

Olga B. Botvinnik

Curriculum Vitae

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Studying the “dark matter” of genomes since 2017. PhD in single-cell RNA-sequencing. “Grand unified theory of cells,” hashing, sequencing weird creatures, STEM outreach. MIT, Broad Institute, UCSC, UCSD, Chan Zuckerberg Biohub. Open science/data/source.

Experience

Jan 2022 – **Bridge Bio Pharma**, San Francisco, CA, Senior Computational Biologist.

Present Analyzed next-generation sequencing data to prioritize therapeutic targets for genetic diseases with unmet needs.

- Analyzed PacBio long-read IsoSeq data of transcriptomes in cell models using Python (`gffutils`, `pandas`, `scikit-learn`, `Biopython`, `sourmash` in Jupyter Notebook).
- Wrote Nextflow Workflows for long- and short-read sequencing data to support gene therapy programs in capsid evolution and AAV population sequencing.
- Deployed Nextflow Workflows on Amazon Web Services Batch.

Jul – Oct **Arcadia Science**, San Francisco, CA, Advisor.

2021 Provided advice to startup founders on data science and bioinformatics needs.

2017–2021 **Chan Zuckerberg Biohub**, *Data Sciences*, San Francisco, CA, Bioinformatics Scientist II.

Investigated biological datasets via machine learning algorithms using a hodgepodge of tools such as Git/GitHub, Rust, Python (`scikit-learn`, `pandas`, `jupyter notebook`, *et al*), AWS, Docker, workflow management languages (Nextflow, Reflow), mentored junior scientists and bioinformaticians as part of a fast-paced, diverse, and integrated team.

Projects:

- Analyzed large single-cell transcriptome of mouse organs in collaboration with 50+ domain experts on *Tabula Muris* resource (github.com/czbiohub/tabula-muris), published in *Nature*
- Collaborated with a multidisciplinary team on *Tabula Microcebus* the first single-cell atlas of a nonhuman primate, Mouse Lemur (tabula-microcebus.ds.czbiohub.org)
- Contributed Python and Rust code to “sourmash” software for genomic and metagenomic *k*-mer analyses (github.com/dib-lab/sourmash)
- Developed “orpheus” (github.com/olgabot/orpheum) tool to extract likely protein-coding reading frames from RNA-seq data.
- Led cross-species analyses projects to study “dark matter” of transcriptomes using subsampled *k*-mers from translated RNA-seq reads in a reduced amino acid alphabet, to find putative homologous genes across millions of years of evolution (open draft manuscript)
- Pioneered weekly “BioinformaticsBeyonce” Twitch channel showcasing open source bioinformatics tools and research (twitch.tv/bioinformaticsbeyonce)
- Spearheaded weekly internal “Cupcakes & Coding” sessions, alternating between facilitating tutorials taught by junior programmers to share coding knowledge, and pair programming sessions (github.com/czbiohub/cupcakes)

- 2010–2011 **Jill Mesirov Laboratory**, *Broad Institute of Harvard and MIT*, Cambridge, MA, Bioinformatics Research Assistant.
Created REVEALER algorithm to unveil candidate oncogenic activators, published in *Nature Biotechnology*. Contributed to papers published in *Science Signaling* and *Journal of Hematology & Oncology*.

Education

- 2017 **Ph.D., Bioinformatics and Systems Biology**, *University of California, San Diego*, La Jolla, CA.
Dissertation: Computational analysis of single-cell alternative splicing
- 2012 **M.S., Bioinformatics and Biomolecular Engineering**, *University of California, Santa Cruz*, Santa Cruz, CA.
- 2010 **S.B., Biological Engineering**, *Massachusetts Institute of Technology*, Cambridge, MA.
- 2010 **S.B., Mathematics**, *Massachusetts Institute of Technology*, Cambridge, MA.

Research Training

- 2013–2017 **Gene Yeo Laboratory**, *University of California, San Diego*, La Jolla, CA.
Led machine-learning analyses of single-cell motor neuron differentiation mRNA-seq data, in collaboration with wet-lab researchers. Independently developed several software packages written in Python for alternative splicing analyses
- 2012–2013 **Research Rotations**, *University of California, San Diego*, La Jolla, CA.
Worked in Profs. Trey Ideker, Gene Yeo, and Pavel Pevzner's laboratories
- 2012 **Nader Pourmand Laboratory**, *University of California, Santa Cruz*, Santa Cruz, CA.
Analyzed single-cell response of breast cancer drug resistance to paclitaxel
- 2010 **Sebastian Seung Laboratory**, *MIT Department of Brain and Cognitive Sciences*, Cambridge, MA.
Computed directionality of neurons in electron microscopy of rabbit retina
- 2009 **David Gifford Laboratory**, *MIT Computer Science and Artificial Intelligence Laboratory*, Cambridge, MA.
Tested whether information flow can predict gene lethality in genomic networks
- 2008 **Sean Eddy Laboratory**, *Howard Hughes Medical Institute Janelia Farm Research Campus*, Ashburn, VA.
Used Hidden Markov Models to improve protein homology search with robust null models
- 2007 **Martha Bulyk Laboratory**, *Brigham and Women's Hospital, Division of Genetics*, Boston, MA.
Analyzed DNA binding specificities of mouse homeodomain transcription factors

Awards

Fellowships

- 2017 University of Washington eScience Institute - Moore/Sloan Data Science and Washington Research Foundation Innovation in Data Science Postdoctoral Fellowship (declined)
- 2014 NumFocus John Hunter Technical Fellowship for Open Source Science

2013–2016 National Defense Science and Engineering Graduate Fellowship

Honors

2016 100 Awesome Women In The Open-Source Community You Should Know, sourced.com

2013 Fannie and John Hertz Foundation Fellowship Finalist

2012 National Science Foundation Graduate Research Fellowship: Honorable Mention

2012 University of California Regents Scholarship

2009 Bernard M. Gordon-MIT Engineering Leadership Program

2008 Howard Hughes Medical Institute Janelia Farm Research Summer Scholar

Publications

Journal Articles

- [1] The Tabula Microcebus Consortium, Camille Ezran, Shixuan Liu, Jingsi Ming, Lisbeth A Guethlein, Michael F Z Wang, Roozbeh Dehghannasiri, Julia Olivieri, Hannah K Frank, Alexander Tarashansky, Winston Koh, Qiuyu Jing, **Olga B Botvinnik**, Jane Antony, Stephen Chang, Angela Oliveira Pisco, Jim Karkanias, Can Yang, James E Ferrell, Scott D Boyd, Peter Parham, Jonathan Z Long, Bo Wang, Julia Salzman, Iwijn De Vlaminck, Angela Wu, Stephen R Quake, and Mark A Krasnow. Mouse lemur transcriptomic atlas elucidates primate genes, physiology, disease, and evolution. *bioRxiv*, page 2022.08.06.503035, Aug. 2022.
- [2] Tabula Sapiens Consortium. The Tabula Sapiens: A multiple-organ, single-cell transcriptomic atlas of humans. *Science*, 376(6594):eabl4896, May 2022.
- [3] Taylor E Reiter, N Tessa Pierce-Ward, Luiz Irber, **Olga B Botvinnik**, and C Titus Brown. Protein k-mers enable assembly-free microbial metapangenomics. *bioRxiv*, page 2022.06.27.497795, June 2022.
- [4] C Ezran, S Liu, S Chang, J Ming, **Olga B Botvinnik**, and others. Tabula Microcebus: A transcriptomic cell atlas of mouse lemur, an emerging primate model organism. *bioRxiv*, 2021.
- [5] **Olga B Botvinnik**, Venkata Naga Pranathi Vemuri, N Tessa Pierce, Phoenix Aja Logan, Saba Nafees, Lekha Karanam, Kyle Joseph Travaglini, Camille Sophie Ezran, Lili Ren, Yanyi Juang, Jianwei Wang, Jianbin Wang, and C Titus Brown. Single-cell transcriptomics for the 99.9% of species without reference genomes. *bioRxiv*, page 2021.07.09.450799, July 2021.
- [6] Sachin J Shah, Peter N Barish, Priya A Prasad, Amy Kistler, Norma Neff, Jack Kamm, Lucy M Li, Charles Y Chiu, Jennifer M Babik, Margaret C Fang, Yumiko Abe-Jones, Narges Alipanah, Francisco N Alvarez, **Olga B Botvinnik**, Gloria Castaneda, CZB CLIAhub Consortium, Rand M Dadasovich, Jennifer Davis, Xianding Deng, Joseph L DeRisi, Angela M Detweiler, Scot Federman, John Haliburton, Samantha Hao, Andrew D Kerkhoff, G Renuka Kumar, Katherine B Malcolm, Sabrina A Mann, Sandra Martinez, Rupa K Mary, Eran Mick, Lusajo Mwakibete, Nader Najafi, Michael J Peluso, Maira Phelps, Angela Oliveira Pisco, Kalani Ratnasiri, Luis A Rubio, Anna Sellas, Kyla D Sherwood, Jonathan Sheu, Natasha Spottiswoode, Michelle Tan, Guixia Yu, Kirsten Neudo-

- erffer Kangelaris, and Charles Langelier. Clinical features, diagnostics, and outcomes of patients presenting with acute respiratory illness: A retrospective cohort study of patients with and without COVID-19. *EClinicalMedicine*, 27:100518, Oct. 2020.
- [7] Lincoln Harris, Rohan Vanheusden, **Olga B Botvinnik**, and Spyros Darmanis. cerebra: A tool for fast and accurate summarizing of variant calling format (VCF) files. *J. Open Source Softw.*, 5(54):2432, Oct. 2020.
 - [8] Tabula Muris Consortium. Single-cell transcriptomics of 20 mouse organs creates a Tabula Muris. *Nature*, pages 1–25, Oct. 2018, <https://www.biorxiv.org/content/early/2017/12/20/237446.full.pdf>.
 - [9] D V Klopfenstein, Liangsheng Zhang, Brent S Pedersen, Fidel Ramírez, Alex Warwick Vesztrocy, Aurélien Naldi, Christopher J Mungall, Jeffrey M Yunes, **Olga B Botvinnik**, Mark Weigel, Will Dampier, Christophe Dessimoz, Patrick Flick, and Haibao Tang. GOATOOLS: A Python library for Gene Ontology analyses. *Sci. Rep.*, 8(1):10872, July 2018.
 - [10] Yan Song*, **Olga B Botvinnik***, Michael T Lovci, Boyko Kakaradov, Patrick Liu, Jia L Xu, and Gene Yeo. Single-Cell Alternative Splicing Analysis with Expedition Reveals Splicing Dynamics during Neuron Differentiation. *Molecular Cell*, 2017. * These authors contributed equally to this work.
 - [11] Curtis A Nutter, Elizabeth A Jaworski, Sunil K Verma, Vaibhav Deshmukh, Qiongling Wang, **Olga B Botvinnik**, Mario J Lozano, Ismail J Abass, Talha Ijaz, Allan R Brasier, Nisha J Garg, Xander H T Wehrens, Gene W Yeo, and Muge N Kuyumcu-Martinez. Dysregulation of RBFOX2 Is an Early Event in Cardiac Pathogenesis of Diabetes. *Cell Reports*, 15(10):2200–2213, 2016.
 - [12] Jong Wook Kim*, **Olga B Botvinnik***, Omar Abudayyeh, Chet Birger, Joseph Rosenbluh, Yashaswi Shrestha, Mohamed E Abazeed, Peter S Hammerman, Daniel DiCara, David J Konieczkowski, et al. Characterizing genomic alterations in cancer by complementary functional associations. *Nature Biotechnology*, 2016. * These authors contributed equally to this work.
 - [13] Kris C Wood, David J Konieczkowski, Cory M Johannessen, Jesse S Boehm, Pablo Tamayo, **Olga B Botvinnik**, Jill P Mesirov, William C Hahn, David E Root, Levi A Garraway, et al. MicroSCALE screening reveals genetic modifiers of therapeutic response in melanoma. *Science Signaling*, 5(224):rs4, 2012.
 - [14] A Goncarencu, P Grynberg, **Olga B Botvinnik**, Geoff Macintyre, and Thomas Abeel. Highlights from the Eighth International Society for Computational Biology (ISCB) Student Council Symposium 2012. *BMC Bioinformatics*, 2012.
 - [15] Naomi Galili, Pablo Tamayo, **Olga B Botvinnik**, Jill P Mesirov, Margarita R Brooks, Gail Brown, and Azra Raza. Prediction of response to therapy with ezatiostat in lower risk myelodysplastic syndrome. *Journal of Hematology & Oncology*, 5(1):1, 2012.
 - [16] Naomi Galili, Pablo Tamayo, **Olga B Botvinnik**, Jill P Mesirov, Jennifer Zikria, Gail Brown, and Azra Raza. Gene Expression Studies May Identify Lower Risk Myelodys-

plastic Syndrome Patients Likely to Respond to Therapy with Ezatiostat Hydrochloride (TLK199). *Blood*, 118(21):2779–2779, 2011.

- [17] Michael F Berger, Gwenael Badis, Andrew R Gehrke, Shaheynoor Talukder, Anthony A Philippakis, Lourdes Pena-Castillo, Trevis M Alleyne, Sanie Mnaimneh, **Olga B Botvinnik**, Esther T Chan, et al. Variation in homeodomain DNA binding revealed by high-resolution analysis of sequence preferences. *Cell*, 133(7):1266–1276, 2008.

Books

- [1] P Compeau and P Pevzner. *Bioinformatics Algorithms Volume 1*, volume 1 of *An Active Learning Approach*. Active Learning Publishers LLC, 2 edition, 2015. Contributed text, figures, problems and code solutions, primarily to “Chapter 4: How Do We Sequence Antibiotics?”.

Conference Posters

- [1] **Olga B Botvinnik**, Yan Song, Michael T Lovci, Boyko Kakaradov, Patrick Liu, Jia L Xu, and Gene W Yeo. Single-cell alternative splicing analysis using Expedition reveals splicing dynamics during neuron differentiation. In *RNA Society*, Kyoto, Japan, June 2016.
- [2] **Olga B Botvinnik**, Yan Song, Michael T Lovci, Boyko Kakaradov, Patrick Liu, Leen Jamal, and Gene W Yeo. Novel computational metrics for population-wide differences in alternative splicing in single cells. In *Stem Cell Genomics California Institute of Regenerative Medicine Retreat*, La Jolla, CA, Apr. 2016.
- [3] **Olga B Botvinnik**, Yan Song, Michael T Lovci, Boyko Kakaradov, Patrick Liu, Leen Jamal, and Gene W Yeo. Single-cell alternative splicing analysis using Expedition reveals splicing dynamics during neuron differentiation. In *Single Cell Analysis Investigators Meeting*, Bethesda, MD, Apr. 2015.
- [4] **Olga B Botvinnik**, Jonathan Kim, Wendy Lee, Paola Castro, and Nader Pourmand. Single-cell differential expression pipeline. In *Intelligent Systems for Molecular Biology (ISMB)*, Long Beach, CA, June 2012.
- [5] **Olga B Botvinnik**, Pablo Tamayo, and Jill P Mesirov. Discovery of novel candidate oncogenic activators with REVEALER. In *Intelligent Systems for Molecular Biology (ISMB)*, Vienna, Austria, June 2011.

Talks

- 2020 **Biology of Genomes**, *Cold Spring Harbor Laboratory*, Long Island, New York, Functional prediction of transcriptomic “dark matter” across species.
Slides: speakerdeck.com/olgabot/functional-prediction-of-transcriptomic-dark-matter-across-species
- 2019 **The Identity and Evolution of Cell Types**, *European Molecular Biology Laboratory*, Heidelberg, Germany, Reference-free comparative transcriptomics.
Slides: speakerdeck.com/olgabot/reference-free-comparative-transcriptomics
- 2019 **Data Intensive Biology Summer Institute (Invited speaker)**, *University of California, Davis*, Davis, CA, Single-cell RNA-seq: To Infinity and Beyond!.
Slides: osf.io/gdzuy/, Video: youtu.be/hAqa8DztxSU

- 2018 **Biological Data Science**, *Cold Spring Harbor Laboratories*, Cold Spring Harbor, NY, Fast approximate cell type identification via MinHash sketches of k-mers in single cell RNA-seq.
Slides: Google slides
- 2018 **Current Progress in Biotechnology Seminar Series (Invited speaker)**, *University of California, Davis*, Davis, CA, If you liked it, you should have put a Seq on it: Job-seq and lessons learned.
Slides: slideshare.net/olgabotvinnik/if-you-liked-it-you-should-have-put-a-seq-on-it
- 2017 **Open Data Science Conference**, *San Francisco Hyatt Regency*, San Francisco, CA, Co-evolution of algorithms and data in biology.
Slides: speakerdeck.com/olgabot/co-evolution-of-algorithms-and-data-in-biology
- 2016 **Festival of Genomics California**, *San Diego Convention Center*, San Diego, CA.
- 2016 **Fluidigm User Group Meeting**, *City of Hope Hospital*, Los Angeles, CA.
- 2016 **Bioinformatics and Systems Biology Bootcamp**, *University of California, San Diego*, La Jolla, CA, Dr. You or How I Learned to Stop Worrying and Love the Ph.D..
Slides: slideshare.net/olgabotvinnik/dr-you-or-how-i-learned-to-stop-worry-and-love-the-phd
- 2016 **Bioinformatics and Systems Biology Ph.D. Program Recruitment**, *University of California, San Diego*, La Jolla, CA.
- 2015 **Bioinformatics and Systems Biology Bootcamp**, *University of California, San Diego*, La Jolla, CA, Dr. You or How I Learned to Stop Worrying and Love the Ph.D..
Slides: slideshare.net/olgabotvinnik/dr-you-or-how-i-learned-to-stop-worry-and-love-the-phd
- 2015 **San Diego Bioinformatics User Group**, *University of California, San Diego*, La Jolla, CA, Open-source software for single-cell and other large-scale transcriptomic datasets.
Slides: <http://nbviewer.jupyter.org/format/slides/gist/olgabot/2ee1087d74df46c842df/> (same as below)
- 2015 **CodeNeuro**, *New Museum*, New York, NY, Flotilla: Data-driven conversations in biology.
Slides: <http://nbviewer.jupyter.org/format/slides/gist/olgabot/2ee1087d74df46c842df/>
- 2015 **AmpNeuro**, *Amplifying Neuroscience Symposium*, La Jolla, CA, Open-source software for single-cell and other large-scale transcriptomic datasets.
Slides: <http://nbviewer.jupyter.org/format/slides/gist/olgabot/ba6970fbfa2babd79f55/>
- 2015 **Bioinformatics Exchange**, *University of California, San Diego*, La Jolla, CA.
- 2015 **Bioinformatics and Systems Biology Ph.D. Program Recruitment**, *University of California, San Diego*, La Jolla, CA.
- 2014 **RNA Club**, *University of California, San Diego*, La Jolla, CA.
- 2014 **Bioinformatics EXPO**, *University of California, San Diego*, La Jolla, CA.
Best Talk, 2nd place
- 2014 **PyData**, *401 Park Ave. South*, New York, NY.
Presentation: https://www.youtube.com/watch?v=IQksDvF12_8. Slides:
<https://github.com/olgabot/pydata2014biodata>

Teaching, Outreach, and Leadership

- 2018– **Core member**, *nf-core*, *nf-co.re*.
Contributed to a community effort to collect a curated set of analysis pipelines built using Nextflow.
- 2017–2019 **Dancer**, *SoulForce Dance Company*, San Francisco, CA.
Member of 11-piece hip-hop dance company. Performed in twice annual shows and assisted in beginner dance classes.
- 2015–2017 **Principal Cellist**, *UCSD Chamber Orchestra*, La Jolla, CA.
First cellist out of six. Led cello section during rehearsals.
- 2016–2017 **Teaching Assistant**, *Cold Spring Harbor Laboratories*, Cold Spring Harbor, NY.
Developed and led bioinformatics coursework of *Single Cell Analysis Course* including alignment, machine learning, Python, and basic command line tools to an audience largely with little to no programming experience. Course materials available at <http://github.com/YeoLab/single-cell-bioinformatics>
- 2016 **Guest Instructor**, *Quantitative Methods in Genetics and Genomics*, La Jolla, CA, .
Taught three weeks of *git*, RNA-seq and analysis methods to graduate-level UCSD course of 30 students, mostly with limited programming experience. Course materials available at <http://github.com/biom262/biom262-2016>
- 2015–2016 **Speaker and Co-Organizer**, *CodeNeuro*, New York, NY and San Francisco, CA.
Presented *flotilla* software, taught “coding for neuroscientists” tutorial (<http://github.com/codeneuro/gitgoing>), and advanced data analysis tutorial
- 2015–2016 **President and Co-Founder**, *Graduate Bioinformatics Council*, La Jolla, CA.
Founded graduate student council organization for UCSD Bioinformatics and Systems Biology Program. Advocated for student voices, organized “town hall” meetings, social hours, fellowship peer review, and led a team of eight vice presidents and representatives.
- 2015 **Guest Instructor**, *Quantitative Methods in Genetics and Genomics*, La Jolla, CA, .
Taught “data cleaning” and plotting course using Python to graduate-level UCSD course of 10 students, mostly with limited programming experience.
- 2013–2016 **Volunteer**, *San Diego Science and Engineering Festival*, San Diego, CA.
Developed and demonstrated bioinformatics modules to all ages at UCSD Bioinformatics booth.
- 2013–2014 **Instructor**, *Bioinformatics Algorithms*, Coursera.org.
Developed interactive curriculum for online Bioinformatics Algorithms Coursera class and textbook. Advisors: Pavel Pevzner and Phillip Compeau
- 2011–2012 **Mentor**, *We Teach Science*, San Jose, CA.
Weekly algebra tutoring to an 8th grader
- 2011–2012 **Guest Instructor**, *Pacific Collegiate School*, Santa Cruz, CA.
Created bioinformatics modules to engage students in tying genotype to phenotype for high school AP Biology
- 2012 **Co-Chair**, *Intelligent Systems for Molecular Biology Student Council Symposium*, Long Beach, CA.
- 2012 **Instructor**, *Minority Access to Research Careers*, Santa Cruz, CA.
Taught inquiry-based stem cell bioinformatics curriculum to undergraduate researchers
- 2011 **Volunteer**, *Science Club for Girls*, Cambridge, MA.
Co-led after-school biology science club for a class of 16 2nd graders
- 2009–2011 **Choreographer**, *MIT DanceTroupe*, Cambridge, MA.
Taught beginner to intermediate hip-hop choreography to fellow students

2008–2010 **Publicity Chair**, *MIT DanceTroupe*, Cambridge, MA.

Designed posters and T-shirts to publicize and promote DanceTroupe concert attendance

2008 **Social Chair**, *Baker House*, Cambridge, MA.

Organized social events for students, including a popular “Dormal” event with catered dinner and jazz music performances

Software

All software is written in Python and open source, licensed under the 3-clause BSD license, except where noted.

anchor Categorizes alternative splicing data into “modes”—bimodal, unimodal, or uniform. <http://github.com/YeoLab/anchor>

bonvoyage Transforms 1d splicing profiles into 2d space to maximize interpretability of change in signal. <http://github.com/YeoLab/bonvoyage>

dobby Dobby is a free and open source package for converting and managing plate reader fluorescence outputs, cDNA concentration files, ECHO pick lists, and creating sample sheets for Illumina sequencing. <http://github.com/czbiohub/dobby>

flotilla All-in-one package to perform machine learning analyses on large-scale molecular profiling datasets such as gene expression and alternative splicing. <http://github.com/YeoLab/flotilla> (72 stars on GitHub)

hermione Compare multiple distributions with horizon plots (also known as ridge plots) <http://github.com/czbiohub/hermione> (6 stars on GitHub)

kvector Counts k -mers in DNA or RNA as k -mer vectors, transforms position weight matrices (PWMs) to k -mer vectors. <http://github.com/olgabot/kvector> (5 stars on GitHub)

nf-core A collection of high quality Nextflow pipelines. Contributed to **rnaseq**, **scrnaseq** and wrote **kmermaid pipeline** <http://github.com/nf-core>

outrigger Fast *de novo* alternative exon detection and quantification. <http://github.com/YeoLab/outrigger> (9 stars on GitHub)

qtools Submit jobs to the supercomputer cluster from within Python. <http://github.com/YeoLab/qtools> (11 stars on GitHub)

poshsplice Annotates alternative splicing events with biological features such as translated protein product. <http://github.com/olgabot/poshsplice> (2 stars on GitHub)

prettyplotlib Painlessly create beautiful matplotlib plots. <http://github.com/olgabot/prettyplotlib> (1,159 stars on GitHub)

pyhomer Utility functions to work with output from the HOMER motif finding program. <https://github.com/olgabot/pyhomer>

seaborn Statistical visualization library. Contributor, wrote clustered heatmap classes and function. <http://github.com/mwaskom/seaborn> (3,602 stars on GitHub)

sourmash Compute and compare MinHash signatures for DNA data sets. Contributor, wrote reduced amino acid alphabet and other protein fixes. <https://github.com/dib-lab/sourmash> (199 stars on GitHub)

wasabiplot* Plot coverage and junction reads for any bam file and any region. *Derivative of SashimiPlot, and thus under the GNU General Public License (GPL).
<http://github.com/olgabot/wasabiplot>

Mentees

- 2019 **Saba Nafees**, *Chan Zuckerberg Biohub*, San Francisco, CA, PhD Intern.
- 2018 **Gerry Meixong**, *Chan Zuckerberg Biohub*, San Francisco, CA, Undergraduate Intern.
- 2014–2017 **Jessica Lettes**, *University of California, San Diego*, La Jolla, CA, Undergraduate Student.
- 2013 **Natalia La Spada**, *University of California, San Diego*, La Jolla, CA, High School Summer Student.