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].

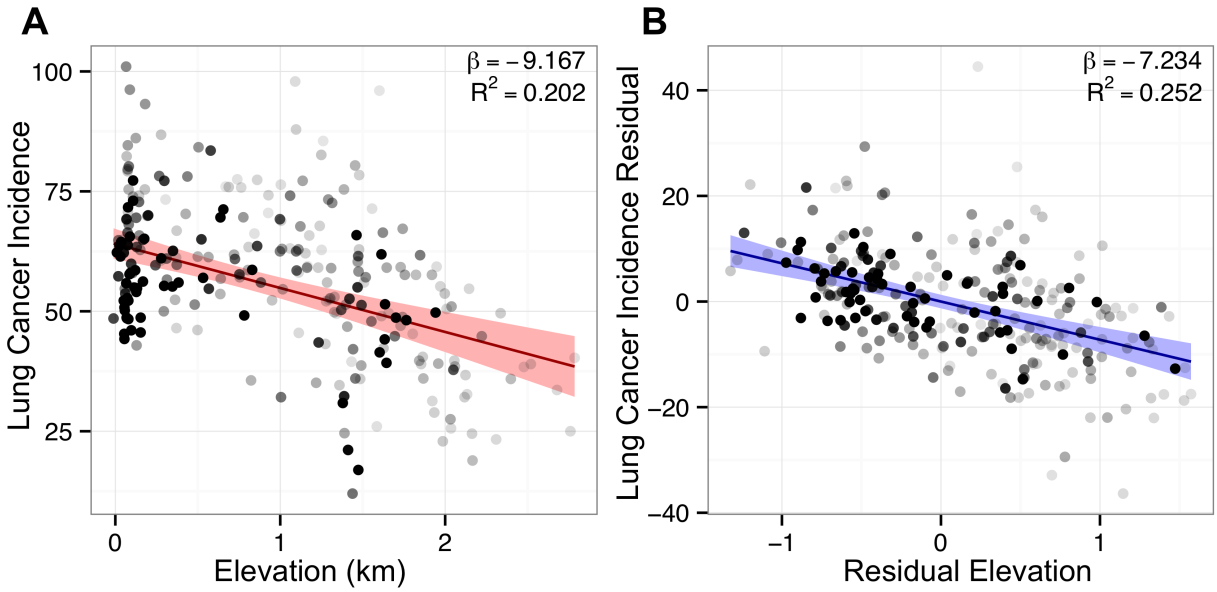


Figure 1: The association between elevation and lung cancer across Western U.S. counties. This figure is reused from here under its CC BY 4.0 License.

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:

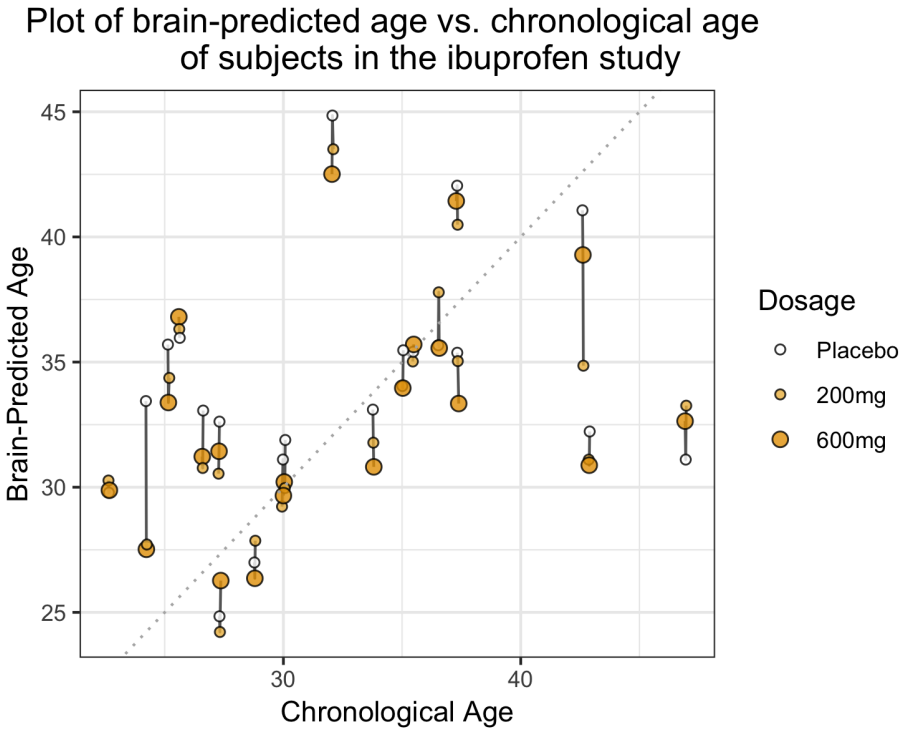
  ```
  M = dec2bin(0:2^(n*n)-1,n*n)
  ```

  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:

  $a^p \equiv a \mod p$

  Anyone recognize this theorem?
- And a figure with a caption:



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.

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