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 also produces joint callsets, performs automated cursory statistical analysis, and generates QC metrics. To date, 1.2 million exomes have had CNV calls generated using GATK-gCNV.
- 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 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 a computational model for evolution of satellite DNA arrays to infer how recombination rates and fitness functions drive expansion and collapse of individual arrays across large timescales.
- Developed computational tools to measure the age of satellite arrays to study factors driving evolution of satellite DNA in *Drosophila.*

PUBLICATIONS

- 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.
- 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

IN PRESS

- Mehrtash B, Fu J, *et al.* GATK-gCNV: A Rare Copy Number Variant Discovery Algorithm and Its Application to Exome Sequencing in the UK Biobank. *Nature Genetics.* 2023*.* doi: 10.1101/2022.08.25.504851

TECHINICAL SKILLS

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