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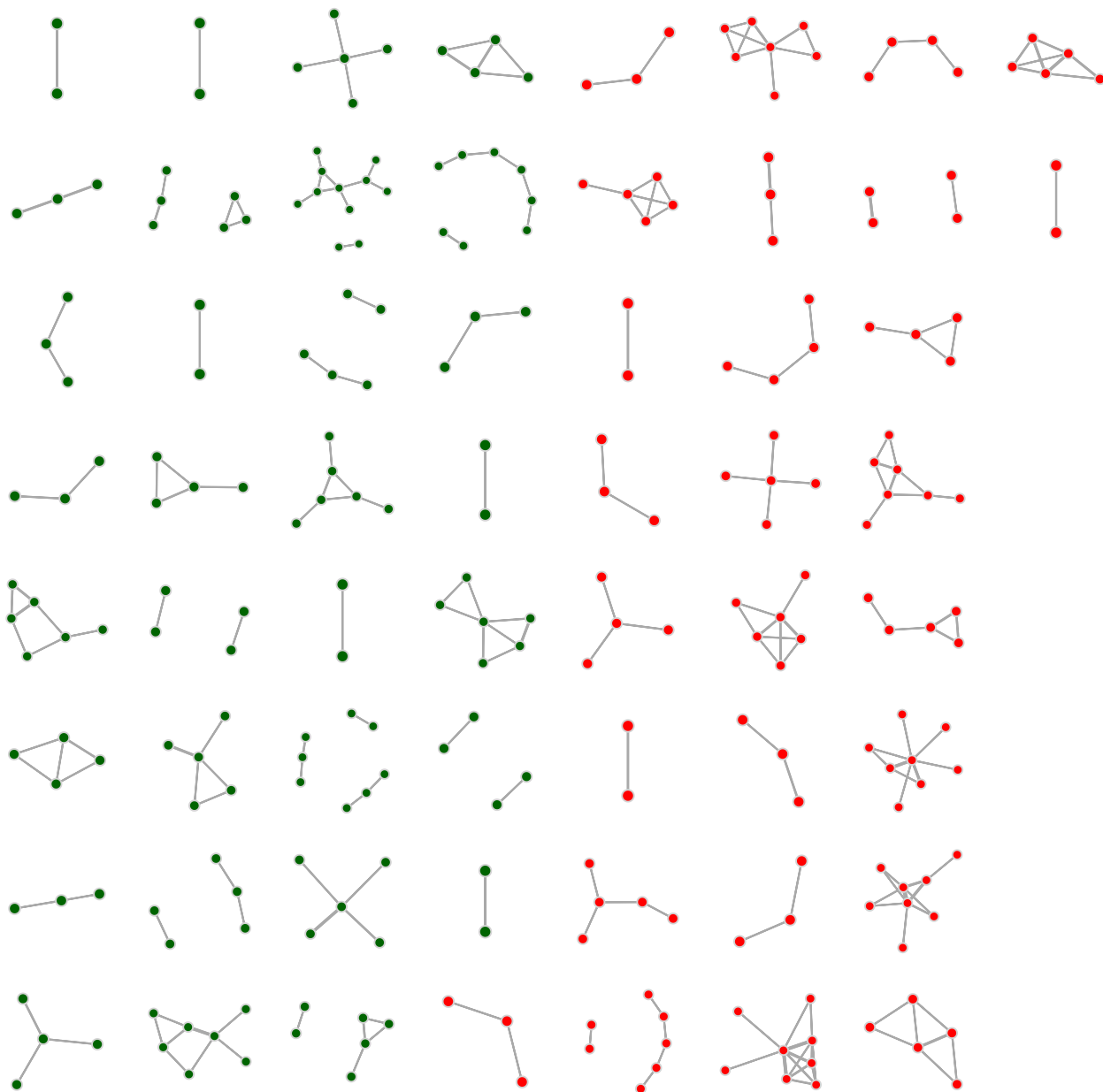
```r
t.test(I(liv.cen-sen.cen))
```

```
##
##  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.

```r
# 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)
```
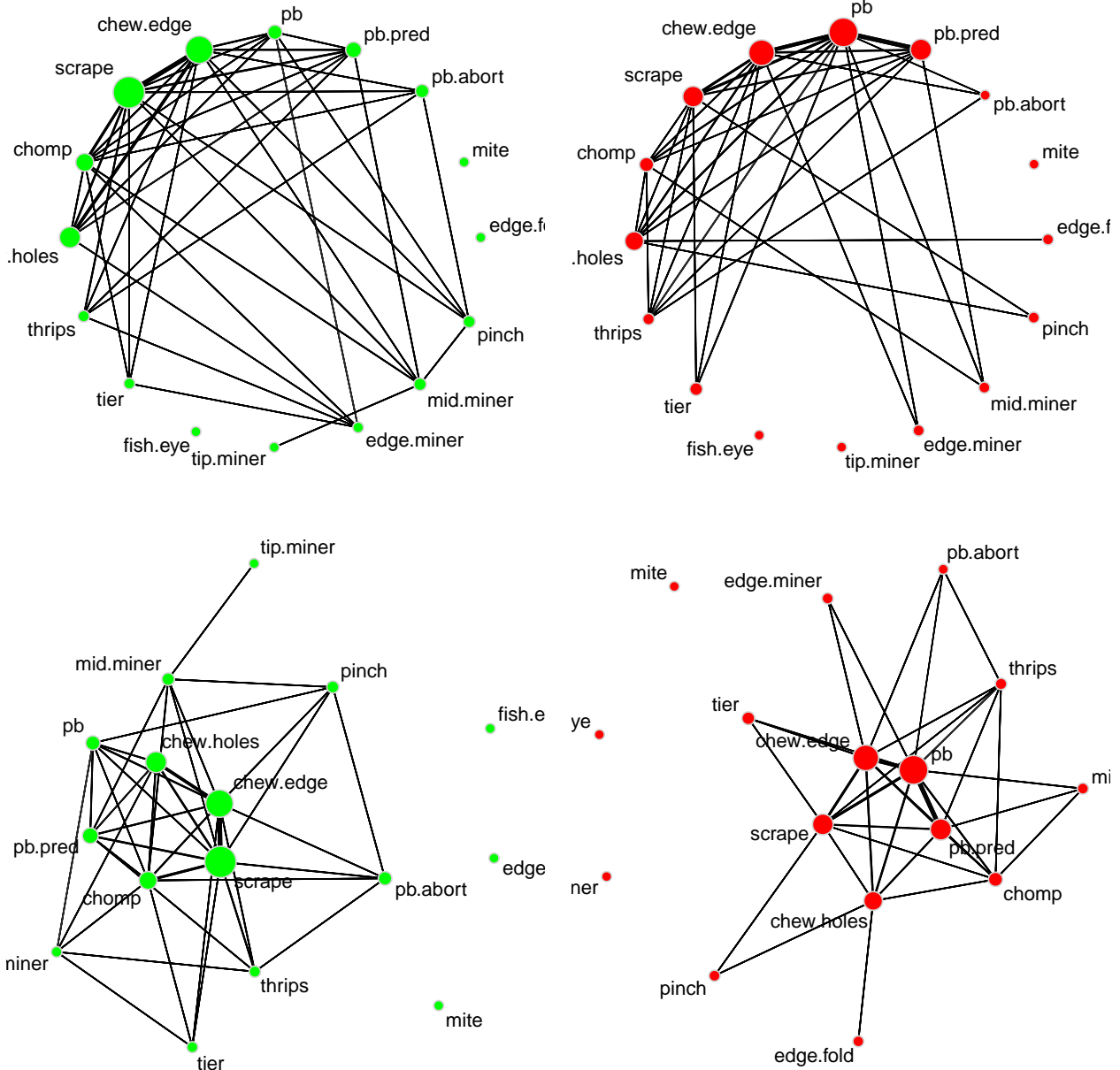
Number of senescing leaves influences the order but not the centrality (eigen) of the networks or the network similarity of senescing leaves.

```
n.lfs <- tree.info$leaves[tree.info$leaf.type == 'sen']
cor.test(n.lfs,I(liv.cen-sen.cen))
```

```
##
##  Pearson's product-moment correlation
##
## data:  n.lfs and I(liv.cen - sen.cen)
## t = -1.5167, df = 34, p-value = 0.1386
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.53594682  0.08372385
## sample estimates:
```

```
##        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  0.178
## 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)))
```
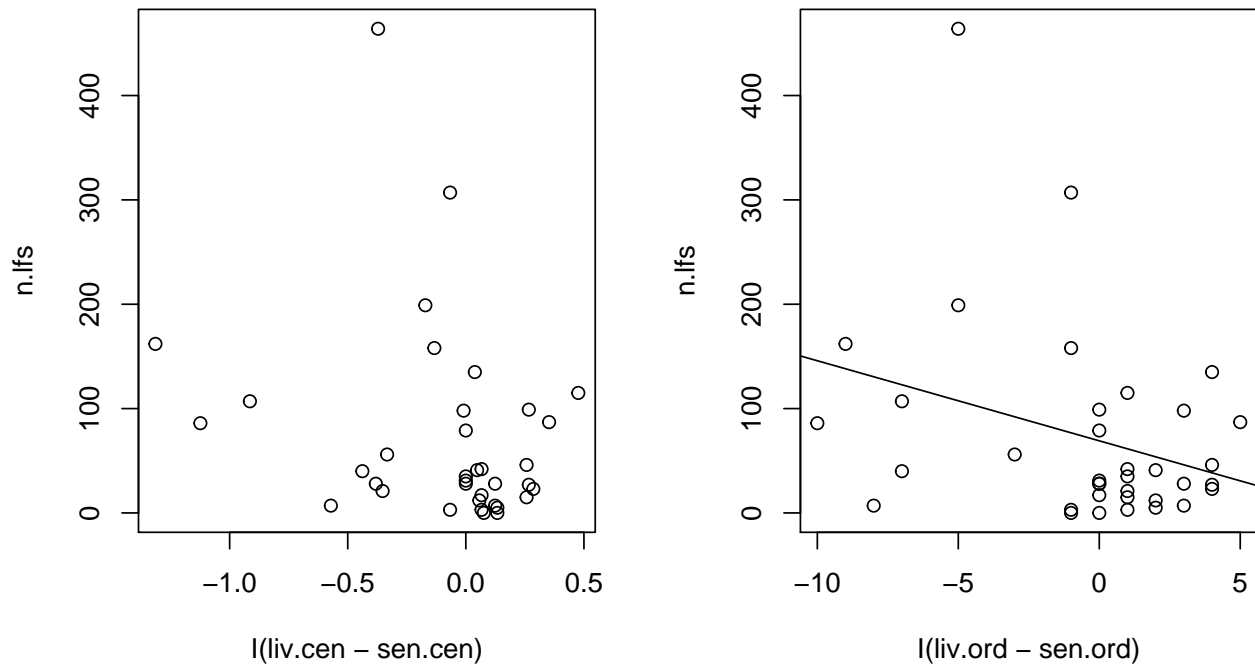
How much variance in network structure does genotype explain?

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.

```r
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  0.004
## factor(leaf.type):factor(geno) 7    116.79  16.684  0.7505 0.07282  0.624
## 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
```

```r
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:  0.1602291
## r^2 for minimum stress configuration:  0.9441925
```

```r
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)))
```
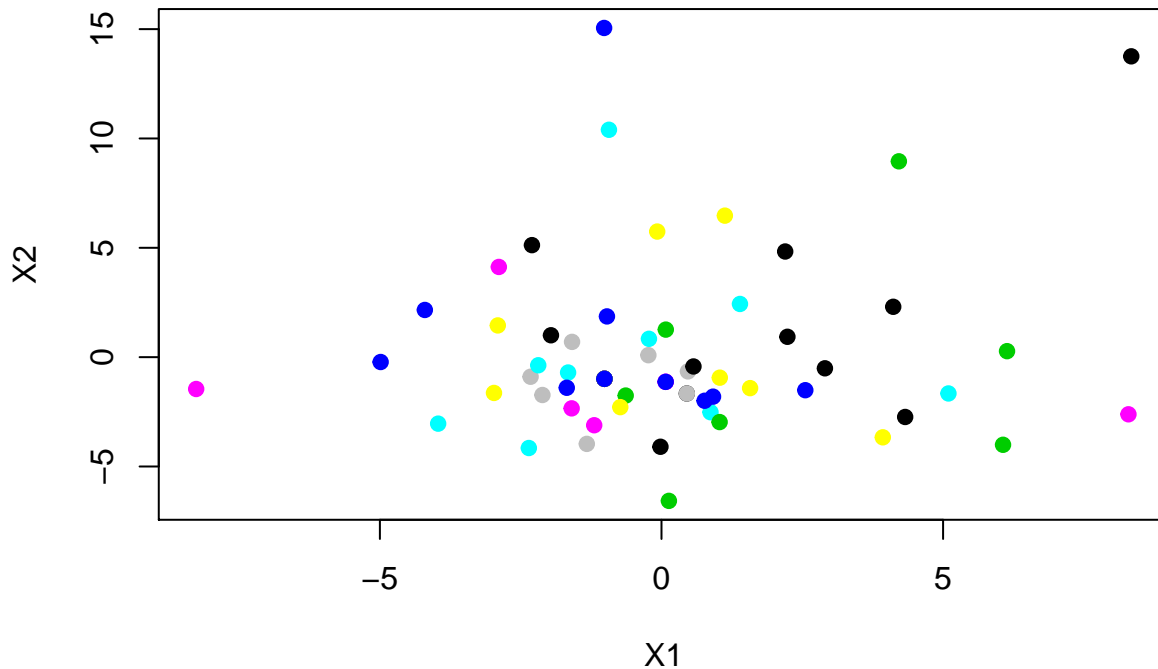


```r
mu <- ch.plot(ord.tree,factor(tree.info$geno))
points(mu,col=as.numeric(factor(unique(tree.info$geno))),pch=19,cex=1.5)
plot(spp.vectors,col='darkgrey')
legend('topright',legend=unique(tree.info$geno),
       col=as.numeric(factor(unique(tree.info$geno))),
       pch=19,bty='d',bg='white',box.col='lightgrey')
```
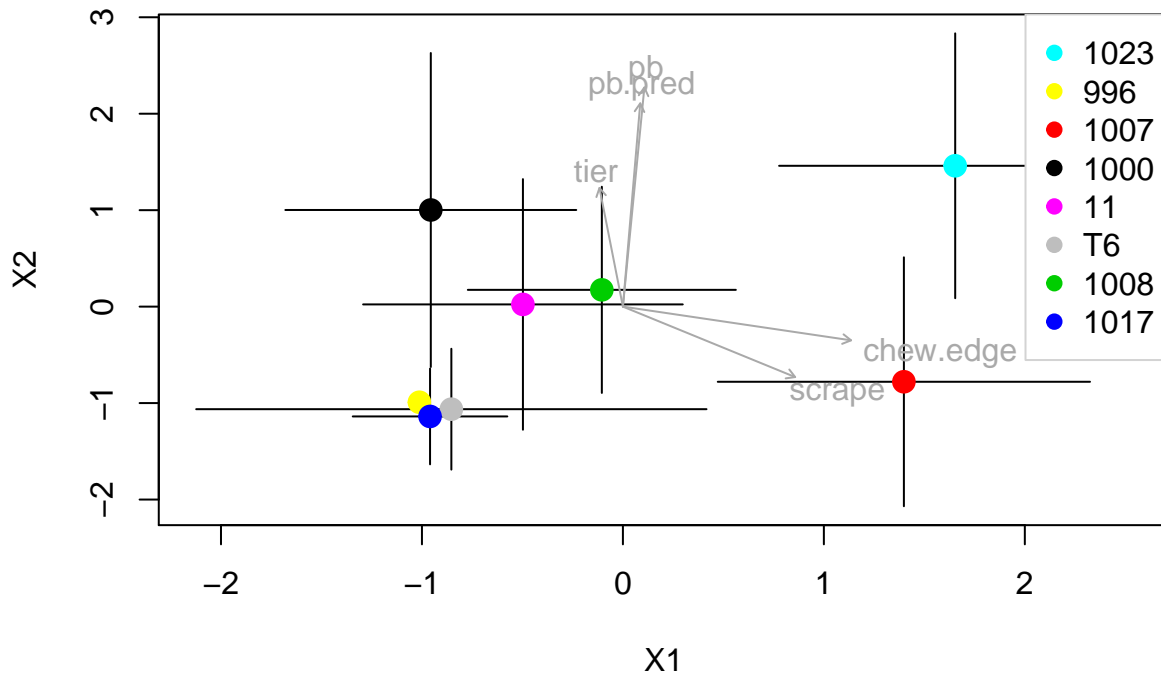
```
library(bipartite)
### centrality
tree.cen <- unlist(lapply(tree.nets,function(x) centralization(x,FUN='degree')))
tree.mod <- dget(file='../data/tree.mod') # see src/treeMods.R

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',]))
```
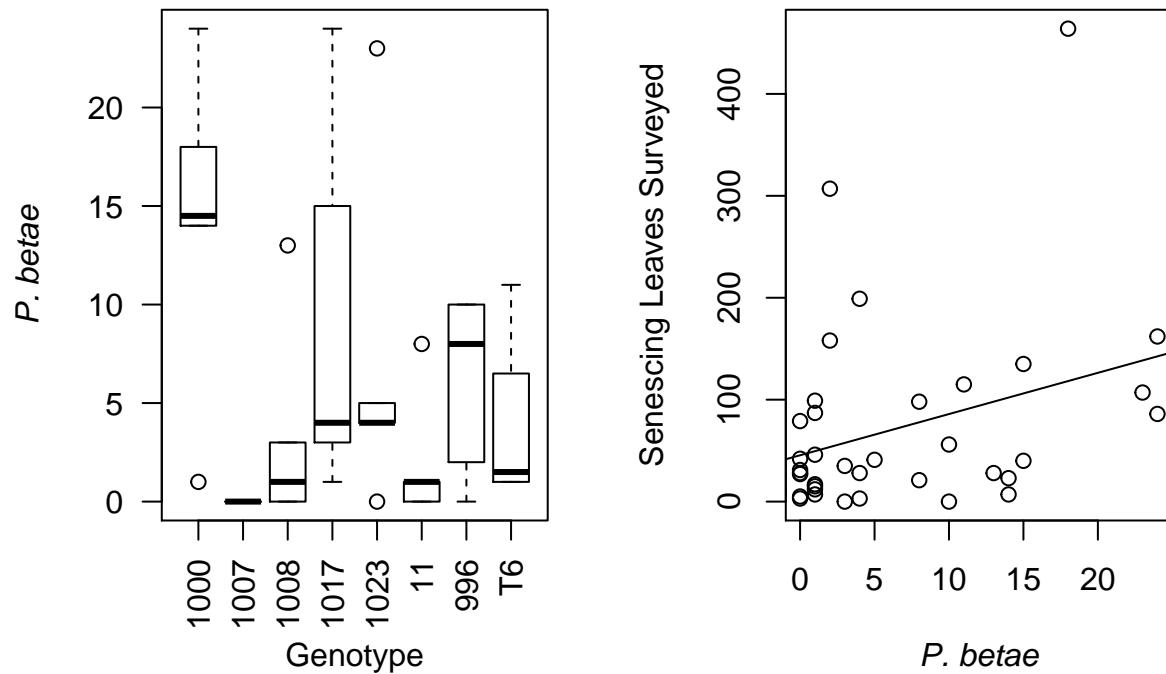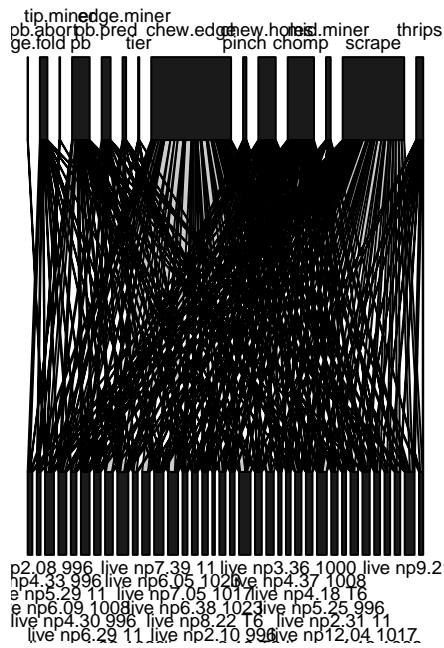
Stand level network modularity

```
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')
```
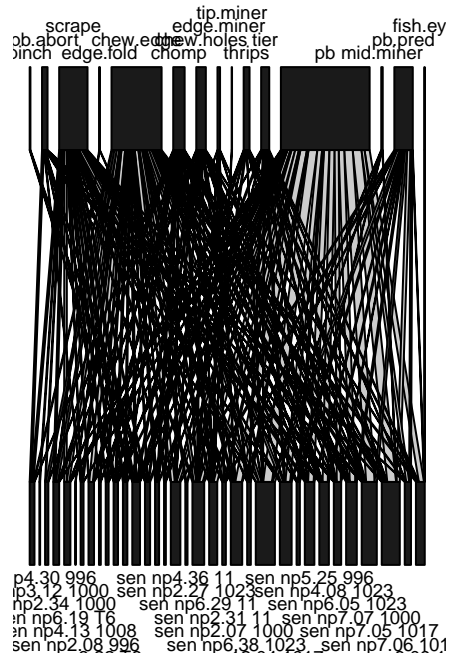
**Live**   **Senescent**

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

```r
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)
```
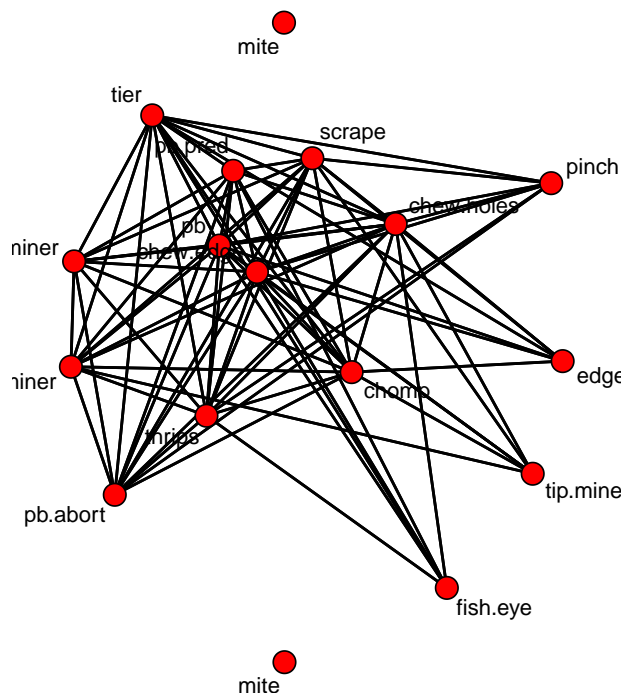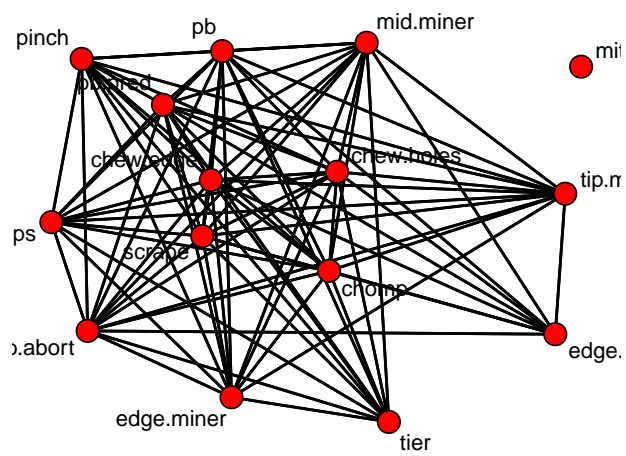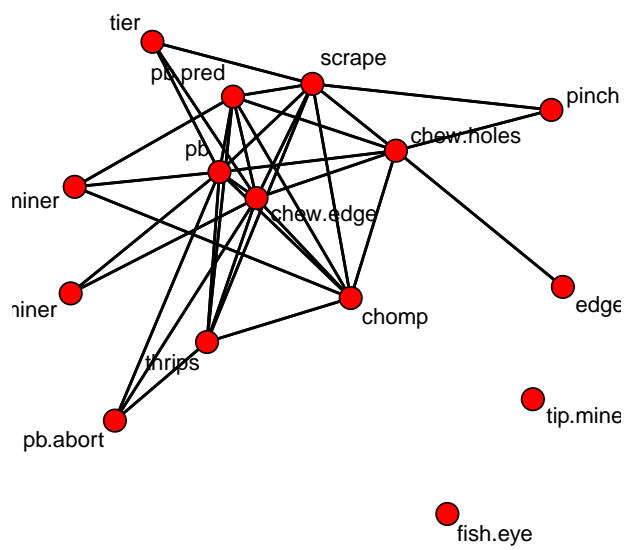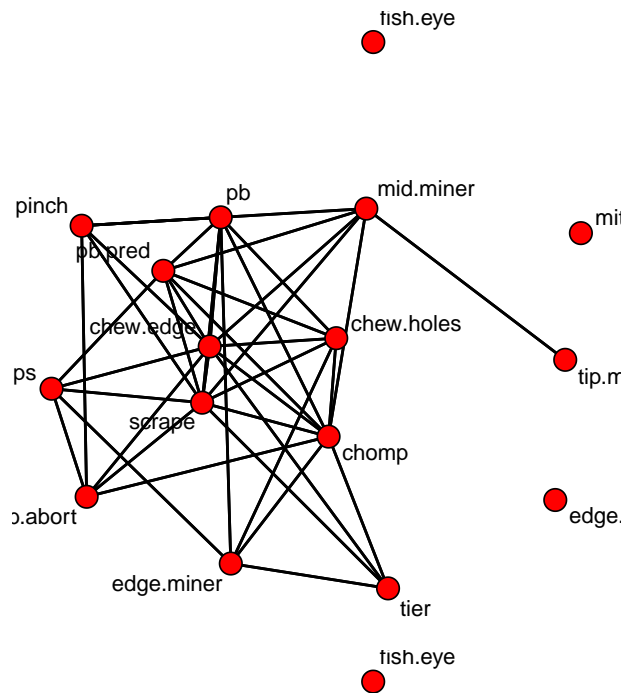
This question isn't very interesting since the effect of genotype doesn't differ between live and senescing leaves.

What does the unipartite projection look like for the trees and genotypes?

```r
```{r error=FALSE,message=FALSE,warning=FALSE, fig.height=5,fig.width=8}
library(RColorBrewer)
liv.b2ut <- liv.bpn %% t(liv.bpn) ## sen.b2ut <- sen.bpn %% t(sen.bpn)
liv.dn <- distNet(tree.nets[tree.info$leaf.type == 'live'],dist.obj=FALSE)
liv.dn <- liv.dn/max(liv.dn)
sen.dn <- distNet(tree.nets[tree.info$leaf.type == 'sen'],dist.obj=FALSE)
sen.dn <- sen.dn/max(sen.dn)
gc.liv <- as.numeric(factor(as.character(do.call(rbind,sapply(rownames(liv.b2ut),strsplit,spli
gc.liv <- brewer.pal(max(gc.liv),name='Set1')
gc.sen <- as.numeric(factor(as.character(do.call(rbind,sapply(rownames(sen.b2ut),strsplit,sp
gc.sen <- brewer.pal(max(gc.sen),name='Set1')
par(mfrow=c(2,2),mai=rep(0.1,4))
gplot(liv.b2ut,gmode='graph',
edge.lwd=(liv.b2ut/max(liv.b2ut)) + 1,vertex.col=gc.liv,
vertex.border='lightgrey',
edge.col='grey')
gplot(sen.b2ut,gmode='graph',
edge.lwd=(sen.b2ut/max(sen.b2ut)) + 1,vertex.col=gc.sen,
vertex.border='lightgrey',
edge.col='grey')
gplot(liv.dn,gmode='graph',
edge.lwd=(liv.dn) + 1,vertex.col=gc.liv,
vertex.border='lightgrey',
edge.col='grey')
```

```r
gplot(sen.dn,gmode='graph',
edge.lwd=(sen.dn) + 1,vertex.col=gc.sen,
```