

# Olga Botvinnik

## Curriculum Vitae

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Research Interests: Molecular and cellular heterogeneity of biological systems

### Education

- 2012–**Ph.D. Candidate, Bioinformatics and Systems Biology**, *University of California, San Diego*, La Jolla, CA.  
Present 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**, *University of California, San Diego*, 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*, Boston, MA.  
Analyzed DNA binding specificities of mouse homeodomain transcription factors

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## Honors and Awards

- 2016 100 Awesome Women In The Open-Source Community You Should Know, sourced.com
- 2014 NumFocus John Hunter Technical Fellowship for Open Source Science
- 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

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## Publications

### Journal Articles

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.

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.

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.

Naomi Galili, Pablo Tamayo, **Olga B Botvinnik**, Jill P Mesirov, Jennifer Zikria, Gail Brown, and Azra 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.

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

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

**Olga B Botvinnik**, Yan Song, Michael T Lovci, Boyko Kakaradov, 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.

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### 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.
- 2016 **Bioinformatics and Systems Biology Ph.D. Program Recruitment**, *University of California, San Diego*, La Jolla, CA.
- 2015 **CodeNeuro**, *New Museum*, New York, NY.
- 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.

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### 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. 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.
- 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

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## 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>