

Samantha Zarate

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Work and Research Experience

Current Aug 2016	Scientist at DNAexus , Mountain View, CA <ul style="list-style-type: none">• Implement popular bioinformatics tools on the DNAexus platform, including structural variation tools such as Parliament2• Lead platform documentation, including writing and editing pages on the DNAexus wiki (https://wiki.dnanexus.com/Home)• Provide scientific and bioinformatics services for all customers in the country of Singapore, including the Genome Institute of Singapore and the National University of Singapore• Work with various other customers to support, accelerate, and productionize their bioinformatics pipelines• Mentored a summer intern, helping her develop and productionize a DNAexus-recommended RNA-seq analysis workflow
Sept 2015 June 2015	Bioinformatics Intern at DNAexus , Mountain View, CA <ul style="list-style-type: none">• Productionized and parallelized tools for the DNAexus platform including WGSa, CNVnator, and SomaticSniper• Productionized and parallelized structural variant calling and analysis tools for the DNAexus 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 <i>Rai1</i> <ul style="list-style-type: none">• Using Mosaic Analysis with Double Markers (MADM) in mice, conducted dendritic spine density analysis and cell quantification in various regions of the brain• Analyzed <i>Rai1</i> expression in embryonic carcinoma murine stem cells differentiated into neurites and muscle cells and differential expression of <i>Rai1</i> using RNA-seq transcription and microarray data• Conducted bioinformatics analysis of RNA-Seq and microarray data

Projects

Parliament2. Runs a combination of tools (BreakSeq, Breakdancer, CNVnator, Delly, Lumpy, Manta) to generate structural variant calls on whole-genome sequencing data.

- [GitHub](#): <https://github.com/dnanexus/parliament2>
- [DockerHub](#): <https://hub.docker.com/r/dnanexus/parliament2/>
- [Preprint](https://www.biorxiv.org/content/early/2018/09/23/424267): <https://www.biorxiv.org/content/early/2018/09/23/424267>

Education

June 2016	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.
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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:** Technical writing, moderate grasp of Spanish