

Olga Botvinnik

Curriculum Vitae

University of California, San Diego
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Education

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

Research Positions

- 2013–**Gene Yeo Laboratory**, *Sanford Consortium for Regenerative Medicine*, La Jolla, CA.
Present Collaborated with wet-lab researchers to analyze single-cell motor neuron differentiation mRNA-seq data. 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.
Developed pipeline to analyze RNA-Seq data, applied to single-cell analysis of breast cancer drug resistance to paclitaxel
- 2010–2011 **Jill Mesirov Laboratory**, *Broad Institute of Harvard and MIT*, Cambridge, MA.
Created REVEALER algorithm to unveil candidate oncogenic activators
- 2010 **Sebastian Seung Laboratory**, *MIT Department of Brain and Cognitive Sciences*, Cambridge, MA.
Computed directionality of neurons in electron microscopy of rabbit retina inner plexiform layer slices
- 2009 **David Gifford Laboratory**, *MIT Computer Science and Artificial Intelligence Laboratory*, Cambridge, MA.
Tested whether measures of information flow can predict gene lethality in different genomic networks
- 2008 **Sean Eddy Laboratory**, *Howard Hughes Medical Institute Janelia Farm Research Campus*, Ashburn, VA.
Improved protein homology search by creating a better null homology model with Hidden Markov Models

- 2007 **Martha Bulyk Laboratory**, *Brigham and Women's Hospital, Division of Genetics*, Ashburn, VA.
Analyzed DNA binding specificities of mouse homeodomain transcription factors

Honors and Awards

- 2016 100 Awesome Women In The Open-Source Community You Should Know, sourced.com
2014 NumFocus John Hunter Technical Fellowship
2013–2016 National Defense Science and Engineering Graduate Fellowship
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

Y. Song*, O. B. Botvinnik*, M. T. Lovci, B. Kakaradov, P. Liu, J. L. Xu, and G. W. Yeo. Single-cell alternative splicing analysis with *Expedition* reveals splicing dynamics during neuron differentiation. In Review. * These authors contributed equally to this work.

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?".

J. W. Kim*, O. B. Botvinnik*, O. Abudayyeh, C. Birger, J. Rosenbluh, Y. Shrestha, M. E. Abazeed, P. S. Hammerman, D. DiCara, D. J. Konieczkowski, et al. Characterizing genomic alterations in cancer by complementary functional associations. *Nature Biotechnology*, 2016. * These authors contributed equally to this work.

K. C. Wood, D. J. Konieczkowski, C. M. Johannessen, J. S. Boehm, P. Tamayo, O. B. Botvinnik, J. P. Mesirov, W. C. Hahn, D. E. Root, L. A. Garraway, et al. Microscale screening reveals genetic modifiers of therapeutic response in melanoma. *Science Signaling*, 5(224):rs4, 2012.

N. Galili, P. Tamayo, O. B. Botvinnik, J. P. Mesirov, M. R. Brooks, G. Brown, and A. Raza. Prediction of response to therapy with ezatiostat in lower risk myelodysplastic syndrome. *Journal of Hematology & Oncology*, 5(1):1, 2012.

N. Galili, P. Tamayo, O. B. Botvinnik, J. P. Mesirov, J. Zikria, G. Brown, and A. Raza. Gene expression studies may identify lower risk myelodysplastic syndrome patients likely to respond to therapy with ezatiostat hydrochloride (tlk199). *Blood*, 118(21):2779–2779, 2011.

M. F. Berger, G. Badis, A. R. Gehrke, S. Talukder, A. A. Philippakis, L. Pena-Castillo, T. M. Alleyne, S. Mnaimneh, O. B. Botvinnik, E. T. Chan, et al. Variation in homeodomain dna binding revealed by high-resolution analysis of sequence preferences. *Cell*, 133(7):1266–1276, 2008.

Talks

- 2016 , *Festival of Genomics California*, San Diego Convention Center, San Diego, CA.
2016 , *Fluidigm User Group Meeting*, City of Hope Hospital, Los Angeles, CA.

Teaching, Outreach, and Leadership

- 2016 **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
- 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.
- 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 reinforce biology concepts in 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

Software

- 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>
- 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>
- kvector** Calculates k -mers in DNA, transforms position weight matrices (PWMs) to k -mer vectors.
<http://github.com/olgabot/kvector>

`outrigger` Fast *De novo* alternative exon detection and quantification. <http://github.com/YeoLab/outrigger>

`poshsplice` Annotates alternative splicing events with biological features such as translated protein product. <http://github.com/olgabot/poshsplice>

`prettyplotlib` Painlessly create beautiful `matplotlib` plots. <http://github.com/olgabot/prettyplotlib>

`seaborn` Contributor, wrote clustered heatmap classes and function. <http://github.com/mwaskom/seaborn>