Danny Antaki

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Education

2013-2018 **PhD, Biomedical Sciences** Advisor: Jonathan Sebat **University of California San Diego**

- Discovered noncoding deletions transmitted from fathers contributed risk for Autism
- Built pipelines to analyze structural variation in >10,000 human whole genomes on AWS
- Developed a machine learning algorithm to genotype structural variation, leading to an updated estimate of the rate of de novo structural variation in humans
- Analyzed microarrays, paired-end short-read genomes, and long-read PacBio and Oxford Nanopore genomes
- Collaborated with 1000 Genomes Project and the Psychiatric Genomics Consortium

2009-2013 **BS, General Biology** **Purdue University**

- Dean's List & Honors Biology Research Program Advisor: John Anderson
- Howard Hughes Medical Institute Summer Intern Advisor: Daisuke Kihara

Experience

2018-Present **Postdoctoral Scholar** Advisor: Joe Gleeson **Rady Children's Institute for Genomic Medicine**

- Processed deeply sequenced (200-300x) whole genomes for somatic variation analysis in sperm of fathers with children with Autism and biopsies from postmortem human brain
- Analyzed rare variants and polygenic risk scores in an Autism cohort of >37,000 individuals
- Mentored a visiting bioinformatics Masters student from SDSU; developed a machine-learning tool for somatic structural variation detection

Select Publications

Google Scholar

2021 MW Breuss*, X Yang*, **D Antaki***, JCM Schlachetzki*, et al. Somatic mosaicism in the mature brain reveals clonal cellular distributions during cortical development. ***bioRxiv*** (in review ***Nature***) * Authors contributed equally to this work

2020 MW Breuss, **D Antaki**, et al. Autism risk in offspring can be assessed through quantification of male sperm mosaicism. ***Nature Medicine***

2018 WM Brandler*, **D Antaki***, M Gujral*, et al. Paternally inherited cis-regulatory structural variants are associated with autism. ***Science*** * Authors contributed equally to this work

2018 **D Antaki**, WM Brandler, J Sebat. SV^2: accurate structural variation genotyping and de novo mutation detection from whole genomes. ***Bioinformatics***

2016 WM Brandler*, **D Antaki***, M Gujral*, et al. Frequency and complexity of de novo structural mutation in autism. ***American Journal of Human Genetics*** * Authors contributed equally to this work

Qualifications and Skills

Python (excellent)

htslib Integration (`pysam`) | Data Analysis (`numpy`, `pandas`) | Machine Learning/Deep Learning (`scikit-learn, keras, TensorFlow`) | Performance/C-integration (`cython`) | Visualization (`matplotlib, seaborn`) | Package Distribution (`setuptools`, pypi)

Perl (excellent) | **R** (very good) | **C/C++** (good) | **Bash** (excellent) | **AWS** (very good) | **Git** (very good) | **HTML** (good)

SAMtools | BCFtools | BEDtools | GATK | Plink | Structural Variation Analysis | De Novo Mutation Calling | Rare Variant Analysis | Variant Annotation (VEP, Annovar) | Next Generation Sequencing Analysis | Single Molecule Long Read Sequencing Analysis | RNAseq | QTL2 | Adobe Photoshop | Adobe Illustrator |LaTeX