

Pitcher Networks

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Sped read Ellison et al. 2014 Sys Bot

- Could building syngamen networks using hybridization and trait information tell us about the ecological and evolutionary responses of pitcher plants?
- Genetic responses to climate change?
- Community genetics?

2 28 Mar 2014

Mouquet network mutualism analysis:

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```
library(enaR) table1 <- t(read.csv('../data/mouq;ng_v;alues.txt'))math.values <-  
-data.frame(t(table1))colnames(math.values) <- -sapply(colnames(t(table1)), function(x)unlist(st  
System Biomass',cex=1,font.lab=2,col='grey') plot(log(tot.biomass) tro.ascASC.CAP,pch =  
19,xlab =' Ascendency',ylab =' TotalSystemBiomass(logscale)',cex = 0.75,font.lab =
```

```

2)plot(log(tot.biomass) log(tro.ascASC),pch=19,xlab='Ascendency', ylab='Total Sys-
tem Biomass',cex=1,font.lab=2,col=grey(0.3), xlim=c(3,17)) points(log(inqC.ascASC), log(sum(inqC.
white',breaks = 10,col = grey(0.3),xlim = c(0.2,0.9),ylim = c(0,15),main ="
,xlab =",ylab =" )points(inqC.ascASC.CAP,1,pch=19) arrows((inqC.ascASC.CAP-
0.0095), 3, (inqC.ascASC.CAP-0.0095),1.5,lwd=5,col='red') detach(math.values) fig
4 flow <- matrix(c(0,0,0, 5,0,0, 5,5,0), nrow=3) input <- c(10,0,0) export <- rep(0,nrow(flow))
respiration <- c(0,0,10) storage <- c(10,10,10) living <- c(TRUE,TRUE,TRUE) test1
<- pack(flow=flow, input=input, output=(export+respiration), export=export, res-
piration=respiration, storage=storage, living=living) flow <- matrix(c(0,0,0, 10,0,0,
0,10,0), nrow=3) input <- c(10,0,0) export <- rep(0,nrow(flow)) respiration <- c(0,0,10)
storage <- c(10,10,10) living <- c(TRUE,TRUE,TRUE) test2 <- pack(flow=flow, in-
put=input, output=(export+respiration), export=export, respiration=respiration,
storage=storage, living=living) enaAscendency(test2) - enaAscendency(test1)

```

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