

Initial Analysis of White Sage Data

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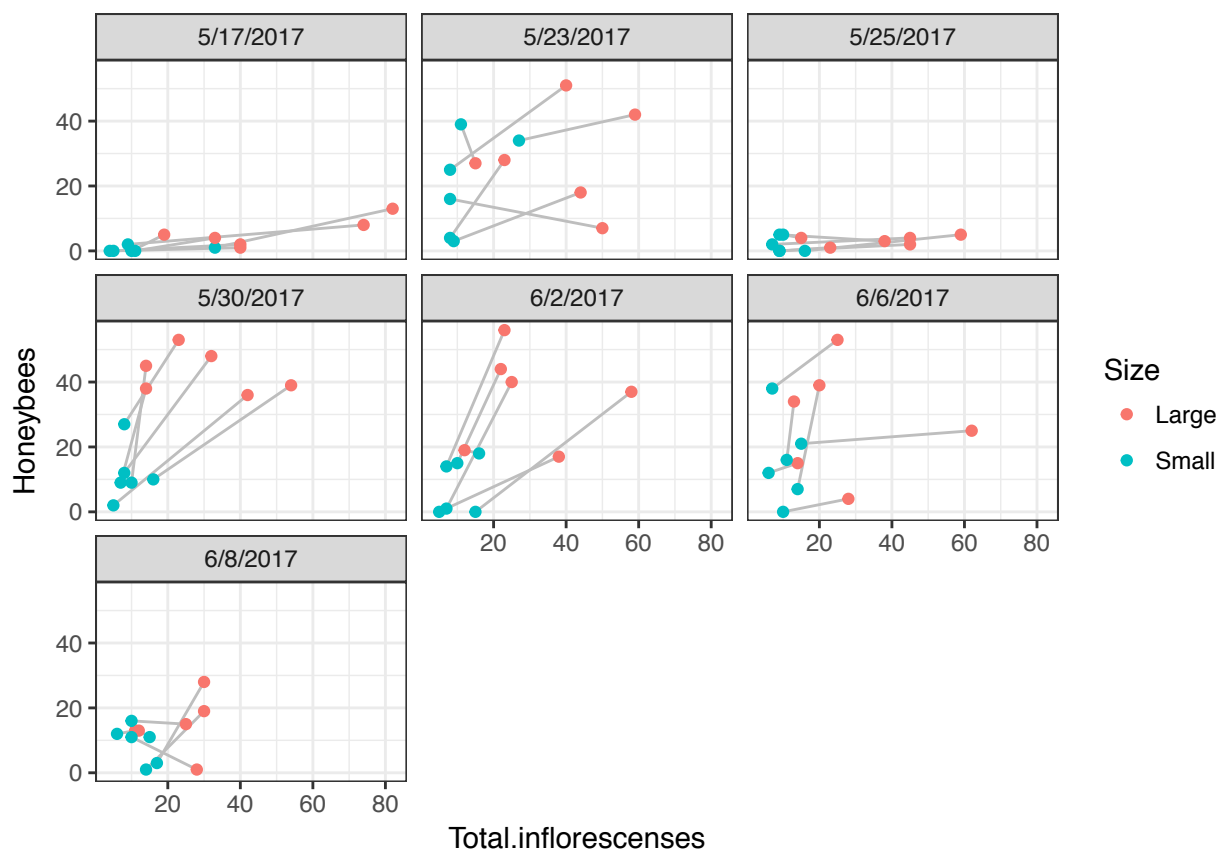
6/20/2017

Load in the clean dataset

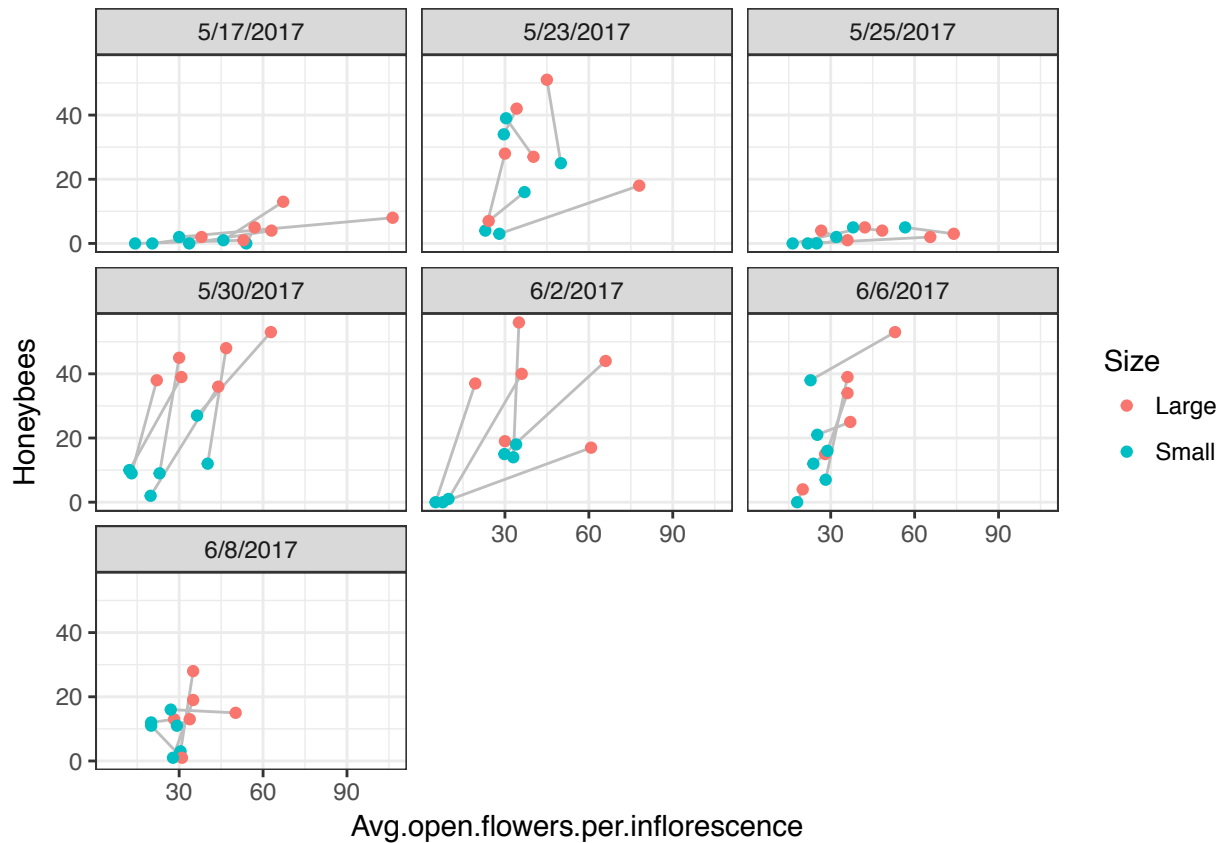
```
setwd('~/.bee/')  
mydat_small=read.csv('pollinator_visitation_fullData.csv')
```

Plot Honeybees vs. Explanatory variable, with groupings

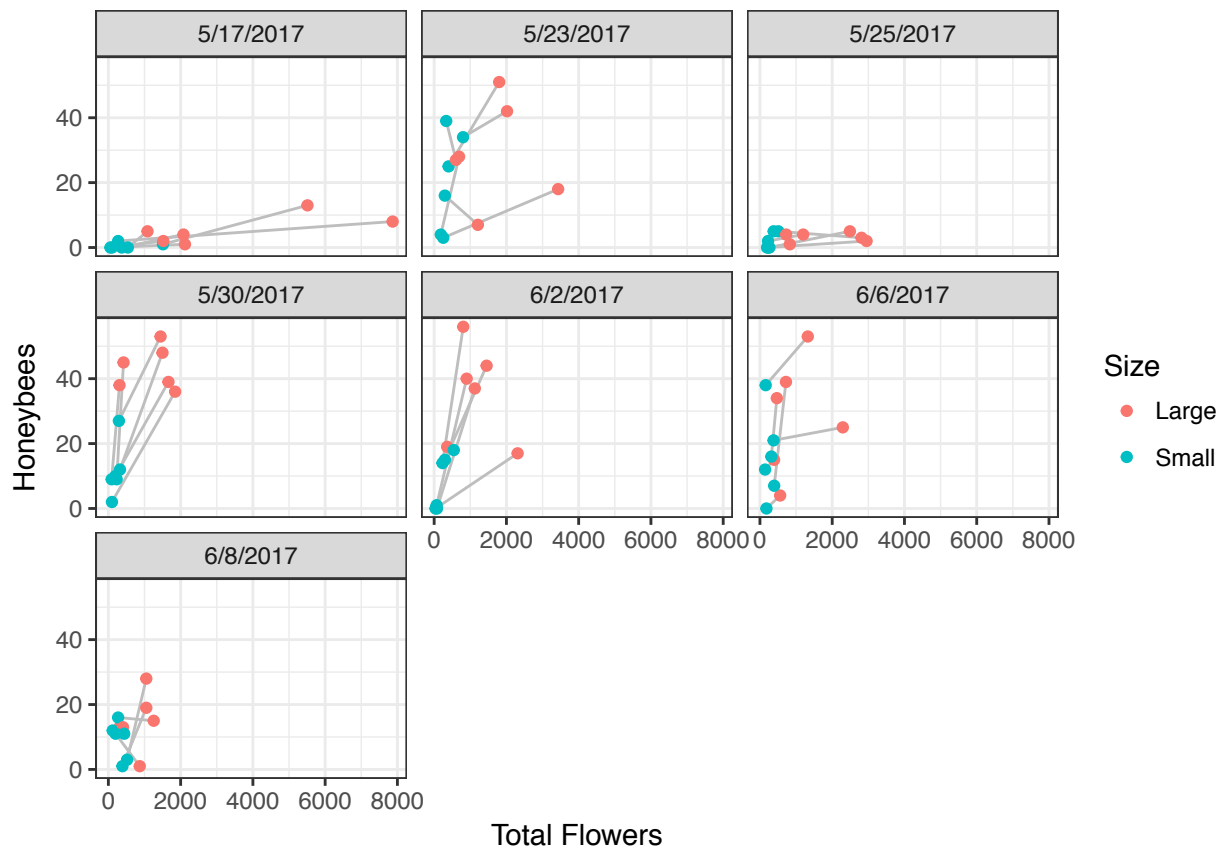
```
ggplot(mydat_small, aes(x=Total.inflorescences, y=Honeybees, color=Size, group=Pair))+  
  geom_line(color='gray')+  
  geom_point()+  
  facet_wrap(~Date)+  
  theme_bw()
```



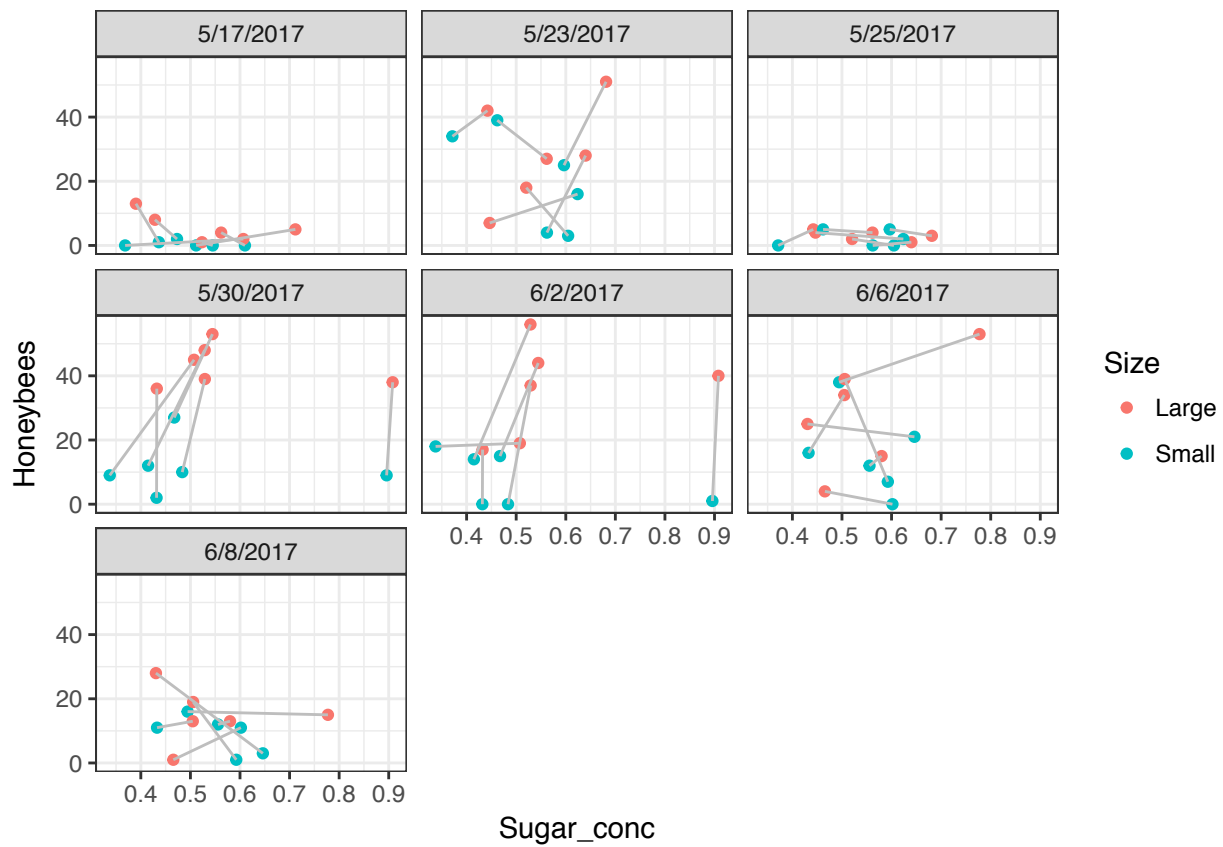
```
ggplot(mydat_small, aes(x=Avg.open.flowers.per.inflorescence, y=Honeybees, color=Size, group=Pair))+  
  geom_line(color='gray')+  
  geom_point()+  
  facet_wrap(~Date)+  
  theme_bw()
```



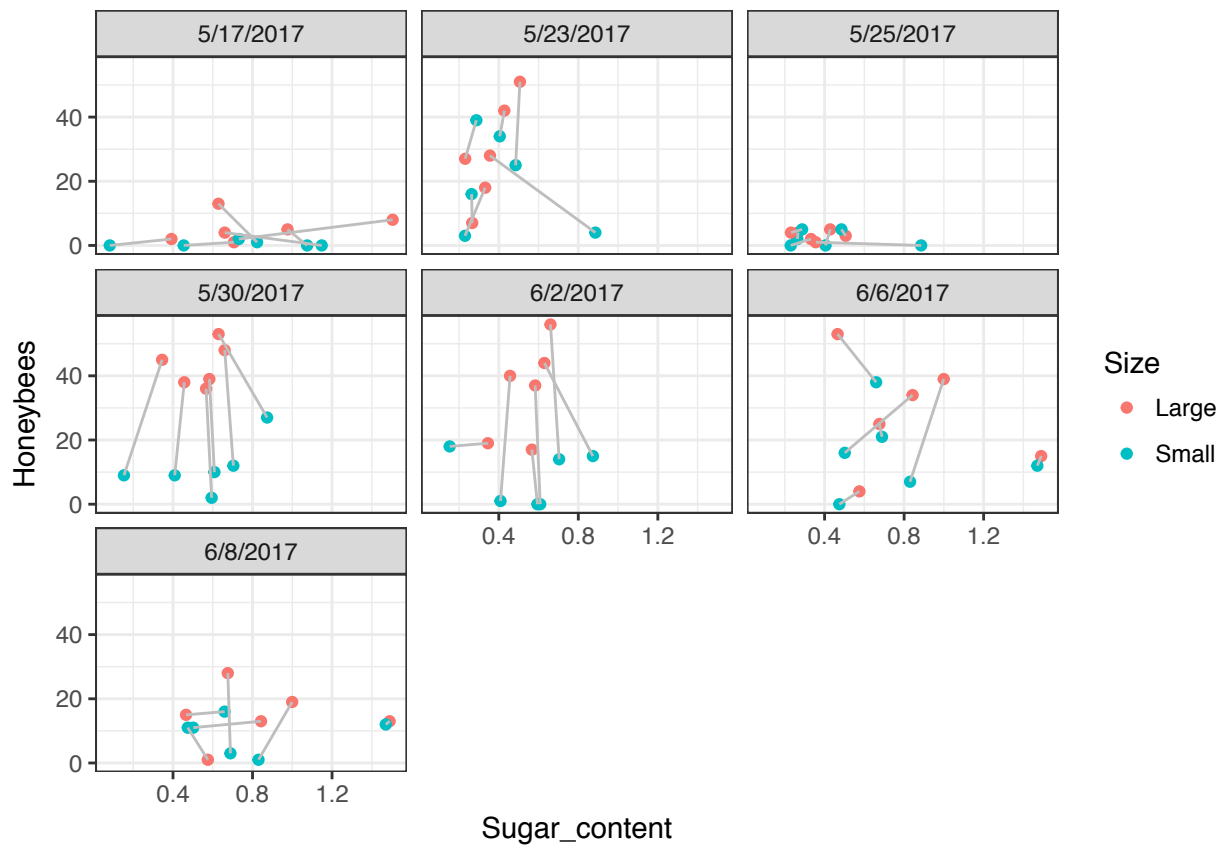
```
ggplot(mydat_small, aes(x=Total.Flowers, y=Honeybees, color=Size, group=Pair))+
  geom_line(color='gray')+
  geom_point()+
  facet_wrap(~Date)+
  labs(x="Total Flowers")+
  theme_bw()
```



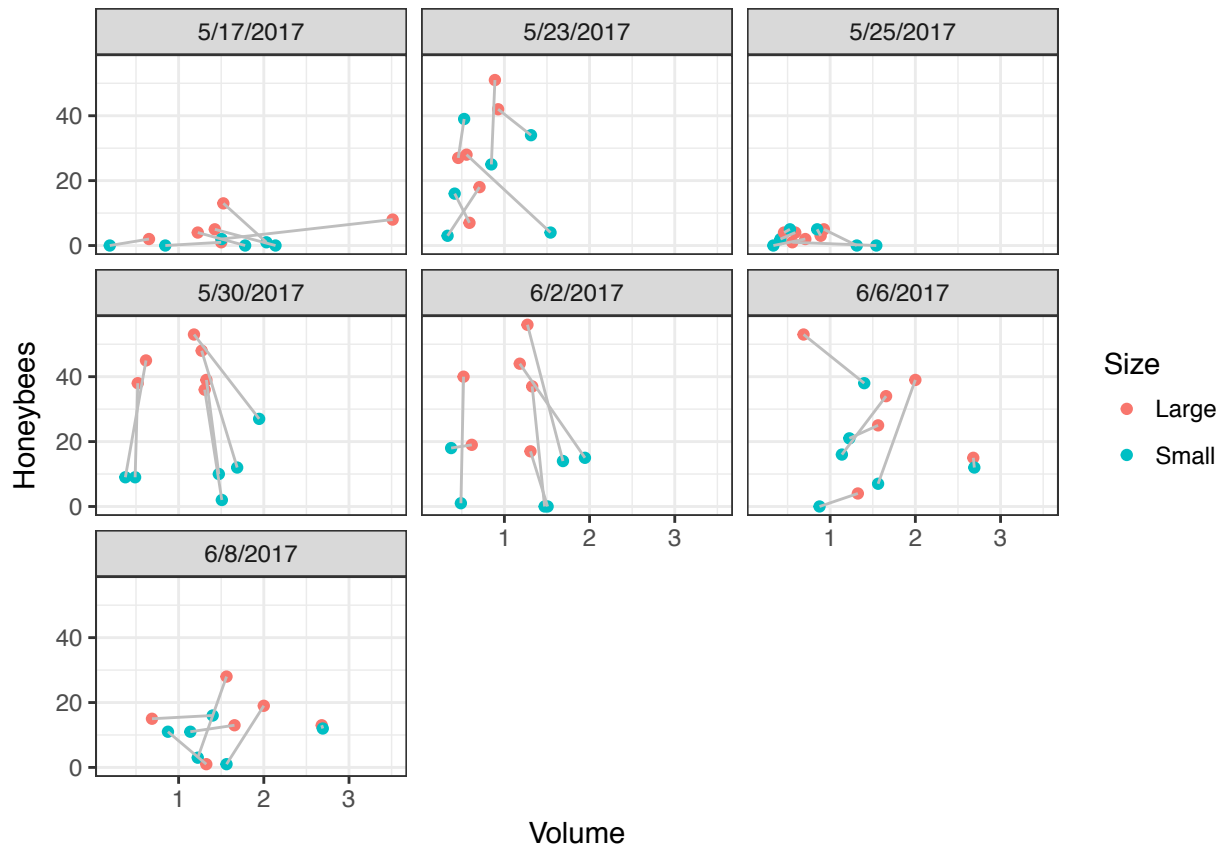
```
ggplot(mydat_small, aes(x=Sugar_conc, y=Honeybees, group=Pair, color=Size))+
  geom_point()+
  geom_line(color='gray')+
  facet_wrap(~Date)+
  theme_bw()
```



```
ggplot(mydat_small, aes(x=Sugar_content, y=Honeybees, group=Pair, color=Size))+
  geom_point()+
  geom_line(color='gray')+
  facet_wrap(~Date)+
  theme_bw()
```



```
ggplot(mydat_small, aes(x=Volume, y=Honeybees, group=Pair, color=Size))+
  geom_point()+
  geom_line(color='gray')+
  facet_wrap(~Date)+
  theme_bw()
```



Load in the raw nectar data from Gdrive

```
url='docs.google.com/spreadsheets/d/1LKr8Ken8p1jpTGpbn2a_napP6uNJ4sEnN8gdDSEQGxY/edit#gid=212997740'
nect=read.csv(text=gsheet2text(url, format='csv'))
```

```
## No encoding supplied: defaulting to UTF-8.
```

```
head(nect)
```

```
##      Date Experiment.Week Observer Patch.ID..color.code.      Location
## 1 5/18/2017              1   Joanna          BOB Pair 1 Small
## 2 5/18/2017              1   Joanna          BOB Pair 1 Small
## 3 5/18/2017              1   Joanna          BOB Pair 1 Small
## 4 5/18/2017              1   Joanna          BOB Pair 1 Small
## 5 5/18/2017              1   Joanna          BOB Pair 1 Small
## 6 5/18/2017              1   Joanna          BOY Pair 1 Large
## Plant.number Species..4.letter.code. Number.of.flowers.used
## 1           1          Sa Ap                      1
## 2           1          Sa Ap                      1
## 3           1          Sa Ap                      1
## 4           1          Sa Ap                      1
## 5           1          Sa Ap                      1
## 6           1          Sa Ap                      1
## Size.of.Microcap..uL. Nectar.collected..cm.  BRIX      Notes
## 1                   2                   3.1 0.210
## 2                   2                   2.2 0.210
```

```
## 3          2          0.0 0.000 no data; evaporated
## 4          2          2.7 0.240
## 5          2          5.0 0.170
## 6          2          2.6 0.205
## Length.of.Microcap..cm. volume.of.nectar..pl. sugar.concentration
## 1          3.2          1.9375          0.4267741935
## 2          3.2          1.3750          0.5154545455
## 3          3.2          0.0000          #DIV/0!
## 4          3.2          1.6875          0.5244444444
## 5          3.2          3.1250          0.2788
## 6          3.2          1.6250          0.4573076923
## sugar.content..pg. X X.1 X.2 X.3 X.4 X.5
## 1          0.826875 NA NA NA NA NA NA
## 2          0.70875 NA NA NA NA NA NA
## 3          #DIV/0! NA NA NA NA NA NA
## 4          0.885 NA NA NA NA NA NA
## 5          0.87125 NA NA NA NA NA NA
## 6          0.743125 NA NA NA NA NA NA
```

```
size=strsplit(as.character(nect$Location), ' ')
df=as.data.frame(t(matrix(unlist(size), 3)))
names(df)=c('non', 'Pair', 'Size')
nect=cbind(nect, df[,2:3])
nect$sugar.concentration=as.numeric(as.character(nect$sugar.concentration))
```

```
## Warning: NAs introduced by coercion
```

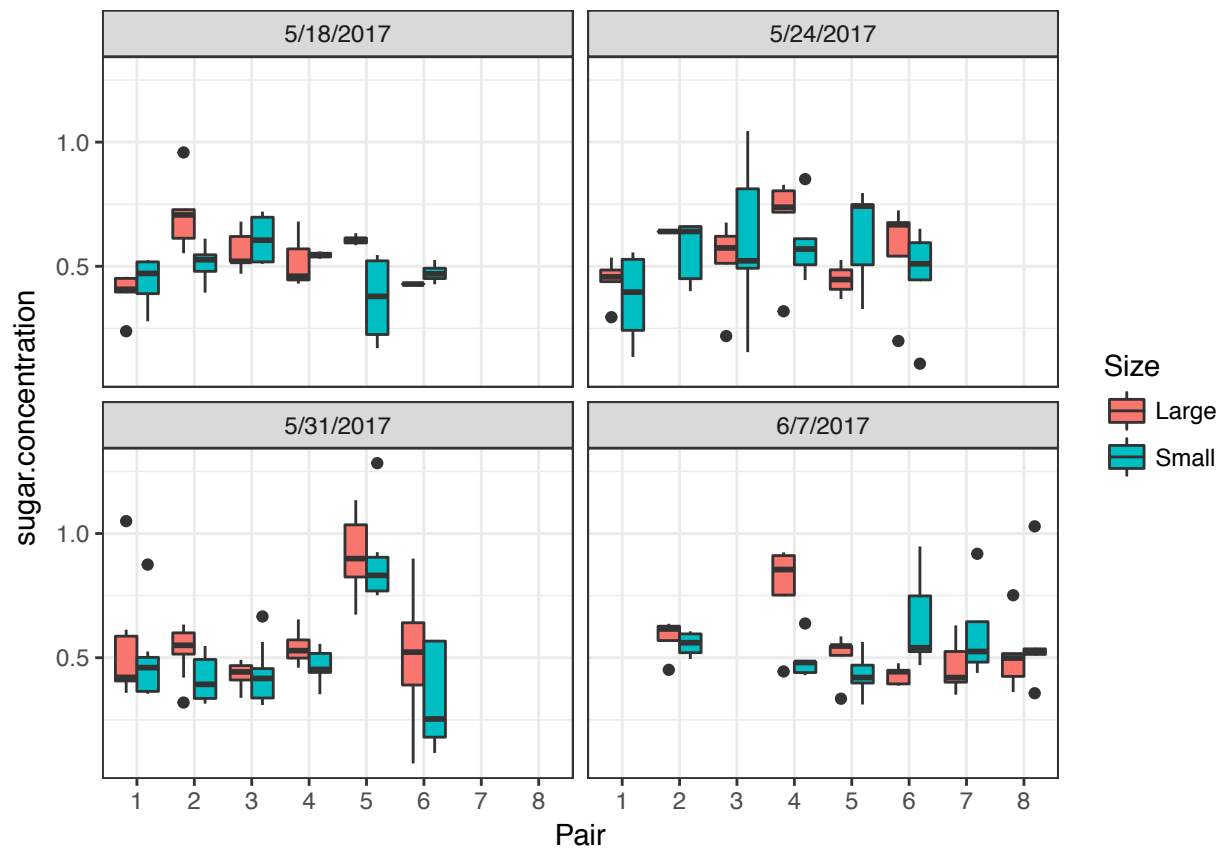
```
nect$sugar.content..pg.=as.numeric(as.character(nect$sugar.content..pg.))
```

```
## Warning: NAs introduced by coercion
```

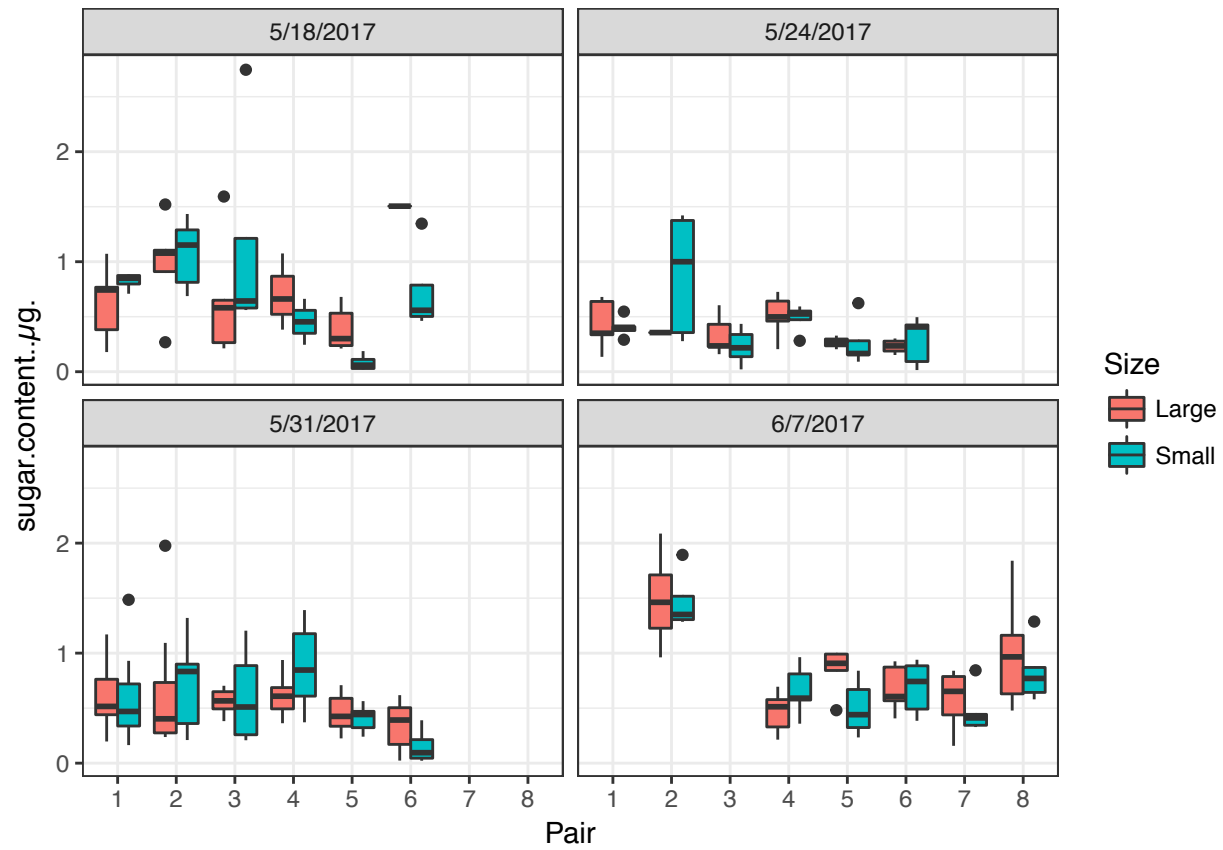
```
#Clean up outliers
nect=nect[which(nect$sugar.concentration<1.9),]
zeros=which(nect$sugar.concentration==0)
nect=nect[-zeros, ]
```

Make some boxplots

```
ggplot(nect, aes(y=sugar.concentration, x=Pair, fill=Size))+
  geom_boxplot()+
  facet_wrap(~Date)+
  theme_bw()
```



```
ggplot(nect, aes(y=sugar.content..pg., x=Pair, fill=Size))+
  geom_boxplot()+
  facet_wrap(~Date)+
  theme_bw()
```

```
ggplot(nect, aes(y=volume.of.nectar..μl., x=Pair, fill=Size))+
  geom_boxplot()+
  facet_wrap(~Date)+
  theme_bw()
```

