

A8_Pollock_Caleb

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https://github.com/caleb-pollock/BIOL432_Assignment8 (https://github.com/caleb-pollock/BIOL432_Assignment8)

Begin by importing the data and observe the structure and head of the data.

```
library(vegan)
```

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

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

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

```
library(ape)  
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  
##  
## Guangchuang Yu, Tommy Tsan-Yuk Lam, Huachen Zhu, Yi Guan. Two methods  
## for mapping and visualizing associated data on phylogeny using ggtree.  
## Molecular Biology and Evolution. 2018, 35(12):3041-3043.  
## doi:10.1093/molbev/msy194  
##  
## LG Wang, TTY Lam, S Xu, Z Dai, L Zhou, T Feng, P Guo, CW Dunn, BR  
## Jones, T Bradley, H Zhu, Y Guan, Y Jiang, G Yu. treeio: an R package  
## for phylogenetic tree input and output with richly annotated and  
## associated data. Molecular Biology and Evolution. 2020, 37(2):599-603.  
## doi: 10.1093/molbev/msz240
```

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

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

```
library(ggplot2)
```

```
# Import the data
```

```
Samples <- read.csv("./data/FloristicSurvey.csv", header = T)
```

```
Samples$Population <- as.factor(Samples$Population)
```

```
str(Samples)
```

```
## 'data.frame':   30 obs. of  44 variables:
## $ Quadrage : chr  "7o3" "7o1" "7o2" "7i3" ...
## $ Population : Factor w/ 5 levels "1","3","7","13",...: 3 3 3 3 3 3 2 2 2 2 ...
## $ Location : chr  "o" "o" "o" "i" ...
## $ Rosettes : int  0 0 0 14 3 0 14 0 0 0 ...
## $ Bolting : int  0 0 0 8 18 3 3 12 26 0 ...
## $ Budding : int  0 0 0 157 184 122 11 23 19 0 ...
## $ Bud_Flw : int  0 0 0 0 0 0 0 0 0 0 ...
## $ Flower : int  0 0 0 0 0 0 0 0 0 0 ...
## $ Flw_Sil : int  0 0 0 0 0 0 0 0 0 0 ...
## $ Silique : int  0 0 0 0 0 0 0 0 0 0 ...
## $ Claytonia_virginiana : int  38 29 57 22 54 44 0 0 0 0 ...
## $ Anemone_hepatica : int  8 7 3 0 0 0 0 0 0 0 ...
## $ Grass_tuft : int  14 22 6 10 3 0 0 0 0 0 ...
## $ Trillium_grandifolium : int  9 30 8 0 0 0 0 0 0 0 ...
## $ Erythronium_trout_lily : int  25 10 5 16 18 7 0 0 0 0 ...
## $ Acer_saccharum : int  5 10 74 0 2 0 66 60 26 71 ...
## $ Dicentra_cucularia : int  0 22 23 0 0 0 0 0 0 0 ...
## $ Bloodroot : int  0 4 0 0 1 0 0 0 0 0 ...
## $ Gallium_aparine : int  0 27 8 17 22 21 2 0 0 0 ...
## $ Ulmus_americanus : int  0 3 0 88 150 133 0 0 0 0 ...
## $ Unknown_1 : int  0 1 0 0 0 0 0 0 0 0 ...
## $ Unknown_2 : int  0 0 0 5 4 4 0 0 0 0 ...
## $ Unknown_3.ranunculaceae : int  0 0 0 0 0 0 0 0 0 0 ...
## $ Unknown_4 : int  0 0 0 0 0 0 1 0 0 0 ...
## $ Dryopteris_marginalis : int  0 0 0 0 0 0 0 1 0 0 ...
## $ Ostrich_fern : int  0 0 0 0 0 0 0 0 0 0 ...
## $ Plantago_lanceolata : int  0 0 0 0 0 0 0 0 0 0 ...
## $ Violet : int  0 0 0 0 0 0 0 0 0 0 ...
## $ Rhamnus_frangula : int  0 0 0 0 0 0 0 0 0 0 ...
## $ Raspberry : int  0 0 0 0 0 0 0 0 0 0 ...
## $ Unknown_5 : int  0 0 0 0 0 0 0 0 0 0 ...
## $ Unknown_6 : int  0 0 0 0 0 0 0 0 0 0 ...
## $ Solidago_canadensis : int  0 0 0 0 0 0 0 0 0 0 ...
## $ Unknown_7 : int  0 0 0 0 0 0 0 0 0 0 ...
## $ Dandelion : int  0 0 0 0 0 0 0 0 0 0 ...
## $ grass : int  0 0 0 0 0 0 0 0 0 0 ...
## $ vicia_cracca : int  0 0 0 0 0 0 0 0 0 0 ...
## $ herb_robert : int  0 0 0 0 0 0 0 0 0 0 ...
## $ thorny_ash : int  0 0 0 0 0 0 0 0 0 0 ...
## $ rhamnus_cathartica : int  0 0 0 0 0 0 0 0 0 0 ...
## $ rhubarb : int  0 0 0 0 0 0 0 0 0 0 ...
## $ Unknown_8 : int  0 0 0 0 0 0 0 0 0 0 ...
## $ Unknown_9 : int  0 0 0 0 0 0 0 0 0 0 ...
## $ maianthemum_racemosum : int  0 0 0 0 0 0 0 0 0 0 ...
```

```
head(Samples)
```

##	Quadrat	Population	Location	Rosettes	Bolting	Budding	Bud_Flw	Flower	Flw_Sil
## 1	7o3	7	o	0	0	0	0	0	0
## 2	7o1	7	o	0	0	0	0	0	0
## 3	7o2	7	o	0	0	0	0	0	0
## 4	7i3	7	i	14	8	157	0	0	0
## 5	7i2	7	i	3	18	184	0	0	0
## 6	7i1	7	i	0	3	122	0	0	0
##	Sillique	Claytonia_virginiana	Anemone_hepatica	Grass_tuft					
## 1	0		38		8	14			
## 2	0		29		7	22			
## 3	0		57		3	6			
## 4	0		22		0	10			
## 5	0		54		0	3			
## 6	0		44		0	0			
##	Trillium_grandifolium	Erythronium.trout.lily.	Acer_saccharum						
## 1		9			25	5			
## 2		30			10	10			
## 3		8			5	74			
## 4		0			16	0			
## 5		0			18	2			
## 6		0			7	0			
##	Dicentra_cucularia	Bloodroot	Gallium_aparine	Ulmus_american	Unknown_1				
## 1		0	0	0	0	0			
## 2		22	4	27	3	1			
## 3		23	0	8	0	0			
## 4		0	0	17	88	0			
## 5		0	1	22	150	0			
## 6		0	0	21	133	0			
##	Unknown_2	Unknown_3.ranunculaceae.	Unknown_4	Dryopteris_marginalis					
## 1	0		0	0		0			
## 2	0		0	0		0			
## 3	0		0	0		0			
## 4	5		0	0		0			
## 5	4		0	0		0			
## 6	4		0	0		0			
##	Ostrich_fern	Plantago_lanceolata	Violet	Rhamnus_frangula	Raspberry	Unknown_5			
## 1	0		0	0	0	0			
## 2	0		0	0	0	0			
## 3	0		0	0	0	0			
## 4	0		0	0	0	0			
## 5	0		0	0	0	0			
## 6	0		0	0	0	0			
##	Unknown_6	Solidago_canadensis	Unknown_7	Dandelion	grass	vicia_cracca			
## 1	0		0	0	0	0			
## 2	0		0	0	0	0			
## 3	0		0	0	0	0			
## 4	0		0	0	0	0			
## 5	0		0	0	0	0			
## 6	0		0	0	0	0			
##	herb_robert	thorny_ash	rhamnus_cathartica	rhubarb	Unknown_8	Unknown_9			
## 1	0	0		0	0	0			
## 2	0	0		0	0	0			

## 3	0	0	0	0	0	0
## 4	0	0	0	0	0	0
## 5	0	0	0	0	0	0
## 6	0	0	0	0	0	0
##	maianthenum_racemosum					
## 1		0				
## 2		0				
## 3		0				
## 4		0				
## 5		0				
## 6		0				

```
# Create a subset of the data that only includes the abundance of each species
abunDat <- Samples[,11:41]
View(abunDat)
```

```
# Convert all of that data to binary
binDat <- ifelse(abunDat==0,0,1)
View(binDat)
```

```
# Calculate the bray-curtis dissimilarity matrix.
```

```
DissMat <- vegdist(binDat, method = "bray")
```

```
# Perform nmds
set.seed(13)
NMDSdat <- metaMDS(DissMat, k=2, trymax = 100)
```

```
## Run 0 stress 0.1320993
## Run 1 stress 0.1518731
## Run 2 stress 0.131928
## ... New best solution
## ... Procrustes: rmse 0.01304373 max resid 0.06408223
## Run 3 stress 0.1370518
## Run 4 stress 0.1451358
## Run 5 stress 0.136929
## Run 6 stress 0.1375842
## Run 7 stress 0.1375842
## Run 8 stress 0.1380588
## Run 9 stress 0.1371053
## Run 10 stress 0.1320991
## ... Procrustes: rmse 0.01303531 max resid 0.06378416
## Run 11 stress 0.1558795
## Run 12 stress 0.1478325
## Run 13 stress 0.1320992
## ... Procrustes: rmse 0.01303836 max resid 0.06380445
## Run 14 stress 0.1605772
## Run 15 stress 0.1451357
## Run 16 stress 0.1476793
## Run 17 stress 0.1427941
## Run 18 stress 0.1366233
## Run 19 stress 0.1632422
## Run 20 stress 0.1366233
## Run 21 stress 0.131928
## ... New best solution
## ... Procrustes: rmse 2.576148e-05 max resid 8.202853e-05
## ... Similar to previous best
## *** Best solution repeated 1 times
```

Create a plot and group by Budding

```
ggplot(Samples, aes(x=NMDSdat$points[,1], y=NMDSdat$points[,2], colour=Budding)) +
  geom_point() +
  labs(x="NMDS 1", y="NMDS 2", title="NMDS of Garlics Mustards affects on Plant Community by Budding") +
  theme_bw()
```

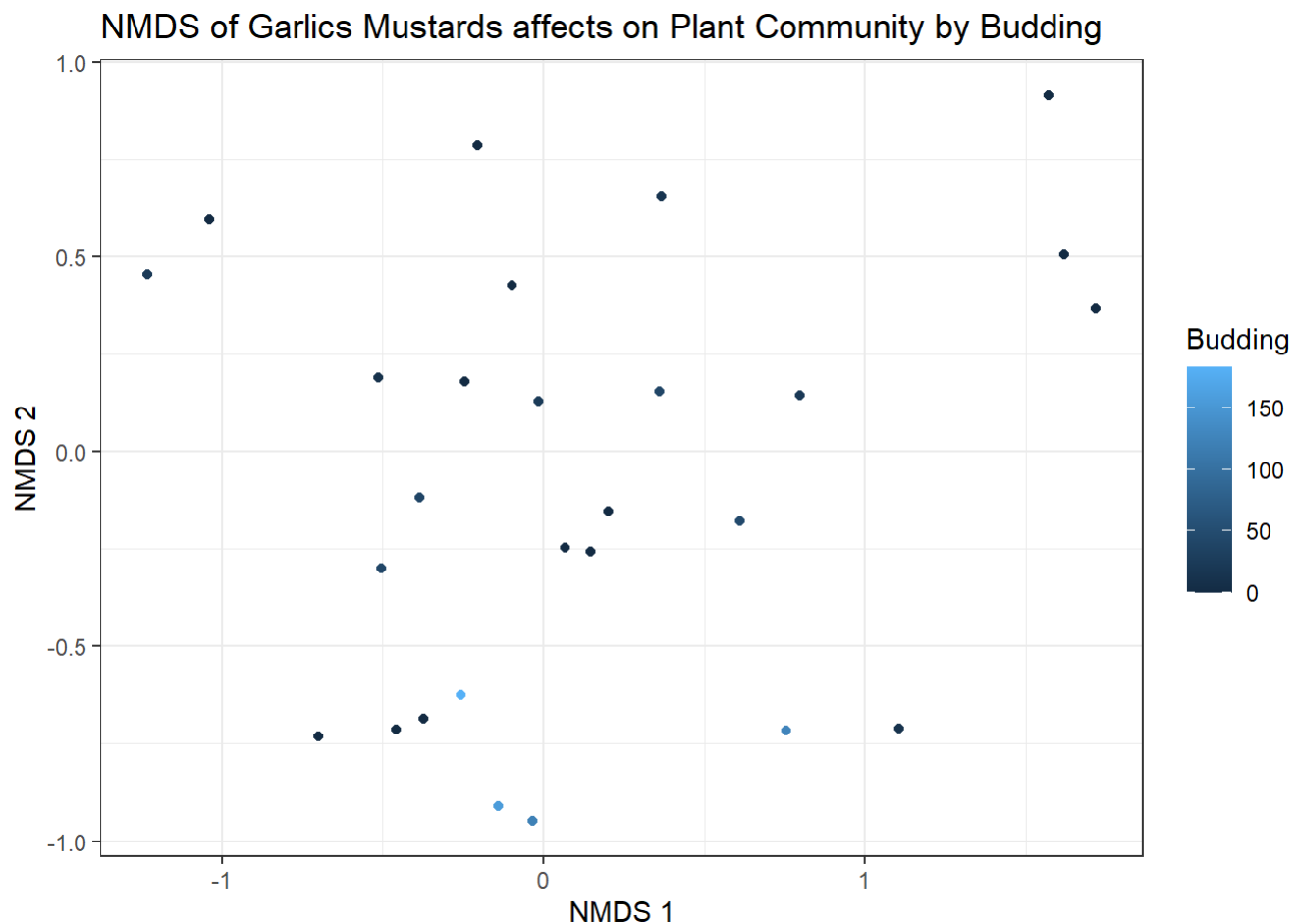


Figure 1: A NMDS analysis to determine what effects garlic mustard has on plant community. Colour separated by budding level data was collected from.

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

Garlic mustards effects on plant community does not appear to have an effect on plant community. From observing the figure, there is not concentration of points which would indicate that the presence of garlic mustard is harming the plant community. Additionally, the plot is coloured by budding of garlic mustard, which would indicate the level of garlic mustard in any given quadrant. There is no discernible relationship between level of budding and harm to plant communities.

```
# Create a plot and group by location

ggplot(Samples, aes(x=NMDSdat$points[,1], y=NMDSdat$points[,2], colour=Location)) +
  geom_point() +
  labs(x="NMDS 1", y="NMDS 2", title="NMDS of Garlics Mustards affects on Plant Community by Location") +
  theme_bw()
```

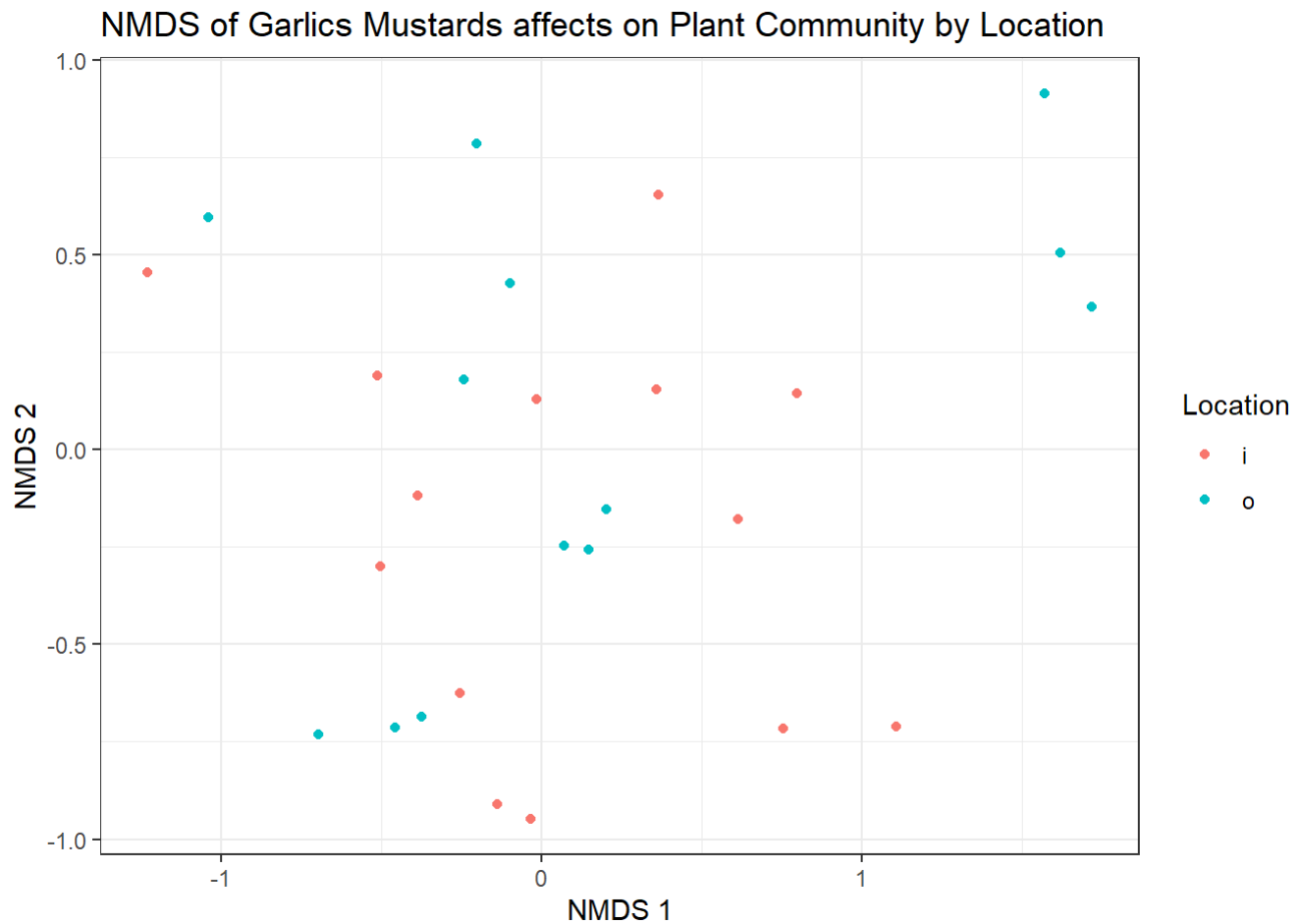


Figure 2: A NMDS analysis to determine what effects garlic mustard has on plant community. Colour separated by location data was collected from.

```
# Create a plot and group sampling population

ggplot(Samples, aes(x=NMDSdat$points[,1], y=NMDSdat$points[,2], colour=Population)) +
  geom_point() +
  labs(x="NMDS 1", y="NMDS 2", title="NMDS of Garlics Mustards affects on Plant Community by Population ") +
  theme_bw()
```

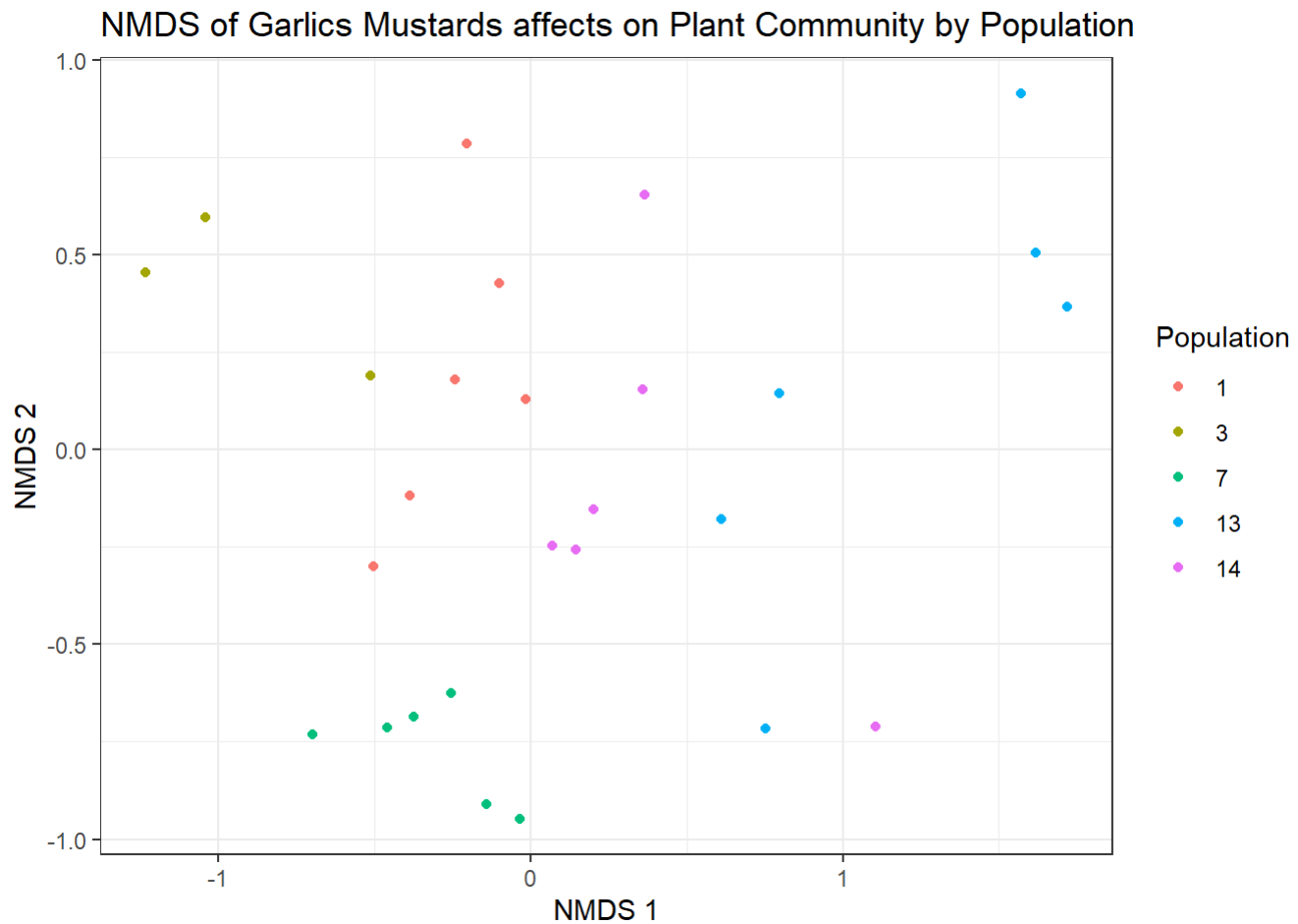



Figure 3: A NMDS analysis to determine what effects garlic mustard has on plant community. Colour separated by population data was collected from.

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

Creating plots which separate the NMDS data for both presence/absence of garlic mustard as well as sampling populations, it is much more likely that sampling population has a stronger effect on plant communities. This is due to a much higher level of grouping of traits observed when sorting the plot by sampling population compared to sorting by location.