Samantha Zarate

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Education

Current *Aug 2019*	Graduate Student in Computational Biology Department of Computer Science, **Johns Hopkins University**
June 2016 *Sept 2012*	Bachelor of Science in Biomedical Computation, **Stanford University** Relevant classes: Computational Molecular Biology (BIOCHEM 218), Representations and Algorithms for Computational Molecular Biology (BIOMEDIN 214), Translational Bioinformatics (BIOMEDIN 217), A Computational Tour of the Human Genome (BIOMEDIN 273A), Design and Analysis of Algorithms (CS 161) Completed a Notation in Science Communication, creating an ePortfolio of artifacts depicting growth and development in the realm of science communication.

Work and Research Experience

Aug 2019 *Aug 2016*	Scientist at **DNAnexus**, Mountain View, CA

- Implemented popular bioinformatics tools on the DNAnexus platform, including structural variation tools such as Parliament2
- Documentation co-lead, including structuring the content, writing and editing pages, and helping prioritize product documentation (http://documentation.dnanexus.com)
- Provided scientific and bioinformatics services for all customers in the country of Singapore, including the Genome Institute of Singapore and the National University of Singapore
- Worked with various other customers to support, accelerate, and productionize their bioinformatics pipelines
- Mentored a summer intern, helping her develop and productionize a DNAnexus-recommended RNA-seq analysis workflow

Sept 2015 *June 2015*	Bioinformatics Intern at **DNAnexus**, Mountain View, CA

- Productionized and parallelized tools for the DNAnexus platform including WGSA, CNVnator, and SomaticSniper
- Productionized and parallelized structural variant calling and analysis tools for the DNAnexus platform such as Parliament, Lumpy, Delly, and Pindel
- Attended the PacBio SMRT Informatics developers' conference as well as the Genome in a Bottle conference, both at the National Institute for Standards and Technology in Gaithersburg, MD, where work on Parliament was presented

June 2015 *Apr 2013*	Research Assistant at **Luo Lab**, Stanford University, Stanford, CA Understanding the function of *Rai1*

- Using Mosaic Analysis with Double Markers (MADM) in mice, conducted dendritic spine density analysis and cell quantification in various regions of the brain
- Analyzed *Rai1* expression in embryonic carcinoma murine stem cells differentiated into neurites and muscle cells and differential expression of *Rai1* using RNA-seq transcription and microarray data
- Conducted bioinformatics analysis of RNA-Seq and microarray data

Skills

- **Scientific:** R, SciPy, NumPy, MATLAB, LaTeX, popular bioinformatics software such as BWA-MEM, Samtools, GATK, etc., structural variant callers such as Lumpy, Breakdancer, Delly, etc.
- **Technical:** Python, Bash, Docker, C, C++, Java, version control (GitHub, Git, Mercurial), cloud software (AWS, Google Cloud)
- **Other:** Scientific communication and technical writing, moderate grasp of Spanish