

Working with collections of communities (0.1-631)

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2016-10-10

Contents

| | | |
|----------|--|-----------|
| 1 | Introduction | 1 |
| 2 | Datasets | 1 |
| 3 | Community collection representation | 2 |
| 3.1 | Basic operations | 2 |
| 3.2 | Subsets | 3 |
| 3.3 | Community properties | 4 |
| 3.4 | Node properties | 10 |
| 3.5 | Trophic link properties | 11 |
| 4 | Plotting | 13 |
| 4.1 | Plot-per-community | 13 |
| 5 | Modifying communities | 16 |
| 6 | Ordering collections | 19 |
| 7 | Aggregating communities | 21 |
| 8 | ‘Global’ node IDs | 25 |
| 8.1 | Create IDs | 25 |
| 8.2 | Table of properties | 25 |
| 8.3 | Plot IDs | 28 |

1 Introduction

Cheddar provides functions for managing collections of communities, allowing you to perform inter-web comparisons such as examining changes in community structure over environmental, temporal and spatial gradients. You should read the ‘CheddarQuickstart’ and ‘Community’ vignettes before reading this one. The ‘ImportExport’ vignette shows how to get collections of communities in to Cheddar.

2 Datasets

Cheddar contains some published empirical food web collection datasets (Table 1).

| Community | Notes | References |
|------------|---|--|
| Millstream | The control and drought treatments from one replicate of a long-running study investigating how drought affects community structure | Ledger et al. (2011) Ledger et al. (2012) Woodward et al. (2012) |
| pHWebs | Ten of the twenty stream communities sampled across a wide pH gradient | Layer et al. (2010) |

Table 1: Community collection data in Cheddar

3 Community collection representation

3.1 Basic operations

Cheddar's `CommunityCollection` is a sub-class of R's `list`.

```
> data(pHWebs)
> pHWebs
```

A collection of 10 communities

Each element in a `CommunityCollection` is a Cheddar `Community`. Many of the usual `list` operations can be used.

```
> length(pHWebs)
```

```
[1] 10
```

```
> is.list(pHWebs)
```

```
[1] TRUE
```

```
> names(pHWebs)
```

```
[1] "Old Lodge"      "Afon Hafren"    "Broadstone"    "Dargall Lane"
[5] "Mosedal Beck"  "Duddon Pike Beck" "Allt a'Mharcaidh" "Hardknott Gill"
[9] "Bere Stream"   "Mill Stream"
```

```
> # Access first community in the collection
```

```
> pHWebs[[1]]
```

Old Lodge containing 23 nodes and 137 trophic links

```
> # Access a community by name
```

```
> pHWebs[['Broadstone']]
```

Broadstone containing 25 nodes and 178 trophic links

```
> # The number of trophic links in Broadstone
```

```
> NumberOfTrophicLinks(pHWebs[['Broadstone']])
```

```
[1] 178
```

```
> # The number of trophic links in each of the ten webs
> sapply(pHWebs, 'NumberOfTrophicLinks')
```

| | | | | |
|------------------|------------------|----------------|--------------|--------------|
| Old Lodge | Afon Hafren | Broadstone | Dargall Lane | Mosedal Beck |
| 137 | 135 | 178 | 99 | 108 |
| Duddon Pike Beck | Allt a'Mharcaidh | Hardknott Gill | Bere Stream | Mill Stream |
| 286 | 334 | 386 | 943 | 1654 |

In contrast to R's lists, you can't change collections directly. This is because many checks are enforced when community collection objects are created, so you can not, for example, modify a collection's length or insert values in to the collection. The following operations would raise errors if executed.

```
> length(pHWebs) <- 2 # You can't do this
> pHWebs[1] <- "This will not work"
```

CommunityCollection guarantees that the title of each Community will be unique within a collection. The following will therefore always be TRUE.

```
> all(FALSE==duplicated(names(pHWebs)))
```

```
[1] TRUE
```

If the Community objects within a collection have body mass, CommunityCollection also guarantees that they will have the same units, as given in the community property 'M.units'. Similarly, all communities in a collection will have the same 'N.units', if they contain numerical abundance data.

3.2 Subsets

You can use list operators to take subsets of collections or to reorder them.

```
> # Returns a new CommunityCollection that contains every other web
> pHWebs[seq(1, 10, by=2)]
```

A collection of 5 communities

```
> # Returns a new CommunityCollection with the order reversed
> pHWebs[10:1]
```

A collection of 10 communities

```
> # Returns a new CommunityCollection containing only these two webs
> pHWebs[c('Old Lodge', 'Bere Stream')]
```

A collection of 2 communities

3.3 Community properties

The `CollectionCPS` (for **Collection** Community **PropertieS**) returns a `data.frame` of properties.

```
> CollectionCPS(pHWebs)
```

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

The table above shows all ‘first-class’ properties in all of the contained communities. `CommunityCollection` places no restrictions on first-class properties such as pH - it is possible for a `Community` within a collection to not have the pH property, to have a pH of NA or even to have an invalid pH, for example a negative value.

`CollectionCPS` takes a ‘properties’ parameter that defines which properties will be returned. The properties argument is a vector whose entries are either names of first-class properties or names of functions which take as single required argument a `CommunityCollection` and return a single value. If properties is NULL, all first-class properties are included in the returned `data.frame`. Just as with `CPS`, properties can be both ‘first-class’ and computed. `CollectionCPS` is a powerful function that allows you to build up a `data.frame` of predictors and responses. For example, the code fragment below allows us to see how diversity varies with pH.

```
> res <- CollectionCPS(pHWebs, properties=c('pH', 'NumberOfNodes'))
> res
```

| | pH | NumberOfNodes |
|------------------|-----|---------------|
| Old Lodge | 5.0 | 23 |
| Afon Hafren | 5.3 | 25 |
| Broadstone | 5.5 | 25 |
| Dargall Lane | 5.8 | 21 |
| Mosedal Beck | 5.9 | 21 |
| Duddon Pike Beck | 6.1 | 35 |
| Allt a'Mharcaidh | 6.5 | 40 |
| Hardknott Gill | 7.0 | 44 |
| Bere Stream | 7.5 | 66 |
| Mill Stream | 8.4 | 87 |

We can use R’s `lm` function to fit a linear regression model to this data.

```
> model <- lm(NumberOfNodes ~ pH, data=res)
> model
```

```
Call:
lm(formula = NumberOfNodes ~ pH, data = res)
```

```
Coefficients:
(Intercept)      pH
    -85.25      19.68
```

Let's examine the model's fit to the data.

```
> summary(model)
```

```
Call:
lm(formula = NumberOfNodes ~ pH, data = res)
```

```
Residuals:
    Min       1Q   Median       3Q      Max
-9.830 -6.556  1.138  5.404  9.878
```

```
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  -85.254     14.794   -5.763 0.000423 ***
pH             19.675       2.319    8.485 2.85e-05 ***
---

```

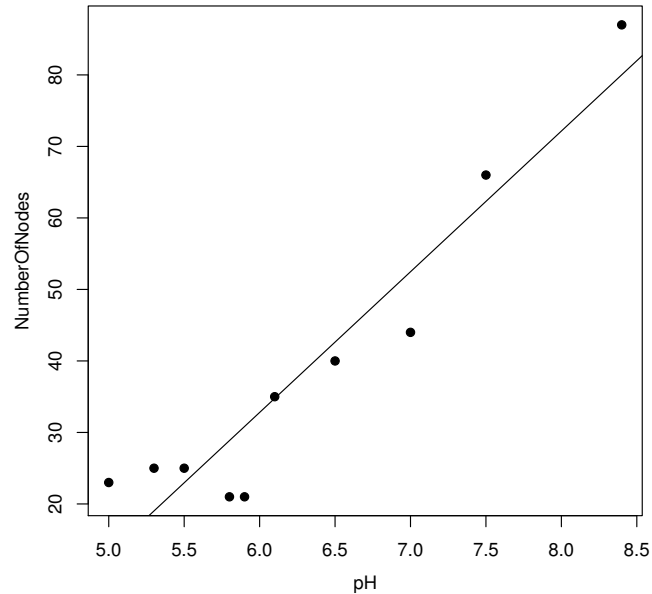
```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 7.391 on 8 degrees of freedom
Multiple R-squared:  0.9,    Adjusted R-squared:  0.8875
F-statistic: 72 on 1 and 8 DF, p-value: 2.852e-05
```

pH has a significant effect on number of nodes.

Let's plot the data and the model regression line.

```
> with(res, plot(pH, NumberOfNodes, pch=19))
> abline(model)
```



The above figure is similar to (Layer et al., 2010), Fig. 4A (p 281). Cheddar's pHWebs dataset contains ten of the twenty food webs analysed by Layer et al. (2010) so the plot is not an exact recreation of the published figure.

The example below uses `CollectionCPS` to assemble a table of four computed properties.

```
> CollectionCPS(pHWebs, c('pH',
  'NumberOfNodes',
  'NumberOfTrophicLinks',
  'DirectedConnectance',
  'NvMSlope'))
```

| | pH | NumberOfNodes | NumberOfTrophicLinks | DirectedConnectance | NvMSlope |
|------------------|-----|---------------|----------------------|---------------------|------------|
| Old Lodge | 5.0 | 23 | 137 | 0.2589792 | -0.6561601 |
| Afon Hafren | 5.3 | 25 | 135 | 0.2160000 | -0.7078312 |
| Broadstone | 5.5 | 25 | 178 | 0.2848000 | -0.5853852 |
| Dargall Lane | 5.8 | 21 | 99 | 0.2244898 | -0.7379515 |
| Mosedal Beck | 5.9 | 21 | 108 | 0.2448980 | -0.7026522 |
| Duddon Pike Beck | 6.1 | 35 | 286 | 0.2334694 | -0.5673022 |
| Allt a'Mharcaidh | 6.5 | 40 | 334 | 0.2087500 | -0.7655290 |
| Hardknott Gill | 7.0 | 44 | 386 | 0.1993802 | -0.7548597 |
| Bere Stream | 7.5 | 66 | 943 | 0.2164830 | -0.6501359 |
| Mill Stream | 8.4 | 87 | 1654 | 0.2185229 | -0.9192528 |

We can use a named vector to get shorter column titles.

```
> CollectionCPS(pHWebs, c('pH',
                           S='NumberOfNodes',
                           L='NumberOfTrophicLinks',
                           C='DirectedConnectance',
                           Slope='NvMSlope'))
```

| | pH | S | L | C | Slope |
|------------------|-----|----|------|-----------|------------|
| Old Lodge | 5.0 | 23 | 137 | 0.2589792 | -0.6561601 |
| Afon Hafren | 5.3 | 25 | 135 | 0.2160000 | -0.7078312 |
| Broadstone | 5.5 | 25 | 178 | 0.2848000 | -0.5853852 |
| Dargall Lane | 5.8 | 21 | 99 | 0.2244898 | -0.7379515 |
| Mosedal Beck | 5.9 | 21 | 108 | 0.2448980 | -0.7026522 |
| Duddon Pike Beck | 6.1 | 35 | 286 | 0.2334694 | -0.5673022 |
| Allt a'Mharcaidh | 6.5 | 40 | 334 | 0.2087500 | -0.7655290 |
| Hardknott Gill | 7.0 | 44 | 386 | 0.1993802 | -0.7548597 |
| Bere Stream | 7.5 | 66 | 943 | 0.2164830 | -0.6501359 |
| Mill Stream | 8.4 | 87 | 1654 | 0.2185229 | -0.9192528 |

The functions in the above examples each return a single value. Functions are permitted to return more than one value, such as `SumBiomassByClass`, which returns the total biomass in each class; the default class is 'category'. Some pHWebs communities contain nodes (detritus and the like) that do not have a category. These appear in '<unnamed>'.
</p>
</div>
<div data-bbox="88 454 558 555" data-label="Text">
<pre>> CollectionCPS(pHWebs, c('pH',
 S='NumberOfNodes',
 L='NumberOfTrophicLinks',
 C='DirectedConnectance',
 Slope='NvMSlope',
 'SumBiomassByClass'))</pre>
</div>
<div data-bbox="86 570 893 893" data-label="Text">
<table>
<thead>
<tr>
<th></th>
<th>pH</th>
<th>S</th>
<th>L</th>
<th>C</th>
<th>Slope</th>
<th><unnamed></th>
<th>invertebrate</th>
<th>producer</th>
</tr>
</thead>
<tbody>
<tr>
<td>Old Lodge</td>
<td>5.0</td>
<td>23</td>
<td>137</td>
<td>0.2589792</td>
<td>-0.6561601</td>
<td>NA</td>
<td>NA</td>
<td>3.450502e-01</td>
</tr>
<tr>
<td>Afon Hafren</td>
<td>5.3</td>
<td>25</td>
<td>135</td>
<td>0.2160000</td>
<td>-0.7078312</td>
<td>NA</td>
<td>321.74544</td>
<td>4.029557e-02</td>
</tr>
<tr>
<td>Broadstone</td>
<td>5.5</td>
<td>25</td>
<td>178</td>
<td>0.2848000</td>
<td>-0.5853852</td>
<td>NA</td>
<td>296.95697</td>
<td>2.487247e-03</td>
</tr>
<tr>
<td>Dargall Lane</td>
<td>5.8</td>
<td>21</td>
<td>99</td>
<td>0.2244898</td>
<td>-0.7379515</td>
<td>NA</td>
<td>75.99819</td>
<td>1.198280e+00</td>
</tr>
<tr>
<td>Mosedal Beck</td>
<td>5.9</td>
<td>21</td>
<td>108</td>
<td>0.2448980</td>
<td>-0.7026522</td>
<td>NA</td>
<td>147.07552</td>
<td>9.363093e-02</td>
</tr>
<tr>
<td>Duddon Pike Beck</td>
<td>6.1</td>
<td>35</td>
<td>286</td>
<td>0.2334694</td>
<td>-0.5673022</td>
<td>NA</td>
<td>981.83475</td>
<td>4.037737e-03</td>
</tr>
<tr>
<td>Allt a'Mharcaidh</td>
<td>6.5</td>
<td>40</td>
<td>334</td>
<td>0.2087500</td>
<td>-0.7655290</td>
<td>NA</td>
<td>NA</td>
<td>3.933786e+00</td>
</tr>
<tr>
<td>Hardknott Gill</td>
<td>7.0</td>
<td>44</td>
<td>386</td>
<td>0.1993802</td>
<td>-0.7548597</td>
<td>NA</td>
<td>522.77646</td>
<td>4.266116e-01</td>
</tr>
<tr>
<td>Bere Stream</td>
<td>7.5</td>
<td>66</td>
<td>943</td>
<td>0.2164830</td>
<td>-0.6501359</td>
<td>NA</td>
<td>4991.18212</td>
<td>6.782687e+00</td>
</tr>
<tr>
<td>Mill Stream</td>
<td>8.4</td>
<td>87</td>
<td>1654</td>
<td>0.2185229</td>
<td>-0.9192528</td>
<td>NA</td>
<td>NA</td>
<td>4.425616e+02</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>vert.ecto</th>
</tr>
</thead>
<tbody>
<tr>
<td>Old Lodge</td>
<td>3500.00000</td>
</tr>
<tr>
<td>Afon Hafren</td>
<td>3200.00000</td>
</tr>
<tr>
<td>Broadstone</td>
<td>97.50000</td>
</tr>
<tr>
<td>Dargall Lane</td>
<td>366666.66667</td>
</tr>
<tr>
<td>Mosedal Beck</td>
<td>500.00000</td>
</tr>
<tr>
<td>Duddon Pike Beck</td>
<td>300.00000</td>
</tr>
<tr>
<td>Allt a'Mharcaidh</td>
<td>412.50000</td>
</tr>
</tbody>
</table>
</div>
<div data-bbox="490 915 506 931" data-label="Page-Footer">
<p>7</p>
</div>

```
Hardknott Gill      4550.00000
Bere Stream        17.94913
Mill Stream        14200.00000
```

We can use a named vector to prefix column titles of values returned by `SumBiomassByClass`.

```
> CollectionCPS(pHWebs, c('pH',
                           S='NumberOfNodes',
                           L='NumberOfTrophicLinks',
                           C='DirectedConnectance',
                           Slope='NvMSlope',
                           B='SumBiomassByClass'))
```

| | pH | S | L | C | Slope | B.<unnamed> | B.invertebrate | B.producer |
|------------------|-----|----|--------------|-----------|------------|-------------|----------------|--------------|
| Old Lodge | 5.0 | 23 | 137 | 0.2589792 | -0.6561601 | NA | NA | 3.450502e-01 |
| Afon Hafren | 5.3 | 25 | 135 | 0.2160000 | -0.7078312 | NA | 321.74544 | 4.029557e-02 |
| Broadstone | 5.5 | 25 | 178 | 0.2848000 | -0.5853852 | NA | 296.95697 | 2.487247e-03 |
| Dargall Lane | 5.8 | 21 | 99 | 0.2244898 | -0.7379515 | NA | 75.99819 | 1.198280e+00 |
| Mosedal Beck | 5.9 | 21 | 108 | 0.2448980 | -0.7026522 | NA | 147.07552 | 9.363093e-02 |
| Duddon Pike Beck | 6.1 | 35 | 286 | 0.2334694 | -0.5673022 | NA | 981.83475 | 4.037737e-03 |
| Allt a'Mharcaidh | 6.5 | 40 | 334 | 0.2087500 | -0.7655290 | NA | NA | 3.933786e+00 |
| Hardknott Gill | 7.0 | 44 | 386 | 0.1993802 | -0.7548597 | NA | 522.77646 | 4.266116e-01 |
| Bere Stream | 7.5 | 66 | 943 | 0.2164830 | -0.6501359 | NA | 4991.18212 | 6.782687e+00 |
| Mill Stream | 8.4 | 87 | 1654 | 0.2185229 | -0.9192528 | NA | NA | 4.425616e+02 |
| | | | B.vert.ecto | | | | | |
| Old Lodge | | | 3500.00000 | | | | | |
| Afon Hafren | | | 3200.00000 | | | | | |
| Broadstone | | | 97.50000 | | | | | |
| Dargall Lane | | | 366666.66667 | | | | | |
| Mosedal Beck | | | 500.00000 | | | | | |
| Duddon Pike Beck | | | 300.00000 | | | | | |
| Allt a'Mharcaidh | | | 412.50000 | | | | | |
| Hardknott Gill | | | 4550.00000 | | | | | |
| Bere Stream | | | 17.94913 | | | | | |
| Mill Stream | | | 14200.00000 | | | | | |

The Old Lodge, Allt a'Mharcaidh and Mill Stream communities each have some invertebrates without *M* and/or *N* either because not enough individuals could be sampled to compute these properties reliably or because no data could be found in the literature. The biomasses for these nodes is `NA` and the summed biomasses for invertebrates in Old Lodge, Allt a'Mharcaidh and Mill Stream are therefore `NA`. We can ignore missing values by setting the 'na.rm' parameter.

```
> CollectionCPS(pHWebs, list('pH',
                              S='NumberOfNodes',
                              L='NumberOfTrophicLinks',
                              C='DirectedConnectance',
                              Slope='NvMSlope',
                              B=list('SumBiomassByClass', na.rm=TRUE)))
```


| | pH | S | L | C | Slope | B.<unnamed> | B.invertebrate | B.producer |
|------------------|-----|----|--------------|-----------|------------|-------------|----------------|--------------|
| Old Lodge | 5.0 | 23 | 137 | 0.2589792 | -0.6561601 | 0 | 507.73598 | 3.450502e-01 |
| Afon Hafren | 5.3 | 25 | 135 | 0.2160000 | -0.7078312 | 0 | 321.74544 | 4.029557e-02 |
| Broadstone | 5.5 | 25 | 178 | 0.2848000 | -0.5853852 | 0 | 296.95697 | 2.487247e-03 |
| Dargall Lane | 5.8 | 21 | 99 | 0.2244898 | -0.7379515 | 0 | 75.99819 | 1.198280e+00 |
| Mosedal Beck | 5.9 | 21 | 108 | 0.2448980 | -0.7026522 | 0 | 147.07552 | 9.363093e-02 |
| Duddon Pike Beck | 6.1 | 35 | 286 | 0.2334694 | -0.5673022 | 0 | 981.83475 | 4.037737e-03 |
| Allt a'Mharcaidh | 6.5 | 40 | 334 | 0.2087500 | -0.7655290 | 0 | 1531.10251 | 3.933786e+00 |
| Hardknott Gill | 7.0 | 44 | 386 | 0.1993802 | -0.7548597 | 0 | 522.77646 | 4.266116e-01 |
| Bere Stream | 7.5 | 66 | 943 | 0.2164830 | -0.6501359 | 0 | 4991.18212 | 6.782687e+00 |
| Mill Stream | 8.4 | 87 | 1654 | 0.2185229 | -0.9192528 | 0 | 2590.88439 | 4.425616e+02 |
| | | | | | | | | |
| | | | B.vert.ecto | | | | | |
| Old Lodge | | | 3500.00000 | | | | | |
| Afon Hafren | | | 3200.00000 | | | | | |
| Broadstone | | | 97.50000 | | | | | |
| Dargall Lane | | | 366666.66667 | | | | | |
| Mosedal Beck | | | 500.00000 | | | | | |
| Duddon Pike Beck | | | 300.00000 | | | | | |
| Allt a'Mharcaidh | | | 412.50000 | | | | | |
| Hardknott Gill | | | 4550.00000 | | | | | |
| Bere Stream | | | 17.94913 | | | | | |
| Mill Stream | | | 14200.00000 | | | | | |

The example below shows a table of 'node connectivity' for each community.

```
> CollectionCPS(pHWebs, c(Basal='FractionBasalNodes',
                           Intermediate='FractionIntermediateNodes',
                           TopLevel='FractionTopLevelNodes',
                           Isolated='FractionIsolatedNodes'))
```

| | Basal | Intermediate | TopLevel | Isolated |
|------------------|-----------|--------------|------------|------------|
| Old Lodge | 0.5217391 | 0.3913043 | 0.08695652 | 0.00000000 |
| Afon Hafren | 0.4000000 | 0.4800000 | 0.12000000 | 0.00000000 |
| Broadstone | 0.3200000 | 0.6000000 | 0.08000000 | 0.00000000 |
| Dargall Lane | 0.4285714 | 0.5238095 | 0.04761905 | 0.00000000 |
| Mosedal Beck | 0.4761905 | 0.4285714 | 0.09523810 | 0.00000000 |
| Duddon Pike Beck | 0.3714286 | 0.4857143 | 0.14285714 | 0.00000000 |
| Allt a'Mharcaidh | 0.3500000 | 0.5250000 | 0.12500000 | 0.00000000 |
| Hardknott Gill | 0.3409091 | 0.6136364 | 0.04545455 | 0.00000000 |
| Bere Stream | 0.3939394 | 0.4393939 | 0.15151515 | 0.01515152 |
| Mill Stream | 0.3793103 | 0.5172414 | 0.10344828 | 0.00000000 |

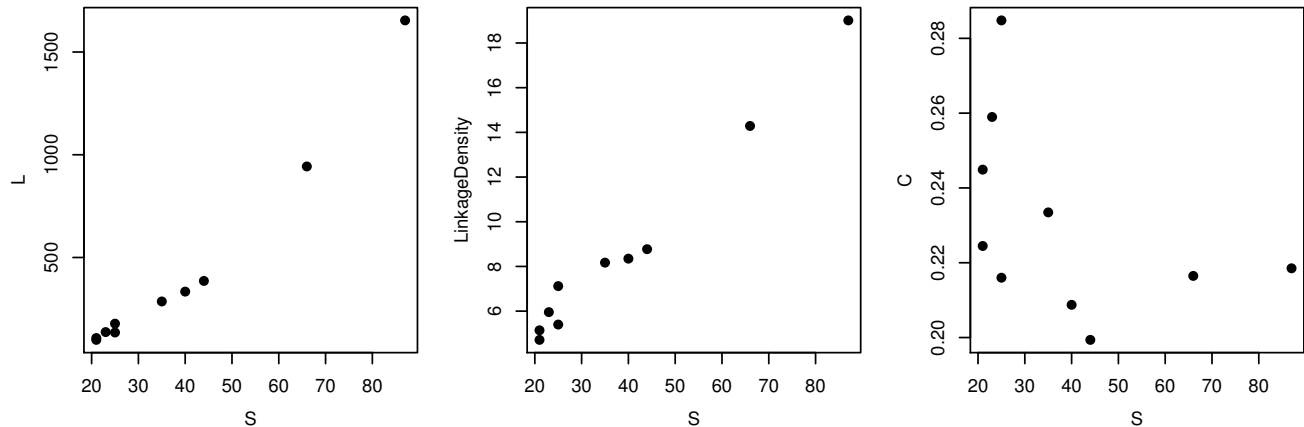
The plot below shows the relationship between the number of links and diversity of the pHWebs communities.

```
> properties <- CollectionCPS(pHWebs, c(S='NumberOfNodes',
                                           L='NumberOfTrophicLinks',
                                           'LinkageDensity',
                                           C='DirectedConnectance'))
```

```

> par(mfrow=c(1,3))
> with(properties, plot(S, L, pch=19))
> with(properties, plot(S, LinkageDensity, pch=19))
> with(properties, plot(S, C, pch=19))

```



These plots are similar to those in Riede et al. (2010), Fig. 1 (p 143) and Brown et al. (2011), Fig. 7 (p 891) but using different data.

3.4 Node properties

CollectionNPS returns a data.frame with a row for every node in every community.

```

> head(CollectionNPS(pHWebs))

```

| | community | node | M | N | category |
|---|-----------|---------------------|--------------|------------|----------|
| 1 | Old Lodge | CPOM | NA | NA | |
| 2 | Old Lodge | FPOM | NA | NA | |
| 3 | Old Lodge | Eunotia exigua | 1.910441e-12 | 2067974311 | producer |
| 4 | Old Lodge | Eunotia rhomboidea | 6.820054e-13 | 210924209 | producer |
| 5 | Old Lodge | Eunotia vanheurckii | 4.290173e-12 | 862038072 | producer |
| 6 | Old Lodge | Eunotia incisa | 1.992908e-11 | 220094827 | producer |

As with CollectionCPS, you can get columns for both first-class and computed properties.

```

> # A subset of first-class properties
> head(CollectionNPS(pHWebs, 'M'))

```

| | community | node | M |
|---|-----------|---------------------|--------------|
| 1 | Old Lodge | CPOM | NA |
| 2 | Old Lodge | FPOM | NA |
| 3 | Old Lodge | Eunotia exigua | 1.910441e-12 |
| 4 | Old Lodge | Eunotia rhomboidea | 6.820054e-13 |
| 5 | Old Lodge | Eunotia vanheurckii | 4.290173e-12 |
| 6 | Old Lodge | Eunotia incisa | 1.992908e-11 |

```
> # Several properties
> head(CollectionNPS(pHWebs, c('M', 'N', 'Biomass', 'Degree', 'IsBasalNode')))
```

| | community | node | M | N | Biomass | Degree | IsBasalNode |
|---|-----------|---------------------|--------------|------------|--------------|--------|-------------|
| 1 | Old Lodge | CPOM | NA | NA | NA | 4 | TRUE |
| 2 | Old Lodge | FPOM | NA | NA | NA | 8 | TRUE |
| 3 | Old Lodge | Eunotia exigua | 1.910441e-12 | 2067974311 | 0.0039507435 | 9 | TRUE |
| 4 | Old Lodge | Eunotia rhomboidea | 6.820054e-13 | 210924209 | 0.0001438514 | 9 | TRUE |
| 5 | Old Lodge | Eunotia vanheurckii | 4.290173e-12 | 862038072 | 0.0036982924 | 9 | TRUE |
| 6 | Old Lodge | Eunotia incisa | 1.992908e-11 | 220094827 | 0.0043862864 | 9 | TRUE |

```
> # Named properties
> head(CollectionNPS(pHWebs, c('M', 'N', B='Biomass', 'Degree', Basal='IsBasalNode')))
```

| | community | node | M | N | B | Degree | Basal |
|---|-----------|---------------------|--------------|------------|--------------|--------|-------|
| 1 | Old Lodge | CPOM | NA | NA | NA | 4 | TRUE |
| 2 | Old Lodge | FPOM | NA | NA | NA | 8 | TRUE |
| 3 | Old Lodge | Eunotia exigua | 1.910441e-12 | 2067974311 | 0.0039507435 | 9 | TRUE |
| 4 | Old Lodge | Eunotia rhomboidea | 6.820054e-13 | 210924209 | 0.0001438514 | 9 | TRUE |
| 5 | Old Lodge | Eunotia vanheurckii | 4.290173e-12 | 862038072 | 0.0036982924 | 9 | TRUE |
| 6 | Old Lodge | Eunotia incisa | 1.992908e-11 | 220094827 | 0.0043862864 | 9 | TRUE |

3.5 Trophic link properties

CollectionTLPS returns a data.frame containing a row for every trophic link in every community:

```
> head(CollectionTLPS(pHWebs))
```

| | community | resource | consumer |
|---|-----------|---------------------|-------------------------|
| 1 | Old Lodge | Chironomidae undet. | Siphonoperla torrentium |
| 2 | Old Lodge | Leuctra nigra | Siphonoperla torrentium |
| 3 | Old Lodge | Nemoura cinerea | Siphonoperla torrentium |
| 4 | Old Lodge | Simuliidae gra | Siphonoperla torrentium |
| 5 | Old Lodge | Simuliidae grb | Siphonoperla torrentium |
| 6 | Old Lodge | Simuliidae grc | Siphonoperla torrentium |

Community names and resource and consumer *M*:

```
> head(CollectionTLPS(pHWebs, 'M'))
```

| | community | resource | consumer | resource.M | consumer.M |
|---|-----------|---------------------|-------------------------|------------|------------|
| 1 | Old Lodge | Chironomidae undet. | Siphonoperla torrentium | 0.07809028 | 1.03837 |
| 2 | Old Lodge | Leuctra nigra | Siphonoperla torrentium | 0.94124878 | 1.03837 |
| 3 | Old Lodge | Nemoura cinerea | Siphonoperla torrentium | 0.35536589 | 1.03837 |
| 4 | Old Lodge | Simuliidae gra | Siphonoperla torrentium | 0.17317064 | 1.03837 |
| 5 | Old Lodge | Simuliidae grb | Siphonoperla torrentium | 0.18357370 | 1.03837 |
| 6 | Old Lodge | Simuliidae grc | Siphonoperla torrentium | 0.22403767 | 1.03837 |

Several properties:

```
> head(CollectionTLPS(pHWebs, c('M', 'N', 'Biomass', 'Degree', 'IsBasalNode')))
```

| | community | resource | consumer | resource.M | resource.N |
|---|------------------|---------------------|-------------------------|------------|------------|
| 1 | Old Lodge | Chironomidae undet. | Siphonoperla torrentium | 0.07809028 | 64.0 |
| 2 | Old Lodge | Leuctra nigra | Siphonoperla torrentium | 0.94124878 | 214.4 |
| 3 | Old Lodge | Nemoura cinerea | Siphonoperla torrentium | 0.35536589 | 342.4 |
| 4 | Old Lodge | Simuliidae gra | Siphonoperla torrentium | 0.17317064 | 6.4 |
| 5 | Old Lodge | Simuliidae grb | Siphonoperla torrentium | 0.18357370 | 83.2 |
| 6 | Old Lodge | Simuliidae grc | Siphonoperla torrentium | 0.22403767 | 3.2 |
| | resource.Biomass | resource.Degree | resource.IsBasalNode | consumer.M | consumer.N |
| 1 | 4.9977782 | 16 | FALSE | 1.03837 | 16 |
| 2 | 201.8037377 | 16 | FALSE | 1.03837 | 16 |
| 3 | 121.6772793 | 16 | FALSE | 1.03837 | 16 |
| 4 | 1.1082921 | 15 | FALSE | 1.03837 | 16 |
| 5 | 15.2733322 | 15 | FALSE | 1.03837 | 16 |
| 6 | 0.7169205 | 15 | FALSE | 1.03837 | 16 |
| | consumer.Biomass | consumer.Degree | consumer.IsBasalNode | | |
| 1 | 16.61392 | 11 | FALSE | | |
| 2 | 16.61392 | 11 | FALSE | | |
| 3 | 16.61392 | 11 | FALSE | | |
| 4 | 16.61392 | 11 | FALSE | | |
| 5 | 16.61392 | 11 | FALSE | | |
| 6 | 16.61392 | 11 | FALSE | | |

Several properties with shorter column names:

```
> head(CollectionTLPS(pHWebs, c('M','N', B='Biomass', D='Degree', Basal='IsBasalNode')))
```

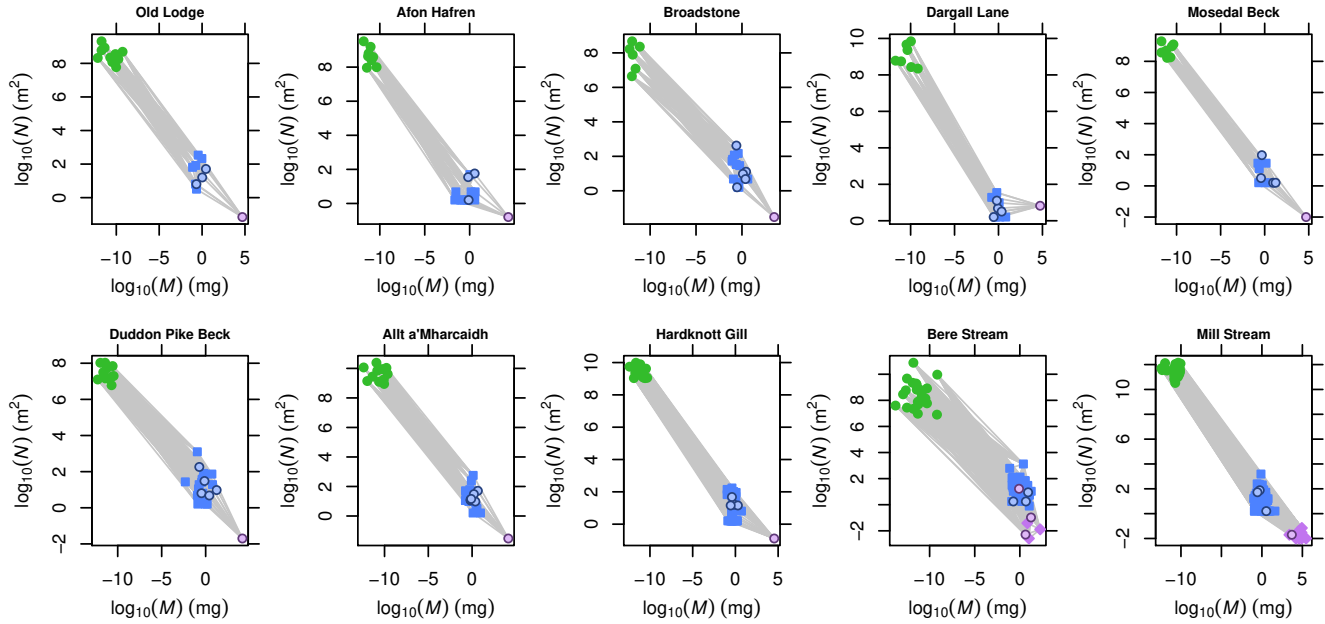
| | community | resource | consumer | resource.M | resource.N | resource.B | |
|---|------------|---------------------|-------------------------|------------|------------|-------------|----------------|
| 1 | Old Lodge | Chironomidae undet. | Siphonoperla torrentium | 0.07809028 | 64.0 | 4.9977782 | |
| 2 | Old Lodge | Leuctra nigra | Siphonoperla torrentium | 0.94124878 | 214.4 | 201.8037377 | |
| 3 | Old Lodge | Nemoura cinerea | Siphonoperla torrentium | 0.35536589 | 342.4 | 121.6772793 | |
| 4 | Old Lodge | Simuliidae gra | Siphonoperla torrentium | 0.17317064 | 6.4 | 1.1082921 | |
| 5 | Old Lodge | Simuliidae grb | Siphonoperla torrentium | 0.18357370 | 83.2 | 15.2733322 | |
| 6 | Old Lodge | Simuliidae grc | Siphonoperla torrentium | 0.22403767 | 3.2 | 0.7169205 | |
| | resource.D | resource.Basal | consumer.M | consumer.N | consumer.B | consumer.D | consumer.Basal |
| 1 | 16 | FALSE | 1.03837 | 16 | 16.61392 | 11 | FALSE |
| 2 | 16 | FALSE | 1.03837 | 16 | 16.61392 | 11 | FALSE |
| 3 | 16 | FALSE | 1.03837 | 16 | 16.61392 | 11 | FALSE |
| 4 | 15 | FALSE | 1.03837 | 16 | 16.61392 | 11 | FALSE |
| 5 | 15 | FALSE | 1.03837 | 16 | 16.61392 | 11 | FALSE |
| 6 | 15 | FALSE | 1.03837 | 16 | 16.61392 | 11 | FALSE |

4 Plotting

4.1 Plot-per-community

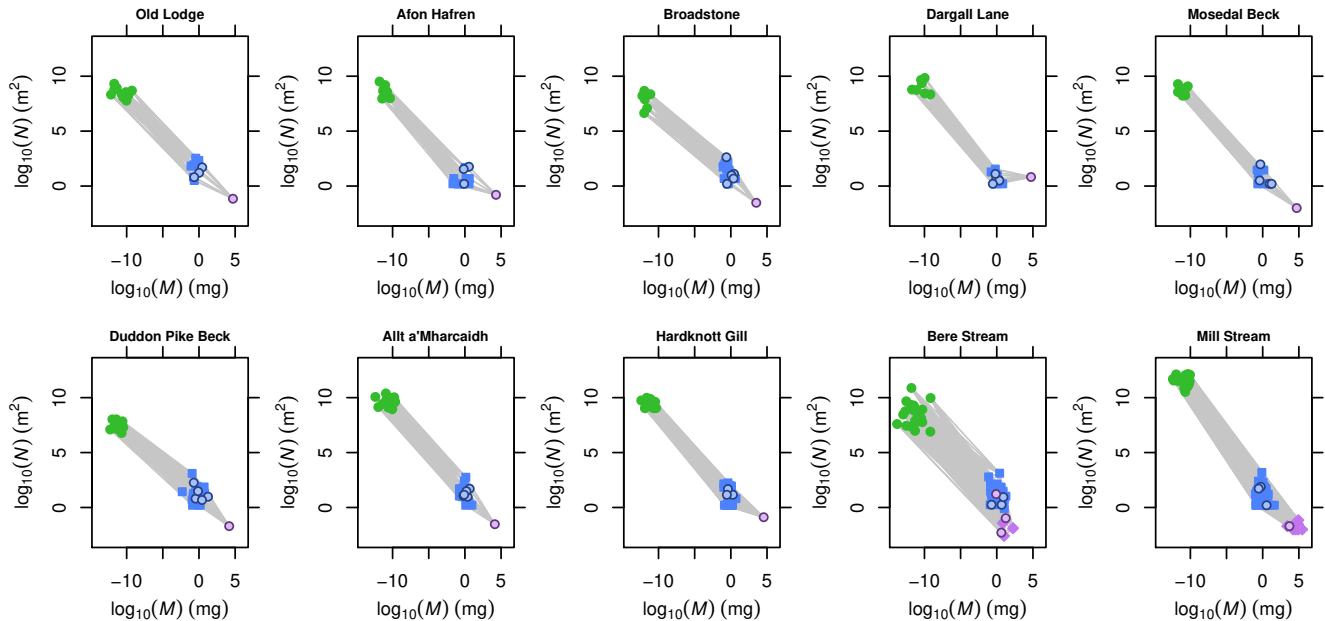
You can use R's `plot` function to 'eyeball' webs in a collection.

```
> plot(pHWebs)
```



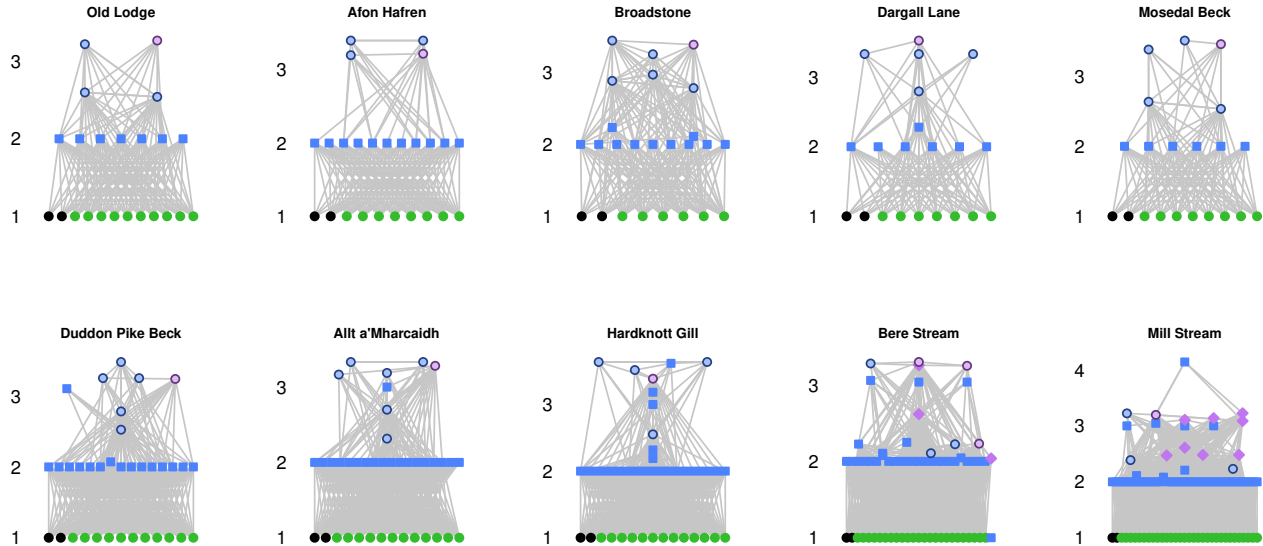
You can use R's plot parameters 'xlim' and 'ylim' to set limits for the x and y axes.

```
> plot(pHWebs, xlim=c(-14,6), ylim=c(-3,13))
```



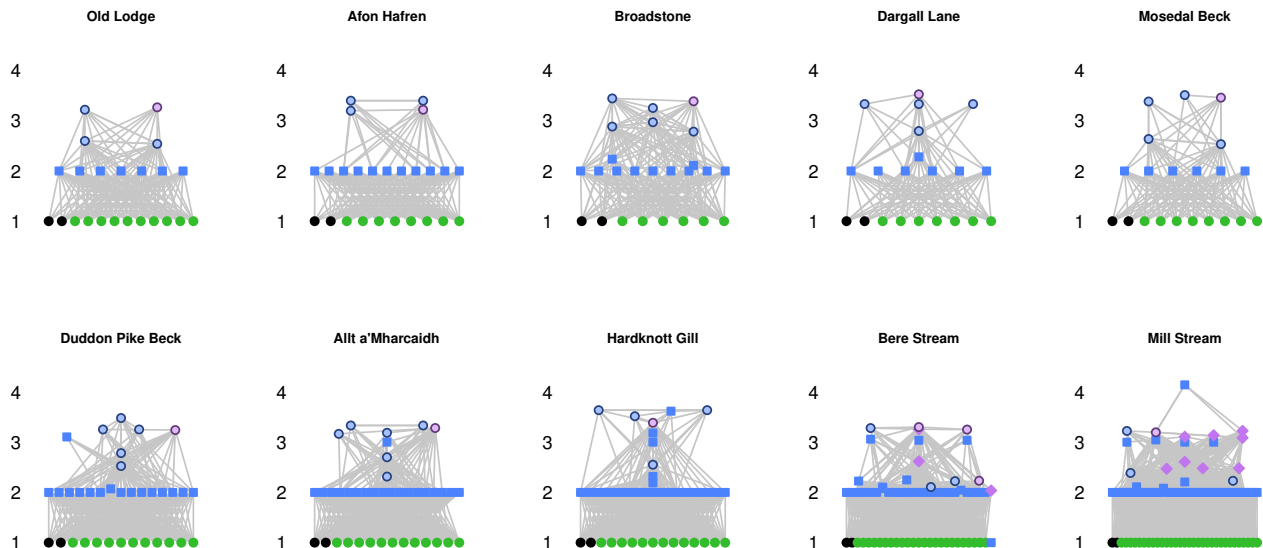
Cheddar examines the properties of the communities in the collection in order to decide which Community-level plot function to use. You can change this behaviour using the ‘plot.fn’ parameter. The PlotWebByLevel allows the webs to be viewed by trophic level.

```
> plot(pHwebs, plot.fn=PlotWebByLevel)
```



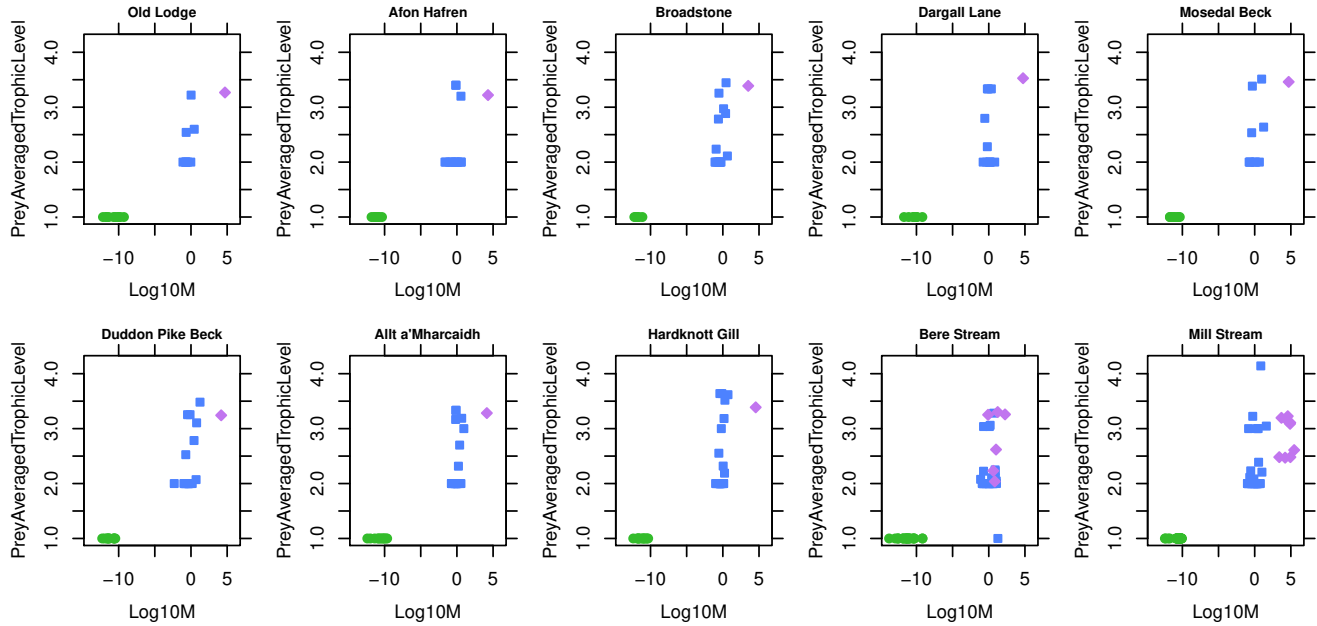
As in the previous example, the y axis limits can be made consistent.

```
> plot(pHwebs, plot.fn=PlotWebByLevel, ylim=c(1, 4.5))
```



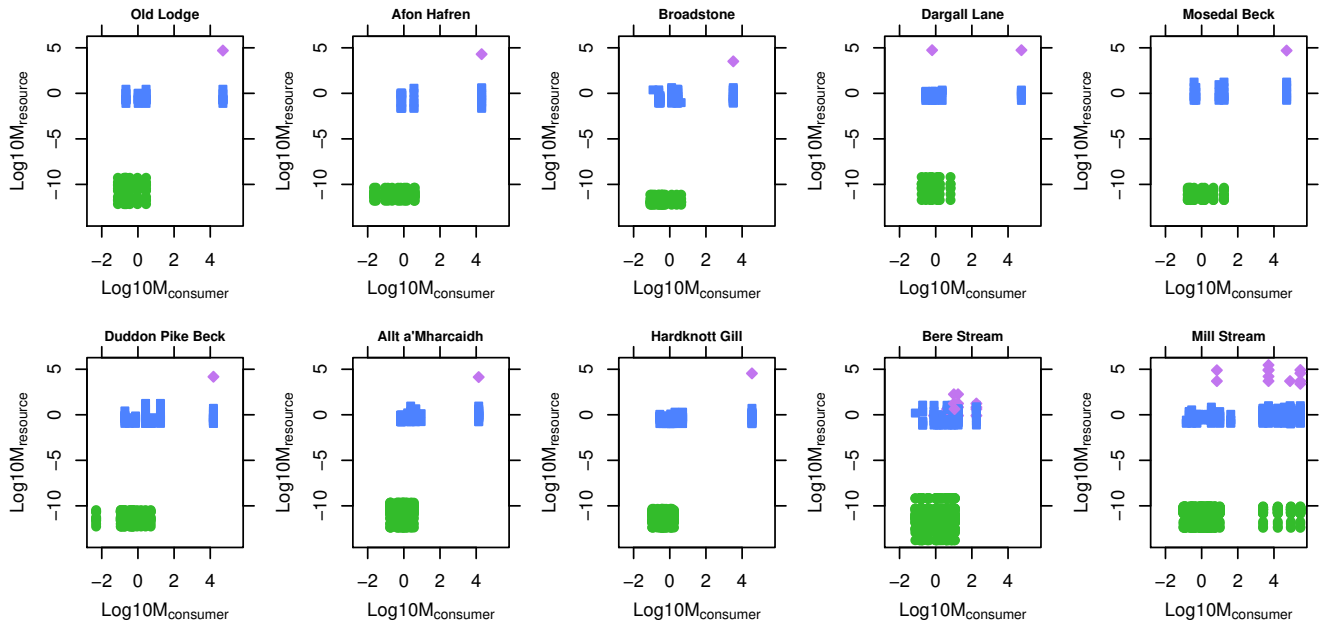
We can use the general-purpose function `PlotNPS` to plot any node properties that we like and all of the power of `PlotNPS` is available. The example below plots trophic level as a function of \log_{10} -transformed body mass. Each plot has the same axis limits. We have turned off plotting of the food web and highlighting of cannibals.

```
> plot(pHWebs, plot.fn=PlotNPS, X='Log10M', Y='PreyAveragedTrophicLevel',
      show.web=FALSE, highlight.nodes=NULL, xlim=c(-14,6), ylim=c(1,4.2))
```



We can also use `PlotTLPS`, as shown below.

```
> plot(pHWebs, plot.fn=PlotTLPS, X='consumer.Log10M',
      Y='resource.Log10M', xlim=c(-2.5, 5.5), ylim=c(-13.8, 5.5))
```



5 Modifying communities

The `CollectionApply` function allows communities within collections to be modified. For example, with certain analyses it can be desirable to remove isolated nodes.

```
> # Bere Stream has some isolated nodes
> CollectionCPS(pHWebs, 'FractionIsolatedNodes')
```

| | FractionIsolatedNodes |
|------------------|-----------------------|
| Old Lodge | 0.00000000 |
| Afon Hafren | 0.00000000 |
| Broadstone | 0.00000000 |
| Dargall Lane | 0.00000000 |
| Mosedal Beck | 0.00000000 |
| Duddon Pike Beck | 0.00000000 |
| Allt a'Mharcaidh | 0.00000000 |
| Hardknott Gill | 0.00000000 |
| Bere Stream | 0.01515152 |
| Mill Stream | 0.00000000 |

```
> pHWebs.no.iso <- CollectionApply(pHWebs, RemoveIsolatedNodes)
> CollectionCPS(pHWebs.no.iso, 'FractionIsolatedNodes') # All 0
```

| | FractionIsolatedNodes |
|--------------------------------------|-----------------------|
| Old Lodge | 0 |
| Afon Hafren | 0 |
| Broadstone | 0 |
| Dargall Lane | 0 |
| Mosedal Beck | 0 |
| Duddon Pike Beck | 0 |
| Allt a'Mharcaidh | 0 |
| Hardknott Gill | 0 |
| Bere Stream (isolated nodes removed) | 0 |
| Mill Stream | 0 |

The `CollectionApply` function can be used with any function that modifies communities, such as `RemoveCannibalisticLinks`.

```
> # The number of cannibals in each community
> sapply(pHWebs, function(community) length(Cannibals(community)))
```

| | | | | |
|------------------|------------------|----------------|--------------|--------------|
| Old Lodge | Afon Hafren | Broadstone | Dargall Lane | Mosedal Beck |
| 4 | 4 | 6 | 5 | 5 |
| Duddon Pike Beck | Allt a'Mharcaidh | Hardknott Gill | Bere Stream | Mill Stream |
| 6 | 7 | 5 | 6 | 4 |

```
> pHWebs.no.can <- CollectionApply(pHWebs, RemoveCannibalisticLinks)
> sapply(pHWebs.no.can, function(community) length(Cannibals(community)))
```



```

      Old Lodge (cannibalistic links removed)
      0
    Afon Hafren (cannibalistic links removed)
      0
    Broadstone (cannibalistic links removed)
      0
    Dargall Lane (cannibalistic links removed)
      0
    Mosedal Beck (cannibalistic links removed)
      0
    Duddon Pike Beck (cannibalistic links removed)
      0
    Allt a'Mharcaidh (cannibalistic links removed)
      0
    Hardknott Gill (cannibalistic links removed)
      0
    Bere Stream (cannibalistic links removed)
      0
    Mill Stream (cannibalistic links removed)
      0

```

The function to be applied to each community can also take additional parameters. The following example reorders each community's nodes by body mass.

```
> head(CollectionNPS(pHWebs))
```

| | community | node | M | N | category |
|---|-----------|---------------------|--------------|------------|----------|
| 1 | Old Lodge | CPOM | NA | NA | |
| 2 | Old Lodge | FPOM | NA | NA | |
| 3 | Old Lodge | Eunotia exigua | 1.910441e-12 | 2067974311 | producer |
| 4 | Old Lodge | Eunotia rhomboidea | 6.820054e-13 | 210924209 | producer |
| 5 | Old Lodge | Eunotia vanheurckii | 4.290173e-12 | 862038072 | producer |
| 6 | Old Lodge | Eunotia incisa | 1.992908e-11 | 220094827 | producer |

```
> pHWebs.by.M <- CollectionApply(pHWebs, OrderCommunity, 'M')
> head(CollectionNPS(pHWebs.by.M))
```

| | community | node | M | N | category |
|---|-----------------------|------------------------|--------------|------------|----------|
| 1 | Old Lodge (reordered) | Eunotia rhomboidea | 6.820054e-13 | 210924209 | producer |
| 2 | Old Lodge (reordered) | Eunotia exigua | 1.910441e-12 | 2067974311 | producer |
| 3 | Old Lodge (reordered) | Brachysira vitrea | 1.910441e-12 | 600675465 | producer |
| 4 | Old Lodge (reordered) | Eunotia vanheurckii | 4.290173e-12 | 862038072 | producer |
| 5 | Old Lodge (reordered) | Eunotia incisa | 1.992908e-11 | 220094827 | producer |
| 6 | Old Lodge (reordered) | Brachysira brebissonii | 3.426856e-11 | 119218031 | producer |

We can put the nodes lacking *M* first.

```
> pHWebs.by.M <- CollectionApply(pHWebs, OrderCommunity, 'M', na.last=FALSE)
> head(CollectionNPS(pHWebs.by.M))
```

| | community | node | M | N | category |
|---|-----------------------|--------------------|--------------|------------|--------------|
| 1 | Old Lodge (reordered) | CPOM | NA | NA | |
| 2 | Old Lodge (reordered) | FPOM | NA | NA | |
| 3 | Old Lodge (reordered) | Leuctra sp. | NA | NA | invertebrate |
| 4 | Old Lodge (reordered) | Eunotia rhomboidea | 6.820054e-13 | 210924209 | producer |
| 5 | Old Lodge (reordered) | Eunotia exigua | 1.910441e-12 | 2067974311 | producer |
| 6 | Old Lodge (reordered) | Brachysira vitrea | 1.910441e-12 | 600675465 | producer |

6 Ordering collections

`OrderCollection` allows you to order collections by whatever properties you please. To order the webs by decreasing pH:

```
> pHWebs.decreasing.pH <- OrderCollection(pHWebs, 'pH', decreasing=TRUE)
> CollectionCPS(pHWebs.decreasing.pH)
```

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

To order alphabetically by community name.

```
> pHWebs.name <- OrderCollection(pHWebs, 'title')
> CollectionCPS(pHWebs.name)
```

| | 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 |

You can sort on computed properties, such as the number of nodes.

```
> pHWebs.n.nodes <- OrderCollection(pHWebs, 'NumberOfNodes')
> CollectionCPS(pHWebs.n.nodes, c('pH', 'lat', 'NumberOfNodes'))
```

| | pH | lat | NumberOfNodes |
|------------------|-----|-------|---------------|
| Dargall Lane | 5.8 | 55.08 | 21 |
| Mosedal Beck | 5.9 | 54.41 | 21 |
| Old Lodge | 5.0 | 51.04 | 23 |
| Afon Hafren | 5.3 | 52.47 | 25 |
| Broadstone | 5.5 | 51.08 | 25 |
| Duddon Pike Beck | 6.1 | 54.41 | 35 |
| Allt a'Mharcaidh | 6.5 | 57.12 | 40 |

| | | | |
|----------------|-----|-------|----|
| Hardknott Gill | 7.0 | 54.40 | 44 |
| Bere Stream | 7.5 | 50.73 | 66 |
| Mill Stream | 8.4 | 50.68 | 87 |

Two communities have 21 nodes and two have 25. We can sort on more than one property to break ties. This example sorts by number of nodes and the latitude within number of nodes.

```
> pHWebs.n.nodes.and.lat <- OrderCollection(pHWebs, 'NumberOfNodes', 'lat')
> CollectionCPS(pHWebs.n.nodes.and.lat, c('pH', 'lat', 'NumberOfNodes'))
```

| | pH | lat | NumberOfNodes |
|------------------|-----|-------|---------------|
| Mosedal Beck | 5.9 | 54.41 | 21 |
| Dargall Lane | 5.8 | 55.08 | 21 |
| Old Lodge | 5.0 | 51.04 | 23 |
| Broadstone | 5.5 | 51.08 | 25 |
| Afon Hafren | 5.3 | 52.47 | 25 |
| Duddon Pike Beck | 6.1 | 54.41 | 35 |
| Allt a'Mharcaidh | 6.5 | 57.12 | 40 |
| Hardknott Gill | 7.0 | 54.40 | 44 |
| Bere Stream | 7.5 | 50.73 | 66 |
| Mill Stream | 8.4 | 50.68 | 87 |

7 Aggregating communities

`AggregateCommunities` aggregates the communities within a collection in to a new single community object. The way that node, trophic link and community properties are aggregated are shown here using the `Millstream` data set (?Ledger et al., 2011). The ‘c4’ community was a control and the ‘d4’ community was exposed to a drought treatment.

```
> data(Millstream)
> Millstream
```

A collection of 2 communities

```
> names(Millstream)
```

```
[1] "c4" "d4"
```

The herbivorous insect *Synorthocladius* sp. appears in both communities but with a different mean M and N .

```
> nps <- CollectionNPS(Millstream)
> nps['Synorthocladius sp.'==nps$node,c('community','M','N')]
```

| | community | M | N |
|-----|-----------|------------|-----------|
| 56 | c4 | 0.02099907 | 32.92305 |
| 114 | d4 | 0.03868121 | 206.58558 |

Now let’s perform the aggregation of these two communities, weighting by N :

```
> aggregation1 <- AggregateCommunities(Millstream, weight.by='N')
> # Satisfy ourselves that each node has been included in the aggregated community
> all(sort(unique(nps$node))==sort(NPS(aggregation1)$node))
```

```
[1] TRUE
```

Now let’s examine how ‘M’ and ‘N’ have been computed for *Synorthocladius* sp.:

```
> NPS(aggregation1)['Synorthocladius sp.',c('M','N')]
```

| | M | N |
|---------------------|-----------|----------|
| Synorthocladius sp. | 0.0362506 | 119.7543 |

These values were computed from the values in the collection as follows:

```
> # Arithmetic mean of N
> mean(nps['Synorthocladius sp.'==nps$node,'N'])
```

```
[1] 119.7543
```

```
> # N-weighted mean of M
> weighted.mean(nps['Synorthocladius sp.'==nps$node,'M'],
  nps['Synorthocladius sp.'==nps$node,'N'])
```

```
[1] 0.0362506
```

Now let's see what happens when we perform the aggregation of these two communities without any weighting:

```
> aggregation2 <- AggregateCommunities(Millstream, weight.by=NULL)
> NPS(aggregation2)['Synorthocladius sp.',c('M','N')]
```

```

               M               N
Synorthocladius sp. 0.02984014 119.7543
```

```
> # Arithmetic mean of M
> mean(nps['Synorthocladius sp.'==nps$node,'M'])
```

```
[1] 0.02984014
```

```
> # Arithmetic mean of N
> mean(nps['Synorthocladius sp.'==nps$node,'N'])
```

```
[1] 119.7543
```

`AggregateCommunities` combines character and logical node properties by joining unique values with a `'.'`. `AggregateCommunities` aggregates trophic links by taking the union of links across all communities. There are twelve trophic links in to and out of *Synorthocladius sp.* in 'c4' and 'd4'.

```
> ttps <- CollectionTLPS(Millstream)
> ttps['Synorthocladius sp.'==ttps$resource |
      'Synorthocladius sp.'==ttps$consumer,]
```

| | community | resource | consumer |
|-----|-----------|---------------------------|------------------------------|
| 283 | c4 | Synorthocladius sp. | Polycentropus flavomaculatus |
| 355 | c4 | Amorphous detritus (FPOM) | Synorthocladius sp. |
| 356 | c4 | Plant fragments (CPOM) | Synorthocladius sp. |
| 357 | c4 | Navicula gregaria | Synorthocladius sp. |
| 358 | c4 | Navicula tripunctata | Synorthocladius sp. |
| 359 | c4 | Gomphonema olivaceum | Synorthocladius sp. |
| 360 | c4 | Cocconeis placentula | Synorthocladius sp. |
| 361 | c4 | Rhoicosphenia abbreviata | Synorthocladius sp. |
| 362 | c4 | Gongrosira incrustans | Synorthocladius sp. |
| 617 | d4 | Amorphous detritus (FPOM) | Synorthocladius sp. |
| 618 | d4 | Plant fragments (CPOM) | Synorthocladius sp. |
| 619 | d4 | Gongrosira incrustans | Synorthocladius sp. |

The union of these twelve trophic links gives nine unique links:

```
> TrophicLinksForNodes(aggregation1, 'Synorthocladius sp.')
```

| | resource | consumer |
|---|---------------------------|------------------------------|
| 1 | Synorthocladius sp. | Polycentropus flavomaculatus |
| 2 | Amorphous detritus (FPOM) | Synorthocladius sp. |
| 3 | Plant fragments (CPOM) | Synorthocladius sp. |

| | | |
|---|--------------------------|--------------------|
| 4 | Navicula gregaria | Synorthocladus sp. |
| 5 | Navicula tripunctata | Synorthocladus sp. |
| 6 | Gomphonema olivaceum | Synorthocladus sp. |
| 7 | Cocconeis placentula | Synorthocladus sp. |
| 8 | Rhoicosphenia abbreviata | Synorthocladus sp. |
| 9 | Gongrosira incrustans | Synorthocladus sp. |

Community properties are aggregated by computing the arithmetic mean of numeric values and by joining unique character and logical together with a ‘,’:

```
> CollectionCPS(Millstream)
```

| | title | M.units | N.units | treatment | block |
|----|-------|---------|-----------------|-----------|-------|
| c4 | c4 | mg | m ⁻² | control | 4 |
| d4 | d4 | mg | m ⁻² | disturbed | 4 |

```
> data.frame(CPS(aggregation1))
```

| | title | M.units | N.units | treatment | block |
|---|----------------------|---------|-----------------|-------------------|-------|
| 1 | Aggregation of c4,d4 | mg | m ⁻² | control,disturbed | 4 |

AggregateCommunitiesBy aggregates by a single property, either first-class or computed, of the contained communities. Each food web in the pHWebs dataset has a different pH, so aggregating by pH would result in a collection of the same ten communities. The Duddon Pike Beck and Mosedal Beck communities share the same latitude and have pH values of 6.1 and 5.9 respectively.

```
> CollectionCPS(pHWebs[c('Duddon Pike Beck', 'Mosedal Beck')])
```

| | title | M.units | N.units | code | pH | lat | long |
|------------------|------------------|---------|----------------|------|-----|-------|-------|
| Duddon Pike Beck | Duddon Pike Beck | mg | m ² | DUD1 | 6.1 | 54.41 | -3.17 |
| Mosedal Beck | Mosedal Beck | mg | m ² | DUD3 | 5.9 | 54.41 | -3.14 |

Aggregating by the ‘lat’ property therefore results in a new collection of nine communities.

```
> CollectionCPS(AggregateCommunitiesBy(pHWebs, 'lat'))
```

| | title | M.units | N.units | code | pH | lat | long |
|--|--|---------|----------------|------|-----|-------|--------|
| Aggregation of Old Lodge | Aggregation of Old Lodge | | | | | | |
| Aggregation of Afon Hafren | Aggregation of Afon Hafren | | | | | | |
| Aggregation of Broadstone | Aggregation of Broadstone | | | | | | |
| Aggregation of Dargall Lane | Aggregation of Dargall Lane | | | | | | |
| Aggregation of Mosedal Beck,Duddon Pike Beck | Aggregation of Mosedal Beck,Duddon Pike Beck | | | | | | |
| Aggregation of Allt a'Mharcaidh | Aggregation of Allt a'Mharcaidh | | | | | | |
| Aggregation of Hardknott Gill | Aggregation of Hardknott Gill | | | | | | |
| Aggregation of Bere Stream | Aggregation of Bere Stream | | | | | | |
| Aggregation of Mill Stream | Aggregation of Mill Stream | | | | | | |
| | | M.units | N.units | code | pH | lat | long |
| Aggregation of Old Lodge | | mg | m ² | OLD | 5.0 | 51.04 | 0.080 |
| Aggregation of Afon Hafren | | mg | m ² | HAF | 5.3 | 52.47 | -3.700 |
| Aggregation of Broadstone | | mg | m ² | BRO | 5.5 | 51.08 | 0.053 |

| | | | | | | |
|--|----|----------------|-----------|-----|-------|--------|
| Aggregation of Dargall Lane | mg | m ² | DAR | 5.8 | 55.08 | -4.430 |
| Aggregation of Mosedal Beck,Duddon Pike Beck | mg | m ² | DUD3,DUD1 | 6.0 | 54.41 | -3.155 |
| Aggregation of Allt a'Mharcaidh | mg | m ² | MHA | 6.5 | 57.12 | -3.850 |
| Aggregation of Hardknott Gill | mg | m ² | DUD2 | 7.0 | 54.40 | -3.170 |
| Aggregation of Bere Stream | mg | m ² | BER | 7.5 | 50.73 | -2.210 |
| Aggregation of Mill Stream | mg | m ² | MIL | 8.4 | 50.68 | -2.180 |

The aggregation of Duddon Pike Beck and Mosedal Beck has a pH of 6: the arithmetic mean of the two pH values of the two communities.

8 ‘Global’ node IDs

This section describes how to assign a unique ID number to every species in a `CommunityCollection`. This is a common requirement for studies of multiple communities.

8.1 Create IDs

This code fragment creates a mapping from species names to global IDs. The IDs are assigned starting with producers, then invertebrates, then fish, sorted alphabetically within each category.

```
> data(TL84, TL86)
> TL <- CommunityCollection(list(TL84, TL86))
> # TL.aggregated is a new Community object containing every species in the TL
> all.TL <- AggregateCommunities(TL)
> # Generate a factor of categories
> nps <- NPS(all.TL, c('node', 'category'))
> categories <- factor(nps$category, levels=c('producer', 'invertebrate',
                                              'vert.ecto'))
> # Order all.TL by categories
> all.TL <- OrderCommunity(all.TL, new.order=order(categories, nps$node))
> # Create the mapping from node name to ID
> map <- 1:NumberOfNodes(all.TL)
> names(map) <- unname(NP(all.TL, 'node'))
```

8.2 Table of properties

This code fragment creates a table showing species’ names, categories and IDs.

```
> data.frame(ID=1:NumberOfNodes(all.TL),
             NPS(all.TL, c(Species='node', Category='category',
                           'M', 'N', TL='PreyAveragedTrophicLevel')),
             row.names=NULL)
```

| | ID | Species | Category | M | N | TL |
|----|----|-------------------------------|----------|--------------|-----------|----------|
| 1 | 1 | Anabaena circinalis | producer | 1.910000e-13 | 3.000e+06 | 1.000000 |
| 2 | 2 | Ankyra judayi | producer | 1.530000e-13 | 6.500e+06 | 1.000000 |
| 3 | 3 | Arthrodemus sp. | producer | 1.520000e-12 | 2.450e+07 | 1.000000 |
| 4 | 4 | Asterionella formosa | producer | 1.120000e-12 | 2.500e+06 | 1.000000 |
| 5 | 5 | Chromulina sp. | producer | 3.030000e-14 | 1.790e+08 | 1.000000 |
| 6 | 6 | Chroococcus dispersus | producer | 2.390000e-13 | 1.250e+07 | 1.000000 |
| 7 | 7 | Chroococcus limneticus | producer | 1.310000e-12 | 8.000e+06 | 1.000000 |
| 8 | 8 | Chrysosphaerella longispina | producer | 6.736000e-10 | 2.500e+06 | 1.000000 |
| 9 | 9 | Closteriopsis longissimus | producer | 2.366139e-13 | 5.050e+07 | 1.000000 |
| 10 | 10 | Cosmarium sp. | producer | 3.710000e-12 | 5.000e+05 | 1.000000 |
| 11 | 11 | Cryptomonas sp. 1 | producer | 2.308969e-13 | 4.850e+07 | 1.000000 |
| 12 | 12 | Cryptomonas sp. 2 | producer | 1.510000e-12 | 1.400e+07 | 1.000000 |
| 13 | 13 | Cryptomonas sp. 3 | producer | 6.720000e-13 | 9.000e+06 | 1.000000 |
| 14 | 14 | Cryptomonas sp. 4 | producer | 1.640000e-12 | 1.400e+07 | 1.000000 |
| 15 | 15 | Dactylococcopsis fascicularis | producer | 1.320000e-13 | 2.350e+07 | 1.000000 |
| 16 | 16 | Diceras sp. | producer | 1.530000e-13 | 7.500e+06 | 1.000000 |

| | | | | | | |
|----|----|---------------------------------------|--------------|--------------|-----------|----------|
| 17 | 17 | <i>Dictyosphaerium pulchellum</i> | producer | 4.998571e-13 | 7.000e+06 | 1.000000 |
| 18 | 18 | <i>Dinobryon bavaricum</i> | producer | 3.040000e-12 | 1.900e+07 | 1.000000 |
| 19 | 19 | <i>Dinobryon cylindricum</i> | producer | 4.355286e-12 | 3.500e+07 | 1.000000 |
| 20 | 20 | <i>Dinobryon sertularia</i> | producer | 1.074000e-11 | 2.000e+06 | 1.000000 |
| 21 | 21 | <i>Dinobryon sociale</i> | producer | 6.410000e-13 | 1.400e+07 | 1.000000 |
| 22 | 22 | <i>Glenodinium pulvisculus</i> | producer | 5.200000e-12 | 4.000e+06 | 1.000000 |
| 23 | 23 | <i>Glenodinium quadridens</i> | producer | 7.540000e-12 | 3.350e+07 | 1.000000 |
| 24 | 24 | <i>Gloeocystis</i> sp. | producer | 9.460000e-11 | 2.500e+06 | 1.000000 |
| 25 | 25 | <i>Mallomonas</i> sp. 1 | producer | 1.030000e-12 | 9.500e+06 | 1.000000 |
| 26 | 26 | <i>Mallomonas</i> sp. 2 | producer | 1.410000e-12 | 1.135e+07 | 1.000000 |
| 27 | 27 | <i>Mallomonas</i> -spiny sp. 1 | producer | 2.220000e-12 | 1.050e+07 | 1.000000 |
| 28 | 28 | <i>Mallomonas</i> -spiny sp. 2 | producer | 2.220000e-12 | 1.300e+07 | 1.000000 |
| 29 | 29 | <i>Microcystis aeruginosa</i> | producer | 1.620000e-11 | 7.500e+06 | 1.000000 |
| 30 | 30 | <i>Nostoc</i> sp. | producer | 7.970000e-13 | 1.000e+06 | 1.000000 |
| 31 | 31 | <i>Oocystis</i> sp. 1 | producer | 3.860000e-12 | 1.200e+07 | 1.000000 |
| 32 | 32 | <i>Oocystis</i> sp. 2 | producer | 6.320000e-12 | 1.500e+06 | 1.000000 |
| 33 | 33 | <i>Oscillatoria</i> sp. | producer | 1.610000e-12 | 3.000e+06 | 1.000000 |
| 34 | 34 | <i>Peridinium cinctum</i> | producer | 4.060000e-11 | 4.000e+06 | 1.000000 |
| 35 | 35 | <i>Peridinium limbatum</i> | producer | 6.460000e-11 | 9.000e+06 | 1.000000 |
| 36 | 36 | <i>Peridinium pulsillum</i> | producer | 1.580000e-12 | 6.200e+07 | 1.000000 |
| 37 | 37 | <i>Peridinium wisconsinense</i> | producer | 3.560000e-11 | 7.000e+06 | 1.000000 |
| 38 | 38 | <i>Quadrigula lacustris</i> | producer | 7.130000e-12 | 5.150e+07 | 1.000000 |
| 39 | 39 | <i>Quadrigula</i> sp. 2 | producer | 9.480000e-13 | 5.500e+06 | 1.000000 |
| 40 | 40 | <i>Rhizosolenia</i> sp. | producer | 6.860000e-13 | 2.800e+07 | 1.000000 |
| 41 | 41 | <i>Schroederia setigera</i> | producer | 6.370000e-13 | 4.450e+07 | 1.000000 |
| 42 | 42 | <i>Selenastrum minutum</i> | producer | 2.720000e-13 | 1.055e+08 | 1.000000 |
| 43 | 43 | <i>Sphaerocystis schroeteri</i> | producer | 1.080000e-11 | 1.000e+06 | 1.000000 |
| 44 | 44 | <i>Spinocosmarium</i> sp. | producer | 3.710000e-12 | 1.000e+06 | 1.000000 |
| 45 | 45 | <i>Staurostrum</i> sp. | producer | 4.300000e-12 | 4.500e+06 | 1.000000 |
| 46 | 46 | <i>Synedra</i> sp. | producer | 3.087467e-11 | 1.500e+06 | 1.000000 |
| 47 | 47 | <i>Synura</i> sp. | producer | 5.070000e-12 | 5.000e+05 | 1.000000 |
| 48 | 48 | <i>Trachelomonas</i> sp. | producer | 1.750000e-13 | 1.110e+08 | 1.000000 |
| 49 | 49 | Unclassified flagellates | producer | 3.460000e-13 | 9.400e+08 | 1.000000 |
| 50 | 50 | Unclassified microflagellates | producer | 1.020000e-13 | 6.300e+07 | 1.000000 |
| 51 | 51 | <i>Ascomorpha eucadis</i> | invertebrate | 2.968966e-10 | 1.740e+04 | 2.000000 |
| 52 | 52 | <i>Bosmina longirostris</i> | invertebrate | 1.550000e-09 | 7.750e+04 | 2.000000 |
| 53 | 53 | <i>Chaoborus punctipennis</i> | invertebrate | 2.550000e-07 | 1.200e+04 | 3.142379 |
| 54 | 54 | <i>Conochiloides dossuarius</i> | invertebrate | 1.600000e-10 | 1.184e+05 | 2.000000 |
| 55 | 55 | <i>Conochilus</i> (colonial) | invertebrate | 1.460000e-08 | 2.100e+03 | 2.000000 |
| 56 | 56 | <i>Conochilus</i> (solitary) | invertebrate | 3.500000e-11 | 1.800e+04 | 2.000000 |
| 57 | 57 | <i>Cyclops varians rubellus</i> | invertebrate | 2.134118e-08 | 5.100e+03 | 3.166667 |
| 58 | 58 | <i>Daphnia pulex</i> | invertebrate | 4.697241e-08 | 8.700e+03 | 2.071429 |
| 59 | 59 | <i>Daphnia rosea</i> | invertebrate | 1.360000e-08 | 1.200e+03 | 2.130435 |
| 60 | 60 | <i>Diaphanosoma leuchtenbergianum</i> | invertebrate | 2.240000e-09 | 7.200e+03 | 2.000000 |
| 61 | 61 | <i>Diaptomus oregonensis</i> | invertebrate | 1.440000e-08 | 3.000e+02 | 2.000000 |
| 62 | 62 | <i>Filinia longispina</i> | invertebrate | 1.800000e-10 | 1.200e+03 | 2.000000 |
| 63 | 63 | <i>Gastropus hyptopus</i> | invertebrate | 1.350000e-10 | 9.000e+02 | 2.000000 |
| 64 | 64 | <i>Gastropus stylifer</i> | invertebrate | 1.264744e-10 | 2.340e+04 | 2.000000 |

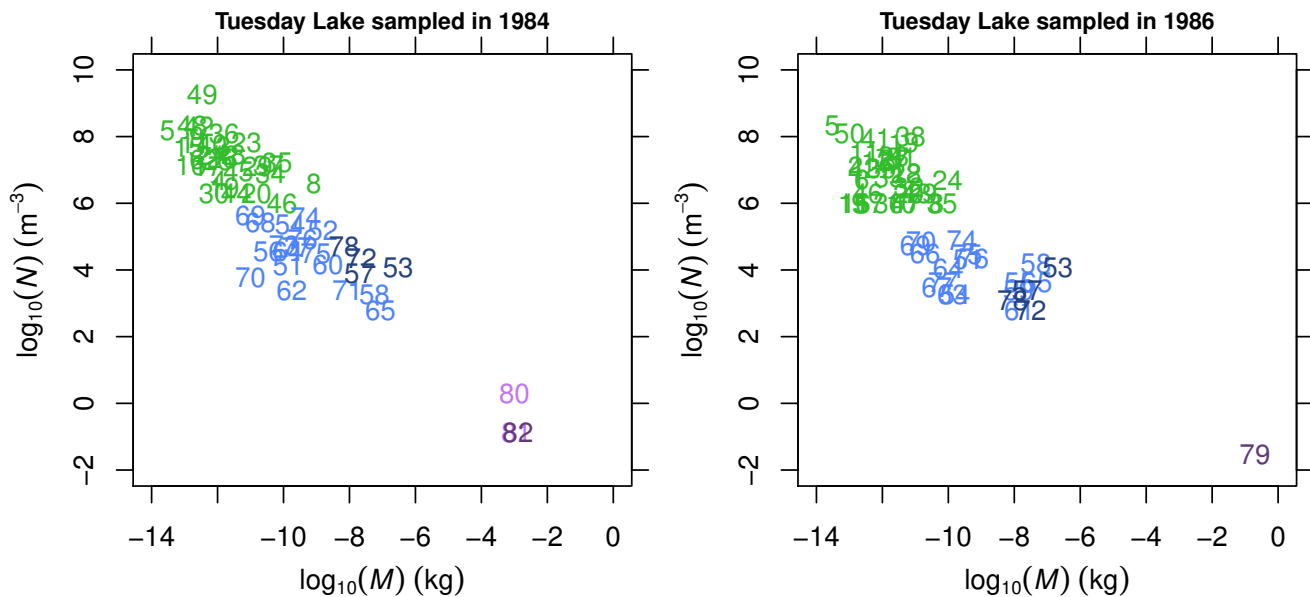
| | | | | | | |
|----|----|---------------------------|--------------|--------------|-----------|----------|
| 65 | 65 | Holopedium gibberum | invertebrate | 5.372500e-08 | 2.400e+03 | 2.000000 |
| 66 | 66 | Kellicottia bostoniensis | invertebrate | 2.000000e-11 | 1.590e+04 | 2.000000 |
| 67 | 67 | Kellicottia longispina | invertebrate | 4.500000e-11 | 1.500e+03 | 2.000000 |
| 68 | 68 | Kellicottia sp. | invertebrate | 2.000000e-11 | 1.280e+05 | 2.000000 |
| 69 | 69 | Keratella cochlearis | invertebrate | 1.000000e-11 | 2.399e+05 | 2.000000 |
| 70 | 70 | Keratella testudo | invertebrate | 1.460317e-11 | 3.780e+04 | 2.000000 |
| 71 | 71 | Leptodiaptomus siciloides | invertebrate | 8.800000e-09 | 1.200e+03 | 2.000000 |
| 72 | 72 | Orthocyclops modestus | invertebrate | 2.313846e-08 | 1.170e+04 | 3.166667 |
| 73 | 73 | Ploesoma sp. | invertebrate | 1.050000e-10 | 2.790e+04 | 2.000000 |
| 74 | 74 | Polyarthra vulgaris | invertebrate | 4.306820e-10 | 2.258e+05 | 2.000000 |
| 75 | 75 | Synchaeta sp. | invertebrate | 6.629293e-10 | 2.970e+04 | 2.000000 |
| 76 | 76 | Trichocerca cylindrica | invertebrate | 4.249133e-10 | 5.190e+04 | 2.000000 |
| 77 | 77 | Trichocerca multiepinis | invertebrate | 2.351765e-10 | 2.550e+04 | 2.000000 |
| 78 | 78 | Tropocyclops prasinus | invertebrate | 6.900000e-09 | 2.520e+04 | 3.166667 |
| 79 | 79 | Micropterus salmoides | vert.ecto | 2.000000e-01 | 1.500e-02 | 3.737936 |
| 80 | 80 | Phoxinus eos | vert.ecto | 1.010000e-03 | 9.850e-01 | 3.523756 |
| 81 | 81 | Phoxinus neogaeus | vert.ecto | 1.170000e-03 | 6.650e-02 | 3.523756 |
| 82 | 82 | Umbra limi | vert.ecto | 1.290000e-03 | 6.600e-02 | 3.796484 |

This code fragment could be easily extended to include any node property that NPS can compute.

8.3 Plot IDs

The following code fragment show how to produce a plot of the two communities side by side, showing global IDs.

```
> par(mfrow=c(1,2))
> for(community in TL)
{
  PlotNmM(community, show.nodes.as='labels', show.web=FALSE,
          node.labels=map[NP(community, 'node')], xlim=c(-14, 0),
          ylim=c(-2, 10))
}
```



By default `PlotNm` highlights species that are cannibals, which are shown in a darker colour. See help for the `PlotNPS` function and the ‘PlotsAndStats’ vignette for more information.

References

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