

Trouble on Tatooine: constructing a plausible fantasy food web

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Purpose: A half-baked experimnt on trying to construct a food web for Tatooine using real world data.

Motivation: I'm going through a Star Wars moment™.

Conceptally: What if we're dealing with realy poor data coveragw for a location can we still salvage *something*

Plan: Take a species list for Tatooine, assign some traits and use that as the transfer medium from real-world trait and interaction data.

Outcome?: Maybe we can also identify some missing species based on trophic levels/links are missing

Challenges: What to treat as a complete species list for Tatooine, reconciling the fact that species were developed based on 'narrative need' as opposed to 'ecological need

1 This template uses pandoc (and a few additional python glue scripts) to facilitate the production of
2 scientific articles using a standard markdown file. The objective is to ensure that standard markdown
3 (with the important exception of the pandoc-crossref citation markup) will be rendered into an
4 interactive website (which allows collaborative annotations with the `hypothes.is` platform), a “draft”
5 style PDF (double-spaced, numbered lines, figures at the end), and a “preprint” style PDF (with slightly
6 more reader-friendly pagination).

7 The core bit of configuration is the `metadata.json` file, which handles information about authorship,
8 affiliations, the abstract, keywords, etc. All documents will be deployed to gh-pages *only* on push events
9 from the main branch. All of the artifacts will be built when doing pull requests, so you can check that
10 merging a branch is *not* going to cause the compilation of the documents to fail; indeed, you can download
11 the artifacts produced during the run, to check the PDF and html files. The website is only updated from
12 the main branch.

13 The workflow is *very* GitHub based, and so the manuscript file is the `README.md` - this is not going to be a
14 huge issue as 90% of the markdown is standard, with the exception of the citations and mathematics, so
15 this will render (mostly) like a normal README file.

16 **Deploying the template**

17 The process of deploying this template has been *greatly* streamlined from previous versions:

- 18 • Click on the “Use this template” button
- 19 • Edit `README.md` with your own text, commit, and push
- 20 • This push will trigger the first build - the builds are only active on the main branch (*not* master!),
21 and on pull requests
- 22 • Go to `http://you.github.io/repo-name/` to view the html version, and get access to the PDFs
- 23 • Add your references to the `references.bib` file
- 24 • Edit the `metadata.json` file to add the title, abstract, authors

25 In particular, note that *you do not need* to create a personal access token to deploy to gh-pages (from
26 where the website is served).

27 **The metadata file**

28 **General information**

29 The title is a field in the metadata.json:

```
{  
  "title": "Preprint template"  
}
```

30 **Authorship**

31 Authors are listed as objects in the authors block. Each author is specified as follows:

```
{  
  "familyname": "Bob",  
  "givennames": "Alice",  
  "email": "alice.bob@u.edu",  
  "orcid": "0000-0000-0000-0001",  
  "affiliations": [  
    "Affiliation 1",  
    "Affiliation 2"  
  ],  
  "status": ["corresponding", "equal"]  
}
```

32 The email field is recommended for all authors. The status field is only useful for the corresponding
33 author, and to denote equal contributions. These informations are rendered on the initial page. If an
34 orcid is given, it will be linked on the HTML and PDF versions.

35 Note that there is *no need* to number the affiliations - a small python script will take care of this
36 automatically.

37 Abstract

38 This template supports three types of abstracts, indicated in the metadata file as abstract:

39 A regular abstract is defined as

```
"abstract": "A very long string"
```

40 An itemized abstract is an array of strings, each representing a bullet point:

```
"abstract": [  
  "Point 1",  
  "Point 2"  
]
```

41 A structured abstract is an object with key-value pairs :

```
"abstract": {  
  "Location": "Worldwide",  
  "Organisms": "Mammals"  
}
```

42 Citation style

43 The citationstyle key corresponds to the name, with .cs1 omitted, of a CSL stylesheet stored in the
44 [citation style language](#) repository. Note that there is no difference between main and dependent styles, the
45 build engine will take the correct steps to get the correct style. The default is "citationstyle":
46 "ecology-letters". There is a longer section about references management later on.

47 References management

48 The references are managed by pandoc. Note that we *do not* use pandoc-citeproc, which was an external
49 module for older pandoc versions. References *must* be stored in a references.bib file, and that it would
50 make sense to order it alphabetically by key.

51 We use [Zotero](#) for references management, and for the lab's manuscripts, we work from folders in a shared
52 library (with a folder for every manuscript).

53 It is recommended to use the [Better BibTeX](#) plugin for citation key generations, and auto-export of the
54 shared library to the references.bib file. We use a citation key format meant to convey information on
55 the author (first author full name), date (complete year), and title (first three letters of the first two non-stop
56 words). It must be set in the Better BibTeX preferences as (you might need to remove the line changes):

```
57 [auth:fold]
58 [year]
59 [title:fold:nopunctordash:skipwords:lower:select=1,1:substring=1,3:capitalize]
60 [title:fold:nopunctordash:skipwords:lower:select=2,2:substring=1,3:capitalize]
```

61 It is a good idea to configure Better BibTeX to auto-export on change, and to remove a lot of fields that are
62 not strictly speaking required for references. The list of fields we usually ignore is:

```
63 abstract,copyright,annotation,file,pmid,month,shorttitle,keywords
```

64 The citations are done using the normal markdown syntax, where @Elton1927AniEco produces
65 (Elton1927AniEco?), and [@Camerano1880EquViv] produces (Camerano1880EquViv?).

66 **Figures, Tables, and other floats**

67 Note that you can wrap the text of legends for both figures and tables. This avoids the issue of having very
68 long lines.

69 **Mathematics**

70 The following equation

$$J'(p) = \frac{1}{\log(S)} \times \left(- \sum p \times \log(p) \right) \quad (1)$$

71 is produced using

85 **Example text**

86 Connectance, defined as the ratio of realized interactions on the total number of potential interactions, is
87 one of the most common descriptor of network structure. In a bipartite network with T species at the top,
88 and B at the bottom, having a total of L interactions, it is defined as $Co = L/(T \times B)$. Connectance has a
89 lower bound, as the network cannot have fewer interactions than the number of species in its more
90 speciose level – the minimal connectance is therefore $c_m = \max(T, B)$. This makes the connectance of
91 networks of different sizes difficult to compare, especially since bipartite networks tend to have a low
92 connectance. For this reason, we used a corrected version of connectance, defined as

$$Co^* = \frac{L - c_m}{T \times B - c_m} . \quad (2)$$

93 **This is a subsection**

94 This takes values between 0 (the network has the minimal number of interactions) and 1 (all species are
95 connected), but is robust to variations in species richness.

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98 connected), but is robust to variations in species richness.

99 **Some non-standard maths**

100 The phylogenetic reconstruction of $\hat{\mathcal{L}}$ and $\hat{\mathcal{R}}$ has an associated uncertainty, represented by the breadth of
101 the uniform distribution associated to each of their entries. Therefore, we can use this information to
102 assemble a *probabilistic* metaweb in the sense of (Poisot2016StrPro?), *i.e.* in which every interaction is
103 represented as a single, independent, Bernoulli event of probability p .

104 Specifically, we have adopted the following approach. For every entry in $\hat{\mathcal{L}}$ and $\hat{\mathcal{R}}$, we draw a value from
105 its distribution. This results in one instance of the possible left ($\hat{\ell}$) and right (\hat{r}) subspaces for the
106 Canadian metaweb. These can be multiplied, to produce one matrix of real values. Because the entries in

107 $\hat{\ell}$ and \hat{r} are in the same space where \mathcal{L} and \mathcal{R} were originally predicted, it follows that the threshold ρ
108 estimated for the European metaweb also applies. We use this information to produce one random
109 Canadian metaweb, $N = \mathcal{L}\hat{\mathcal{R}}' \geq \rho$.

110 Because the intervals around some trait values can be broad (in fact, probably broader than what they
111 would actually be, see *e.g.* **Garland1999IntPhy?**), we repeat the above process 2×10^5 times, which
112 results in a probabilistic metaweb P , where the probability of an interaction (here conveying our degree of
113 trust that it exists given the inferred trait distributions) is given by the number of times where it appears
114 across all random draws N , divided by the number of samples. An interaction with $P_{i,j} = 1$ means that
115 these two species were predicted to interact in all 2×10^5 random draws, etc..

116 **References**



Figure 1: This is the legend of the figure, which will be shown in the margin in preprint mode, and underneath the figure in draft mode. The legend can contain references, etc. It is advised to use a resolution of at least 600dpi for the figures.