

BioHackathon Europe 2021 #1: CiTO annotations in BioHackrXiv

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Keywords

Cito, Biohackrxiv, Markdown, Pandoc, Biohakeu12

Abstract

Serendipity. I did not plan this hack at the BioHackathon Europe 2021 but it happened anyway. Based on earlier work in the Journal of Cheminformatics, extending on the work by Krewinkel et al. I looked into the idea of using the Lua filter for BioHackrXiv, a preprint server for BioHackathons. Actually, I started by looking at the Citation Styling Language file used by the BioHackrXiv tools. But that was just wrong.

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chem-bla-ics

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Long story short: [it worked!](#) Thanks to the encouragements from [Pjotr](#) and [Tazro](#) and suggestions from [Lars](#) and some code on how to [dump a Lua data structure to stdout](#).

In the Markdown/BibTeX combination you would normally write `[@bibtexkey]` to add the reference to the article with the given key in the `.bib` file. To type the citation (to state the intention why you cite that source), for example because you use a method in it, you write `[@usesMethodIn:bibtexkey]`. This is different from [how it currently works for the Journal of Cheminformatics](#), where the intention cannot be given at citation level yet. You can even use more than one intention, e.g. `[@usesMethodIn:extends:bibtexkey]`.

If you want to try it, just create a compatible Markdown file with BibTeX file in a new GitHub repository, and post the repository URL on this [cool preview website](#).

Here's what the created PDF could look like:

References

Bolleman, J. T., Mungall, C. J., Strozzi, F., Baran, J., Dumontier, M., Bonnal, R. J., Buels, R., Hoehndorf, R., Fujisawa, T., Katayama, T., & Cock, P. J. (2016). FALDO: a semantic standard for describing the location of nucleotide and protein feature annotation. *J Biomed Semantics*, 7, 39. <https://doi.org/10.1186/s13326-016-0067-z> [cito:agreesWith]

Byrd, W. E. (2009). *Relational programming in miniKanren: Techniques, applications, and implementations* [PhD thesis]. Indiana University.



Chiba, H., Nishide, H., & Uchiyama, I. (2015). Construction of an ortholog database using the semantic web technology for integrative analysis of genomic data. *PLOS ONE*, 10(4), e0122802. <https://doi.org/10.1371/journal.pone.0122802> [cito:usesMethodIn] [cito:agreesWith]

Friedman, D. P., Byrd, W. E., Kiselyov, O., & Hemann, J. (2018). *The Reasoned Schemer* (second edition). MIT Press. ISBN: 9780262535519 [cito:usesMethodIn] [cito:agreesWith]

Queralt-Rosinach, N., Pinero, J., Bravo, À., Sanz, F., & Furlong, L. I. (2016). DisGeNET-RDF: harnessing the innovative power of the Semantic Web to explore the genetic basis of diseases. *Bioinformatics*, 32(14), 2236–2238. <https://doi.org/10.1093/bioinformatics/btw214>

Wielemaker, J., Beek, W., Hildebrand, M., & Ossenbruggen, J. van. (2016). ClioPatria: A SWI-Prolog infrastructure for the Semantic Web. *Semantic Web*, 7(5), 529–541. <https://doi.org/10.3233/SW-150191>