Working with collections of communities (0.1-639)

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2024-07-24

Contents

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 C**ommunity **P**ropertie**S**) 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
```

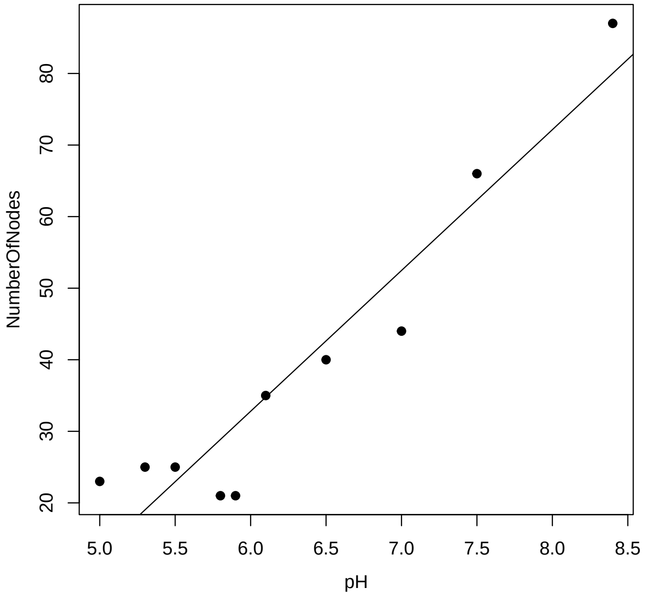
Let's examine the model's fit to the data.

```
> 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>'.

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

                  pH  S    L         C      Slope <unnamed> invertebrate     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
                    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
```

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 computed 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.

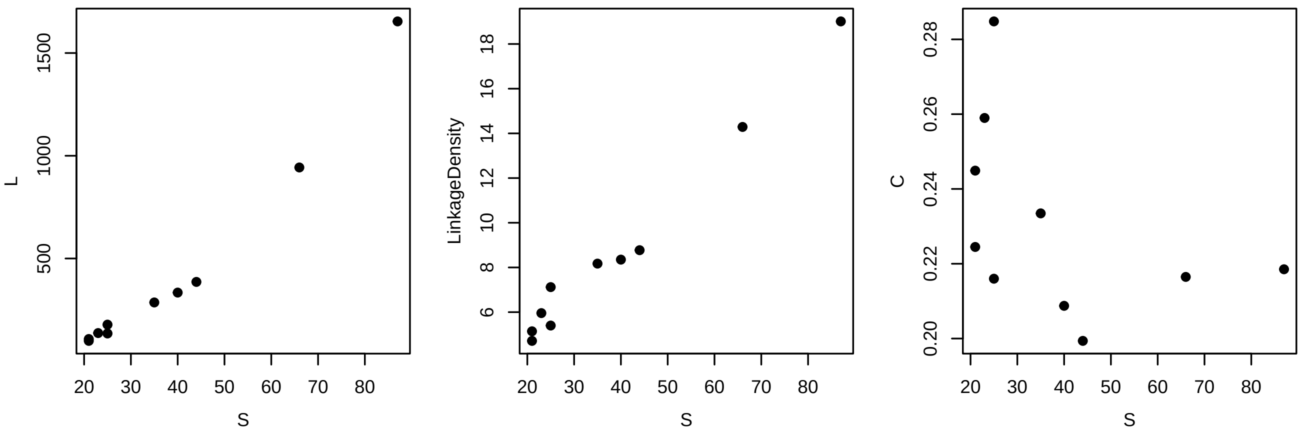
```
> CollectionCPS(pHWebs, c(Basal='FractionBasalNodes',
                          Intermediate='FractionIntermediateNodes',
                          TopLevel='FractionTopLevelNodes',
                          Isolated='FractionIsolatedNodes'))
```

```
                     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')))
```

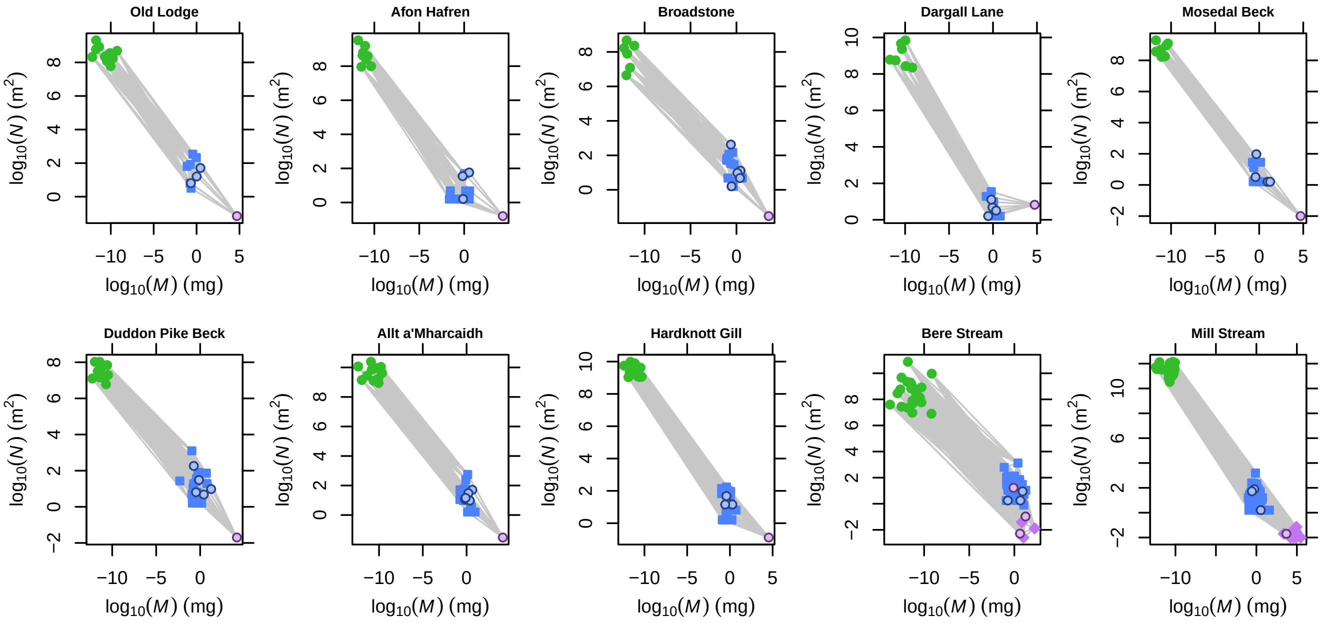
```
  community            resource                consumer resource.M resource.N  resource.B
1 Old Lodge Chironomidae undet. Siphonoperla torrentium 0.07809028       64.0   4.9977782
2 Old Lodge       Leuctra nigra Siphonoperla torrentium 0.94124878      214.4 201.8037377
3 Old Lodge     Nemoura cinerea 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

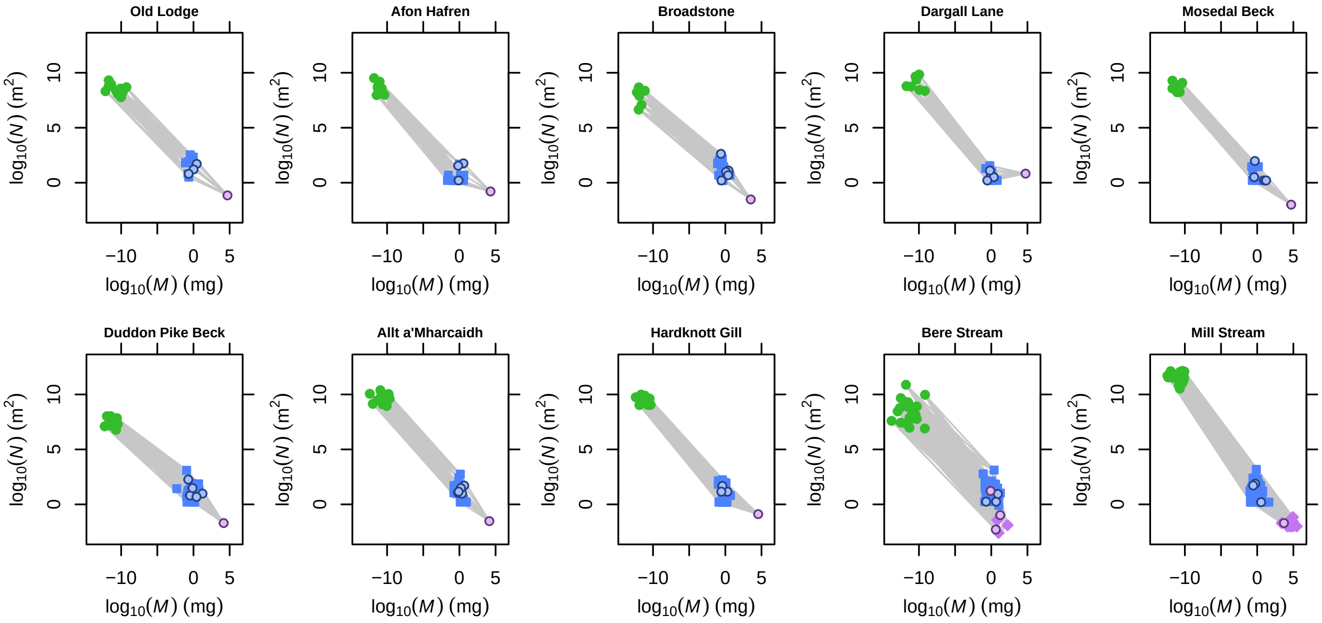
You can use R's `plot` function to 'eyeball' webs in a collection.

```
> plot(pHWebs)
```



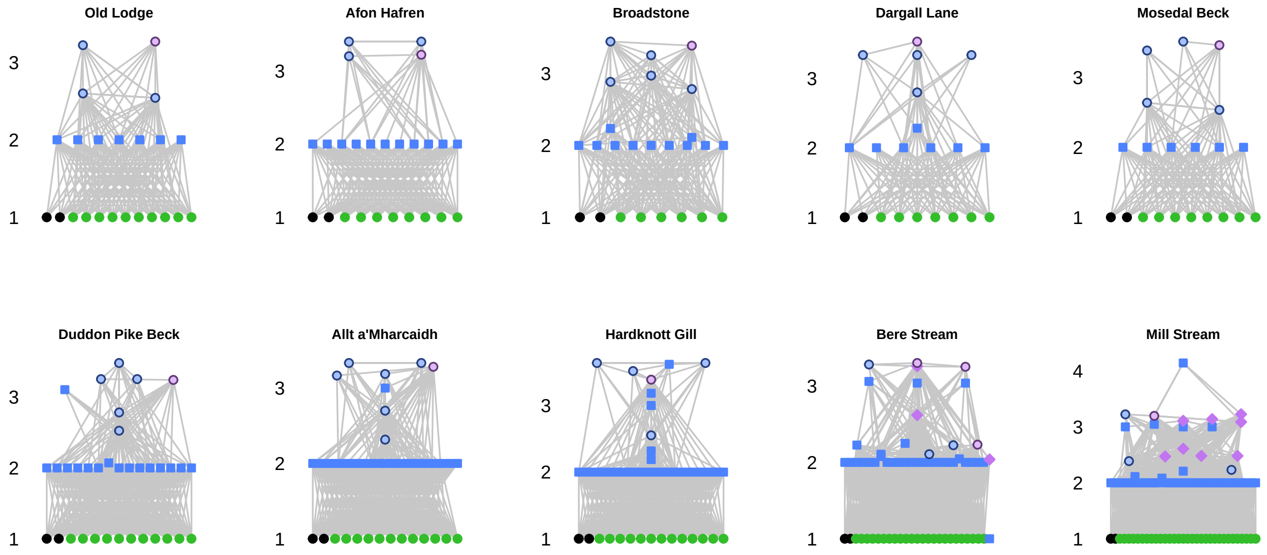
You can use R's plot parameters 'xlim' and 'ylim' to set limits for the x and y axes.

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



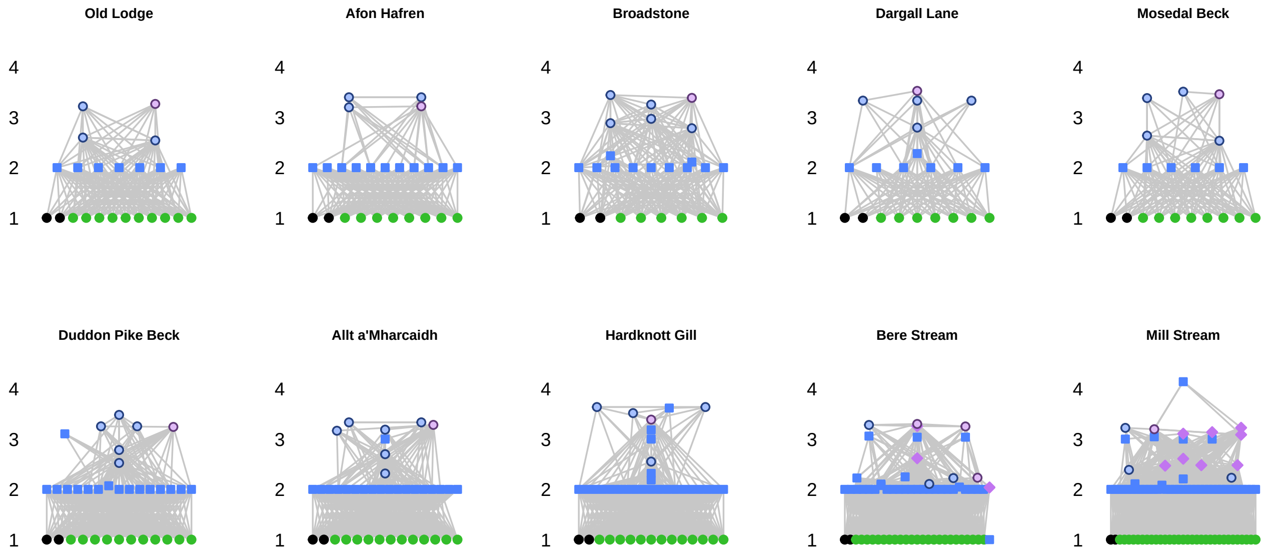
Cheddar examines the properties of the communities in the collection in order to decide which `Community`-level plot function to use. You can change this behaviour using the ‘plot.fn’ parameter. The `PlotWebByLevel` allows the webs to be viewed by trophic level.

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



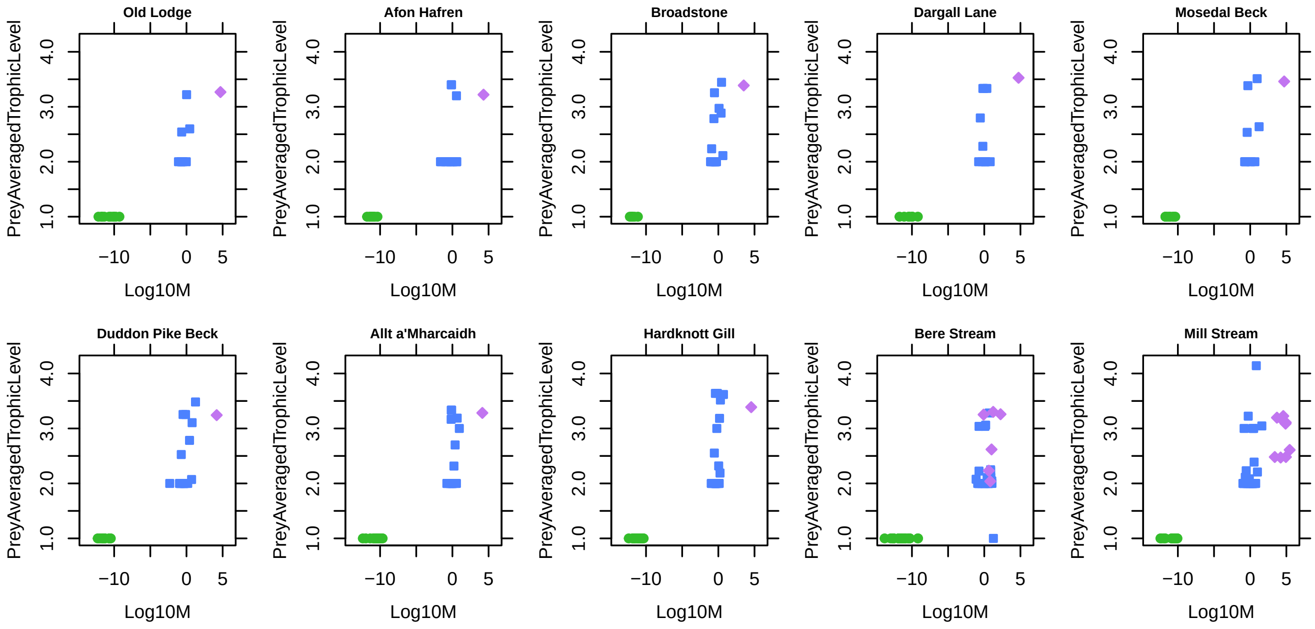
As in the previous example, the y axis limits can be made consistent.

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



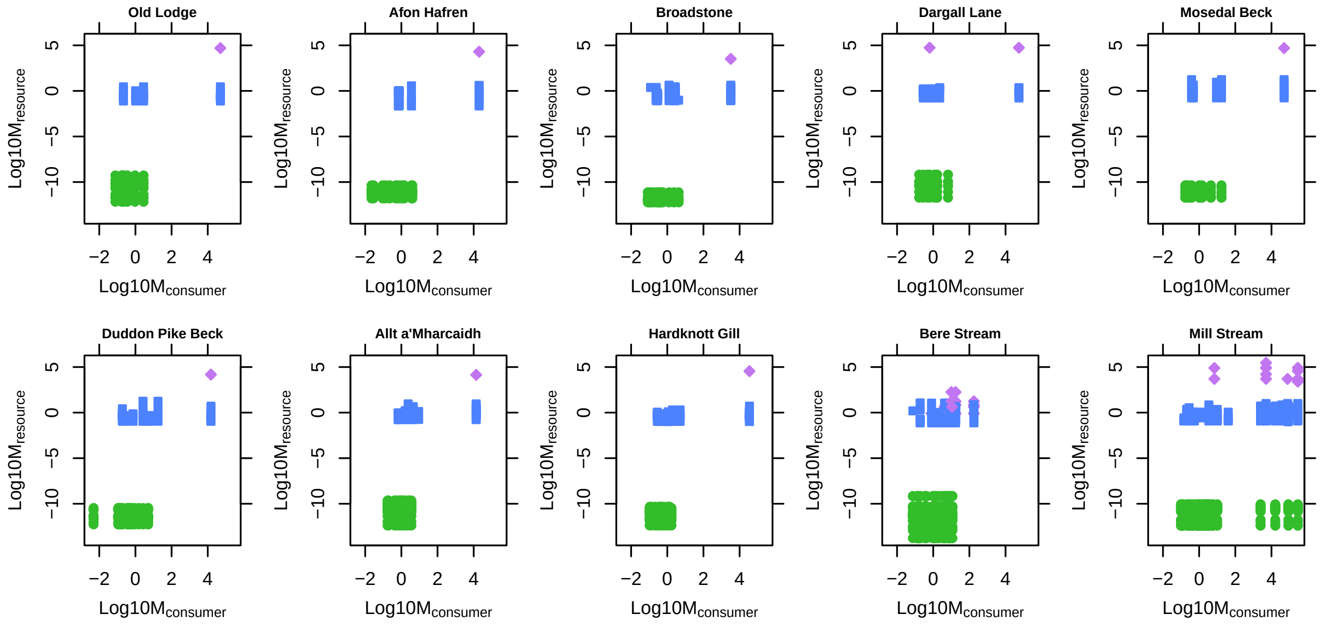
We can use the general-purpose function `PlotNPS` to plot any node properties that we like and all of the power of `PlotNPS` is available. The example below plots trophic level as a function of $\log_{10}$-transformed body mass. Each plot has the same axis limits. We have turned off plotting of the food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

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

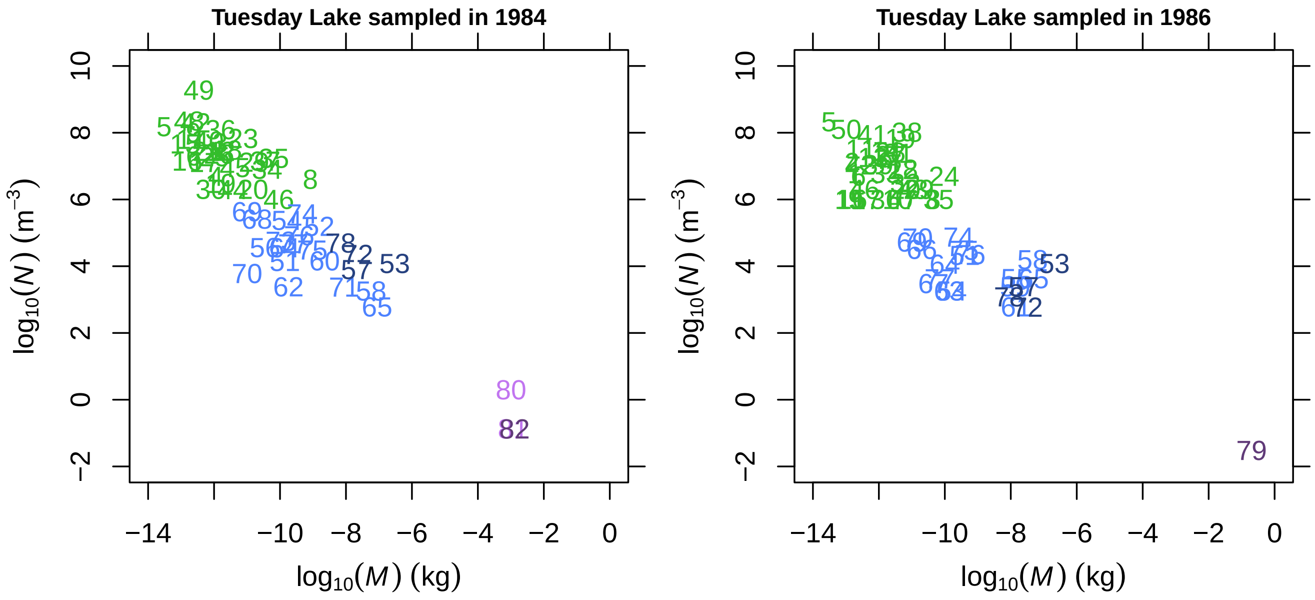
```
65 65            Holopedium gibberum invertebrate 5.372500e-08 2.400e+03 2.000000
66 66       Kellicottia bostoniensis invertebrate 2.000000e-11 1.590e+04 2.000000
67 67         Kellicottia longispina invertebrate 4.500000e-11 1.500e+03 2.000000
68 68                Kellicottia sp. invertebrate 2.000000e-11 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 multicrinis 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)
 {
     PlotNvM(community, show.nodes.as='labels', show.web=FALSE,
             node.labels=map[NP(community, 'node')], xlim=c(-14, 0),
             ylim=c(-2, 10))
 }
```



By default PlotNvM 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.

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