

Natalie Davidson

PhD. Candidate

Expected Graduation Jan. 2019

Biomedical Informatics Group
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Education

Weill Medical College, Cornell University, Memorial Sloan-Kettering Cancer, Tri-Institutional Program in Computational Biology and Medicine (GPA: 3.8)

PhD. Computational Biology and Medicine

Advisor: Dr. Gunnar Rätsch

2013 - Present, Expected Graduation January 2019

University of California, Los Angeles (GPA: 3.68)

M.S. Computer Science, focus: Computational Biology

Advisor: Dr. Jason Ernst

2011 - 2013

University of California, Santa Barbara (Major GPA: 3.8)

B.S. Computer Science and Minor in Mathematics

2006 - 2011

Research

ETH Zürich / Biomedical Informatics Lab / Research Assistant

April 2016 - PRESENT

My research is focused on using and extending statistical models to understand transcriptional dysregulation in cancer. In addition to continuing my research projects from MSKCC, described below, I began two new projects: 1) Method to identify hypoxic signatures; 2) Method to estimate protein abundance from MS-SWATH data.

Memorial Sloan Kettering Cancer Center (MSKCC) / Rätsch Lab / Research assistant

June 2014 - April 2016

My research focused on understanding transcriptional and translational dysregulation in cancer; I utilized RNA-Seq and Ribo-Seq. I also participated in the International Cancer Genome Consortium where I integrate multiple transcriptional aberrations in over 1,000 samples to identify cancer relevant genes and alteration patterns.

Cornell University / Keinan Lab / Rotation Student

March 2014 - June 2014

As a rotation student I helped to conduct comprehensive genome-wide analysis to research the genetics of Bene Israel peoples from India and determine extent of both Jewish and Indian ancestry.

UCLA / Ernst Lab / Master's Student

June 2011 - June 2013

My master's thesis focused on creating a method to predict transcription factor binding patterns. The method utilized LASSO regression (glmnet), motif finding (MEME), and chromatin states (ChromHMM).

Publications

Davidson, Natalie R.*, et al. "Genomic basis for RNA alterations revealed by whole-genome analyses of 27 cancer types." *bioRxiv* (2018). Under review at *Nature*.

Davidson, Natalie R.*, Markolin, P.* , et al. "Discovery of a HIF dependent and hypoxia-inducible long isoform of SLC35A3". *In preparation*.

Krishnamoorthy, G.* , **Davidson, Natalie R.**, et al. "EIF1AX and RAS mutations cooperate to drive thyroid tumorigenesis through ATF4 and c-MYC". Under review at *Cancer Discovery*.

Waldman, Y Y.* , Bindadda A., **Davidson, Natalie R.**, et al. "The genetics of Bene Israel from India reveals both substantial Jewish and Indian ancestry." *PLoS One* 11.3 (2016): e0152056.

Davidson, Natalie R.*, et al. "DISTING: A web application for fast algorithmic computation of alternative indistinguishable linear compartmental models." *Computer methods and programs in biomedicine* 143 (2017): 129-135.

Davidson, Natalie R.*, et al. "Integrative Analysis of Transcriptome Variation in Uterine Carcinosarcoma and Comparison to Sarcoma and Endometrial Carcinoma." *bioRxiv* (2014): 012708. *In preparation*.

Presentations

Identification and Characterization of hypoxia-inducible Factor (HIF) -Dependent Alternative Splicing Events in Pancreatic Cancer
ISMB Student Council Symposium (Talk), RegSys (Poster)
July 2018

Integrating Diverse Transcriptomic Alterations to Identify Cancer-Relevant Genes
ISMB HiTSeq and Student Council Symposium (Talk)
Voted best student talk
July 2017
RECOMB Computational Cancer Biology (Talk)
April 2018

Differential Expression Method for Related Samples
ISMB Student Council Symposium (Talk), Integrative RNA Biology (Poster)
Voted 3rd best student talk
April 2016

Integrative Analysis of Transcriptome Variation in Uterine Carcinosarcoma and Comparison to Sarcoma and Endometrial Carcinoma
The Cancer Genome Atlas' 4th Scientific Symposium (Poster)
May 2015

Work

UCLA International Institute IT Group / Web Developer

2011 - 2013

AT&T Government Solutions / Intern

2009 - 2011

My work consisted of working on GUIs, modifying and working with network algorithms. All work was done in C++.

Mentorship

Co-Adviser Rotation Student / 3 months

2018

Project Title: Identifying hypoxic, RAS, and P53 pathway activation in TCGA data and predicting drug resistance in external cohorts.

Co-Adviser Master Student / 6 months

2017

Thesis Title: Identifying subpopulations of cancer cells and their interactions using proteomic single-cell data

Teaching

Learning and Intelligent Systems / Teaching Assistant

Fall 2017

Intro to Machine Learning / Teaching Assistant

Spring 2017 & 2018

Skills

Programming

High proficiency in R. Experience with Bash scripting, Java, C/C++, Python, VB.NET.. Experienced in Linux, Windows, and Mac environments.

Bioinformatic

Experienced with RNA-seq processing software for QC, alignment, quantification, and downstream analyses. These software include: STAR, FastQC, htseq, biomaRt, IGV, Picard Tools, MEME, and GSEA. I have previously worked with other data analysis softwares such as VarScan, PLINK, and ChromHMM.

Honors

Best Student Talk / ISMB Student Council

2017

3rd Best Student Talk / ISMB Student Council

2016

Selected to Participate / Leena Peltonen School of Human Genetics

2016

Service

GRASSHOPR Mentor, Cornell University, 2013-2014**Yoga Club Organizer, Weill Cornell Graduate School, 2015-2016****Social Chair, Tri-I Computational Biology and Medicine, 2014-2015**