Isaac Wong

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EDUCATION

University of Rochester **May 2019**

- Bachelor of Science in Computational Biology
- Bachelor of Arts in Computer Science

RESEARCH EXPERIENCE

Massachusetts General Hospital – Center for Genomic Medicine **Boston, Massachusetts**

Bioinformatics Specialist II – Talkowski lab *July 2019 – present*

- Worked on development of GATK-gCNV, a cloud based computational pipeline to call copy number variants from exome sequencing data. The pipeline produces joint callsets, performs automated cursory statistical analysis, and generates QC metrics.
- Managed the storage of the Talkowski lab's local HPC cluster, totaling 800TB across 45 users.
- Developed general purpose, scalable computational methods for the processing of WGS data with a focus on analyzing SNVs and structural variants.
- Developed methods for processing and analyzing cell free fetal DNA for use in prenatal diagnostics.
- Trained new hires in lab protocols and standard operating procedures.

University of Rochester – Department of Biology **Rochester, New York**

Research Assistant – Larracuente Lab *October 2016 – May 2019*

- Developed computational models to study factors driving the evolution of satellite DNA arrays in *Drosophila* to better understand how recombination rates and fitness functions drive expansion and collapse of individual arrays across large timescales.

PUBLICATIONS

- Mehrtash B and Fu, *et al*. GATK-gCNV enables the discovery of rare copy number variants from exome sequencing data. *Nature Genetics.* August 2023. doi: 10.1038/s41588-023-01449-0.
- Lower C and Valkanas E, *et al.* Systematic evaluation of genome sequencing for the diagnostic assessment of autism spectrum disorder and fetal structural anomalies. *American Journal of Human Genetics*. August 2023. doi: 10.1016/j.ajhg.2023.07.010.
- Duyzend M, *et al.* O39: Comprehensive, high-resolution, and non-invasive prenatal screening of coding variation. *Genetics in Medicine Open.* January 2023. doi: 10.1016/j.gimo.2023.100646.
- Baxter S, *et al*. Centers for Mendelian Genomics: A decade of facilitating gene discovery. *Genetics in Medicine*. 2022. doi: 10.1016/j.gim.2021.12.005.
- Akula S, et al. Exome Sequencing and the Identification of New Genes and Shared Mechanisms in Polymicrogyria. *JAMA Neurology*. July 2023. doi: 10.1001/jamaneurol.2023.2363.
- Stamou M, et al. Contribution of Copy Number Variation in Idiopathic Hypogonadotropic Hypogonadism. *J Endocr Soc*. 2021. doi:10.1210/jendso/bvab048.1537.
- Dyment D, *et al*. Alternative genomic diagnoses for individuals with a clinical diagnosis of Dubowitz syndrome. *Am J Med Genet Part A*. October 2020. doi: 10.1002/ajmg.a.61926.
- Hu S, *et al*. Whole exome sequencing analyses reveal gene–microbiota interactions in the context of IBD. *Gut*. July 2020. doi: 10.1136/gutjnl-2019-319706.
- Sproul J, *et* al. Dynamic Evolution of Euchromatic Satellites on the X Chromosome vin *Drosophila melanogaster* and the *simulans* Clade. *Molecular Biology and Evolution*. August 2020. doi: 10.1093/molbev/msaa078.
- Fallon T, *et al*. Firefly genomes illuminate parallel origins of bioluminescence in beetles. *eLife*. October 2018. doi: 10.7554/eLife.36495

TECHINICAL SKILLS

- R, Java, Python, WDL, Bash, Docker, Google Cloud Platform