Isaac Wong

[iwong1@mgh.harvard.edu] • [iwong@broadinstitute.org] • [github.com/theisaacwong]

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*
- Developed a cloud based computational pipeline to call copy number variants from exome sequencing data, generate joint callsets, and perform automated cursory statistical analysis and QC. To date, I have produced CNV callsets spanning 1,400,00 exomes.
- 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.

University of Rochester – Department of Biology **Rochester, New York**
Undergraduate research – 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.*
- Developed computational methods for predicting individual satellite DNA array size from WGS data to study factors driving evolution of satellite DNA in *Drosophila.*

PUBLICATIONS

- Baxter S, Posey J, Lake N, *et al*. Centers for Mendelian Genomics: A decade of facilitating gene discovery. *Genetics in Medicine*. 2022. https://doi.org/10.1016/j.gim.2021.12.005.
- Stamou M, Brand H, Lippincott MF, et al. Contribution of Copy Number Variation in Idiopathic Hypogonadotropic Hypogonadism. *J Endocr Soc*. 2021. doi:10.1210/jendso/bvab048.1537
- Dyment, DA, O'Donnell-Luria, A, Agrawal, PB, *et al*. Alternative genomic diagnoses for individuals with a clinical diagnosis of Dubowitz syndrome. *Am J Med Genet Part A*. October 2020. doi.org/10.1002/ajmg.a.61926
- Hu S, Vich Vila A, Gacesa R, *et al*. Whole exome sequencing analyses reveal gene–microbiota interactions in the context of IBD. *Gut*. July 2020. dx.doi.org/10.1136/gutjnl-2019-319706
- Sproul J, Khost D, Eickbush D, *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.org/10.1093/molbev/msaa078
- Fallon T, Lower S, Chang C, *et al*. Firefly genomes illuminate parallel origins of bioluminescence in beetles. *eLife*. October 2018. doi.org/10.7554/eLife.36495

IN REVIEW

- 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. *Biorxiv*. 2022. https://doi.org/10.1101/2022.08.25.504851

TECHINICAL SKILLS

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