Cheddar plots and statistics (0.1-619)

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Contents

1 Introduction

This vignette describes Cheddar's flexible system for plotting properties of ecological communities. You should read the 'Community' vignette before reading this one. Cheddar's plotting system is built upon two general-purpose functions: `PlotNPS` (for **Plot N**ode **P**ropertie**S**) and `PlotTLPS` (**Plot T**rophic-**L**ink **P**ropertie**S**), which allow a range of properties, first-class and computed, Cheddar-provided and user-defined, to be plotted in a variety of ways. `PlotNPS` and `PlotTLPS` are used by a large number of convenience 'wrapper' functions that provide different views of a community, focussing on food web data that are augmented with estimates of body mass, M, and/or numerical abundance, N, following Cohen et al. (2003) (Table 1). You can use whatever mixture of `PlotNPS`, `PlotTLPS` and the functions in Table

Trophic links	M	N	Plot function	Description
	✓		`PlotMvRankM`	$\log_{10}(M)$ versus rank(M)
	✓		`PlotMDistribution`	Distribution of $\log_{10}(M)$
		✓	`PlotNvRankN`	$\log_{10}(N)$ versus rank(N)
		✓	`PlotNDistribution`	Distribution of $\log_{10}(N)$
	✓	✓	`PlotBvRankB`	$\log_{10}(B)$ versus rank(B)
	✓	✓	`PlotBDistribution`	Distribution of $\log_{10}(B)$
	✓	✓	`PlotNSpectrum`	Approximate numerical abundance spectrum
	✓	✓	`PlotNvM` *	$\log_{10}(N)$ versus $\log_{10}(M)$
	✓	✓	`PlotBSpectrum`	Approximate biomass abundance spectrum
	✓	✓	`PlotBvM` *	$\log_{10}(B)$ versus $\log_{10}(M)$
✓			`PlotPredationMatrix`	Predation matrix
✓			`PlotWebByLevel`	Food web plotted vertically by trophic level
✓			`PlotDegreeDistribution`	Histogram of node degree
✓			`PlotCircularWeb`	An overview of complexity
✓	✓		`PlotMRvMC` *	$\log_{10}(M)$ of resource versus $\log_{10}(M)$ of consumer
✓		✓	`PlotNRvNC` *	$\log_{10}(N)$ of resource versus $\log_{10}(N)$ of consumer
✓		✓	`PlotNPyramid`	$\log_{10}(\sum(N))$ by trophic level
✓	✓	✓	`PlotBRvBC` *	$\log_{10}(B)$ of resource versus $\log_{10}(B)$ of consumer
✓	✓	✓	`PlotBPyramid`	$\log_{10}(\sum(B))$ by trophic level
✓	✓	✓	`PlotAlowervAupper`	Upper link-angle against lower link angle

Table 1: Cheddar's high-level plot functions.

1 that meets your needs and fits your data. The examples below use the datasets from the two pelagic epilimnion communities of Tuesday Lake, Michigan, USA (Carpenter and Kitchell, 1996; Cohen et al., 2003; Jonsson et al., 2005) and the community of Ythan Estuary in north Scotland (Hall and Raffaelli, 1991; Emmerson and Raffaelli, 2004).

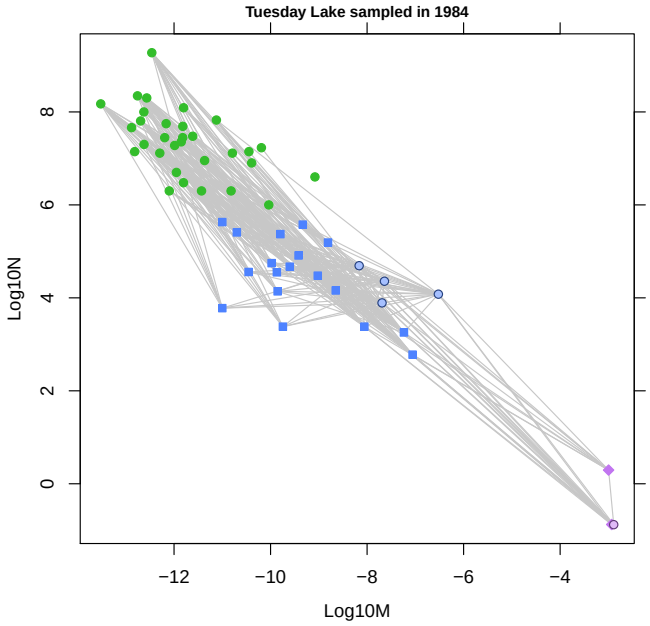
2 Plotting node properties

2.1 PlotNPS

`PlotNPS` plots one node property against another. Every Cheddar function that plots one point per node delegates the job of plotting to `PlotNPS` and all of its power and flexibility are available to all of the functions discussed in this section. `PlotNPS` function accepts the names of properties to plot on the x and y axes. These can be either 'first-class' properties, such as body mass, M, and numerical abundance, N, or they can be the names of functions that compute and return node properties.

The relationship between species-level log-transformed N and M has implications for Reuman et al. (2008) and ecosystem-level Brown et al. (2004) theories. We can plot $\log_{10}(N)$ against $\log_{10}(M)$ by using `PlotNPS` together with the `Log10M` and `Log10N` functions.

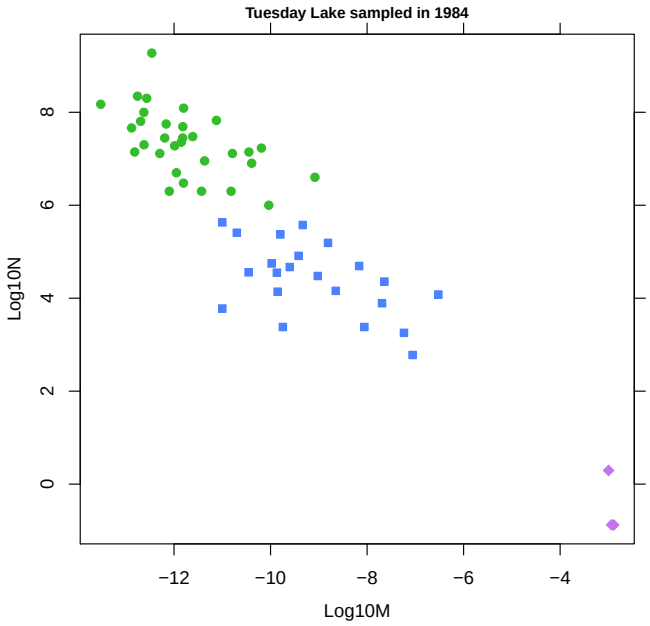
```
> data(TL84)
> PlotNPS(TL84, 'Log10M', 'Log10N')
```



`PlotNPS` uses the 'category' node property, if present, to decide plotting colours and symbols. Producers are shown by green circles, invertebrates by blue squares and vertebrate ectotherms by purple diamonds. Many of Cheddar's plotting an 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. This is explored more in Section 2.4.

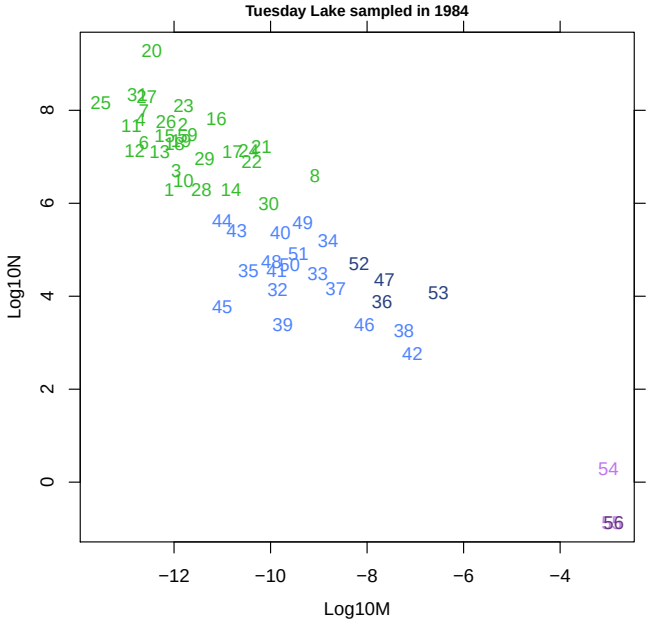
The TL84 datasets include trophic links so PlotNPS will show the food web and highlights cannibals by plotting them in a light-coloured filled circle with a dark border, as shown in the previous example. We can turn off these behaviours.

```
> PlotNPS(TL84, 'Log10M', 'Log10N', show.web=FALSE, highlight.nodes=NULL)
```



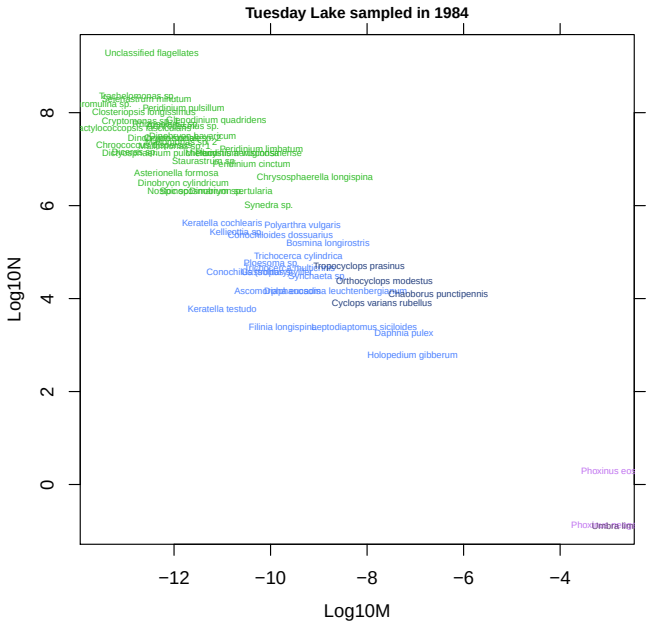
We can plots labels rather than points. When plotting labels, nodes given by 'highlight.nodes' (by default, those nodes that are cannibals) are shown in a darker colour.

```
> PlotNPS(TL84, 'Log10M', 'Log10N', show.nodes.as='labels', show.web=FALSE)
```



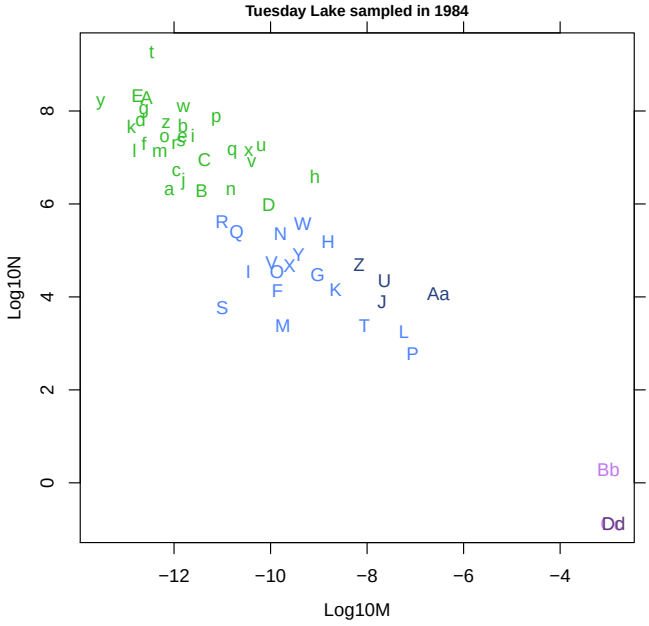
In the above example, labels are taken from the order of the nodes in the `TL84` community. We can plot a different label by setting the 'node.labels' property. The example below plots node names.

```
> PlotNPS(TL84, 'Log10M', 'Log10N', show.nodes.as='labels', show.web=FALSE,
        node.labels='node', cex=0.5)
```



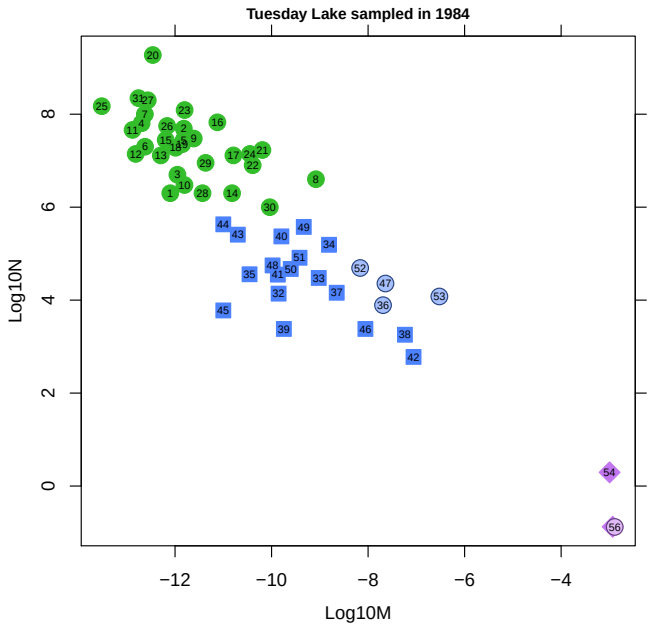
The parameter `node.labels` also accepts a vector of labels, so we could use letters to label the nodes.

```
> lots.of.letters <- c(letters, LETTERS, paste(LETTERS,letters,sep=''))
> PlotNPS(TL84, 'Log10M', 'Log10N', show.nodes.as='labels', show.web=FALSE,
        node.labels=lots.of.letters[1:NumberOfNodes(TL84)])
```



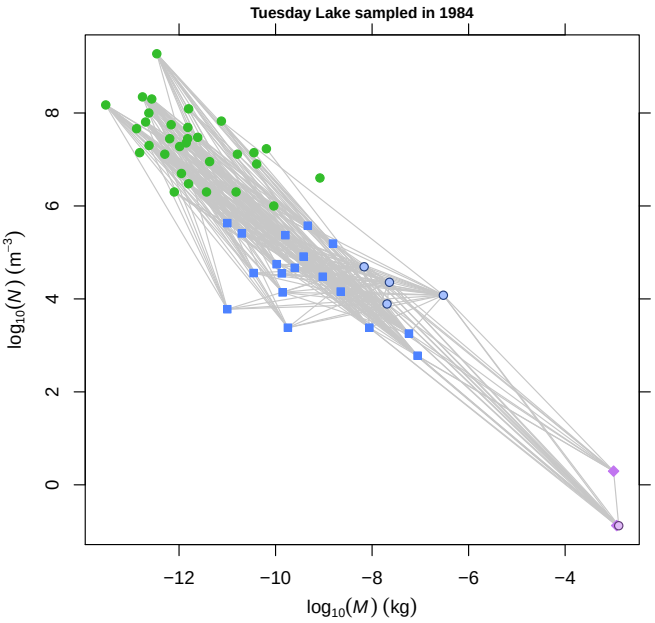
`PlotNPS` can plot both symbols and labels.

```
> PlotNPS(TL84, 'Log10M', 'Log10N', show.nodes.as='both', show.web=FALSE, cex=2)
```



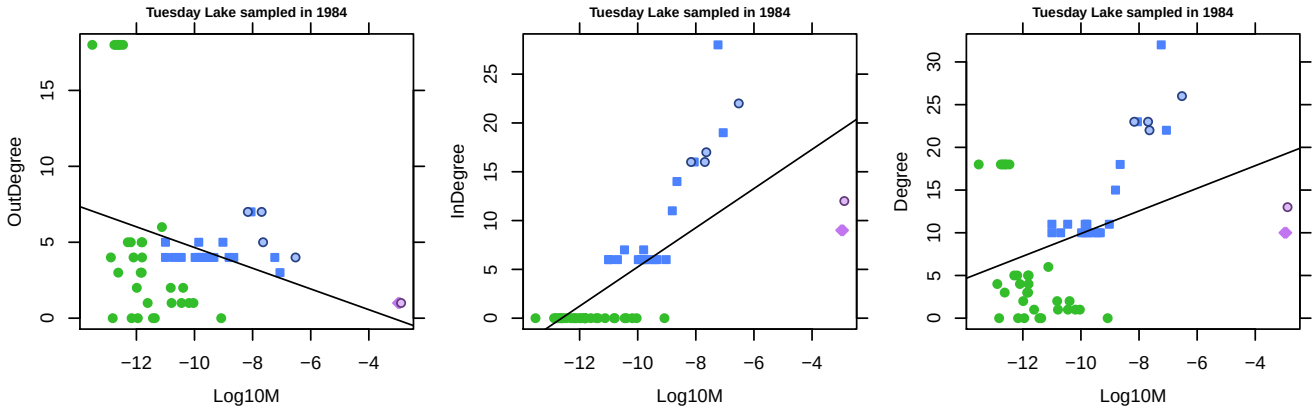
When `show.nodes.as` is 'both', the size and colours of labels are goverened by `label.cex` and `label.colour`, the latter discussed further in Section 2.4. The axes titles in the above examples are taken from the names of the properties. Cheddar provides some functions for producing nicely-formatted labels, shown below.

```
> PlotNPS(TL84, 'Log10M', 'Log10N', xlab=Log10MLabel(TL84),
        ylab=Log10NLabel(TL84))
```



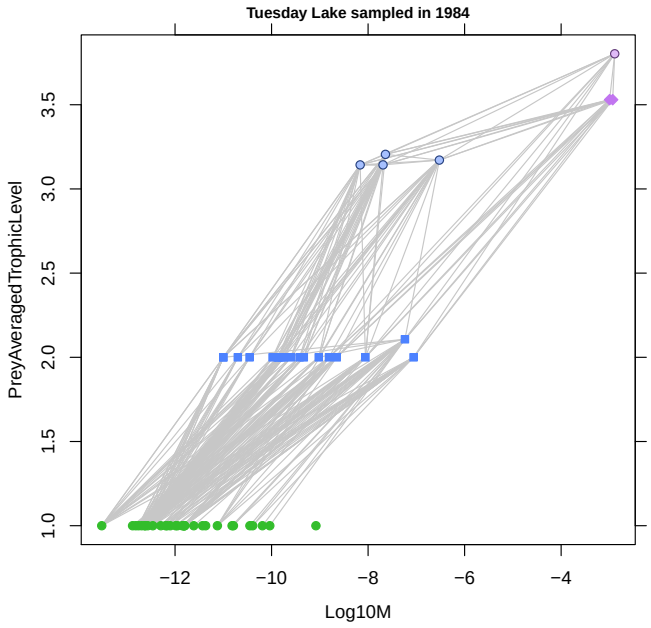
`PlotNPS` can plot any computed node property. For example, we can examine allometric degree distributions (Jonsson et al., 2005; Otto et al., 2007; Digel et al., 2011), which describe how species' numbers of trophic links scale with their log-transformed body masses.

```
> par(mfrow=c(1,3))
> PlotNPS(TL84, 'Log10M', 'OutDegree', show.web=FALSE)
> abline(lm(OutDegree(TL84) ~ Log10M(TL84)))
> PlotNPS(TL84, 'Log10M', 'InDegree', show.web=FALSE)
> abline(lm(InDegree(TL84) ~ Log10M(TL84)))
> PlotNPS(TL84, 'Log10M', 'Degree', show.web=FALSE)
> abline(lm(Degree(TL84) ~ Log10M(TL84)))
```



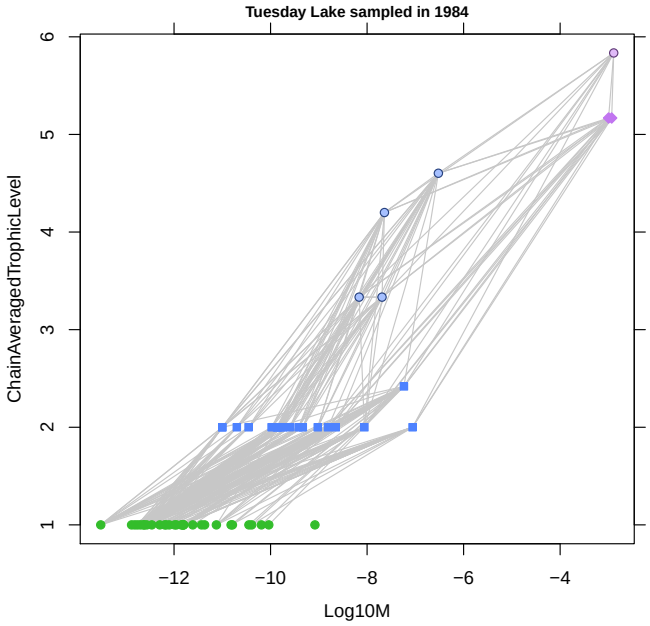
To examine the relationship between trophic structure and body mass (Cohen et al., 2003; Jonsson et al., 2005; Gilljam et al., 2011; Jacob et al., 2011; Riede et al., 2011; de Visser et al., 2011) we can plot trophic level against log-transformed body mass. The `PreyAveragedTrophicLevel` uses the matrix-inversion method of Levine (1980) to compute trophic levels.

```
> PlotNPS(TL84, 'Log10M', 'PreyAveragedTrophicLevel')
```



An alternative measure of trophic level is provided by `ChainAveragedTrophicLevel`, which computes the mean position of each node in every chain in the food web.

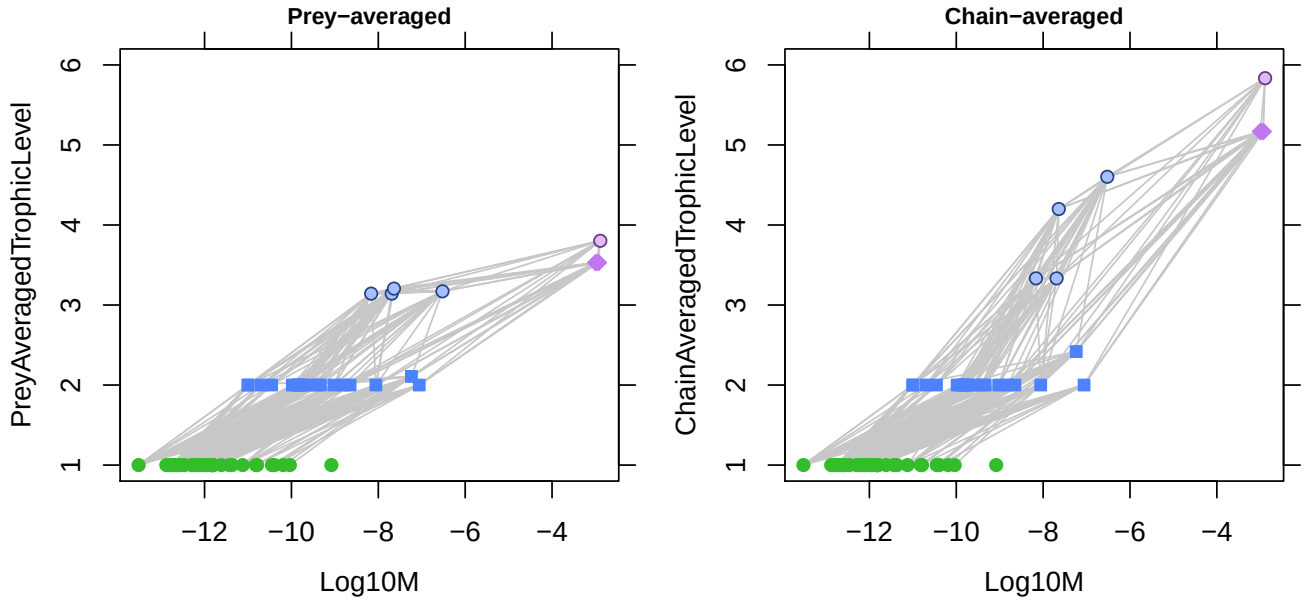
```
> PlotNPS(TL84, 'Log10M', 'ChainAveragedTrophicLevel')
```



Cheddar offers the six different measures of trophic level described by Williams and Martinez (2004); see the 'Communities' vignette and the help page for `TrophicLevels` for details.

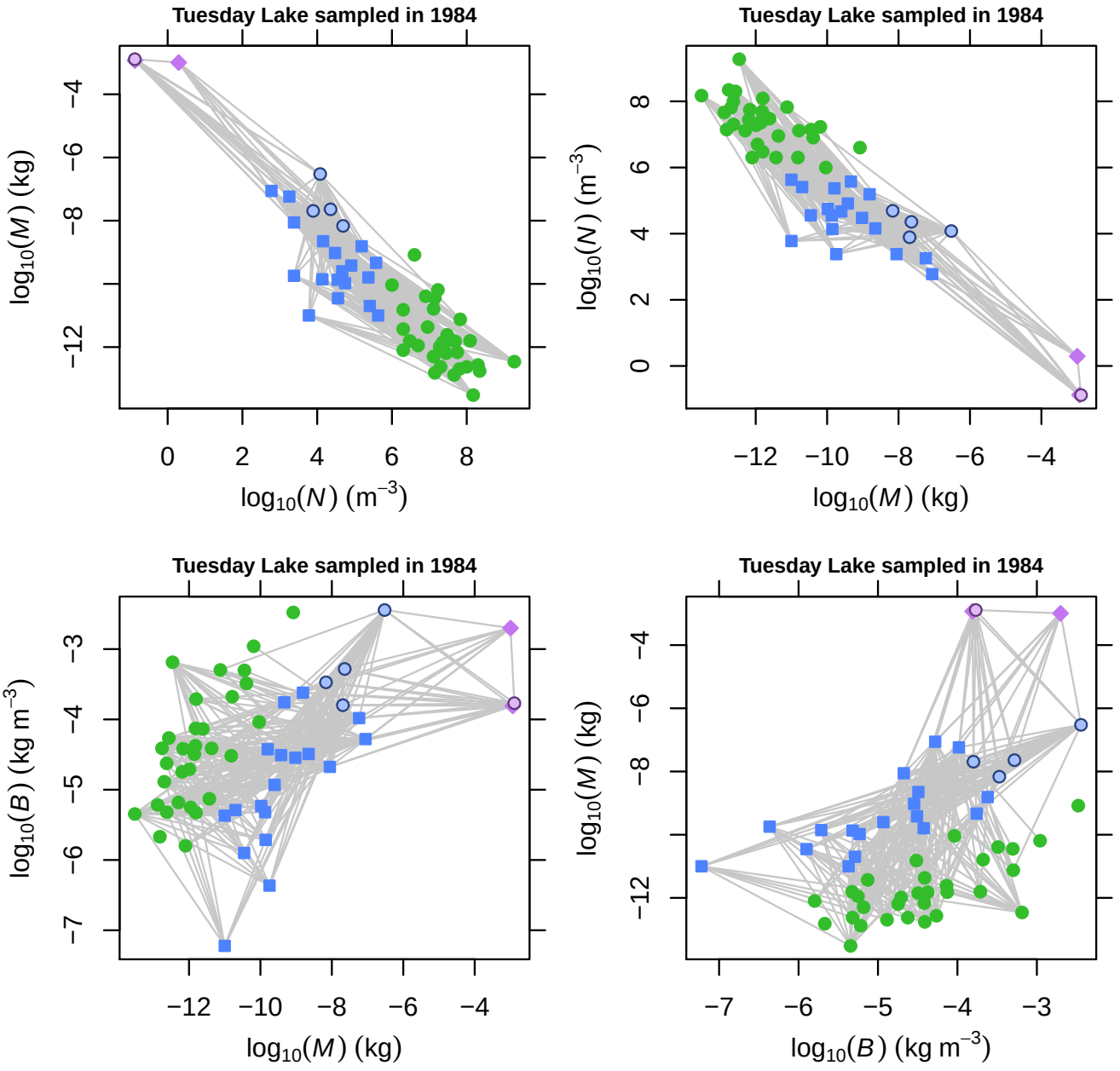
`PlotNPS` accepts the range of graphical parameters provided by R 's plotting system, such as `ylim` and `main`. To directly compare prey-averaged and chain-averaged trophic level we can produce side-by-side plots with the same y-axis limits.

```
> par(mfrow=c(1,2))
> PlotNPS(TL84, 'Log10M', 'PreyAveragedTrophicLevel', ylim=c(1, 6),
          main='Prey-averaged')
> PlotNPS(TL84, 'Log10M', 'ChainAveragedTrophicLevel', ylim=c(1, 6),
          main='Chain-averaged')
```



It is common to plot some combination of $\log_{10}$-transformed body mass, M, numerical abundance, N, or biomass, B (e.g. Cohen et al., 2003; Jonsson et al., 2005; Woodward et al., 2005). The convenience functions `PlotMvN`, `PlotNvM`, `PlotBvM` and `PlotMvB` are 'wrappers' around `PlotNPS` that create these plots.

```
> par(mfrow=c(2,2))
> PlotMvN(TL84)
> PlotNvM(TL84)
> PlotBvM(TL84)
> PlotMvB(TL84)
```

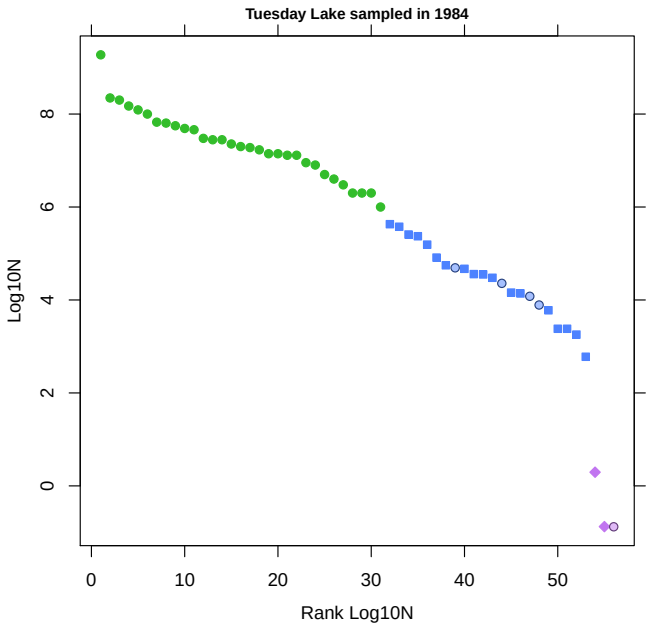


All of the modifying parameters that can be sent to `PlotNPS` to do things like changing the highlighting etc., can also be sent to to these convenience functions.

2.2 Rank of properties

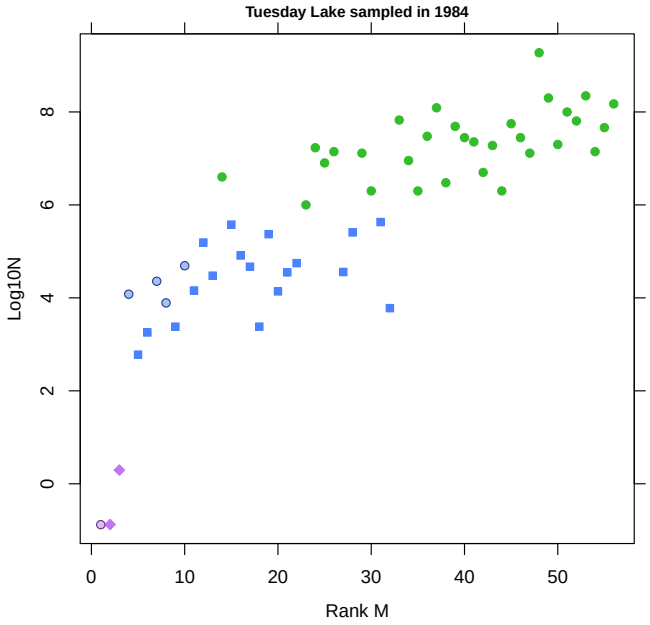
`PlotRankNPS` plots the rank of a property. As with `PlotNPS`, properties can be either first-class or computed. To plot $\log_{10}(N)$ against the rank of N (Jonsson et al., 2005):

```
> PlotRankNPS(TL84, 'Log10N')
```



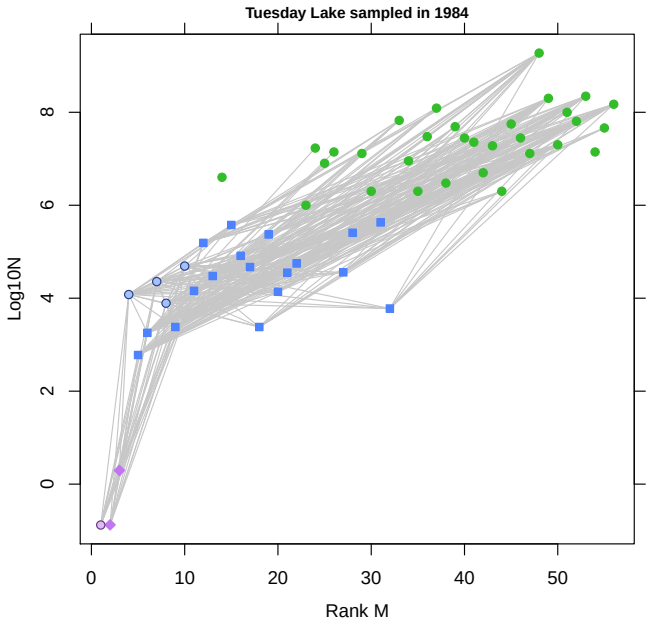
To plot $\log_{10}(N)$ against the rank of M:

```
> PlotRankNPS(TL84, 'Log10N', rank.by='M')
```



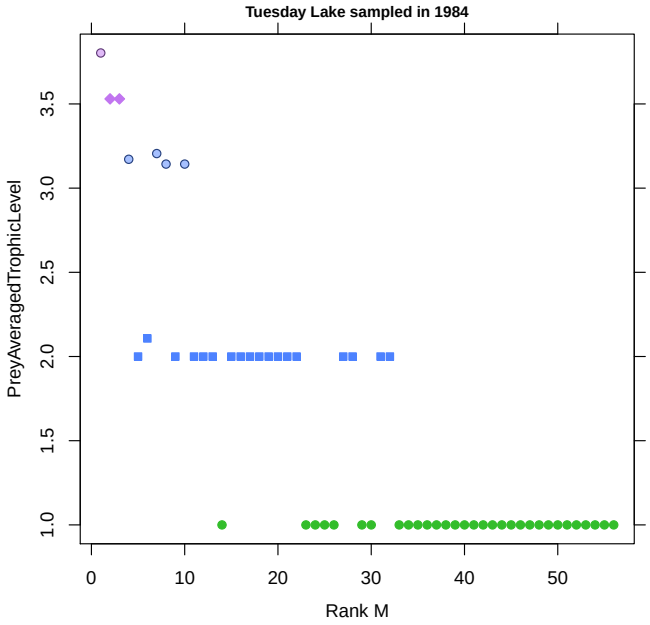
`PlotRankNPS` uses `PlotNPS` to do the actual plotting so all of `PlotNPS`'s power and parameters available. For example, the default behaviour of `PlotRankNPS` is to not show the food web. We can use `PlotNPS`'s 'show.web' parameter to show the food web.

```
> PlotRankNPS(TL84, 'Log10N', rank.by='M', show.web=TRUE)
```



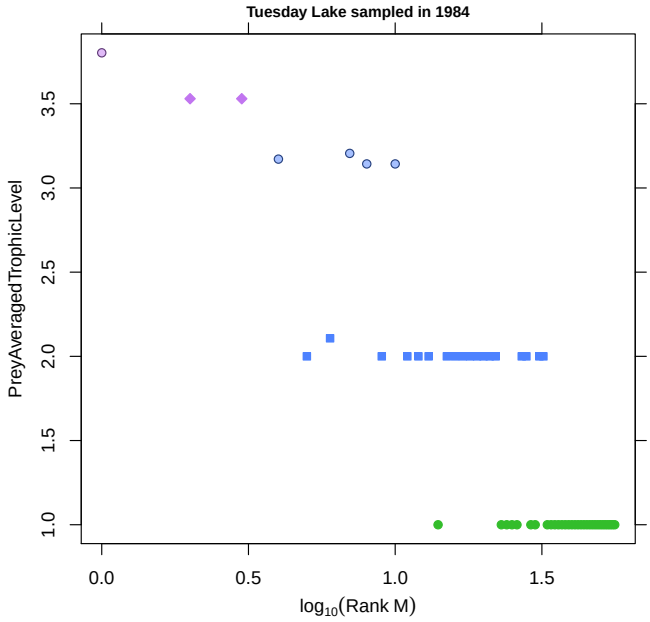
To plot trophic level against rank of M (Jonsson et al., 2005):

```
> PlotRankNPS(TL84, 'PreyAveragedTrophicLevel', rank.by='M')
```



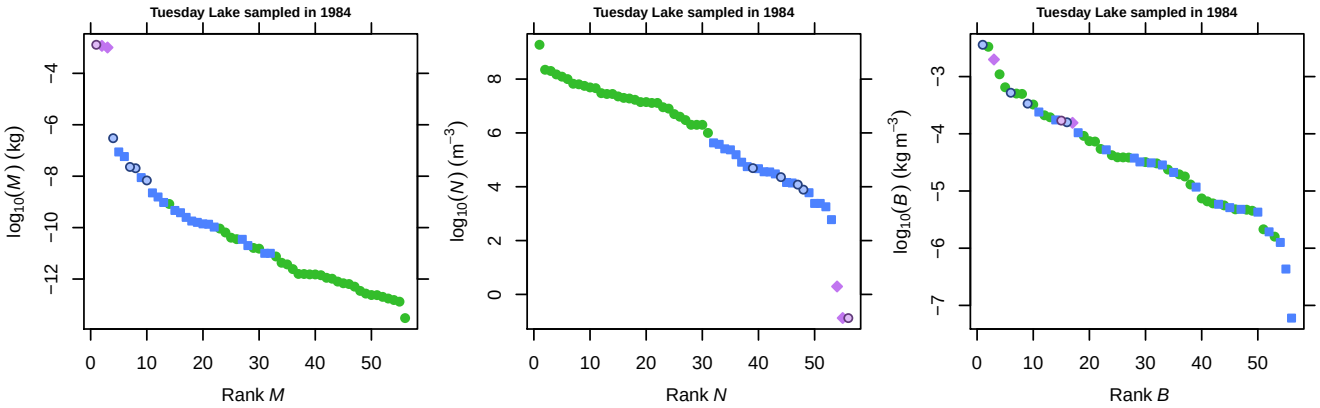
The `PlotRankNPS` function can log-transform the rank values shown on the x axis (Jonsson et al., 2005):

```
> PlotRankNPS(TL84, 'PreyAveragedTrophicLevel', rank.by='M', log10.rank=TRUE)
```



The convenience functions `PlotMvRankM`, `PlotNvRankN` and `PlotBvRankB` are 'wrappers' around `PlotRankNPS` that plot rank $\log_{10}$-transformed body mass, M, numerical abundance, N, or biomass, B (Jonsson et al., 2005).

```
> par(mfrow=c(1,3))
> PlotMvRankM(TL84)
> PlotNvRankN(TL84)
> PlotBvRankB(TL84)
```

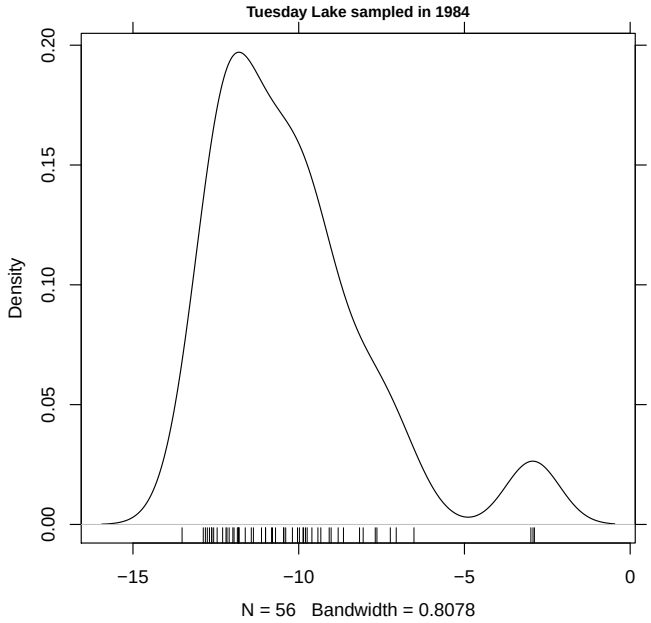


All of the modifying parameters that can be sent to `PlotNPS` to do things like changing the highlighting etc., can also be sent to to these convenience functions.

2.3 Distribution of a property

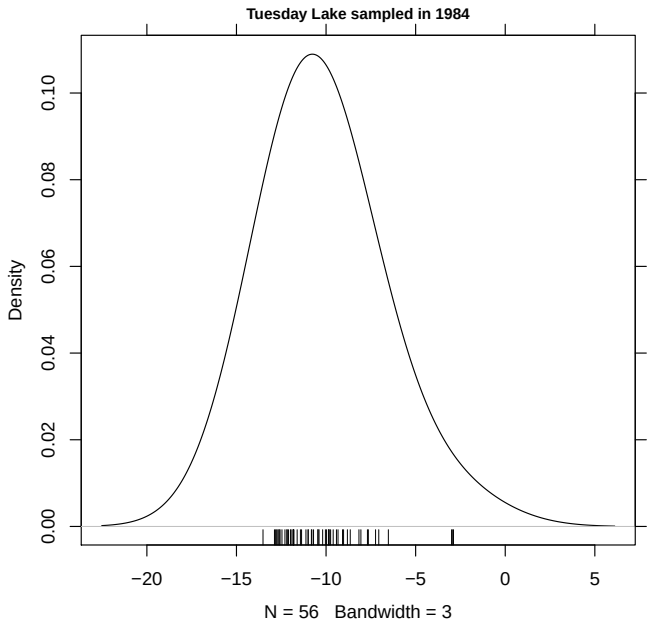
The `PlotNPSDistribution` function plots the distribution of a node property.

```
> PlotNPSDistribution(TL84, 'Log10M')
```



You can pass arguments to R 's `density` function using `density.args`, to change the bandwidth, for example:

```
> PlotNPSDistribution(TL84, 'Log10M', density.args=list(bw=3))
```

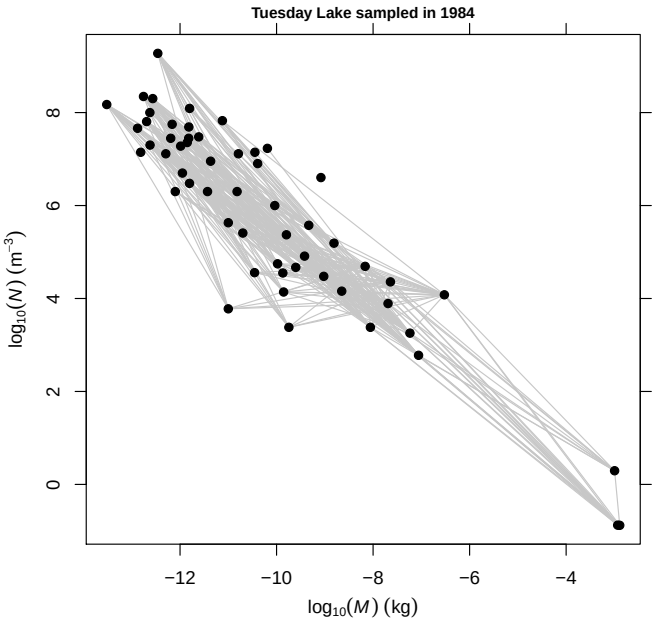


The convenience 'wrapper' functions `PlotMDistribution`, `PlotNDistribution` and `PlotBDistribution` plot $\log_{10}$-transformed body mass, numerical abundance and biomass abundance respectively.

2.4 Colours and symbols

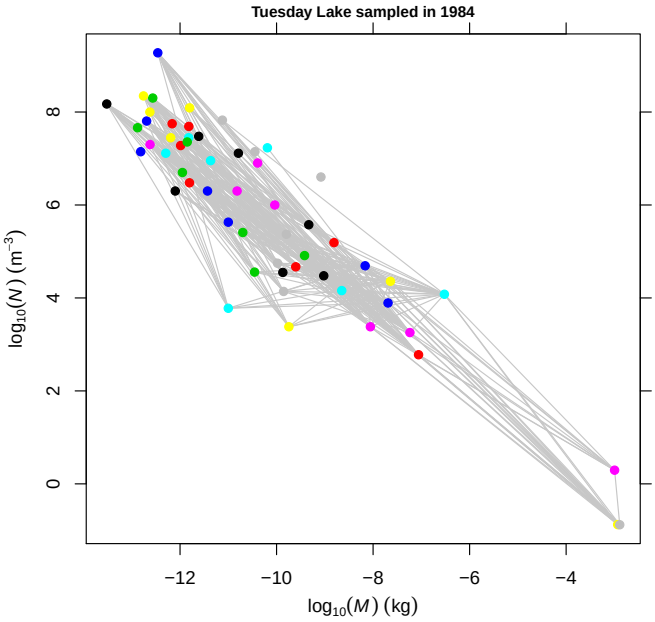
Cheddar builds on R 's highly flexible plotting mechanisms. Symbol, outline colour, fill colour and symbol size can controlled either by a first-class property, such as 'category' or taxonomic resolution, or by a computed property such as trophic species numbers. As with any R plot, you can directly set colours, symbols, a graph title etc. If the community being plotted has a node property called 'category' the function uses 'category' to decide plotting colours and symbols using the specifications given in `DefaultCategoryColours` and `DefaultCategorySymbols`.

```
> PlotNvM(TL84, col=1, pch=19, highlight.nodes=NULL)
```



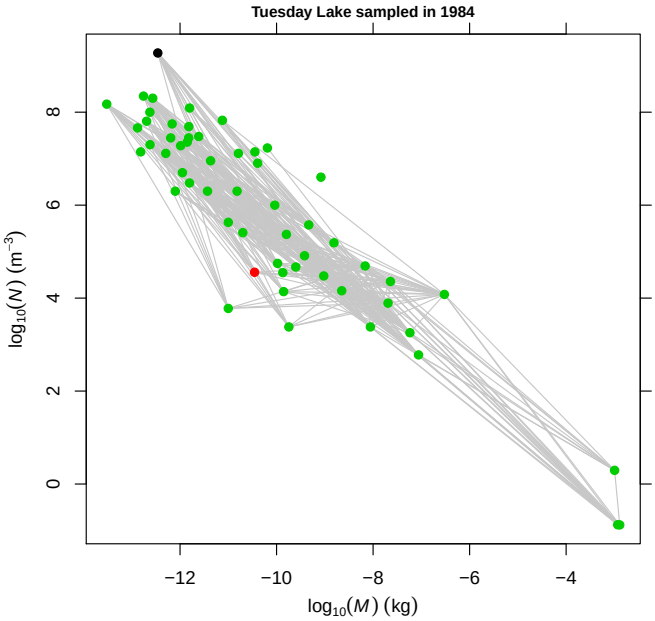
Plot each node in different colour by providing a vector of colours.

```
> PlotNvM(TL84, col=1:56, pch=19, highlight.nodes=NULL)
```



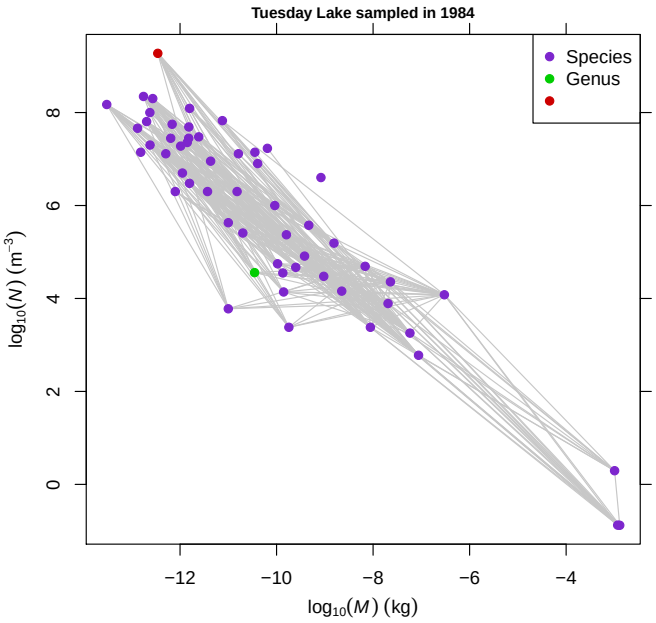
Plot each level of taxonomic resolution in a different colour. In this example, a value of 'colour.spec' is not given so `PlotNPS` converts the values of the first-class node property 'resolved.to' to a factor and uses the factor levels to colour each node. This is a 'quick and dirty' way to set node colours.

```
> PlotNvM(TL84, colour.by='resolved.to', pch=19, highlight.nodes=NULL)
```



We can improve on this by showing each level of taxonomic resolution in a specific colour by providing the 'colour.spec' parameter.

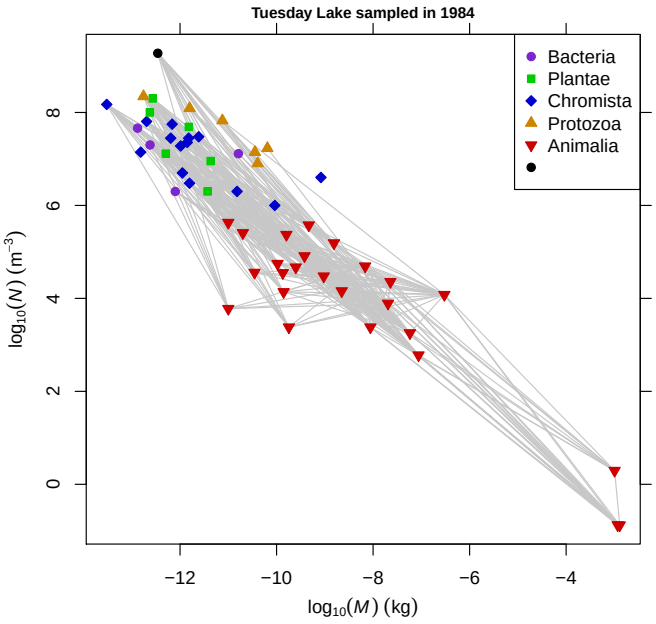
```
> colour.spec <- c(Species='purple3', Genus='green3', 'red3')
> PlotNvM(TL84, colour.by='resolved.to', colour.spec=colour.spec, pch=19,
        highlight.nodes=NULL)
> legend("topright", legend=names(colour.spec), pch=19, col=colour.spec)
```



The 'Unclassified flagellates' node does not have a taxonomic resolution. This node is matched by the unnamed value in `colour.spec` and so is shown in red.

The example below uses the 'kingdom' level of classification to determine node colours and symbols.

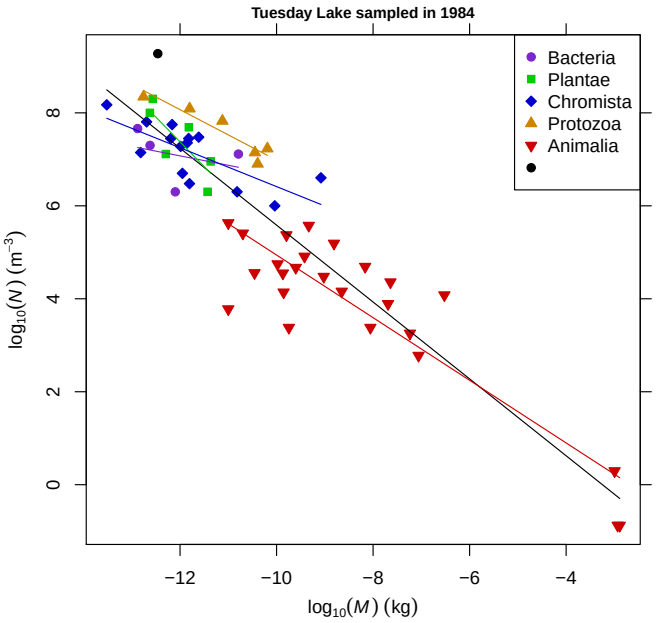
```
> symbol.spec = c(Bacteria=21, Plantae=22, Chromista=23,
                  Protozoa=24, Animalia=25, 19)
> colour.spec = c(Bacteria='purple3', Plantae='green3',
                  Chromista='blue3', Protozoa='orange3',
                  Animalia='red3', 'black')
> PlotNvM(TL84,
          symbol.by='kingdom', symbol.spec=symbol.spec,
          bg.by='kingdom', bg.spec=colour.spec,
          colour.by='kingdom', colour.spec=colour.spec,
          highlight.nodes=NULL)
> legend("topright", legend=names(colour.spec), pch=symbol.spec,
         col=colour.spec, pt.bg=colour.spec)
```



The 'Unclassified flagellates' node does not have a classification so is matched by the unnamed values in `symbol.spec` and `colour.spec` and is shown by a black circle.

We can fit and plot linear regressions for each kingdom by using the `NvMLinearRegressions` and `PlotLinearModels` functions. The food web is not shown in this plot to make the regression lines clearer.

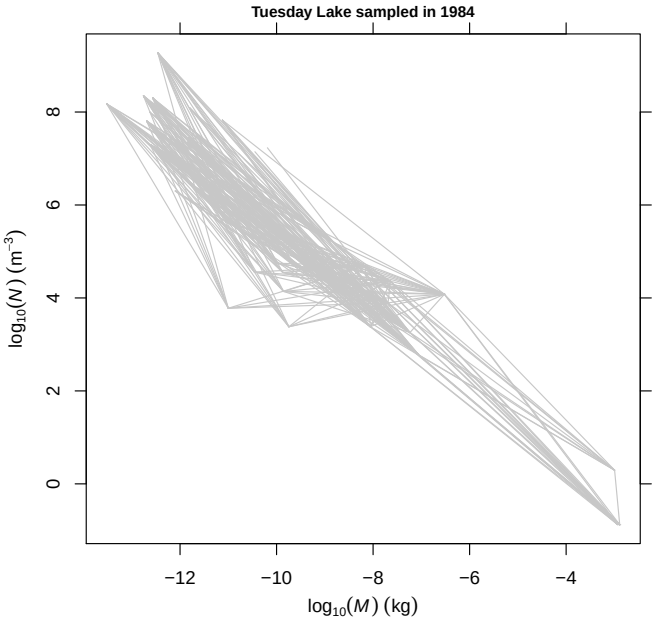
```
> symbol.spec = c(Bacteria=21, Plantae=22, Chromista=23,
                  Protozoa=24, Animalia=25, 19)
> colour.spec = c(Bacteria='purple3', Plantae='green3',
                  Chromista='blue3', Protozoa='orange3',
                  Animalia='red3', 'black')
> PlotNvM(TL84,
          symbol.by='kingdom', symbol.spec=symbol.spec,
          bg.by='kingdom', bg.spec=colour.spec,
          colour.by='kingdom', colour.spec=colour.spec,
          highlight.nodes=NULL, show.web=FALSE)
> legend("topright", legend=names(colour.spec), pch=symbol.spec,
         col=colour.spec, pt.bg=colour.spec)
> models <- NvMLinearRegressions(TL84, class='kingdom')
> colours <- PlotLinearModels(models, colour.spec=colour.spec)
```



The model fitted through all data points is matched by the empty value in `colour.spec` so is drawn in black. `NvMLinearRegressions` is described in more detail in Section 5.

You can use `pch=NA` to turn off symbols and just show the food web.

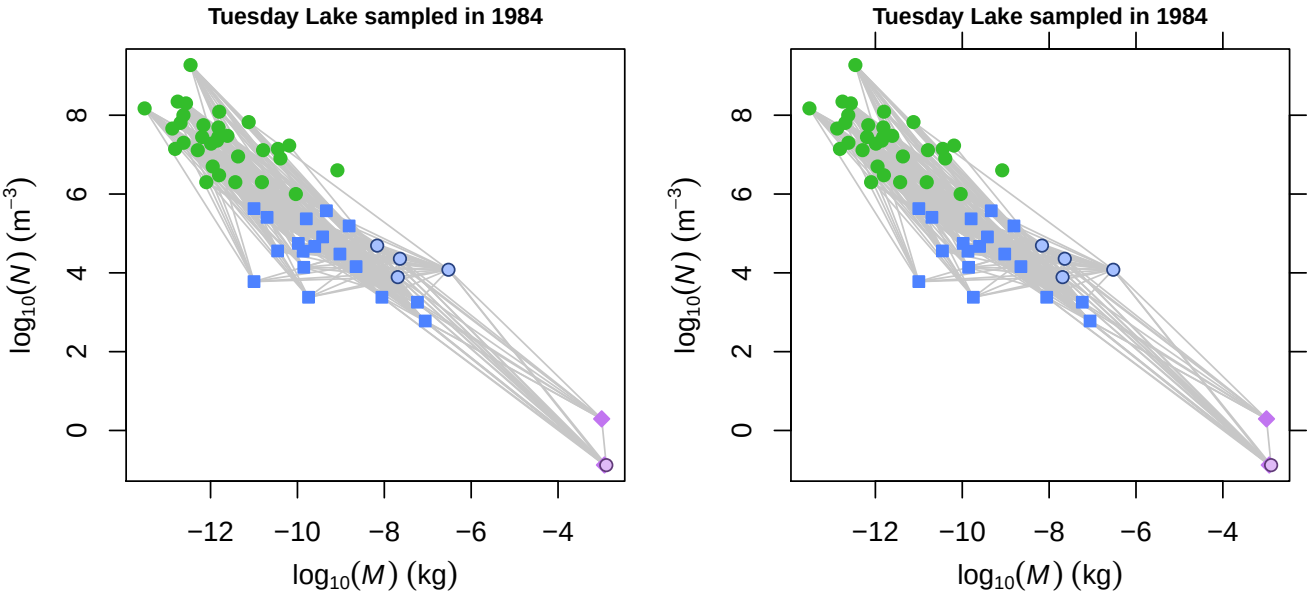
```
> PlotNvM(TL84, pch=NA, highlight.nodes=NULL)
```



See the help page for the R `par` function for more information about colours and symbols.

All of Cheddar's plot functions add axis ticks to the top and right of the plot by default. This can be turned off by using the `cheddarTopAndRightTicks` option.

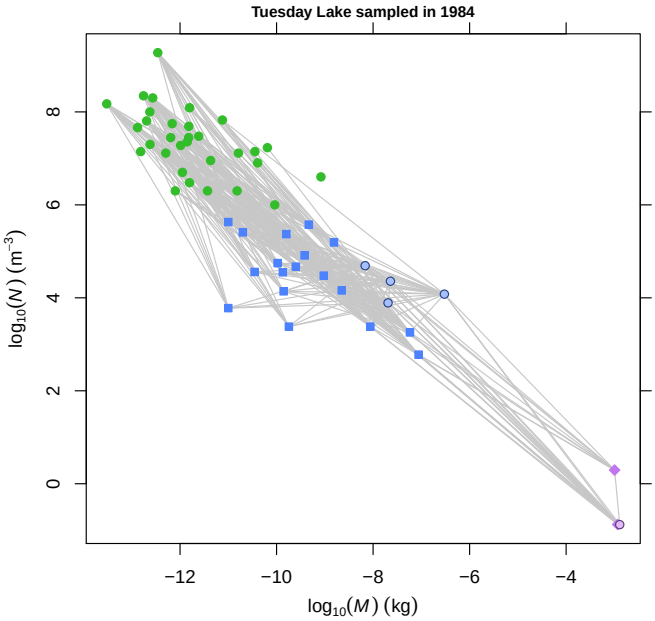
```
> par(mfrow=c(1,2))
> # Don't add ticks
> options(cheddarTopAndRightTicks=FALSE)
> PlotNvM(TL84)
> # Add ticks
> options(cheddarTopAndRightTicks=TRUE)
> PlotNvM(TL84)
```



2.5 Highlights and lowlights

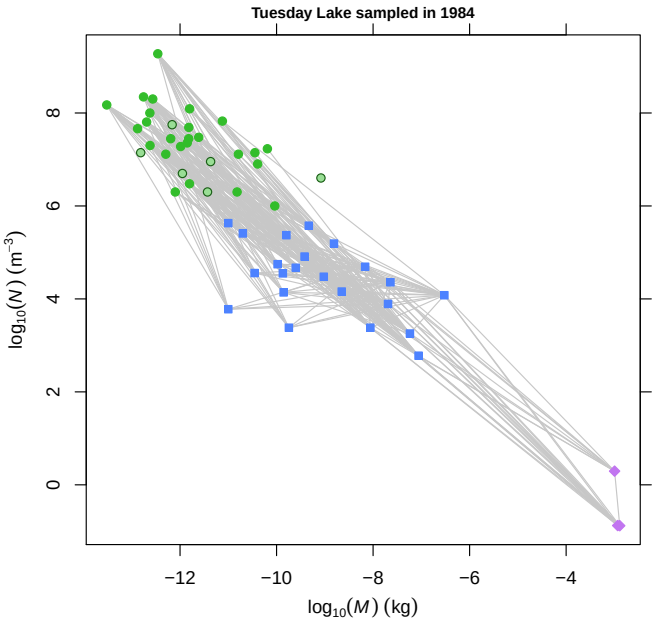
`PlotNPS` (and by extension all of the other node plotting functions) allow individual nodes to be highlighted or lowlighted using the `highlight.nodes` and `lowlight.nodes` parameters. These parameters accept functions. Functions should take a single `Community` object and return node names. Cheddar provides many such functions, such as `Cannibals`, which returns the names of all nodes that consume themselves.

```
> PlotNvM(TL84, highlight.nodes=Cannibals)
```



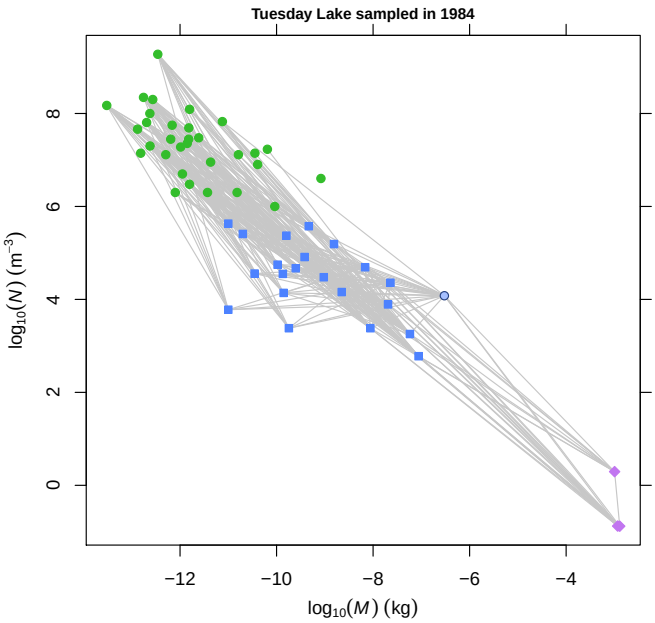
To highlight nodes without trophic-links to any other nodes we can use the `IsolatedNodes` function.

```
> PlotNvM(TL84, highlight.nodes=IsolatedNodes)
```



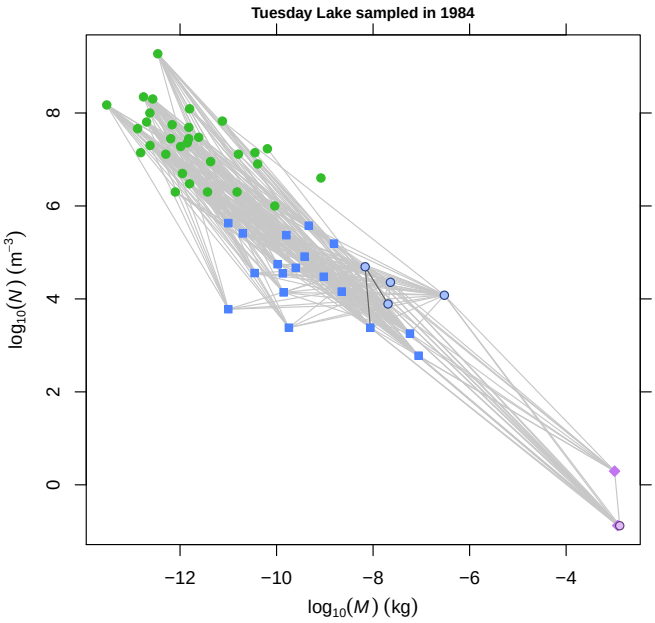
These parameters also accept the names or IDs of nodes. We can highlight an individual node.

```
> PlotNvM(TL84, highlight.nodes='Chaoborus punctipennis')
```



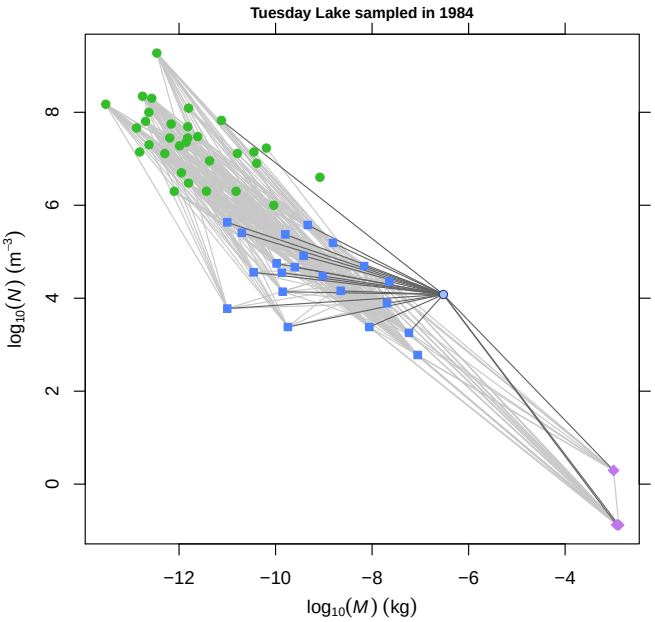
`PlotNPS` also allows trophic links to be highlighted. The `highlight.links` parameter accepts either a `data.frame` with the columns 'resource' and 'consumer' or a function that accepts a single community as its only parameters and returns such a `data.frame`. One such function is `ResourceLargerThanConsumer`, which returns a `data.frame` containing trophic links in which the resource has a larger body mass, M, than its consumer. To highlight these links we would simply pass this function as the `highlight.links` parameter.

```
> PlotNvM(TL84, highlight.links=ResourceLargerThanConsumer)
```



The example below uses the helper function `TrophicLinksForNodes` to highlight all links in to and out of *Chaoborus punctipennis*.

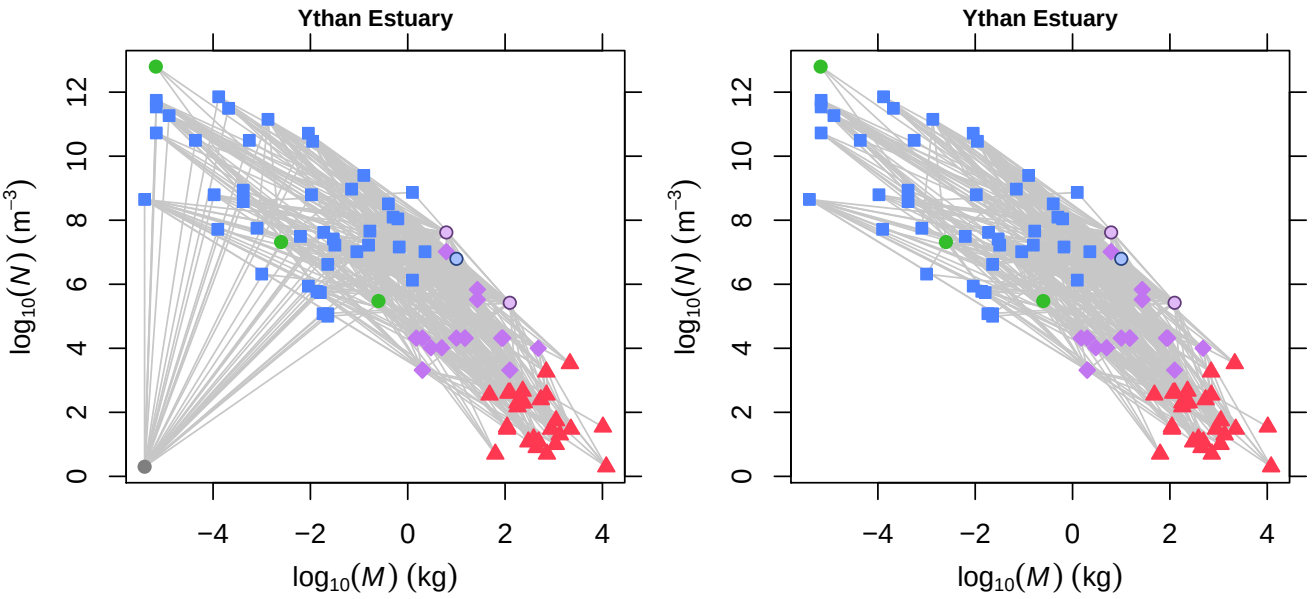
```
> PlotNvM(TL84, highlight.nodes='Chaoborus punctipennis',
        highlight.links=TrophicLinksForNodes(TL84, 'Chaoborus punctipennis'))
```



2.6 Nodes that lack properties

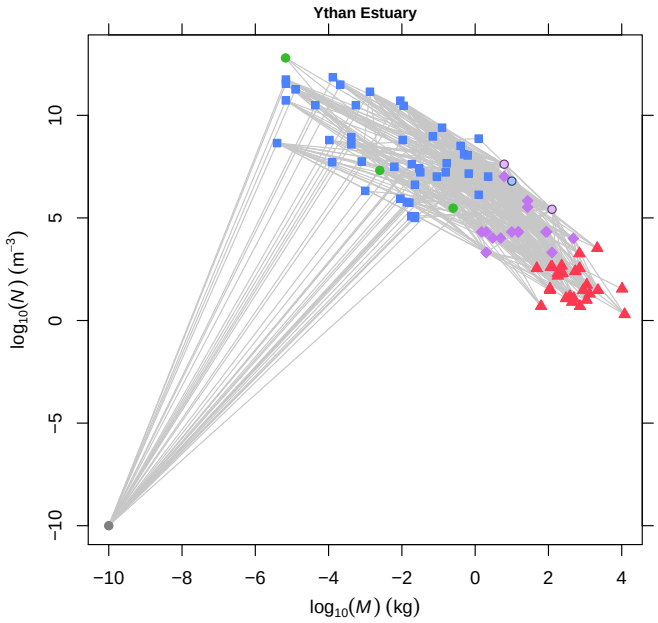
Communities are never completely sampled and some species may be represented by too few individuals for properties such as M and N to be accurately estimated. Other resources such as detritus, commonly eaten by primary consumers in many communities, have no clearly-defined M or N. Many datasets will therefore contain food-web nodes that lack one or more properties, for example Ythan Estuary dataset has a large number of primary consumers that depend upon detritus, which has no M or N. `PlotNPS`, and hence the higher-level functions that use it, will place nodes without a property at the lowest extent of the relevant axis if the 'show.na' parameter is `TRUE`. The `PlotNvM`, `PlotMvN`, `PlotBvM` and `PlotMvB` functions all set 'show.na' to `TRUE` by default. All other functions that delegate to `PlotNPS` set 'show.na' to `FALSE` by default. The first of the $\log_{10}(N)$-versus-$\log_{10}(M)$ plots below show detritus at the bottom-left of the plot.

```
> data(YthanEstuary)
> par(mfrow=c(1,2))
> PlotNvM(YthanEstuary)
> PlotNvM(YthanEstuary, show.na=FALSE)
```



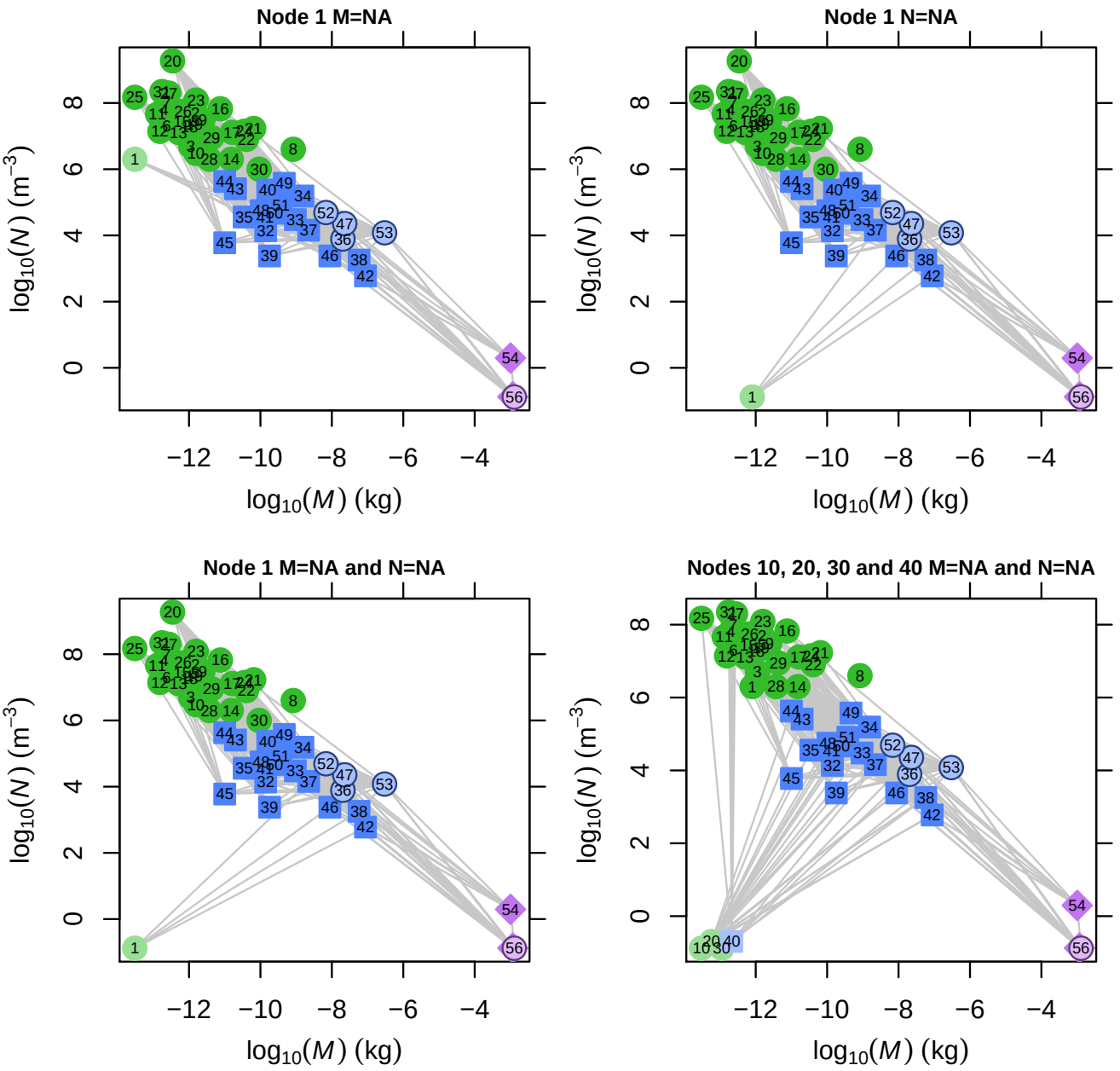
The location of the detritus node is determined by the extent of the data, or by the axes limits, if given.

```
> PlotNvM(YthanEstuary, xlim=c(-10, 4), ylim=c(-10, 13))
```



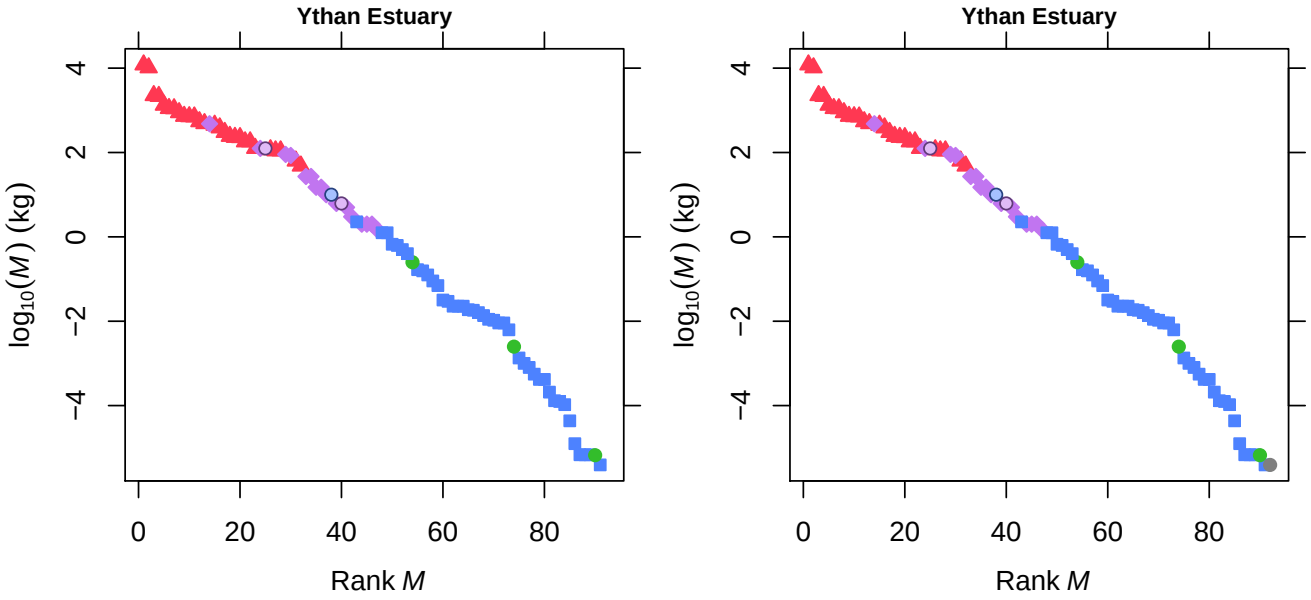
The example below shows how `PlotNPS` behaves in four different cases - node lacks x property, node lacks y property, node lacks both x and y properties and many nodes lack both x and y properties. `lowlight.nodes` defaults to nodes that lack either one of the properties being plotted, so the plots below lowlight the node(s) lacking M and/or N.

```
> par(mfrow=c(2,2))
> np <- NPS(TL84)
> np[1,'M'] <- NA
> PlotNvM(Community(nodes=np, trophic.links=TLPS(TL84), properties=CPS(TL84)),
        main='Node 1 M=NA', show.nodes.as='both',cex=2)
> np <- NPS(TL84)
> np[1,'N'] <- NA
> PlotNvM(Community(nodes=np, trophic.links=TLPS(TL84), properties=CPS(TL84)),
        main='Node 1 N=NA', show.nodes.as='both',cex=2)
> np <- NPS(TL84)
> np[1,'M'] <- NA
> np[1,'N'] <- NA
> PlotNvM(Community(nodes=np, trophic.links=TLPS(TL84), properties=CPS(TL84)),
        main='Node 1 M=NA and N=NA', show.nodes.as='both',cex=2)
> np <- NPS(TL84)
> np[c(10, 20, 30, 40),'M'] <- NA
> np[c(10, 20, 30, 40),'N'] <- NA
> PlotNvM(Community(nodes=np, trophic.links=TLPS(TL84), properties=CPS(TL84)),
        main='Nodes 10, 20, 30 and 40 M=NA and N=NA', show.nodes.as='both',
        cex=2)
```


Node 1 M=NA
Node 1 N=NA
Node 1 M=NA and N=NA
Nodes 10, 20, 30 and 40 M=NA and N=NA
log10(N) (m−3)
log10(M) (kg)
0
2
4
6
8
−12
−10
−8
−6
−4

The `PlotMvRankM` function delegates work to `PlotNPS`. The behaviour of 'show.na' for `PlotMvRankM` is shown below. The left-hand plot does not show the detritus node whereas the right-hand plot shows it as a grey circle.

```
> data(YthanEstuary)
> par(mfrow=c(1,2))
> PlotMvRankM(YthanEstuary)
> PlotMvRankM(YthanEstuary, show.na=TRUE)
```



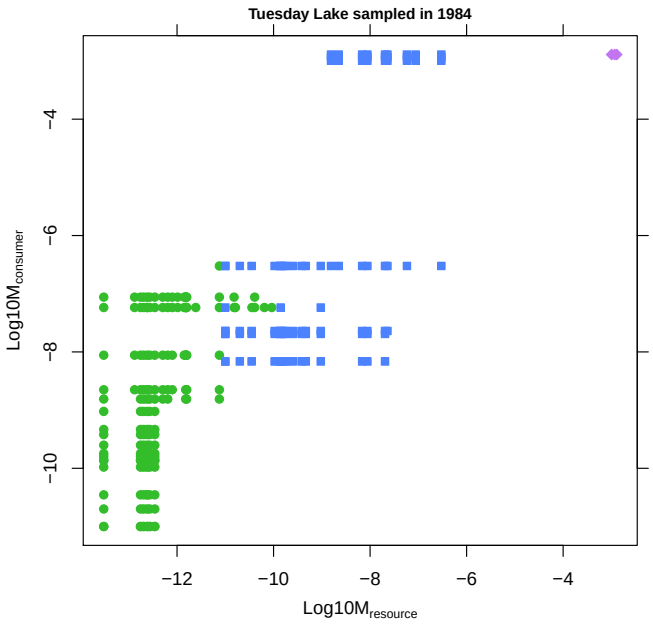
3 Plotting trophic-link properties

3.1 PlotTLPS

`PlotTLPS` (for **Plot** **T**rophic-**L**ink **P**ropertie**S**) plots one trophic-link property against another. Every Cheddar function that plots a point per trophic link delegates the job of plotting to `PlotTLPS` and all of its power and flexibility are available to all of the functions discussed in this section.

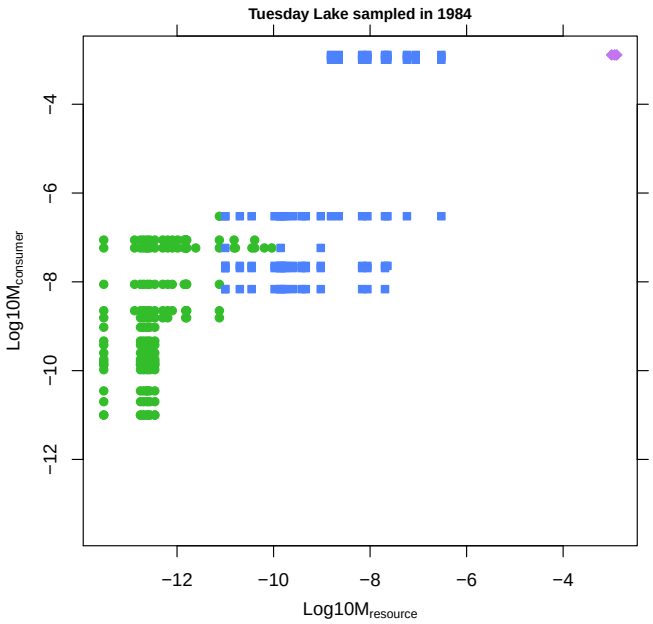
`PlotTLPS` accepts the names of properties to plot on the x and y axes. These can be both 'first-class' and computed properties of trophic links or nodes (where node properties are here viewed as properties of the trophic link of which the node is a part). If a property name begins with either 'resource.' or 'consumer.' then the remainder of the name is assumed to be a node property. For example, to plot $\log_{10}(M)$ of consumers against $\log_{10}(M)$ of consumers we can use the helper function `Log10M`.

```
> PlotTLPS(TL84, 'resource.Log10M', 'consumer.Log10M')
```



We can make the plot more informative if the the limits of both the x and y axes are the same. Setting the 'axes.limits.equal' parameter to `TRUE` instructs `PlotTLPS` to do just that, as shown below.

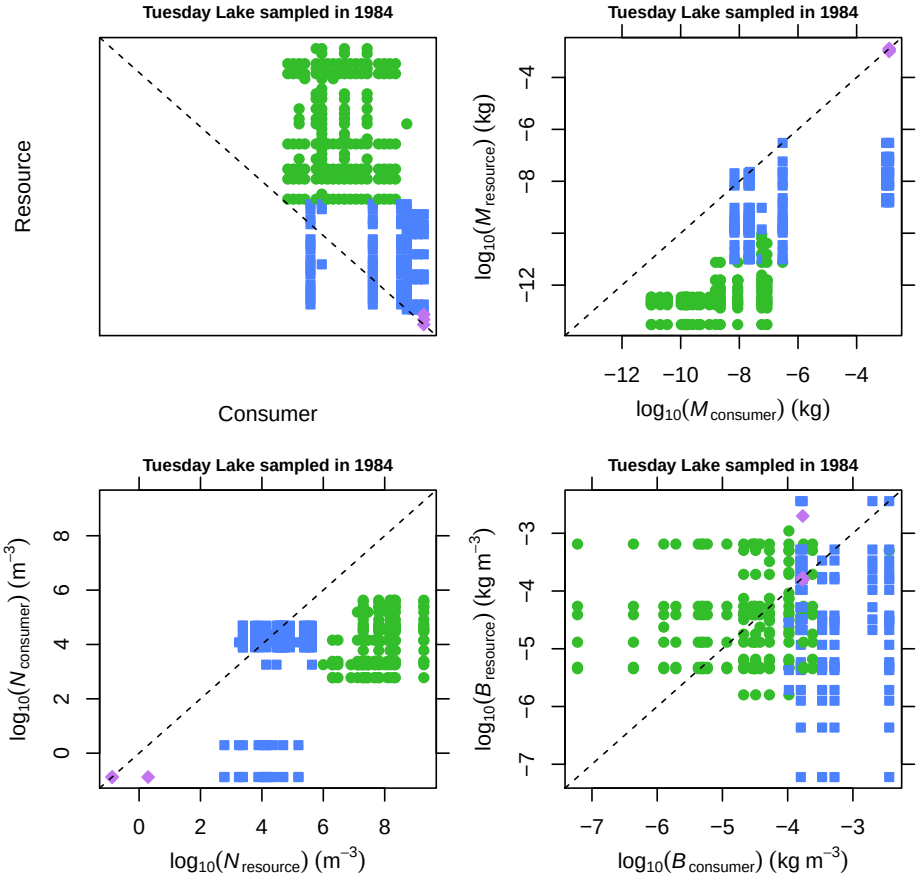
```
> PlotTLPS(TL84, 'resource.Log10M', 'consumer.Log10M', axes.limits.equal=TRUE)
```



`PlotTLPS` uses the `TLPS` function to assemble data for plotting. `PlotTLPS` uses the `category` node property of resources, if present, to decide plotting colours and symbols. Resources that are producers are shown by green circles, invertebrates by blue squares and vertebrate ectotherms by purple diamonds. This is explored more in Section 2.4.

The convenience functions `PlotPredationMatrix`, `PlotMRvMC`, `PlotMCvMR`, `PlotNRvNC`, `PlotNCvNR`, `PlotBRvBC`, `PlotBCvBR` are 'wrappers' around `PlotTLPS` that plot a predation matrix (a binary matrix with species shown in node order, starting at the top-left, points on the dashed line are cannibals) or $\log_{10}$-transformed body mass, M, numerical abundance, N, or biomass, B.

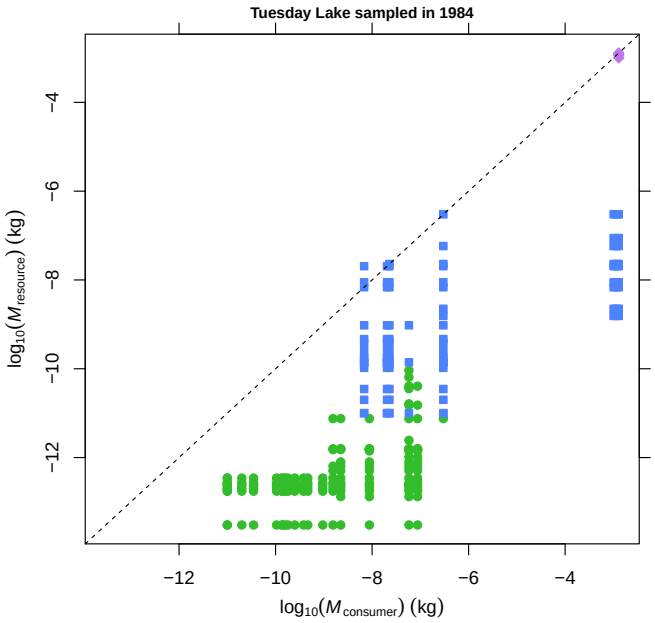
```
> par(mfrow=c(2,2))
> PlotPredationMatrix(TL84)
> PlotMRvMC(TL84)
> PlotNCvNR(TL84)
> PlotBRvBC(TL84)
```



3.2 Colours and symbols

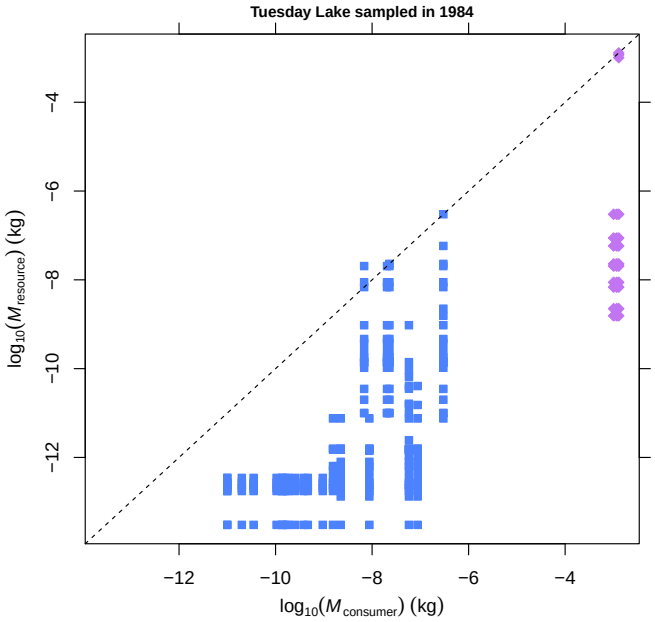
`PlotTLPS` uses a similar mechanism to `PlotNPS`. If the community being plotted has a node property called 'category' the function uses 'resource.category' to decide plotting colours and symbols using the specifications given in `DefaultCategoryColours` and `DefaultCategorySymbols`, as shown by this plot of consumer-versus-resource $\log_{10}$-transormed body mass.

```
> PlotMRvMC(TL84)
```



To plot the same data using the consumer's category to decide colours and symbols.

```
> PlotMRvMC(TL84, colour.by='consumer.category', bg.by='consumer.category',
          symbol.by='consumer.category')
```



The `bg.by` parameter is used to determine the background colour of each point. See the section for 'bg' in the help page for the R `par` function for more information.

4 Values by class

Cheddar provides functions that compute values over classes of nodes. For example, we can examine the total M, N and biomass in each category.

```
> SumMByClass(TL84)

invertebrate     producer    vert.ecto
5.110800e-07 1.127248e-09 3.470000e-03

> SumNByClass(TL84)

invertebrate     producer    vert.ecto
  1.8678e+06   3.2107e+09   2.2350e+00

> SumBiomassByClass(TL84)

invertebrate     producer    vert.ecto
 0.005376146  0.007438267  0.002315590
```

These functions can show the sums by any property of the community so we could look at the same totals by kingdom.

```
> SumMByClass(TL84, 'kingdom')

   <unnamed>     Animalia     Bacteria    Chromista      Plantae     Protozoa
3.460000e-13 3.470511e-03 1.736800e-11 9.488933e-10 1.054600e-11 1.500950e-10

> SumNByClass(TL84, 'kingdom')

 <unnamed>   Animalia   Bacteria  Chromista    Plantae   Protozoa
1880000000    1867802   81000000  425700000  373000000  451000000

> SumBiomassByClass(TL84, 'kingdom')

  <unnamed>    Animalia    Bacteria   Chromista     Plantae    Protozoa
0.000650480 0.007691736 0.000223046 0.003699680 0.000205291 0.002659770
```

The 'Unclassified flagellates' node does not have a kingdom, and the resulting value is labelled '<unnamed>'. These convenience functions are 'wrappers' around the more general-purpose `ApplyByClass` function. The following two calls produce the same result.

```
> SumBiomassByClass(TL84)

invertebrate     producer    vert.ecto
 0.005376146  0.007438267  0.002315590

> ApplyByClass(TL84, 'Biomass', 'category', sum)

invertebrate     producer    vert.ecto
 0.005376146  0.007438267  0.002315590
```

See the help page for `ApplyByClass` for more examples.

5 $\log_{10}(N)$-versus-$\log_{10}(M)$ statistics

Cheddar contains some helper functions that assist in the commonly-performed $\log_{10}(N)$-versus-$\log_{10}(M)$ statistics. `NvMLinearRegressions` returns a list of linear regressions through $\log_{10}(N)$-versus-$\log_{10}(M)$ node data. By default it fits a regression through all of the nodes (called 'all') and a separate regression through each node category.

```
> models <- NvMLinearRegressions(TL84)
> names(models)

[1] "all"          "producer"     "invertebrate" "vert.ecto"
```

You can extract the slopes and intercepts for each of these regression models.

```
> sapply(models, 'coef')

                   all   producer invertebrate vert.ecto
(Intercept) -2.6862753  2.5583364    1.4656062 -34.66097
x           -0.8271145 -0.4071509   -0.3243168 -11.62787
```

The 'class' parameter defines the sets of nodes to which `NvMLinearRegressions` fits regressions. This defaults to 'category', if this is present in the community. You can set the 'class' parameter to fit regressions through different sets of nodes, such as through each phylum as shown below.

```
> models <- NvMLinearRegressions(TL84, class='phylum')
> names(models)

 [1] "all"           "Cyanobacteria" "Charophyta"    "Ochrophyta"    "Cryptophyta"
 [6] "Chlorophyta"   "Myzozoa"       "<unnamed>"     "Euglenozoa"    "Rotifera"
[11] "Arthropoda"    "Chordata"
```

The '<unnamed>' label refers to a model fitted to nodes that do not have a phylum - just the 'unclassifiied flagellates' node in this case. It is not possible to fit a linear regression to a single data point and `NvMLinearRegressions` returns `NULL` for classes that contain just a single node. The data contain one node in phylum Euglenozoa and one node without a phylum, so these entries are `NULL`.

```
> sapply(models, is.null)

          all Cyanobacteria    Charophyta    Ochrophyta   Cryptophyta   Chlorophyta
        FALSE         FALSE         FALSE         FALSE         FALSE         FALSE
      Myzozoa     <unnamed>    Euglenozoa      Rotifera    Arthropoda      Chordata
        FALSE          TRUE          TRUE         FALSE         FALSE         FALSE
```

`NvMLinearRegressions` also returns `NULL` for classes where all or all bar one of the nodes have M and/or M of `NA`. The Broadstone stream dataset contains detrital and algal nodes that all lack both M and N; these nodes are in the <unnamed> category.

```
> data(BroadstoneStream)
> models <- NvMLinearRegressions(BroadstoneStream)
> sapply(models, is.null)
```

```
         all invertebrate    <unnamed>     producer
       FALSE        FALSE         TRUE         TRUE
```

Three helper functions return the slope and/or intercept of an ordinary linear regression through all data.

```
> NvMSlope(TL84)

[1] -0.8271145

> NvMIntercept(TL84)

[1] -2.686275

> NvMSlopeAndIntercept(TL84)

     slope  intercept
-0.8271145 -2.6862753
```

Three more helper functions extract these coefficients for each class.

```
> NvMSlopeByClass(TL84)

         slope.all     slope.producer slope.invertebrate    slope.vert.ecto
       -0.8271145         -0.4071509         -0.3243168        -11.6278709

> NvMInterceptByClass(TL84)

         intercept.all     intercept.producer intercept.invertebrate
             -2.686275               2.558336               1.465606
   intercept.vert.ecto
            -34.660973

> NvMSlopeAndInterceptByClass(TL84)

             slope.all         slope.producer     slope.invertebrate
            -0.8271145             -0.4071509             -0.3243168
       slope.vert.ecto          intercept.all     intercept.producer
           -11.6278709             -2.6862753              2.5583364
intercept.invertebrate    intercept.vert.ecto
             1.4656062            -34.6609728
```

You can fit regressions to whatever class you like.

```
> NvMSlopeByClass(TL84, class='kingdom')

      slope.all  slope.Bacteria   slope.Plantae slope.Chromista  slope.Protozoa
     -0.8271145      -0.2028766      -1.0654368      -0.4177200      -0.5434582
slope.<unnamed>  slope.Animalia
             NA      -0.6737747

> NvMInterceptByClass(TL84, class='kingdom')
```

```
      intercept.all  intercept.Bacteria   intercept.Plantae intercept.Chromista
          -2.686275            4.640388           -5.409768            2.236353
 intercept.Protozoa intercept.<unnamed>  intercept.Animalia
           1.547918                  NA           -1.796438
```

```
> NvMSlopeAndInterceptByClass(TL84, class='kingdom')
```

```
          slope.all      slope.Bacteria       slope.Plantae     slope.Chromista
         -0.8271145          -0.2028766          -1.0654368          -0.4177200
     slope.Protozoa     slope.<unnamed>      slope.Animalia       intercept.all
         -0.5434582                  NA          -0.6737747          -2.6862753
 intercept.Bacteria   intercept.Plantae intercept.Chromista  intercept.Protozoa
          4.6403880          -5.4097680           2.2363526           1.5479185
intercept.<unnamed>  intercept.Animalia
                 NA          -1.7964381
```

6 Tri-trophic statistics

Cohen et al. (2009) proposed a novel analysis that simultaneously considers body mass, M, numerical abundance, N, and the community's food web. The `NvMTriTrophicStatistics` function provides this analysis. It takes a single community as its only parameter. Cannibalistic links and all nodes with an N or M of `NA` are removed before statistics are computed. It returns a list containing three matrices: 'links', 'three.node.chains' and 'trophic.chains'. The examples in Section 7.4 show how to use this function and the three matrices that it returns to reconstruct the important figures and tables from Cohen et al. (2009).

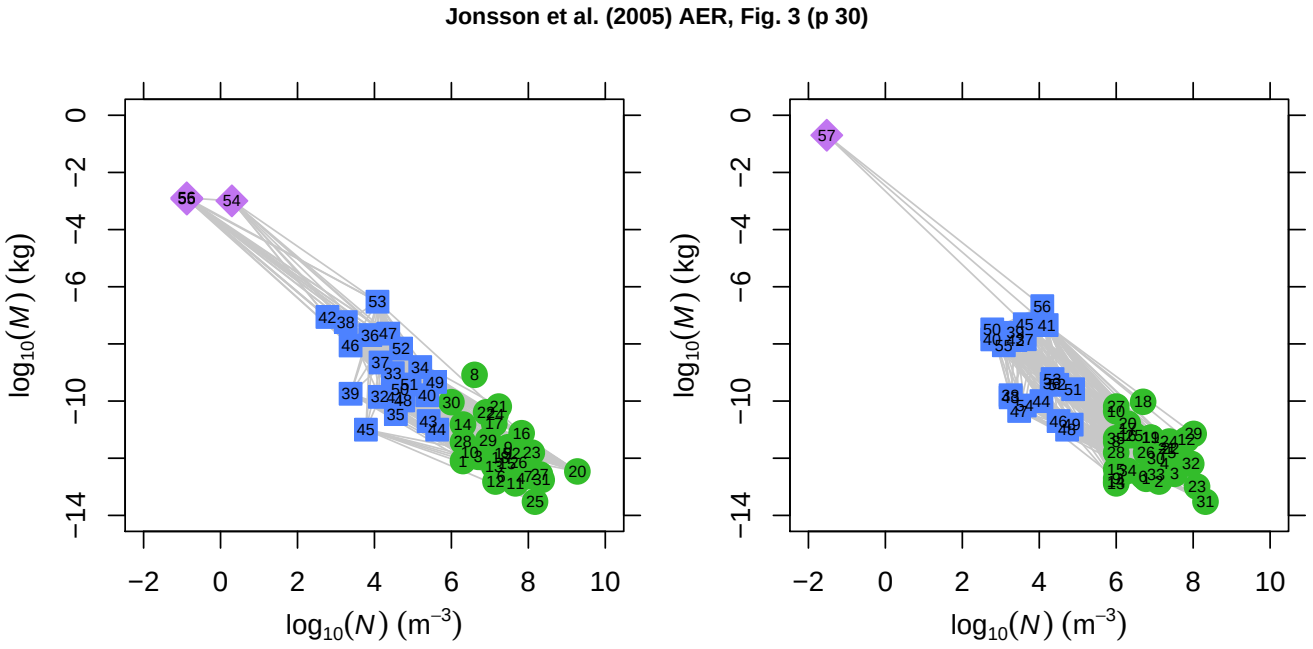
7 Examples through recreating figures and tables from published articles

The following sections show how to use Cheddar to recreate some published figures.

7.1 Jonsson et al. (2005)

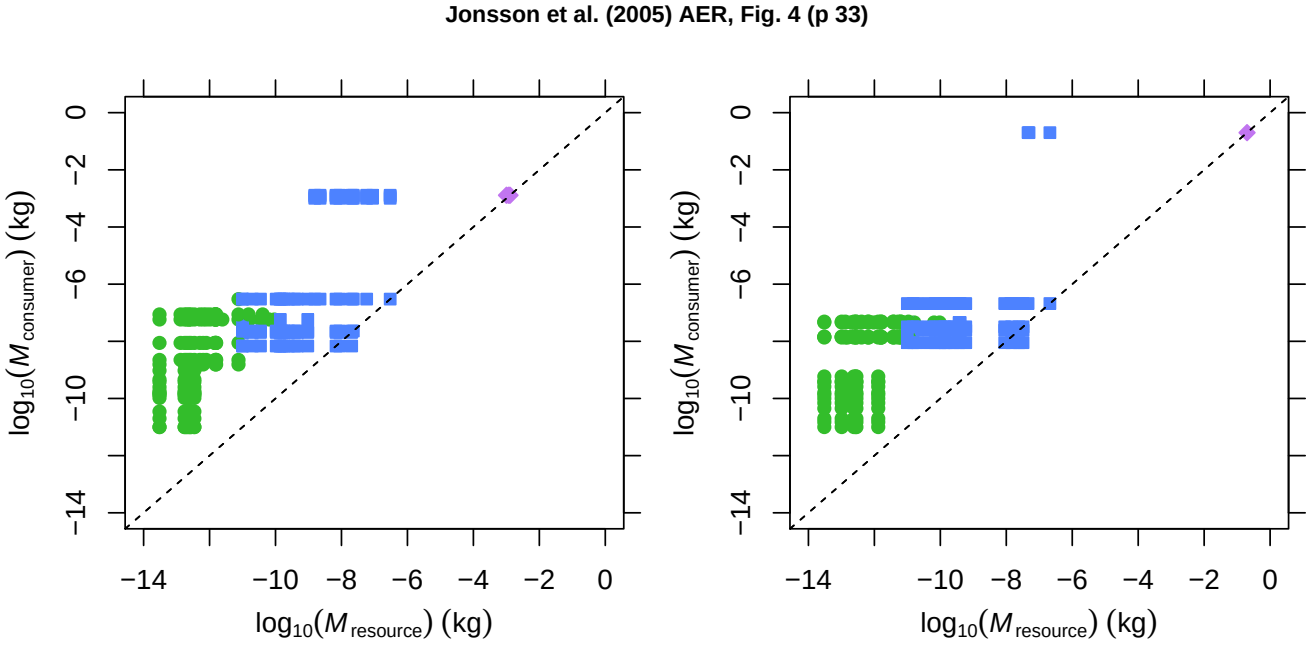
7.1.1 Jonsson et al. (2005), Fig. 3 (p 30)

```
> data(TL84, TL86)
> par(mfrow=c(1,2))
> PlotMvN(TL84, show.nodes.as='both', cex=2, xlim=c(-2, 10), ylim=c(-14, 0),
        highlight.nodes=NULL, highlight.links=NULL, main='')
> PlotMvN(TL86, show.nodes.as='both', cex=2, xlim=c(-2, 10), ylim=c(-14, 0),
        highlight.nodes=NULL, highlight.links=NULL, main='')
> title(main='Jonsson et al. (2005) AER, Fig. 3 (p 30)', outer=TRUE)
```



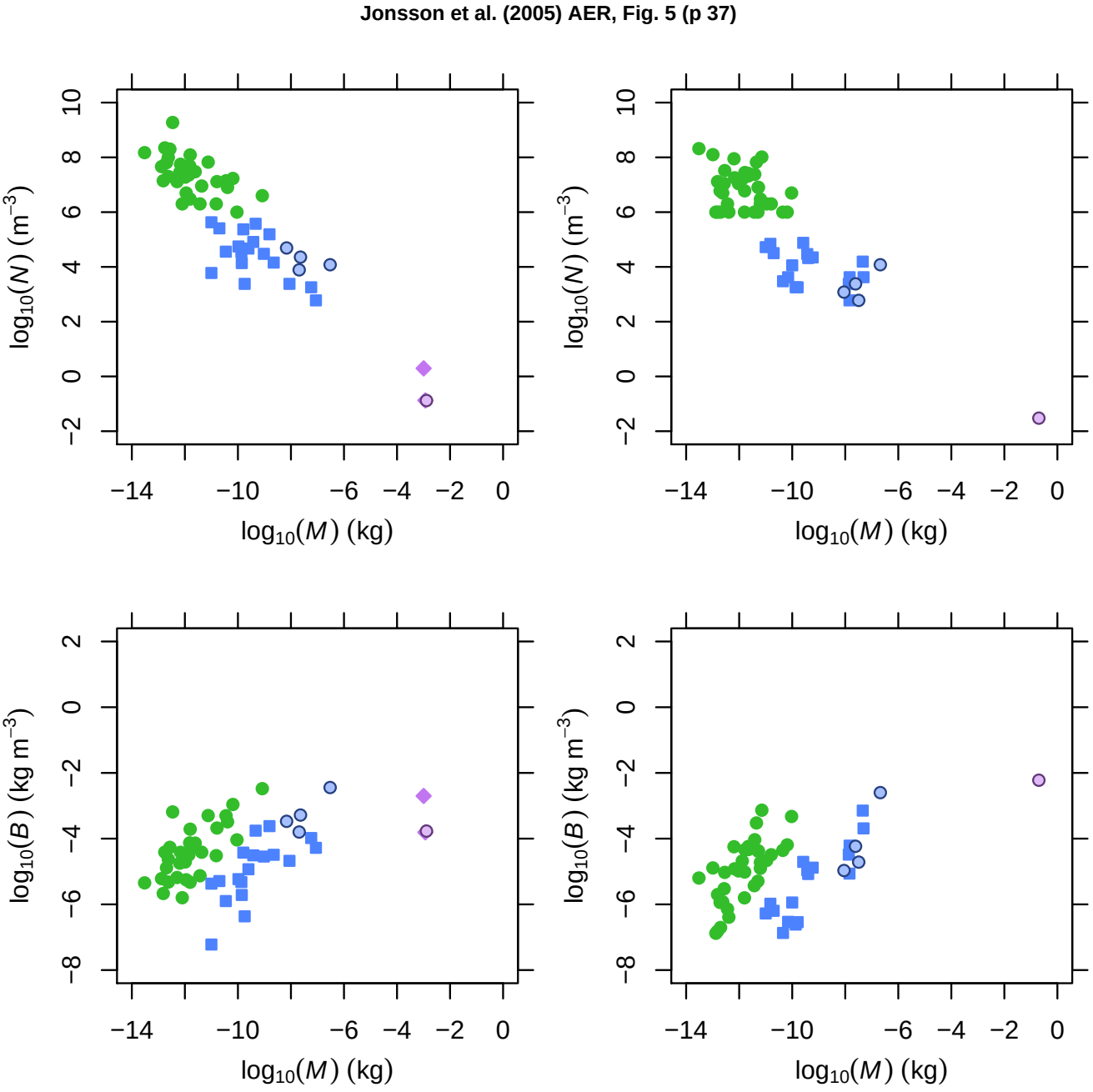
7.1.2 Jonsson et al. (2005), Fig. 4 (p 33)

```
> par(mfrow=c(1,2))
> PlotMCvMR(TL84, xlim=c(-14, 0), ylim=c(-14, 0), main='')
> abline(a=0, b=1, lty=2)
> PlotMCvMR(TL86, xlim=c(-14, 0), ylim=c(-14, 0), main='')
> abline(a=0, b=1, lty=2)
> title(main='Jonsson et al. (2005) AER, Fig. 4 (p 33)', outer=TRUE)
```



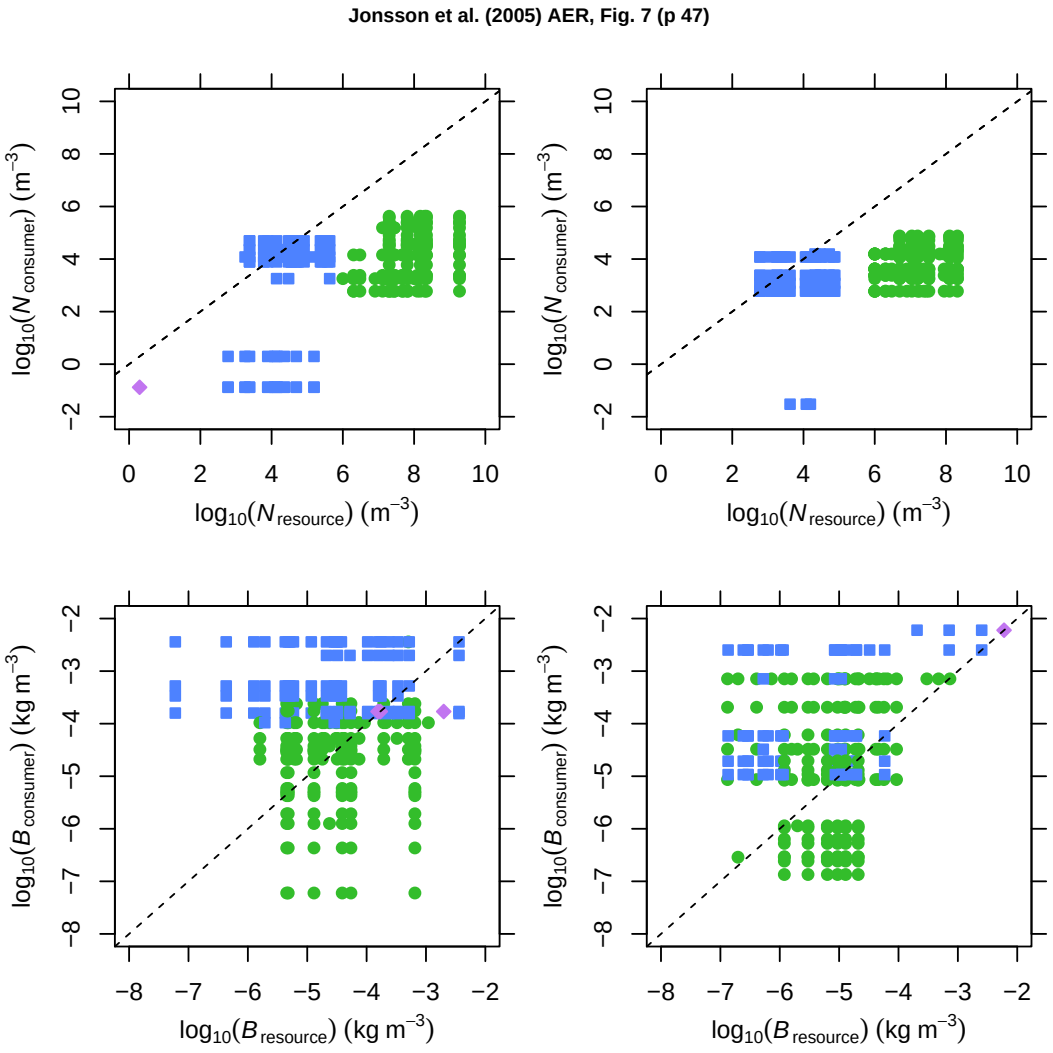
7.1.3 Jonsson et al. (2005), Fig. 5 (p 37)

```
> par(mfrow=c(2,2))
> PlotNvM(TL84, xlim=c(-14, 0), ylim=c(-2,10), show.web=FALSE, main='')
> PlotNvM(TL86, xlim=c(-14, 0), ylim=c(-2,10), show.web=FALSE, main='')
> PlotBvM(TL84, xlim=c(-14, 0), ylim=c(-8,2), show.web=FALSE, main='')
> PlotBvM(TL86, xlim=c(-14, 0), ylim=c(-8,2), show.web=FALSE, main='')
> title(main='Jonsson et al. (2005) AER, Fig. 5 (p 37)', outer=TRUE)
```



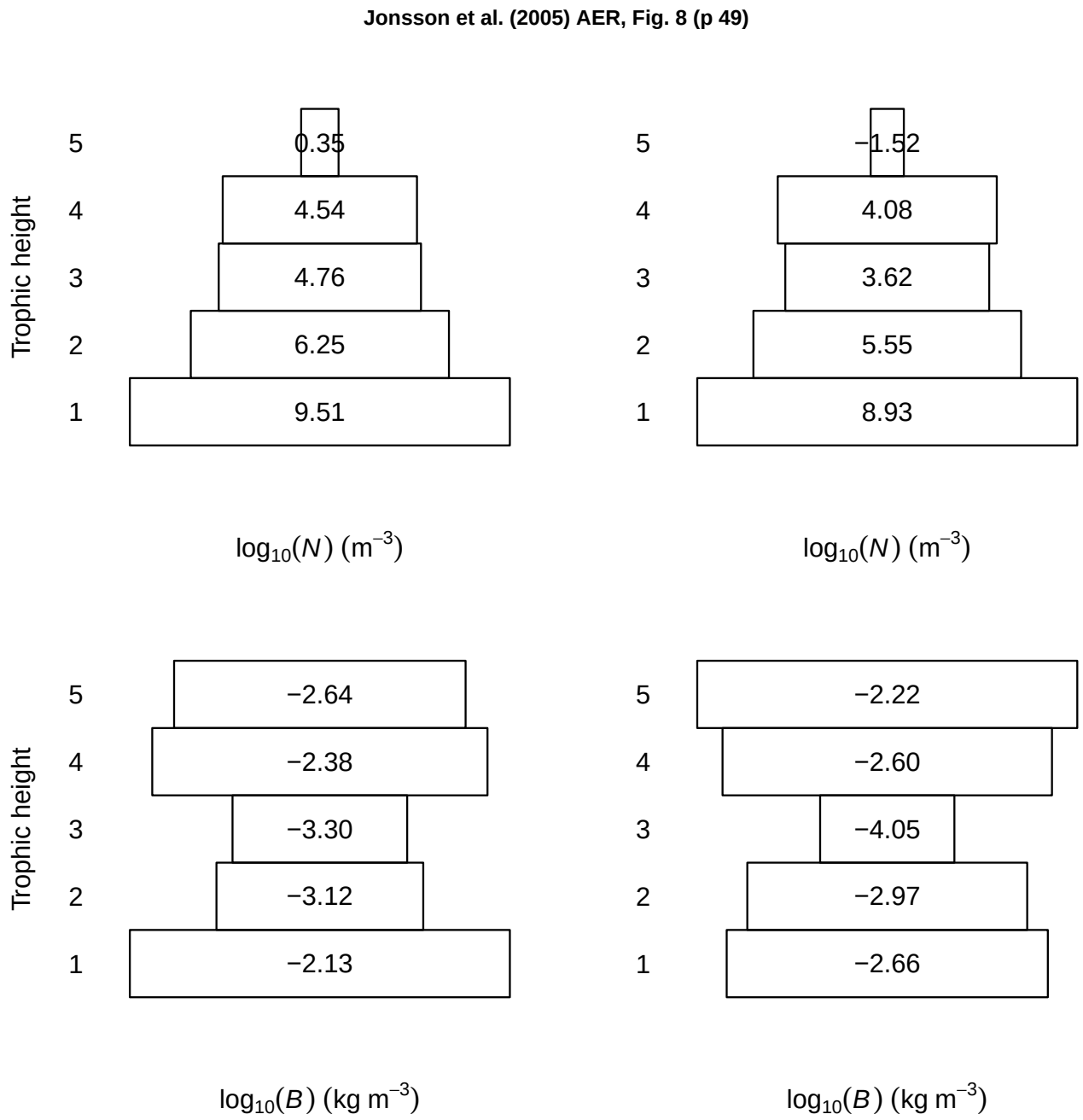
7.1.4 Jonsson et al. (2005), Fig. 7 (p 47)

```
> par(mfrow=c(2,2))
> PlotNCvNR(TL84, xlim=c(0, 10), ylim=c(-2,10), main='')
> abline(a=0, b=1, lty=2)
> PlotNCvNR(TL86, xlim=c(0, 10), ylim=c(-2,10), main='')
> abline(a=0, b=1, lty=2)
> PlotBCvBR(TL84, xlim=c(-8, -2), ylim=c(-8, -2), main='')
> abline(a=0, b=1, lty=2)
> PlotBCvBR(TL86, xlim=c(-8, -2), ylim=c(-8, -2), main='')
> abline(a=0, b=1, lty=2)
> title(main='Jonsson et al. (2005) AER, Fig. 7 (p 47)', outer=TRUE)
```



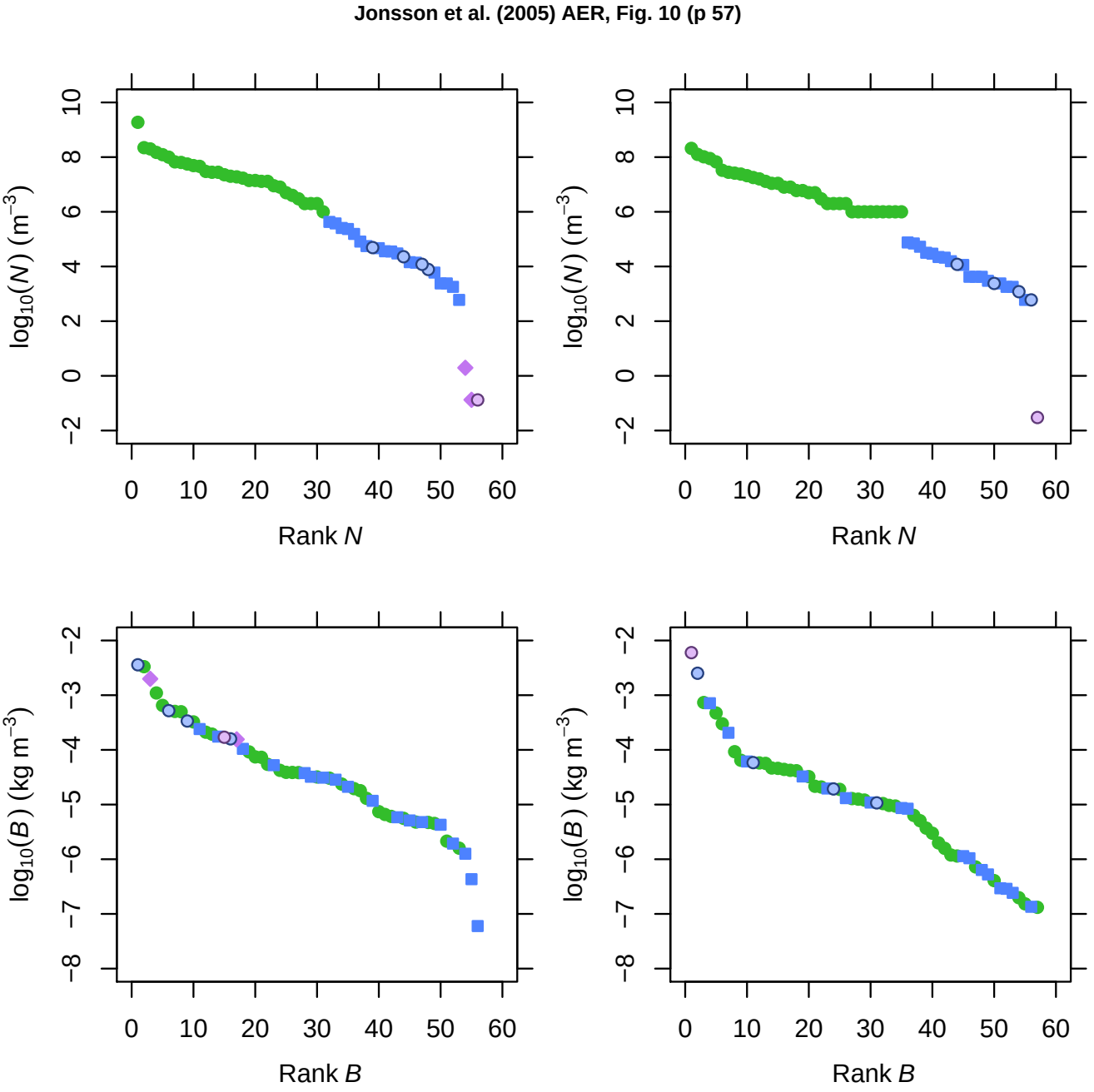
7.1.5 Jonsson et al. (2005), Fig. 8 (p 49)

```
> par(mfrow=c(2,2))
> tl84.levels <- floor(TrophicHeight(TL84))
> tl86.levels <- floor(TrophicHeight(TL86))
> PlotNPyramid(TL84, level=tl84.levels, main='', ylab='Trophic height')
> PlotNPyramid(TL86, level=tl86.levels, main='')
> PlotBPyramid(TL84, level=tl84.levels, main='', ylab='Trophic height')
> PlotBPyramid(TL86, level=tl86.levels, main='')
> title(main='Jonsson et al. (2005) AER, Fig. 8 (p 49)', outer=TRUE)
```



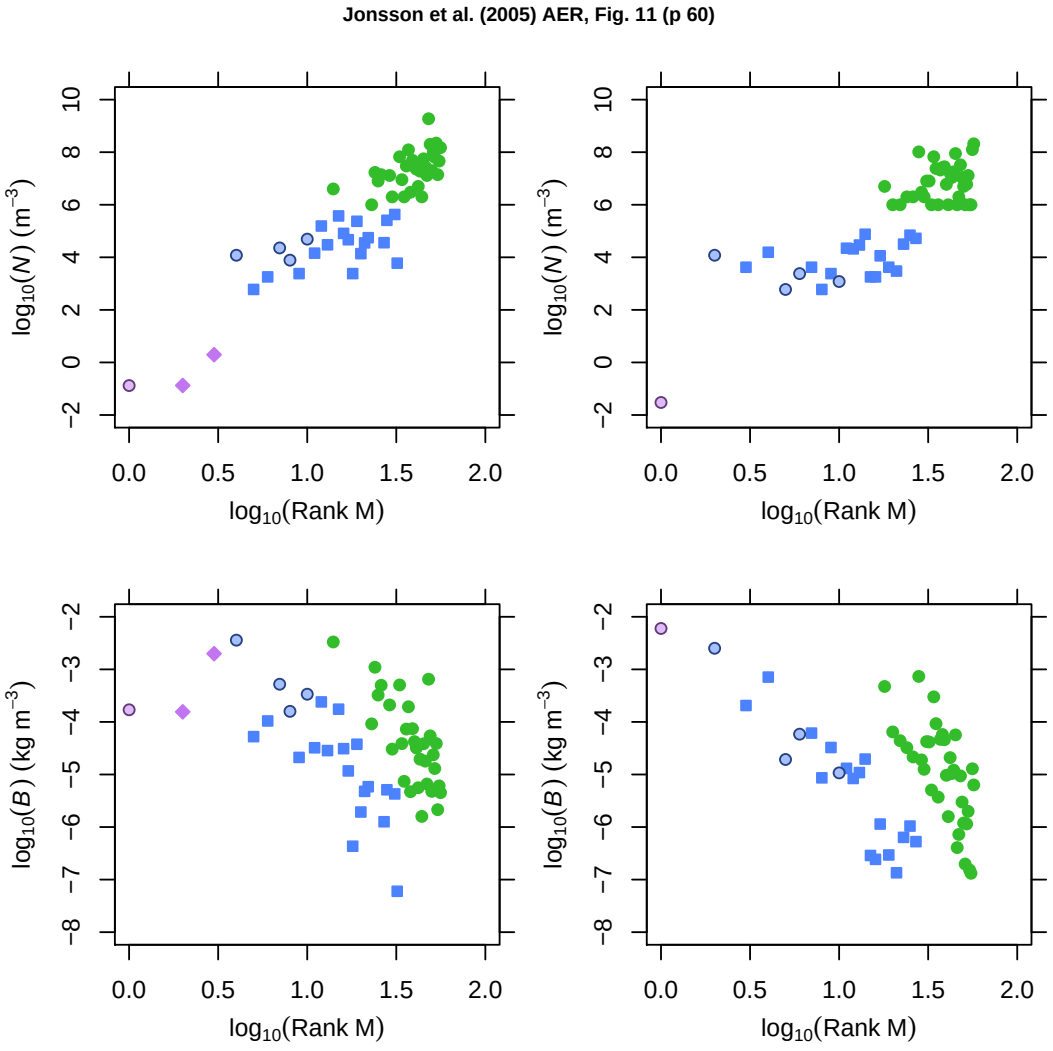
7.1.6 Jonsson et al. (2005), Fig. 10 (p 57)

```
> par(mfrow=c(2,2))
> PlotNvRankN(TL84, xlim=c(0,60), ylim=c(-2, 10), main='')
> PlotNvRankN(TL86, xlim=c(0,60), ylim=c(-2, 10), main='')
> PlotBvRankB(TL84, xlim=c(0,60), ylim=c(-8, -2), main='')
> PlotBvRankB(TL86, xlim=c(0,60), ylim=c(-8, -2), main='')
> title(main='Jonsson et al. (2005) AER, Fig. 10 (p 57)', outer=TRUE)
```



7.1.7 Jonsson et al. (2005), Fig. 11 (p 60)

```
> par(mfrow=c(2,2))
> PlotRankNPS(TL84, property='Log10N', rank.by='M', log10.rank=TRUE,
              xlim=c(0,2), ylim=c(-2, 10), ylab=Log10NLabel(TL84), main='')
> PlotRankNPS(TL86, property='Log10N', rank.by='M', log10.rank=TRUE,
              xlim=c(0,2), ylim=c(-2, 10), ylab=Log10NLabel(TL84), main='')
> PlotRankNPS(TL84, property='Log10Biomass', rank.by='M',
              log10.rank=TRUE, xlim=c(0,2), ylim=c(-8, -2),
              ylab=Log10BLabel(TL84), main='')
> PlotRankNPS(TL86, property='Log10Biomass', rank.by='M',
              log10.rank=TRUE, xlim=c(0,2), ylim=c(-8, -2),
              ylab=Log10BLabel(TL84), main='')
> title(main='Jonsson et al. (2005) AER, Fig. 11 (p 60)', outer=TRUE)
```

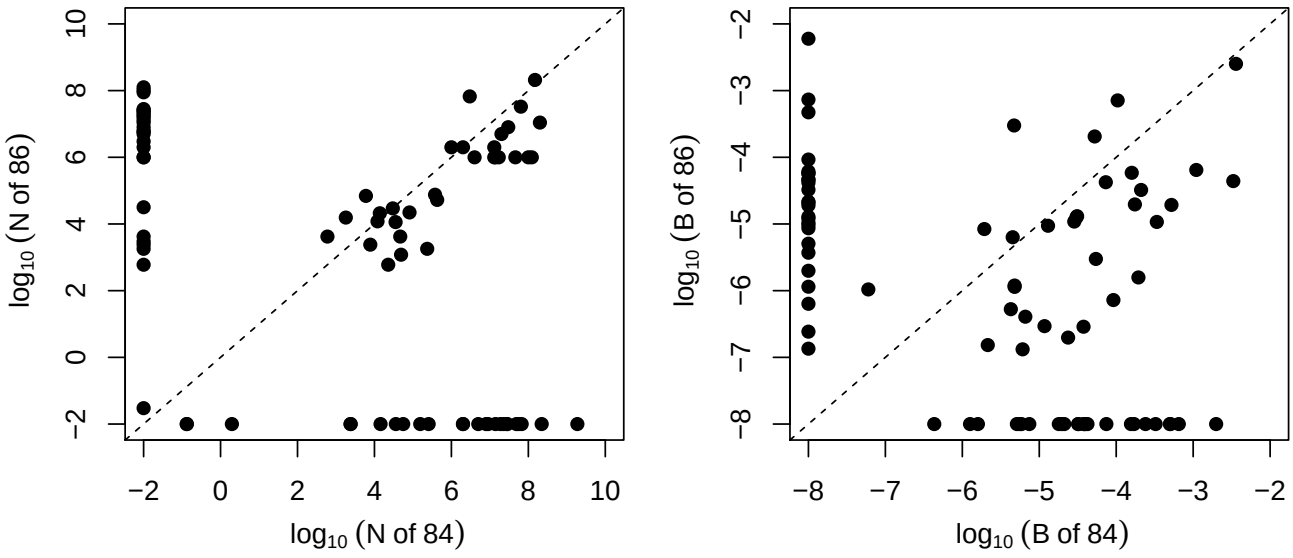


7.1.8 Jonsson et al. (2005), Fig. 12 (p 61)

In this example, we write a small function that plots one community against another.

```
> PlotCommunityVCommunity <- function(a, b, property, xlim=NULL, ylim=NULL, ...)
 {
     a.nodes <- NP(a, 'node')
     b.nodes <- NP(b, 'node')
     all.nodes <- union(a.nodes, b.nodes)

     a.values <- NPS(a, property)[,property]
     names(a.values) <- a.nodes
     b.values <- NPS(b, property)[,property]
     names(b.values) <- b.nodes
     points <- PlaceMissingPoints(a.values[all.nodes], xlim,
                                  b.values[all.nodes], ylim)
     plot(points[,1], points[,2], xlim=xlim, ylim=ylim, ...)

     abline(a=0, b=1, lty=2)
 }
> par(mfrow=c(1,2))
> PlotCommunityVCommunity(TL84, TL86, 'Log10N', xlim=c(-2,10), ylim=c(-2,10),
                          xlab=~log[10]~(N~of~84), ylab=~log[10]~(N~of~86),pch=19)
> PlotCommunityVCommunity(TL84, TL86, 'Log10Biomass',
                          xlim=c(-8,-2), ylim=c(-8,-2),
                          xlab=~log[10]~(B~of~84), ylab=~log[10]~(B~of~86),pch=19)
> title(main='Jonsson et al. (2005) AER, Fig. 12 (p 61)', outer=TRUE)
```

Jonsson et al. (2005) AER, Fig. 12 (p 61)

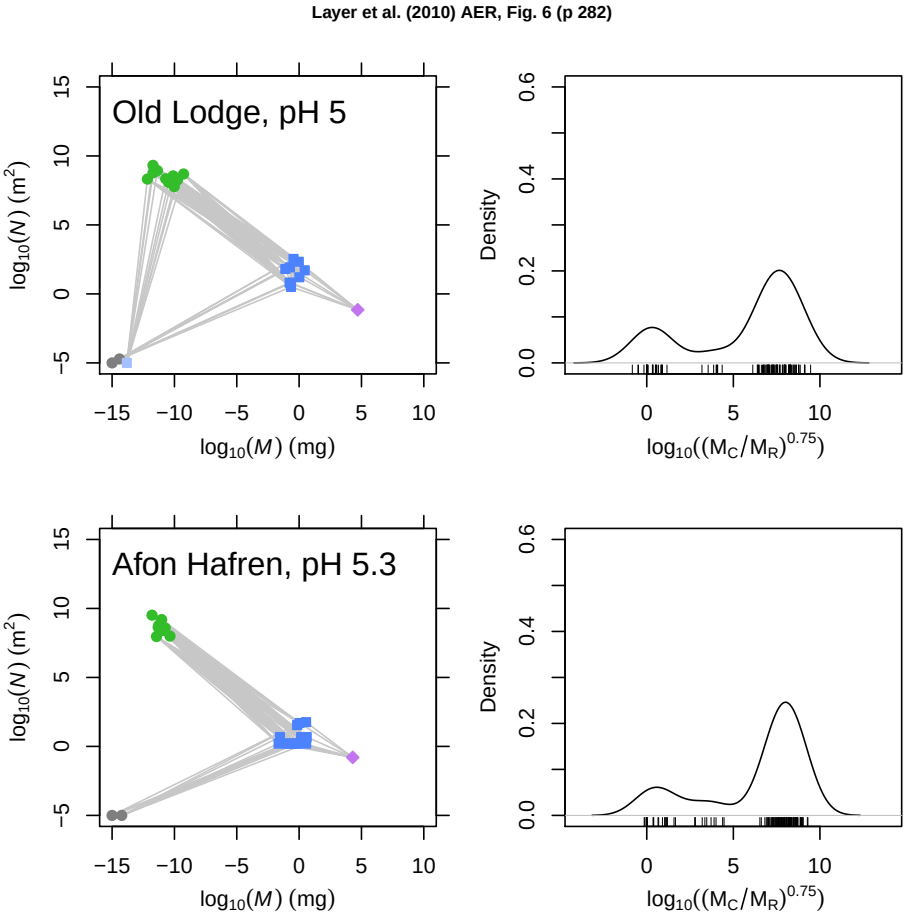


7.2 Layer et al. (2010)

7.2.1 Layer et al. (2010), Fig. 6 (p 282)

Four of the panels from the published figure. This example uses the 'pHWebs' community collection dataset; see the 'Collections' vignette for more information about community collections.

```
> data(pHWebs)
> par(mfrow=c(2,2))
> for(community in pHWebs[1:2])
 {
     PlotNvM(community, xlim=c(-15, 10), ylim=c(-5,15), main='',
             highlight.nodes=NULL)
     text(-15, 13, with(CPS(community), paste(title, ', pH ', pH, sep='')),
          adj=0, cex=1.5)
     tlps <- TLPS(community, node.properties='M')
     tlps <- tlps[!is.na(tlps$resource.M) & !is.na(tlps$consumer.M),]
     interaction.strength <- log10( (tlps$consumer.M / tlps$resource.M)^0.75 )
     plot(density(interaction.strength), xlim=c(-4,14), ylim=c(0,0.6),
          main='', xlab=~log[10]((M[C]/M[R])^0.75))
     rug(interaction.strength)
 }
> title(main='Layer et al. (2010) AER, Fig. 6 (p 282)', outer=TRUE)
```

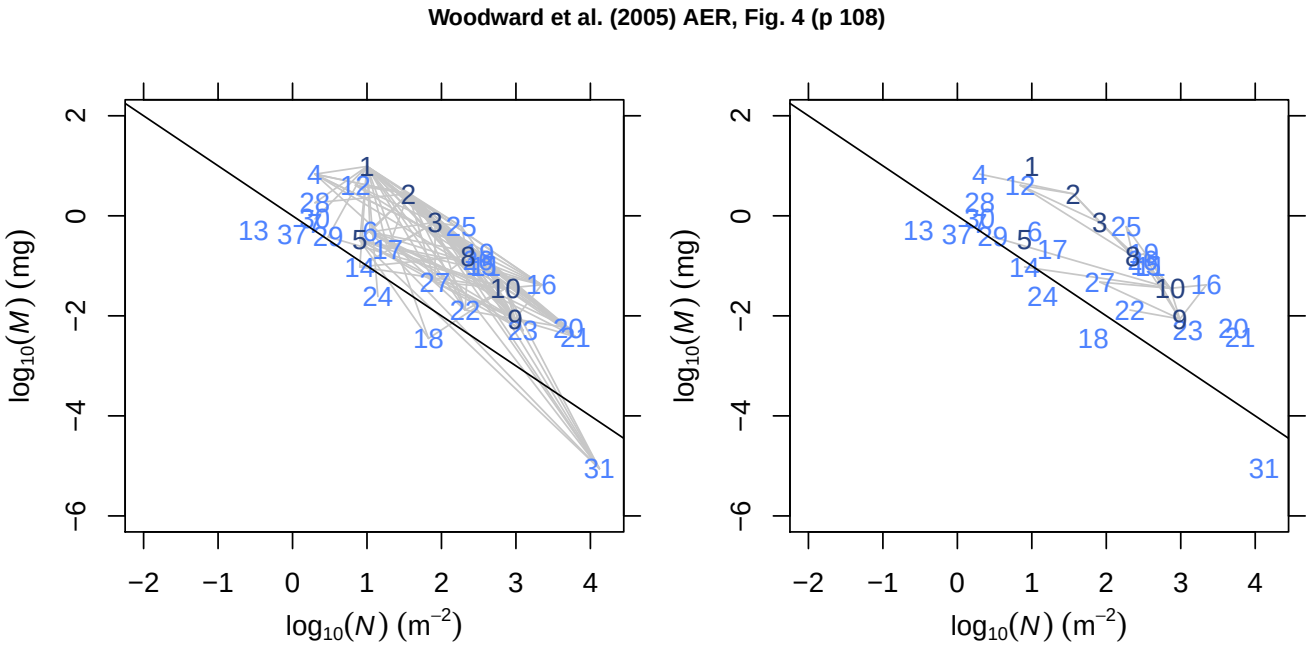


7.3 Woodward et al. (2005)

7.3.1 Woodward et al. (2005), Fig. 4. (p 108)

The left panel shows all trophic links. The right panel shows just links for which the resource has a larger body mass than the consumer.

```
> data(BroadstoneStream)
> par(mfrow=c(1,2))
> PlotMvN(BroadstoneStream, show.nodes.as='labels', label.cex=0.8,
          xlim=c(-2, 4.2), ylim=c(-6,2), main='', show.na=FALSE,
          highlight.links=NULL)
> abline(a=0, b=-1)
> tlps <- TLPS(BroadstoneStream, node.properties='M')
> lty <- rep(0, NumberOfTrophicLinks(BroadstoneStream))
> lty[tlps$resource.M > tlps$consumer.M] <- 1
> PlotMvN(BroadstoneStream, show.nodes.as='labels', label.cex=0.8,
          xlim=c(-2, 4.2), ylim=c(-6,2), main='', show.na=FALSE,
          highlight.links=NULL, link.lty=lty)
> abline(a=0, b=-1)
> title(main='Woodward et al. (2005) AER, Fig. 4 (p 108)', outer=TRUE)
```



7.4 Cohen et al. (2009)

7.4.1 Cohen et al. (2009), Table 1 (p 22338)

This code removes isolated nodes from communities for consistency with the paper. `NvMTriTrophicStatistics` does this for us anyway so the M - N tritrophic statistics are not affected but the network statistics in the last four rows of the table would be different to those in the paper.

```
> data(TL84, TL86, YthanEstuary)
> res <- lapply(list(TL84, TL86, YthanEstuary), function(community)
 {
     community <- RemoveNodes(community, remove=with(NPS(community), node[is.na(M) | is.na(N)]))
     community <- RemoveCannibalisticLinks(community)
     community <- RemoveIsolatedNodes(community)

     tts<-NvMTriTrophicStatistics(community)
     lp <- tts[['links']]
     tncp <- tts[['three.node.chains']]
     tcp <- tts[['trophic.chains']]

     community.span <- diff(range(Log10M(community))) +
                       diff(range(Log10N(community)))

     wiggling <- mean(tcp$sum.chain.length) / mean(tcp$chain.span)

     UnsafeMean <- function(x)
     {
         ifelse(is.null(x), NA, mean(x))
     }

     return (c(
      'Mean link length'=mean(lp$length),
      'Mean L upper'=UnsafeMean(tncp$Lupper),
      'Mean L lower'=UnsafeMean(tncp$Llower),
      '2 x mean link length'=2*mean(lp$length),
      'Mean 2-span'=UnsafeMean(tncp$two.span),
      'Mean L upper + L lower'=UnsafeMean(tncp$Lupper + tncp$Llower),
      '2 x mean link length / mean 2-span'=
             2 * mean(lp$length) / UnsafeMean(tncp$two.span),
      'Mean L upper + L lower/ mean 2-span'=
             UnsafeMean(tncp$Lupper + tncp$Llower) / UnsafeMean(tncp$two.span),
      'Mean count chain length'=mean(tcp$count.chain.length),
      'Mean count chain length x mean link length'=
             mean(tcp$count.chain.length)*mean(lp$length),
      'Community span'=community.span,
      'Mean count chain length x mean link length / community span'=
             mean(tcp$count.chain.length) * mean(lp$length)/community.span,
      'Mean sum chain lengths'=mean(tcp$sum.chain.length),
```

```
      'Mean chain span'=mean(tcp$chain.span),
      'Mean chain span / community span'=mean(tcp$chain.span) / community.span,
      'Mean sum chain lengths / mean chain span'=
            mean(tcp$sum.chain.length) / mean(tcp$chain.span),
      'Mean sum chain lengths / community span'=
            mean(tcp$sum.chain.length) / community.span,
      'L'=NumberOfTrophicLinks(community),
      'S^2'=NumberOfNodes(community)^2,
      'L/S^2'=DirectedConnectance(community),
      'L/S'=LinkageDensity(community)))
 })
> res <- do.call('cbind', res)
> colnames(res) <- c('TL84', 'TL86', 'Ythan Estuary')
> print(round(res,2))
```

	TL84	TL86	Ythan Estuary
Mean link length	6.33	5.90	7.29
Mean L upper	5.41	3.43	5.06
Mean L lower	5.99	5.69	6.15
2 x mean link length	12.67	11.79	14.57
Mean 2-span	11.02	8.65	10.51
Mean L upper + L lower	11.40	9.12	11.20
2 x mean link length / mean 2-span	1.15	1.36	1.39
Mean L upper + L lower/ mean 2-span	1.03	1.05	1.07
Mean count chain length	4.84	4.84	4.43
Mean count chain length x mean link length	30.62	28.56	32.31
Community span	20.78	22.66	21.98
Mean count chain length x mean link length / community span	1.47	1.26	1.47
Mean sum chain lengths	19.96	23.33	16.88
Mean chain span	18.71	20.63	13.18
Mean chain span / community span	0.90	0.91	0.60
Mean sum chain lengths / mean chain span	1.07	1.13	1.28
Mean sum chain lengths / community span	0.96	1.03	0.77
L	264.00	236.00	379.00
S^2	2500.00	2601.00	8281.00
L/S^2	0.11	0.09	0.05
L/S	5.28	4.63	4.16

7.4.2 Cohen et al. (2009), Table S3 (p 8)

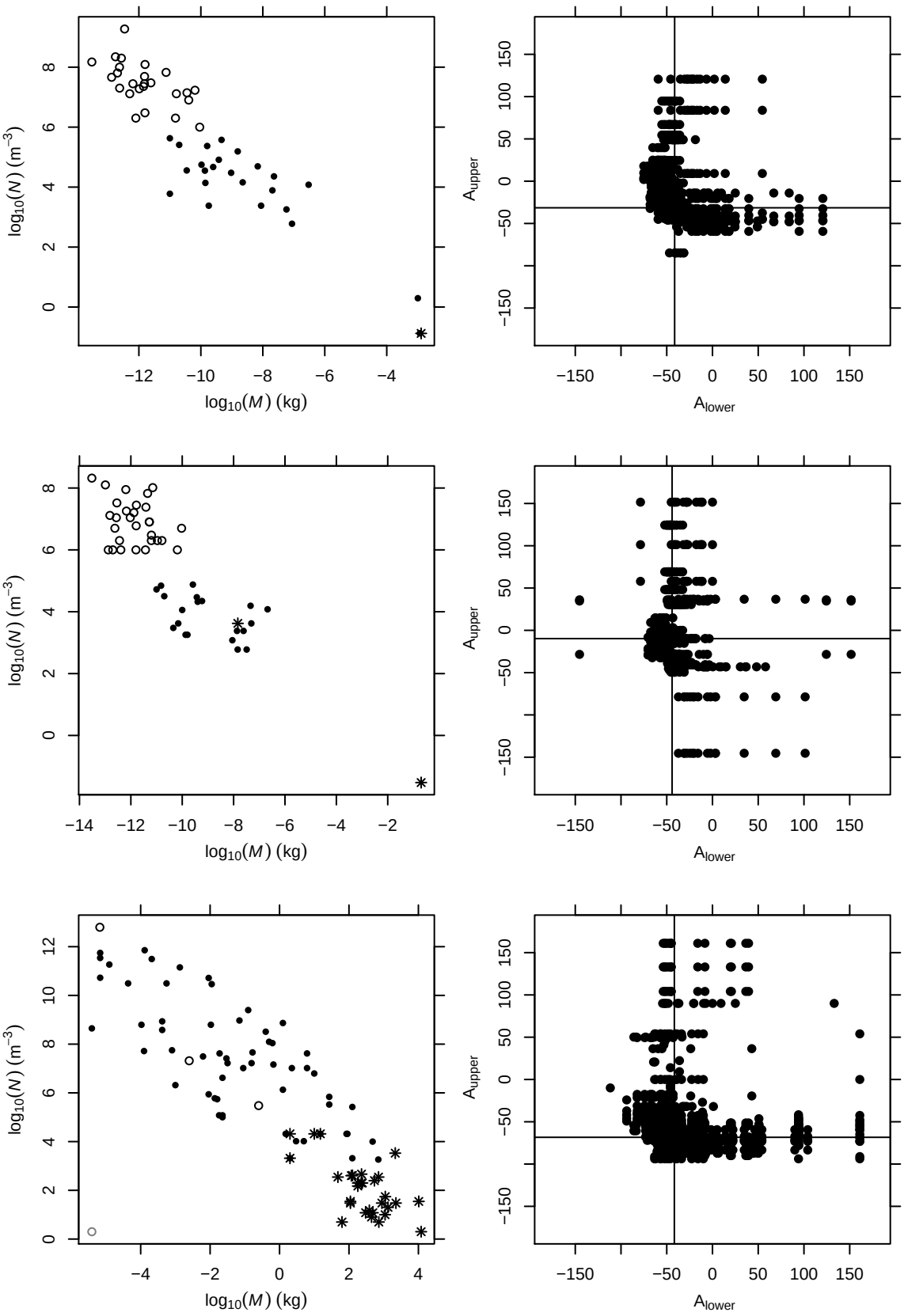
```
> res <- lapply(list(TL84, TL86, YthanEstuary), function(community)
 {
     community <- RemoveNodes(community, remove=with(NPS(community), node[is.na(M) | is.na(N)]))
     community <- RemoveCannibalisticLinks(community)
     community <- RemoveIsolatedNodes(community)

     chains <- ThreeNodeChains(community, node.properties='M')
     MR <- chains$bottom.M
     MI <- chains$intermediate.M
```

```
     MC <- chains$top.M

     lp <- TLPS(community, node.properties='M')

     return (c('MR<=MI<=MC'=sum(MR<=MI & MI<=MC),
               'MR<=MC<MI'=sum(MR<=MC & MC<MI),
               'MI<MR<=MC'=sum(MI<MR  & MR<=MC),
               'MI<=MC<MR'=sum(MI<=MC & MC<MR),
               'MC<MR<MI'=sum(MC<MR  & MR<MI),
               'MC<MI<MR'=sum(MC<MI  & MI<MR),
               'All 2-chains'=nrow(chains),
               'MR<MC'=sum(lp$resource.M<lp$consumer.M),
               'MR=MC'=sum(lp$resource.M==lp$consumer.M),
               'MR>MC'=sum(lp$resource.M>lp$consumer.M),
               'All links'=nrow(lp)))
 })
> res <- do.call('cbind', res)
> colnames(res) <- c('TL84', 'TL86', 'Ythan Estuary')
> print(round(res,2))

             TL84 TL86 Ythan Estuary
MR<=MI<=MC   1001  577          1232
MR<=MC<MI      30   59            65
MI<MR<=MC      12   10            68
MI<=MC<MR       0    1             3
MC<MR<MI        1    3             0
MC<MI<MR        0    1             3
All 2-chains 1044  651          1371
MR<MC         262  232           368
MR=MC           0    0             2
MR>MC           2    4             9
All links     264  236           379
```

7.4.3 Cohen et al. (2009), Fig. 1, (p 22336)

```
> data(TL84, TL86, YthanEstuary)
> par(mfrow=c(3,2))
> for(community in list(TL84, TL86, YthanEstuary))
 {
     community <- RemoveIsolatedNodes(community)
     pch <- rep(1, NumberOfNodes(community))
     pch[IsIntermediateNode(community)] <- 20
     pch[IsTopLevelNode(community)] <- 8
     PlotNvM(community, col=1, highlight.nodes=NULL, show.web=FALSE,
             main='', pch=pch)
     PlotAuppervAlower(community, main='')
 }
> title(main='Cohen et al. (2009) PNAS, Fig. 1 (p 22336)', outer=TRUE)
```

Cohen et al. (2009) PNAS, Fig. 1 (p 22336)



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