

# Samantha Zarate

+1 (651) 230-3680 • slzarate@jhu.edu • [GitHub](#): slzarate • [in](#): slzarate

---

## Education

Current Aug 2019	Graduate Student in Computational Biology Department of Computer Science, <b>Johns Hopkins University</b>
June 2016 Sept 2012	Bachelor of Science in Biomedical Computation, <b>Stanford University</b> 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 <b>DNAexus</b> , Mountain View, CA <ul style="list-style-type: none"><li>Implemented popular bioinformatics tools on the DNAexus platform, including structural variation tools such as Parliament2</li><li>Documentation co-lead, including structuring the content, writing and editing pages, and helping prioritize product documentation (<a href="http://documentation.dnanexus.com">http://documentation.dnanexus.com</a>)</li><li>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</li><li>Worked with various other customers to support, accelerate, and productionize their bioinformatics pipelines</li><li>Mentored a summer intern, helping her develop and productionize a DNAexus-recommended RNA-seq analysis workflow</li></ul>
Sept 2015 June 2015	Bioinformatics Intern at <b>DNAexus</b> , Mountain View, CA <ul style="list-style-type: none"><li>Productionized and parallelized tools for the DNAexus platform including WGSa, CNVnator, and SomaticSniper</li><li>Productionized and parallelized structural variant calling and analysis tools for the DNAexus platform such as Parliament, Lumpy, Delly, and Pindel</li><li>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</li></ul>
June 2015 Apr 2013	Research Assistant at <b>Luo Lab</b> , Stanford University, Stanford, CA Understanding the function of <i>Rai1</i> <ul style="list-style-type: none"><li>Using Mosaic Analysis with Double Markers (MADM) in mice, conducted dendritic spine density analysis and cell quantification in various regions of the brain</li><li>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</li><li>Conducted bioinformatics analysis of RNA-Seq and microarray data</li></ul>

## Preprints & Manuscripts

P1. Parliament2: Fast Structural Variant Calling Using Optimized Combinations of Callers. **S. Zarate**, A. Carroll, O. Krasheninina, F. J. Sedlazeck, G. Jun, W. Salerno, E. Boerwinkle, R Gibbs (2018) *bioRxiv* doi: <https://doi.org/10.1101/424267>

## Posters

- Parliament2: Fast Structural Variant Calling Using Optimized Combinations of Callers. **S. Zarate**, A. Carroll, O. Krasheninina, F. Sedlazeck, G. Jun, W. J. Salerno, E. Boerwinkle, R. A. Gibbs (2019) Advances in Genome Biology and Technology (AGBT), Marco Island, FL.

- Parliament2: Benchmarking a Structural Variant Consensus Caller Compared to Individual Methods. A. Carroll, **S. Zarate**, W. J. Salerno, F. Sedlazeck, O. Krasheninina, R. Gibbs (2018) 23andMe Genome Research Day, Mountain View, CA.
- Parliament2: Benchmarking a Structural Variant Consensus Caller Compared to Individual Methods. A. Carroll, **S. Zarate**, W. J. Salerno, F. Sedlazeck, O. Krasheninina, R. Gibbs (2018) Biology of Genomes, Cold Spring Harbor, NY.
- CHORUS: Enabling the sharing of federated genomic data associated with subjects from varied Singapore ethnic groups. **S. Zarate**, J. Ow, Y. Hwang, Y. Men, P. Lim, P. Ng (2017) Biology of Genomes, Cold Spring Harbor, NY.
- Analyzing the function of Smith Magenis Syndrome-associated gene *Rai1*. **S. Zarate**, C. Guenther, L. Luo (2014) SURPS (Symposium of Undergraduate Research and Public Service) poster session, Stanford, CA.
- Understanding the function of RAI1 through genetic mosaic analysis in mice. **S. Zarate**, C. Guenther, L. Luo (2013) Bio-X Undergraduate Fellow poster session, Stanford, CA.

## 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