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Olga Borisovna Botvinnik

Education

UNIVERSITY OF CALIFORNIA, SAN DIEGO SAN DIEGO, CA
PH.D. IN BIOINFORMATICS AND SYSTEMS BIOLOGY JUNE 2017 (EXPECTED)
Advisor: Prof. Gene Yeo
Dissertation: Computational analysis of single-cell alternative splicing in motor neuron development
Coursework: Algorithm Analysis and Design; Structural Bioinf.; Bioinf. Algorithms; Quant. Mol. Biology; Stat. Methods in Bioinf.; Genomics, Proteomics, and Network Biology; Current Concepts in Stem Cell Biology

UNIVERSITY OF CALIFORNIA, SANTA CRUZ SANTA CRUZ, CA
M.S. IN BIOMOLECULAR ENGINEERING AND BIOINFORMATICS JUNE 2012
Thesis: Single-cell analysis of breast cancer drug resistance (Advised by Prof. Nader Pourmand)

MASSACHUSETTS INSTITUTE OF TECHNOLOGY CAMBRIDGE, MA
S.B. IN MATHEMATICS JUNE 2010
S.B. IN BIOLOGICAL ENGINEERING JUNE 2010

Research

UNIVERSITY OF CALIFORNIA, SAN DIEGO SAN DIEGO, CA
GENE YEO LAB July 2013 – Present
- Collaborated with wet-lab researchers to analyzed single-cell motor neuron differentiation mRNA-seq data
- Independently developed several software packages written in Python for alternative splicing analyses

UNIVERSITY OF CALIFORNIA, SAN DIEGO SAN DIEGO, CA
RESEARCH ROTATIONS September 2012 – June 2013
- Worked in Profs. Trey Ideker, Gene Yeo, and Pavel Pevzner's laboratories.

UNIVERSITY OF CALIFORNIA, SANTA CRUZ SANTA CRUZ, CA
NADER POURMAND LAB January 2011 – June 2011
- Developed pipeline to analyze RNA-Seq data, applied to single-cell analysis of breast cancer drug resistance

BROAD INSTITUTE OF HARVARD AND MIT CAMBRIDGE, MA
JILL MESIROV LAB November 2010 – August 2011
- Created REVEALER algorithm to unveil candidate oncogenic activators , paper accepted at *Nature Biotechnology*
- Contributed to papers accepted in *Science Signaling* and *J Hematology & Oncology*

MIT DEPARTMENT OF BRAIN AND COGNITIVE SCIENCES CAMBRIDGE, MA
SEBASTIAN SEUNG LAB January - June 2010
- Computed directionality of neurons in electron microscopy of rabbit retina inner plexiform layer slices

MIT COMPUTER SCIENCE AND ARTIFICIAL INTELLIGENCE LABORATORY CAMBRIDGE, MA
COMPUTATIONAL GENOMICS GROUP (DAVID GIFFORD LAB) January – December 2009
- Tested whether measures of information flow can predict gene lethality in different genomic networks

HOWARD HUGHES MEDICAL INSTITUTE JANELIA FARM RESEARCH CAMPUS ASHBURN, VA
SEAN EDDY LAB Summer 2008
- Improved protein homology search by creating a better null homology model with Hidden Markov Models

BRIGHAM AND WOMEN'S HOSPITAL, DIVISION OF GENETICS BOSTON, MA
MARTHA BULYK LAB Summer 2007
- Analyzed DNA binding specificities of mouse homeodomain transcription factors, resulted in a publication in *Cell*

Publications

1. Kim JW*, **Botvinnk OB*,** Birger C, Rosenbluh J, Y. Shrestha, M. Abazeed, P. Hammerman, D. J. Konieczkowski, C. Johannessen, G. Alexe, A. Aguirre, M. Ghandi, G. Kryukov, H. Greulich, F. Vazquez, B.A. Weir, E. Van Allen, A. Liberzon, D. DiCara, O. Abudayyeh, A. Tsherniak, D. D. Shao, T. I. Zack, M. Noble, G. Getz, R. Beroukhim, L. A. Garraway, M. Meyerson, D. A. Barbie, J. Boehm, W. C. Hahn, J. P. Mesirov, and P. Tamayo. Mapping Genomic Alterations to Functional Profiles of Pathway Activation, Gene Dependency and Drug Sensitivity. *(accepted, Nature Biotechnology)* *These authors contributed equally to this work.
2. Goncearenco A, Grynberg P, **Botvinnik OB**, Macintyre G, Abeel T. Highlights from the 8th ISCB Student Council Symposium, Long Beach, California, USA, July 13 2012. BMC Bioinformatics.
3. Galili N, Tamayo P, **Botvinnik OB,** Mesirov JP, Brown G, Raza A. Gene expression studies may identify lower risk myelodysplastic syndrome patients likely to respond to therapy with ezatiostat hydrochloride (TLK199). *J Hematology & Oncology* (2012)
4. Wood KC, Konieczkowski DJ, Johannessen CM, Boehm JS, Tamayo P, **Botvinnik OB**, Mesirov JP, Hahn WC, Root D.E, Garraway LA, Sabatini DM. Miniaturized functional screening reveals genetic modifiers of therapeutic response in melanoma. *Science Signaling* (2012)

5. **Botvinnik OB**, Tamayo P, Mesirov JP. Discovery of novel candidate oncogenic activators with REVEALER. *Intelligent Systems for Molecular Biology* (ISMB) Conference. Vienna, Austria (2011)

6. Berger MF, Badis G, Gehrke AR, Talukder S, Philippakis AA, Peña-Castillo L, Alleyne TM, Mnaimneh S, **Botvinnik OB**, Chan ET, Khalid F, Zhang W, Newburger D, Jaeger SA, Morris QD, Bulyk ML, Hughes TR. Variation in homeodomain DNA binding revealed by high-resolution analysis of sequence preferences. *Cell* (2008)

Online Courses

- CalTech's Learning from Data (Fall 2013)
- Stanford's Probabilistic Graphical Models from Coursera (Spring 2013)

Community Outreach

- Volunteer for UCSD Bioinformatics booth at San Diego Science and Engineering Festival (2013-2016)
- Created bioinformatics modules to reinforce biology concepts in high school AP Biology (2011-2012)
- Mentor for *We Teach Science*, weekly algebra tutoring to an 8th grader in San Jose, CA (2011-2012)
- Taught inquiry-based stem cell curriculum to Minority Access to Research Careers students (2012)

Teaching

- Taught 3 weeks of a graduate-level UCSD course for 30 students as the sole student instructor (all others being professors)
- Developed interactive curriculum for online Bioinformatics Algorithms Coursera class

Professional and Leadership

- President and co-founder of Graduate Bioinformatics Council (GBIC) at UCSD
- Co-organized CodeNeuro SF 2015 Conference and taught an advanced data analysis tutorial
- Presented *flotilla* data analysis software at CodeNeuro NYC 2015 Conference and taught an introductory programming and version control tutorial
- Co-chaired ISMB Student Council Symposium 2012
- Member, RNA Society

Software (Python language)

- *flotilla* – All-in-one package to perform machine learning analyses on large-scale biological datasets
- *outrigger* – Creates custom alternative splicing indices and calculate percent spliced-in of junction reads
- *anchor* – Categorizes alternative splicing data into "modes" – bimodal, unimodal, or uniform
- *bonvoyage* – Transforms 1d splicing profiles into 2d space to maximize interpretability of change in signal
- *poshsplice* – Annotates alternative splicing events with biological features such as translated protein product
- *kvector* – Calculates k-mers in DNA, transforms position weight matrices (PWMs) to k-mer vectors
- *seaborn* contributor – Wrote hierarchical clustered heatmap function and classes
- *prettyplotlib* - painlessly create beautiful matplotlib plots (no longer maintaining)

Awards and Honors

- NumFOCUS John Hunter Technical Fellow (1 chosen, International Award)   *Graduate*
- National Defense Science and Engineering Graduate Fellow (top 6%)
- Hertz Foundation Fellowship Finalist (top 6%)
- National Science Foundation Graduate Research Fellowship: Honorable Mention (top 20%)
- University of California Regents Scholarship (2011)

- Bernard M. Gordon-MIT Engineering Leadership Program (2009)   *Undergraduate*
- Howard Hughes Medical Institute Janelia Farm Research Campus Summer Scholar (2008)

Skills

Programming   Python, git, R, bash, LaTeX
Design   Adobe Illustrator, OmniGraffle, Adobe Photoshop, Adobe LightRoom
Languages   Certified Russian-English medical interpreter (via Harvard Pilgrim Culture InSight program)

Extracurriculars

Graduate: Cello - Principal cellist of UCSD Chamber Orchestra, member of *Choro Científico* Brazillian folk improvisation group
Undergraduate: Lightweight Men's Crew (Coxswain), Everett Moore Baker House Executive Committee (Social Chair), Kappa Alpha Theta Women's Fraternity (Zeta Mu chapter), DanceTroupe (Choreographer, Publicity Chair)