

Working with communities (0.1-631.1)

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Contents

| | | |
|----------|---|-----------|
| 1 | Introduction | 1 |
| 2 | Datasets | 2 |
| 3 | Community representation | 2 |
| 3.1 | Community properties | 3 |
| 3.2 | Nodes | 5 |
| 3.3 | Food web | 10 |
| 3.3.1 | Resource-consumer pairs | 10 |
| 3.3.2 | Trophic-link properties | 12 |
| 3.3.3 | Predation matrix | 13 |
| 3.3.4 | Node connectivity | 14 |
| 3.3.5 | Trophic chains | 16 |
| 3.3.6 | Large numbers of trophic chains | 21 |
| 3.3.7 | Trophic level | 23 |
| 3.3.8 | Link strengths | 24 |
| 4 | Community manipulations | 28 |
| 4.1 | Node order | 28 |
| 4.2 | Node order and intervality | 29 |
| 4.3 | Removing nodes | 31 |
| 4.4 | Removing cannibalistic links | 34 |
| 4.5 | Lumping nodes | 34 |

1 Introduction

The core of the package is a flexible, extendable representation of an ecological community, described in this vignette. Cheddar’s system for plotting communities and statistical analysis of communities is covered in the ‘PlotsAndStats’ vignette. The ‘ImportExport’ vignette covers getting community data in to and out of Cheddar. If you are working with collections, for example to see how community structure changes through time, across environmental gradients or resulting from experimental manipulation, read the ‘Collections’ vignette.

2 Datasets

Cheddar contains several published empirical food-web datasets (Table 1).

| Community | Notes | References |
|------------------|---|---|
| Benguela | Crude estimate of M ; trophic links have diet fraction | Yodzis (1998) |
| BroadstoneStream | M and N ; nodes are well resolved | Woodward et al. (2005) |
| TL84 and TL86 | M and N ; nodes are well resolved | Carpenter and Kitchell (1996) Cohen et al. (2003) Jonsson et al. (2005) |
| SkipwithPond | No M or N ; trophic links have ‘link.evidence’ and ‘link.life.stage’ properties | Warren (1989) |
| YthanEstuary | M and N for all nodes except detritus; nodes are well-resolved at high trophic levels but poorly resolved at low trophic levels | Hall and Raffaelli (1991) Emmerson and Raffaelli (2004) |

Table 1: Community data in Cheddar. M : body mass. N : numerical abundance.

3 Community representation

A Cheddar community has three aspects:

- *community properties* such as sampling date, lat & long, altitude, temperature and pH,
- *nodes*, which are the names of species together with any associated properties such as mean body mass, M , and mean numerical abundance, N , and taxonomic classification,
- the *food web*, defined as the names of each resource-consumer node pair, together with properties such as evidence for the link (e.g. empirically observed or inferred from literature).

The final aspect is optional - Cheddar communities need not contain trophic links. The `LoadCommunity` and `SaveCommunity` functions provide a standard data format, with each aspect stored in its own CSV (Comma-Separated Value) file, described further in the ‘ImportExport’ vignette. Cheddar allows user-defined data to be added to any of these three aspects simply by adding the data to the relevant CSV file. Any data so added will be available to Cheddar’s plotting and analysis functions. Each aspect is accessed using the functions `CPS` (for **C**ommunity **P**roperty**S**), `NPS` (for **N**ode **P**roperty**S**) and `TLPS` (for **T**rophic **L**ink **P**roperty**S**) (Table 2). Each of the three community aspects are discussed below. The following examples use the TL84 dataset, which is from Tuesday Lake in Michigan, USA, sampled in 1984 (Carpenter and Kitchell, 1996; Cohen et al., 2003; Jonsson et al., 2005). The data contain estimates of body mass, M , and numerical abundance, N , for each species.

```
> data(TL84) # Load the dataset
> print(TL84) # A description of the data
```

Tuesday Lake sampled in 1984 containing 56 nodes and 269 trophic links

| Aspect | Accessor function | PlotFunction | CSV file |
|------------|-------------------|--------------|-------------------|
| Properties | CPS | n/a | properties.csv |
| Nodes | NPS | PlotNPS | nodes.csv |
| Food web | TLPS | PlotTLPS | trophic.links.csv |

Table 2: Aspects of a Cheddar community

3.1 Community properties

The `CommunityPropertyNames` function returns the names of the community properties.

```
> CommunityPropertyNames(TL84)
```

```
[1] "title"    "M.units" "N.units" "lat"      "long"     "habitat"
```

‘title’ is the only property that a community is guaranteed to contain. The function `CPS` (for **C**ommunity **P**roperty **S**) returns a list of values.

```
> CPS(TL84)
```

```
$title
```

```
[1] "Tuesday Lake sampled in 1984"
```

```
$M.units
```

```
[1] "kg"
```

```
$N.units
```

```
[1] "m^-3"
```

```
$lat
```

```
[1] 46.21667
```

```
$long
```

```
[1] 89.53333
```

```
$habitat
```

```
[1] "Freshwater pelagic"
```

This shows the latitude and longitude of the lake and tells us the units for body mass, M , and numerical abundance, N , are kg and individuals per metre cubed, respectively. Many of the provided communities (Table 1) contain lat, long and habitat. Some communities have more properties. `CPS` lets you get a subset of community properties. For example, to see only the lat and long.

```
> CPS(TL84, c('lat', 'long'))
```

```
$lat
```

```
[1] 46.21667
```

```
$long
```

```
[1] 89.53333
```

CPS also accepts the names of functions that compute community properties. Two such functions are `NumberOfNodes` and `NumberOfTrophicLinks`.

```
> NumberOfNodes(TL84)

[1] 56

> NumberOfTrophicLinks(TL84)

[1] 269

> # A list containing lat, long, number of nodes and number of trophic links
> CPS(TL84, c('lat', 'long', 'NumberOfNodes', 'NumberOfTrophicLinks'))

$lat
[1] 46.21667

$long
[1] 89.53333

$NumberOfNodes
[1] 56

$NumberOfTrophicLinks
[1] 269
```

A named vector can be used to rename values.

```
> CPS(TL84, c('lat', 'long', S='NumberOfNodes', L='NumberOfTrophicLinks'))

$lat
[1] 46.21667

$long
[1] 89.53333

$S
[1] 56

$L
[1] 269
```

Names that are neither properties of the community nor function names result in NA.

```
> # Returns a list containing 'not a property'=NA
> CPS(TL84, c('not a property'))

$`not a property`
[1] NA
```

The related function `CollectionCPS` will be of interest if you are examining collections of communities, described in the ‘Collections’ vignette.

3.2 Nodes

Let's use two more Cheddar functions to get some more information about TL84's nodes.

```
> NumberOfNodes(TL84)
```

```
[1] 56
```

```
> NodePropertyNames(TL84)
```

```
[1] "node"      "category"  "M"         "N"         "kingdom"   "phylum"
[7] "class"     "order"     "family"    "genus"     "species"   "resolved.to"
```

The data contains 56 nodes and `NodePropertyNames` tells us that TL84 contains a lot of information about each node. We can get a table of these node properties by using the `NPS` function. To avoid printing the full table of 56 rows, the examples below use R's `head` and `tail` functions to show just the first or last six rows of the `data.frame` returned by `NPS`.

```
> head(NPS(TL84))
```

| | node | category | M | N | kingdom |
|-----------------------|-----------------------|----------|----------|---------|-----------|
| Nostoc sp. | Nostoc sp. | producer | 7.97e-13 | 2.0e+06 | Bacteria |
| Arthrodesmus sp. | Arthrodesmus sp. | producer | 1.52e-12 | 4.9e+07 | Plantae |
| Asterionella formosa | Asterionella formosa | producer | 1.12e-12 | 5.0e+06 | Chromista |
| Cryptomonas sp. 1 | Cryptomonas sp. 1 | producer | 2.03e-13 | 6.4e+07 | Chromista |
| Cryptomonas sp. 2 | Cryptomonas sp. 2 | producer | 1.51e-12 | 2.8e+07 | Chromista |
| Chroococcus dispersus | Chroococcus dispersus | producer | 2.39e-13 | 2.0e+07 | Bacteria |

| | phylum | class | order | family |
|-----------------------|---------------|--------------------|-----------------|------------------|
| Nostoc sp. | Cyanobacteria | Cyanophyceae | Nostocales | Nostocaceae |
| Arthrodesmus sp. | Charophyta | Zygnematomyphyceae | Desmidiiales | Desmidiaceae |
| Asterionella formosa | Ochrophyta | Bacillariophyceae | Fragilariales | Fragilariaceae |
| Cryptomonas sp. 1 | Cryptophyta | Cryptophyceae | Cryptomonadales | Cryptomonadaceae |
| Cryptomonas sp. 2 | Cryptophyta | Cryptophyceae | Cryptomonadales | Cryptomonadaceae |
| Chroococcus dispersus | Cyanobacteria | Cyanophyceae | Chroococcales | Chroococcaceae |

| | genus | species | resolved.to |
|-----------------------|--------------|-----------|-------------|
| Nostoc sp. | Nostoc | | Species |
| Arthrodesmus sp. | Arthrodesmus | | Species |
| Asterionella formosa | Asterionella | formosa | Species |
| Cryptomonas sp. 1 | Cryptomonas | | Species |
| Cryptomonas sp. 2 | Cryptomonas | | Species |
| Chroococcus dispersus | Chroococcus | dispersus | Species |

'node' is the only node property that a community is guaranteed to contain. Many of Cheddar's plotting and analysis functions make use of the 'category' node property; this property is optional but, if included in a community, it should contain one of 'producer', 'invertebrate', 'vert.ecto', 'vert.endo' or should be empty.

```
> # Just body mass
```

```
> head(NPS(TL84, 'M'))
```

```

M
Nostoc sp. 7.97e-13
Arthrodesmus sp. 1.52e-12
Asterionella formosa 1.12e-12
Cryptomonas sp. 1 2.03e-13
Cryptomonas sp. 2 1.51e-12
Chroococcus dispersus 2.39e-13

> # Body mass and numerical abundance.
> head(NPS(TL84, c('M', 'N')))
```

```

M N
Nostoc sp. 7.97e-13 2.0e+06
Arthrodesmus sp. 1.52e-12 4.9e+07
Asterionella formosa 1.12e-12 5.0e+06
Cryptomonas sp. 1 2.03e-13 6.4e+07
Cryptomonas sp. 2 1.51e-12 2.8e+07
Chroococcus dispersus 2.39e-13 2.0e+07
```

In addition to first-class node properties like M and N , you can also use `NPS` to assemble computed node properties by passing in the name(s) of function(s) that take a community object as the only parameter and return either a vector of length `NumberOfNodes` or a `matrix` or `data.frame` with `NumberOfNodes` rows. Cheddar contains many suitable functions and you can also write your own. For example, it is common to \log_{10} -transformation M and N , which we can do using the `Log10M` and `Log10N` functions.

```

> tail(NPS(TL84, c('Log10M', 'Log10N')))
```

| | Log10M | Log10N |
|------------------------|-----------|------------|
| Trichocerca cylindrica | -9.420216 | 4.9116902 |
| Tropocyclops prasinus | -8.164309 | 4.6919651 |
| Chaoborus punctipennis | -6.522879 | 4.0791812 |
| Phoxinus eos | -2.995679 | 0.2944662 |
| Phoxinus neogaeus | -2.931814 | -0.8761484 |
| Umbra limi | -2.889410 | -0.8794261 |

You can provide a mix of property and function names.

```

> tail(NPS(TL84, c('Log10M', 'Log10N', 'category', 'phylum')))
```

| | Log10M | Log10N | category | phylum |
|------------------------|-----------|------------|--------------|------------|
| Trichocerca cylindrica | -9.420216 | 4.9116902 | invertebrate | Rotifera |
| Tropocyclops prasinus | -8.164309 | 4.6919651 | invertebrate | Arthropoda |
| Chaoborus punctipennis | -6.522879 | 4.0791812 | invertebrate | Arthropoda |
| Phoxinus eos | -2.995679 | 0.2944662 | vert.ecto | Chordata |
| Phoxinus neogaeus | -2.931814 | -0.8761484 | vert.ecto | Chordata |
| Umbra limi | -2.889410 | -0.8794261 | vert.ecto | Chordata |

The `Log10MNBiomass` function returns a `matrix` of \log_{10} -transformed body mass, M , numerical abundance, N , and biomass, B , and is a convenient way to get all three of these properties in to a table.

```
> tail(NPS(TL84, c('Log10MNBiomass')))
```

| | Log10M | Log10N | Log10Biomass |
|------------------------|-----------|------------|--------------|
| Trichocerca cylindrica | -9.420216 | 4.9116902 | -4.508526 |
| Tropocyclops prasinus | -8.164309 | 4.6919651 | -3.472344 |
| Chaoborus punctipennis | -6.522879 | 4.0791812 | -2.443697 |
| Phoxinus eos | -2.995679 | 0.2944662 | -2.701212 |
| Phoxinus neogaeus | -2.931814 | -0.8761484 | -3.807962 |
| Umbra limi | -2.889410 | -0.8794261 | -3.768836 |

We can use NPS to assemble a table showing node degree: the number of trophic links in to and out of that node. Cheddar contains three functions that compute a different aspect of node degree.

```
> nps <- NPS(TL84, c('InDegree', 'OutDegree', 'Degree'))
> head(nps)
```

| | InDegree | OutDegree | Degree |
|-----------------------|----------|-----------|--------|
| Nostoc sp. | 0 | 4 | 4 |
| Arthrodesmus sp. | 0 | 3 | 3 |
| Asterionella formosa | 0 | 0 | 0 |
| Cryptomonas sp. 1 | 0 | 18 | 18 |
| Cryptomonas sp. 2 | 0 | 5 | 5 |
| Chroococcus dispersus | 0 | 18 | 18 |

```
> # This is always true for all nodes
> all(nps$Degree == nps$InDegree+nps$OutDegree)
```

```
[1] TRUE
```

Some readers will be more familiar with the terms ‘trophic vulnerability’ and ‘trophic generality’; the functions `TrophicVulnerability` and `TrophicGenerality` are synonyms for `OutDegree` and `InDegree` respectively. Cannibalistic links count twice towards `Degree` - one link going out and one going in. The cannibalistic fish *Umbra limi* in TL84 has no consumers other than itself so it has an `OutDegree` of one.

```
> IsCannibal(TL84)['Umbra limi']
```

```
Umbra limi
      TRUE
```

```
> InDegree(TL84)["Umbra limi"]
```

```
Umbra limi
      12
```

```
> OutDegree(TL84)["Umbra limi"]
```

```
Umbra limi
      1
```

```
> Degree(TL84)["Umbra limi"]
```

Umbra limi
13

We can combine some of these functions to investigate allometric degree distribution (Jonsson et al., 2005; Otto et al., 2007; Digel et al., 2011; Jacob et al., 2011), which describe how species' numbers of trophic links scale with their log-transformed body masses.

```
> tail(NPS(TL84, c('Log10M', 'OutDegree', 'InDegree', 'Degree')))
```

| | Log10M | OutDegree | InDegree | Degree |
|------------------------|-----------|-----------|----------|--------|
| Trichocerca cylindrica | -9.420216 | 4 | 6 | 10 |
| Tropocyclops prasinus | -8.164309 | 7 | 16 | 23 |
| Chaoborus punctipennis | -6.522879 | 4 | 22 | 26 |
| Phoxinus eos | -2.995679 | 1 | 9 | 10 |
| Phoxinus neogaeus | -2.931814 | 1 | 9 | 10 |
| Umbra limi | -2.889410 | 1 | 12 | 13 |

Some authors have been interested in how trophic level varies with body mass (Jacob et al., 2011). Two more functions suitable for use with NPS are `PreyAveragedTrophicLevel` and `ChainAveragedTrophicLevel`, which give different measures of each node's trophic level in the food web; these two functions, and others related to trophic level, are discussed further in section 3.3.

```
> tail(NPS(TL84, c('Log10M', 'PreyAveragedTrophicLevel',  
  'ChainAveragedTrophicLevel')))
```

| | Log10M | PreyAveragedTrophicLevel | ChainAveragedTrophicLevel |
|------------------------|-----------|--------------------------|---------------------------|
| Trichocerca cylindrica | -9.420216 | 2.000000 | 2.000000 |
| Tropocyclops prasinus | -8.164309 | 3.142857 | 3.333333 |
| Chaoborus punctipennis | -6.522879 | 3.171344 | 4.602527 |
| Phoxinus eos | -2.995679 | 3.529951 | 5.168337 |
| Phoxinus neogaeus | -2.931814 | 3.529951 | 5.168337 |
| Umbra limi | -2.889410 | 3.802678 | 5.835003 |

The column titles for the trophic-level measures are very long. We can use a named vector to get shortened column titles.

```
> tail(NPS(TL84, c('Log10M', PATL='PreyAveragedTrophicLevel',  
  CATL='ChainAveragedTrophicLevel')))
```

| | Log10M | PATL | CATL |
|------------------------|-----------|----------|----------|
| Trichocerca cylindrica | -9.420216 | 2.000000 | 2.000000 |
| Tropocyclops prasinus | -8.164309 | 3.142857 | 3.333333 |
| Chaoborus punctipennis | -6.522879 | 3.171344 | 4.602527 |
| Phoxinus eos | -2.995679 | 3.529951 | 5.168337 |
| Phoxinus neogaeus | -2.931814 | 3.529951 | 5.168337 |
| Umbra limi | -2.889410 | 3.802678 | 5.835003 |

NPS also allows parameters to be passed to functions. This is demonstrated using the `TrophicSpecies` function: in order to account for different levels of taxonomic resolution and other biases, researchers often lump biological species together. Species in the food web that have the same resources and consumers are the same 'trophic species' (Briand and Cohen, 1984; Pimm et al., 1991; Williams and Martinez, 2000). The `TrophicSpecies` function computes these IDs.


```
> tail(TrophicSpecies(TL84))
```

| | | |
|------------------------|-----------------------|------------------------|
| Trichocerca cylindrica | Tropocyclops prasinus | Chaoborus punctipennis |
| 16 | 13 | 20 |
| Phoxinus eos | Phoxinus neogaeus | Umbra limi |
| 21 | 21 | 22 |

Some analyses (e.g. Jonsson et al., 2005) exclude isolated species when computing trophic species numbers. Isolated species are those nodes that consume no others and have no consumers (Section 3.3.4). To compare the effect of including or excluding isolated species we can pass the function to NPS twice, once setting the ‘include.isolated’ parameter.

```
> head(NPS(TL84, list(TS.iso='TrophicSpecies',
                      TS.no.iso=list('TrophicSpecies', include.isolated=FALSE))))
```

| | TS.iso | TS.no.iso |
|-----------------------|--------|-----------|
| Nostoc sp. | 1 | 1 |
| Arthrodemus sp. | 2 | 2 |
| Asterionella formosa | 3 | NA |
| Cryptomonas sp. 1 | 4 | 3 |
| Cryptomonas sp. 2 | 5 | 4 |
| Chroococcus dispersus | 4 | 3 |

Asterionella formosa is an isolated species so has been given a trophic species of NA in the ‘TS.no.iso’ column. The `LumpTrophicSpecies` function lumps nodes together using these IDs (Section 4.5). The second argument to NPS can therefore be defined as a list containing either names of first class properties, names of functions that take only a community or lists in which the first element is the name of a function that takes a community and subsequent elements are *named* arguments to that function. Names of the list are column names in the returned `data.frame`.

NPS therefore makes it very easy to assemble tables of properties either for analysis or for presentation in a manuscript. The example below recreates the first ten rows of Jonsson et al. (2005), Appendix 1A (p74–75).

```
> head(NPS(TL84, list('category', BM='M', 'NA'='N',
                      TS=list('TrophicSpecies', include.isolated=FALSE),
                      TH=list('TrophicHeight', include.isolated=FALSE))))
```

10)

| | category | BM | NA | TS | TH |
|-----------------------------|----------|----------|---------|----|----|
| Nostoc sp. | producer | 7.97e-13 | 2.0e+06 | 1 | 1 |
| Arthrodemus sp. | producer | 1.52e-12 | 4.9e+07 | 2 | 1 |
| Asterionella formosa | producer | 1.12e-12 | 5.0e+06 | NA | NA |
| Cryptomonas sp. 1 | producer | 2.03e-13 | 6.4e+07 | 3 | 1 |
| Cryptomonas sp. 2 | producer | 1.51e-12 | 2.8e+07 | 4 | 1 |
| Chroococcus dispersus | producer | 2.39e-13 | 2.0e+07 | 3 | 1 |
| Closteriopsis longissimus | producer | 2.37e-13 | 1.0e+08 | 5 | 1 |
| Chrysosphaerella longispina | producer | 8.31e-10 | 4.0e+06 | NA | NA |
| Dinobryon bavaricum | producer | 2.44e-12 | 3.0e+07 | 6 | 1 |
| Dinobryon cylindricum | producer | 1.57e-12 | 3.0e+06 | 1 | 1 |

Some values in this table are different to those presented by Jonsson et al. (2005) in their Appendix 1A. Firstly, the numerical abundance values for zooplankton are different. Values in their table "...should be multiplied by 6 to convert them to concentrations in the epilimnion" (Jonsson et al., 2005), and our data incorporate that conversion. Secondly, the values of trophic height presented are slightly different for species at higher trophic levels because of the different methods used to break cycles (see the help for Cheddar's `TrophicSpecies` function). It is not clear from the text of Jonsson et al. (2005) exactly how they broke cycles. Because Cheddar is open source, users can refer readers to the function and version used to completely specify the algorithm used.

NPS returns NA for any names that are neither a first-class property of the community nor the name of a function.

```
> head(NPS(TL84, c('Not a property or function')))
```

| | Not a property or function |
|-----------------------|----------------------------|
| Nostoc sp. | NA |
| Arthrodesmus sp. | NA |
| Asterionella formosa | NA |
| Cryptomonas sp. 1 | NA |
| Cryptomonas sp. 2 | NA |
| Chroococcus dispersus | NA |

3.3 Food web

`NumberOfTrophicLinks` returns the number of trophic links that the community contains.

```
> NumberOfTrophicLinks(TL84)
```

```
[1] 269
```

Cheddar communities need not contain trophic links so this function might return zero. The following sections describe some different ways in which to view and analyse food webs in cheddar.

3.3.1 Resource-consumer pairs

`TLPS` (for **T**rophic **L**ink **P**roperty**S**) returns a `data.frame` of trophic links pairs (or NULL if the community has no food web). The `data.frame` always contains the columns 'resource' and 'consumer'.

```
> head(TLPS(TL84))
```

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

`TLPS` takes a parameter `node.properties`, which should be a vector of names suitable for passing to `NPS`. You can therefore use functions and names and can pass parameters to functions, just as in the `NPS` examples above.

```
> head(TLPS(TL84, node.properties='M'))
```

| | resource | consumer | resource.M |
|--------------------------|--------------------------|--------------------|------------|
| Cryptomonas sp. 1 | Cryptomonas sp. 1 | Ascomorpha eucadis | 2.03e-13 |
| Chroococcus dispersus | Chroococcus dispersus | Ascomorpha eucadis | 2.39e-13 |
| Unclassified flagellates | Unclassified flagellates | Ascomorpha eucadis | 3.46e-13 |
| Chromulina sp. | Chromulina sp. | Ascomorpha eucadis | 3.03e-14 |
| Selenastrum minutum | Selenastrum minutum | Ascomorpha eucadis | 2.72e-13 |
| Trachelomonas sp. | Trachelomonas sp. | Ascomorpha eucadis | 1.75e-13 |
| | consumer.M | | |
| Cryptomonas sp. 1 | 1.4e-10 | | |
| Chroococcus dispersus | 1.4e-10 | | |
| Unclassified flagellates | 1.4e-10 | | |
| Chromulina sp. | 1.4e-10 | | |
| Selenastrum minutum | 1.4e-10 | | |
| Trachelomonas sp. | 1.4e-10 | | |

```
> head(TLPS(TL84, node.properties=c('M','Biomass')))
```

| | resource | consumer | resource.M |
|--------------------------|--------------------------|--------------------|------------------|
| Cryptomonas sp. 1 | Cryptomonas sp. 1 | Ascomorpha eucadis | 2.03e-13 |
| Chroococcus dispersus | Chroococcus dispersus | Ascomorpha eucadis | 2.39e-13 |
| Unclassified flagellates | Unclassified flagellates | Ascomorpha eucadis | 3.46e-13 |
| Chromulina sp. | Chromulina sp. | Ascomorpha eucadis | 3.03e-14 |
| Selenastrum minutum | Selenastrum minutum | Ascomorpha eucadis | 2.72e-13 |
| Trachelomonas sp. | Trachelomonas sp. | Ascomorpha eucadis | 1.75e-13 |
| | resource.Biomass | consumer.M | consumer.Biomass |
| Cryptomonas sp. 1 | 1.2992e-05 | 1.4e-10 | 1.932e-06 |
| Chroococcus dispersus | 4.7800e-06 | 1.4e-10 | 1.932e-06 |
| Unclassified flagellates | 6.5048e-04 | 1.4e-10 | 1.932e-06 |
| Chromulina sp. | 4.5147e-06 | 1.4e-10 | 1.932e-06 |
| Selenastrum minutum | 5.4400e-05 | 1.4e-10 | 1.932e-06 |
| Trachelomonas sp. | 3.8850e-05 | 1.4e-10 | 1.932e-06 |

```
> head(TLPS(TL84, node.properties=c('M', B='Biomass')))
```

| | resource | consumer | resource.M |
|--------------------------|--------------------------|--------------------|------------|
| Cryptomonas sp. 1 | Cryptomonas sp. 1 | Ascomorpha eucadis | 2.03e-13 |
| Chroococcus dispersus | Chroococcus dispersus | Ascomorpha eucadis | 2.39e-13 |
| Unclassified flagellates | Unclassified flagellates | Ascomorpha eucadis | 3.46e-13 |
| Chromulina sp. | Chromulina sp. | Ascomorpha eucadis | 3.03e-14 |
| Selenastrum minutum | Selenastrum minutum | Ascomorpha eucadis | 2.72e-13 |
| Trachelomonas sp. | Trachelomonas sp. | Ascomorpha eucadis | 1.75e-13 |
| | resource.B | consumer.M | consumer.B |
| Cryptomonas sp. 1 | 1.2992e-05 | 1.4e-10 | 1.932e-06 |
| Chroococcus dispersus | 4.7800e-06 | 1.4e-10 | 1.932e-06 |
| Unclassified flagellates | 6.5048e-04 | 1.4e-10 | 1.932e-06 |
| Chromulina sp. | 4.5147e-06 | 1.4e-10 | 1.932e-06 |
| Selenastrum minutum | 5.4400e-05 | 1.4e-10 | 1.932e-06 |
| Trachelomonas sp. | 3.8850e-05 | 1.4e-10 | 1.932e-06 |

TLPS takes a parameter `link.properties`, which should be a vector of names that are either first-class trophic-link properties or are functions. Functions should take a community as the first parameter and a second parameter that is a `data.frame` containing the columns ‘resource’ and ‘consumer’. They should return either a vector of length `NumberOfTrophicLinks` or a matrix or `data.frame` with `NumberOfTrophicLinks` rows.

3.3.2 Trophic-link properties

Food web data in Cheddar communities can be augmented with extra information. The dataset of SkipwithPond (Warren, 1989) contains two such properties: ‘link.evidence’ and ‘link.life.stage’.

```
> data(SkipwithPond)
> head(TLPS(SkipwithPond))
```

| | resource | consumer | link.evidence |
|---|--|------------------|---------------|
| 1 | Small oligochaetes (principally Enchytraeidae) | Polycelis tenuis | Inferred |
| 2 | Lumbriculus variegatus | Polycelis tenuis | Inferred |
| 3 | Procladius sagittalis | Polycelis tenuis | Inferred |
| 4 | Corynoneura scutellata | Polycelis tenuis | Inferred |
| 5 | Chironomus dorsalis | Polycelis tenuis | Known |
| 6 | Glyptotendipes pallens | Polycelis tenuis | Known |

```
link.life.stage
1 All life stages
2 All life stages
3 All life stages
4 All life stages
5 All life stages
6 All life stages
```

`TrophicLinkPropertyNames` returns the names of the trophic-link properties in a community.

```
> TrophicLinkPropertyNames(SkipwithPond)
```

| | | | | |
|-----|------------|------------|-----------------|-------------------|
| [1] | "resource" | "consumer" | "link.evidence" | "link.life.stage" |
|-----|------------|------------|-----------------|-------------------|

TLPS accepts a ‘link.properties’ parameter. You can use this to get a subset of the first-class link properties. The columns ‘resource’ and ‘consumer’ are always returned.

```
> head(TLPS(SkipwithPond, link.properties='link.evidence'))
```

| | resource | consumer | link.evidence |
|---|--|------------------|---------------|
| 1 | Small oligochaetes (principally Enchytraeidae) | Polycelis tenuis | Inferred |
| 2 | Lumbriculus variegatus | Polycelis tenuis | Inferred |
| 3 | Procladius sagittalis | Polycelis tenuis | Inferred |
| 4 | Corynoneura scutellata | Polycelis tenuis | Inferred |
| 5 | Chironomus dorsalis | Polycelis tenuis | Known |
| 6 | Glyptotendipes pallens | Polycelis tenuis | Known |

TLPS takes a parameter `link.properties`, which should be a vector of names that are either first-class trophic-link properties or are functions. Functions should take a community as the only parameter.

They should return either a vector of length `NumberOfTrophicLinks` or a matrix or data.frame with `NumberOfTrophicLinks` rows. This is illustrated by the code fragment below, which uses the `Log10RCMRatio` function to get the \log_{10} -transformed ratio between body mass of the resource and consumer in each trophic link in TL84.

```
> head(TLPS(TL84, link.properties='Log10RCMRatio'))
```

| | resource | consumer | Log10RCMRatio |
|---|--------------------------|--------------------|---------------|
| 1 | Cryptomonas sp. 1 | Ascomorpha eucadis | -2.838632 |
| 2 | Chroococcus dispersus | Ascomorpha eucadis | -2.767730 |
| 3 | Unclassified flagellates | Ascomorpha eucadis | -2.607052 |
| 4 | Chromulina sp. | Ascomorpha eucadis | -3.664685 |
| 5 | Selenastrum minutum | Ascomorpha eucadis | -2.711559 |
| 6 | Trachelomonas sp. | Ascomorpha eucadis | -2.903090 |

You can combine `node.properties` and `link.properties`.

```
> head(TLPS(TL84, node.properties='Log10M', link.properties='Log10RCMRatio'))
```

| | resource | consumer | Log10RCMRatio | resource.Log10M |
|---|--------------------------|--------------------|---------------|-----------------|
| 1 | Cryptomonas sp. 1 | Ascomorpha eucadis | -2.838632 | -12.69250 |
| 2 | Chroococcus dispersus | Ascomorpha eucadis | -2.767730 | -12.62160 |
| 3 | Unclassified flagellates | Ascomorpha eucadis | -2.607052 | -12.46092 |
| 4 | Chromulina sp. | Ascomorpha eucadis | -3.664685 | -13.51856 |
| 5 | Selenastrum minutum | Ascomorpha eucadis | -2.711559 | -12.56543 |
| 6 | Trachelomonas sp. | Ascomorpha eucadis | -2.903090 | -12.75696 |

| | consumer.Log10M |
|---|-----------------|
| 1 | -9.853872 |
| 2 | -9.853872 |
| 3 | -9.853872 |
| 4 | -9.853872 |
| 5 | -9.853872 |
| 6 | -9.853872 |

3.3.3 Predation matrix

The `PredationMatrix` function returns an R matrix object. The matrix returned by the code fragment below is 56 x 56 and so is not shown for brevity.

```
> pm <- PredationMatrix(TL84)
```

In the example above, all entries in 'pm' are either 0 or 1. This summation below computes the number of 1s in the matrix, which is the same as the number of trophic links in the community.

```
> sum(pm)
```

```
[1] 269
```

```
> NumberOfTrophicLinks(TL84)
```

```
[1] 269
```

Data that contain estimates of link strength can be used to construct a weighted predation matrix, such as the *Benguela* dataset, which contains the ‘diet.fraction’ node property (Yodzis, 1998).

```
> data(Benguela)
> pm <- PredationMatrix(Benguela, weight='diet.fraction')
```

More information about link strengths is in Section 3.3.8.

3.3.4 Node connectivity

A node in a community can be defined as falling in to one of four categories (Table 3). A node will

| Category | Description |
|--------------|---|
| Isolated | No resources or consumers |
| Basal | No resources and one or more consumers |
| Top-level | One or more resources and no consumers |
| Intermediate | Nodes not fitting any of the above categories |

Table 3: Node connectivity. Cannibalistic links are disregarded.

satisfy only one of the above four definitions. These definitions allow three additional definitions (Table 4). For each of the seven definitions (Tables 3 and 4), ‘X’, there are three functions: *IsXNode*, *XNodes*

| Category | Description |
|---------------|-------------------------------------|
| Connected | Basal, Intermediate or Top-level |
| Non-basal | Isolated, Intermediate or Top-level |
| Non-top-level | Isolated, Basal or Intermediate |

Table 4: Additional node connectivity

and *FractionXNodes*. The first returns a vector of type *logical* of length *NumberOfNodes*; values are *TRUE* for nodes that fit the definition of ‘X’. The second returns the names of nodes for which *IsXNode* returns *TRUE*. The third returns the proportion of nodes in the community that fit the definition of ‘X’. For example, a community’s isolated species can be accessed by using *IsolatedNodes*.

```
> IsolatedNodes(TL84)

[1] "Asterionella formosa"      "Chrysosphaerella longispina"
[3] "Diceras sp."              "Rhizosolenia sp."
[5] "Spinocosmarium sp."       "Staurostrum sp."
```

We can use the *IsXNode* functions together with *NPS* to see a table of connectivity for the whole community.

```
> connectivity <- NPS(TL84, c(Basal='IsBasalNode',
                             Isolated='IsIsolatedNode',
                             Intermediate='IsIntermediateNode',
                             TopLevel='IsTopLevelNode'))
> connectivity
```

| | Basal | Isolated | Intermediate | TopLevel |
|--------------------------------|-------|----------|--------------|----------|
| Nostoc sp. | TRUE | FALSE | FALSE | FALSE |
| Arthrodesmus sp. | TRUE | FALSE | FALSE | FALSE |
| Asterionella formosa | FALSE | TRUE | FALSE | FALSE |
| Cryptomonas sp. 1 | TRUE | FALSE | FALSE | FALSE |
| Cryptomonas sp. 2 | TRUE | FALSE | FALSE | FALSE |
| Chroococcus dispersus | TRUE | FALSE | FALSE | FALSE |
| Closteriopsis longissimus | TRUE | FALSE | FALSE | FALSE |
| Chrysosphaerella longispina | FALSE | TRUE | FALSE | FALSE |
| Dinobryon bavaricum | TRUE | FALSE | FALSE | FALSE |
| Dinobryon cylindricum | TRUE | FALSE | FALSE | FALSE |
| Dactylococcopsis fascicularis | TRUE | FALSE | FALSE | FALSE |
| Diceras sp. | FALSE | TRUE | FALSE | FALSE |
| Dictyosphaerium pulchellum | TRUE | FALSE | FALSE | FALSE |
| Dinobryon sertularia | TRUE | FALSE | FALSE | FALSE |
| Dinobryon sociale | TRUE | FALSE | FALSE | FALSE |
| Glenodinium quadridens | TRUE | FALSE | FALSE | FALSE |
| Microcystis aeruginosa | TRUE | FALSE | FALSE | FALSE |
| Mallomonas sp. 1 | TRUE | FALSE | FALSE | FALSE |
| Mallomonas sp. 2 | TRUE | FALSE | FALSE | FALSE |
| Unclassified flagellates | TRUE | FALSE | FALSE | FALSE |
| Peridinium limbatum | TRUE | FALSE | FALSE | FALSE |
| Peridinium cinctum | TRUE | FALSE | FALSE | FALSE |
| Peridinium pulsillum | TRUE | FALSE | FALSE | FALSE |
| Peridinium wisconsinense | TRUE | FALSE | FALSE | FALSE |
| Chromulina sp. | TRUE | FALSE | FALSE | FALSE |
| Rhizosolenia sp. | FALSE | TRUE | FALSE | FALSE |
| Selenastrum minutum | TRUE | FALSE | FALSE | FALSE |
| Spinocosmarium sp. | FALSE | TRUE | FALSE | FALSE |
| Staurostrum sp. | FALSE | TRUE | FALSE | FALSE |
| Synedra sp. | TRUE | FALSE | FALSE | FALSE |
| Trachelomonas sp. | TRUE | FALSE | FALSE | FALSE |
| Ascomorpha eucadis | FALSE | FALSE | TRUE | FALSE |
| Synchaeta sp. | FALSE | FALSE | TRUE | FALSE |
| Bosmina longirostris | FALSE | FALSE | TRUE | FALSE |
| Conochilus (solitary) | FALSE | FALSE | TRUE | FALSE |
| Cyclops varians rubellus | FALSE | FALSE | TRUE | FALSE |
| Diaphanosoma leuchtenbergianum | FALSE | FALSE | TRUE | FALSE |
| Daphnia pulex | FALSE | FALSE | TRUE | FALSE |
| Filinia longispina | FALSE | FALSE | TRUE | FALSE |
| Conochiloides dossuarius | FALSE | FALSE | TRUE | FALSE |
| Gastropus styliifer | FALSE | FALSE | TRUE | FALSE |
| Holopedium gibberum | FALSE | FALSE | TRUE | FALSE |
| Kellicottia sp. | FALSE | FALSE | TRUE | FALSE |
| Keratella cochlearis | FALSE | FALSE | TRUE | FALSE |
| Keratella testudo | FALSE | FALSE | TRUE | FALSE |
| Leptodiaptomus siciloides | FALSE | FALSE | TRUE | FALSE |
| Orthocyclops modestus | FALSE | FALSE | TRUE | FALSE |

| | | | | |
|--------------------------|-------|-------|-------|-------|
| Ploesoma sp. | FALSE | FALSE | TRUE | FALSE |
| Polyarthra vulgaris | FALSE | FALSE | TRUE | FALSE |
| Trichocerca multicroinis | FALSE | FALSE | TRUE | FALSE |
| Trichocerca cylindrica | FALSE | FALSE | TRUE | FALSE |
| Tropocyclops prasinus | FALSE | FALSE | TRUE | FALSE |
| Chaoborus punctipennis | FALSE | FALSE | TRUE | FALSE |
| Phoxinus eos | FALSE | FALSE | TRUE | FALSE |
| Phoxinus neogaeus | FALSE | FALSE | TRUE | FALSE |
| Umbra limi | FALSE | FALSE | FALSE | TRUE |

Because nodes can fit only one of the definitions in Table 3, each row in the `connectivity data.frame` should have one, and only one, value of `TRUE`. We can verify this by summing each row using R's `apply` function.

```
> all(1==apply(connectivity, 1, sum))
```

```
[1] TRUE
```

The following summations are also 1.

```
> sum(FractionBasalNodes(TL84),
      FractionIntermediateNodes(TL84),
      FractionTopLevelNodes(TL84),
      FractionIsolatedNodes(TL84))
```

```
[1] 1
```

```
> sum(FractionConnectedNodes(TL84),
      FractionIsolatedNodes(TL84))
```

```
[1] 1
```

```
> sum(FractionBasalNodes(TL84),
      FractionNonBasalNodes(TL84))
```

```
[1] 1
```

```
> sum(FractionTopLevelNodes(TL84),
      FractionNonTopLevelNodes(TL84))
```

```
[1] 1
```

3.3.5 Trophic chains

Some network properties and analyses require knowledge of every unique path - 'trophic chain' - through the food-web. A trophic chain starts with a basal node (Section 3.3.4) and ends when it is not possible to add nodes that are not already in the chain. Loops and cannibalism are therefore ignored when computing trophic chains. For communities that have one or more top-level nodes each trophic chain will end with a top-level node. The 'length' of a chain is defined as the number of links that it contains, i.e. the number of nodes in the chain minus one.

Cheddar provides two functions for examining trophic chains. The `TrophicChains` function returns a `data.frame` of trophic chains.


```
> tc <- TrophicChains(TL84)
> dim(tc)
```

```
[1] 5988      8
```

There are 5988 unique chains in the food web and the longest chains contain 8 nodes. Let's look at the first 20 chains.

```
> head(tc, 20)
```

| | Node.1 | Node.2 | Node.3 | Node.4 |
|----|---|---------------------------|--------------------------|--------------|
| 1 | Nostoc sp. Diaphanosoma leuchtenbergianum | | Umbra limi | |
| 2 | Nostoc sp. | Daphnia pulex | Umbra limi | |
| 3 | Nostoc sp. | Holopedium gibberum | Umbra limi | |
| 4 | Nostoc sp. | Leptodiaptomus siciloides | Umbra limi | |
| 5 | Nostoc sp. Diaphanosoma leuchtenbergianum | Chaoborus punctipennis | | Umbra limi |
| 6 | Nostoc sp. Diaphanosoma leuchtenbergianum | Phoxinus eos | | Umbra limi |
| 7 | Nostoc sp. Diaphanosoma leuchtenbergianum | Phoxinus neogaeus | | Umbra limi |
| 8 | Nostoc sp. | Daphnia pulex | Chaoborus punctipennis | Umbra limi |
| 9 | Nostoc sp. | Daphnia pulex | Phoxinus eos | Umbra limi |
| 10 | Nostoc sp. | Daphnia pulex | Phoxinus neogaeus | Umbra limi |
| 11 | Nostoc sp. | Holopedium gibberum | Phoxinus eos | Umbra limi |
| 12 | Nostoc sp. | Holopedium gibberum | Phoxinus neogaeus | Umbra limi |
| 13 | Nostoc sp. | Leptodiaptomus siciloides | Cyclops varians rubellus | Umbra limi |
| 14 | Nostoc sp. | Leptodiaptomus siciloides | Orthocyclops modestus | Umbra limi |
| 15 | Nostoc sp. | Leptodiaptomus siciloides | Tropocyclops prasinus | Umbra limi |
| 16 | Nostoc sp. | Leptodiaptomus siciloides | Chaoborus punctipennis | Umbra limi |
| 17 | Nostoc sp. | Leptodiaptomus siciloides | Phoxinus eos | Umbra limi |
| 18 | Nostoc sp. | Leptodiaptomus siciloides | Phoxinus neogaeus | Umbra limi |
| 19 | Nostoc sp. Diaphanosoma leuchtenbergianum | Chaoborus punctipennis | | Phoxinus eos |
| 20 | Nostoc sp. Diaphanosoma leuchtenbergianum | Chaoborus punctipennis | Phoxinus neogaeus | |

| | Node.5 | Node.6 | Node.7 | Node.8 |
|----|--------|--------|--------|--------|
| 1 | | | | |
| 2 | | | | |
| 3 | | | | |
| 4 | | | | |
| 5 | | | | |
| 6 | | | | |
| 7 | | | | |
| 8 | | | | |
| 9 | | | | |
| 10 | | | | |
| 11 | | | | |
| 12 | | | | |
| 13 | | | | |
| 14 | | | | |
| 15 | | | | |
| 16 | | | | |
| 17 | | | | |

```

18
19 Umbra limi
20 Umbra limi

```

Every chain starts with a basal node.

```

> BasalNodes(TL84)

[1] "Nostoc sp." "Arthrodesmus sp."
[3] "Cryptomonas sp. 1" "Cryptomonas sp. 2"
[5] "Chroococcus dispersus" "Closteriopsis longissimus"
[7] "Dinobryon bavaricum" "Dinobryon cylindricum"
[9] "Dactylococcopsis fascicularis" "Dictyosphaerium pulchellum"
[11] "Dinobryon sertularia" "Dinobryon sociale"
[13] "Glenodinium quadridens" "Microcystis aeruginosa"
[15] "Mallomonas sp. 1" "Mallomonas sp. 2"
[17] "Unclassified flagellates" "Peridinium limbatum"
[19] "Peridinium cinctum" "Peridinium pulsillum"
[21] "Peridinium wisconsinense" "Chromulina sp."
[23] "Selenastrum minutum" "Synedra sp."
[25] "Trachelomonas sp."

> # The first node in each chain
> first <- tc[,1]
> all(unique(first) %in% BasalNodes(TL84)) # TRUE

[1] TRUE

```

Tuesday Lake 1984 has a single top-level consumer so every trophic chain ends with this consumer.

```

> TopLevelNodes(TL84)

[1] "Umbra limi"

> # The last node in each chain
> last <- apply(tc, 1, function(row) row[max(which("!"=row))])
> unique(last)

[1] "Umbra limi"

```

Just as with TLPS, `TrophicChains` accepts a 'node.properties' parameter that you can use to add node properties to the returned. For example, to get a table containing the \log_{10} -transformed body mass of each node in every chain.

```

> tc.with.log10M <- TrophicChains(TL84, node.properties='Log10M')

```

The food web of the Benguela marine ecosystem (Yodzis, 1998) does not have any top-level nodes. All chains start with a basal node (by definition) but, for this community, all chains end with an intermediate node.

```

> data(Benguela)
> TopLevelNodes(Benguela)

```

```

character(0)

> tc <- TrophicChains(Benguela)
> last <- apply(tc, 1, function(row) row[max(which("!"=row))])
> unique(last)

[1] "Sharks" "Seals" "Birds"

> IsIntermediateNode(Benguela)[unique(last)]

Sharks Seals Birds
TRUE TRUE TRUE

```

The second function - `TrophicChainsStats` - returns a list of simple statistics about trophic chains.

```

> chain.stats <- TrophicChainsStats(TL84)

The 'chain.lengths' item contains the length of every unique food chain.

> length(chain.stats$chain.lengths) # 5,988 chains

[1] 5988

> summary(chain.stats$chain.lengths)

```

| Min. | 1st Qu. | Median | Mean | 3rd Qu. | Max. |
|-------|---------|--------|-------|---------|-------|
| 2.000 | 4.000 | 5.000 | 4.835 | 6.000 | 7.000 |

The 'node.pos.counts' item is a matrix of `NumberOfNodes` rows and `1+max(chain.lengths)` columns. Elements are the number of chains in which a node appear in that position.

```

> dim(chain.stats$node.pos.counts) # 56 nodes. Longest chain contains 8 nodes

[1] 56 8

```

Basal nodes only have counts in the first column.

```

> chain.stats$node.pos.counts[BasalNodes(TL84),]

```

| | [,1] | [,2] | [,3] | [,4] | [,5] | [,6] | [,7] | [,8] |
|-------------------------------|------|------|------|------|------|------|------|------|
| Nostoc sp. | 75 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Arthrodesmus sp. | 69 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Cryptomonas sp. 1 | 840 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Cryptomonas sp. 2 | 81 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Chroococcus dispersus | 840 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Closteriopsis longissimus | 120 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Dinobryon bavaricum | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Dinobryon cylindricum | 75 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Dactylococcopsis fascicularis | 75 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Dictyosphaerium pulchellum | 81 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Dinobryon sertularia | 9 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Dinobryon sociale | 81 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

| | | | | | | | | |
|--------------------------|-----|---|---|---|---|---|---|---|
| Glenodinium quadridens | 84 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Microcystis aeruginosa | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Mallomonas sp. 1 | 9 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Mallomonas sp. 2 | 69 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Unclassified flagellates | 840 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Peridinium limbatum | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Peridinium cinctum | 9 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Peridinium pulsillum | 81 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Peridinium wisconsinense | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Chromulina sp. | 840 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Selenastrum minutum | 840 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Synedra sp. | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Trachelomonas sp. | 840 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Consumers only have counts in columns two and higher.

```
> chain.stats$node.pos.counts[c(IntermediateNodes(TL84), TopLevelNodes(TL84)),]
```

| | [,1] | [,2] | [,3] | [,4] | [,5] | [,6] | [,7] | [,8] |
|--------------------------------|------|------|------|------|------|------|------|------|
| Ascomorpha eucadis | 0 | 378 | 0 | 0 | 0 | 0 | 0 | 0 |
| Synchaeta sp. | 0 | 378 | 0 | 0 | 0 | 0 | 0 | 0 |
| Bosmina longirostris | 0 | 66 | 0 | 0 | 0 | 0 | 0 | 0 |
| Conochilus (solitary) | 0 | 399 | 0 | 0 | 0 | 0 | 0 | 0 |
| Cyclops varians rubellus | 0 | 0 | 2304 | 1152 | 0 | 0 | 0 | 0 |
| Diaphanosoma leuchtenbergianum | 0 | 84 | 0 | 0 | 0 | 0 | 0 | 0 |
| Daphnia pulex | 0 | 150 | 108 | 0 | 0 | 0 | 0 | 0 |
| Filinia longispina | 0 | 342 | 0 | 0 | 0 | 0 | 0 | 0 |
| Conochiloides dossuarius | 0 | 399 | 0 | 0 | 0 | 0 | 0 | 0 |
| Gastropus stylifer | 0 | 342 | 0 | 0 | 0 | 0 | 0 | 0 |
| Holopedium gibberum | 0 | 57 | 0 | 0 | 0 | 0 | 0 | 0 |
| Kellicottia sp. | 0 | 342 | 0 | 0 | 0 | 0 | 0 | 0 |
| Keratella cochlearis | 0 | 378 | 0 | 0 | 0 | 0 | 0 | 0 |
| Keratella testudo | 0 | 342 | 0 | 0 | 0 | 0 | 0 | 0 |
| Leptodiaptomus siciloides | 0 | 960 | 0 | 0 | 0 | 0 | 0 | 0 |
| Orthocyclops modestus | 0 | 0 | 576 | 1152 | 1152 | 0 | 0 | 0 |
| Ploesoma sp. | 0 | 342 | 0 | 0 | 0 | 0 | 0 | 0 |
| Polyarthra vulgaris | 0 | 342 | 0 | 0 | 0 | 0 | 0 | 0 |
| Trichocerca multicroinis | 0 | 342 | 0 | 0 | 0 | 0 | 0 | 0 |
| Trichocerca cylindrica | 0 | 342 | 0 | 0 | 0 | 0 | 0 | 0 |
| Tropocyclops prasinus | 0 | 0 | 2304 | 1152 | 0 | 0 | 0 | 0 |
| Chaoborus punctipennis | 0 | 3 | 438 | 918 | 1152 | 576 | 0 | 0 |
| Phoxinus eos | 0 | 0 | 86 | 452 | 690 | 576 | 192 | 0 |
| Phoxinus neogaeus | 0 | 0 | 86 | 452 | 690 | 576 | 192 | 0 |
| Umbra limi | 0 | 0 | 86 | 624 | 1594 | 1956 | 1344 | 384 |

All counts are zero for isolated nodes.

```
> chain.stats$node.pos.counts[IsolatedNodes(TL84),]
```

| | [,1] | [,2] | [,3] | [,4] | [,5] | [,6] | [,7] | [,8] |
|-----------------------------|------|------|------|------|------|------|------|------|
| Asterionella formosa | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Chrysosphaerella longispina | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Diceras sp. | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Rhizosolenia sp. | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Spinocosmarium sp. | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Staurostrum sp. | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

If your analysis requires only simple statistics about trophic chains, the `TrophicChainsStats` function is more suitable than `TrophicChains` because it is faster and requires less memory.

```
> system.time(tc <- TrophicChains(TL84))

  user  system elapsed
0.016   0.000   0.016

> system.time(stats <- TrophicChainsStats(TL84))

  user  system elapsed
0.015   0.000   0.015
```

The difference in speed will be greater for communities that contain a large number of nodes and trophic chains such as the Skipwith Pond dataset, which has more than 10^5 unique chains.

3.3.6 Large numbers of trophic chains

The number of possible trophic chains rapidly increases with the number of nodes and links. Let's examine the relationship between number of trophic chains and number of nodes communities in which every consumer eats every other node.

```
> HighlyConnected <- function(n)
{
  # Returns a community containing a single producer and n consumers, all
  # of whom eat everything else
  consumers <- paste('Consumer', 1:n)
  tl <- data.frame(resource=c(rep('Producer', n), rep(consumers, each=n)),
                  consumer=consumers)
  return (Community(nodes=data.frame(node=c('Producer', consumers)),
                    trophic.links=tl,
                    properties=list(title='test')))
}

> # A list of communities of between 1 and 8 consumers
> n <- 8
> communities <- lapply(1:n, HighlyConnected)
> # A list of statistics about each community
> stats <- lapply(communities, TrophicChainsStats)
> # Extract the chain lengths
> cl <- lapply(stats, '[', 'chain.lengths')
> # The number of chains
> n.chains <- sapply(cl, length)
> # The number of chains in each community
> cbind(n.consumers=1:n, longest.chain=sapply(cl, max), n.chains=n.chains)
```

| | <code>n.consumers</code> | <code>longest.chain</code> | <code>n.chains</code> |
|------|--------------------------|----------------------------|-----------------------|
| [1,] | 1 | 1 | 1 |
| [2,] | 2 | 2 | 2 |
| [3,] | 3 | 3 | 6 |
| [4,] | 4 | 4 | 24 |
| [5,] | 5 | 5 | 120 |
| [6,] | 6 | 6 | 720 |
| [7,] | 7 | 7 | 5040 |
| [8,] | 8 | 8 | 40320 |

So with one consumer there is one chain, two consumers - two chains, three consumers - six chains, four consumers - 24 chains and so on. You may recognise this sequence as factorial.

```
> cbind(n.consumers=1:n, longest.chain=sapply(1:n, function(x) {
  factorial(x)
}), n.chains=factorial(1:n))
```

| | <code>n.consumers</code> | <code>longest.chain</code> | <code>n.chains</code> | <code>factorial.n</code> |
|------|--------------------------|----------------------------|-----------------------|--------------------------|
| [1,] | 1 | 1 | 1 | 1 |
| [2,] | 2 | 2 | 2 | 2 |
| [3,] | 3 | 3 | 6 | 6 |
| [4,] | 4 | 4 | 24 | 24 |
| [5,] | 5 | 5 | 120 | 120 |
| [6,] | 6 | 6 | 720 | 720 |
| [7,] | 7 | 7 | 5040 | 5040 |
| [8,] | 8 | 8 | 40320 | 40320 |

What happens if we have even more consumers?

```
> n <- 20
> cbind(n.consumers=1:n, longest.chain=1:n, factorial.n=factorial(1:n))
```

| | <code>n.consumers</code> | <code>longest.chain</code> | <code>factorial.n</code> |
|-------|--------------------------|----------------------------|--------------------------|
| [1,] | 1 | 1 | 1.000000e+00 |
| [2,] | 2 | 2 | 2.000000e+00 |
| [3,] | 3 | 3 | 6.000000e+00 |
| [4,] | 4 | 4 | 2.400000e+01 |
| [5,] | 5 | 5 | 1.200000e+02 |
| [6,] | 6 | 6 | 7.200000e+02 |
| [7,] | 7 | 7 | 5.040000e+03 |
| [8,] | 8 | 8 | 4.032000e+04 |
| [9,] | 9 | 9 | 3.628800e+05 |
| [10,] | 10 | 10 | 3.628800e+06 |
| [11,] | 11 | 11 | 3.991680e+07 |
| [12,] | 12 | 12 | 4.790016e+08 |
| [13,] | 13 | 13 | 6.227021e+09 |
| [14,] | 14 | 14 | 8.717829e+10 |
| [15,] | 15 | 15 | 1.307674e+12 |
| [16,] | 16 | 16 | 2.092279e+13 |
| [17,] | 17 | 17 | 3.556874e+14 |

| | | |
|-------|----|-----------------|
| [18,] | 18 | 18 6.402374e+15 |
| [19,] | 19 | 19 1.216451e+17 |
| [20,] | 20 | 20 2.432902e+18 |

The number of trophic chains quickly becomes too large to compute within practical time and within available memory, and this for communities with just a single producer. When computing chains, `cheddar` allocates memory as required, with a safety limit to prevent too much of the system's memory from being consumed. If you see an error message 'Unable to compute paths' then this safety limit has been reached. The limit can be altered by setting the 'cheddarMaxQueue' option.

```
> # Set to a low number to illustrate the error
> options(cheddarMaxQueue=10)
> tryCatch(TrophicChains(TL84), error=print)

<simpleError in .TrophicChainsSize(community): Unexpected error>

> # Default value
> options(cheddarMaxQueue=NULL)
> chains <- TrophicChains(TL84)
```

If you encounter this error message you can increase the value of 'cheddarMaxQueue' (from its default of 1e7), but it is likely that the food-web is so complex that it will not be possible to compute all paths. Setting 'cheddarMaxQueue' to 0 disables the safety limit.

3.3.7 Trophic level

Several different measures of trophic level are used (e.g. Williams and Martinez, 2004; Jonsson et al., 2005; Zook et al., 2011.) The `PreyAveragedTrophicLevel` function uses the matrix-inversion method of Levine (1980) to compute trophic levels (Williams and Martinez, 2004). This method is very fast and accounts for flow through loops. A different measure of trophic level is offered by the `ChainAveragedTrophicLevel` function, which enumerates every unique food chain in the web (using `TrophicChainsStats`) and computes the mean position of each node in every chain (Williams and Martinez, 2004). The method of `ChainAveragedTrophicLevel` is the same as that described as 'trophic height' by Jonsson et al. (2005) and the name `TrophicHeight` is a synonym for `ChainAveragedTrophicLevel`. `ChainAveragedTrophicLevel` might be noticeably slower than `PreyAveragedTrophicLevel` for very large and/or highly connected food webs.

```
> tail(NPS(TL84, c('PreyAveragedTrophicLevel', 'ChainAveragedTrophicLevel')), 10)
```

| | PreyAveragedTrophicLevel | ChainAveragedTrophicLevel |
|--------------------------|--------------------------|---------------------------|
| Orthocyclops modestus | 3.205357 | 4.200000 |
| Ploesoma sp. | 2.000000 | 2.000000 |
| Polyarthra vulgaris | 2.000000 | 2.000000 |
| Trichocerca multicroinis | 2.000000 | 2.000000 |
| Trichocerca cylindrica | 2.000000 | 2.000000 |
| Tropocyclops prasinus | 3.142857 | 3.333333 |
| Chaoborus punctipennis | 3.171344 | 4.602527 |
| Phoxinus eos | 3.529951 | 5.168337 |
| Phoxinus neogaeus | 3.529951 | 5.168337 |
| Umbra limi | 3.802678 | 5.835003 |

Cheddar offers the six different measures of trophic level described by Williams and Martinez (2004). A function is provided for each one. The `TrophicLevels` convenience function returns a matrix containing all six.

```
> tail(TrophicLevels(TL84), 10)
```

| | ShortestTL | ShortWeightedTL | LongestTL | LongWeightedTL |
|-------------------------|-----------------|-----------------|-----------|----------------|
| Orthocyclops modestus | 3 | 3.102679 | 5 | 4.102679 |
| Ploesoma sp. | 2 | 2.000000 | 2 | 2.000000 |
| Polyarthra vulgaris | 2 | 2.000000 | 2 | 2.000000 |
| Trichocerca multicrinis | 2 | 2.000000 | 2 | 2.000000 |
| Trichocerca cylindrica | 2 | 2.000000 | 2 | 2.000000 |
| Tropocyclops prasinus | 3 | 3.071429 | 4 | 3.571429 |
| Chaoborus punctipennis | 2 | 2.585672 | 6 | 4.585672 |
| Phoxinus eos | 3 | 3.264975 | 7 | 5.264975 |
| Phoxinus neogaeus | 3 | 3.264975 | 7 | 5.264975 |
| Umbra limi | 3 | 3.401339 | 8 | 5.901339 |
| | ChainAveragedTL | PreyAveragedTL | | |
| Orthocyclops modestus | 4.200000 | 3.205357 | | |
| Ploesoma sp. | 2.000000 | 2.000000 | | |
| Polyarthra vulgaris | 2.000000 | 2.000000 | | |
| Trichocerca multicrinis | 2.000000 | 2.000000 | | |
| Trichocerca cylindrica | 2.000000 | 2.000000 | | |
| Tropocyclops prasinus | 3.333333 | 3.142857 | | |
| Chaoborus punctipennis | 4.602527 | 3.171344 | | |
| Phoxinus eos | 5.168337 | 3.529951 | | |
| Phoxinus neogaeus | 5.168337 | 3.529951 | | |
| Umbra limi | 5.835003 | 3.802678 | | |

See the help page for `TrophicLevels` for more information on these different measures.

3.3.8 Link strengths

Cheddar's data format allows zero, one or many measures of link strength to be defined simply by adding additional columns to the `trophic.links.csv` file (Section 3). It is also possible to define and use theoretical measures of link strength. Cheddar's `PredationMatrix` and `FlowBasedTrophicLevel` functions allow empirical and/or theoretical link strengths to be used.

The *Benguela* dataset contains empirical estimates of diet fraction for each trophic link (Yodzis, 1998), available as the 'diet.fraction' property.

```
> data(Benguela)
```

```
> head(TLPS(Benguela))
```

| | resource | consumer | diet.fraction |
|---|------------------------|--------------------|---------------|
| 1 | Phytoplankton | Bacteria | 98.8 |
| 2 | Benthic filter feeders | Benthic carnivores | 100.0 |
| 3 | Phytoplankton | Microzooplankton | 30.6 |
| 4 | Bacteria | Microzooplankton | 29.7 |
| 5 | Microzooplankton | Microzooplankton | 29.7 |
| 6 | Phytoplankton | Mesozooplankton | 45.0 |

A binary predation matrix contains just '0' and '1'.

```
> pm <- PredationMatrix(Benguela)
```

We can weight the predation matrix by empirical diet fractions.

```
> pm <- PredationMatrix(Benguela, weight='diet.fraction')
```

These matrices are 29 x 29 and so are not shown for brevity.

The `FlowBasedTrophicLevel` function uses the same matrix inversion technique as `PreyAveragedTrophicLevel` and uses the 'weight.by' node property to provide an estimate of energy flow through each trophic link. We can easily compare these two different ways of computing trophic level.

```
> cbind(PreyAveragedTrophicLevel(Benguela),
        FlowBasedTrophicLevel(Benguela, weight.by='diet.fraction'))
```

| | [,1] | [,2] |
|------------------------|----------|----------|
| Phytoplankton | 1.000000 | 1.000000 |
| Benthic filter feeders | 1.000000 | 1.000000 |
| Bacteria | 2.000000 | 2.000000 |
| Benthic carnivores | 2.000000 | 2.000000 |
| Microzooplankton | 3.000000 | 2.985075 |
| Mesozooplankton | 3.000000 | 2.992537 |
| Macrozooplankton | 3.000000 | 2.797015 |
| Gelatinous zooplankton | 3.250000 | 3.244403 |
| Anchovy | 3.500000 | 3.826134 |
| Pilchard | 3.333333 | 2.651672 |
| Round herring | 4.000000 | 3.914328 |
| Lightfish | 4.000000 | 3.875224 |
| Lanternfish | 4.000000 | 3.875224 |
| Goby | 3.500000 | 3.238903 |
| Other pelagics | 3.812500 | 3.952869 |
| Horse mackerel | 4.000000 | 3.908589 |
| Chub mackerel | 4.250000 | 4.165017 |
| Other groundfish | 4.776994 | 4.144872 |
| Hakes | 4.930366 | 4.767544 |
| Squid | 4.804069 | 4.609870 |
| Tunas | 4.844189 | 4.421241 |
| Snoek | 4.733434 | 4.713249 |
| Kob | 4.909476 | 4.658580 |
| Yellowtail | 4.897690 | 4.719394 |
| Geelbek | 4.865726 | 4.526048 |
| Whales and dolphins | 4.888027 | 4.769149 |
| Birds | 4.985516 | 4.737059 |
| Seals | 5.113082 | 4.829057 |
| Sharks | 5.183100 | 4.933519 |

Theoretical per capita interaction strengths can be computed from body-mass ratios raised to a power, typically taken to be 2/3 or 3/4 (Emmerson and Raffaelli, 2004; Reuman and Cohen, 2005; Layer et al., 2010). We can define a function to compute these theoretical interaction strengths and use it in computation of trophic levels.

```

> InteractionStrength <- function(community)
{
  ttps <- TLPS(community, node.properties='M')
  return ((ttps$consumer.M / ttps$resource.M)^3/4)
}
> # The InteractionStrength() function can be used together with TLPS() to
> # compute the theoretical interaction strength between each resource-consumer pair
> head(TLPS(Benguela, link.properties='InteractionStrength'))

```

| | resource | consumer | InteractionStrength |
|---|------------------------|--------------------|---------------------|
| 1 | Phytoplankton | Bacteria | 2.5e-13 |
| 2 | Benthic filter feeders | Benthic carnivores | 2.5e-01 |
| 3 | Phytoplankton | Microzooplankton | 2.5e-01 |
| 4 | Bacteria | Microzooplankton | 2.5e+11 |
| 5 | Microzooplankton | Microzooplankton | 2.5e-01 |
| 6 | Phytoplankton | Mesozooplankton | 2.5e+05 |

We can use this measure of interaction strength to compute flow-based trophic level.

```

> cbind(PreyAveragedTrophicLevel(Benguela),
  FlowBasedTrophicLevel(Benguela, weight.by='diet.fraction'),
  FlowBasedTrophicLevel(Benguela, weight.by='InteractionStrength'))

```

| | [,1] | [,2] | [,3] |
|------------------------|----------|----------|----------|
| Phytoplankton | 1.000000 | 1.000000 | 1.000000 |
| Benthic filter feeders | 1.000000 | 1.000000 | 1.000000 |
| Bacteria | 2.000000 | 2.000000 | 2.000000 |
| Benthic carnivores | 2.000000 | 2.000000 | 2.000000 |
| Microzooplankton | 3.000000 | 2.985075 | 3.000000 |
| Mesozooplankton | 3.000000 | 2.992537 | 3.000000 |
| Macrozooplankton | 3.000000 | 2.797015 | 2.000002 |
| Gelatinous zooplankton | 3.250000 | 3.244403 | 3.000000 |
| Anchovy | 3.500000 | 3.826134 | 3.000000 |
| Pilchard | 3.333333 | 2.651672 | 2.000002 |
| Round herring | 4.000000 | 3.914328 | 3.999999 |
| Lightfish | 4.000000 | 3.875224 | 3.999999 |
| Lanternfish | 4.000000 | 3.875224 | 3.999999 |
| Goby | 3.500000 | 3.238903 | 3.000000 |
| Other pelagics | 3.812500 | 3.952869 | 3.999999 |
| Horse mackerel | 4.000000 | 3.908589 | 3.999999 |
| Chub mackerel | 4.250000 | 4.165017 | 3.999999 |
| Other groundfish | 4.776994 | 4.144872 | 3.999999 |
| Hakes | 4.930366 | 4.767544 | 3.999999 |
| Squid | 4.804069 | 4.609870 | 3.018712 |
| Tunas | 4.844189 | 4.421241 | 4.796740 |
| Snoek | 4.733434 | 4.713249 | 3.024660 |
| Kob | 4.909476 | 4.658580 | 3.000829 |
| Yellowtail | 4.897690 | 4.719394 | 3.000830 |
| Geelbek | 4.865726 | 4.526048 | 3.453351 |

| | | | |
|---------------------|----------|----------|----------|
| Whales and dolphins | 4.888027 | 4.769149 | 3.006892 |
| Birds | 4.985516 | 4.737059 | 3.999999 |
| Seals | 5.113082 | 4.829057 | 4.796740 |
| Sharks | 5.183100 | 4.933519 | 3.999999 |

The weighting functionality offered by the `PredationMatrix` and `FlowBasedTrophicLevel` functions make it possible to use multiple empirical and/or theoretical link strengths and interaction strengths in analyses.

4 Community manipulations

4.1 Node order

The ordering of nodes within a community can be important both for presentation and analysis. Cheddar's `OrderCommunity` function reorders nodes and returns a new community object. `OrderCommunity` accepts names that meets the criteria of the `properties` parameter of the `NPS` function. This includes the names of 'first-class' properties, such as *M*, and the names of functions that take a single community and return a value for each node, such as `Degree`, which returns the number of trophic links for each node. The following examples order TL84 by increasing body mass and by increasing degree.

```
> TL84.increasing.M <- OrderCommunity(TL84, 'M', title='Increasing M')
> head(NPS(TL84.increasing.M, c('M', 'Degree')))
```

| | M | Degree |
|-------------------------------|----------|--------|
| Chromulina sp. | 3.03e-14 | 18 |
| Dactylococcopsis fascicularis | 1.32e-13 | 4 |
| Diceras sp. | 1.53e-13 | 0 |
| Trachelomonas sp. | 1.75e-13 | 18 |
| Cryptomonas sp. 1 | 2.03e-13 | 18 |
| Closteriopsis longissimus | 2.37e-13 | 3 |

```
> TL84.increasing.degree <- OrderCommunity(TL84, 'Degree',
                                             title='Increasing degree')
> head(NPS(TL84.increasing.degree, c('M', 'Degree')))
```

| | M | Degree |
|-----------------------------|----------|--------|
| Asterionella formosa | 1.12e-12 | 0 |
| Chrysosphaerella longispina | 8.31e-10 | 0 |
| Diceras sp. | 1.53e-13 | 0 |
| Rhizosolenia sp. | 6.86e-13 | 0 |
| Spinocosmarium sp. | 3.71e-12 | 0 |
| Staurostrum sp. | 4.30e-12 | 0 |

Similar to R's `order` function, `OrderCommunity` can sort by more than one name with subsequent names used to break ties. We can use this to sort alphabetically by category and then by increasing *M* within each category.

```
> TL84.category.then.M <- OrderCommunity(TL84, 'category', 'M')
> head(NPS(TL84.category.then.M, c('category', 'M')))
```

| | category | M |
|-----------------------|--------------|----------|
| Keratella cochlearis | invertebrate | 1.00e-11 |
| Keratella testudo | invertebrate | 1.00e-11 |
| Kellicottia sp. | invertebrate | 2.00e-11 |
| Conochilus (solitary) | invertebrate | 3.50e-11 |
| Ploesoma sp. | invertebrate | 1.05e-10 |
| Gastropus stylifer | invertebrate | 1.35e-10 |

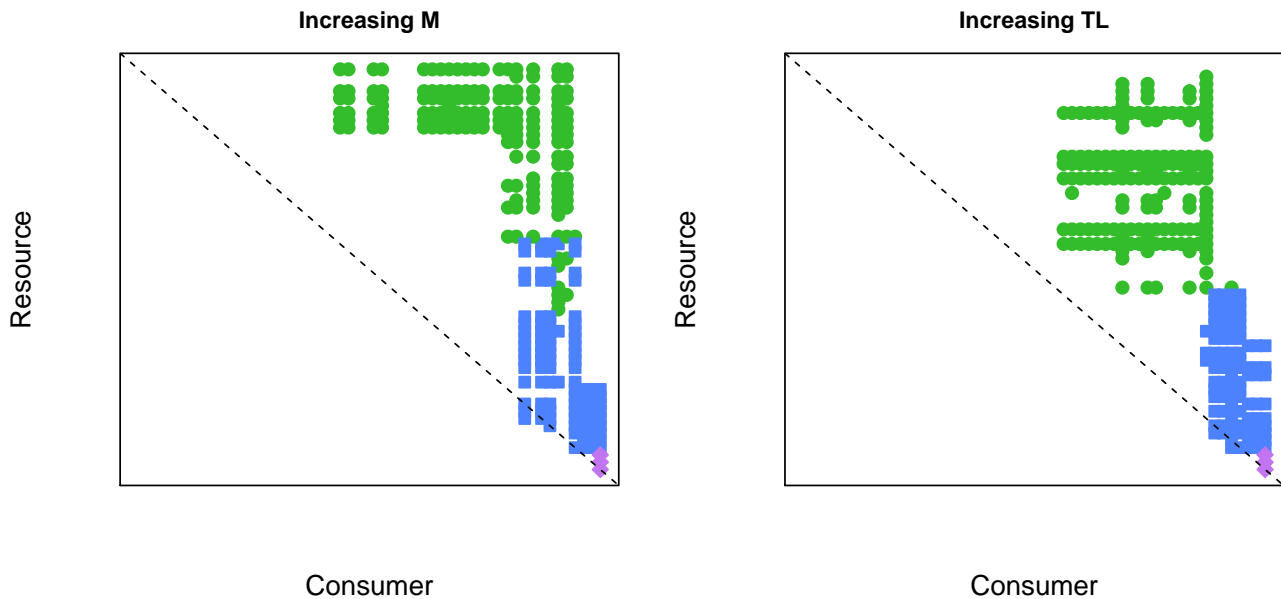
4.2 Node order and intervality

Visualising the food web as a predation matrix is central to many analyses and theories. There has been much recent interest in the relationship between food web structure and species' niches, in particular the role of body size on determining a species' position in a food web and the effect on intervality - a measure of the adjacency of resources and consumers in the food web (Williams and Martinez, 2000; Stouffer et al., 2006; Zook et al., 2011). We can use `OrderCommunity` to explore the effect ordering species along different niche axes. The code fragment below creates two new orderings of `TL84`, one by increasing body mass and the other by increasing trophic level, with random ordering within ties for trophic level (Zook et al., 2011).

```
> # Increasing M
> TL84.increasing.M <- OrderCommunity(TL84, 'M', title='Increasing M')
> new.order <- order(PreyAveragedTrophicLevel(TL84), sample(1:56))
> TL84.increasing.TL <- OrderCommunity(TL84, new.order=new.order,
                                         title='Increasing TL')
```

We could use any of Cheddar's different measure of trophic level (Section 3.3.7). The `PlotPredationMatrix` function allows us to graphically compare the effect of these different orderings.

```
> par(mfrow=c(1,2))
> PlotPredationMatrix(TL84.increasing.M)
> PlotPredationMatrix(TL84.increasing.TL)
```



The total number of gaps in diets (columns) and consumers (rows) (Stouffer et al., 2011; Zook et al., 2011):

```
> SumDietGaps(TL84.increasing.M)
[1] 132
> SumDietGaps(TL84.increasing.TL)
```

[1] 262

```
> SumConsumerGaps(TL84.increasing.M)
```

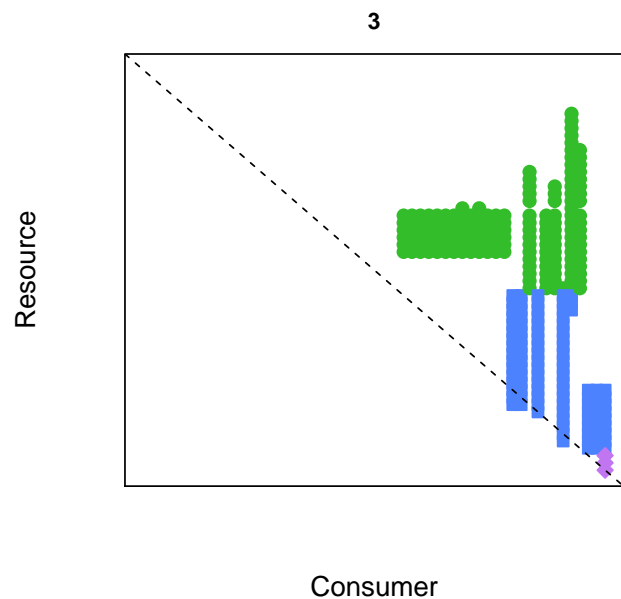
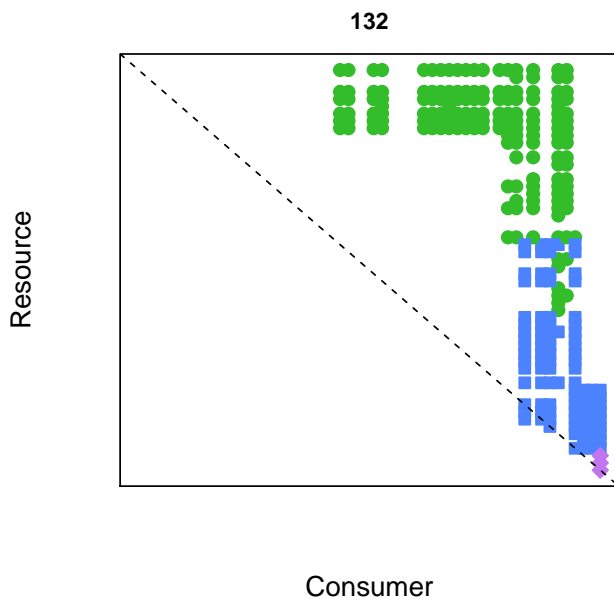
[1] 154

```
> SumConsumerGaps(TL84.increasing.TL)
```

[1] 114

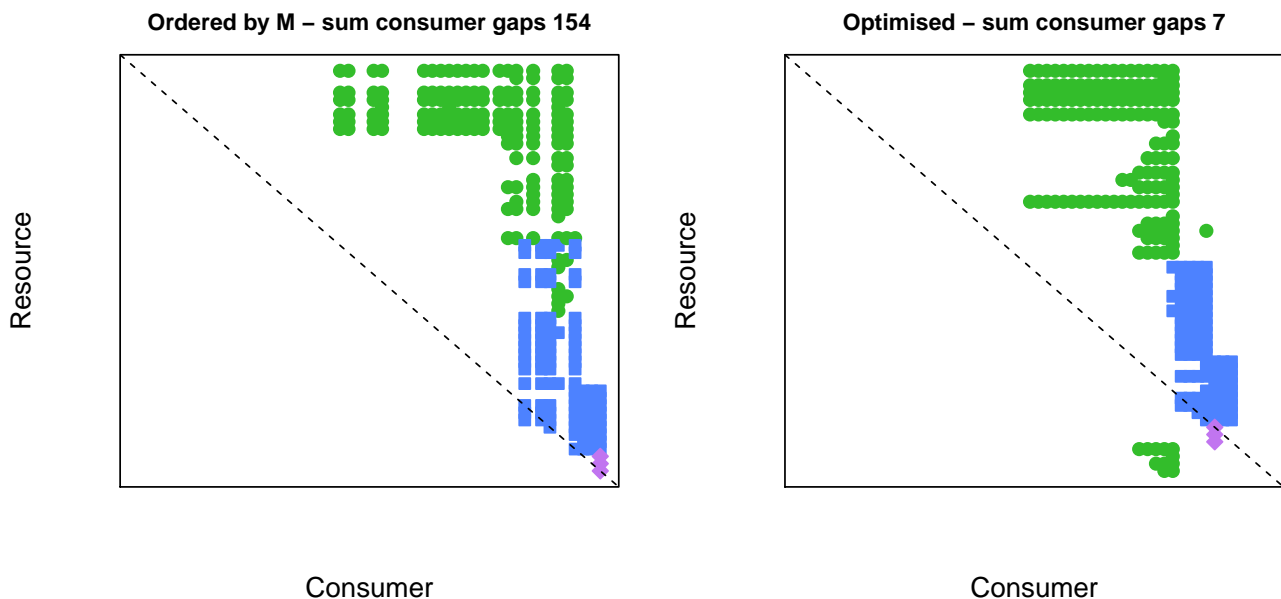
The `MinimiseSumDietGaps` function implements simulated annealing learning to minimise `SumDietGaps`, as described by Stouffer et al. (2006). Simulated annealing learning is a stochastic method so several optimisations might be required to find the global minimum; this is done by setting the ‘n’ parameter greater than 1:

```
> par(mfrow=c(1,2))
> PlotPredationMatrix(TL84.increasing.M, main=SumDietGaps(TL84.increasing.M))
> res <- MinimiseSumDietGaps(TL84, n=10)
> PlotPredationMatrix(res$reordered, main=SumDietGaps(res$reordered))
```



`MinimiseSumConsumerGaps` uses the same method to minimise the gaps in each species' consumers (Zook et al., 2011).

```
> par(mfrow=c(1,2))
> PlotPredationMatrix(TL84.increasing.M,
  main=paste('Ordered by M - sum consumer gaps',
    SumConsumerGaps(TL84.increasing.M)))
> res <- MinimiseSumConsumerGaps(TL84, n=10)
> PlotPredationMatrix(res$reordered,
  main=paste('Optimised - sum consumer gaps',
    SumConsumerGaps(res$reordered)))
```



4.3 Removing nodes

Isolated nodes are often removed from food-web analyses (e.g. Jonsson et al., 2005). `RemoveIsolatedNodes` is a convenience function that returns a new `Community` with isolated nodes removed.

```
> NumberOfNodes(TL84)

[1] 56

> IsolatedNodes(TL84)

[1] "Asterionella formosa"      "Chrysosphaerella longispina"
[3] "Diceras sp."              "Rhizosolenia sp."
[5] "Spinocosmarium sp."       "Staurostrum sp."

> NumberOfTrophicLinks(TL84)

[1] 269
```

```

> TL84.no.isolated <- RemoveIsolatedNodes(TL84)
> NumberOfNodes(TL84.no.isolated)          # Six fewer species

[1] 50

> IsolatedNodes(TL84.no.isolated)          # No isolated species

character(0)

> NumberOfTrophicLinks(TL84.no.isolated)  # Number of trophic links unchanged

[1] 269

```

The general-purpose `RemoveNodes` function returns a new `Community` object with one or more nodes removed.

```

> NumberOfNodes(TL84)

[1] 56

> NumberOfTrophicLinks(TL84)

[1] 269

> # Remove the first ten nodes
> TL84.r <- RemoveNodes(TL84, 1:10)
> NumberOfNodes(TL84.r)

[1] 46

> NumberOfTrophicLinks(TL84.r)

[1] 213

> # Remove producers
> TL84.r <- RemoveNodes(TL84, 'producer'==NP(TL84, 'category'))
> NumberOfNodes(TL84.r)

[1] 25

> NumberOfTrophicLinks(TL84.r)

[1] 103

> # Remove species by name
> to.remove <- c("Cryptomonas sp. 1", "Chroococcus dispersus",
               "Unclassified flagellates", "Chromulina sp.",
               "Selenastrum minutum", "Trachelomonas sp.")
> TL84.r <- RemoveNodes(TL84, to.remove)
> NumberOfNodes(TL84.r)

[1] 50

```



```
> NumberOfTrophicLinks(TL84.r)
```

```
[1] 161
```

```
> # Three different ways of removing node 56 (Umbra limi)
```

```
> TL84.ra <- RemoveNodes(TL84, 56)
```

```
> TL84.rb <- RemoveNodes(TL84, 'Umbra limi')
```

```
> TL84.rc <- RemoveNodes(TL84, c(rep(FALSE,55), TRUE))
```

```
> identical(TL84.ra, TL84.rb) # TRUE
```

```
[1] TRUE
```

```
> identical(TL84.ra, TL84.rc) # TRUE
```

```
[1] TRUE
```

The `RemoveNodes` function takes an argument called 'method', which indicates how removals should be propagated through the food web. If 'method' is 'direct' (the default), only the nodes in `remove` are removed. If 'method' is 'secondary', secondarily extinct nodes - those that directly consume one or more nodes in 'remove' and that no longer have any resources (except themselves) after the removal - are also removed. If 'method' is 'cascade', a multistep version of 'secondary' is applied. This has the effect of propagating extinctions through the community - all consumers that are ultimately dependent upon all species in 'remove', and upon no other nodes (except themselves), will be removed.

```
> # The behaviours of the different methods
```

```
> NumberOfNodes(TL84) # 56 nodes in total
```

```
[1] 56
```

```
> length(BasalNodes(TL84)) # 25 basal nodes
```

```
[1] 25
```

```
> length(IsolatedNodes(TL84)) # 6 isolated nodes
```

```
[1] 6
```

```
> RemoveNodes(TL84, BasalNodes(TL84)) # 56 - 25 = 31 nodes remain
```

Tuesday Lake sampled in 1984 (25 nodes directly removed) containing 31 nodes and 103 trophic links

```
> RemoveNodes(TL84, BasalNodes(TL84), method='secondary') # 14 nodes remain
```

Tuesday Lake sampled in 1984 (25 nodes directly removed) containing 14 nodes and 30 trophic links

```
> RemoveNodes(TL84, BasalNodes(TL84), method='cascade') # The 6 isolated nodes remain
```

Tuesday Lake sampled in 1984 (25 nodes directly removed) containing 6 nodes

4.4 Removing cannibalistic links

`RemoveCannibalisticLinks` returns a new `Community` without those trophic links in which a node consumes itself.

```
> NumberOfNodes(TL84)

[1] 56

> Cannibals(TL84)          # 5 species

[1] "Cyclops varians rubellus" "Orthocyclops modestus"  "Tropocyclops prasinus"
[4] "Chaoborus punctipennis"  "Umbra limi"

> NumberOfTrophicLinks(TL84)

[1] 269

> TL84.no.cannibals <- RemoveCannibalisticLinks(TL84)
> NumberOfNodes(TL84.no.cannibals)          # Number of nodes unchanged

[1] 56

> Cannibals(TL84.no.cannibals)              # No species

character(0)

> NumberOfTrophicLinks(TL84.no.cannibals)  # 5 fewer trophic links

[1] 264
```

4.5 Lumping nodes

Certain analyses call for food-web nodes to be merged. In order to reduce biases, nodes that share the same resources and consumers, so-called ‘trophic species’, are commonly lumped together (Briand and Cohen, 1984; Pimm et al., 1991; Williams and Martinez, 2000). The `LumpTrophicSpecies` performs this task and returns a new `Community` object.

```
> NumberOfNodes(TL84)

[1] 56

> TL84.lumped <- LumpTrophicSpecies(TL84)
> length(unique(TrophicSpecies(TL84)))    # 22 trophic species in TL84...

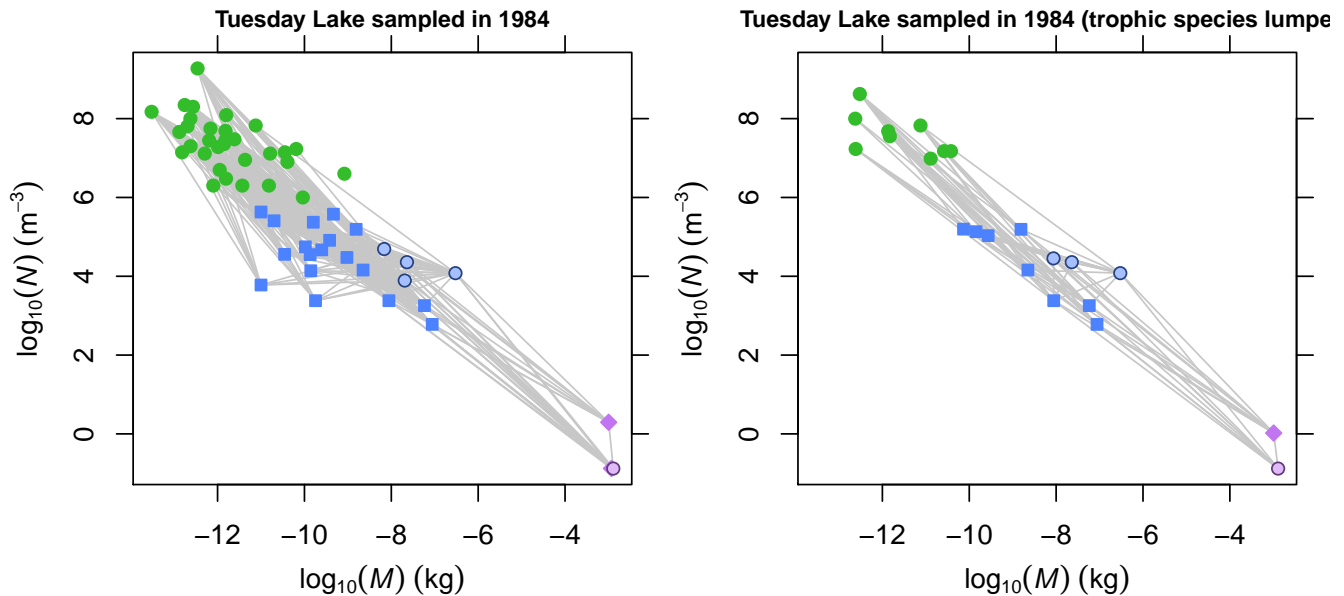
[1] 22

> NumberOfNodes(TL84.lumped)              # ... and 22 nodes in the lumped web

[1] 22
```

The plot below shows the lumped and unlumped webs.

```
> par(mfrow=c(1,2))
> plot(TL84)
> plot(TL84.lumped, xlim=range(Log10M(TL84)), ylim=range(Log10N(TL84)))
```



The `LumpNodes` function is a more general-purpose function that allows any nodes in a community to be lumped together. It takes a parameter 'lump', which should be a vector of length `NumberOfNodes`. Nodes with the same value of 'lump' will be merged together. This example lumps together isolated species in TL84.

```
> length(which(IsIsolatedNode(TL84))) # 6 isolated species

[1] 6

> IsolatedNodes(TL84) # Names of isolated nodes

[1] "Asterionella formosa" "Chrysosphaerella longispina"
[3] "Diceras sp."         "Rhizosolenia sp."
[5] "Spinocosmarium sp."  "Staurostrum sp."

> lump <- NP(TL84, 'node') # Existing node names
> # Give isolated nodes the same lump value
> lump[IsolatedNodes(TL84)] <- 'Isolated nodes lumped together'
> TL84.lumped <- LumpNodes(TL84, lump)
> NumberOfNodes(TL84) # 56 nodes in unlumped web

[1] 56

> NumberOfNodes(TL84.lumped) # 51 nodes in lumped web
```

```
[1] 51
```

```
> IsolatedNodes(TL84.lumped) # A single node
```

```
[1] "Isolated nodes lumped together"
```

By default, numeric values are weighted by numerical abundance, N .

This trivial example shows that no nodes are lumped if values in lump are unique to each node.

```
> lump <- NP(TL84, 'node')
```

```
> identical(TL84, LumpNodes(TL84, lump, title=CP(TL84, 'title')))
```

```
[1] FALSE
```

The Ythan Estuary dataset contains two species that are split by life stage: *Platichthys flesus* (european flounder) and *Somateria mollissima* (common eider). The code fragment below shows how to lump these in to a single node for each species.

```
> data(YthanEstuary)
```

```
> # The names of nodes in YthanEstuary
```

```
> lump <- NP(YthanEstuary, 'node')
```

```
> # European flounder:
```

```
> # "Platichthys flesus" and "Platichthys flesus (juvenile)"
```

```
> # Lump these in to one node
```

```
> lump["Platichthys flesus (juvenile)"==lump] <- "Platichthys flesus"
```

```
> # Common eider:
```

```
> # "Somateria mollissima" and "Somateria mollissima (juvenile)"
```

```
> # Lump these in to one node
```

```
> lump["Somateria mollissima (juvenile)"==lump] <- "Somateria mollissima"
```

```
> YthanEstuary.lumped <- LumpNodes(YthanEstuary, lump)
```

```
> NumberOfNodes(YthanEstuary) # 92
```

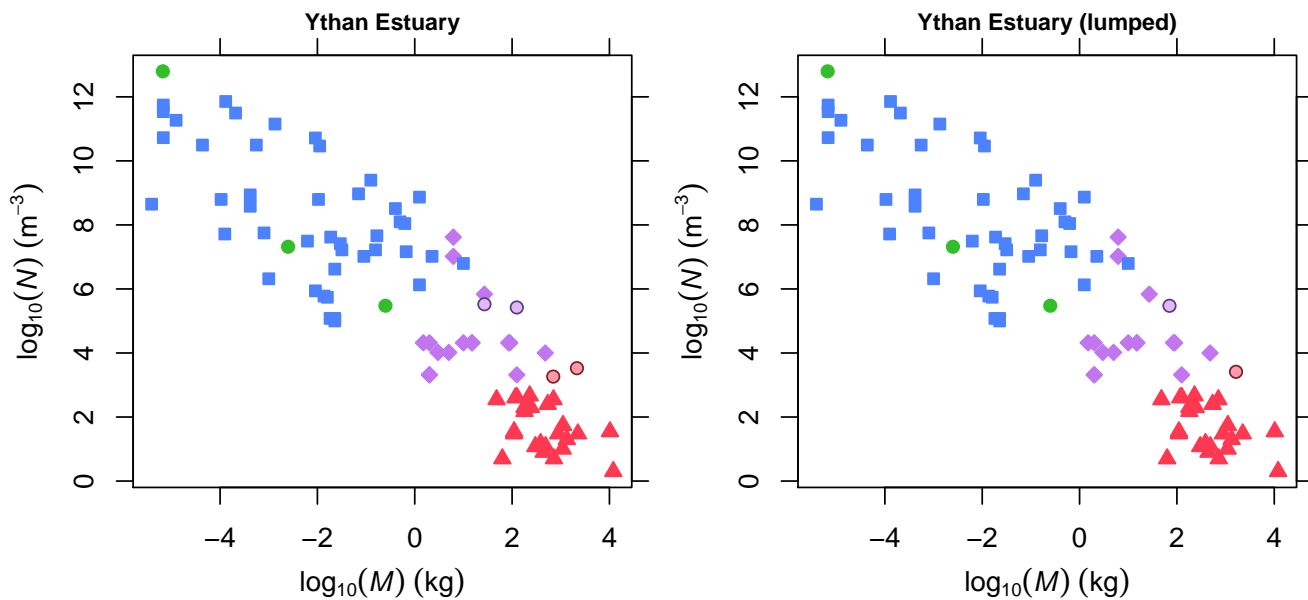
```
[1] 92
```

```
> NumberOfNodes(YthanEstuary.lumped) # 90
```

```
[1] 90
```

Graphically compare the two communities.

```
> # Plot the original and lumped communities
> par(mfrow=c(1,2))
> plot(YthanEstuary, highlight.nodes=c("Platichthys flesus",
                                       "Platichthys flesus (juvenile)",
                                       "Somateria mollissima",
                                       "Somateria mollissima (juvenile)"),
       show.web=FALSE)
> plot(YthanEstuary.lumped, highlight.nodes=c("Platichthys flesus",
                                              "Somateria mollissima"),
       show.web=FALSE)
```



The default behaviour of `LumpNodes` and `LumpTrophicSpecies` is to aggregate numeric node properties by computing the N -weighted mean.

```
> NPS(YthanEstuary.lumped)["Platichthys flesus", c('M','N')]
```

```

               M           N
Platichthys flesus 70.36585 298480
```

```
> # These values were computed as follows
> nps <- NPS(YthanEstuary)
> M <- nps[c("Platichthys flesus", "Platichthys flesus (juvenile)", 'M')]
> N <- nps[c("Platichthys flesus", "Platichthys flesus (juvenile)", 'N')]
> # Arithmetic mean of N
> mean(N)
```

```
[1] 298480
```

```
> # N-weighted mean of M
> weighted.mean(M, N)
```

```
[1] 70.36585
```

The ‘weight.by’ parameter controls this behaviour:

```
> YthanEstuary.lumped2 <- LumpNodes(YthanEstuary, lump, weight.by=NULL)
> NPS(YthanEstuary.lumped2)["Platichthys flesus", c('M','N')]
```

```

              M      N
Platichthys flesus 76 298480
```

```
> # Computed as the arithmetic means of M and N
> mean(M)
```

```
[1] 76
```

```
> mean(N)
```

```
[1] 298480
```

```
>
```

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