ms\_willow\_network\_supplement

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The code below replicates the analyses for the qualitative and quantitative network data.

##   
## Attaching package: 'reshape'  
##   
## The following objects are masked from 'package:reshape2':  
##   
## colsplit, melt, recast  
##   
##   
## Attaching package: 'plyr'  
##   
## The following objects are masked from 'package:reshape':  
##   
## rename, round\_any  
##   
##   
## Attaching package: 'dplyr'  
##   
## The following objects are masked from 'package:plyr':  
##   
## arrange, desc, failwith, id, mutate, summarise, summarize  
##   
## The following objects are masked from 'package:stats':  
##   
## filter, lag  
##   
## The following objects are masked from 'package:base':  
##   
## intersect, setdiff, setequal, union  
##   
## Joining by: c("Gender", "Genotype", "plant.position")  
## Joining by: c("Genotype", "plant.position")  
## Loading required package: permute  
## Loading required package: lattice  
## This is vegan 2.0-10

## [1] "aSG\_Tory" "rG\_Eulo" "rG\_Lestodip" "rG\_Mesopol" "rG\_Platy"   
## [6] "rG\_Tory" "SG\_Platy" "vLG\_Eulo" "vLG\_Mesopol" "vLG\_Mymarid"  
## [11] "vLG\_Platy" "vLG\_Tory"

##   
## \* A B D E F G H I J K L M N O P Q R S T U V W X Y Z   
## 4 2 5 3 2 2 1 1 5 1 6 4 1 1 1 1 3 1 5 2 0 5 3 5 3 7

Table 1: Quantitative full data set with euclidean distance

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | df | SS | MS | F | P |
| log(shootEst.no18) | 1 | 1.76 | 1.76 | 2.62 | 0.028 |
| Genotype | 25 | 38.16 | 1.53 | 2.27 | 0.001 |
| Residuals | 118 | 79.25 | 0.67 | NA | NA |
| Total | 144 | 119.17 | NA | NA | NA |

Table S2: Quantitative data subset, euclidean

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | df | SS | MS | F | P |
| log(shootEst.no18) | 1 | 2.74 | 2.74 | 2.28 | 0.031 |
| Genotype | 12 | 24.58 | 2.05 | 1.70 | 0.004 |
| Residuals | 44 | 52.96 | 1.20 | NA | NA |
| Total | 57 | 80.29 | NA | NA | NA |

Table S3: Quantitative data subset, with bray-curtis dissimilarity

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | df | SS | MS | F | P |
| log(shootEst.no18) | 1 | 0.68 | 0.68 | 2.30 | 0.029 |
| Genotype | 12 | 5.24 | 0.44 | 1.49 | 0.015 |
| Residuals | 44 | 12.93 | 0.29 | NA | NA |
| Total | 57 | 18.85 | NA | NA | NA |

Table S3: Qualitative data subset, with Jaccard dissimilarity

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | df | SS | MS | F | P |
| log(shootEst.no18) | 1 | 0.93 | 0.93 | 3.17 | 0.003 |
| Genotype | 12 | 5.28 | 0.44 | 1.50 | 0.007 |
| Residuals | 44 | 12.89 | 0.29 | NA | NA |
| Total | 57 | 19.09 | NA | NA | NA |

Table S4: Qualitative data subset, with euclidean dissimilarity

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | df | SS | MS | F | P |
| log(shootEst.no18) | 1 | 3.23 | 3.23 | 2.70 | 0.010 |
| Genotype | 12 | 22.31 | 1.86 | 1.55 | 0.001 |
| Residuals | 44 | 52.67 | 1.20 | NA | NA |
| Total | 57 | 78.21 | NA | NA | NA |