

Edit me to practice contributing to a collaborative Manubot manuscript

test edit - hello world. This manuscript ([permalink](#)) was automatically generated from [manubot/try-manubot@b4c4bef](#) on April 1, 2020.

Authors

- **John Doe**

 [XXXX-XXXX-XXXX-XXXX](#) ·  [johndoe](#) ·  [johndoe](#)

Department of Something, University of Whatever · Funded by Grant XXXXXXXX

- **Jane Roe**

 [XXXX-XXXX-XXXX-XXXX](#) ·  [janeroe](#)

Department of Something, University of Whatever; Department of Whatever, University of Something

Abstract

Manubot is an open source tool for writing manuscripts on GitHub in markdown format. Manubot applies the git-based software workflow to scholarly writing, enabling enhanced transparency, collaboration, automation, and reproducibility.

This manuscript is a Manubot demo, intended to give users a playground to practice using Manubot. Everyone is encouraged to try writing with Manubot by editing this manuscript.

Manubot is described in the paper titled “Open collaborative writing with Manubot” [[1](#)].

Test my understanding

Main text

Lorem ipsum text [[2](#)] is a strong introduction for any manuscript.

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Manubot makes it easy to cite this manuscript [[3](#)]. It has been used to write several manuscripts that are now preprints on *bioRxiv* [[4](#),[5](#),[6](#),[7](#)]. Notice that only [[6](#)] has the correct name of the preprint server. Manubot allows authors to overwrite reference information, in this case with a BibTeX file.

Lorem ipsum also makes a strong conclusion.

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References

1. Open collaborative writing with Manubot

Daniel S. Himmelstein, Vincent Rubinetti, David R. Slochower, Dongbo Hu, Venkat S. Malladi, Casey S. Greene, Anthony Gitter

Manubot (2020-01-14) <https://greenelab.github.io/meta-review/>

2. Lorem ipsum

Wikipedia

(2020-03-30) https://en.wikipedia.org/w/index.php?title=Lorem_ipsum&oldid=948079675

3. Edit me to practice contributing to a collaborative Manubot manuscript

John Doe, Jane Roe

(2020-03-31) <https://manubot.github.io/try-manubot/>

4. GimmeMotifs: an analysis framework for transcription factor motif analysis

Niklas Bruse, Simon J. van Heeringen

Cold Spring Harbor Laboratory (2018-11-20) <https://doi.org/gfxrkc>

DOI: [10.1101/474403](https://doi.org/10.1101/474403)

5. Plasmids for independently tunable, low-noise expression of two genes

João P. N. Silva, Soraia Vidigal Lopes, Diogo J. Grilo, Zach Hensel

Cold Spring Harbor Laboratory (2019-01-09) <https://doi.org/gfs47c>

DOI: [10.1101/515940](https://doi.org/10.1101/515940)

6. Scaling tree-based automated machine learning to biomedical big data with a dataset selector

Trang T. Le, Weixuan Fu, Jason H. Moore

bioRxiv (2018-12) <https://www.biorxiv.org/content/10.1101/502484v1>

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7. Genotyping structural variants in pangenome graphs using the vg toolkit

Glenn Hickey, David Heller, Jean Monlong, Jonas A. Sibbesen, Jouni Sirén, Jordan Eizenga, Eric T. Dawson, Erik Garrison, Adam M. Novak, Benedict Paten

Cold Spring Harbor Laboratory (2019-06-01) <https://doi.org/gf3jfm>

DOI: [10.1101/654566](https://doi.org/10.1101/654566)