

Pett_Cheddar

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Cheddar

- Provides a flexible, extendable representation of an ecological community or communities
- Range of functions for analysis and visualization
 - Specifically it focuses on food web dynamics, body mass, and numerical abundance data
 - Allows for inter-web comparisons (changes in community structure over environmental, temporal, or spatial gradient)

Cheddar Introduction

```
# load library
library(cheddar)
# load data
data(TL84)
# whats really nice about cheddar is that it has multiple datasets to work with
```

Before actually getting into analyses and plots in cheddar I first wanted to go over cheddars data set framework.

A community data set in cheddars framework has 3 components. Cheddar works best if you import your 3 components from 3 separate CSVs into a directory and then that directory name will be your dataset name.

To illustrate the cheddar data framework we are going to break down Tuesday Lakes data set into the 3 CSVs in its own subdirectory.

Properties

Contains properties applicable to the community.

- Must contain one row of data and title column
- M & N units must be present if they are present in the nodes csv

```
# First we are going to make a directory to hold the csvs
# create community directory
dir.create("TL84")
```

```
## Warning in dir.create("TL84"): 'TL84' already exists
```

```
# create vectors for each field in properties
title = "Tuesday Lake sampled in 1984"
N.units = "m-3"
M.units = "kg"
lat = 46.21667
long = 89.53333
habitat = "Freshwater pelagic"
# making a data frame with vectors
properties<-data.frame(title, N.units, M.units, lat, long, habitat)
properties
```

```
##               title N.units M.units      lat      long
## 1 Tuesday Lake sampled in 1984    m^-3      kg 46.21667 89.53333
##               habitat
## 1 Freshwater pelagic

# write csv #row.names=FALSE the column names wouldnt line up
write.csv(properties, file="TL84/properties.csv", row.names=FALSE)
```

Nodes

Defines species and associated properties

- Contains one row for every species in the community
- Node column is the only mandatory column (component of food web ex. CPOM) + Column node contains node or species names
- + M & N represent Mass & Numerical Abundance

```
# create vectors that were putting into the data frame
node = TL84$nodes$node
# Cheddar has a really nice function to collapse the community by any of these categories
M = TL84$nodes$M
N = TL84$nodes$N
kingdom = TL84$nodes$kingdom
phylum = TL84$nodes$phylum
class = TL84$nodes$class
order = TL84$nodes$order
family = TL84$nodes$family
genus = TL84$nodes$genus
species = TL84$nodes$species
# making a data frame with vectors
nodes<-data.frame(node,
                  M, N, kingdom, phylum, class, order, family, genus, species)
head(nodes)
```

```
##               node      M      N  kingdom  phylum
## 1      Nostoc sp. 7.97e-13 2.0e+06  Bacteria Cyanobacteria
## 2    Arthrodesmus sp. 1.52e-12 4.9e+07  Plantae  Charophyta
## 3 Asterionella formosa 1.12e-12 5.0e+06 Chromista  Ochrophyta
## 4    Cryptomonas sp. 1 2.03e-13 6.4e+07 Chromista  Cryptophyta
## 5    Cryptomonas sp. 2 1.51e-12 2.8e+07 Chromista  Cryptophyta
## 6 Chroococcus dispersus 2.39e-13 2.0e+07  Bacteria Cyanobacteria
##               class      order      family      genus
## 1    Cyanophyceae  Nostocales  Nostocaceae  Nostoc
## 2 Zygnematophyceae  Desmidiiales  Desmidiaceae Arthrodesmus
## 3 Bacillariophyceae  Fragilariales  Fragilariaceae Asterionella
## 4    Cryptophyceae  Cryptomonadales  Cryptomonadaceae  Cryptomonas
## 5    Cryptophyceae  Cryptomonadales  Cryptomonadaceae  Cryptomonas
## 6    Cyanophyceae  Chroococcales  Chroococcaceae  Chroococcus
##      species
## 1
## 2
## 3  formosa
## 4
## 5
```

```
## 6 dispersus
# write csv
write.csv(nodes, file="TL84/nodes.csv", row.names=FALSE)
```

Trophic.Links

Optional file that defines foodweb (trophic links)

- File contains a row for every resource consumer trophic interaction in the community
- Values in resource & consumer should contain node names

```
# create vector for trophic.links.csv
resource = TL84$trophic.links$resource
consumer = TL84$trophic.links$consumer
trophic.links<-data.frame(resource, consumer)
head(trophic.links)

##              resource              consumer
## 1      Cryptomonas sp. 1 Ascomorpha eucadis
## 2    Chroococcus dispersus Ascomorpha eucadis
## 3 Unclassified flagellates Ascomorpha eucadis
## 4          Chromulina sp. Ascomorpha eucadis
## 5    Selenastrum minutum Ascomorpha eucadis
## 6    Trachelomonas sp. Ascomorpha eucadis

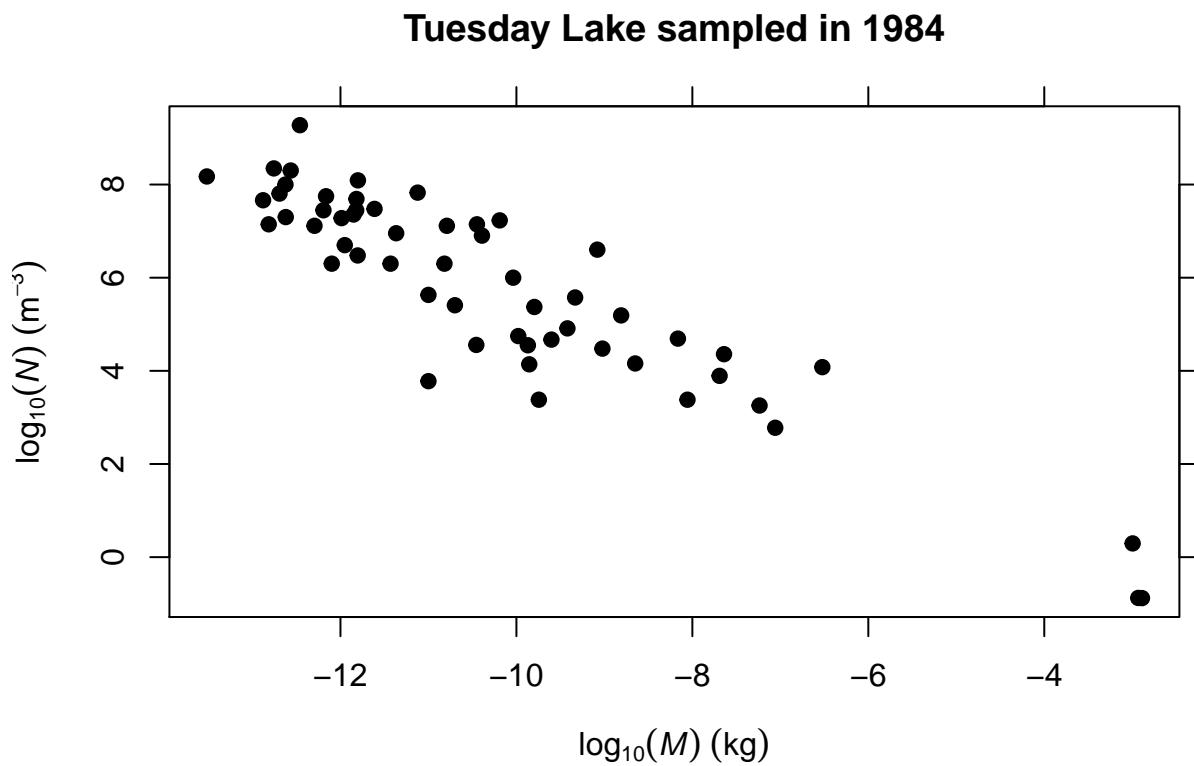
# write csv
write.csv(trophic.links, file="TL84/trophic.links.csv", row.names=FALSE)
# Loading our dataset from the csvs we made
TL84<-LoadCommunity("./TL84", fn='read.csv')
# You can also weight the trophic interaction in this file by adding a new column.
# For example, in the Chesapeakebay dataset there is a biomass.flow column in trophic.links
# load dataset
data(ChesapeakeBay)
# lets take a peak!
head(ChesapeakeBay$trophic.links) ## (biomass.flow=biomass moving from 1 organism to another)

##              resource              consumer
## 1      Free bacteria in water column Heterotrophic microflagellates
## 2              Phytoplankton              Microzooplankton
## 3 Bacteria attached to suspended particles              Microzooplankton
## 4      Heterotrophic microflagellates              Microzooplankton
## 5              Phytoplankton              Zooplankton
## 6 Bacteria attached to suspended particles              Zooplankton
## biomass.flow
## 1      88721.0
## 2      31715.0
## 3       870.9
## 4      31638.0
## 5      37149.0
## 6       1685.4
```

Abundance vs Mass (Network Connection Overlay) Plot

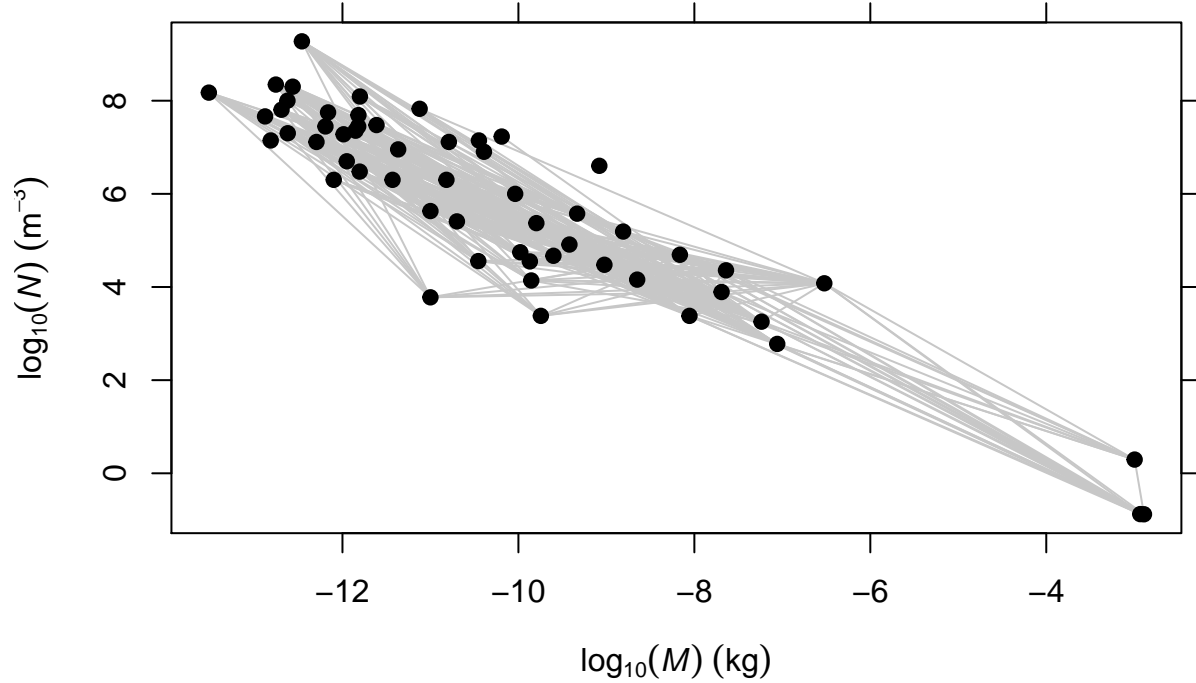
```
# Plot 1 species
```

```
PlotNmM(TL84, col=1, pch=19, highlight.nodes=NULL, show.web=FALSE) # can easily do without cheddar
```



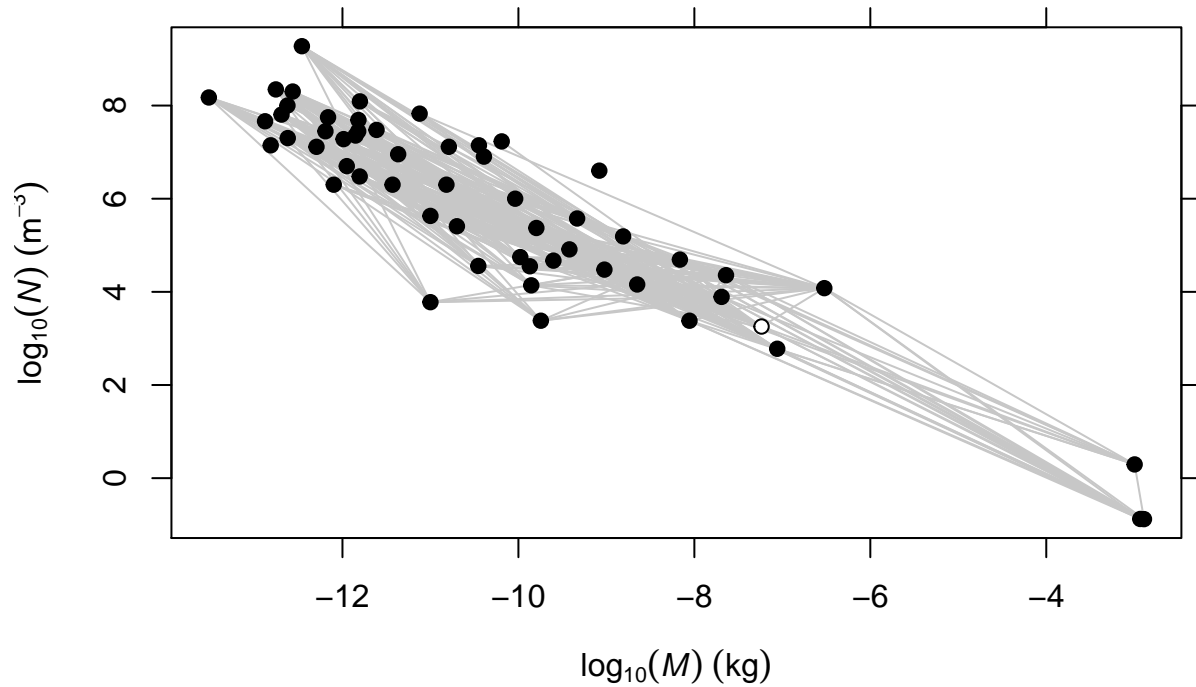
```
PlotNmM(TL84, col=1, pch=19, highlight.nodes=NULL, show.web=TRUE)
```

Tuesday Lake sampled in 1984



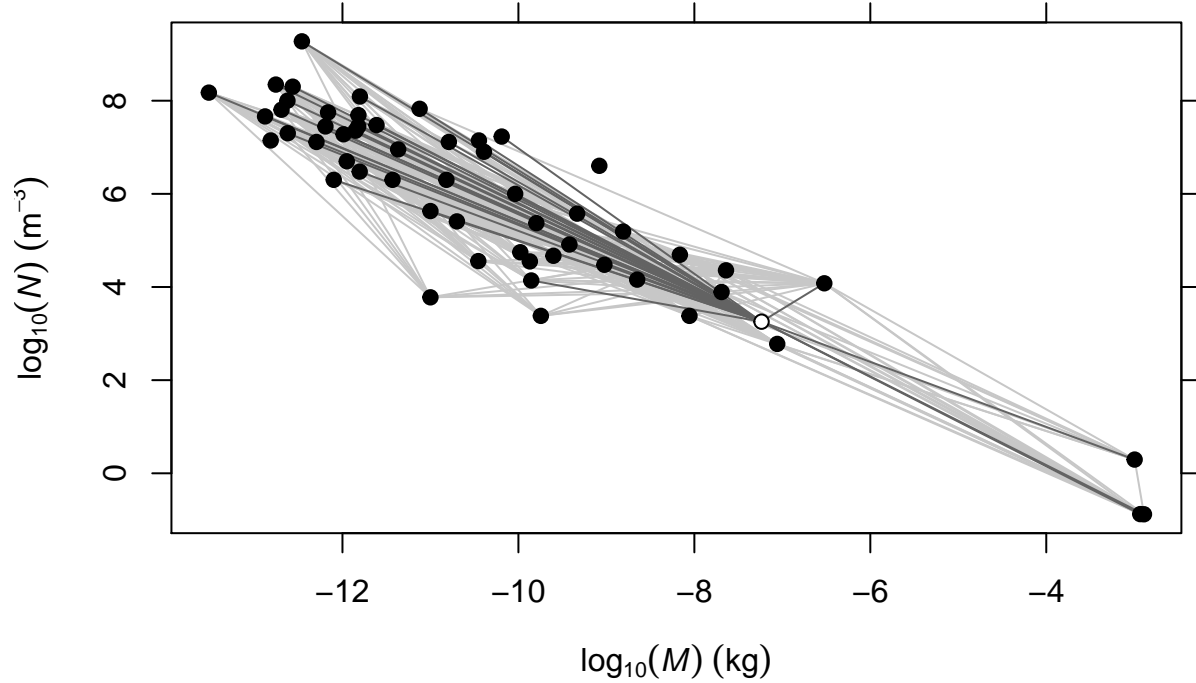
```
PlotNmM(TL84, col=1, pch=19, highlight.nodes='Daphnia pulex') # highlight an individual
```

Tuesday Lake sampled in 1984



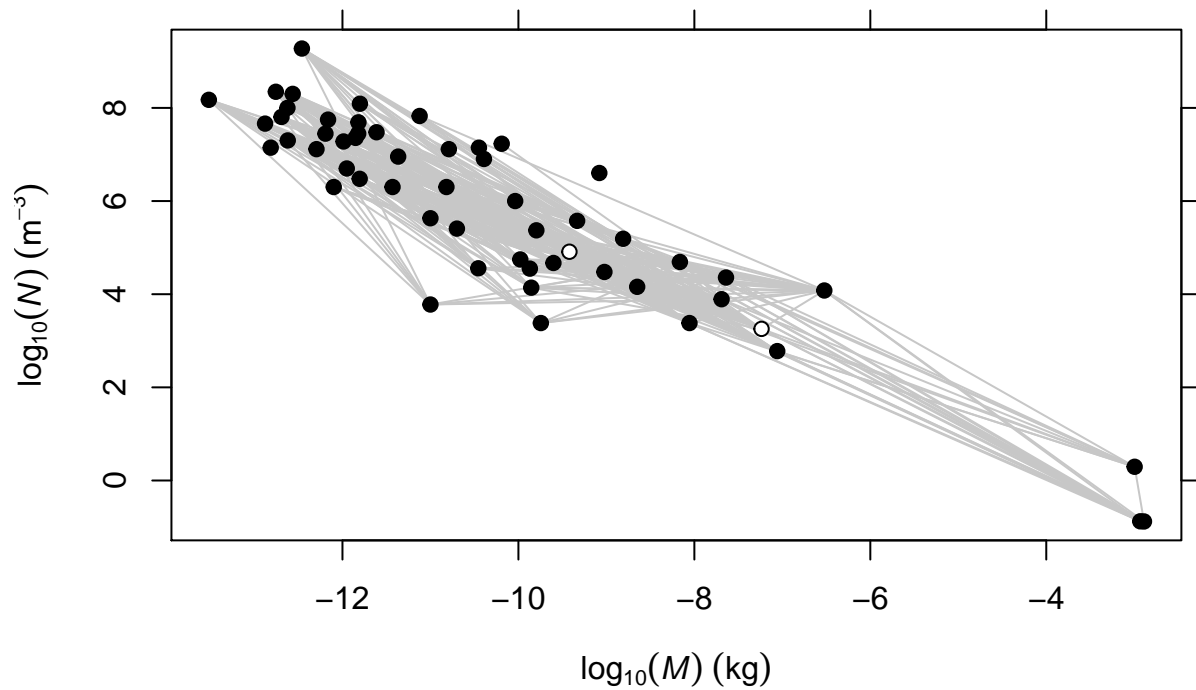
```
PlotNmM(TL84, col=1, pch=19, highlight.nodes='Daphnia pulex',  
highlight.links=TrophicLinksForNodes(TL84, 'Daphnia pulex')) # highlight an individual & links
```

Tuesday Lake sampled in 1984



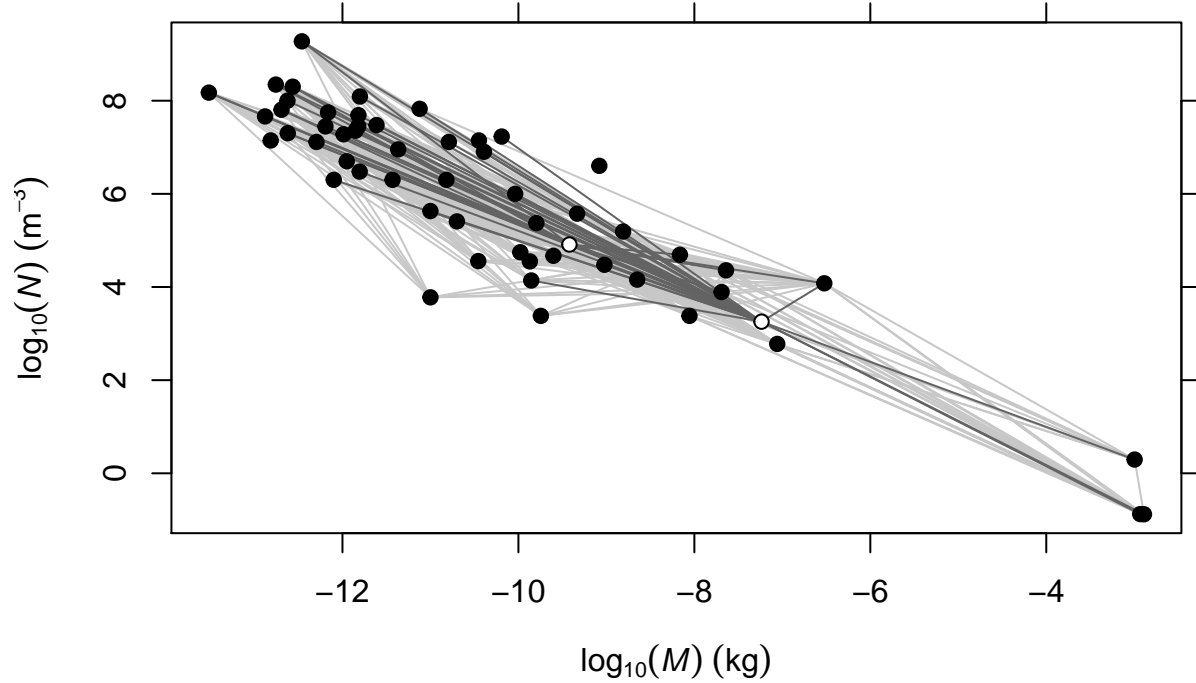
```
# Plot 2 species
PlotNvM(TL84, col=1, pch=19, highlight.nodes=c('Daphnia pulex','Trichocerca cylindrica'))
```

Tuesday Lake sampled in 1984



```
PlotNvM(TL84, col=1, pch=19, highlight.nodes=c('Daphnia pulex','Trichocerca cylindrica'),
  highlight.links=TrophicLinksForNodes(TL84, c('Daphnia pulex','Trichocerca cylindrica')))
```

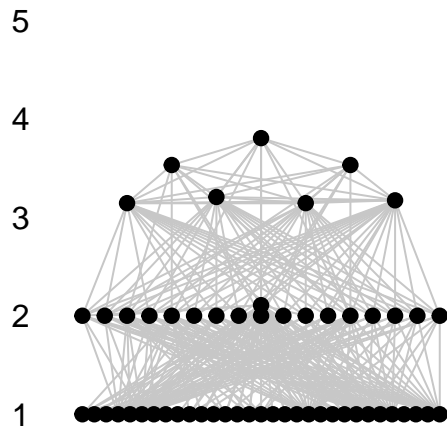
Tuesday Lake sampled in 1984



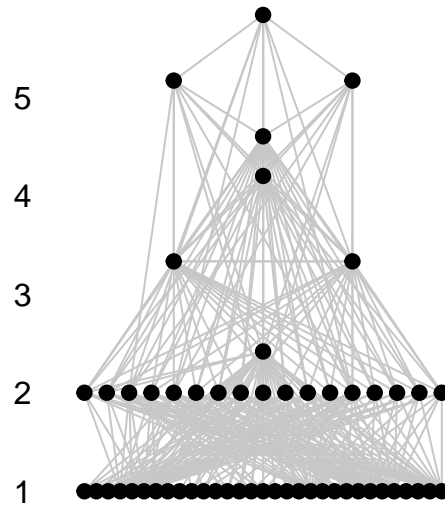
Food-Web By Level Plot

```
# Compare prey-averaged and chain-averaged trophic level
# 2 methodologies to rank trophic levels
# help('PreyAveragedTrophicLevel')
# ylim keeping at default fixed and comparable
par(mfrow=c(1,2)) # setting up 2 plots
PlotWebByLevel(TL84, ylim=c(1,5.8),level='PreyAveragedTrophicLevel', main='Prey-averaged',col=1, pch=19)
PlotWebByLevel(TL84, ylim=c(1,5.8),level='ChainAveragedTrophicLevel', main='Chain-averaged',col=1, pch=19)
```

Prey-averaged



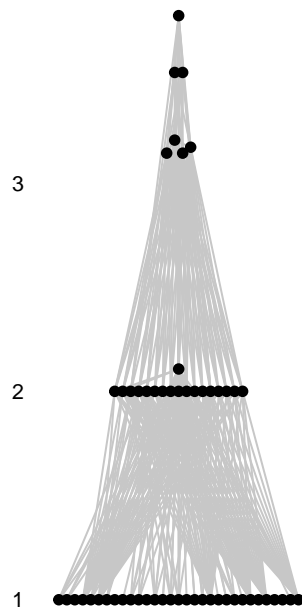
Chain-averaged



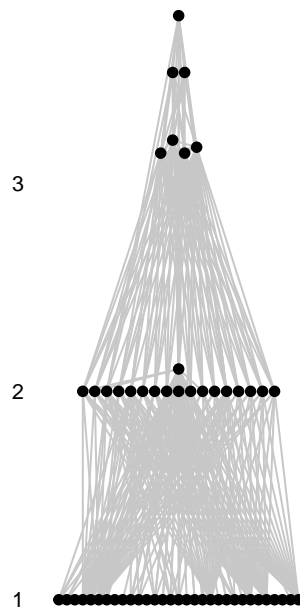
Compare the three different x layouts

```
par(mfrow=c(1,3))
for(x.layout in c('skinny', 'narrow', 'wide'))
{
  PlotWebByLevel(TL84, x.layout=x.layout, main=x.layout, col=1, pch=19, highlight.nodes=NULL)
}
```

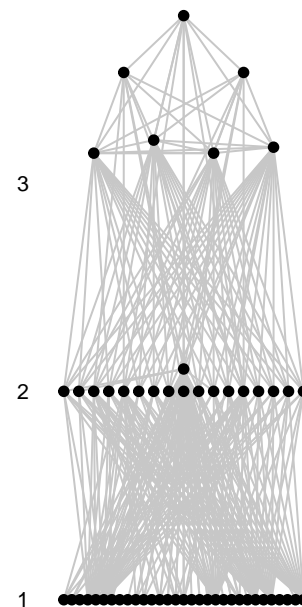
skinny



narrow



wide



Compare the effect of staggering levels

Primary producers are staggered in the second plot

```
par(mfrow=c(1,2))
```

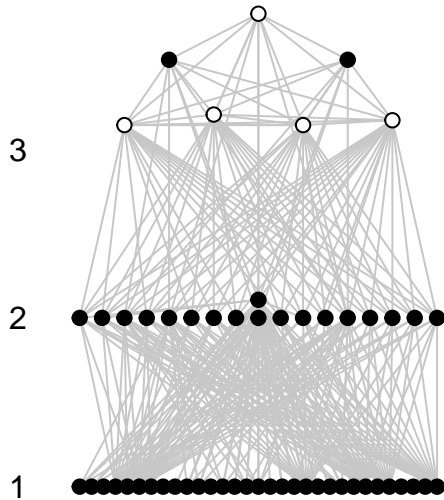
No staggering - stagger and max.nodes.per.row are ignored

```
PlotWebByLevel(TL84, y.layout='compress', col=1, pch=19)
```

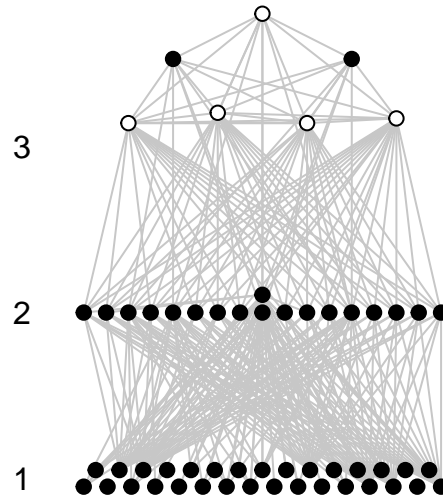
Stagger


```
PlotWebByLevel(TL84, y.layout='stagger', stagger=0.1,col=1, pch=19,
               max.nodes.per.row=20)
```

Tuesday Lake sampled in 1984



Tuesday Lake sampled in 1984

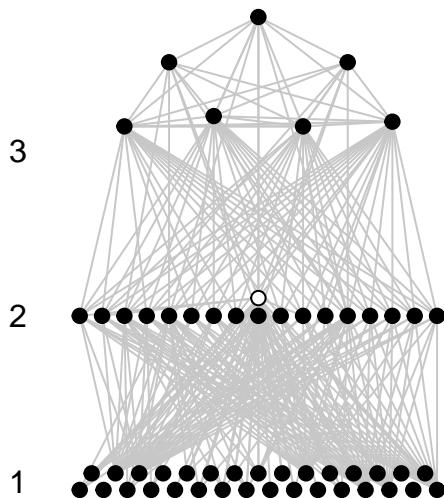


```
# Highlight pulex
```

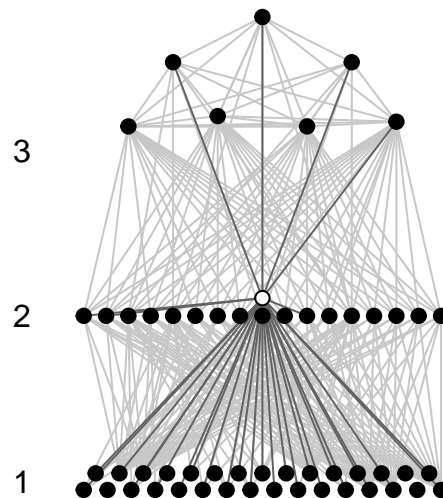
```
PlotWebByLevel(TL84, y.layout='stagger', stagger=0.1,col=1, pch=19,highlight.nodes='Daphnia pulex',
               max.nodes.per.row=20) # just node
```

```
PlotWebByLevel(TL84, y.layout='stagger', stagger=0.1,col=1, pch=19, highlight.nodes='Daphnia pulex', hi
```

Tuesday Lake sampled in 1984



Tuesday Lake sampled in 1984

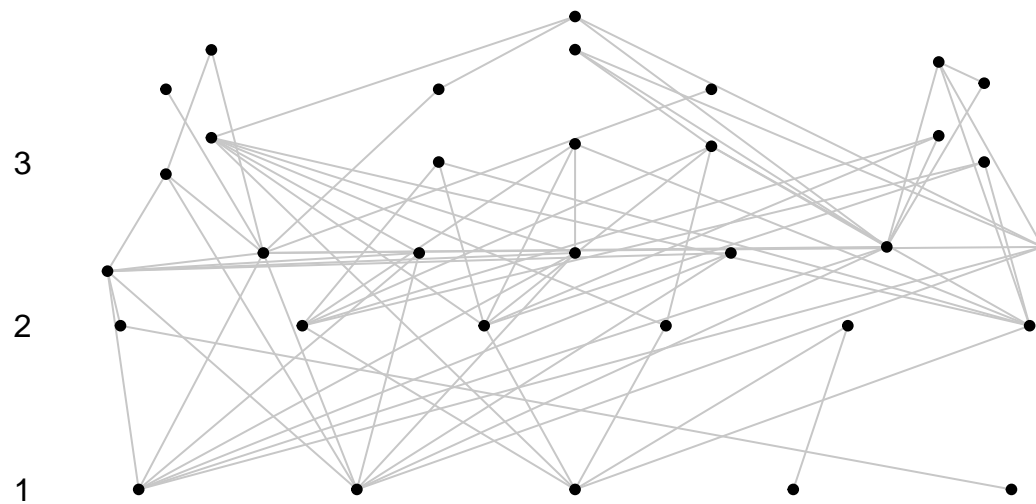


Chesapeake Bay Data, Symbolizing Nodes & Lengths

```
# ChesapeakeBay Data
# citation
data(ChesapeakeBay)
# plot basic food web
```

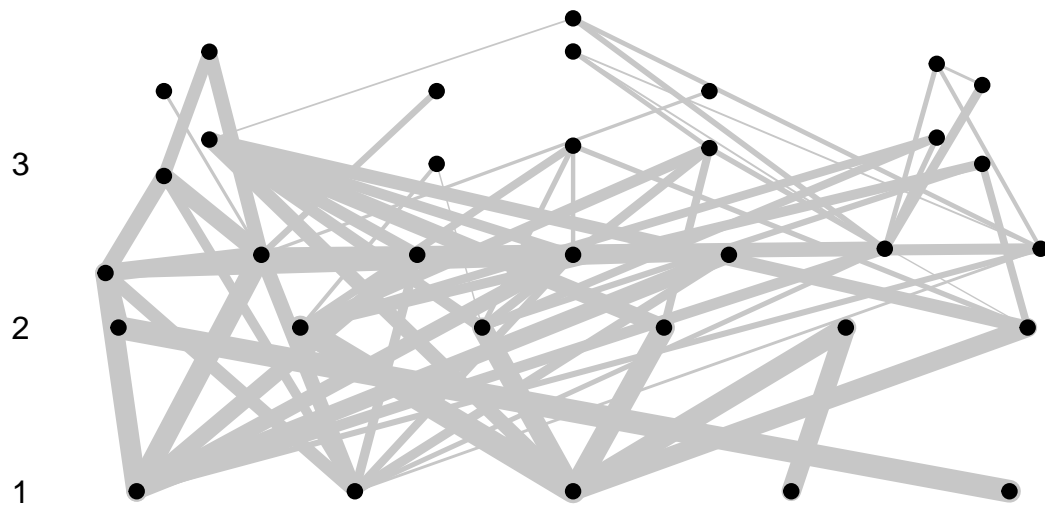
```
PlotWebByLevel(ChesapeakeBay,
               col=1,
               pch=20,
               highlight.nodes=NULL)
```

Chesapeake Bay



```
# develop link line widths based on biomass flow
# log transform for graphical representation
link.lwd=log(ChesapeakeBay$trophic.links$biomass.flow)
# plot food web with link weights
PlotWebByLevel(ChesapeakeBay,
               col=1,
               pch=19,
               highlight.nodes=NULL,
               link.lwd=link.lwd,
               main="Chesapeake Bay Weighted by Flow"
               )
```

Chesapeake Bay Weighted by Flow

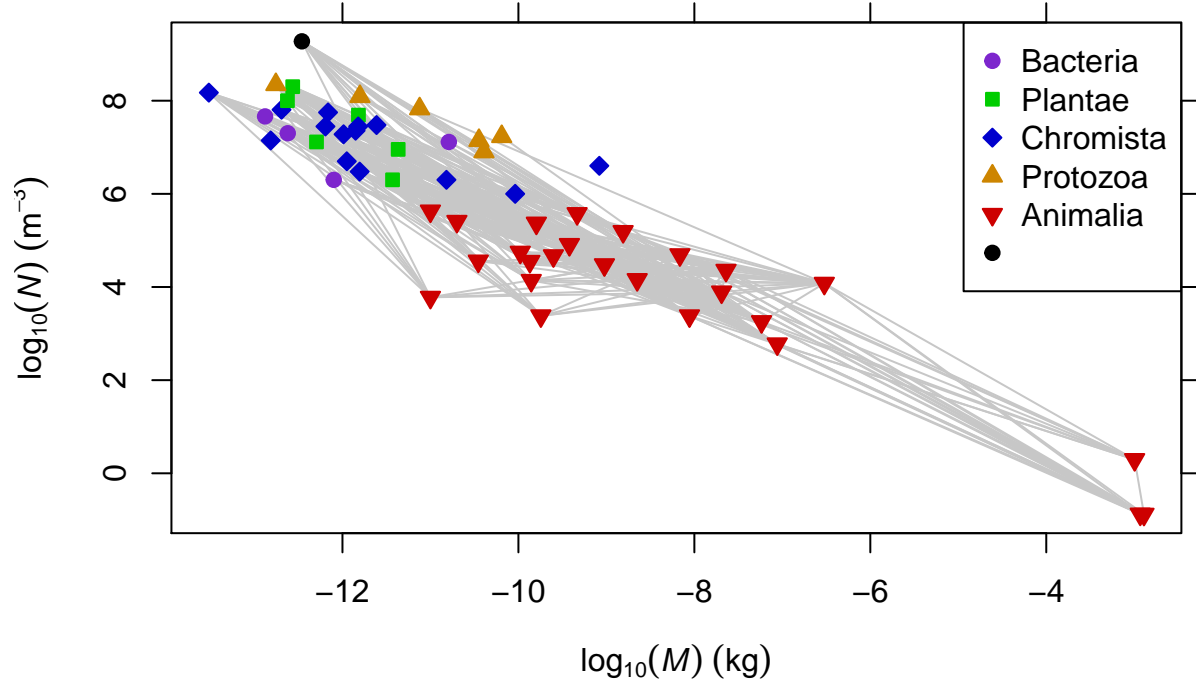


Kingdom Level Regression

```
# custom symbols for each kingdom
symbol.spec = c(Bacteria=21, Plantae=22, Chromista=23,
                 Protozoa=24, Animalia=25, 19)
symbol.spec

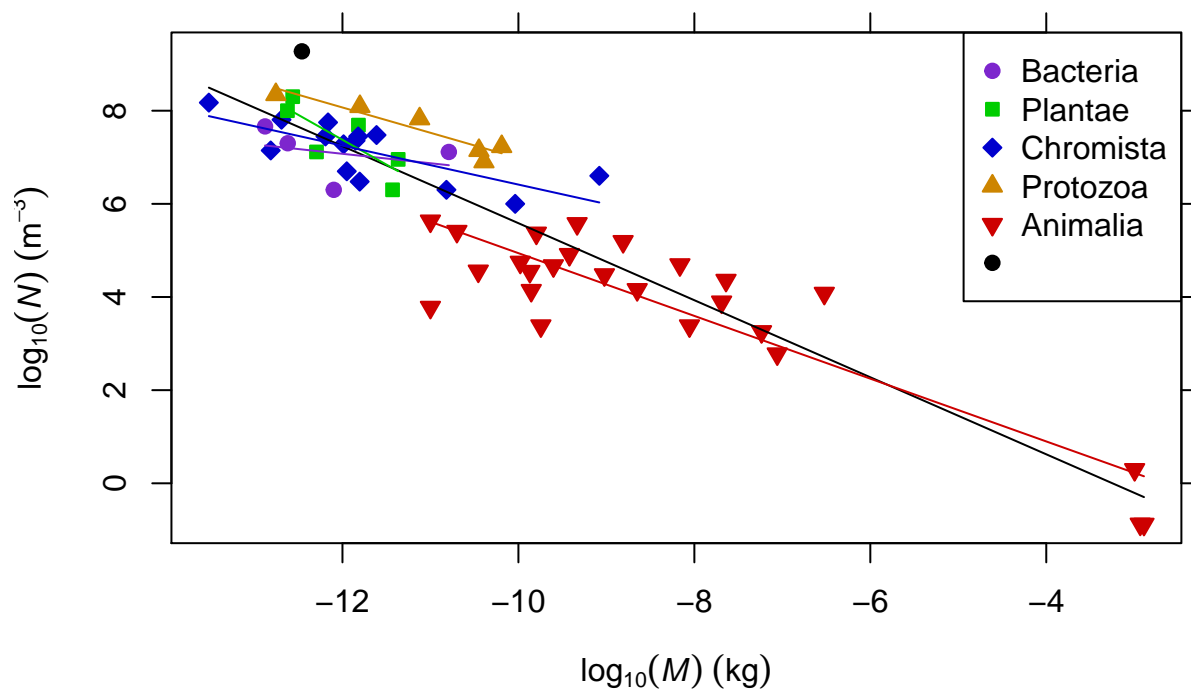
## Bacteria Plantae Chromista Protozoa Animalia
##      21      22      23      24      25      19
colour.spec = c(Bacteria='purple3', Plantae='green3', Chromista='blue3', Protozoa='orange3',
                 Animalia='red3', 'black')
# run plot and legend at same time
PlotNm(TL84,
symbol.by='kingdom', symbol.spec=symbol.spec, bg.by='kingdom', bg.spec=colour.spec, colour.by='kingdom',
legend("topright", legend=names(colour.spec), pch=symbol.spec,
      col=colour.spec, pt.bg=colour.spec)
```

Tuesday Lake sampled in 1984



```
# Run all at once (different regression lines for density and biomass for diff kingdoms)
PlotNm(TL84,
symbol.by='kingdom', symbol.spec=symbol.spec, bg.by='kingdom', bg.spec=colour.spec, colour.by='kingdom',
legend("topright", legend=names(colour.spec), pch=symbol.spec,
col=colour.spec, pt.bg=colour.spec)
models <- NvMLLinearRegressions(TL84, class='kingdom')
colours <- PlotLinearModels(models, colour.spec=colour.spec)
```

Tuesday Lake sampled in 1984



Lumping Communities

```
# Lumping community by order
# Create vector designating lumpage
lump <- NP(TL84, 'order') # NP extracts node/species property
head(lump, 20)
```

```
##          Nostoc sp.          Arthrodesmus sp.
##          "Nostocales"        "Desmidiiales"
##    Asterionella formosa      Cryptomonas sp. 1
##          "Fragilariales"      "Cryptomonadales"
##    Cryptomonas sp. 2        Chroococcus dispersus
##          "Cryptomonadales"      "Chroococcales"
##    Closteriopsis longissimus  Chrysosphaerella longispina
##          "Chlorellales"        "Chromulinales"
##    Dinobryon bavaricum      Dinobryon cylindricum
##          "Chromulinales"      "Chromulinales"
##    Dactylococcopsis fascicularis  Diceras sp.
##          "Chroococcales"      "Hibberdiales"
##    Dictyosphaerium pulchellum  Dinobryon sertularia
##          "Chlorellales"        "Chromulinales"
##    Dinobryon sociale        Glenodinium quadridens
##          "Chromulinales"      "Peridiniales"
##    Microcystis aeruginosa      Mallomonas sp. 1
##          "Chroococcales"      "Synurales"
##    Mallomonas sp. 2          Unclassified flagellates
##          "Synurales"          ""
```

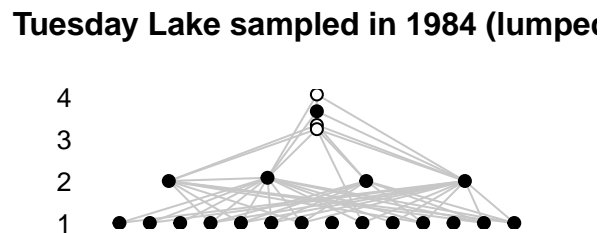
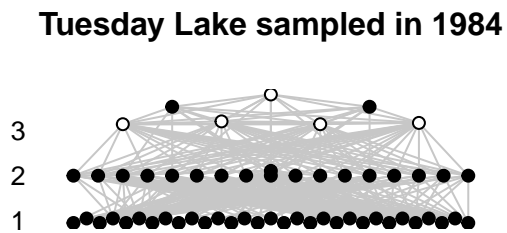
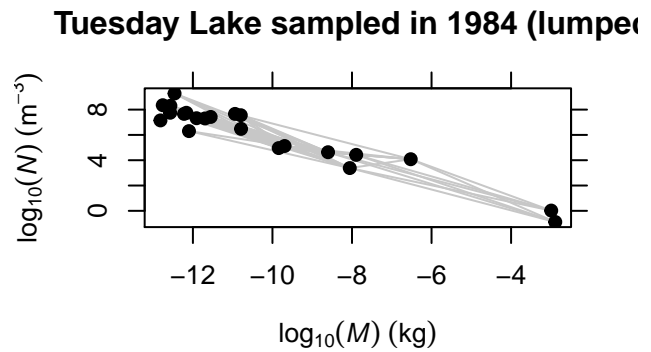
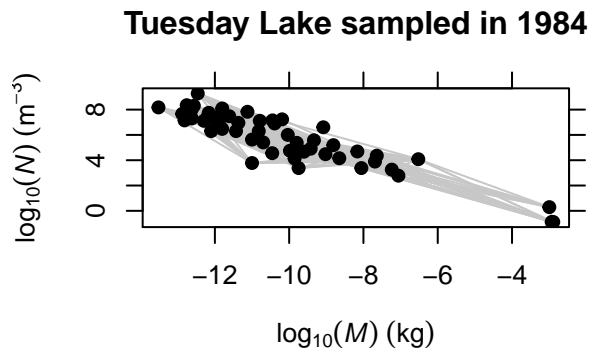
```
# rename parts of vector with "" for order name.
lump[""==lump] <- names(lump[""==lump] )
head(lump, 20)
```

```
##           Nostoc sp.           Arthrodesmus sp.
##           "Nostocales"         "Desmidiiales"
## Asterionella formosa          Cryptomonas sp. 1
##           "Fragilariales"      "Cryptomonadales"
##           Cryptomonas sp. 2     Chroococcus dispersus
##           "Cryptomonadales"     "Chroococcales"
## Closteriopsis longissimus      Chrysosphaerella longispina
##           "Chlorellales"        "Chromulinales"
##           Dinobryon bavaricum   Dinobryon cylindricum
##           "Chromulinales"       "Chromulinales"
## Dactylococcopsis fascicularis  Diceras sp.
##           "Chroococcales"       "Hibberdiales"
## Dictyosphaerium pulchellum     Dinobryon sertularia
##           "Chlorellales"        "Chromulinales"
##           Dinobryon sociale      Glenodinium quadridens
##           "Chromulinales"       "Peridiniales"
## Microcystis aeruginosa         Mallomonas sp. 1
##           "Chroococcales"       "Synurales"
##           Mallomonas sp. 2       Unclassified flagellates
##           "Synurales"           "Unclassified flagellates"
```

```
#create lumped community dataset
TL84.lumped <- LumpNodes(TL84, lump)
TL84.lumped
```

```
## Tuesday Lake sampled in 1984 (lumped) containing 22 nodes and 58 trophic links
```

```
# were gonna make 4 plots to NvM 1 not lumped and 1 lumped
par(mfrow=c(2,2))
PlotNvM(TL84, col=1, pch=19, highlight.nodes=NULL)
PlotNvM(TL84.lumped, col=1, pch=19, highlight.nodes=NULL)
PlotWebByLevel(TL84, y.layout='stagger', stagger=0.1,col=1, pch=19,
max.nodes.per.row=20)
PlotWebByLevel(TL84.lumped, y.layout='stagger', stagger=0.1,col=1, pch=19,
max.nodes.per.row=20)
```



Working With Multiple Communities At ONCE

```
# load dataset
data("pHWebs")
pHWebs
```

```
## A collection of 10 communities
```

```
# example communities (2/10)
pHWebs$`Old Lodge`
```

```
## Old Lodge containing 23 nodes and 137 trophic links
```

```
pHWebs$`Afon Hafren`
```

```
## Afon Hafren containing 25 nodes and 135 trophic links
```

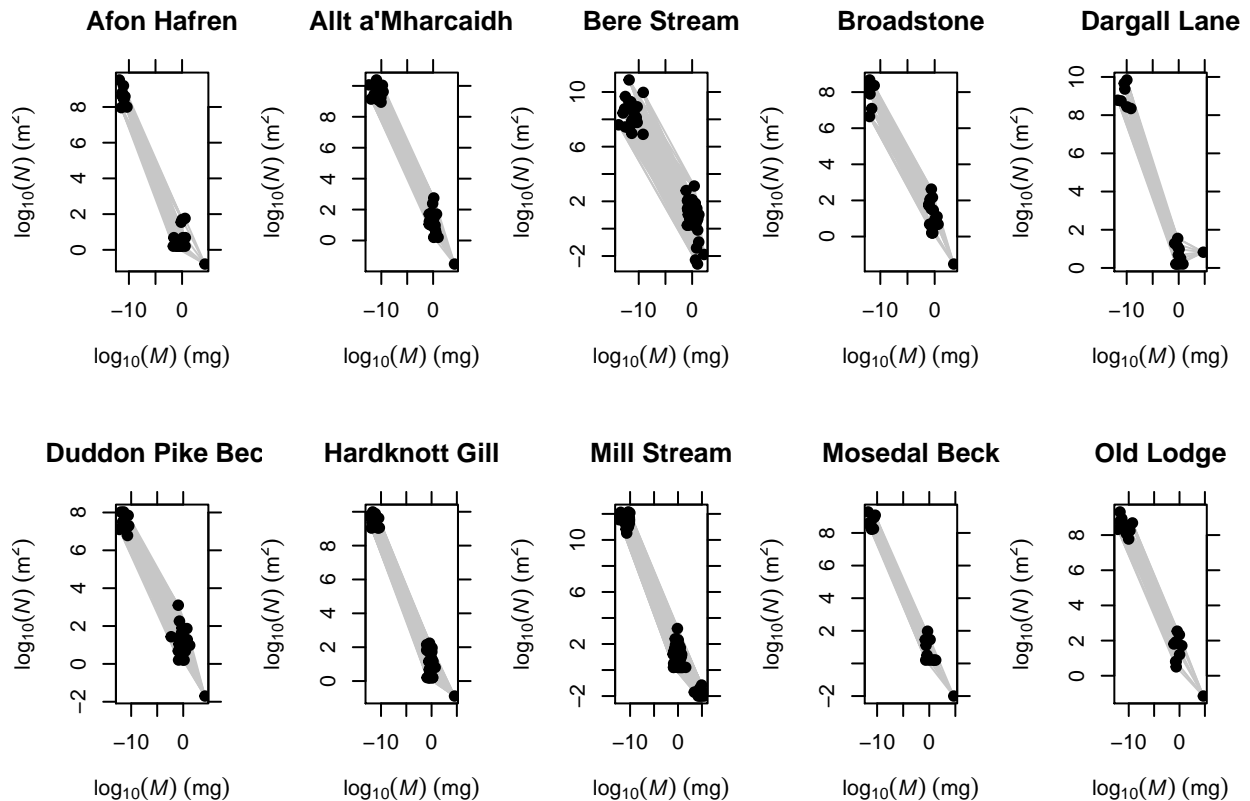
```
pHWebs$`Afon Hafren`$properties
```

```
## $title
## [1] "Afon Hafren"
##
## $M.units
## [1] "mg"
##
## $N.units
## [1] "m^2"
##
## $code
## [1] "HAF"
##
## $pH
## [1] 5.3
##
```

```
## $lat
## [1] 52.47
##
## $long
## [1] -3.7
```

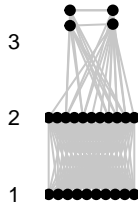
```
# Export pHWebs to a directory
SaveCollection(pHWebs, "./comm")
# Import pHWebs from a directory
pHWebs<-LoadCollection("./comm")

# Biomass by Abundance for multiple communities
plot(pHWebs, col=1, pch=19, highlight.nodes=NULL)
```

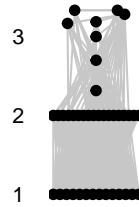


```
# Food Webs for multiple communities
plot(pHWebs, plot.fn=PlotWebByLevel, col=1, pch=19, highlight.nodes=NULL)
```

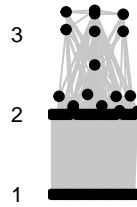

Afon Hafren



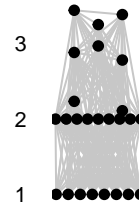
Allt a'Mharcaidh



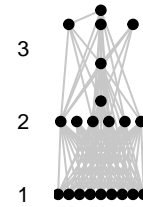
Bere Stream



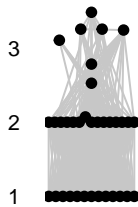
Broadstone



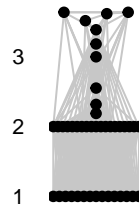
Dargall Lane



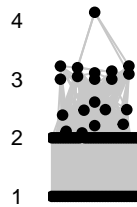
Duddon Pike Bec



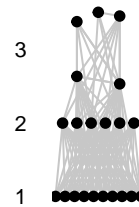
Hardknott Gill



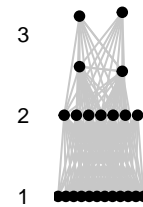
Mill Stream



Mosedal Beck



Old Lodge



Returns a data.frame of first-class and computed properties of communities (Master data frame)
CollectionCPS(pHWebs)

```
##               title M.units N.units code pH  lat  long
## Afon Hafren      Afon Hafren      mg    m^2  HAF 5.3 52.47 -3.700
## Allt a'Mharcaidh Allt a'Mharcaidh  mg    m^2  MHA 6.5 57.12 -3.850
## Bere Stream      Bere Stream      mg    m^2  BER 7.5 50.73 -2.210
## Broadstone       Broadstone       mg    m^2  BRO 5.5 51.08  0.053
## Dargall Lane     Dargall Lane      mg    m^2  DAR 5.8 55.08 -4.430
## Duddon Pike Beck Duddon Pike Beck  mg    m^2  DUD1 6.1 54.41 -3.170
## Hardknott Gill   Hardknott Gill    mg    m^2  DUD2 7.0 54.40 -3.170
## Mill Stream      Mill Stream      mg    m^2  MIL 8.4 50.68 -2.180
## Mosedal Beck     Mosedal Beck     mg    m^2  DUD3 5.9 54.41 -3.140
## Old Lodge        Old Lodge        mg    m^2  OLD 5.0 51.04  0.080
```

community characteristics

```
pH.char<-CollectionCPS(pHWebs, c('pH',                                #Community Property##i.e.: pHWebs$`Old Lodge`$
                                'NumberOfNodes',                      #cheddar function ##i.e.: NumberOfNodes(pHWeb
                                'NumberOfTrophicLinks',                #cheddar function ##...
                                'DirectedConnectance',                 #cheddar function ##...
                                'NvMSlope'))                          #cheddar function ##...
```

head(pH.char)

```
##               pH NumberOfNodes NumberOfTrophicLinks
## Afon Hafren      5.3              25              135
## Allt a'Mharcaidh 6.5              40              334
## Bere Stream      7.5              66              943
## Broadstone       5.5              25              178
## Dargall Lane     5.8              21               99
## Duddon Pike Beck 6.1              35             286
##               DirectedConnectance NvMSlope
## Afon Hafren      0.2160000 -0.7078312
```

```
## Allt a'Mharcaidh      0.2087500 -0.7655290
## Bere Stream           0.2164830 -0.6501359
## Broadstone            0.2848000 -0.5853852
## Dargall Lane          0.2244898 -0.7379515
## Duddon Pike Beck      0.2334694 -0.5673022
```

```
# Node connectivity for all communities
```

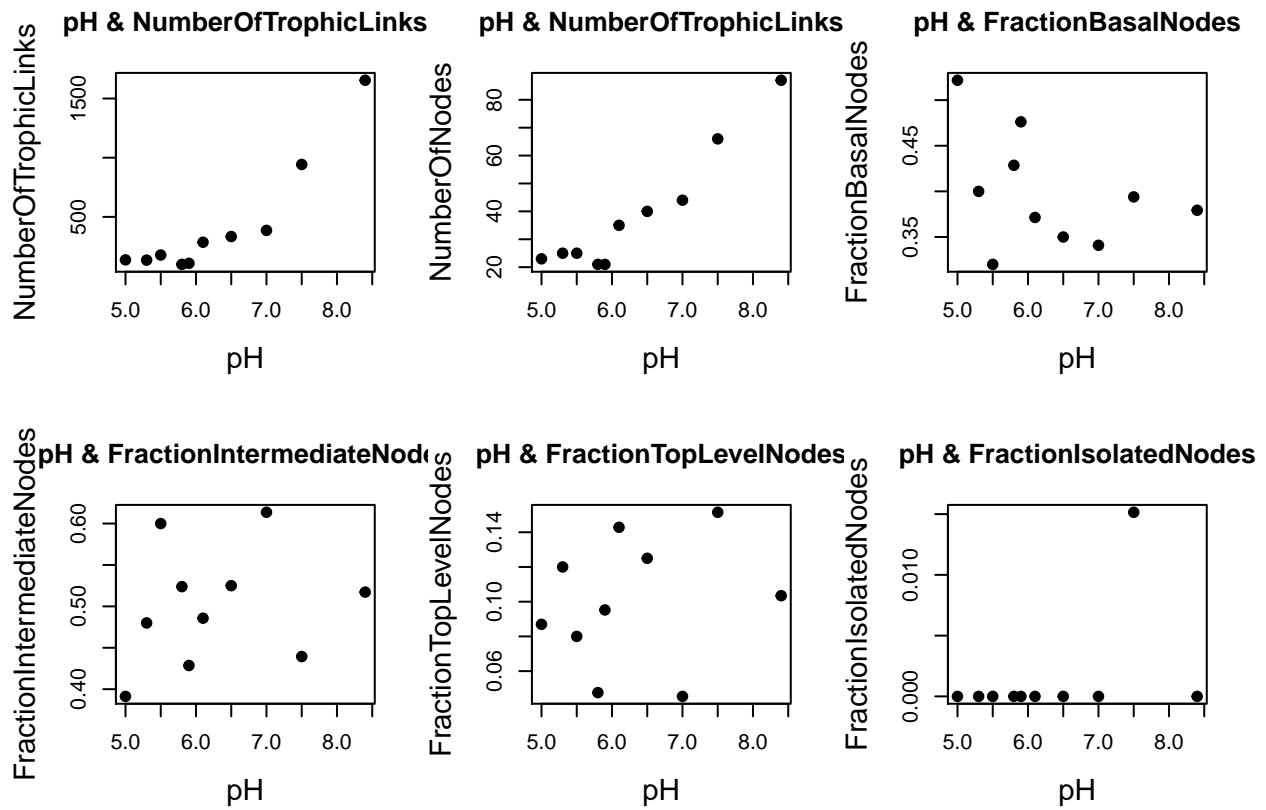
```
pH.conn<-CollectionCPS(pHWebs, c('pH',           #Community Property
                                'FractionBasalNodes', #cheddar function
                                'FractionIntermediateNodes', #cheddar function
                                'FractionTopLevelNodes', #cheddar function
                                'FractionIsolatedNodes')) #cheddar function

head(pH.conn)
```

```
##           pH FractionBasalNodes FractionIntermediateNodes
## Afon Hafren      5.3           0.4000000           0.4800000
## Allt a'Mharcaidh 6.5           0.3500000           0.5250000
## Bere Stream      7.5           0.3939394           0.4393939
## Broadstone       5.5           0.3200000           0.6000000
## Dargall Lane     5.8           0.4285714           0.5238095
## Duddon Pike Beck 6.1           0.3714286           0.4857143
##           FractionTopLevelNodes FractionIsolatedNodes
## Afon Hafren           0.1200000           0.0000000
## Allt a'Mharcaidh      0.1250000           0.0000000
## Bere Stream           0.1515151           0.0151515
## Broadstone            0.0800000           0.0000000
## Dargall Lane          0.04761905          0.0000000
## Duddon Pike Beck      0.14285714          0.0000000
```

```
# Plot relationships between pH and community structure.
```

```
par(mfrow=c(2,3))
with(pH.char, plot(pH, NumberOfTrophicLinks, pch=19, main="pH & NumberOfTrophicLinks", cex.lab=1.4))
with(pH.char, plot(pH, NumberOfNodes, pch=19, main="pH & NumberOfTrophicLinks", cex.lab=1.4))
with(pH.conn, plot(pH, FractionBasalNodes, pch=19, main="pH & FractionBasalNodes", cex.lab=1.4))
with(pH.conn, plot(pH, FractionIntermediateNodes, pch=19, main="pH & FractionIntermediateNodes", cex.lab=1.4))
with(pH.conn, plot(pH, FractionTopLevelNodes, pch=19, main="pH & FractionTopLevelNodes", cex.lab=1.4))
with(pH.conn, plot(pH, FractionIsolatedNodes, pch=19, main="pH & FractionIsolatedNodes", cex.lab=1.4))
```



```
# Order community by pH
pHWebs.d <- OrderCollection(pHWebs, 'pH', decreasing=TRUE)
# Plot food webs ordered by pH
plot(pHWebs.d, plot.fn=PlotWebByLevel, col=1, pch=19, highlight.nodes=NULL)
```

