Final Poster Figures

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7/19/2017

Install Necessary Pakcages and Load Data

```
#install_github("ggbiplot", "vqv")
#library(ggbiplot)
library(lme4)
#install.packages('dplyr')
library(dplyr)
library(devtools)
#devtools::install_github("strengejacke/sjPlot",force = TRUE)
library(sjPlot)
library(sjmisc)
library(reshape2)
library(ggplot2)
library(car)
```

```
##
## Attaching package: 'car'
```

```
## The following object is masked from 'package:dplyr':
##
##     recode
```

```
setwd('../bee')
logData=read.csv('pollinator_visitation_fullData_logTrans.csv')
```

Test Significant of the Difference Between Honeybees Visiting Small vs Large Plants

```
data_dt=split(logData, logData$Date)
#Make a dataframe, summing visits for small and large plants
ttest=data.frame()
for(i in 1:length(data_dt)){
  add=data.frame(Date=names(data_dt)[i],LargeVisit=sum(data_dt[[i]]$Visits&data_dt[[i]]$Size=='Large'),
  ttest=rbind(ttest, add)
}
#peek
ttest
```

```
##        Date LargeVisit SmallVisit
## 1 5/17/2017          5          1
## 2 5/23/2017          4          2
## 3 5/25/2017          4          2
## 4 5/30/2017          6          0
## 5  6/2/2017          5          1
## 6  6/6/2017          4          2
## 7  6/8/2017          5          1
```

Plot and perform one-tailed t test

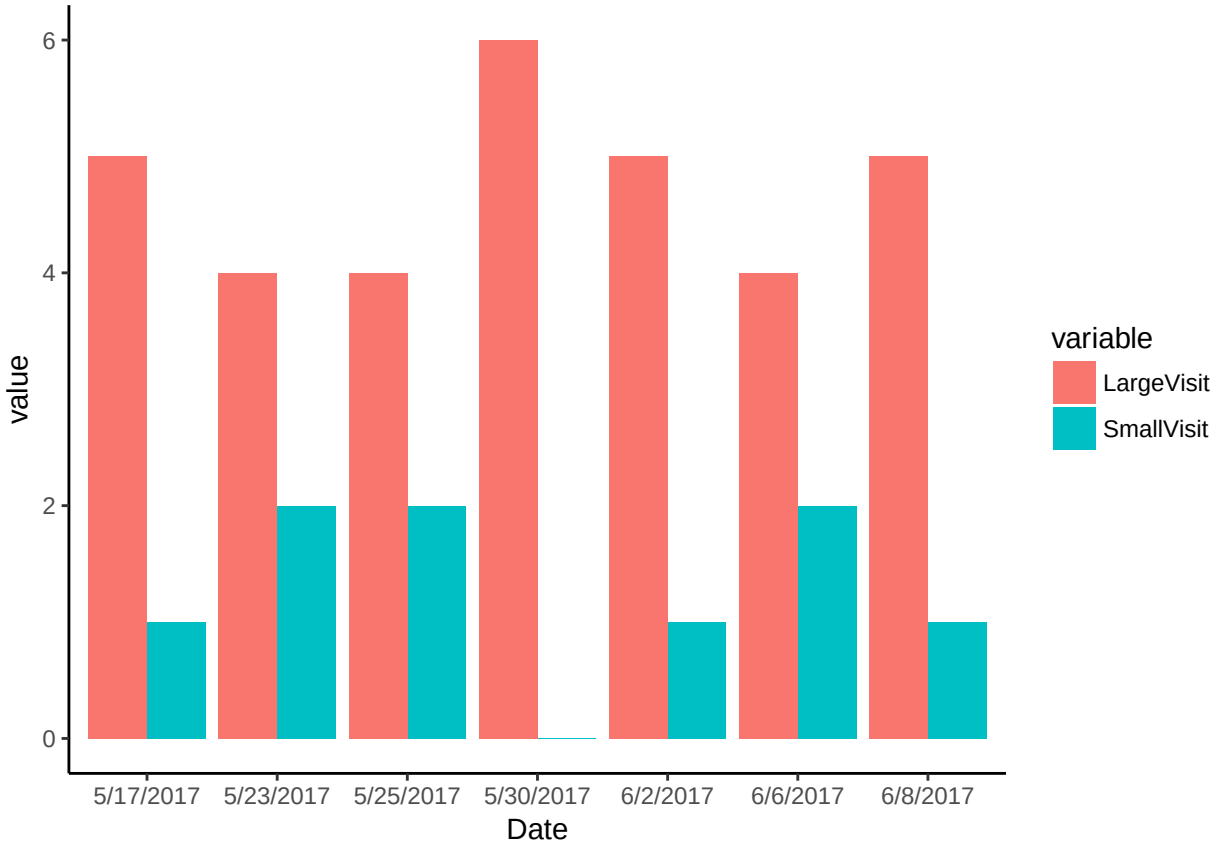
```
t.test(ttest$LargeVisit, ttest$SmallVisit, alternative='greater')
```

```
##
##  Welch Two Sample t-test
##
## data:  ttest$LargeVisit and ttest$SmallVisit
## t = 8.4853, df = 12, p-value = 1.024e-06
## alternative hypothesis: true difference in means is greater than 0
## 95 percent confidence interval:
##  2.708419      Inf
## sample estimates:
## mean of x mean of y
##  4.714286  1.285714
```

```
tmelt=melt(ttest)
```

```
## Using Date as id variables
```

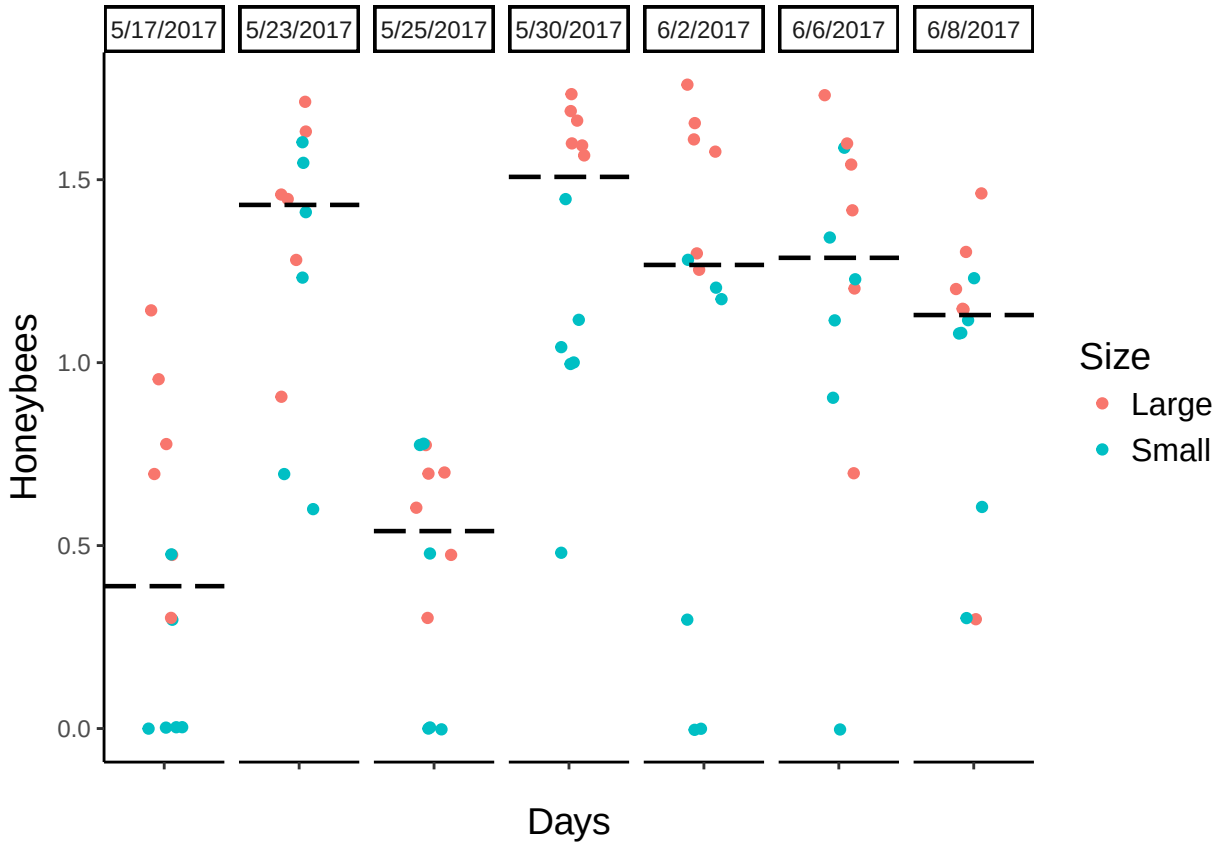
```
ggplot(tmelt, aes(x=Date, y=value, fill=variable))+geom_bar(stat='identity', position='dodge')+theme_cla
```



Make Scatter Plots of Honeybees vs Date, Separated by Large and Small Plants

```
theshold=c()
wholedf=data.frame()
for( i in 1:length(data_dt)){
  theshold[i]=median(data_dt[[i]]$Honeybees)
  data_dt[[i]]$Median=theshold[i]
  wholedf=rbind(wholedf, data_dt[[i]])
}
logData=wholedf

ggplot(data=logData, aes(x='', y=Honeybees, color=Size))+
  geom_jitter(width = 0.15)+
  facet_grid(~Date)+
  geom_hline(aes(yintercept = Median),lty=5, size=0.8)+
  labs(x="Days", size=4)+
  theme_classic()+
  theme(axis.title=element_text(size=14), legend.title=element_text(size=14),legend.text=element_text(s
```



Linear Modeling with Mixed Effects

```
mylogit <- lmer(Honeybees ~
                  Avg.open.flowers.per.inflorescence+
                  Total.inflorescenses+
                  Sugar_content+
                  height+
                  (1|Date), data=logData)

summary(mylogit)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## Honeybees ~ Avg.open.flowers.per.inflorescence + Total.inflorescenses +
##     Sugar_content + height + (1 | Date)
##    Data: logData
##
## REML criterion at convergence: 72
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.7877 -0.7635  0.2402  0.6884  1.8529
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Date     (Intercept) 0.1930   0.4394
##  Residual             0.1053   0.3245
## Number of obs: 84, groups:  Date, 7
##
## Fixed effects:
##                                   Estimate Std. Error t value
## (Intercept)                       -1.10433    0.32694  -3.378
## Avg.open.flowers.per.inflorescence  1.12848    0.21604   5.223
## Total.inflorescenses                0.17775    0.15182   1.171
## Sugar_content                      -0.02303    0.17960  -0.128
## height                              0.55853    0.84131   0.664
##
## Correlation of Fixed Effects:
##             (Intr) Av.... Ttl.nf Sgr_cn
## Avg.pn.fl.. -0.634
## Ttl.nflrscn  0.025 -0.215
## Sugar_cntnt  0.293 -0.123  0.026
## height      -0.097 -0.348 -0.517 -0.048
```

```
an=Anova(mylogit)
pvals=round(an$`Pr(>Chisq)`,4)
```

Plot Results

```
sjp.setTheme()
vars=c('Avg.open.flowers.per.inflorescence','Total.inflorescenses','Sugar_content',
       'height')
tit=c('Reward+Efficiency','Poential Reward for Colony', 'Reward per Inflorescense','Salience')
```

```
for(i in 1:length(vars)){
  ploot2=sjp.lmer(mylogit, type = "pred", facet.grid = FALSE,
                  vars = c(vars[i],'Date'), prnt.plot=F,show.ci=T)
  ploot2=ploot2[[2]]+
    labs(x=vars[i])+
    ggtitle(tit[i], subtitle=paste0("(p-val = ",pvals[i],')'))+
    theme_classic()+
    scale_color_brewer(palette = 'Paired')+
    theme(title=element_text(size=14, face='bold'),axis.title=element_text(size=14), legend.title=eleme
  #pdf(paste0('forPoster/lmerFull_diffSlope2_',vars[i],'.pdf'))
  plot(ploot2)
  #dev.off()
  #graphics.off()
}
```

```
## Scale for 'colour' is already present. Adding another scale for
## 'colour', which will replace the existing scale.
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## 'colour', which will replace the existing scale.
```
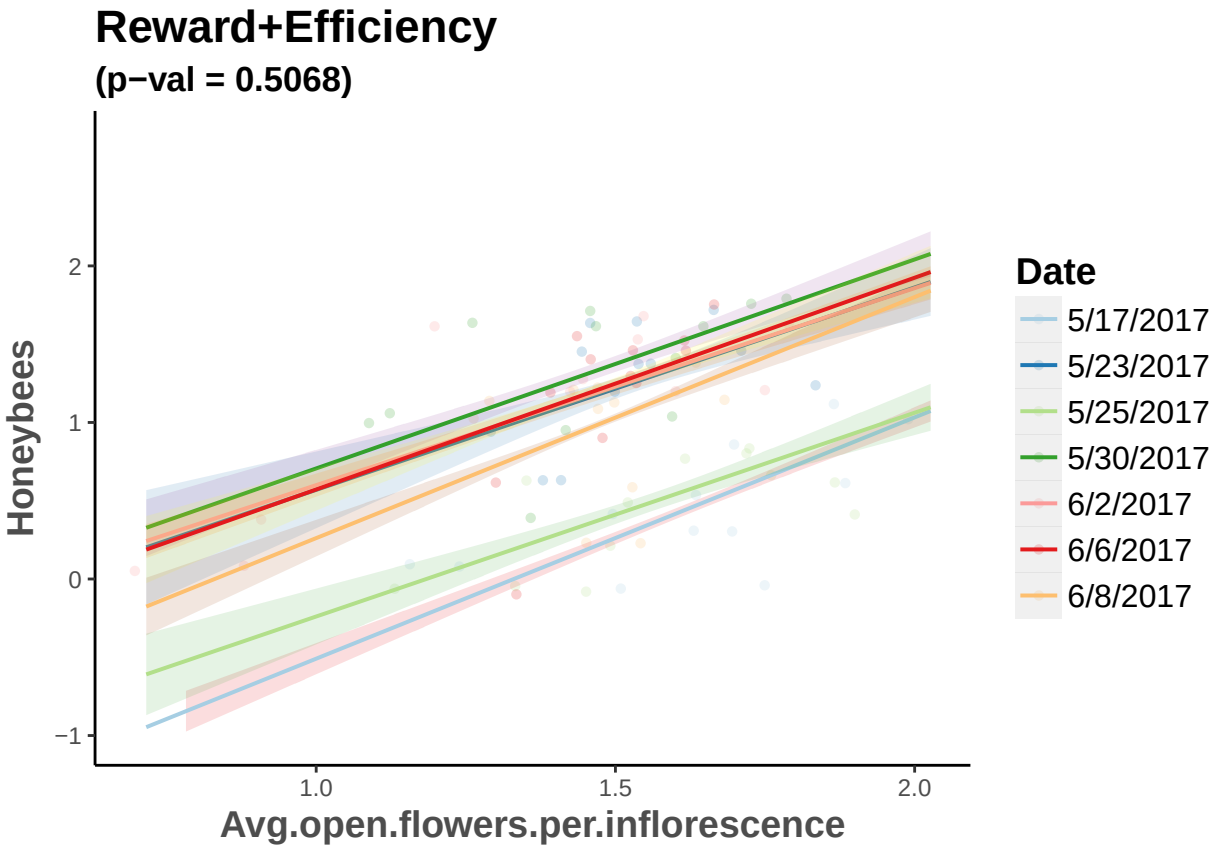
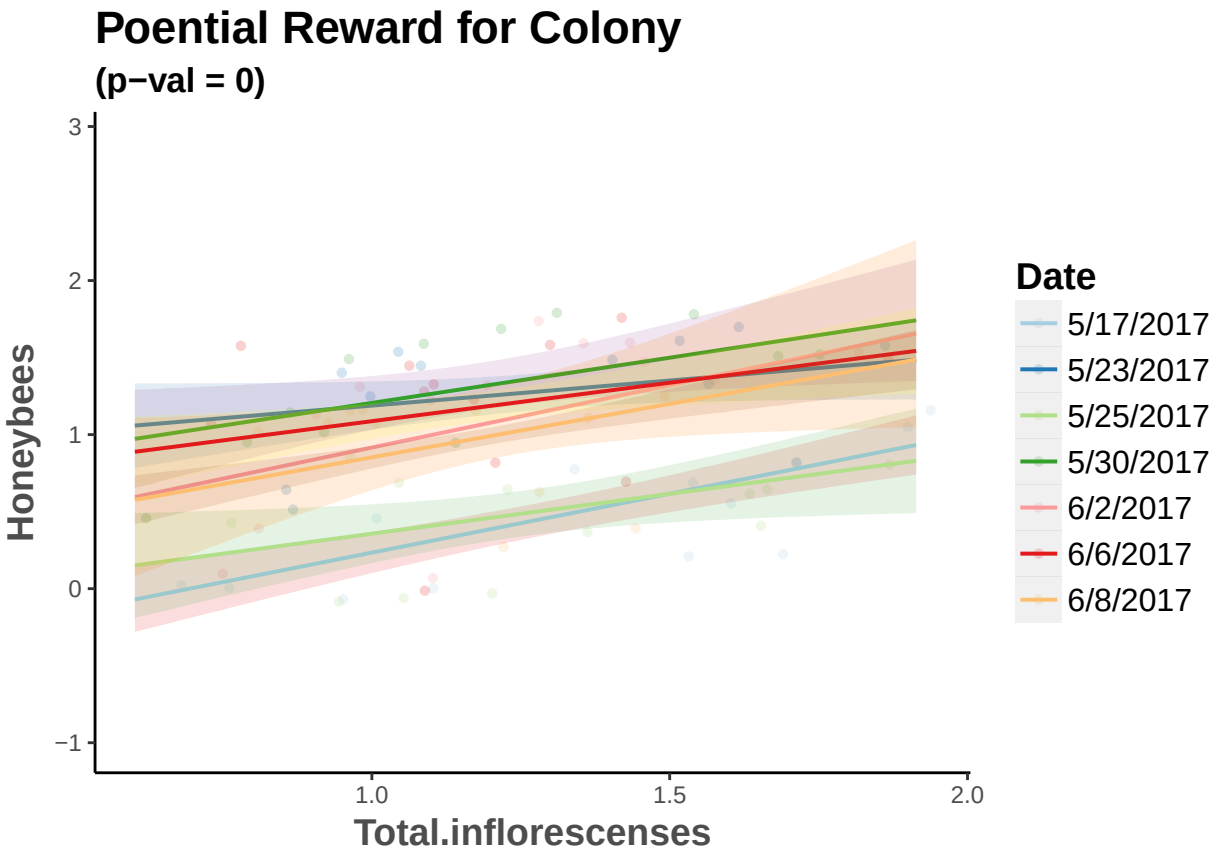




```
## Scale for 'colour' is already present. Adding another scale for
## 'colour', which will replace the existing scale.
```




```
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## 'colour', which will replace the existing scale.
```
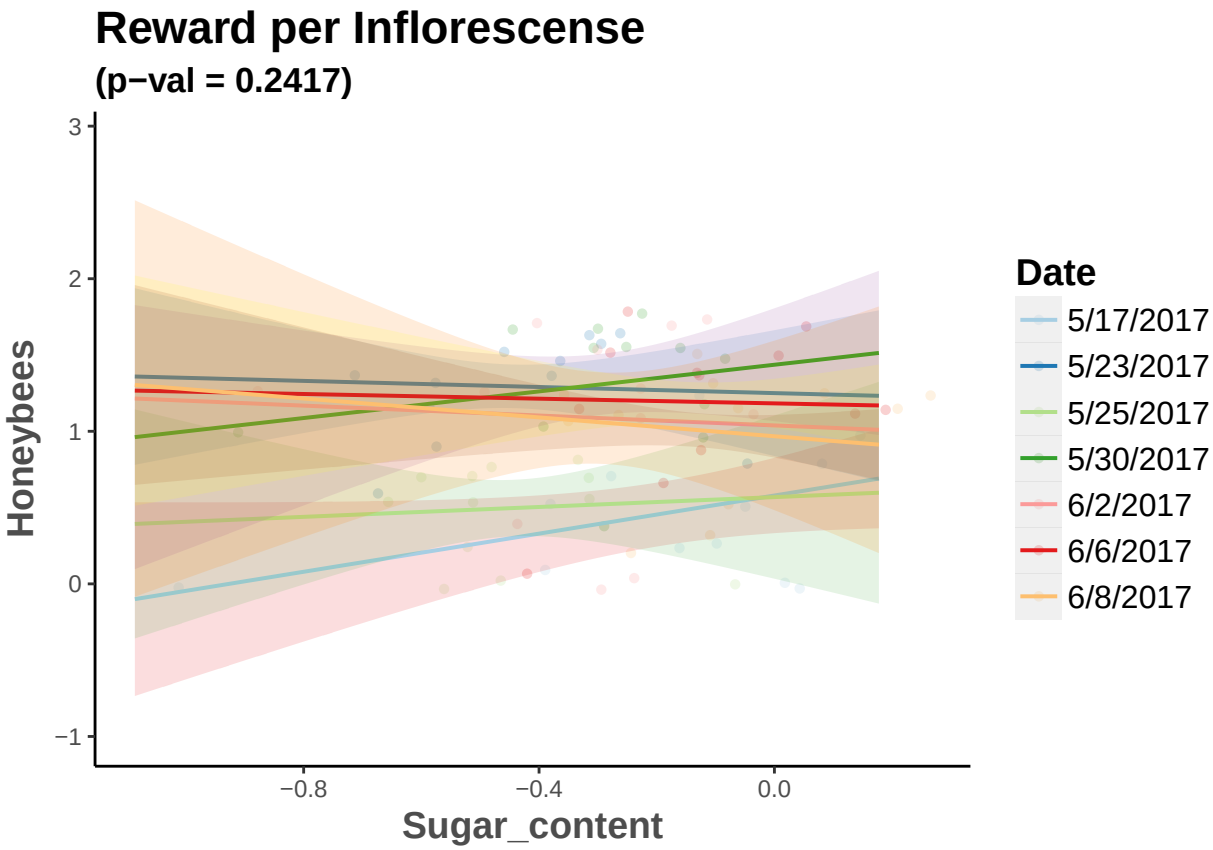
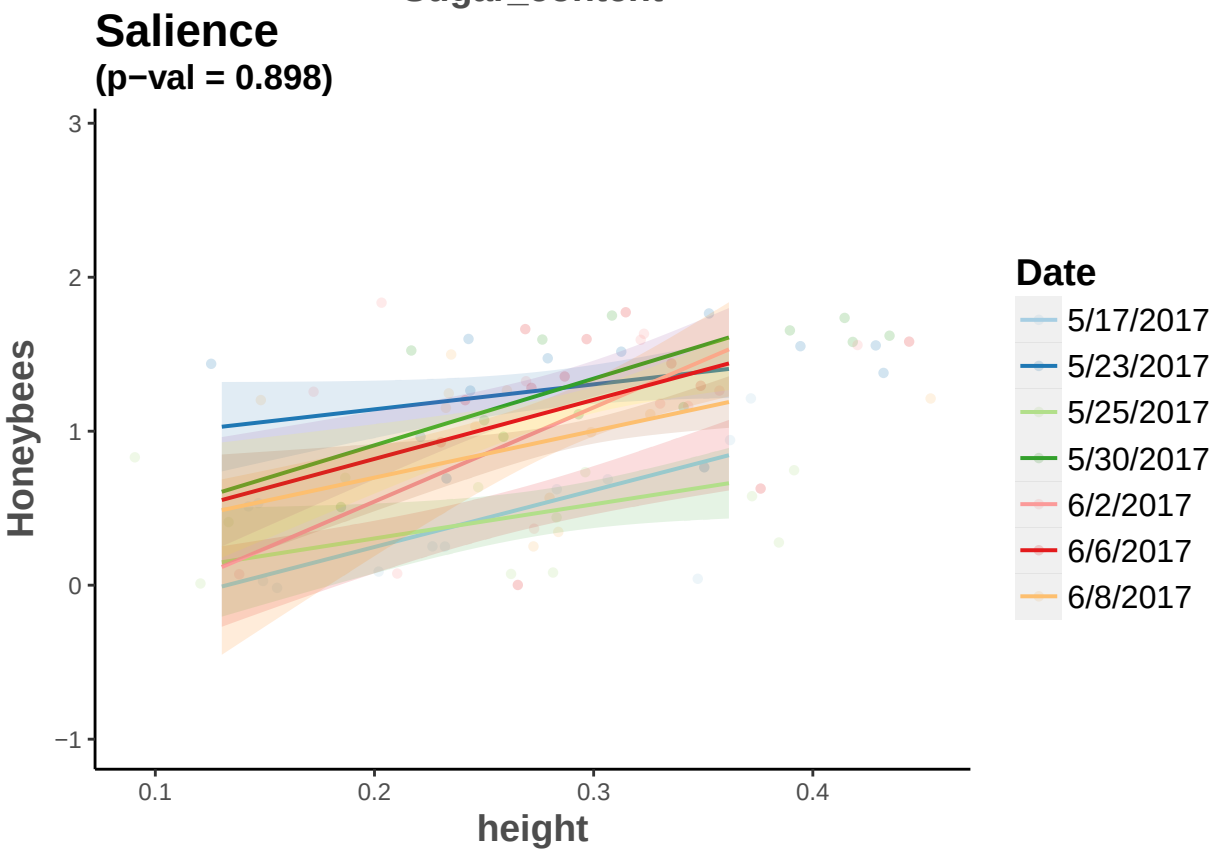


Reward per Inflorescense
(p−val = 0.2417)
Honeybees
Sugar_content
3
2
1
0
−1
−0.8
−0.4
0.0
Date
5/17/2017
5/23/2017
5/25/2017
5/30/2017
6/2/2017
6/6/2017
6/8/2017


Salience
(p−val = 0.898)
Honeybees
height
3
2
1
0
−1
0.1
0.2
0.3
0.4
Date
5/17/2017
5/23/2017
5/25/2017
5/30/2017
6/2/2017
6/6/2017
6/8/2017