

The people of the 24th annual Pacific Symposium on Biocomputing in Hawaii

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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 the result of a *special working group* at the 2019 [Pacific Symposium on Biocomputing](#) that will introduce attendees to collaborative writing with Manubot. Each conference attendee is invited to write a small blurb on themselves and their research, by submitting a pull request to the manuscript repository at <https://github.com/dhimmel/psb-manuscript>.

The working group also [covers](#) how to write your next manuscript [using Manubot](#) and what features of Manubot can help biomedical researchers document and publish their computational research. For example, Manubot enables citation by persistent identifier to automate bibliographic metadata retrieval and formatting as well as allowing templating so results can be directly inserted from the analyses that produced them.

Methods

In this section, PSB 2019 attendees are asked to contribute a bit about themselves and their research. As part of the [special working group](#), we thought this would be a helpful activity to introduce biocomputational scientists to writing with Manubot. For inspiration, here are some prompts:

- Introduce yourself briefly.
- What do you research? Include any relevant links to your lab or personal website.
- What is your favorite study from your career or what study was your biggest discovery?
- What was your first scholarly publication?
- Add a code snippet or mathematical equation.
- Add a figure with a caption. This could be a picture of you in Hawaii or a figure from your previous work if the license is permissive enough to allow reuse.

Self-citations are explicitly encouraged, since one goal of this activity is to introduce attendees to the concept of [citation by persistent identifier](#). By having attendees cite their existing works, we hope to show researchers how references can be created from just persistent identifiers, and how this can assist with collaborative and transparent authoring.

The [markdown manuscript source](#) has a section for each PSB 2019 attendee, generated from the online [attendee list](#). Names are ordered alphabetically by last name. If you'd like to contribute, but are not already in the list, please insert your section at the appropriate alphabetical location.

For questions on how to use Manubot, see the [usage documentation](#). More information on the tool and its inception is available in the project manuscript [1].

Attendees

Weixuan Fu

Aloha, I'm in the [Institute for Biomedical Informatics \(IBI\)](#) at the University of Pennsylvania and the developer of [TPOT](#) and PennAI [2].

My main interest of research is developing automated machine learning tools for the analysis of large scale biomedical/sequencing data. Besides that, I am working on optimizing analysis pipeline of predicting neoantigen specifically presented in tumor cells using DNA and RNA sequencing data, for designing personalized neoantigen vaccines in cancer immunotherapies.

Casey Greene

I run an integrative genomics research lab at the University of of Pennsylvania, and I direct the Childhood Cancer Data Lab for Alex's Lemonade Stand Foundation. The lab at Penn develops methods to integrate large-scale public datasets, primarily from transcriptomic assays, and applies these methods to a broad set of biological questions. We've studied numerous systems, and we currently have active research projects in the application areas of microbial systems [3,4], cancers [5,6,7,8], and rare diseases [9]. At this PSB, a postdoc from the group will present a paper describing Continental Breakfast Included (CBI) effect in the final talk of the final session of this year's meeting [10].

I'm also interested in technologies that enhance the future of scientific communication. Our lab has studied Sci-Hub [11]. We've led a large collaborative review of deep learning in biology and medicine [12]. Members of the lab have developed tools like manubot [1], which you are using now. More publications are available on our [lab website](#).

Daniel Himmelstein

Greetings, I'm in the [Greene Lab](#) at the University of Pennsylvania and am the lead developer of the Manubot project. 2019 is my first PSB and I'm exciting to backpack around the Big Island following the conference.

My main area of research is integrating biomedical knowledge using hetnets [13,14]. However, I've also studied Sci-Hub, finding that it provides access to nearly all paywalled scholarly literature [15]. Perhaps my biggest discovery was observing an epidemiological association that higher elevation counties have lower rates of lung cancer, suggesting that oxygen is an inhaled carcinogen (Figure 1) [16,17].

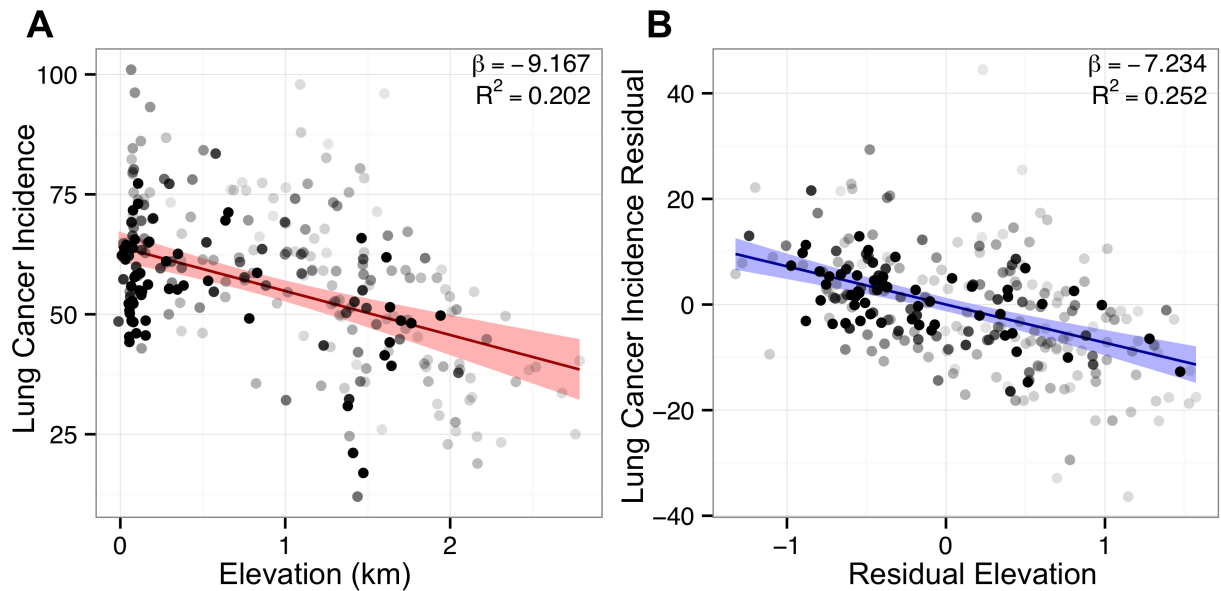


Figure 1: The association between elevation and lung cancer across Western U.S. counties. This figure is reused from [here](#) under its CC BY 4.0 License.

I haven't done much text mining, but I did enjoy extracting attendee names for PSB from the online PDF. Converting the PDF to text in Python was [as easy as](#):

```
# https://stackoverflow.com/a/48673754
import tika.parser
parsed = tika.parser.from_file('attendees.pdf')
text = parsed["content"]
```

Trang Le

Hello from the [Moore lab](#) at the University of Pennsylvania! I'm [a mathematician](#) who's currently excited about automated machine learning.

Here goes the self-citations:

- My own favorite study: Generalization of the Fermi Pseudopotential [\[18\]](#) - a piece of mathematical physics work I got to do when procrastinating writing my dissertation.
- My first (first-author) scholarly publication: Differential privacy-based evaporative cooling feature selection and classification with relief-F and random forests [\[19\]](#). Check out the Github repo for this study [here](#).
- Code snippet I'm most proud of:

```
M = dec2bin(0:2^(n*n)-1,n*n)
```

I will be impressed if you could tell what the language is. This is my answer to a question on [Math StackExchange](#).

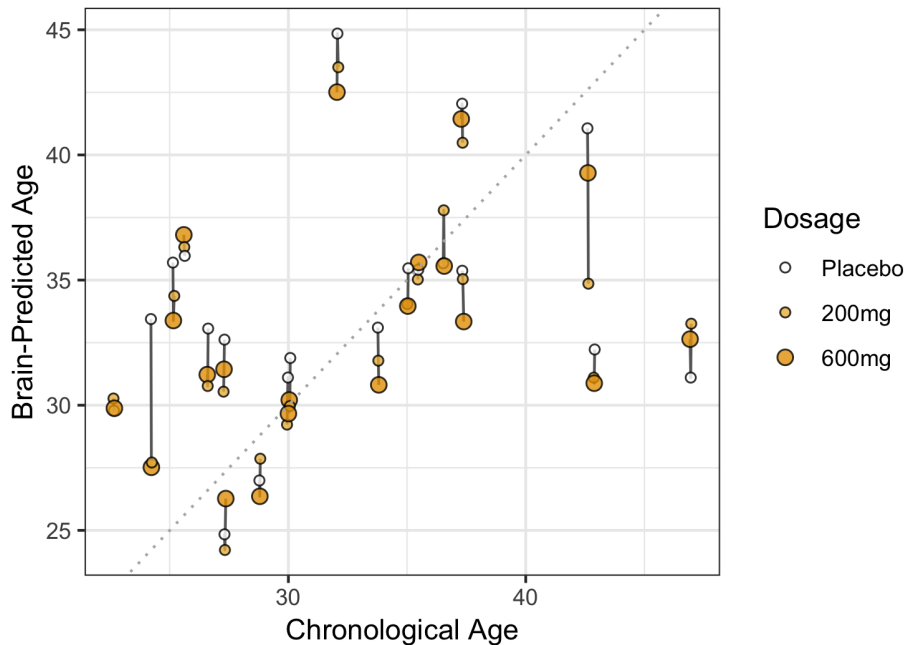
- I have too many favorite mathematical equations, but here's one:

$$a^p \equiv a \pmod{p}$$

Anyone recognize this theorem?

- And a figure with a caption:

Plot of brain-predicted age vs. chronological age of subjects in the ibuprofen study



This is an improved version of my main figure in this interesting study [20].

Aloah from the [Pinello Lab!](#)

I am a computational biologist studying the role of chromatin structure/dynamics and non-coding regions including enhancers, promoters, insulators and their role in gene regulation. The mission of my lab is the integration of omics data to explore and better understand the functional mechanisms of the non-coding genome and to provide accessible tools for the community to accelerate discovery in this field. The long-term goal of my research is to develop innovative computational approaches and to use cutting-edge experimental assays, such as single cell and genome editing, to systematically analyze sources of genetic and epigenetic variation that affect gene regulation in different human traits and diseases. I believe this will further our understanding of disease etiology involving these poorly characterized regions and will provide a foundation for the development of new drugs and more targeted treatments.

I am excited to share during the workshop [Reading between the genes: Interpreting noncoding DNA in high throughput](#) a new computational methods we have recently developed to analyze CRISPR tiling screen called CRISPR-SURF. You can read more on the manuscript that was recently published in Nature Methods [21].

Jaclyn Taroni

I'm a data scientist at the [Childhood Cancer Data Lab](#) (CCDL), an initiative of [Alex's Lemonade Stand Foundation](#). I'm interested in how diverse collections of publicly available transcriptomic data can help us learn about the biology of rare diseases. As a graduate student, I studied systemic sclerosis [22]. In the [PSB 2019 Text Mining and Machine Learning for Precision Medicine Workshop](#), I'll present our MultiPLIER project [9]. With the CCDL, I've been working on [refine.bio](#), a project for uniformly processing transcriptomic data from multiple species.

References

1. Open collaborative writing with Manubot

Daniel S. Himmelstein, David R. Slochower, Venkat S. Malladi, Casey S. Greene, Anthony Gitter
Manubot Preprint (2018-12-31) <https://greenelab.github.io/meta-review/>

2. A System for Accessible Artificial Intelligence

Randal S. Olson, Moshe Sipper, William La Cava, Sharon Tartarone, Steven Vitale, Weixuan Fu, Patryk Orzechowski, Ryan J. Urbanowicz, John H. Holmes, Jason H. Moore
Genetic Programming Theory and Practice XV (2018) <https://doi.org/gfsptm>
DOI: [10.1007/978-3-319-90512-9_8](https://doi.org/10.1007/978-3-319-90512-9_8)

3. ADAGE-Based Integration of Publicly Available Pseudomonas aeruginosa Gene Expression Data with Denoising Autoencoders Illuminates Microbe-Host Interactions

Jie Tan, John H. Hammond, Deborah A. Hogan, Casey S. Greene
mSystems (2016-01-19) <https://doi.org/gcgmbq>
DOI: [10.1128/msystems.00025-15](https://doi.org/10.1128/msystems.00025-15) · PMID: [27822512](https://pubmed.ncbi.nlm.nih.gov/27822512/) · PMCID: [PMC5069748](https://pubmed.ncbi.nlm.nih.gov/PMC5069748/)

4. Unsupervised Extraction of Stable Expression Signatures from Public Compendia with an Ensemble of Neural Networks

Jie Tan, Georgia Doing, Kimberley A. Lewis, Courtney E. Price, Kathleen M. Chen, Kyle C. Cady, Barret Perchuk, Michael T. Laub, Deborah A. Hogan, Casey S. Greene
Cell Systems (2017-07) <https://doi.org/gcw9f4>
DOI: [10.1016/j.cels.2017.06.003](https://doi.org/10.1016/j.cels.2017.06.003) · PMID: [28711280](https://pubmed.ncbi.nlm.nih.gov/28711280/) · PMCID: [PMC5532071](https://pubmed.ncbi.nlm.nih.gov/PMC5532071/)

5. Extracting a biologically relevant latent space from cancer transcriptomes with variational autoencoders

Gregory P. Way, Casey S. Greene
Biocomputing 2018 (2017-11-17) <https://doi.org/gfspd>
DOI: [10.1142/9789813235533_0008](https://doi.org/10.1142/9789813235533_0008)

6. Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas

Gregory P. Way, Francisco Sanchez-Vega, Konnor La, Joshua Armenia, Walid K. Chatila, Augustin Luna, Chris Sander, Andrew D. Cherniack, Marco Mina, Giovanni Ciriello, ... Armaz Mariamidze
Cell Reports (2018-04) <https://doi.org/gfspb>
DOI: [10.1016/j.celrep.2018.03.046](https://doi.org/10.1016/j.celrep.2018.03.046) · PMID: [29617658](https://pubmed.ncbi.nlm.nih.gov/29617658/) · PMCID: [PMC5918694](https://pubmed.ncbi.nlm.nih.gov/PMC5918694/)

7. Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas

Theo A. Knijnenburg, Linghua Wang, Michael T. Zimmermann, Nyasha Chambwe, Galen F. Gao,

Andrew D. Cherniack, Huihui Fan, Hui Shen, Gregory P. Way, Casey S. Greene, ... Armaz Mariamidze

Cell Reports (2018-04) <https://doi.org/gfspsc>

DOI: [10.1016/j.celrep.2018.03.076](https://doi.org/10.1016/j.celrep.2018.03.076) · PMID: [29617664](https://pubmed.ncbi.nlm.nih.gov/29617664/) · PMCID: [PMC5961503](https://pubmed.ncbi.nlm.nih.gov/PMC5961503/)

8. Oncogenic Signaling Pathways in The Cancer Genome Atlas

Francisco Sanchez-Vega, Marco Mina, Joshua Armenia, Walid K. Chatila, Augustin Luna, Konnor C. La, Sofia Dimitriadou, David L. Liu, Havish S. Kantheti, Sadegh Saghafein, ... Armaz Mariamidze

Cell (2018-04) <https://doi.org/gc7r9b>

DOI: [10.1016/j.cell.2018.03.035](https://doi.org/10.1016/j.cell.2018.03.035) · PMID: [29625050](https://pubmed.ncbi.nlm.nih.gov/29625050/) · PMCID: [PMC6070353](https://pubmed.ncbi.nlm.nih.gov/PMC6070353/)

9. MultiPLIER: a transfer learning framework reveals systemic features of rare autoimmune disease

Jaclyn N Taroni, Peter C Grayson, Qiwen Hu, Sean Eddy, Matthias Kretzler, Peter A Merkel, Casey S Greene

Cold Spring Harbor Laboratory (2018-08-20) <https://doi.org/gfc9bb>

DOI: [10.1101/395947](https://doi.org/10.1101/395947)

10. Parameter tuning is a key part of dimensionality reduction via deep variational autoencoders for single cell RNA transcriptomics

Qiwen Hu, Casey S Greene

Cold Spring Harbor Laboratory (2018-08-05) <https://doi.org/gdxxjf>

DOI: [10.1101/385534](https://doi.org/10.1101/385534)

11. Sci-Hub provides access to nearly all scholarly literature

Daniel S Himmelstein, Ariel Rodriguez Romero, Jacob G Levernier, Thomas Anthony Munro, Stephen Reid McLaughlin, Bastian Greshake Tzovaras, Casey S Greene

eLife (2018-03-01) <https://doi.org/ckcj>

DOI: [10.7554/elife.32822](https://doi.org/10.7554/elife.32822) · PMID: [29424689](https://pubmed.ncbi.nlm.nih.gov/29424689/) · PMCID: [PMC5832410](https://pubmed.ncbi.nlm.nih.gov/PMC5832410/)

12. Opportunities and obstacles for deep learning in biology and medicine

Travers Ching, Daniel S. Himmelstein, Brett K. Beaulieu-Jones, Alexandr A. Kalinin, Brian T. Do, Gregory P. Way, Enrico Ferrero, Paul-Michael Agapow, Michael Zietz, Michael M. Hoffman, ... Casey S. Greene

Journal of The Royal Society Interface (2018-04) <https://doi.org/gddkhn>

DOI: [10.1098/rsif.2017.0387](https://doi.org/10.1098/rsif.2017.0387) · PMID: [29618526](https://pubmed.ncbi.nlm.nih.gov/29618526/) · PMCID: [PMC5938574](https://pubmed.ncbi.nlm.nih.gov/PMC5938574/)

13. Heterogeneous Network Edge Prediction: A Data Integration Approach to Prioritize Disease-Associated Genes.

Daniel S Himmelstein, Sergio E Baranzini

PLoS computational biology (2015-07-09) <https://www.ncbi.nlm.nih.gov/pubmed/26158728>

DOI: [10.1371/journal.pcbi.1004259](https://doi.org/10.1371/journal.pcbi.1004259) · PMID: [26158728](https://pubmed.ncbi.nlm.nih.gov/26158728/) · PMCID: [PMC4497619](https://pubmed.ncbi.nlm.nih.gov/PMC4497619/)

14. Systematic integration of biomedical knowledge prioritizes drugs for repurposing

Daniel Scott Himmelstein, Antoine Lizee, Christine Hessler, Leo Brueggeman, Sabrina L Chen, Dexter Hadley, Ari Green, Pouya Khankhanian, Sergio E Baranzini

eLife (2017-09-22) <https://doi.org/cdfk>

DOI: [10.7554/elife.26726](https://doi.org/10.7554/elife.26726) · PMID: [28936969](https://pubmed.ncbi.nlm.nih.gov/28936969/) · PMCID: [PMC5640425](https://pubmed.ncbi.nlm.nih.gov/PMC5640425/)

15. Sci-Hub provides access to nearly all scholarly literature

Daniel S Himmelstein, Ariel Rodriguez Romero, Jacob G Levernier, Thomas Anthony Munro, Stephen Reid McLaughlin, Bastian Greshake Tzovaras, Casey S Greene

eLife (2018-03-01) <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5832410/>

DOI: [10.7554/elife.32822](https://doi.org/10.7554/elife.32822) · PMID: [29424689](https://pubmed.ncbi.nlm.nih.gov/29424689/) · PMCID: [PMC5832410](https://pubmed.ncbi.nlm.nih.gov/PMC5832410/)

16. Lung cancer incidence decreases with elevation: evidence for oxygen as an inhaled carcinogen

Kamen P. Simeonov, Daniel S. Himmelstein

PeerJ (2015-01-13) <https://doi.org/98p>

DOI: [10.7717/peerj.705](https://doi.org/10.7717/peerj.705) · PMID: [25648772](https://pubmed.ncbi.nlm.nih.gov/25648772/) · PMCID: [PMC4304851](https://pubmed.ncbi.nlm.nih.gov/PMC4304851/)

17. Unraveling the Ties of Altitude, Oxygen and Lung Cancer

George Johnson

The New York Times (2016-01-25) <https://www.nytimes.com/2016/01/26/science/unraveling-the-ties-of-altitude-oxygen-and-lung-cancer.html>

18. Generalization of the Fermi Pseudopotential

Trang T. Le, Zach Osman, D. K. Watson, Martin Dunn, B. A. McKinney

arXiv (2018-06-14) <https://arxiv.org/abs/1806.05726v1>

19. Differential privacy-based evaporative cooling feature selection and classification with relief-F and random forests

Trang T Le, W Kyle Simmons, Masaya Misaki, Jerzy Bodurka, Bill C White, Jonathan Savitz, Brett A McKinney

Bioinformatics (2017-05-04) <https://doi.org/f96b8d>

DOI: [10.1093/bioinformatics/btx298](https://doi.org/10.1093/bioinformatics/btx298) · PMID: [28472232](https://pubmed.ncbi.nlm.nih.gov/28472232/) · PMCID: [PMC5870708](https://pubmed.ncbi.nlm.nih.gov/PMC5870708/)

20. Effect of Ibuprofen on BrainAGE: A Randomized, Placebo-Controlled, Dose-Response Exploratory Study

Trang T. Le, Rayus Kuplicki, Hung-Wen Yeh, Robin L. Aupperle, Sahib S. Khalsa, W. Kyle Simmons, Martin P. Paulus

Biological Psychiatry: Cognitive Neuroscience and Neuroimaging (2018-10) <https://doi.org/gfsprv>

DOI: [10.1016/j.bpsc.2018.05.002](https://doi.org/10.1016/j.bpsc.2018.05.002) · PMID: [29941380](https://pubmed.ncbi.nlm.nih.gov/29941380/)

21. CRISPR-SURF: discovering regulatory elements by deconvolution of CRISPR tiling screen data.

Jonathan Y Hsu, Charles P Fulco, Mitchel A Cole, Matthew C Canver, Danilo Pellin, Falak Sher, Rick Farouni, Kendell Clement, Jimmy A Guo, Luca Biasco, ... Luca Pinello

Nature methods (2018-12) <https://www.ncbi.nlm.nih.gov/pubmed/30504875>

DOI: [10.1038/s41592-018-0225-6](https://doi.org/10.1038/s41592-018-0225-6) · PMID: [30504875](https://pubmed.ncbi.nlm.nih.gov/30504875/)

22. A novel multi-network approach reveals tissue-specific cellular modulators of fibrosis in systemic sclerosis

Jaclyn N. Taroni, Casey S. Greene, Viktor Martyanov, Tammara A. Wood, Romy B. Christmann, Harrison W. Farber, Robert A. Lafyatis, Christopher P. Denton, Monique E. Hinchcliff, Patricia A. Pioli, ... Michael L. Whitfield

Genome Medicine (2017-03-23) <https://doi.org/gfsptx>

DOI: [10.1186/s13073-017-0417-1](https://doi.org/10.1186/s13073-017-0417-1) · PMID: [28330499](https://pubmed.ncbi.nlm.nih.gov/28330499/) · PMCID: [PMC5363043](https://pubmed.ncbi.nlm.nih.gov/PMC5363043/)