

# Template to prepare preprints and manuscripts using markdown and github actions

[Timothée Poisot](#) <sup>1</sup> Peregrin Took <sup>2</sup> Merriadoc Brandybuck <sup>3</sup>

<sup>1</sup> Université de Montréal <sup>2</sup> Québec Centre for Biodiversity Sciences <sup>3</sup> Inn of the Prancing Pony

<sup>4</sup> Fellowship of the Ring <sup>5</sup> Green Dragon Inn

<sup>‡</sup> Equal contributions

## Correspondance to:

Timothée Poisot — [timothee.poisot@umontreal.ca](mailto:timothee.poisot@umontreal.ca)

This work is released by its authors under a CC-BY 4.0 license



Last revision: *September 12, 2022*

1 This template uses pandoc (and a few additional *Julia* glue scripts) to facilitate the production of scientific  
2 articles using a standard markdown file. The objective is to ensure that standard markdown (with the  
3 important exception of the pandoc-crossref citation markup) will be rendered into an interactive website  
4 (which allows collaborative annotations with the `hypothesis` platform), a “draft” style PDF  
5 (double-spaced, numbered lines, figures at the end), and a “preprint” style PDF (with more reader-friendly  
6 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 Elton  
65 (1927), and [@Camerano1880EquViv] produces (Camerano 1880).

## 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

```
$$J'(p) = \frac{1}{\text{log}(S)} \times \dots \quad \text{\#eq:eq1}
```

and can be referenced using @eq: eq1, which will result in eq. 1. Note that because we use pandoc-crossref, the label “eq.” will be generated automatically.

## Tables

Table legends go on the line after the table itself. To generate a reference to the table, use {#tbl: id} – then, in the text, you can use {@tbl: id} to refer to the table. For example, the table below is tbl. 1. You can remove the *table* in front by using !@tbl: id, or force it to be capitalized with \\*tbl: id.

Table 1: This is a table, and its identifier is id – we can refer to it using {@tbl: id}. Note that even if the table legend is written below the table itself, it will appear on top in the PDF document.

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
5.1	3.5	1.4	0.2	setosa
5.0	3.6	1.4	0.2	setosa
5.4	3.9	1.7	0.4	setosa

## Figures

Figures can have a legend – all figures *must* be in the figures/ folder of the project, as it is also used for the website. We recommend to use good resolution images, rather than PDFs, or at least to have multiple versions available.

```
![This is the legend of the figure...](figures/figure.png){#fig:figure}
```

[Figure 1 about here.]

We can now use @fig: figure to refer to fig. 1.

## 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.

## 96 **This is another subsection**

97 This takes values between 0 (the network has the minimal number of interactions) and 1 (all species are  
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

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

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

## References

- preCamerano, L. (1880). Dell'equilibrio dei viventi merce la reciproca distruzione. *Atti Della R. Accad. Delle Sci. Torino*, 15, 393–414.
- Elton, C.S. (1927). *Animal ecology*. University of Chicago Press.



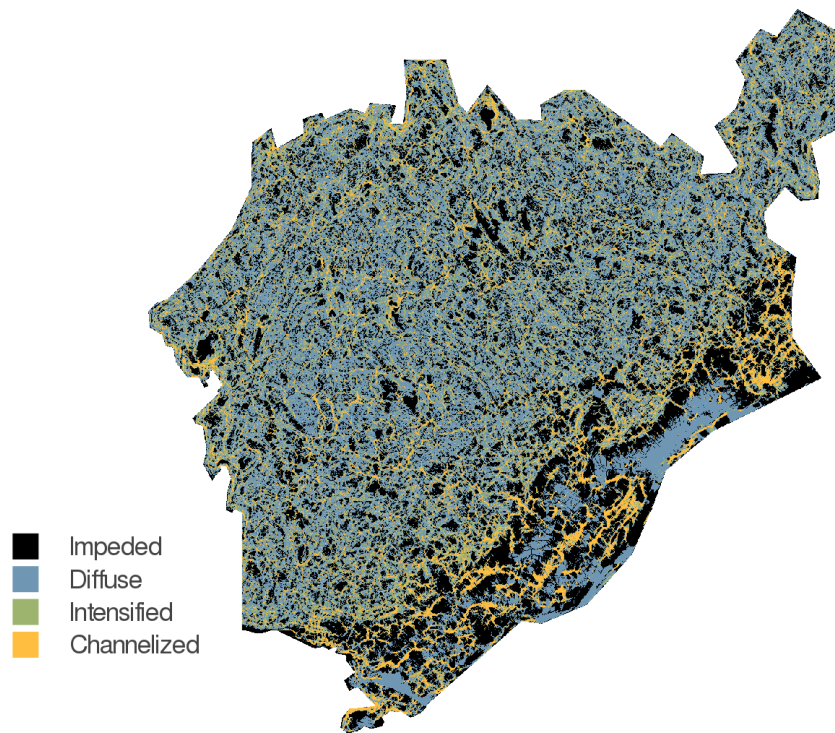


Figure 1: This is the legend of the figure, which will be shown in the margin in preprint mode, and underneath the figure in draft mode. The legend can contain references, etc. It is advised to use a resolution of at least 600dpi for the figures.