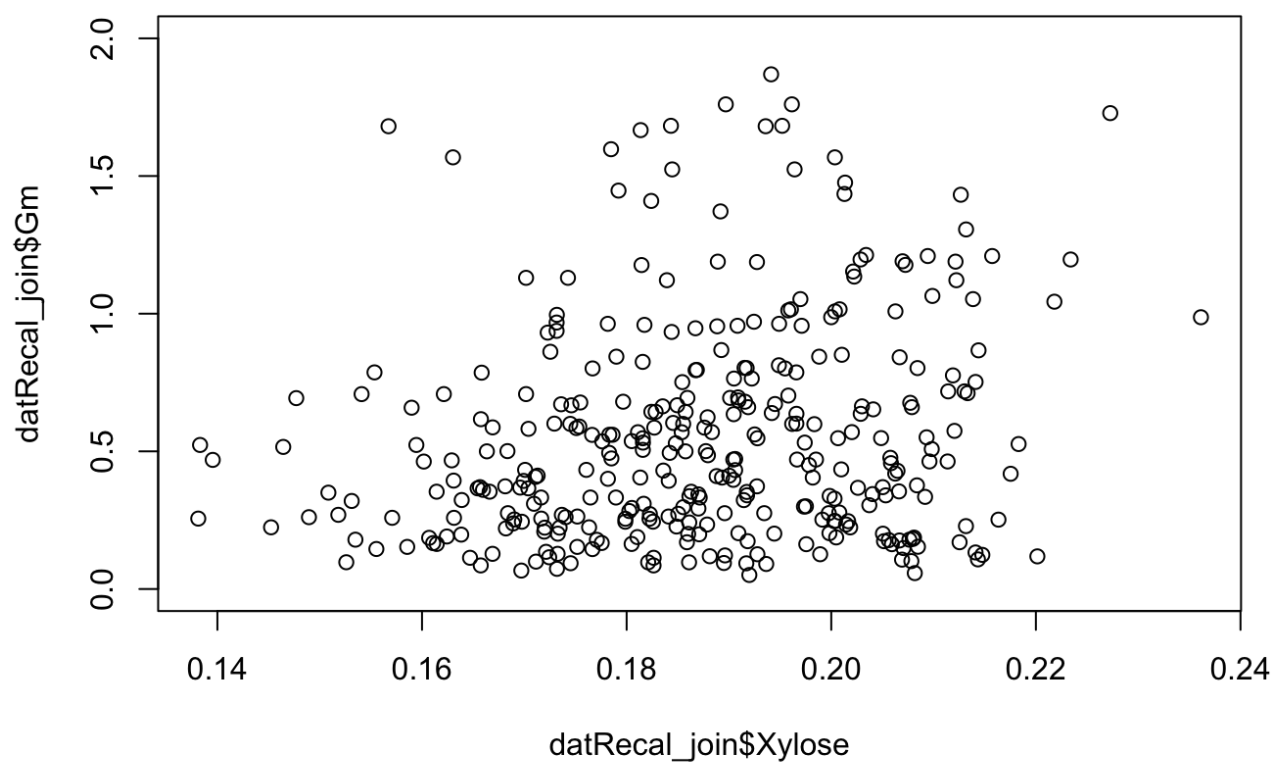


```
plot(datRecal_join$Xylose, datRecal_join$Resistwp25)
```

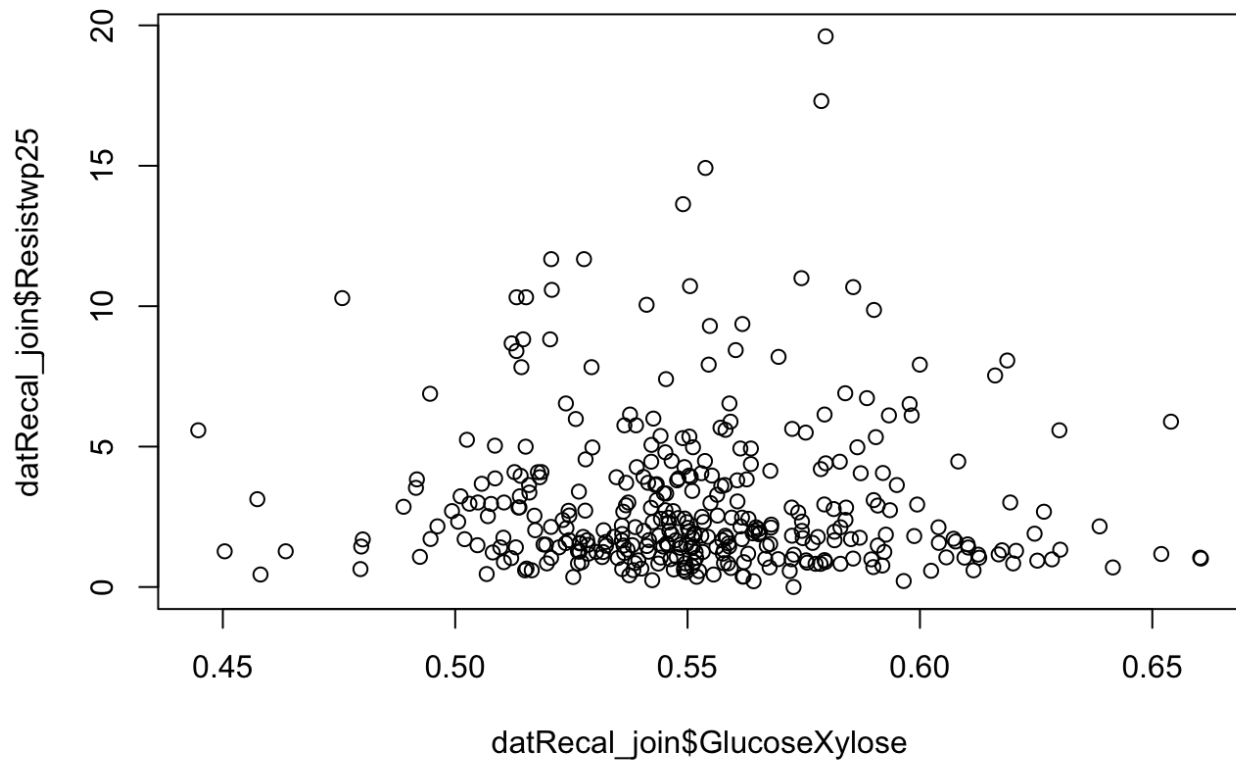




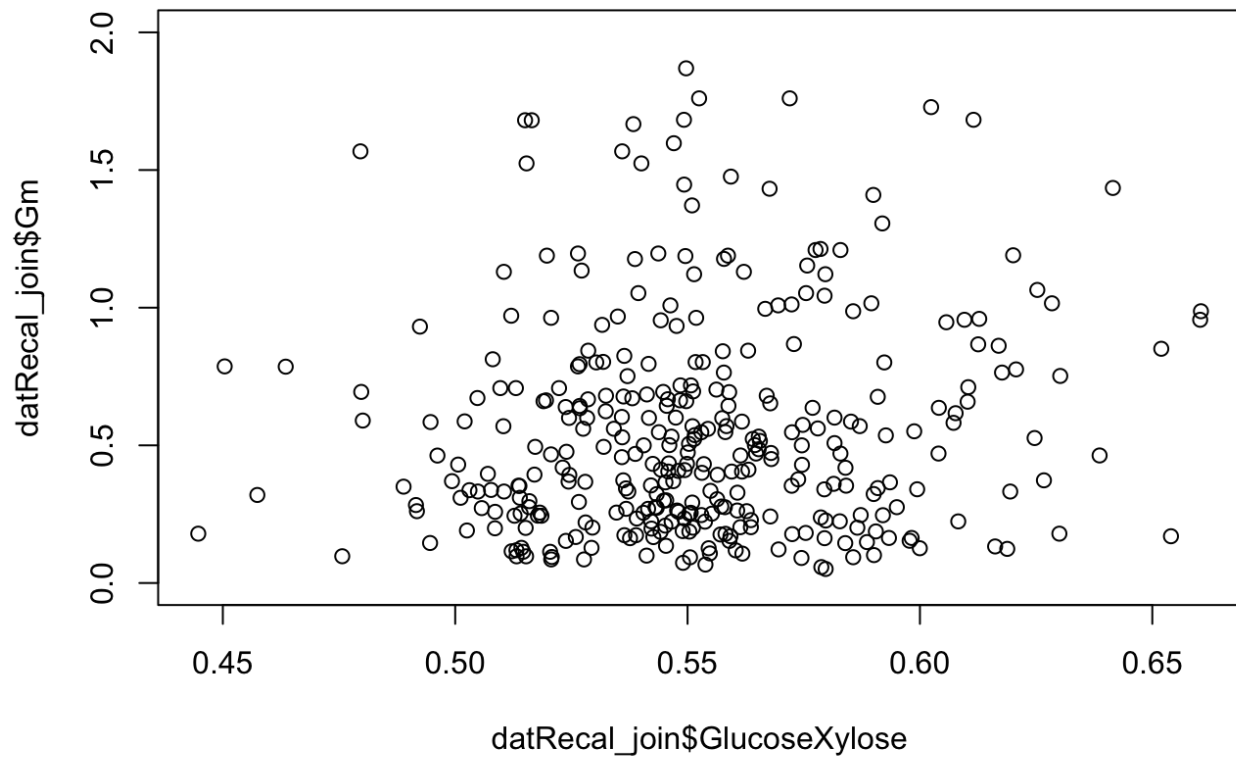
```
plot(datRecal_join$Xylose, datRecal_join$Gm, ylim=c(0,2))
```



```
plot(datRecal_join$ GlucoseXylose, datRecal_join$Resistwp25)
```



```
plot(datRecal_join$ GlucoseXylose, datRecal_join$Gm, ylim=c(0,2))
```



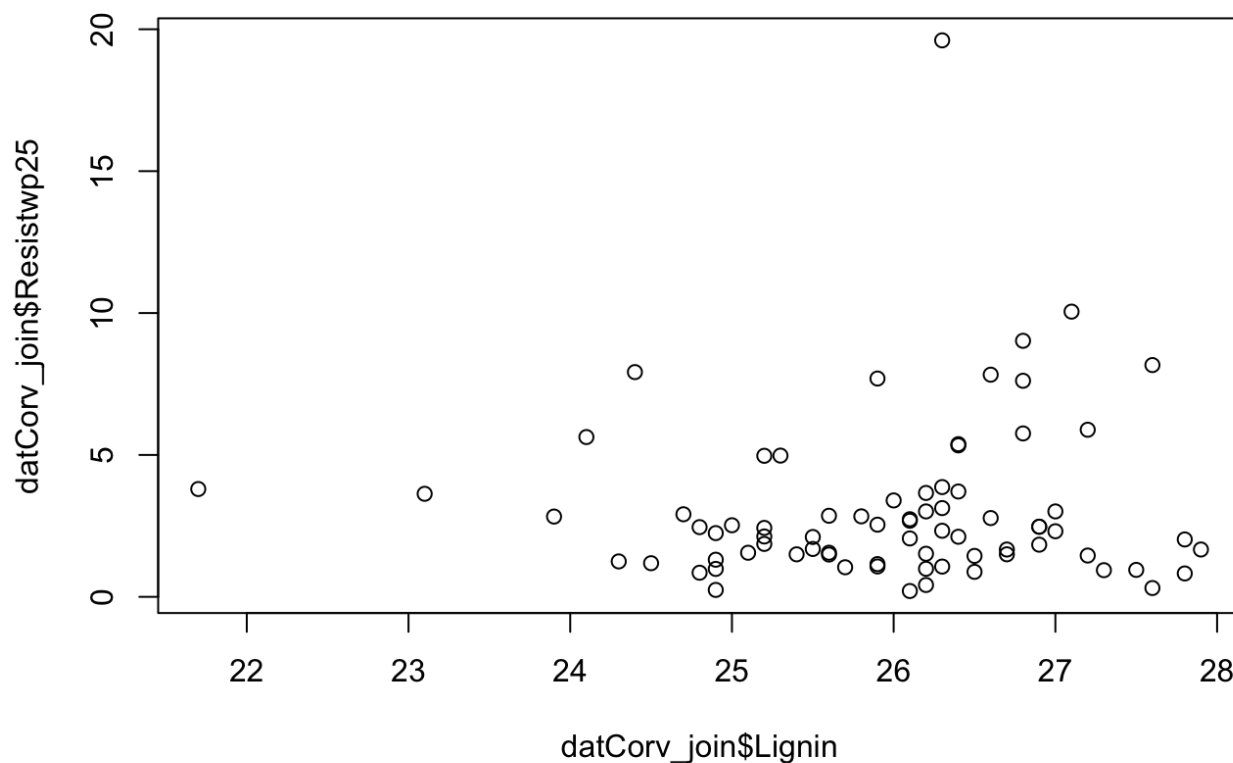
## Plots for Corvallis

Note, not many points in Corvallis\_2010.csv

```
datCorv<-read.csv("Corvallis_2010.csv")
datCorv_join<-inner_join(dat2, datCorv, by = "id")
```

```
## Warning: joining character vector and factor, coercing into character
## vector
```

```
plot(datCorv_join$Lignin, datCorv_join$Resistwp25)
```



```
cor.test(datCorv_join$Lignin, datCorv_join$Resistwp25, method = "spearman")
```

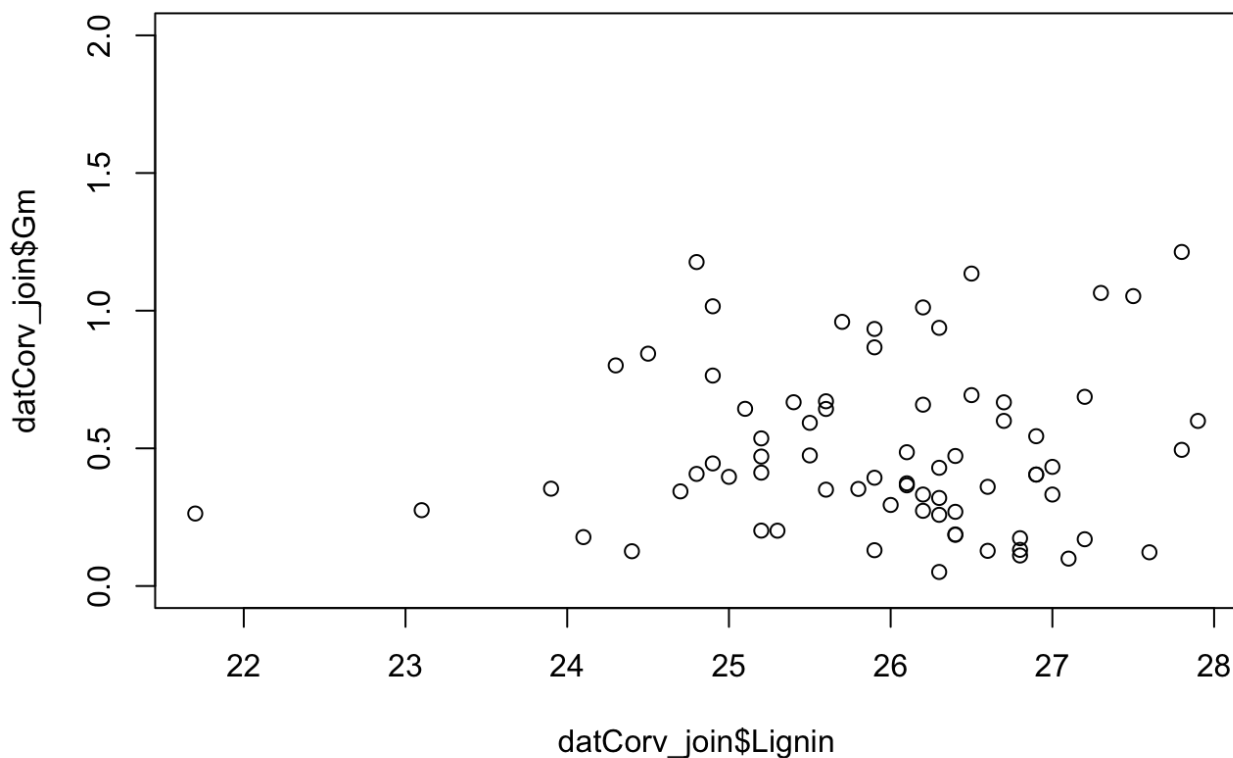
```
## Warning in cor.test.default(datCorv_join$Lignin, datCorv_join$Resistwp25,
## : Cannot compute exact p-value with ties
```

```
##
## Spearman's rank correlation rho
##
## data: datCorv_join$Lignin and datCorv_join$Resistwp25
## S = 70808.22, p-value = 0.7837
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## 0.03201336
```

```
cor.test(datCorv_join$Lignin, datCorv_join$Resistwp25, method = "pearson")
```

```
##
## Pearson's product-moment correlation
##
## data: datCorv_join$Lignin and datCorv_join$Resistwp25
## t = 0.5486, df = 74, p-value = 0.5849
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.1641698 0.2850075
## sample estimates:
## cor
## 0.06364132
```

```
plot(datCorv_join$Lignin, datCorv_join$Gm, ylim=c(0,2))
```



```
cor.test(datCorv_join$Lignin, datCorv_join$Gm, method = "spearman")
```

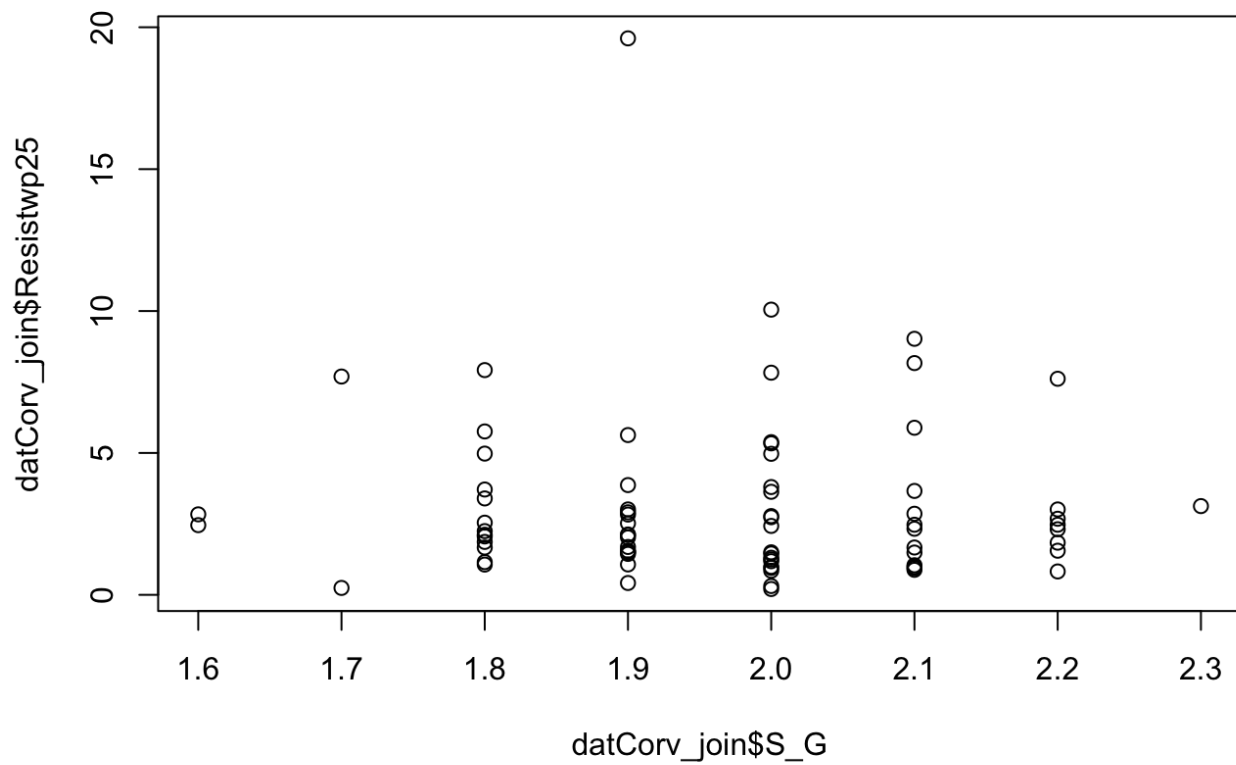
```
## Warning in cor.test.default(datCorv_join$Lignin, datCorv_join$Gm, method =
## "spearman"): Cannot compute exact p-value with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data: datCorv_join$Lignin and datCorv_join$Gm  
## S = 75491.78, p-value = 0.7837  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## -0.03201336
```

```
cor.test(datCorv_join$Lignin, datCorv_join$Gm, method = "pearson")
```

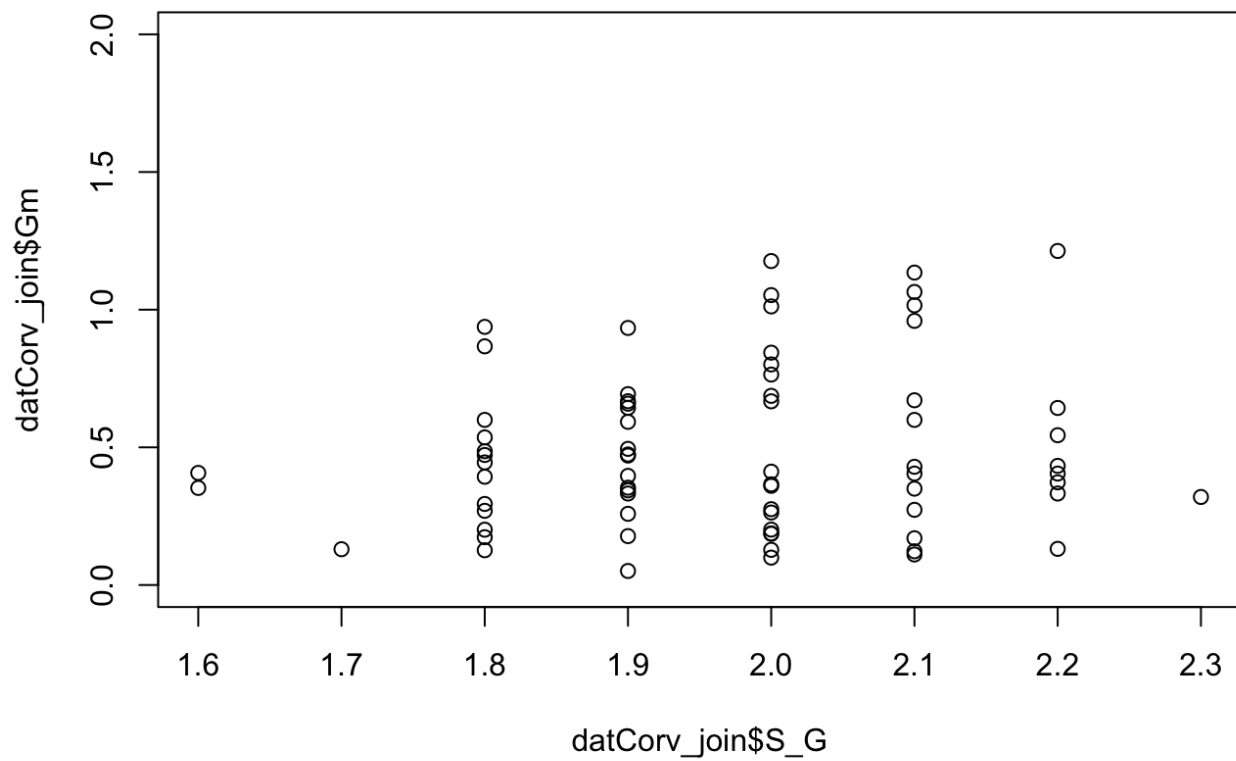
```
##  
## Pearson's product-moment correlation  
##  
## data: datCorv_join$Lignin and datCorv_join$Gm  
## t = 0.4119, df = 74, p-value = 0.6816  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.1795674 0.2703647  
## sample estimates:  
## cor  
## 0.04782431
```

```
plot(datCorv_join$S_G, datCorv_join$Resistwp25)
```

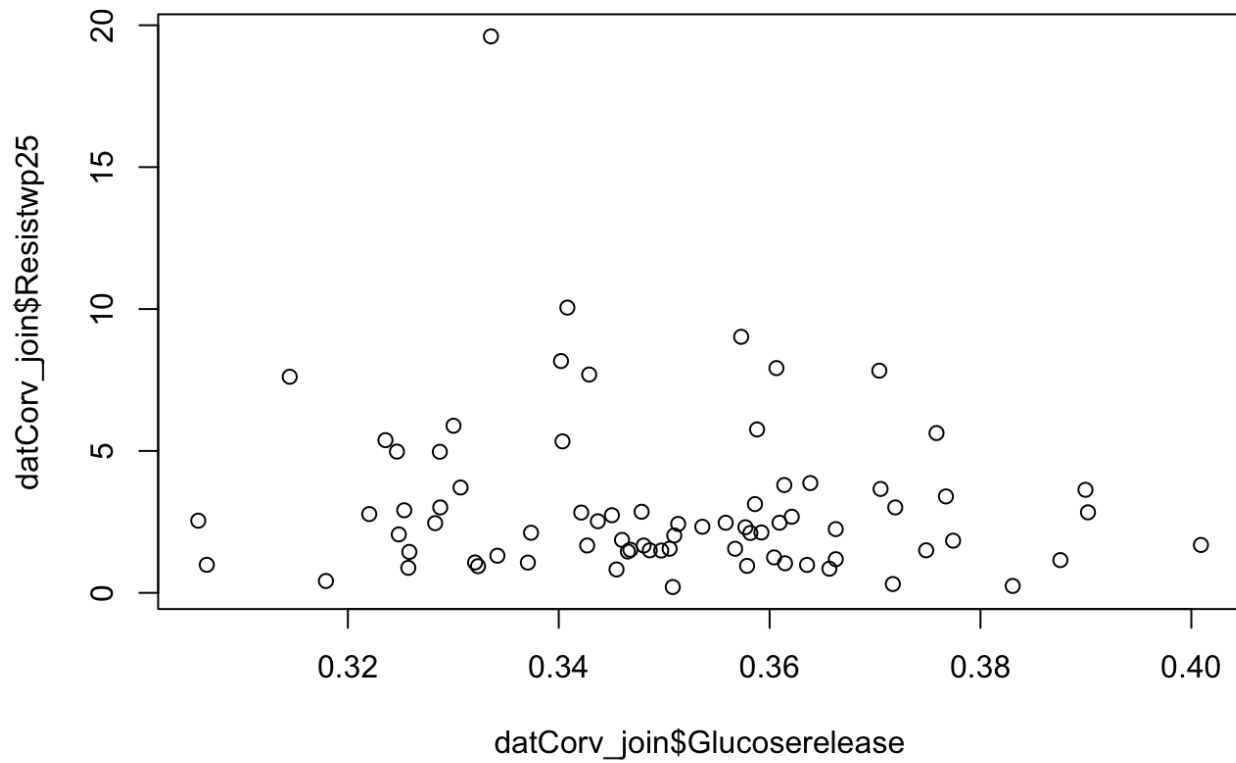


```
plot(datCorv_join$S_G, datCorv_join$Gm, ylim=c(0,2))
```

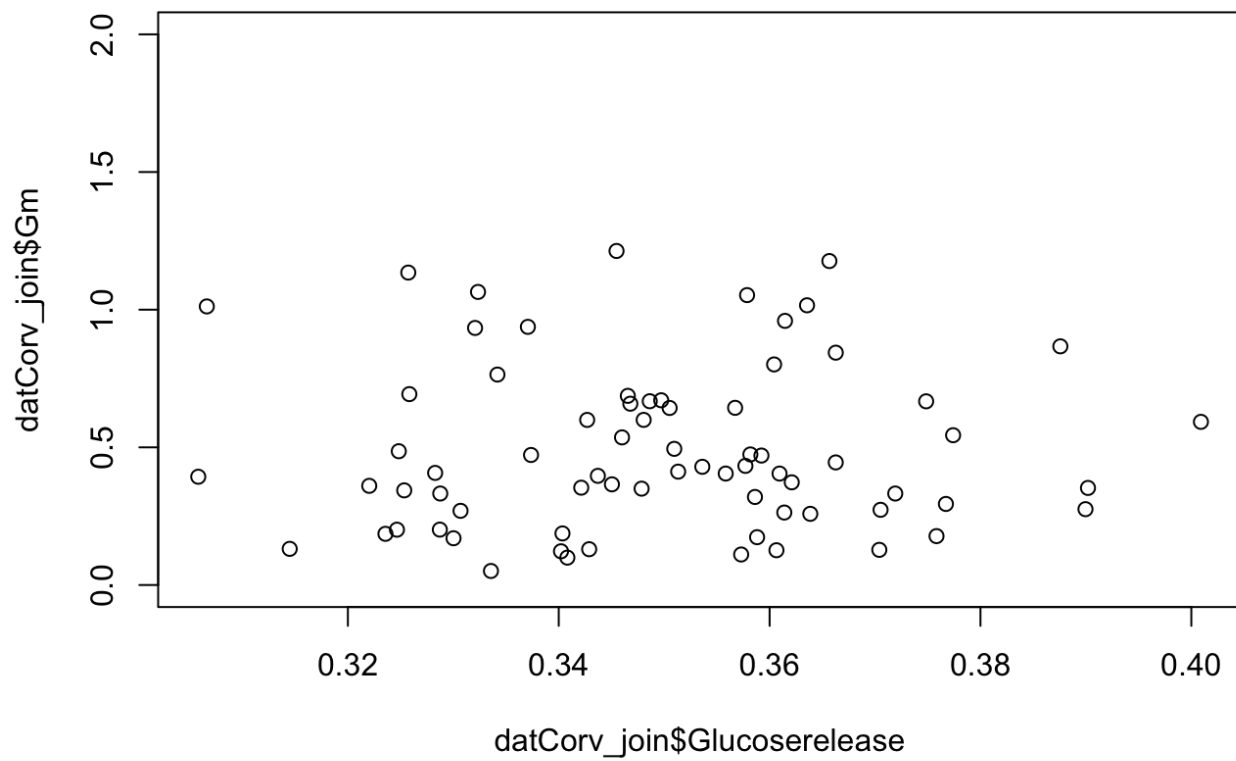




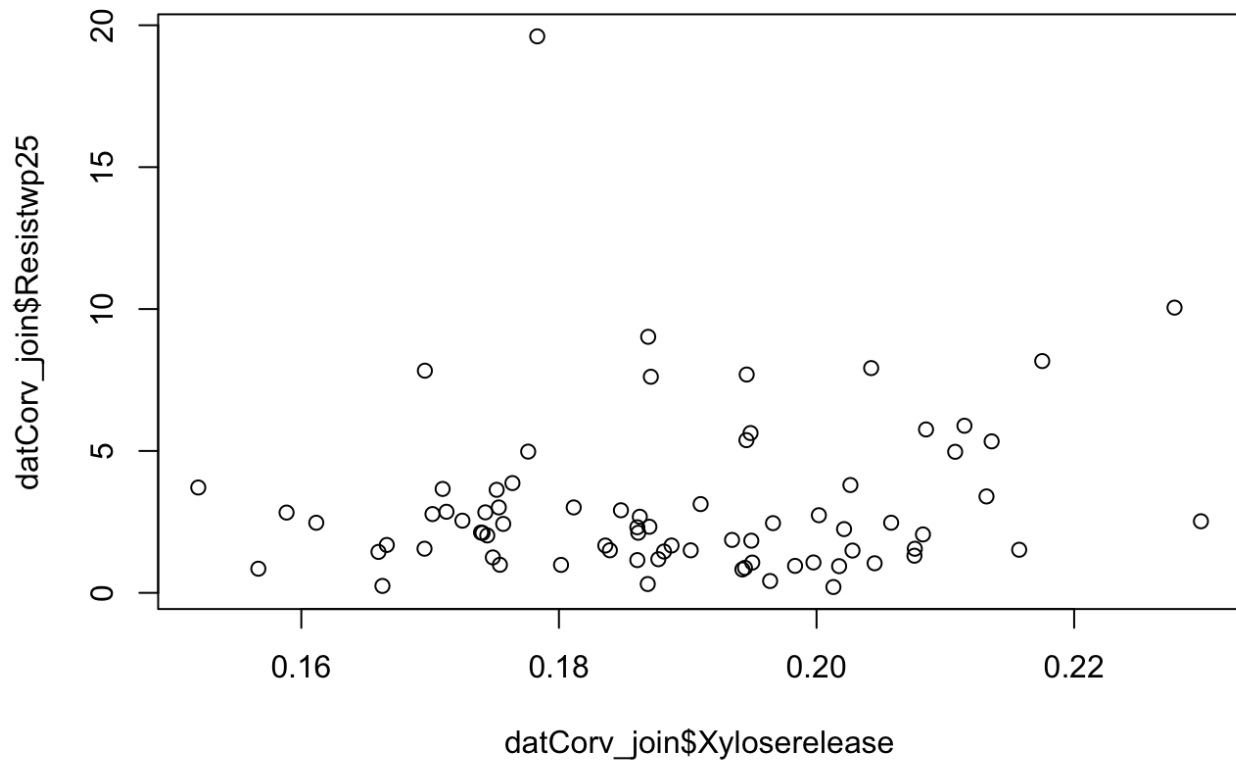
```
plot(datCorv_join$Glucoserelease, datCorv_join$Resistwp25)
```



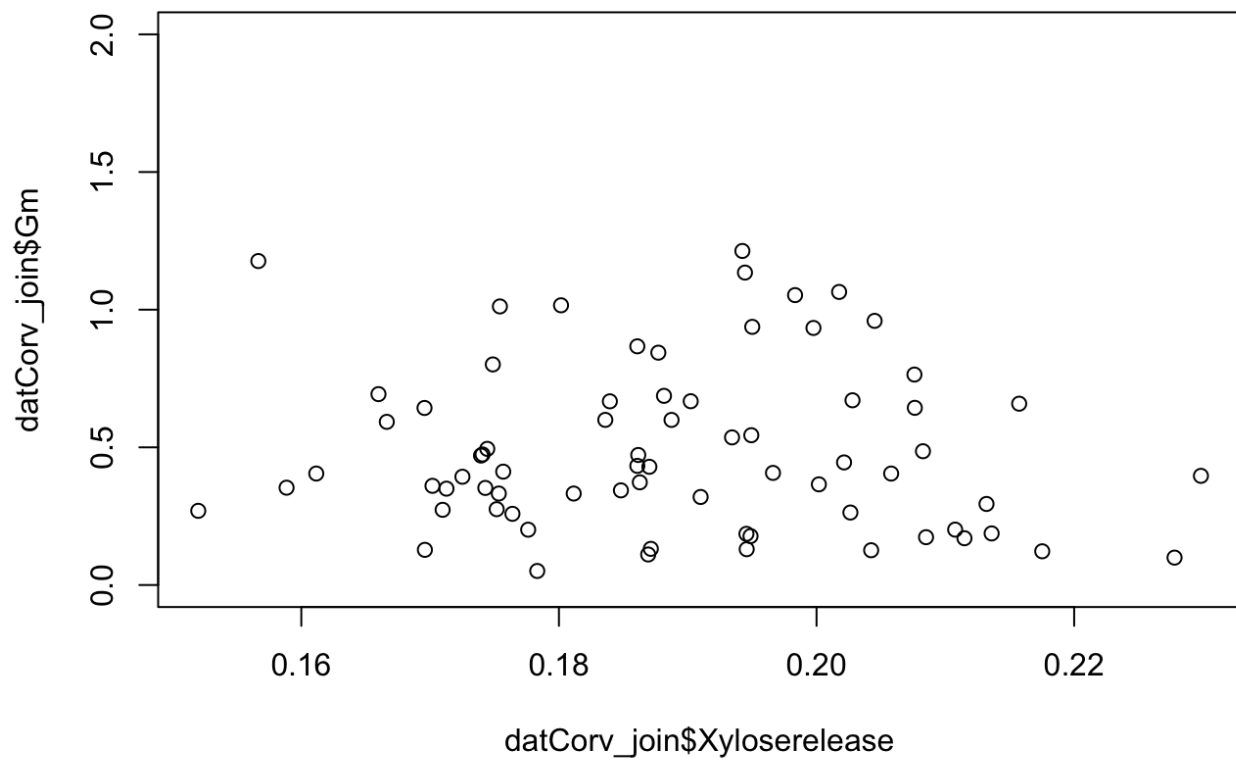
```
plot(datCorv_join$Glucoserelease, datCorv_join$Gm, ylim=c(0,2))
```



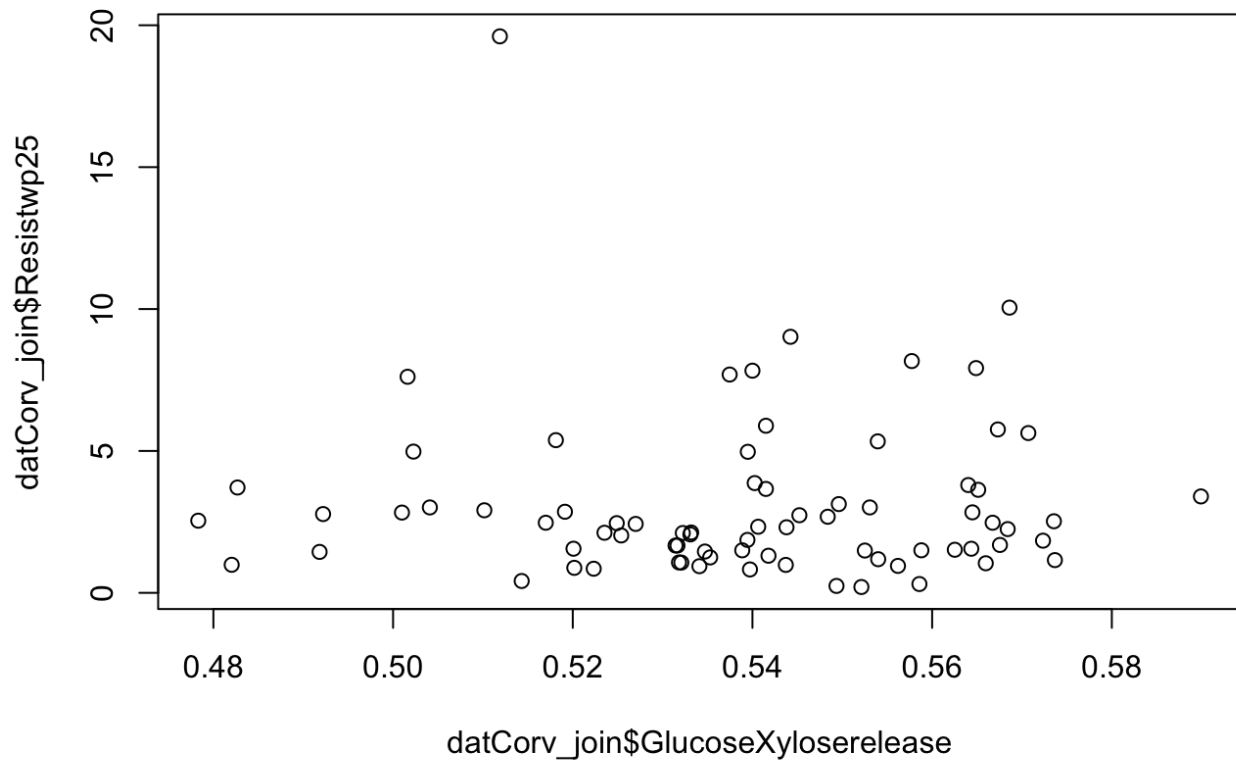
```
plot(datCorv_join$Xyloserelease, datCorv_join$Resistwp25)
```



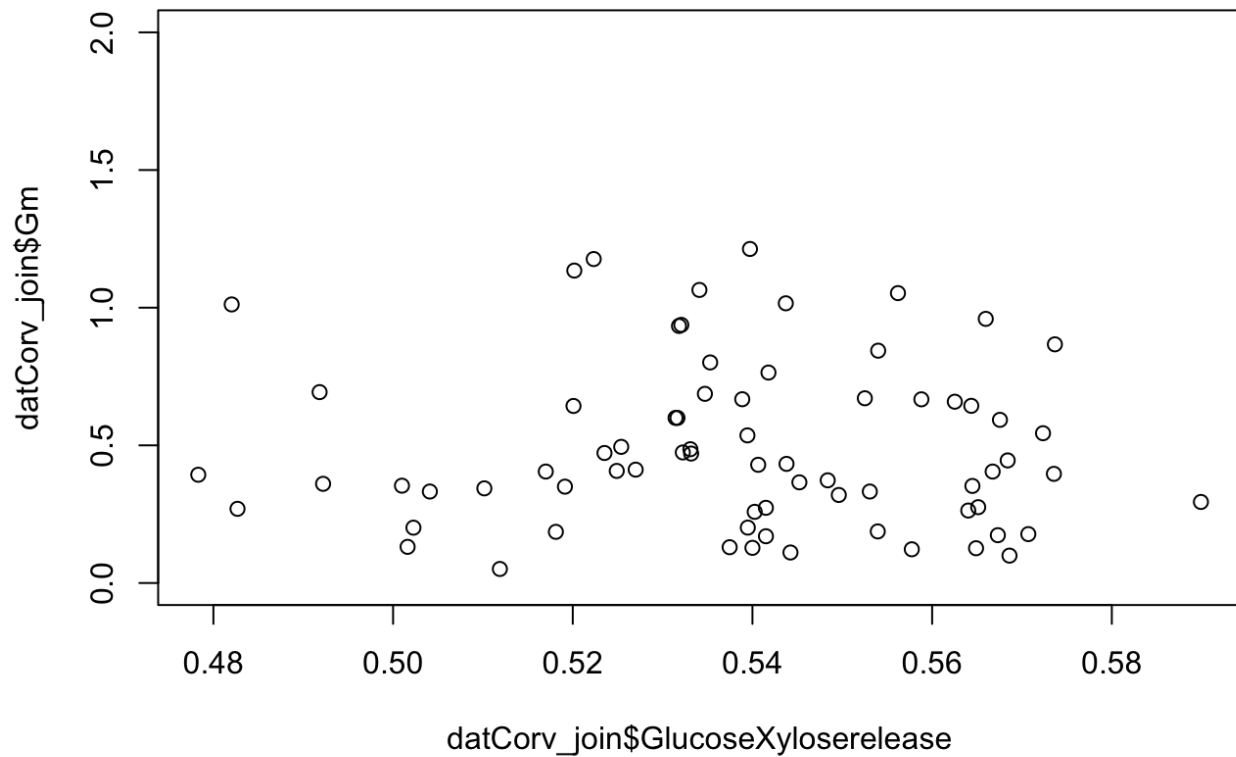
```
plot(datCorv_join$Xyloserelease, datCorv_join$Gm, ylim=c(0,2))
```



```
plot(datCorv_join$GlucoseXyloserelease, datCorv_join$Resistwp25)
```



```
plot(datCorv_join$GlucoseXyloserelease, datCorv_join$Gm, ylim=c(0,2))
```



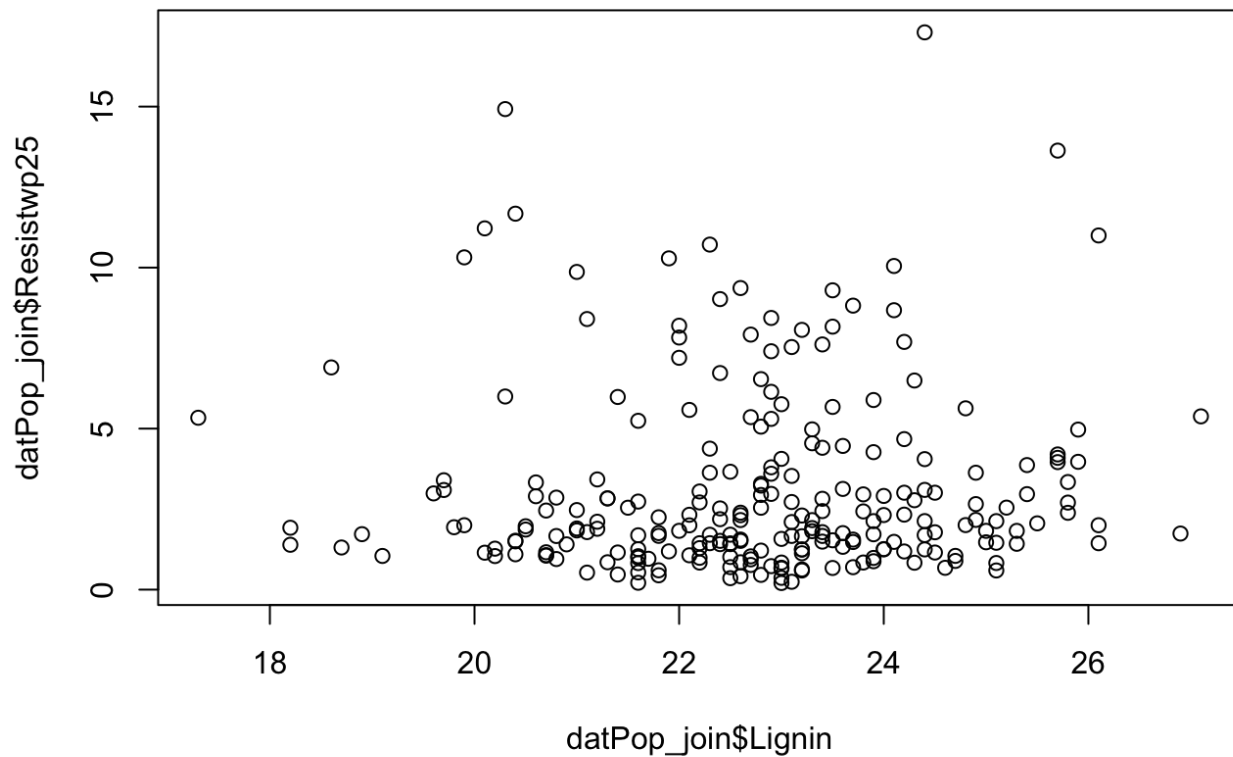
## the Poplar\_C5\_C6\_12\_20\_11.csv dataset

details unknown

```
datPop<-read.csv("Poplar_C5_C6_12_20_11.csv")
datPop_join<-inner_join(dat2, datPop, by = "id")
```

```
## Warning: joining character vector and factor, coercing into character
## vector
```

```
plot(datPop_join$Lignin, datPop_join$Resistwp25)
```



```
cor.test(datPop_join$Lignin, datPop_join$Resistwp25, method = "spearman")
```

```
## Warning in cor.test.default(datPop_join$Lignin, datPop_join$Resistwp25, :  
## Cannot compute exact p-value with ties
```

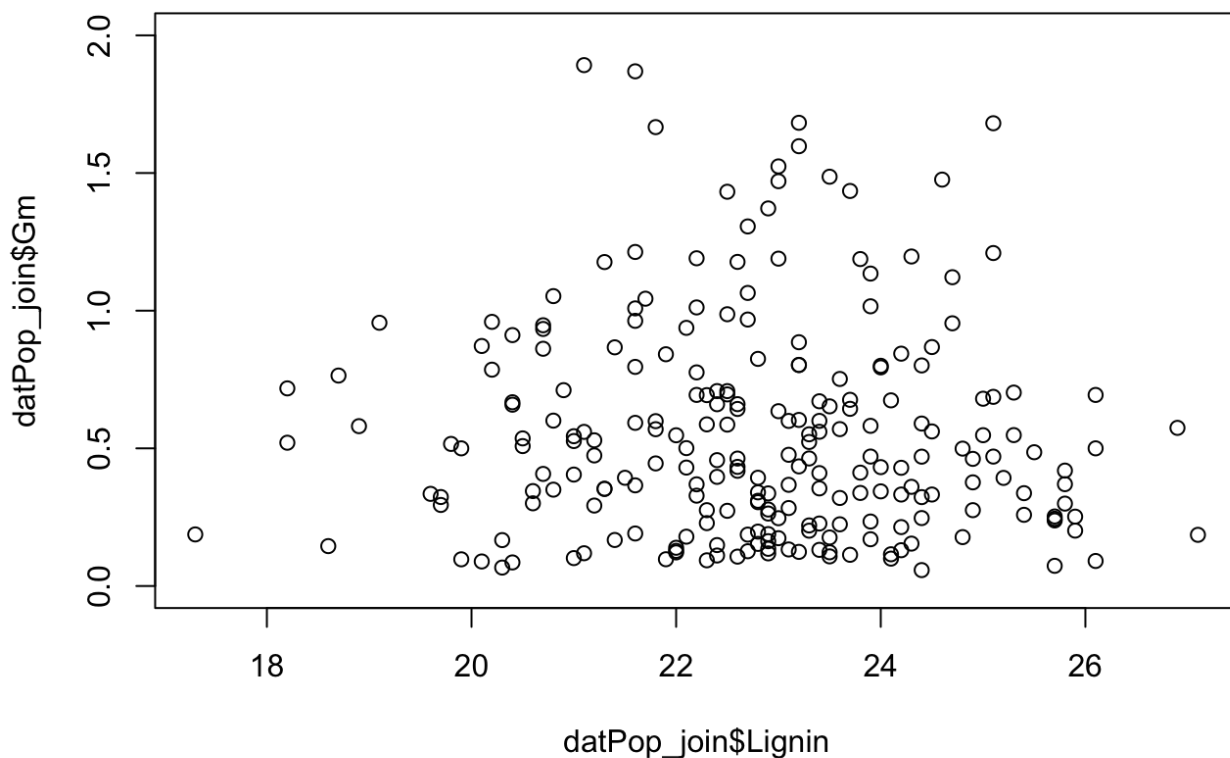
```
##  
## Spearman's rank correlation rho  
##  
## data: datPop_join$Lignin and datPop_join$Resistwp25  
## S = 2211919, p-value = 0.1786  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## 0.08639537
```

```
cor.test(datPop_join$Lignin, datPop_join$Resistwp25, method = "pearson")
```



```
##
## Pearson's product-moment correlation
##
## data: datPop_join$Lignin and datPop_join$Resistwp25
## t = 0.4128, df = 242, p-value = 0.6801
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.09939061 0.15160709
## sample estimates:
##          cor
## 0.02652632
```

```
plot(datPop_join$Lignin, datPop_join$Gm, ylim=c(0,2))
```



```
cor.test(datPop_join$Lignin, datPop_join$Gm, method = "spearman")
```

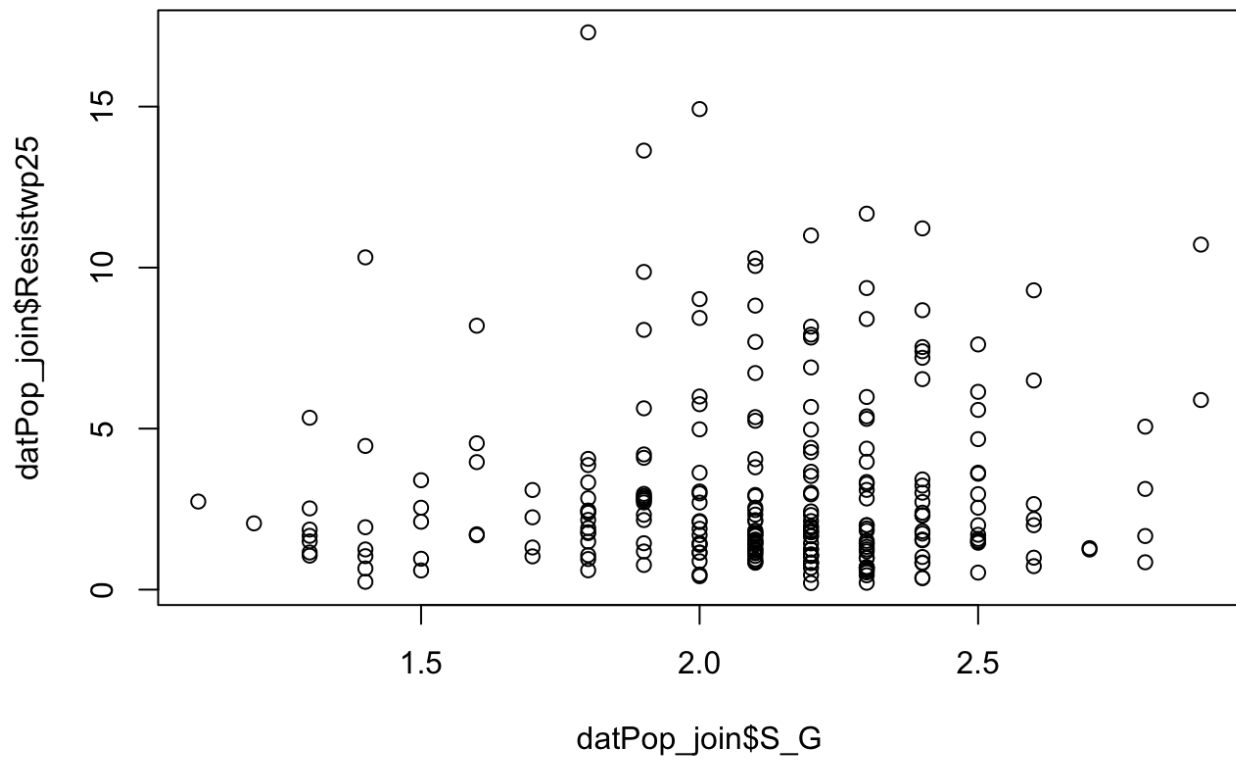
```
## Warning in cor.test.default(datPop_join$Lignin, datPop_join$Gm, method =
## "spearman"): Cannot compute exact p-value with ties
```

```
##  
## Spearman's rank correlation rho  
##  
## data: datPop_join$Lignin and datPop_join$Gm  
## S = 2630261, p-value = 0.1786  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## -0.08639537
```

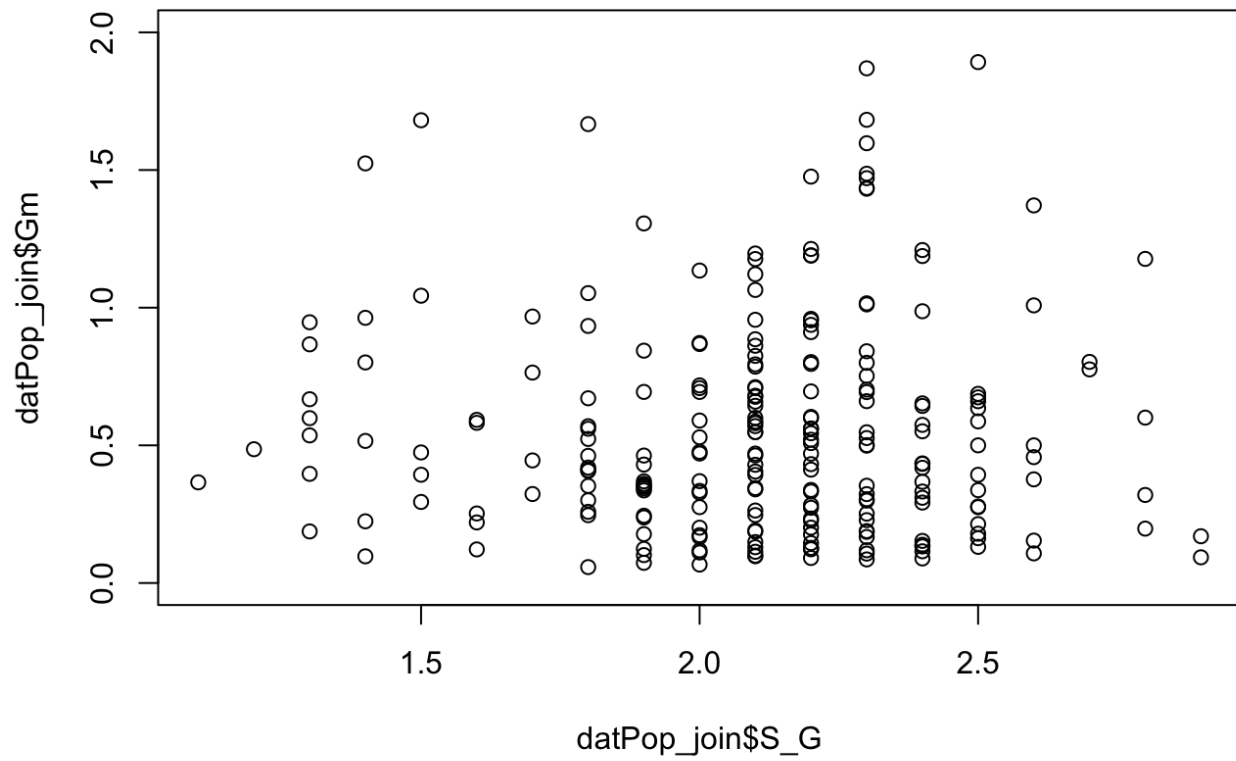
```
cor.test(datPop_join$Lignin, datPop_join$Gm, method = "pearson")
```

```
##  
## Pearson's product-moment correlation  
##  
## data: datPop_join$Lignin and datPop_join$Gm  
## t = -0.9101, df = 242, p-value = 0.3637  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.18264806 0.06768036  
## sample estimates:  
## cor  
## -0.05840186
```

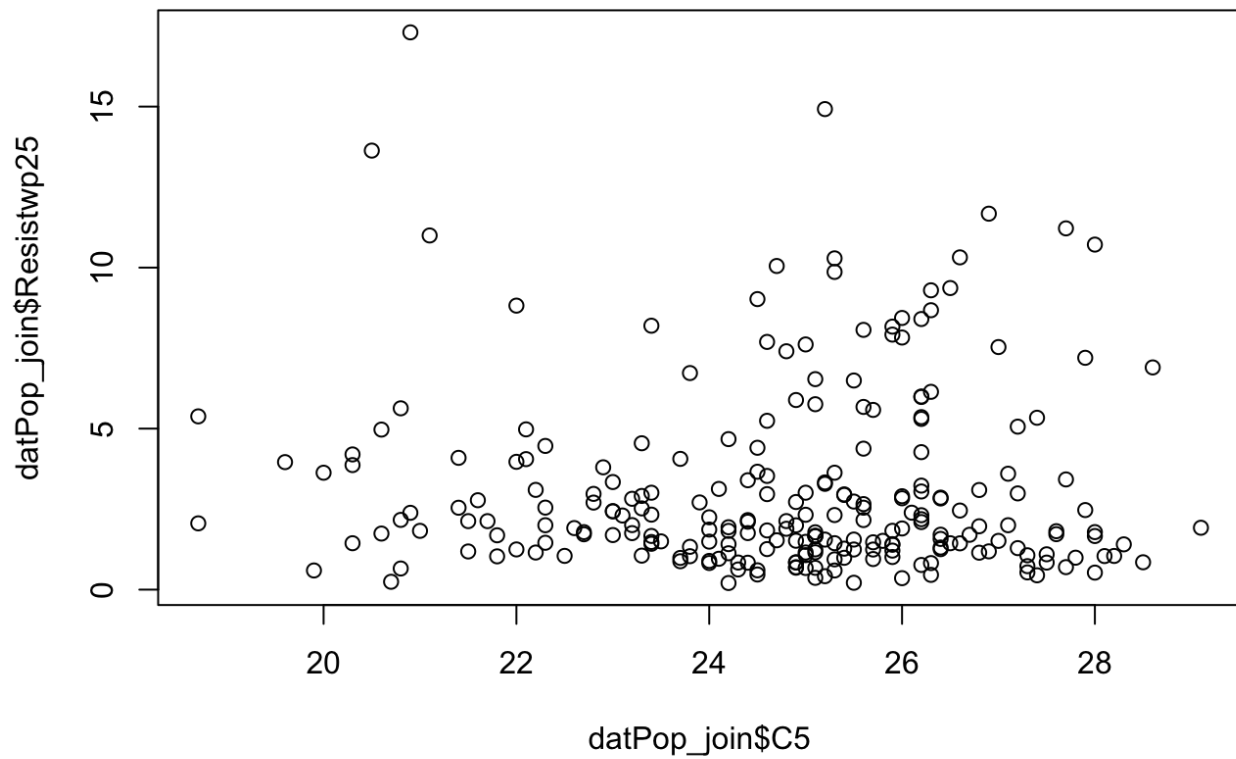
```
plot(datPop_join$S_G, datPop_join$Resistwp25)
```



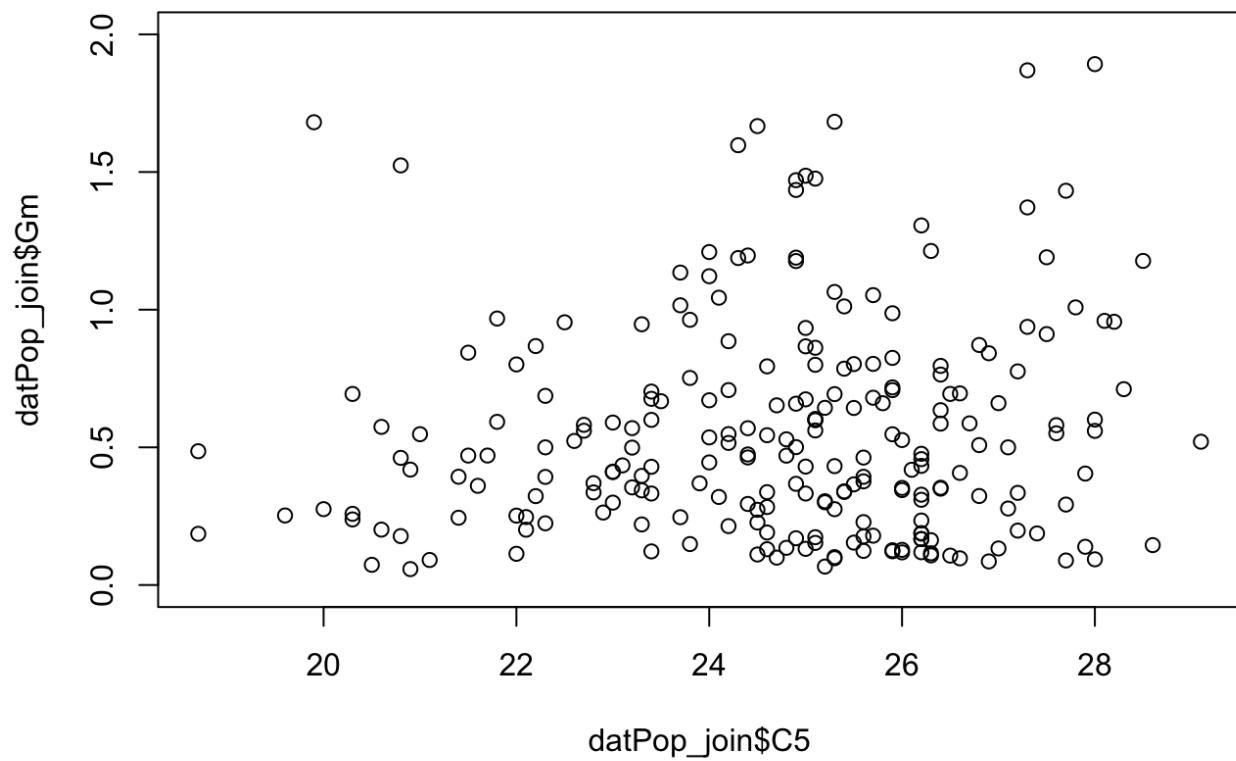
```
plot(datPop_join$S_G, datPop_join$Gm, ylim=c(0,2))
```



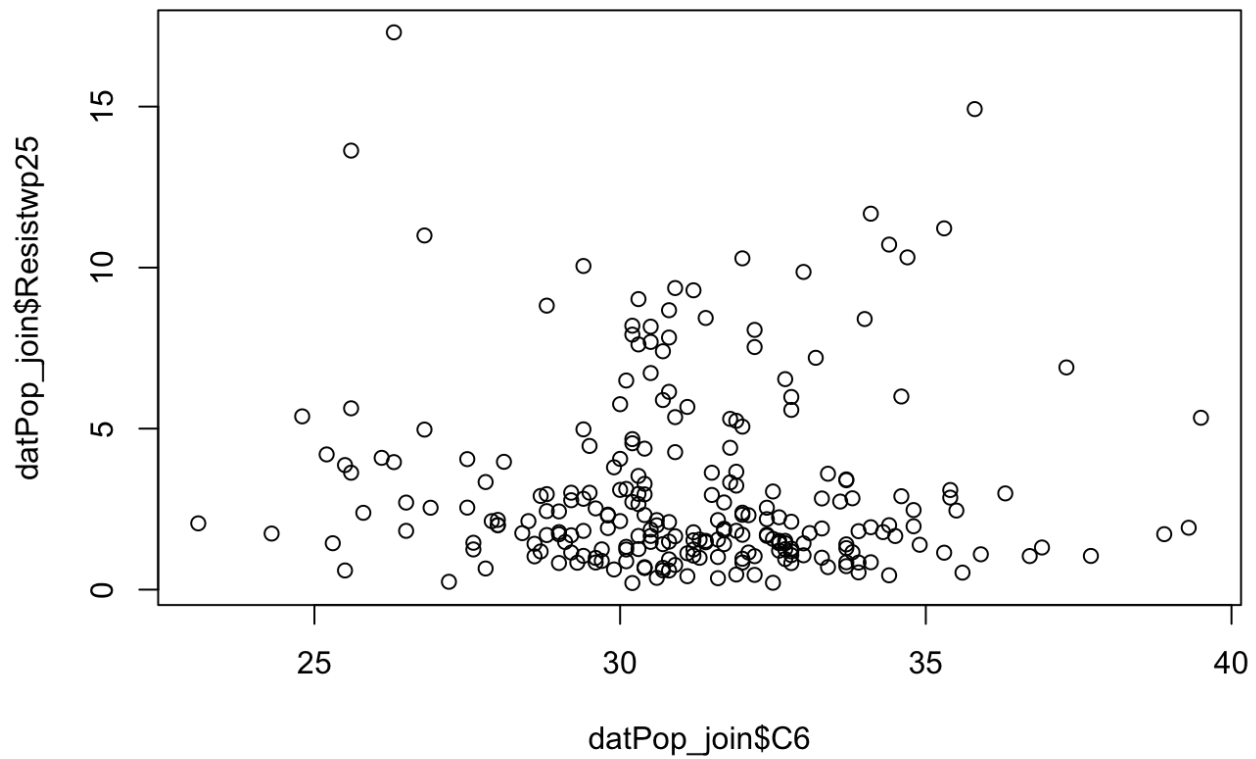
```
plot(datPop_join$C5, datPop_join$Resistwp25)
```



```
plot(datPop_join$C5, datPop_join$Gm, ylim=c(0,2))
```



```
plot(datPop_join$C6, datPop_join$Resistwp25)
```



```
plot(datPop_join$C6, datPop_join$Gm, ylim=c(0,2))
```

