

Shawn Cho

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EDUCATION	Johns Hopkins University MS in Bioinformatics, GPA: 3.967	Baltimore, MD Sept. 2014 — May 2016
	University of California, San Diego BS in Bioengineering: Biotech, GPA: 3.588	La Jolla, CA Sept. 2010 — June 2014

EXPERIENCE	Informatics, Scientist I Samumed	Samumed Apr. 2016 — Present
	<ul style="list-style-type: none">Samumed is a leader in medical research and development for tissue-level regeneration. With our platform's origins in small molecule-based Wnt pathway modulation, we develop therapeutics to address a range of degenerative diseases, regenerative medicine and oncology.	

Founder, Full-Stack Web Developer & Instructor Snipcademy	Snipcademy.com Mar. 2014 — Present
<ul style="list-style-type: none">Built an educational website offering code lessons on the Linux command line, Bash shell scripting, HTML/CSS/JavaScript, Python and more. Bioinformatics lessons on sequencing technologies, pairwise alignments, and sequence file formats.Back-end: Utilized PHP Laravel MVC framework with MySQL Database Management System and Laravel Forge for deployment services.Front-end: Implemented SEO within HTML, Google analytics plugin for user analysis. Styling with JS/JQuery, CSS/SASS and Twitter Bootstrap.	

Bioinformatician UCSD Dept. of Psychiatry and Cellular & Molecular Medicine	Sebat Lab May 2014 — Aug. 2014
<ul style="list-style-type: none">Analyzed facial features of 16p11.2 CNV duplication and deletion cohorts using 3dMD software tools.Performed pairwise comparison statistical analysis correcting for false discovery rate in R.	
May 2012 — June 2013	
<ul style="list-style-type: none">Utilized Random Forests R package and the "leave-one-out" method to identify 16p11.2 copy number variant genotypes in autistic adolescents using clinical variables.Analyzed locomotor behavior, pre-pulse inhibition, and fear conditioning data using linear regression models on transgenic mice with various copies of the <i>VIPR2</i> gene.Developed scripts in R to select fixed nucleotide differences between human and chip genomes while masking SNPs, repeats, and DGVs for primer design.Formulated algorithms to calculate silhouette scores for clustering quality control.	

SKILLSET OVERVIEW

- Languages:** Python, Java, JavaScript (jQuery), SQL, HTML, CSS/SASS (Twitter Bootstrap, Bourbon), PHP (Laravel MVC), Bash (Awk/Sed), R.
- Platforms:** Linux (Ubuntu Desktop & Server), OS X, Windows.
- Software:** Git, Eclipse, Sublime, Vim, MySQLWorkBench, Adobe Photoshop, Indesign & Illustrator.
- Bioinformatics Tools:** Galaxy + Linux command line, SAMtools, BEDtools, Tuxedo Suite, IGV, UCSC Genome Browsers, biological databases: dbSNP, NCBI, Ensembl, OMIM.

AWARDS & CERTS

- Linux+ Certificate and Coursera Genome Data Science Specialization (5/7 courses completed).
- Ranked in Top 100 worldwide (99.7%) on Rosalind, a site that offers challenging bioinformatics problems. Solved with Python 3.4.3, and placed second in Illumina's 2013 Bioinformatics Code Challenge.
- Received the Amgen 2012 Scholar's award, a competitive and fully-funded program for undergraduates to conduct a summer's worth of research with a UCSD professor.

PUBLICATIONS

Kusenda, M., V. Vacic, D. Malhotra, L. Rodgers, K. Pavon, J. Meth, R. A. Kumar, S. L. Christian, H. Peeters, **S. S. Cho**, A. Addington, J. L. Rapoport, and J. Sebat. "The Influence of Microdeletions and Microduplications of 16p11.2 on Global Transcription Profiles." *Journal of Child Neurology* 30.14 (2015): 1947-953.