Working with collections of communities (0.1-613)

Lawrence Hudson

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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. (2008) Ledger et al. (2011) 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.
```

```
> # Access a community by name
> pHWebs[['Broadstone']]
```

```
Broadstone containing 25 nodes.
```

```
> # 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 **C**ollection **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
```
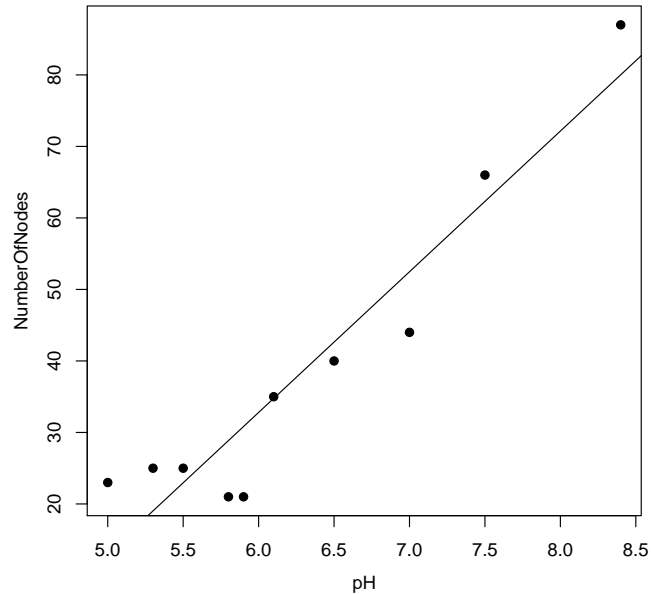
pH has a significant effect on number of nodes.

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, which defaults to 'category'.

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

```
                 pH  S    L         C       Slope V1 invertebrate      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
                    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.V1 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))
```
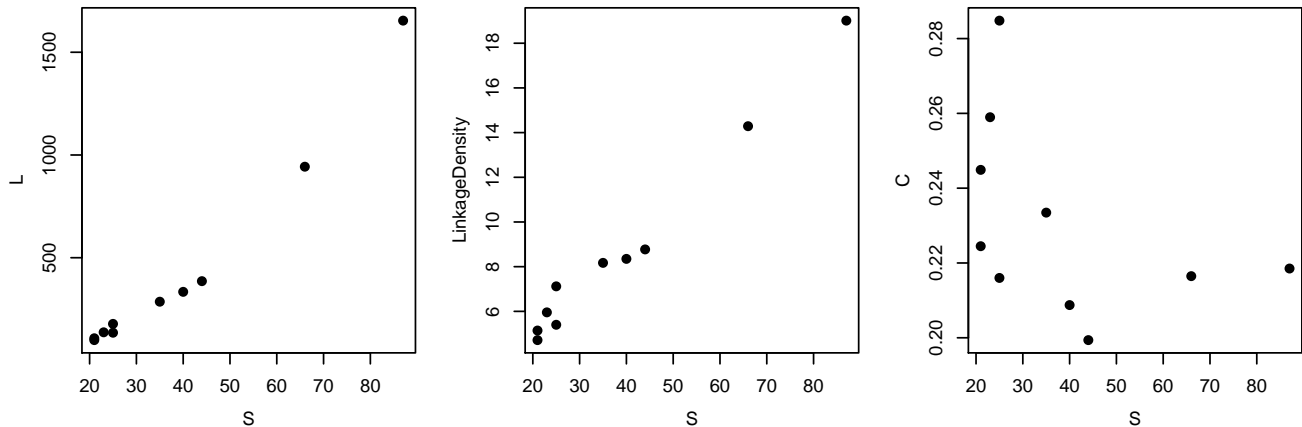

These plots are similar to those in Riede et al. (2010), Fig. 1 (p 143) and Brown et al. (2011), Fig. 7 (p 891) but using different data.

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.

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```
> # 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
```
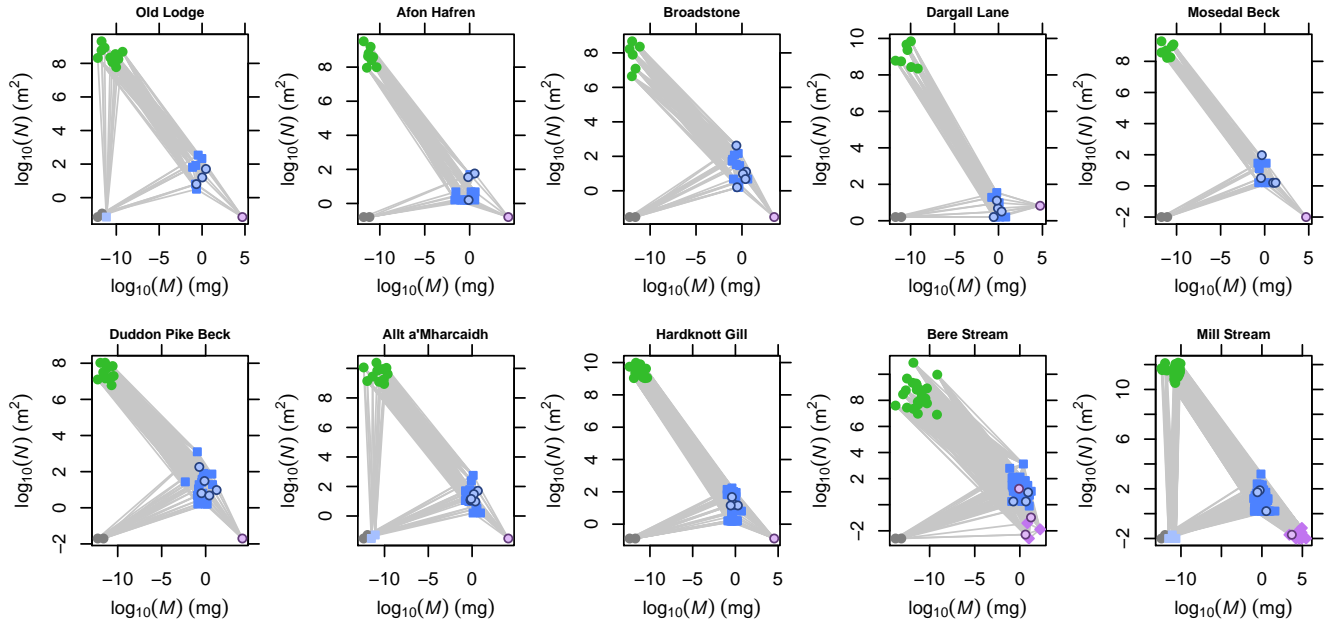
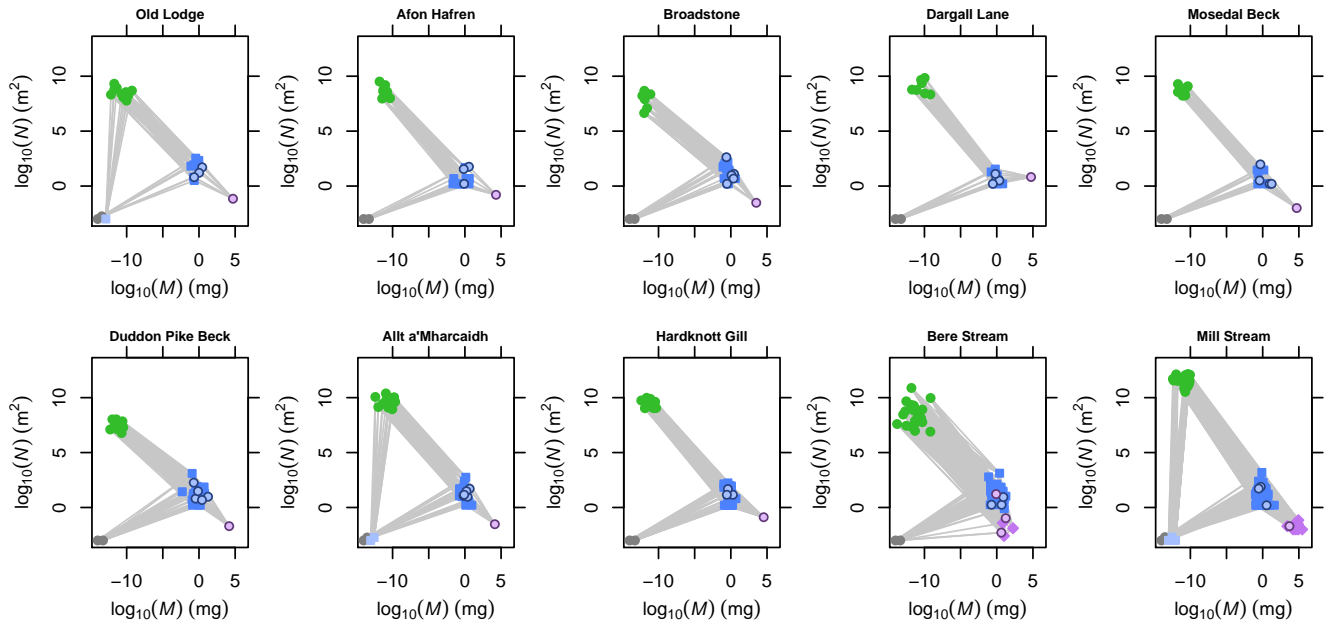| 4 | 15 | FALSE | 1.03837 | 16 | 16.61392 | 11 | FALSE |
| 5 | 15 | FALSE | 1.03837 | 16 | 16.61392 | 11 | FALSE |
| 6 | 15 | FALSE | 1.03837 | 16 | 16.61392 | 11 | FALSE |

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)
```
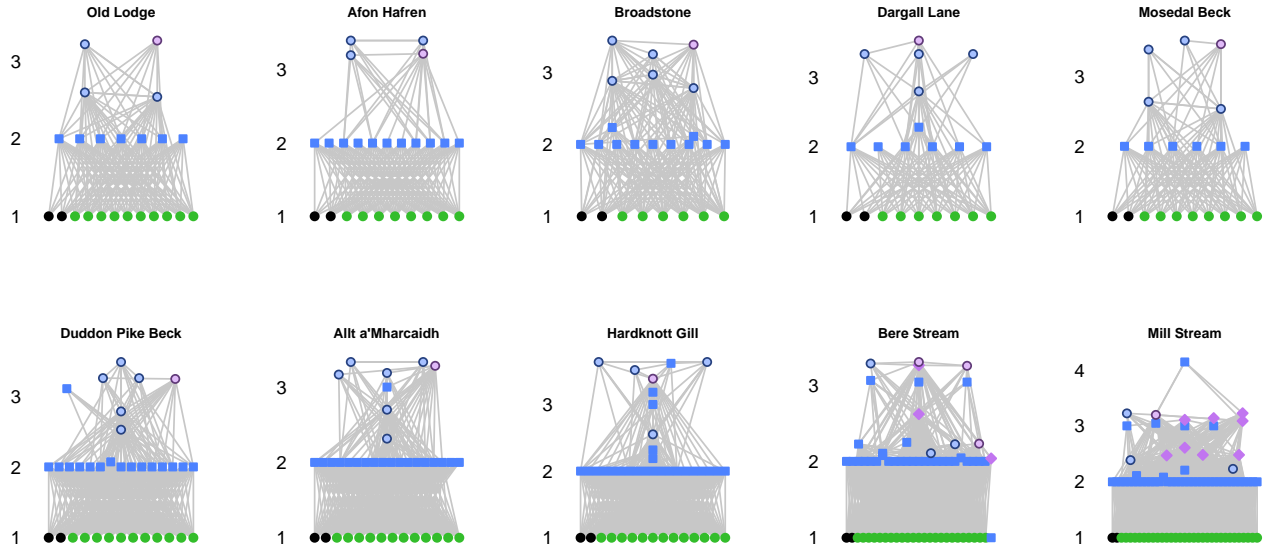

As in the previous example, the y axis limits can be made consistent.

```
> plot(pHWebs, plot.fn=PlotWebByLevel, ylim=c(1, 4.5))
```
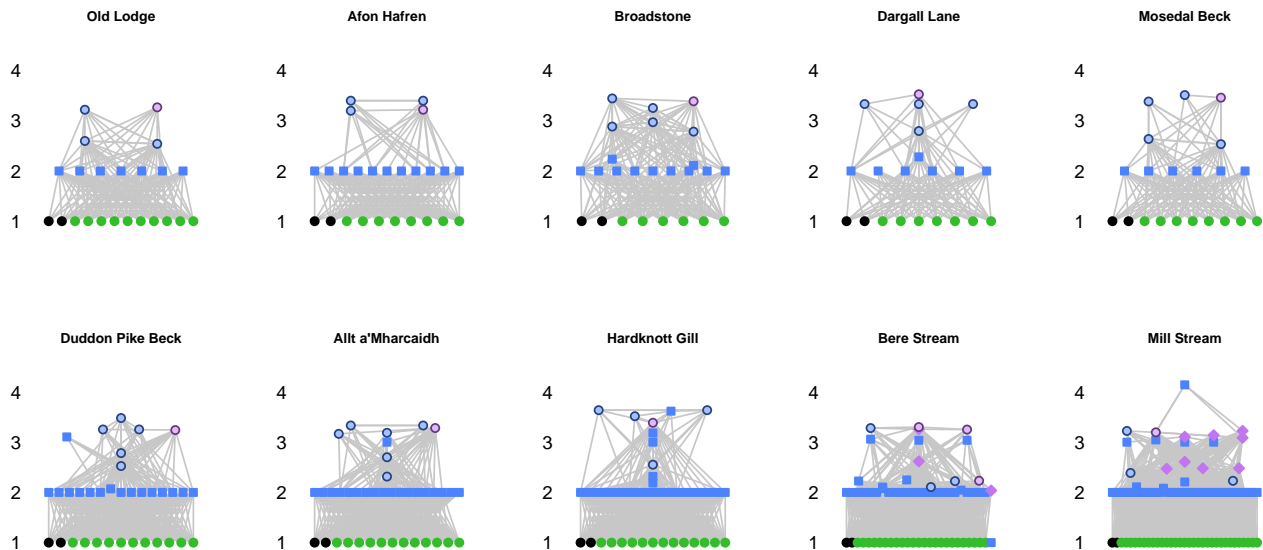
We can use the general-purpose function `PlotNPS` to plot any node properties that we like and all of the power of `PlotNPS` is available. The example below plots trophic level as a function of $\log_{10}$-transformed body mass. Each plot has the same axis limits. We have turned off plotting of the food 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))
```
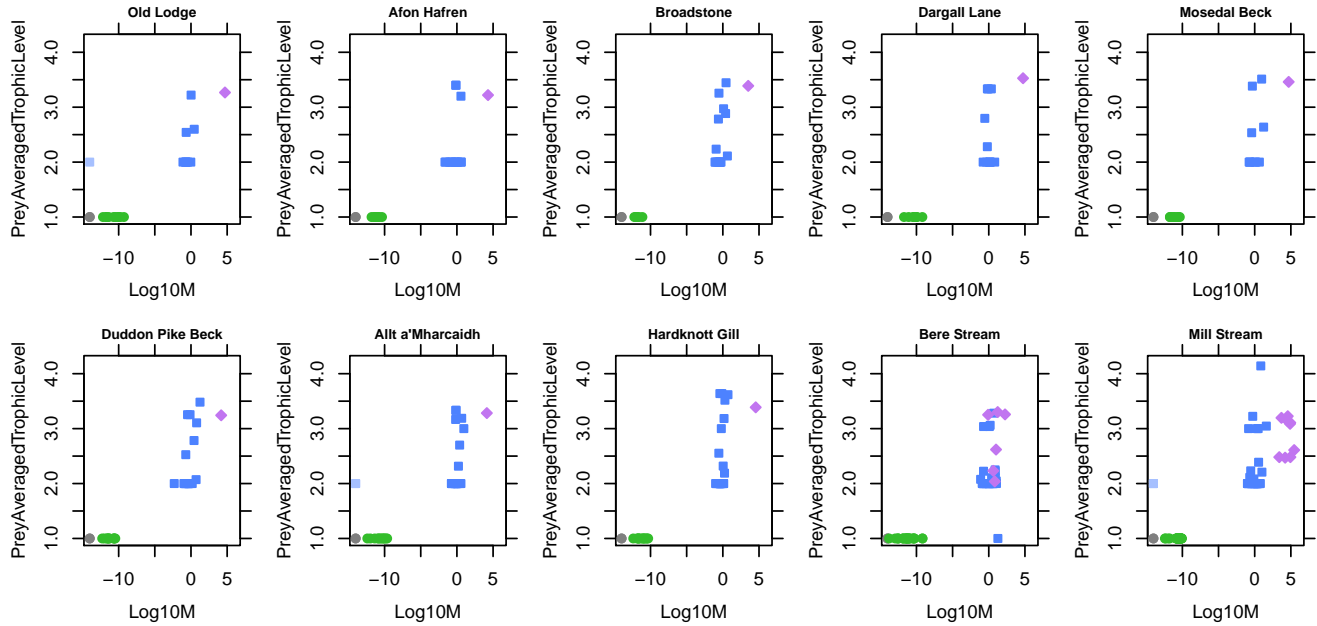

We can also use `PlotTLPS`, as shown below.

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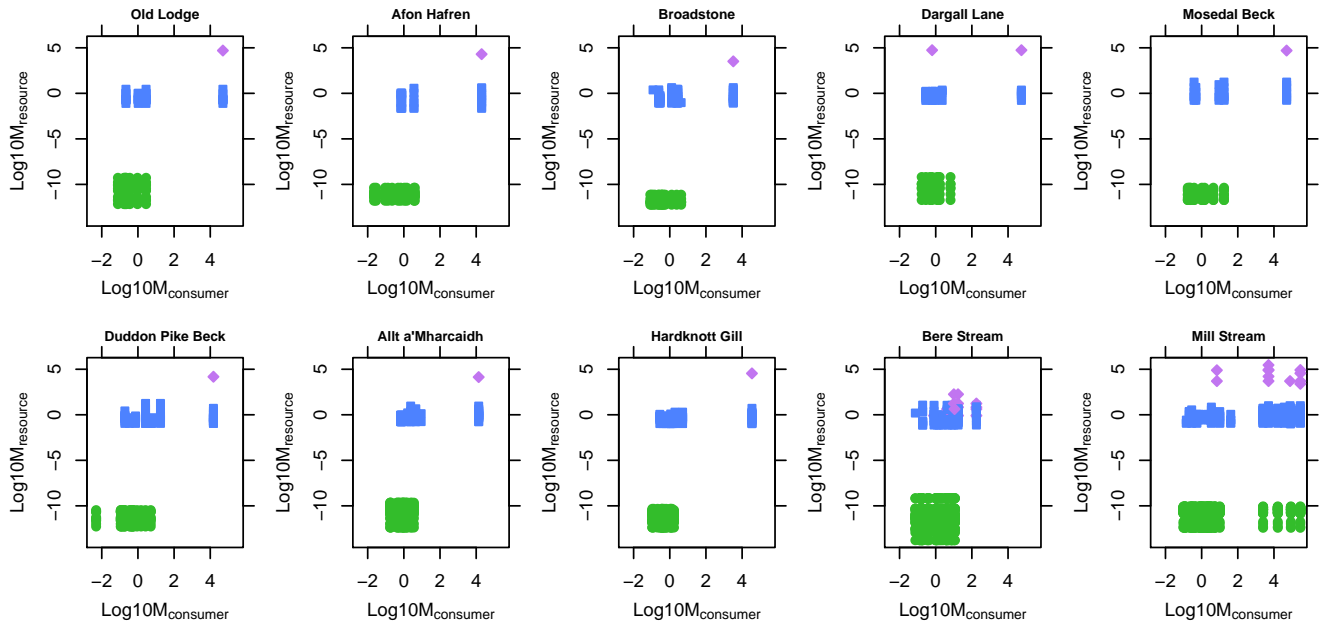
5 Modifying communities

As mentioned previously, collections cannot be modified directly because many checks for data consistency are run when collections are constructed (Section 3.1). However, the function `CollectionApply` is provided to assist with modifying collections. For example, with certain analyses it can be desirable to remove 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')
```

```
                                    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`.

```
> 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 the nodes each community 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
```

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, c('pH', 'NumberOfNodes'))
```

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

To sort by latitude and then by pH.

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

	lat	pH
Mill Stream	50.68	8.4
Bere Stream	50.73	7.5
Old Lodge	51.04	5.0
Broadstone	51.08	5.5
Afon Hafren	52.47	5.3
Hardknott Gill	54.40	7.0
Mosedal Beck	54.41	5.9

```
Duddon Pike Beck 54.41 6.1
Dargall Lane     55.08 5.8
Allt a'Mharcaidh 57.12 6.5
```

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., 2008, 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
283       Synorthocladius sp. Polycentropus flavomaculatus
355 Amorphous detritus (FPOM)         Synorthocladius sp.
356    Plant fragments (CPOM)         Synorthocladius sp.
```

```
357          Navicula gregaria        Synorthocladius sp.
358         Navicula tripunctata      Synorthocladius sp.
359        Gomphonema olivaceum       Synorthocladius sp.
360        Cocconeis placentula       Synorthocladius sp.
361   Rhoicosphenia abbreviata        Synorthocladius sp.
362       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))
  }
```
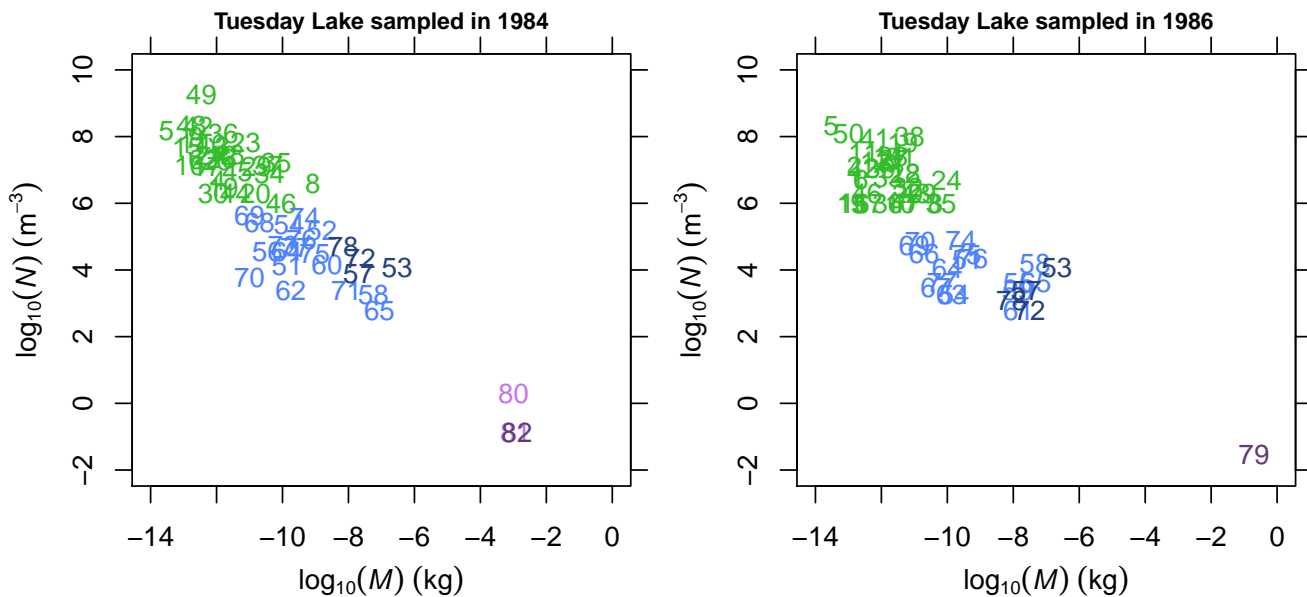

By default `PlotNvM` highlights species that are cannibals, which are shown in a darker colour. See help for the `PlotNPS` function and the 'PlotsAndStats' vignette for more information.

References

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