

Lichen Data Analysis

Tests for average light on each tree as a whole

```
#total light coverage w total lichen coverage --> no signifcant correlation, p>0.05 but 0.11
light_perc<-light_long%>%
  group_by(tree)%>%
  mutate("total_light"=sum(light_cov))%>%
  summarize(total_light,percentcoverage)
```

```
## `summarise()` has grouped output by 'tree'. You can override using the `.groups` argument.
cor.test(light_perc$total_light,light_perc$percentcoverage)
```

```
##
## Pearson's product-moment correlation
##
## data: light_perc$total_light and light_perc$percentcoverage
## t = 1.6049, df = 118, p-value = 0.1112
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.03397556 0.31709031
## sample estimates:
## cor
## 0.1461558
```

```
#total light vs lichen for each species
light_spec<-lichen_long%>%
  group_by(tree)%>%
  filter(lichen_dir=="total")%>%
  summarize("total_light"=sum(north,east,south,west),species,lichen_covprop)
```

```
## `summarise()` has grouped output by 'tree'. You can override using the `.groups` argument.
```

```
#green not significant, p>0.05
green<-light_spec%>%
  filter(species=="green")
cor.test(green$lichen_covprop,green$total_light)
```

```
##
## Pearson's product-moment correlation
##
## data: green$lichen_covprop and green$total_light
## t = 0.82546, df = 28, p-value = 0.4161
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.2182558 0.4873405
## sample estimates:
## cor
## 0.154133
```

```
#yellow not significant p>0.05
yellow<-light_spec%>%
  filter(species=="yellow")
cor.test(yellow$lichen_covprop,yellow$total_light)
```

```
##
## Pearson's product-moment correlation
##
## data: yellow$lichen_covprop and yellow$total_light
## t = 0.49555, df = 28, p-value = 0.6241
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.2763097 0.4387713
## sample estimates:
## cor
## 0.0932413
```

```
#grey not significant p>0.05
gray<-light_spec%>%
  filter(species=="gray")
cor.test(gray$lichen_covprop,gray$total_light)
```

```
##
## Pearson's product-moment correlation
##
## data: gray$lichen_covprop and gray$total_light
## t = 1.0646, df = 28, p-value = 0.2962
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.1755083 0.5205152
## sample estimates:
## cor
## 0.197232
```

```
#total light vs lichen diversity - significant at the p<0.05 level, there is a positive correlation bet
light_div<-light_long%>%
  group_by(tree)%>%
  summarize("total_light"=sum(light_cov),speciesnum=mean(speciesnum))
cor.test(light_div$speciesnum,light_div$total_light)
```

```
##
## Pearson's product-moment correlation
##
## data: light_div$speciesnum and light_div$total_light
## t = 2.5527, df = 28, p-value = 0.01643
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.08801049 0.68719919
## sample estimates:
## cor
## 0.4345027
```

Tests based on tree quadrants

```
#light on north and south - significant difference p-value <0.001
t.test(lichenclean$north,lichenclean$south, paired=TRUE)

##
## Paired t-test
##
## data: lichenclean$north and lichenclean$south
## t = -4.1697, df = 29, p-value = 0.0002519
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -118.51912 -40.51421
## sample estimates:
## mean of the differences
## -79.51667

#lichen on north and south - not significant, p-value>0.05
t.test(lichenclean$north_coverage,lichenclean$south_coverage,paired=TRUE)

##
## Paired t-test
##
## data: lichenclean$north_coverage and lichenclean$south_coverage
## t = 1.1876, df = 29, p-value = 0.2446
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.04710127 0.17754284
## sample estimates:
## mean of the differences
## 0.06522078

#lichen on north and south for green- not significant, p-value >0.05
green_south<-lichen_long%>%
  filter(species=="green",lichen_dir=="south")
green_north<-lichen_long%>%
  filter(species=="green",lichen_dir=="north")
t.test(green_south$lichen_covprop,green_north$lichen_covprop,paired=TRUE)

##
## Paired t-test
##
## data: green_south$lichen_covprop and green_north$lichen_covprop
## t = -1.0024, df = 29, p-value = 0.3245
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.11697962 0.04002891
## sample estimates:
## mean of the differences
## -0.03847536

#for yellow - not significant p>0.05
yellow_south<-lichen_long%>%
  filter(species=="yellow",lichen_dir=="south")
yellow_north<-lichen_long%>%
  filter(species=="yellow",lichen_dir=="north")
```

```

t.test(yellow_south$lichen_covprop,yellow_north$lichen_covprop,paired=TRUE)

##
## Paired t-test
##
## data: yellow_south$lichen_covprop and yellow_north$lichen_covprop
## t = -0.32046, df = 29, p-value = 0.7509
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.013585701 0.009904971
## sample estimates:
## mean of the differences
## -0.001840365

#for grey - significant at the p<0.05, true difference is > 0 (more on south than north)
gray_south<-lichen_long%>%
  filter(species=="gray",lichen_dir=="south")
gray_north<-lichen_long%>%
  filter(species=="gray",lichen_dir=="north")
t.test(gray_south$lichen_covprop,gray_north$lichen_covprop,paired=TRUE)

##
## Paired t-test
##
## data: gray_south$lichen_covprop and gray_north$lichen_covprop
## t = 2.0951, df = 29, p-value = 0.045
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.001362651 0.113039675
## sample estimates:
## mean of the differences
## 0.05720116

#for differences in diversity - not significant, p>0.05
div<-lichen_long%>%
  mutate("lichen_pres"=factor(ifelse(lichen_cov>0, "1", "0")))

div_north<-div%>% #getting species diversity for north side
  filter(lichen_dir=="north")%>%
  filter(species!="total")%>%
  select(tree,lichen_pres)%>%
  mutate("lichen_pres"=as.numeric(lichen_pres)-1)%>%
  group_by(tree)%>%
  summarize("diversity"=sum(lichen_pres))

div_south<-div%>% #getting species diversity for south side
  filter(lichen_dir=="south")%>%
  filter(species!="total")%>%
  select(tree,lichen_pres)%>%
  mutate("lichen_pres"=as.numeric(lichen_pres)-1)%>%
  group_by(tree)%>%
  summarize("diversity"=sum(lichen_pres))

t.test(div_north$diversity,div_south$diversity,paired=TRUE)

```

```
##
## Paired t-test
##
## data: div_north$diversity and div_south$diversity
## t = -0.25414, df = 29, p-value = 0.8012
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.3015866 0.2349199
## sample estimates:
## mean of the differences
## -0.03333333
```

Figures for significant results

Figure 2

```
ggplot(light_div,aes(x=speciesnum,y=total_light))+
  geom_point()+
  geom_smooth(method="lm",se=FALSE)+
  geom_jitter()+
  labs(title="Lichen Diversity Increases with Light Levels",subtitle="cor=0.4345, p<0.05",y="Total Recorded Light")

## `geom_smooth()` using formula 'y ~ x'
```

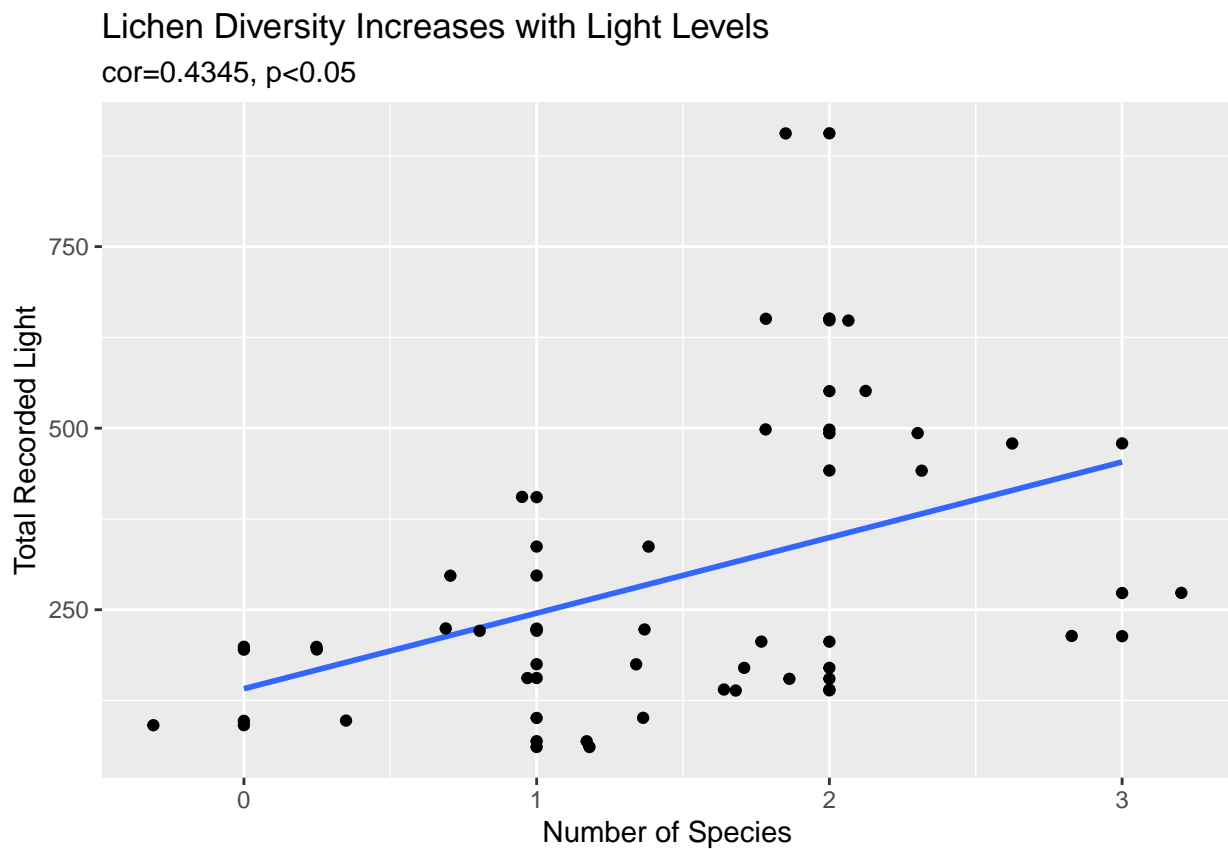


Figure 3

```
light_long_fig<-light_long%>%
  filter(light_dir=="north"|light_dir=="south")
ggplot(light_long_fig)+
  geom_boxplot(aes(x=light_dir,y=light_cov))+
  labs(x="Direction",y="Recorded Light Levels (umols)",title="Difference in Light Levels on North and South Sides of Trees")
```

Difference in Light Levels on North and South Sides of Trees

paired t-test, mean of differences = 79.517, $p < 0.001$

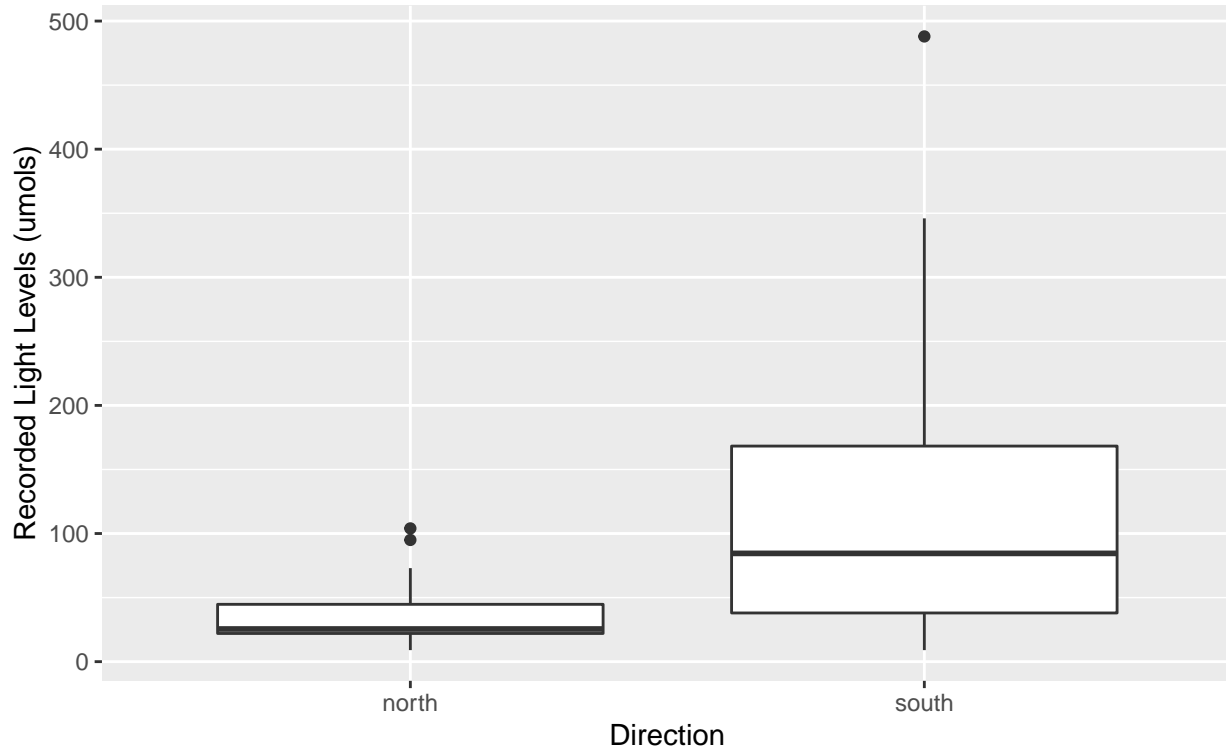


Figure 4

```
gray_south<-gray_south%>%
  select(tree,lichen_covprop)%>%
  mutate("south"=lichen_covprop)%>%
  select(tree,south)
gray_north<-gray_north%>%
  select(tree,lichen_covprop)%>%
  mutate("north"=lichen_covprop)%>%
  select(tree,north)
gray_coverage<-left_join(gray_south,gray_north,by="tree")%>%
  pivot_longer(south:north,names_to="direction",values_to = "coverage_prop")

ggplot(gray_coverage)+
  geom_boxplot(aes(x=direction,y=coverage_prop))+
  labs(title="Difference in Gray Lichen Coverage on North and South Sides of Trees",subtitle="Paired t-test")
```

