Cheddar quick start (0.1-639)

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Contents

1 Introduction

The Cheddar R package provides a flexible, extendable representation of an ecological community and a range of functions for analysis and visualisation, focusing on food web, body mass and numerical abundance data. It also allows inter-web comparisons such as examining changes in community structure over environmental, temporal or spatial gradients. This vignette is a brief introduction to some different areas of Cheddar. Each area is discussed in detail in its own vignette, listed in Section 5.

2 Community basics

The examples below use the pelagic epilimnion community of Tuesday Lake, Michigan, USA sampled in 1984 (Carpenter and Kitchell, 1996; Cohen et al., 2003; Jonsson et al., 2005), available in Cheddar as the TL84 dataset.

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

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

> NumberOfNodes(TL84)

[1] 56

> NumberOfTrophicLinks(TL84)

[1] 269
```

NPS assembles node properties in to an `R data.frame`. Let's look at the first 10 rows of such a table.

```
> head(NPS(TL84, c('category',
                   'Log10MNBiomass',
                   TS='TrophicSpecies',
                   TL='PreyAveragedTrophicLevel')), 10)
```
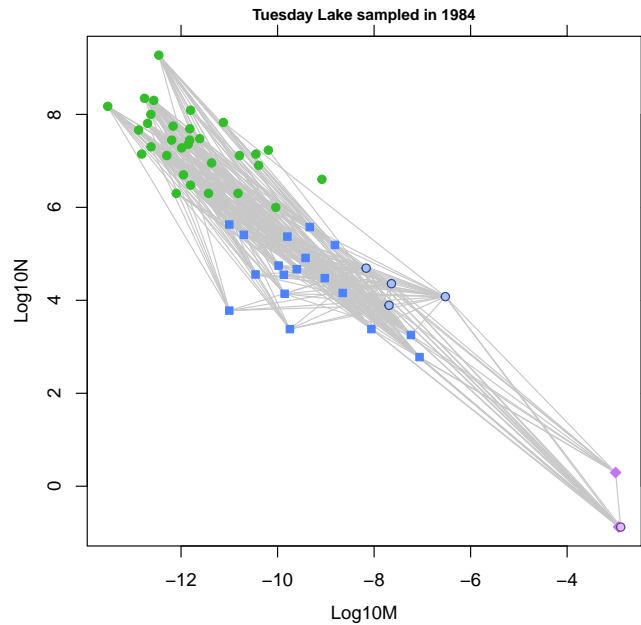
	category	Log10M	Log10N	Log10Biomass	TS	TL
Nostoc sp.	producer	-12.098542	6.301030	-5.797512	1	1
Arthrodesmus sp.	producer	-11.818156	7.690196	-4.127960	2	1
Asterionella formosa	producer	-11.950782	6.698970	-5.251812	3	1
Cryptomonas sp. 1	producer	-12.692504	7.806180	-4.886324	4	1
Cryptomonas sp. 2	producer	-11.821023	7.447158	-4.373865	5	1
Chroococcus dispersus	producer	-12.621602	7.301030	-5.320572	4	1
Closteriopsis longissimus	producer	-12.625252	8.000000	-4.625252	6	1
Chrysosphaerella longispina	producer	-9.080399	6.602060	-2.478339	3	1
Dinobryon bavaricum	producer	-11.612610	7.477121	-4.135489	7	1
Dinobryon cylindricum	producer	-11.804100	6.477121	-5.326979	1	1

3   Community plots

NPS has a corresponding plot function `PlotNPS`, which plots one node property against another. `PlotNPS` takes the names of node properties to plot on the x and y axes. Just as with `NPS`, node properties can be either 'first-class' or computed. The example below plots $\log_{10}$-transformed numerical abundance against $\log_{10}$-transformed body mass.
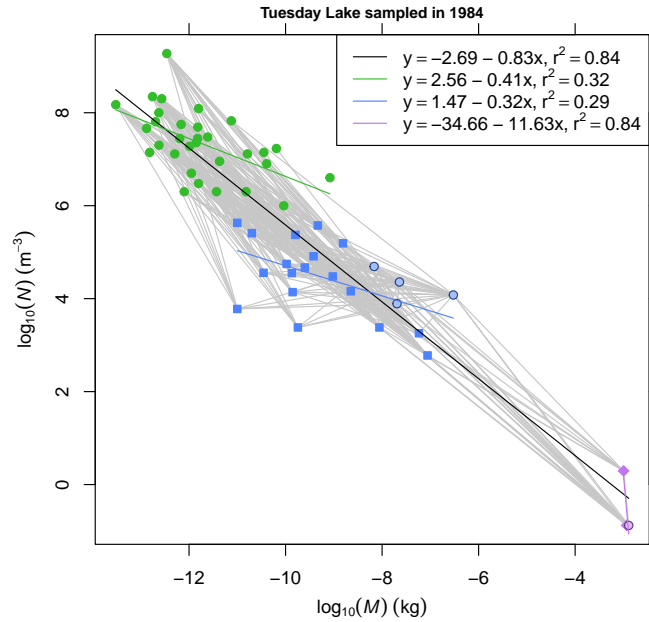
```
> PlotNPS(TL84, 'Log10M', 'Log10N')
```


Producers are shown by green circles, invertebrates by blue squares and vertebrate ectotherms by purple diamonds, cannibals shown by lighter-coloured circles and trophic links shown by grey lines.   The
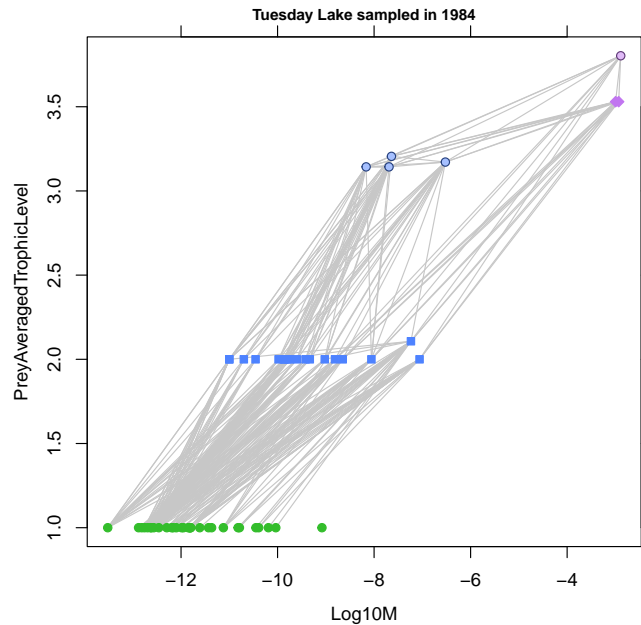
`NvMLinearRegressions` and `PlotLinearModels` functions can be used to add regression lines through each of the three categories.

```
> PlotNvM(TL84)
> models <- NvMLinearRegressions(TL84)
> colours <- PlotLinearModels(models)
> legend("topright", sapply(models, FormatLM), lty=1, col=colours)
```
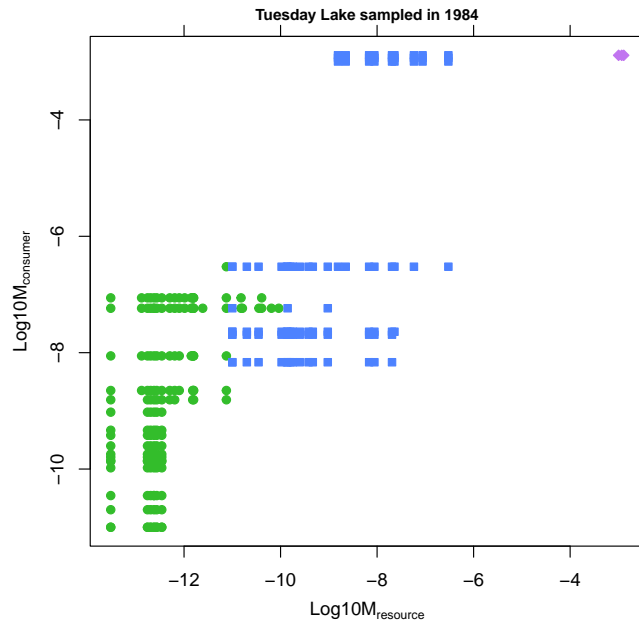

The following example shows trophic level against $\log_{10}$-transformed body mass.

```
> PlotNPS(TL84, 'Log10M', 'PreyAveragedTrophicLevel')
```
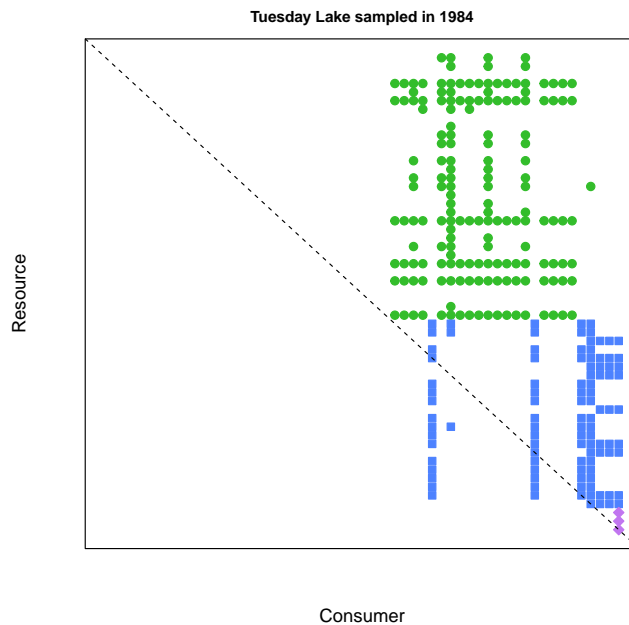
Similarly, `PlotTLPS` plots one trophic-link property against another. Names prefixed with either 'resource.' or 'consumer.' are taken to be node properties. The following example therefore plots the $\log_{10}$-transformed body mass of the consumer against that of the resource for every trophic link in the community.

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


Tuesday Lake sampled in 1984

Colours in this plot are the same as in the `PlotNPS` examples and denote the resource's category. The example below shows the food web as a predation matrix: a binary matrix with species shown in node order, starting at the top-left. Points on the dashed line indicate cannibals.

```
> PlotPredationMatrix(TL84)
```


Tuesday Lake sampled in 1984

4 Collections of communities

Cheddar's `pHWebs` dataset contains ten of the 20 webs sampled across a wide pH gradient by Layer et al. (2010). This example assembles a table of properties for this collection.

```
> data(pHWebs)
> CollectionCPS(pHWebs,
                c('lat',
                  'long',
                  'pH',
                  S='NumberOfNodes',
                  L='NumberOfTrophicLinks',
                  'L/S'='LinkageDensity',
                  C='DirectedConnectance',
                  Slope='NvMSlope',
                  B='FractionBasalNodes',
                  I='FractionIntermediateNodes',
                  T='FractionTopLevelNodes'))
```

	lat	long	pH	S	L	L/S	C	Slope	B
Old Lodge	51.04	0.080	5.0	23	137	5.956522	0.2589792	-0.6561601	0.5217391
Afon Hafren	52.47	-3.700	5.3	25	135	5.400000	0.2160000	-0.7078312	0.4000000
Broadstone	51.08	0.053	5.5	25	178	7.120000	0.2848000	-0.5853852	0.3200000
Dargall Lane	55.08	-4.430	5.8	21	99	4.714286	0.2244898	-0.7379515	0.4285714
Mosedal Beck	54.41	-3.140	5.9	21	108	5.142857	0.2448980	-0.7026522	0.4761905
Duddon Pike Beck	54.41	-3.170	6.1	35	286	8.171429	0.2334694	-0.5673022	0.3714286
Allt a'Mharcaidh	57.12	-3.850	6.5	40	334	8.350000	0.2087500	-0.7655290	0.3500000
Hardknott Gill	54.40	-3.170	7.0	44	386	8.772727	0.1993802	-0.7548597	0.3409091
Bere Stream	50.73	-2.210	7.5	66	943	14.287879	0.2164830	-0.6501359	0.3939394
Mill Stream	50.68	-2.180	8.4	87	1654	19.011494	0.2185229	-0.9192528	0.3793103

	I	T
Old Lodge	0.3913043	0.08695652
Afon Hafren	0.4800000	0.12000000
Broadstone	0.6000000	0.08000000
Dargall Lane	0.5238095	0.04761905
Mosedal Beck	0.4285714	0.09523810
Duddon Pike Beck	0.4857143	0.14285714
Allt a'Mharcaidh	0.5250000	0.12500000
Hardknott Gill	0.6136364	0.04545455
Bere Stream	0.4393939	0.15151515
Mill Stream	0.5172414	0.10344828

5 Further reading

You should read the 'Community' vignette. Plotting and anlysis of communities is covered in the 'PlotsAndStats' vignette. The 'ImportExport' vignette shows how to get your community data in to and out of Cheddar. If you have data from several communities and are interested in seeing how community structure changes among them, read the 'Collections' vignette.

References

S.R. Carpenter and J.F. Kitchell. *The trophic cascade in lakes.* Cambridge University Press, 1996.

J.E. Cohen, T. Jonsson, and S.R. Carpenter. Ecological community description using the food web, species abundance, and body size. *Proceedings of the National Academy of Sciences of the United States of America*, 100(4):1781–1786, 2003. doi: 10.1073/pnas.232715699.

T. Jonsson, J.E. Cohen, and S.R. Carpenter. Food webs, body size, and species abundance in ecological community description. *Advances In Ecological Research*, 36:1–84, 2005. doi: 10.1016/S0065-2504(05) 36001-6.

K. Layer, J.O. Riede, A.G. Hildrew, and G. Woodward. Food web structure and stability in 20 streams across a wide ph gradient. *Advances In Ecological Research*, 42:265–299, 2010. doi: 10.1016/S0065-2504(10)42005-X.