

ACN: Analysis of Leaf-Modifier Interaction Networks



Weighted and probabilistic analyses:

```
### load pit data
source('../src/loadPitdata.R')

head(summary(tree.info))
```

```
##  leaf.type      tree      geno      leaves
##  "live:36 " "np12.04: 2 " "1000  :12 " "Min.   : 0.00 "
##  "sen :36 " "np12.07: 2 " "1008  :10 " "1st Qu.: 38.75 "
##  NA        "np13.10: 2 " "1017  :10 " "Median : 50.00 "
##  NA        "np2.07 : 2 " "1023  :10 " "Mean   : 61.26 "
##  NA        "np2.08 : 2 " "11     :10 " "3rd Qu.: 50.00 "
##  NA        "np2.10 : 2 " "996   :10 " "Max.   :464.00 "
```

```
head(summary(tree.arth))
```

```
##
##      Length Class      Mode
## live np12.04 1017 "16"    "data.frame" "list"
## live np12.07 1017 "16"    "data.frame" "list"
## live np13.10 1017 "16"    "data.frame" "list"
## live np2.07 1000 "16"    "data.frame" "list"
## live np2.08 996  "16"    "data.frame" "list"
## live np2.10 996  "16"    "data.frame" "list"
```

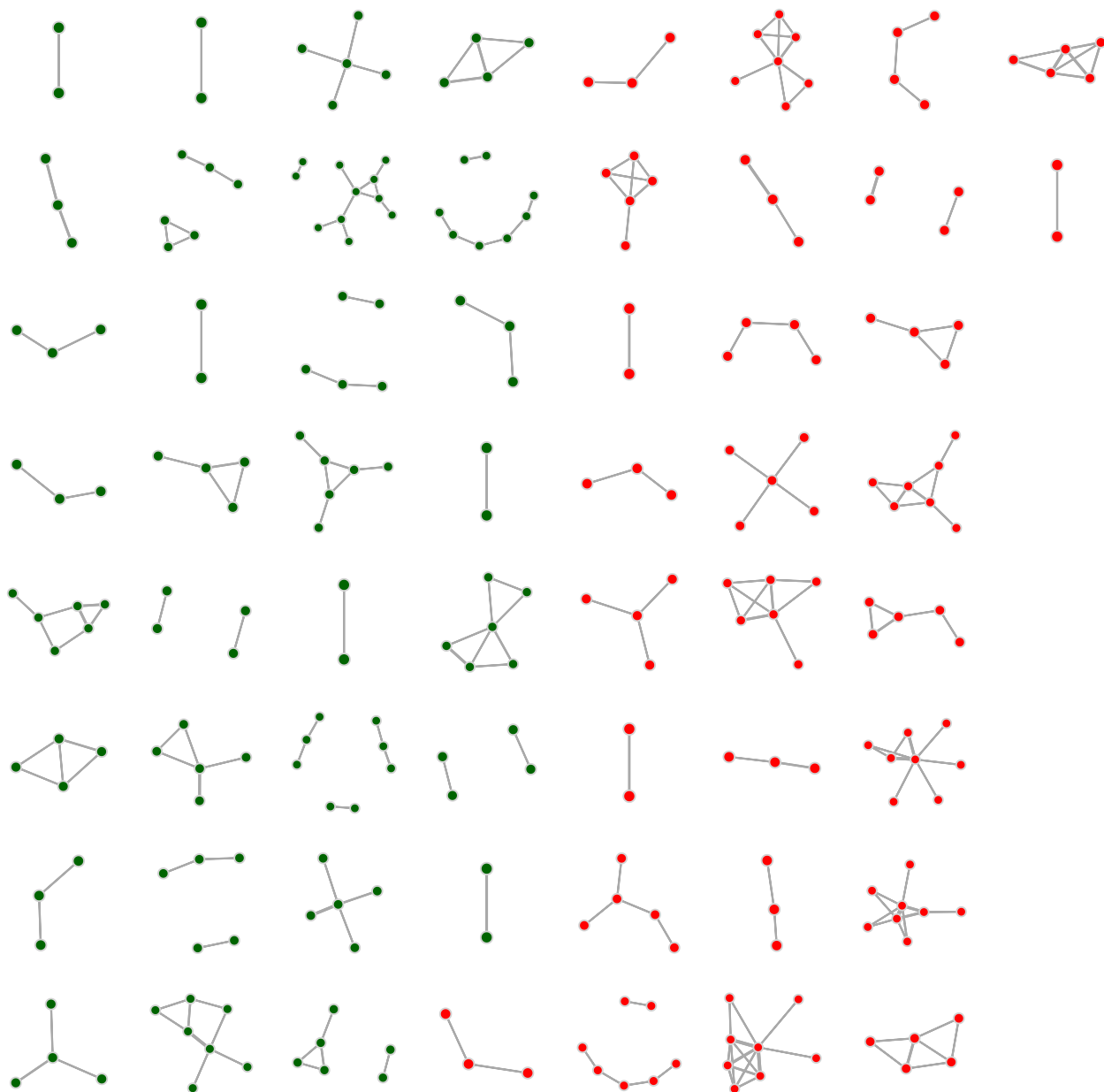
```
head(summary(arth.mats))
```

```
##               Length Class   Mode
## live np12.04 1017 "800"  "-none-" "numeric"
## live np12.07 1017 "800"  "-none-" "numeric"
## live np13.10 1017 "800"  "-none-" "numeric"
## live np2.07 1000 "800"  "-none-" "numeric"
## live np2.08 996  "800"  "-none-" "numeric"
## live np2.10 996  "800"  "-none-" "numeric"
```

Generate the network using the co-occurrences of each arthropod on a leaf.

```
library(sna)
nets.plot <- lapply(tree.nets,rmZeros)

par(mfcol=c(8,9),mai=rep(0.1,4))
for (i in 1:length(nets.plot)){
  if (sum(dim(nets.plot[[i]])) != 0){
    if (tree.info[i,1] == 'sen'){
      vc <- 'red'
    }else{vc <- 'darkgreen'}
    gplot(nets.plot[[i]],gmode='graph',
          edge.col='darkgrey',vertex.col=vc,
          vertex.border='lightgrey',
          edge.lwd=nets.plot[[i]],vertex.cex=2)
  }
}
```



```
t.test(I(liv.cen-sen.cen))
```

```
##
## One Sample t-test
##
## data: I(liv.cen - sen.cen)
## t = -1.3324, df = 35, p-value = 0.1914
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## -0.22098995 0.04585768
## sample estimates:
## mean of x
## -0.08756614
```

Analyze the mean networks for live and senescent leaves.

```
# average structure and variance
liv.mu <- meanNet(liv.nets)
liv.var <- varNet(liv.nets)
sen.mu <- meanNet(sen.nets)
sen.var <- varNet(sen.nets)

par(mfrow=c(2,2),mai=rep(0.1,4))
gplot(liv.mu,gmode='graph',
      edge.lwd=liv.mu/max(liv.mu)*3,vertex.col='green',
      vertex.border='lightgrey',
      edge.col=grey(liv.var/max(liv.var)),
      vertex.cex=apply(liv.spc,2,mean) * 3 + 0.5,
      mode='circle',displaylabels=TRUE)
gplot(sen.mu,gmode='graph',
      edge.lwd=sen.mu/max(sen.mu)*3,vertex.col='red',
      vertex.border='lightgrey',
      edge.col=grey(sen.var/max(sen.var)),
      vertex.cex=apply(sen.spc,2,mean) * 3 + 0.5,
      mode='circle',displaylabels=TRUE)
gplot(liv.mu,gmode='graph',
      edge.lwd=liv.mu/max(liv.mu)*3,vertex.col='green',
      vertex.border='lightgrey',
      edge.col=grey(liv.var/max(liv.var)),
      vertex.cex=apply(liv.spc,2,mean) * 3 + 0.5,
      displaylabels=TRUE)
gplot(sen.mu,gmode='graph',
      edge.lwd=sen.mu/max(sen.mu)*3,vertex.col='red',
      vertex.border='lightgrey',
      edge.col=grey(sen.var/max(sen.var)),
      vertex.cex=apply(sen.spc,2,mean) * 3 + 0.5,
      displaylabels=TRUE)
```



```
##          cor
## -0.2517362
```

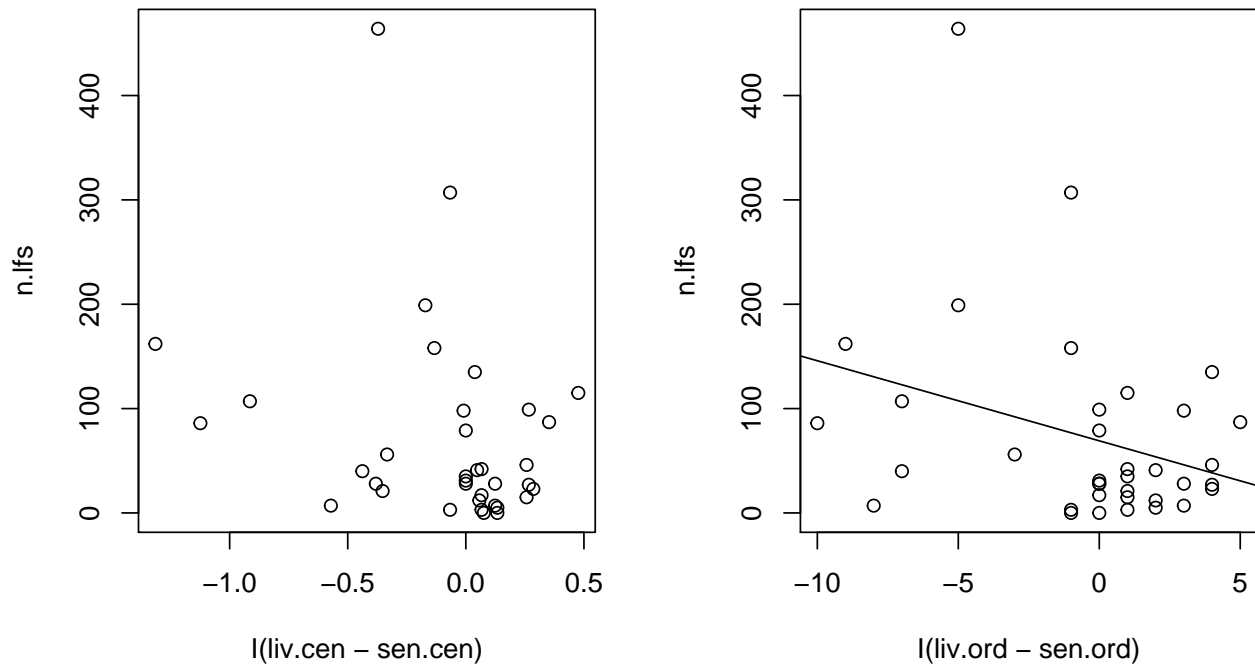
```
cor.test(n.lfs,I(liv.ord-sen.ord))
```

```
##
## Pearson's product-moment correlation
##
## data:  n.lfs and I(liv.ord - sen.ord)
## t = -1.9501, df = 34, p-value = 0.05945
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.5847730  0.0126857
## sample estimates:
##          cor
## -0.3171719
```

```
adonis(distNet(tree.nets[tree.info$leaf.type == 'sen'])~n.lfs)
```

```
##
## Call:
## adonis(formula = distNet(tree.nets[tree.info$leaf.type == "sen"]) ~      n.lfs)
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## n.lfs      1     37.85  37.849  1.3597 0.03845  0.194
## Residuals 34     946.43  27.836      0.96155
## Total     35     984.28      1.00000
```

```
par(mfrow=c(1,2))
plot(I(liv.cen-sen.cen),n.lfs)
plot(I(liv.ord-sen.ord),n.lfs)
abline(lm(n.lfs~I(liv.ord-sen.ord)))
```



How much variance in network structure does genotype explain?

About 8% of the variation in network structure was attributable to tree genotype. This was primarily due to genetic effects on re-wiring of the network rather than changes to the structure. Leaf senescence strongly impacted network modularity.

```
library(BiodiversityR)
library(ecodist)
dn.tree <- distNet(tree.nets)
adonis(dn.tree~factor(leaf.type)*factor(geno),data=tree.info, strata=tree.info$tree)
```

```
##
## Call:
## adonis(formula = dn.tree ~ factor(leaf.type) * factor(geno),      data = tree.info, strata = tree.in
##
## Blocks: strata
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs MeanSqs F.Model    R2 Pr(>F)
## factor(leaf.type)      1    118.53  118.528  5.3315 0.07390 0.001
## factor(geno)           7     123.52   17.646  0.7937 0.07702 0.001
## factor(leaf.type):factor(geno) 7     116.79   16.684  0.7505 0.07282 0.661
## Residuals            56    1244.97   22.232           0.77626
## Total                71    1603.81           1.00000
##
## factor(leaf.type)      ***
## factor(geno)           ***
## factor(leaf.type):factor(geno)
## Residuals
## Total
```

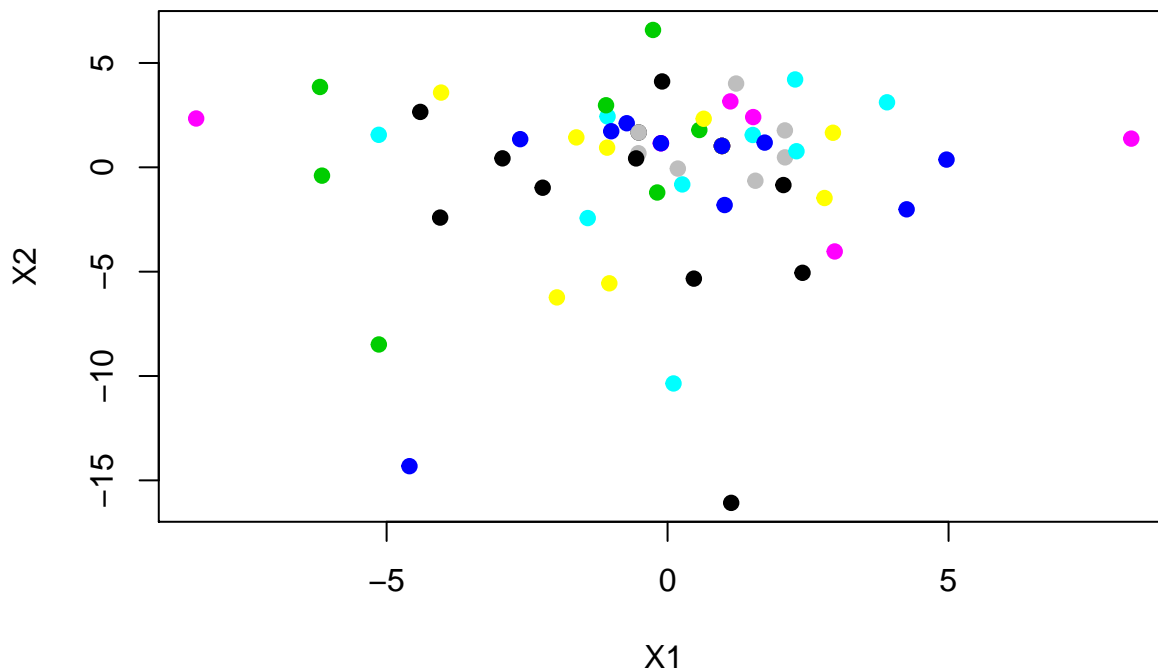
```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ord.tree <- nmds.min(nmds(dn.tree,2,2),dims=2)
```

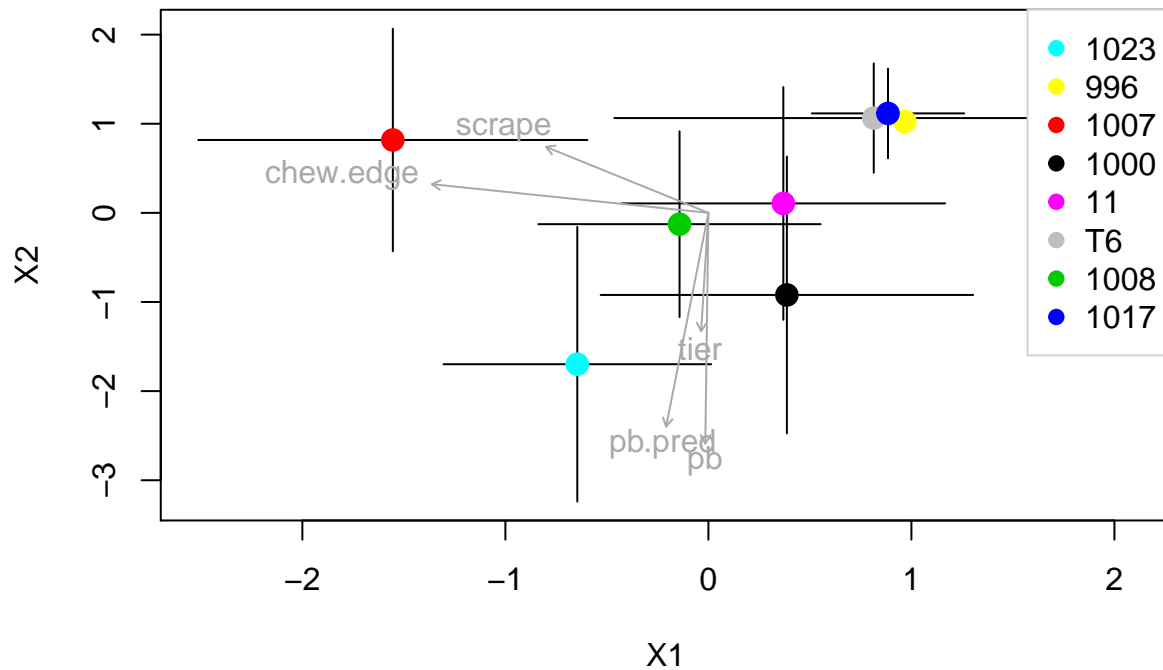
```
## Using random start configuration
## Using random start configuration
## Using random start configuration
## Using random start configuration
## Using random start configuration
## Using random start configuration
## Using random start configuration
## Using random start configuration
## Using random start configuration
## Using random start configuration
## Minimum stress for given dimensionality: 0.16264
## r^2 for minimum stress configuration: 0.9422117
```

```
spp.vectors <- envfit(ord.tree,spp.tot)
spp.vectors <- envfit(ord.tree,spp.tot[,spp.vectors$vectors$pvals <= 0.05])

plot(ord.tree,pch=19,
      col=as.numeric(factor(tree.info$geno)))
```



```
mu <- ch.plot(ord.tree,factor(tree.info$geno))
points(mu,col=as.numeric(factor(unique(tree.info$geno))),pch=19,cex=1.5)
plot(spp.vectors,col='darkgrey')
legend('topright',legend=unique(tree.info$geno),
      col=as.numeric(factor(unique(tree.info$geno))),
      pch=19,bty='d',bg='white',box.col='lightgrey')
```

“{r }

```
adonis(distNet(liv.nets)~factor(geno),data=tree.info[tree.info$leaf.type ==
'live',])
```

```
adonis(distNet(sen.nets)~factor(geno),data=tree.info[tree.info$leaf.type ==
'sen',])
```

““

```
library(bipartite)
### centrality
tree.cen <- unlist(lapply(tree.nets,function(x) centralization(x,FUN='degree'))))
tree.mod <- dget(file='../data/tree.mod') # see src/treeMods.R

summary(aov(tree.cen~tree+factor(leaf.type)*factor(geno),data=tree.info))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## tree	35	2.9209	0.08345	1.311	0.232
## factor(leaf.type)	1	0.1380	0.13802	2.168	0.152
## factor(leaf.type):factor(geno)	7	0.6164	0.08805	1.383	0.251
## Residuals	28	1.7824	0.06366		

```
summary(aov(tree.mod~tree+factor(leaf.type)*factor(geno),data=tree.info))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## tree	35	1.0698	0.0306	0.903	0.616910
## factor(leaf.type)	1	0.5749	0.5749	16.976	0.000304 ***

```
## factor(leaf.type):factor(geno) 7 0.2974 0.0425 1.255 0.307767
## Residuals                      28 0.9482 0.0339
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Genotype does not directly influence senescence, but may indirectly influence senescence through pb.

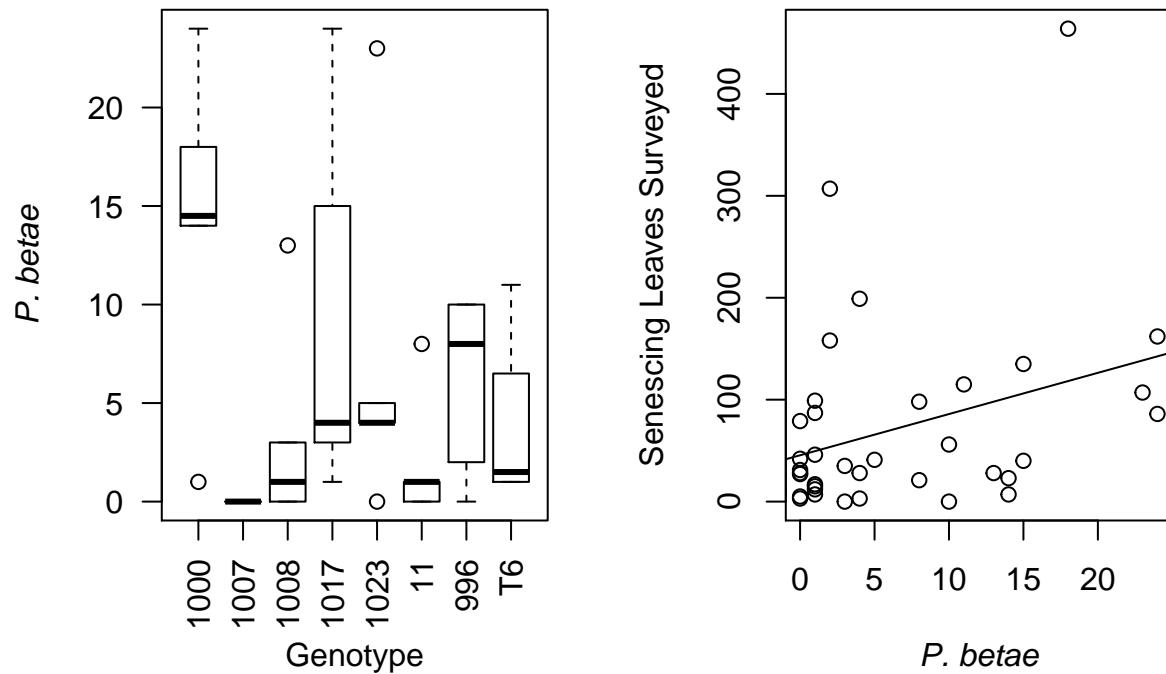
```
summary(aov(I(leaves~0.5)~factor(geno)*pb,
             data=data.frame(tree.info,spp.tot)[tree.info$leaf.type == 'sen',]))
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## factor(geno)   7  171.2    24.46   1.178 0.3564
## pb             1   98.8    98.82   4.760 0.0406 *
## factor(geno):pb 6   79.5    13.25   0.638 0.6985
## Residuals      21  436.0    20.76
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(aov(I(pb~0.5) ~ factor(geno),
             data=data.frame(tree.info,spp.tot)[tree.info$leaf.type == 'sen',]))
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## factor(geno)   7   30.03    4.290   2.114 0.0751 .
## Residuals      28   56.81    2.029
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
par(mfrow=c(1,2))
plot(pb~geno,
     data=data.frame(tree.info,spp.tot)[tree.info$leaf.type == 'sen',],
     xlab='Genotype',ylab=expression(italic('P. betae')),las=2)
plot(leaves~pb,
     data=data.frame(tree.info,spp.tot)[tree.info$leaf.type == 'sen',],
     xlab=expression(italic('P. betae')),ylab='Senescing Leaves Surveyed')
abline(lm(leaves~pb,data=data.frame(tree.info,spp.tot)[
  tree.info$leaf.type == 'sen',]))
```



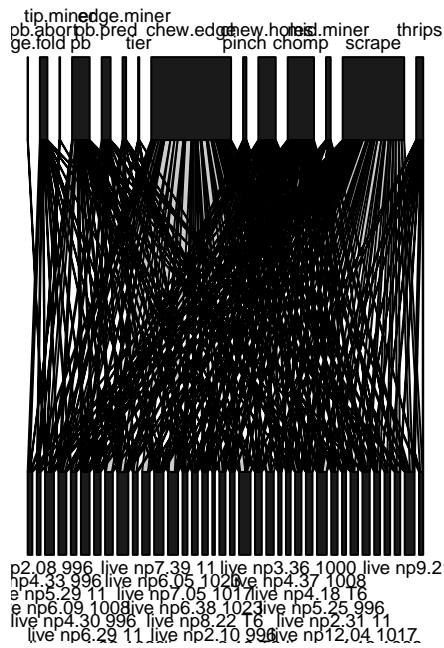
Stand level network modularity

```
liv.bpn <- spp.tot[tree.info$leaf.type == 'live',]
sen.bpn <- spp.tot[tree.info$leaf.type == 'sen',]

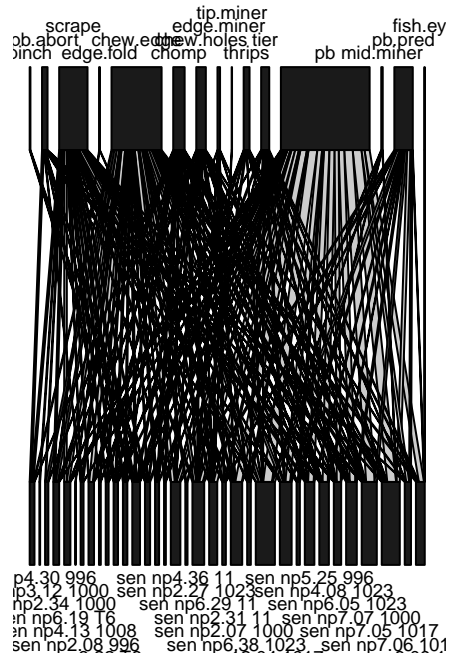
liv.modules <- dget('../data/liv.modules')
sen.modules <- dget('../data/sen.modules')

par(mfrow=c(1,2))
plotweb(liv.bpn);title(main='Live')
plotweb(sen.bpn);title(main='Senescent')
```

Live



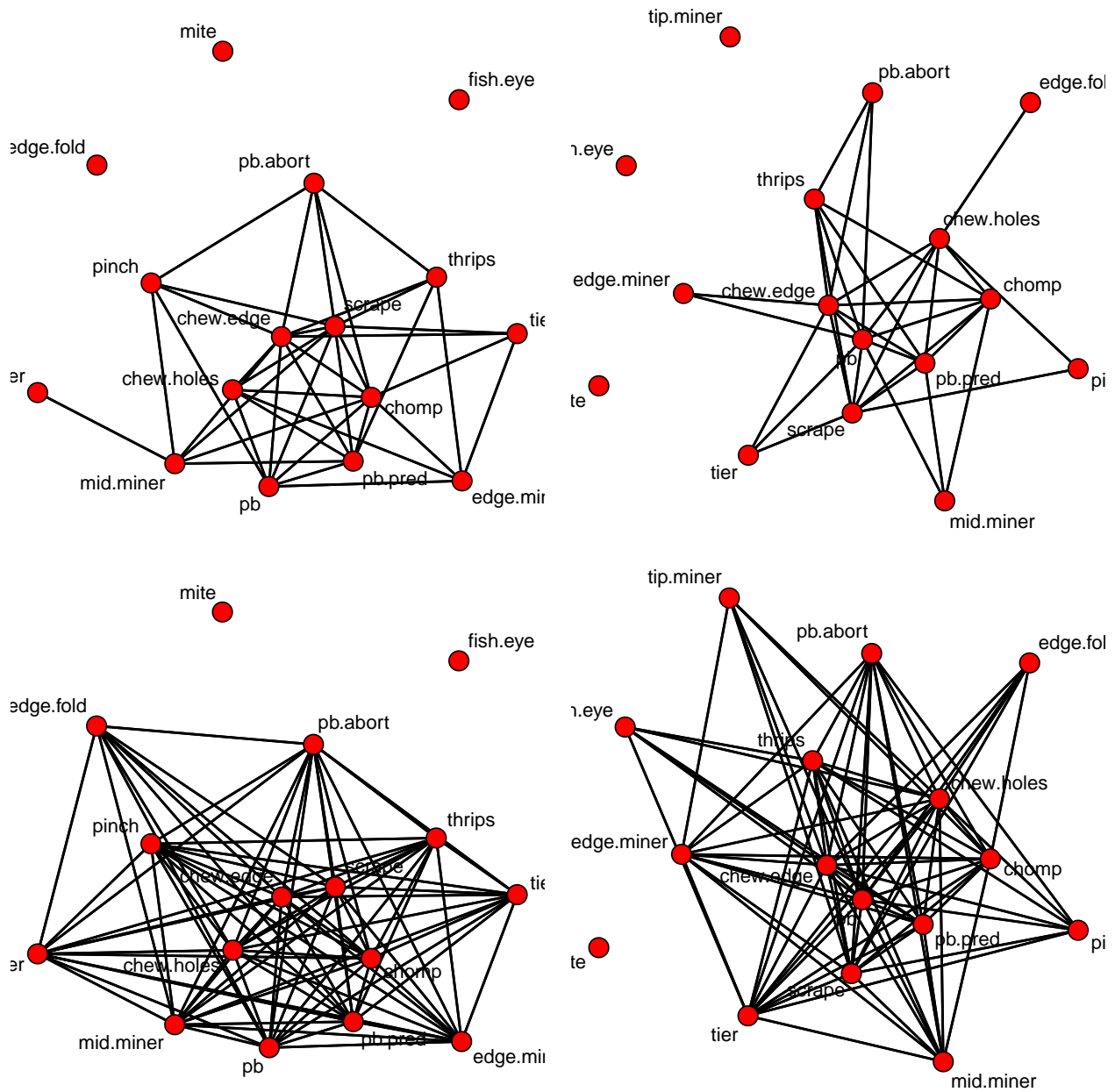
Senescent



How does the mean interaction network compare to the bipartite to unipartite projection?

```
liv.b2u <- t(liv.bpn) %*% liv.bpn
sen.b2u <- t(sen.bpn) %*% sen.bpn

par(mfrow=c(2,2),mai=rep(0.1,4))
liv.coo <- gplot(liv.mu,gmode='graph',displaylabels=TRUE)
sen.coo <- gplot(sen.mu,gmode='graph',displaylabels=TRUE)
gplot(liv.b2u,coord=liv.coo,gmode='graph',displaylabels=TRUE)
gplot(sen.b2u,coord=sen.coo,gmode='graph',displaylabels=TRUE)
```



This question isn't very interesting since the effect of genotype doesn't differ between live and senescing leaves. What does the unipartite projection look like for the trees and genotypes?