

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

- Developed computational pipelines to call copy number variants from exome sequencing data and perform automated cursory statistical analysis. To date, I have processed 1,400,00 exomes.
- Managed the storage and costs for the Talkowski lab's HPC cluster, totaling 800TB across 45 users.
- Developed general purpose, scalable computational methods for the processing of WGS data and analyzing results, with a focus on 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 – Larracuenta 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*.

Freie Universität – Department of Biochemistry

Berlin, Germany

Independent Research – Ewers Lab, DAAD RISE Fellowship

May 2018 – August 2018

- Developed computational tools to measure, analyze, and predict the movement of and forces on magnetic nanoparticles which were bound to cell membrane proteins and then manipulated by an external magnetic.

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/endo/bvab048.1537
- Dymant, 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 in *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

POSTER PRESENTATIONS

- Isaac Wong, “Dynamic evolution of euchromatic satellites on the X chromosome in *Drosophila*” 60th Annual *Drosophila* Research Conference, Dallas, Texas, 2019.
- Isaac Wong, “Complex Satellite DNA variation within and between populations of *Drosophila melanogaster*” 59th Annual *Drosophila* Research Conference, Philadelphia, Pennsylvania, 2018.

TECHNICAL SKILLS

- Programming languages: R, Java, Python 3, scripting in Linux/Bash environment. Workflow languages: WDL