Elliot Gavrin 2023-03-08 https://github.com/19eag3/BIOL432_Assignment8 Libraries library(ape) library(ggplot2) library(vegan) ## Loading required package: permute ## Loading required package: lattice ## This is vegan 2.6-4 library(dplyr) ## Attaching package: 'dplyr' ## The following object is masked from 'package:ape': ## ## where ## The following objects are masked from 'package:stats': ## ## filter, lag ## The following objects are masked from 'package:base': ## ## intersect, setdiff, setequal, union library(BiocManager) 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. Data Integration, Manipulation and Visualization of ## Phylogenetic Trees (1st edition). Chapman and Hall/CRC. 2022, ## doi:10.1201/9781003279242 ## 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 **Exploring Dataset** Samples<-read.csv("C:/Users/egavr/OneDrive/Documents/BIOL432/Csv files/FloristicSurvey.csv") dim(Samples) ## [1] 30 44 head(Samples) Quadrate Population Location Rosettes Bolting Budding Bud_Flw Flower Flw_Sil ## 1 703 7 0 0 0 0 ## 2 701 0 0 0 0 0 ## 3 702 0 0 ## 4 7i3 i 14 157 0 ## 5 7i2 3 18 184 0 0 i 0 7i1 7 0 3 0 ## 122 ## Sillique Claytonia_virginiana Anemone_hepatica Grass_tuft ## 1 0 38 0 29 ## 2 7 22 57 6 ## 3 0 3 0 22 10 ## 4 0 0 54 3 ## 5 0 ## 6 44 Trillium_grandifolium Erythronium.trout.lily. Acer_saccharum ## 1 9 25 ## 2 30 10 10 8 5 ## 3 74 ## 4 0 16 0 ## 5 18 7 0 ## 6 Dicentra_cucularia Bloodroot Gallium_aparine Ulmus_americana Unknown_1 ## ## 1 0 ## 2 22 4 27 3 1 23 ## 3 0 8 0 0 0 0 17 88 ## 4 0 ## 5 1 22 150 0 0 133 Unknown_2 Unknown_3.rannunculaceae. Unknown_4 Dryopteris_marginalis ## 1 0 ## 2 0 0 0 ## 3 0 ## 4 ## 5 ## 6 0 Ostrich_fern Plantago_lanceolata Violet Rhamnus_frangula Raspberry Unknown_5 ## ## 1 0 0 0 0 0 ## 2 0 0 0 ## 3 0 0 0 0 0 0 0 0 ## 4 0 0 0 0 0 0 0 ## 5 0 0 Unknown_6 Solidago_canadensis Unknown_7 Dandelion grass viccia_cracca ## 1 0 0 0 0 0 0 0 ## 2 0 0 ## 3 ## 4 0 0 0 ## 5 0 0 ## 6 herb_robert thorny_ash rhamnus_cathartica rhubarb Unknown_8 Unknown_9 ## 1 0 ## 2 0 0 0 ## 3 0 ## 4 ## 5 0 0 0 maianthenum_racemosum ## 1 ## 2 ## 3 ## 4 ## 5 ## 6 tail(Samples) Quadrate Population Location Rosettes Bolting Budding Bud_Flw Flower Flw_Sil ## 25 1402 ## 26 1401 0 14 0 ## 27 1403 14 ## 28 14i2 14 28 15 ## 29 14i1 14 i 34 12 0 ## 30 **14i3** 14 i 25 41 Sillique Claytonia_virginiana Anemone_hepatica Grass_tuft ## 25 0 5 ## 26 ## 27 1 ## 28 0 ## 29 7 37 ## 30 Trillium_grandifolium Erythronium.trout.lily. Acer_saccharum ## 25 7 ## 26 12 13 22 19 ## 27 0 2 ## 28 ## 29 Dicentra_cucularia Bloodroot Gallium_aparine Ulmus_americana Unknown_1 ## 25 0 0 3 ## 26 ## 27 21 ## 28 0 ## 29 0 0 0 ## 30 0 1 Unknown_2 Unknown_3.rannunculaceae. Unknown_4 Dryopteris_marginalis ## 25 ## 26 1 0 ## 27 2 0 ## 28 0 ## 29 0 Ostrich_fern Plantago_lanceolata Violet Rhamnus_frangula Raspberry Unknown_5 ## 25 0 ## 26 0 ## 27 0 4 13 ## 28 0 0 0 0 ## 29 0 ## 30 0 0 0 1 1 Solidago_canadensis Unknown_7 ## 26 0 ## 27 ## 28 2 4 0 ## 29 30 ## 30 0 0 ## herb_robert thorny_ash rhamnus_cathartica rhubarb Unknown_8 Unknown_9 ## 25 5 ## 26 0 0 ## 27 18 0 0 0 ## 28 1 0 ## 29 0 5 ## 30 maianthenum_racemosum ## 25 ## 26 ## 27 ## 28 ## 29 0 str(Samples) 30 obs. of 44 variables: ## 'data.frame': ## \$ Quadrate : chr "703" "701" "702" "7i3" ... ## \$ Population : int 7777773333... "o" "o" "o" "i" ... ## \$ Location : chr ## \$ Rosettes : int 000143014000... : int 0008183312260... \$ Bolting ## \$ Budding : int 0 0 0 157 184 122 11 23 19 0 ... ## \$ Bud_Flw : int 0000000000... ## \$ Flower : int 0000000000... ## \$ Flw_Sil : int 0000000000... ## \$ Sillique : int 0000000000... ## \$ Claytonia_virginiana : int 38 29 57 22 54 44 0 0 0 0 ... ## \$ Anemone_hepatica : int 8730000000... ## \$ 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 ... : int 5 10 74 0 2 0 66 60 26 71 ... ## \$ Acer_saccharum ## \$ Dicentra_cucularia : int 0 22 23 0 0 0 0 0 0 0 ... ## \$ Bloodroot : int 0400100000... : int 0 27 8 17 22 21 2 0 0 0 ... ## \$ Gallium_aparine ## \$ Ulmus_americana : int 0 3 0 88 150 133 0 0 0 0 ... ## \$ Unknown_1 : int 0100000000... ## \$ Unknown_2 : int 0005440000... ## \$ Unknown_3.rannunculaceae.: int 000000000000... ## \$ Unknown 4 : int 0000001000... ## \$ Dryopteris_marginalis : int 000000100... ## \$ Ostrich_fern : int 0000000000... ## \$ Plantago_lanceolata : int 0000000000... : int 0000000000... ## \$ Violet ## \$ Rhamnus_frangula : int 0000000000... ## \$ Raspberry ## \$ Unknown_5 : int 0000000000... ## \$ Unknown_6 : int 0000000000... ## \$ Solidago_canadensis : int 0000000000... ## \$ Unknown_7 : int 00000000000... ## \$ Dandelion : int 0000000000... ## \$ grass : int 0000000000... : int 0000000000... ## \$ viccia_cracca ## \$ herb robert : int 0000000000... ## \$ thorny_ash : int 00000000000 \$ rhamnus_cathartica : int 0000000000... \$ rhubarb : int 0000000000... \$ Unknown_8 : int 0000000000... \$ Unknown_9 : int 00000000000... \$ maianthenum_racemosum : int 0000000000... summary(Samples) Population Rosettes Quadrate Location Length:30 Min. : 1.0 Length:30 Min. : 0.000 ## Class :character 1st Qu.: 3.0 Class :character 1st Qu.: 0.000 Mode :character Median : 7.0 Mode :character Median : 0.000 Mean : 7.6 ## Mean : 2.733 ## 3rd Qu.:13.0 3rd Qu.: 4.500 ## Max. :14.0 Max. :14.000 Budding Bud_Flw Flw_Sil ## Bolting Flower Min. : 0.000 Min. : 0.00 Min. :0 Min. :0 Min. :0 1st Qu.:0 1st Qu.: 0.000 1st Qu.: 0.00 1st Qu.:0 1st Qu.:0 Median : 1.500 Median :0 Median : 5.50 Median :0 Median :0 Mean : 29.47 Mean : 8.533 Mean :0 Mean :0 Mean :0 3rd Qu.: 36.00 ## 3rd Qu.:16.500 3rd Qu.:0 3rd Qu.:0 3rd Qu.:0 :34.000 Max. :184.00 Max. :0 Max. :0 Max. Sillique Claytonia_virginiana Anemone_hepatica Grass_tuft : 0 Min. : 0.00 Min. : 0.000 Min. :0.0 1st Qu.: 0.00 1st Qu.:0 1st Qu.:0.0 1st Qu.: 0.000 Median : 0.00 Median :0 Median :0.0 Median : 0.000 ## Mean :0 Mean :10.17 Mean :0.6 Mean : 2.133 3rd Qu.:0 3rd Qu.:10.00 3rd Qu.:0.0 3rd Qu.: 1.500 :0 Max. :57.00 Max. :22.000 ## Max. Max. :8.0 Trillium_grandifolium Erythronium.trout.lily. Acer_saccharum Min. : 0.000 Min. : 0.00 Min. : 0.00 1st Qu.: 0.000 1st Qu.: 0.00 1st Qu.: 0.00 Median : 0.000 Median : 0.00 ## Median: 8.00 Mean : 1.567 Mean : 5.60 Mean : 21.03 ## 3rd Qu.: 0.000 3rd Qu.: 9.25 3rd Qu.: 18.50 Max. :30.000 Max. :26.00 Max. :187.00 Bloodroot Gallium_aparine Ulmus_americana Dicentra_cucularia Min. : 0.0 Min. :0.0000 Min. : 0.000 Min. : 0.00 1st Qu.: 0.0 1st Qu.:0.0000 1st Qu.: 0.000 1st Qu.: 0.00 Median: 0.0 Median : 1.500 Median: 0.00 Median :0.0000 Mean : 1.5 Mean :0.1667 Mean : 7.233 Mean : 13.13 3rd Qu.: 0.0 3rd Qu.:0.0000 3rd Qu.:14.750 3rd Qu.: 2.00 Max. :4.0000 Max. :150.00 ## Max. :23.0 Max. :41.000 Unknown_1 Unknown_2 Unknown_3.rannunculaceae. Unknown_4 :0.0 Min. :0.0000 Min. Min. :0.0000 Min. : 0.000 1st Qu.:0.0 1st Qu.: 0.000 ## Median :0.0 Median :0.0000 Median :0.0000 Median : 0.000 Mean :0.1 Mean :0.4333 Mean :0.1667 Mean : 1.267 3rd Qu.:0.0000 ## 3rd Qu.:0.0 3rd Qu.:0.0000 3rd Qu.: 1.000 :5.0000 :4.0000 Max. :15.000 :1.0 Max. Max. Dryopteris_marginalis Ostrich_fern Plantago_lanceolata Violet ## Min. :0.00000 Min. :0.0 Min. : 0.0000 Min. : 0.0 1st Qu.:0.00000 1st Qu.:0.0 1st Qu.: 0.0000 1st Qu.: 0.0 Median : 0.0 Median :0.00000 Median :0.0 Median : 0.0000 Mean :0.03333 ## Mean :0.5 Mean : 0.4333 Mean : 0.7 3rd Qu.:0.00000 3rd Qu.:0.0 3rd Qu.: 0.0000 3rd Qu.: 0.0 :1.00000 Max. :4.0 Max. :13.0000 Max. :17.0 ## Max. Rhamnus_frangula Raspberry Unknown_5 ## Unknown_6 Min. :0.0000 Min. :0.0 Min. : 0.000 Min. : 0.0000 1st Qu.:0.0000 1st Qu.:0.0 1st Qu.: 0.000 1st Qu.: 0.0000 Median :0.0000 Median :0.0 Median : 0.000 Median : 0.0000 Mean :0.4667 Mean :0.3 Mean : 1.667 Mean : 0.7333 3rd Qu.: 0.0000 ## 3rd Qu.:0.0000 3rd Qu.:0.0 3rd Qu.: 0.750 :7.0000 :27.000 :22.0000 Max. :4.0 Max. Max. Solidago_canadensis Unknown_7 Dandelion grass Min. : 0.000 Min. :0.00000 Min. : 0.000 Min. : 0.0 1st Qu.:0.00000 1st Qu.: 0.0 1st Qu.: 0.000 1st Qu.: 0.000 Median: 0.0 Median : 0.000 Median :0.00000 Median : 0.000 Mean :0.06667 Mean : 1.367 Mean : 1.233 Mean : 28.1 3rd Qu.: 0.000 ## 3rd Qu.: 0.000 3rd Qu.:0.00000 3rd Qu.: 14.0 ## Max. :18.000 Max. :2.00000 Max. :14.000 Max. :239.0 viccia_cracca herb_robert thorny_ash ## rhamnus_cathartica :0.00000 Min. : 0.0 :0.0000 ## Min. Min. Min. :0.00000 1st Qu.:0.00000 1st Qu.: 0.0 1st Qu.:0.0000 1st Qu.:0.00000 Median :0.00000 Median : 0.0 Median :0.0000 Median :0.00000 Mean : 1.8 Mean :0.06667 :0.4333 Mean :0.03333 Mean ## 3rd Qu.:0.00000 3rd Qu.: 0.0 3rd Qu.:0.0000 3rd Qu.:0.00000 Max. :2.00000 Max. :18.0 Max. :8.0000 :1.00000 ## rhubarb Unknown_8 Unknown_9 maianthenum_racemosum ## Min. :0.00000 Min. :0.00000 Min. :0.0 Min. :0.0000 1st Qu.:0.00000 1st Qu.:0.00000 1st Qu.:0.0 1st Qu.:0.0000 Median :0.0000 Median :0.00000 Median :0.00000 Median :0.0 ## Mean :0.03333 Mean :0.06667 Mean :0.1 Mean :0.1333 3rd Qu.:0.00000 3rd Qu.:0.00000 3rd Qu.:0.0 3rd Qu.:0.0000 :1.00000 ## Max. :2.00000 Max. :3.0 Max. :4.0000 Max. Converting Factors into Binary Data InDat <-Samples %>% select(-c(Quadrate, Location)) InDat2 <-Samples %>% select(-c(Quadrate)) BinDat2 <-InDat2 BinDat <-InDat for(row in 1:nrow(InDat)){ for(col in 1:ncol(InDat)){ if (BinDat[row,col] > 0){ BinDat[row,col]<-1 } str(BinDat) ## 'data.frame': 30 obs. of 42 variables: \$ Population : num 111111111... \$ Rosettes : num 0001101000... \$ Bolting : num 0001111110 ... : num 0001111110... \$ Budding \$ Bud_Flw : int 00000000000... \$ Flower : int 0000000000... ## \$ Flw_Sil : int 0000000000... \$ Sillique : int 0000000000... \$ Claytonia_virginiana : num 1111110000... \$ Anemone_hepatica : num 1110000000... \$ Grass_tuft 1111100000... \$ Trillium_grandifolium : num 11100000000... \$ Erythronium.trout.lily. : num 1 1 1 1 1 1 0 0 0 0 ... \$ Acer_saccharum 1110101111... \$ Dicentra_cucularia 0 1 1 0 0 0 0 0 0 0 ... : num \$ Bloodroot : num 0 1 0 0 1 0 0 0 0 0 ... \$ Gallium_aparine 0 1 1 1 1 1 1 0 0 0 ... \$ Ulmus_americana 0 1 0 1 1 1 0 0 0 0 ... : num ## \$ Unknown_1 : num 0 1 0 0 0 0 0 0 0 0 ... \$ Unknown_2 0 0 0 1 1 1 0 0 0 0 ... \$ Unknown_3.rannunculaceae.: num 00000000000... : num 0000001000... \$ Unknown_4 \$ Dryopteris_marginalis : num 0 0 0 0 0 0 0 1 0 0 : num 0000000000... ## \$ Ostrich_fern ## \$ Plantago_lanceolata : num 0 0 0 0 0 0 0 0 0 0 ... ## \$ Solidago_canadensis : num 0 0 0 0 0 0 0 0 0 0 ... ## \$ Unknown_7 : num 0 0 0 0 0 0 0 0 0 0 0 ...

\$ Dandelion : num 0 0 0 0 0 0 0 0 0 0 0 ...

\$ grass : num 0 0 0 0 0 0 0 0 0 0 0 ...

\$ viccia_cracca : num 0 0 0 0 0 0 0 0 0 0 ...

\$ thorny_ash : num 0 0 0 0 0 0 0 0 0 0 0 ...

\$ rhamnus_cathartica : num 0 0 0 0 0 0 0 0 0 0 ...

\$ rhubarb : num 0 0 0 0 0 0 0 0 0 0 0 ... : num 0000000000... : num 00000000000... ## \$ Unknown_8 ## \$ Unknown_9 ## \$ maianthenum_racemosum : num 0 0 0 0 0 0 0 0 0 0 ... Q1 - Categorizing by Dissimularity - Highlighting the samples that are taken in and out of mustard plant patches OTU_dist<- vegdist(BinDat, method="bray", binary=F) OTUtree<-nj(OTU_dist) NMDSdat<-metaMDS(OTU_dist, k=2)</pre> ## Run 0 stress 0.1935574 ## Run 1 stress 0.2030529 ## Run 2 stress 0.2031668 ## Run 3 stress 0.1976602 ## Run 4 stress 0.2110441 ## Run 5 stress 0.1976603 ## Run 6 stress 0.211044 ## Run 7 stress 0.1976602 ## Run 8 stress 0.2110963 ## Run 9 stress 0.2030523 ## Run 10 stress 0.2110963 ## Run 11 stress 0.1932304 ## ... New best solution ## ... Procrustes: rmse 0.01444141 max resid 0.06028253 ## Run 12 stress 0.1935574 ## ... Procrustes: rmse 0.01444086 max resid 0.06034636 ## Run 13 stress 0.1932304 ## ... New best solution ## ... Procrustes: rmse 5.089089e-06 max resid 1.753421e-05 ## ... Similar to previous best ## Run 14 stress 0.2259137 ## Run 15 stress 0.1976602 ## Run 16 stress 0.2030526 ## Run 17 stress 0.2468614 ## Run 18 stress 0.1932304 ## ... Procrustes: rmse 1.625149e-05 max resid 6.959699e-05 ## ... Similar to previous best ## Run 19 stress 0.1935574 ## ... Procrustes: rmse 0.01444046 max resid 0.06033852 ## Run 20 stress 0.1975778 ## *** Best solution repeated 2 times ggtree(OTUtree,layout="rectangular") %<+% BinDat2 +</pre> geom_tiplab(aes(colour=Location))+ theme(legend.position = "right") ## ! The tree contained negative edge length. If you want to ignore the edge, you ## can set `options(ignore.negative.edge=TRUE)`, then re-run ggtree. 19 16 22 Location 30 a i 28 Fig. 1: Dissimilarity tree depicting the 29 **a** 0 a NA 26 25 13 14 relationship between each sample. Red samples are samples that are taken from quadrents within mustard plant patches. Grey samples are taken from quadrents outside of mustard plant samples There is influence in plant samples from areas where mustard plants are present. The OUT tree determined the samples that are in the same patches as mustard plants to be the most similar to each other, while plants outside of the mustard patches are not as similar to those within. Q2 Pdat<-data.frame(NMDS1=NMDSdat\$points[,1],</pre> NMDS2=NMDSdat\$points[,2], SampleID=row.names(Samples)) Pdat<-merge(Pdat, Samples, all.x=T, all.y=F)</pre> str(Pdat) 900 obs. of 47 variables: ## 'data.frame': ## \$ NMDS1 : num -0.262 -0.511 -0.413 -0.669 -0.505 ... ## \$ NMDS2 : num -0.7342 -0.6252 -0.6419 0.0108 -0.062 ... ## \$ SampleID : chr "1" "2" "3" "4" ... ## \$ Quadrate : chr "703" "703" "703" "703" ... \$ Population 7777777777... : int \$ Location "0" "0" "0" "0" ... ## \$ Rosettes : int 0000000000... \$ Bolting 0 0 0 0 0 0 0 0 0 0 ... \$ Budding 0 0 0 0 0 0 0 0 0 0 ... \$ Bud_Flw : int 0000000000... ## \$ Flower 0 0 0 0 0 0 0 0 0 0 ... ## \$ Flw_Sil : int 0000000000... ## \$ Sillique : int 0000000000... ## \$ Claytonia_virginiana : int 38 38 38 38 38 38 38 38 38 ... ## \$ Anemone_hepatica : int 888888888... ## \$ Grass_tuft : int 14 14 14 14 14 14 14 14 14 ... ## \$ Trillium_grandifolium : int 9 9 9 9 9 9 9 9 9 ... ## \$ Erythronium.trout.lily. : int 25 25 25 25 25 25 25 25 25 25 ... : int 555555555... ## \$ Acer_saccharum \$ Dicentra_cucularia : int 0000000000... : int 0000000000 ## \$ Bloodroot ## \$ Gallium_aparine : int 0000000000... \$ Ulmus_americana \$ Unknown_1 0 0 0 0 0 0 0 0 0 0 ... \$ Unknown_2 : int 0 0 0 0 0 0 0 0 0 0 . . . \$ Unknown_3.rannunculaceae.: int 00000000000... \$ Unknown_4 : int 0 0 0 0 0 0 0 0 0 0 ... \$ Dryopteris_marginalis : int 0 0 0 0 0 0 0 0 0 0 . . . \$ Ostrich_fern ## \$ Plantago_lanceolata 0 0 0 0 0 0 0 0 0 0 ... ## \$ Violet 0 0 0 0 0 0 0 0 0 0 ... ## \$ Rhamnus_frangula : int 0000000000... ## \$ Raspberry 0 0 0 0 0 0 0 0 0 0 ... ## \$ Unknown_5 0 0 0 0 0 0 0 0 0 0 ... ## \$ Unknown_6 0 0 0 0 0 0 0 0 0 0 ... ## \$ Solidago_canadensis \$ Unknown_7 0 0 0 0 0 0 0 0 0 0 ... ## \$ Dandelion : int 0000000000... ## \$ grass ## \$ viccia_cracca ## \$ herb_robert 0 0 0 0 0 0 0 0 0 0 . . . ## \$ thorny_ash ## \$ rhamnus_cathartica 0 0 0 0 0 0 0 0 0 0 ... : int \$ rhubarb : int 0000000000... \$ Unknown 8 0 0 0 0 0 0 0 0 0 0 ... \$ Unknown_9 : int 0000000000... : int 0000000000... \$ maianthenum_racemosum Pdat\$fLocation <- factor(Pdat\$Location)</pre> ggplot(aes(x=NMDS1, y=NMDS2, color=fLocation, alpha=I(0.6)), data=Pdat)+geom_point()+ geom_jitter()+ $scale_colour_gradient(limits = c(0,14))+$ theme_classic()+ scale_color_manual(values = c("red", "green")) ## Scale for colour is already present. ## Adding another scale for colour, which will replace the existing scale. 8.0 0.4 fLocation NMDS2 Fig. 2: Plot of NMDS2 vs NMDS1. -0.4 -0.8 -0.5 0.0 0.5 1.0 NMDS1 Red dots are where the samples in the prescence of mustard. Green dots are where samples were recorded outside the presence of mustard. ggplot(aes(x=NMDS1,y=NMDS2,colour=Population), data=Pdat)+ geom_point()+ geom_jitter()+ theme_classic() 8.0 0.4 Population NMDS2

10

1.0

-0.4

8.0-

-0.5

categorized by population than by presence of mustard.

0.0

respresnt a higher population of mustard in the area that the sample was taken frmo.

NMDS1

0.5

Fig. 3: Plot of NMDS vs NMDS1. Darker dots represent a lower population of mustard in the area that the sample was taken from. Lighter dots

The figures support that the populaiton has a stronger impact on plant communities, because they are grouped together more tightly when