

Template to prepare preprints and manuscripts using markdown and github actions

[Timothée Poisot](#)^{1,2,‡} Peregrin Took^{3,4} Merriadoc Brandybuck^{5,4,‡}

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

⁴ Fellowship of the Ring ⁵ Green Dragon Inn

‡ These authors contributed equally to the work

Correspondance to:

Timothée Poisot — timothee.poisot@umontreal.ca

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



Last revision: *September 12, 2021*

Purpose: This template provides a series of scripts to render a markdown document into an interactive website and a series of PDFs.

Motivation: It makes collaborating on text with GitHub easier, and means that we never need to think about the output.

Internals: GitHub actions and a series of python scripts. The markdown is handled with pandoc.

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 first three fields are the title, language, and license. It's probably advisable not to change these, and
30 there are chances that the logo on the PDF will not capture the values made here (this will have to be,
31 maybe, fixed at some point).

```
{  
  "title": "Preprint template",  
  "license": "CC-BY",  
  "language": "en"  
}
```

32 **Authorship**

33 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"]  
}
```

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

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

39 **Abstract**

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

41 A regular abstract is defined as

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

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

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

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

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

44 **Citation style**

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

49 **References management**

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

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

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

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

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

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

66 The citations are done using the normal markdown syntax, where @Elton1927AniEco produces Elton
67 (1927), and [@Camerano1880EquViv] produces (Camerano 1880).

68 **Figures, Tables, and other floats**

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

71 Mathematics

72 The following equation

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

73 is produced using

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

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

76 Tables

77 Table legends go on the line after the table itself. To generate a reference to the table, use {#tbl: id} –
78 then, in the text, you can use {@tbl: id} to refer to the table. For example, the table below is tbl. 1. You
79 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 |

80 Figures

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

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

85 [Figure 1 about here.]

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

87 **Example text**

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

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

95 **This is a subsection**

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

98 **This is another subsection**

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

101 **Some non-standard maths**

102 The phylogenetic reconstruction of $\hat{\mathcal{L}}$ and $\hat{\mathcal{R}}$ has an associated uncertainty, represented by the breadth of
103 the uniform distribution associated to each of their entries. Therefore, we can use this information to

104 assemble a *probabilistic* metaweb in the sense of (Poisot2016StrPro?), i.e. in which every interaction is
105 represented as a single, independent, Bernoulli event of probability p .

106 Specifically, we have adopted the following approach. For every entry in $\hat{\mathcal{L}}$ and $\hat{\mathcal{R}}$, we draw a value from
107 its distribution. This results in one instance of the possible left ($\hat{\ell}$) and right (\hat{r}) subspaces for the
108 Canadian metaweb. These can be multiplied, to produce one matrix of real values. Because the entries in
109 $\hat{\ell}$ and \hat{r} are in the same space where \mathcal{L} and \mathcal{R} were originally predicted, it follows that the threshold ρ
110 estimated for the European metaweb also applies. We use this information to produce one random
111 Canadian metaweb, $N = \hat{\mathcal{L}}\hat{\mathcal{R}}' \geq \rho$.

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

118 References

- 119 Camerano, L. (1880). Dell'equilibrio dei viventi merce la reciproca distruzione. *Atti Della R. Accad. Delle*
120 *Sci. Torino*, 15, 393–414.
- 121 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.