

[https://github.com/klynch416/BIOL432\\_A8](https://github.com/klynch416/BIOL432_A8) ([https://github.com/klynch416/BIOL432\\_A8](https://github.com/klynch416/BIOL432_A8))

```
library(dplyr)
```

```
##  
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':  
##  
##   filter, lag
```

```
## The following objects are masked from 'package:base':  
##  
##   intersect, setdiff, setequal, union
```

```
library(ggplot2)  
library(ape)
```

```
##  
## Attaching package: 'ape'
```

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

```
library(ggtree)
```

```
## ggtree v3.6.2 For help: https://yulab-smu.top/treedata-book/  
##  
## If you use the ggtree package suite in published research, please cite  
## the appropriate paper(s):  
##  
## Guangchuang Yu, David Smith, Huachen Zhu, Yi Guan, Tommy Tsan-Yuk Lam.  
## ggtree: an R package for visualization and annotation of phylogenetic  
## trees with their covariates and other associated data. Methods in  
## Ecology and Evolution. 2017, 8(1):28-36. doi:10.1111/2041-210X.12628  
##  
## Shuangbin Xu, Lin Li, Xiao Luo, Meijun Chen, Wenli Tang, Li Zhan, Zehan  
## Dai, Tommy T. Lam, Yi Guan, Guangchuang Yu. Ggtree: A serialized data  
## object for visualization of a phylogenetic tree and annotation data.  
## iMeta 2022, 4(1):e56. doi:10.1002/imt2.56  
##  
## Guangchuang Yu. Using ggtree to visualize data on tree-like structures.  
## Current Protocols in Bioinformatics. 2020, 69:e96. doi:10.1002/cpbi.96
```

```
##  
## Attaching package: 'ggtree'
```

```
## The following object is masked from 'package:ape':  
##  
## rotate
```

```
library(vegan)
```

```
## Loading required package: permute
```

```
## Loading required package: lattice
```

```
## This is vegan 2.6-4
```

### *Loading data set*

```
data <- read.csv("./FloristicSurvey.csv")
```

### *Influence of garlic mustard on total plant species number*

```
totaldata <- data %>% filter(Location == "i") %>% mutate(Total_species = rowSums(across(Claytonia  
a_virginiana:maianthenum_racemosum)), Total_GM = rowSums(across(Rosettes:Sillique))) %>% select  
(!Rosettes:maianthenum_racemosum)
```

```
ggplot(data = totaldata, aes(x = Total_GM, y = Total_species)) +  
  geom_point(aes(colour = as.factor(Population))) +  
  geom_smooth(method = "lm", se = F) +  
  scale_colour_discrete(name = "Population") +  
  scale_x_continuous(name = "Total Garlic Mustard Plants") +  
  scale_y_continuous(name = "Total Species Present") +  
  theme_classic()
```

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

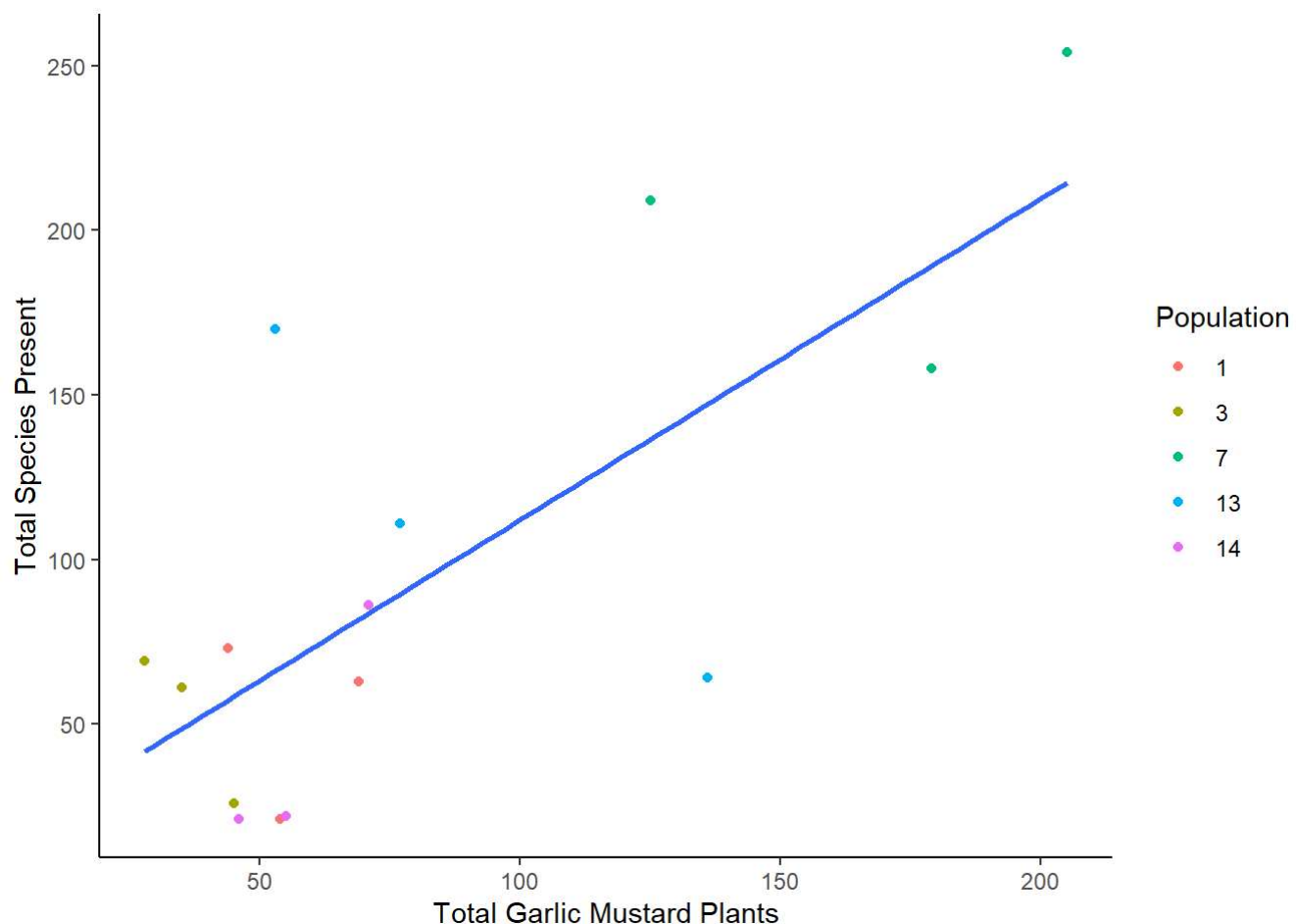


Figure 1. Distribution of the total number of species present with varying Garlic Mustard densities inside their patches. Species were counted across five different populations of Garlic Mustard plants. There is a positive relationship between the number of Garlic Mustard plants present and the total number of species found. There also seems to be an influence of the different Garlic Mustard populations.

What effect (if any) does garlic mustard have on the plant community?

When looking at the change in total number of plant species inside the garlic mustard patches, we find a positive relationship. That is, when garlic mustard plant numbers increase so do total species numbers. We also find that different populations of garlic mustard have a different influence on the number of total species present. Population 7 had the most garlic mustard plants and other species, while population 3 had the least garlic mustard plants and total species count.

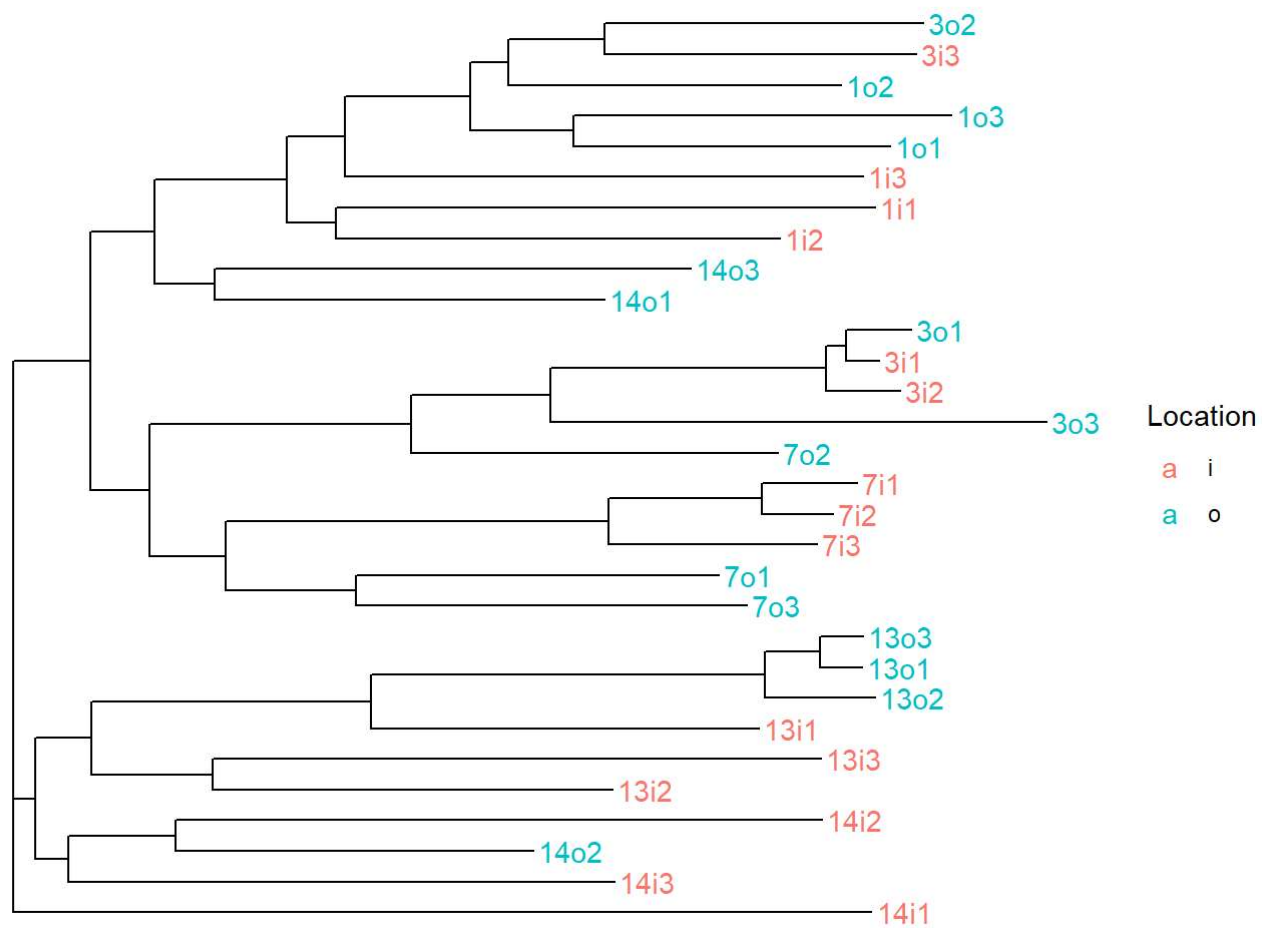
#### Distance matrix

```
quaddata <- data %>% select(!c(Quadrate:Sillique))
row.names(quaddata) <- data$Quadrate

Factors <- data %>% select(Quadrate:Location)

quaddist <- vegdist(quaddata, method = "bray", binary = F)
quadtree <- nj(quaddist)

ggtree(quadtree, layout = "rectangular") %<+% Factors +
  geom_tiplab(aes(colour = Location))
```



### NMDS

```
NMDSdat <- metaMDS(quaddist, k = 2, trymax = 100)
```

```
## Run 0 stress 0.1461135
## Run 1 stress 0.1560521
## Run 2 stress 0.1414388
## ... New best solution
## ... Procrustes: rmse 0.06686128  max resid 0.3092684
## Run 3 stress 0.1489957
## Run 4 stress 0.211273
## Run 5 stress 0.1560521
## Run 6 stress 0.1534442
## Run 7 stress 0.1534441
## Run 8 stress 0.1560521
## Run 9 stress 0.1534442
## Run 10 stress 0.1561093
## Run 11 stress 0.1489954
## Run 12 stress 0.1461136
## Run 13 stress 0.1560521
## Run 14 stress 0.1461135
## Run 15 stress 0.1534442
## Run 16 stress 0.1414388
## ... New best solution
## ... Procrustes: rmse 0.000269717  max resid 0.0009814689
## ... Similar to previous best
## Run 17 stress 0.1414389
## ... Procrustes: rmse 0.000294573  max resid 0.001076371
## ... Similar to previous best
## Run 18 stress 0.1589506
## Run 19 stress 0.141439
## ... Procrustes: rmse 0.0003747331  max resid 0.001377463
## ... Similar to previous best
## Run 20 stress 0.1560521
## *** Best solution repeated 3 times
```

```
PDat <- data.frame(NMDS1 = NMDSdat$points[,1],
                   NMDS2 = NMDSdat$points[,2],
                   Quadrate = row.names(quaddata))

PDat <- merge(PDat, Factors, by = "Quadrate", all.x = T, all.y = F)

ggplot(data = PDat) +
  geom_point(aes(x = NMDS1, y = NMDS2, colour = Location, shape = as.factor(Population))) +
  scale_color_discrete(name = "Location") +
  scale_shape_discrete(name = "Population") +
  theme_classic()
```

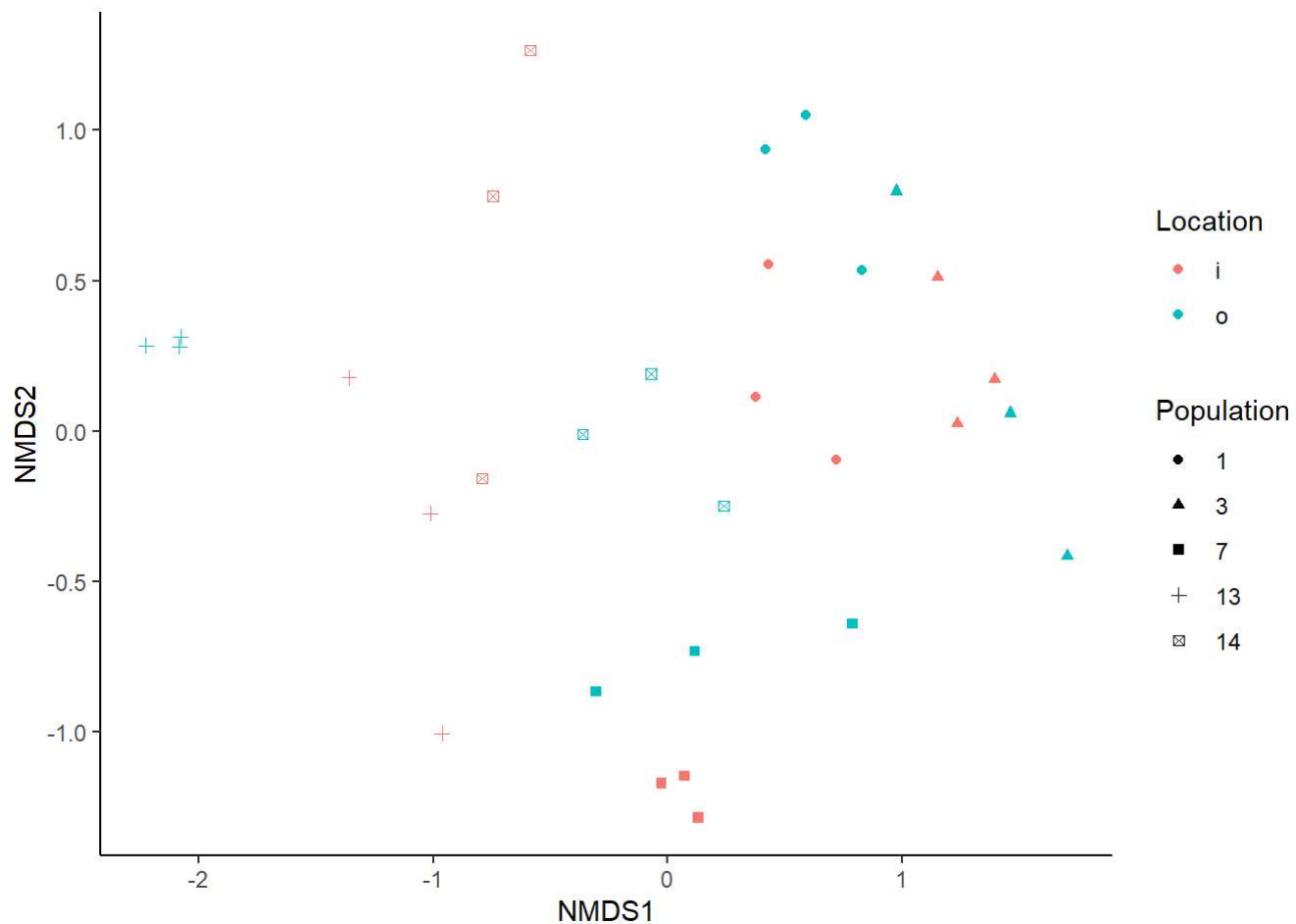


Figure 2. Relationship between the number of different plant species and the quadrature of Garlic mustard. The points were separated by location (i: inside patch, o: outside patch) and population (1,3,13,14). There appears to be no relationship between the number of species between the two locations. However, there may be a relationship between the populations.

What has a stronger effect on plant communities: the presence/absence of garlic mustard (in/out) or sampling population?

The presence or absence of garlic mustard does not create any visible clusters, leading to the conclusion that location of the garlic mustard plants may not have an influence on plant communities. The different populations created more obvious clusters suggesting that population has a stronger influence on plant communities. There may also be an interactive influence of location and population as location-population pairs created more obvious clusters.