Olga Botvinnik

Curriculum Vitae

University of California, San Diego
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Education

2012– Present **Ph.D., Bioinformatics and Systems Biology**, *University of California, San Diego*, 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– Present **Gene Yeo Laboratory**, *Sanford Consortium for Regenerative Medicine*, La Jolla, CA.
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

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, fellowhsip 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 ages 2-18 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**, *XXX High 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`