

XIAOTONG YAO

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1300 York Ave • New York, NY 10065

EDUCATION

- Ph.D., Weill Cornell Medicine, Computational Biology** Jul 2015 - expected **Apr 2021**
• Mentored by Imielinski, M: *Illuminating Rearranged Cancer Genome Structures through Genome Graphs*
- M.S., New York University, Bioinformatics** Aug 2013-May 2015
Overall GPA: 3.9/4.0
New York, NY
• Mentored by Vogel, C: *iSUMO - Integrative Prediction of Functionally Relevant SUMOylated Proteins*
- B.S., Zhejiang University, Biotechnology** Aug 2009-May 2013
Overall GPA: 3.4/4.0
New York, NY
• Mentored by Chen, M: *Optimization of Streptomycin Production in *S. avermitilis* by Metabolic Network Analysis*

WORK EXPERIENCE

- Weill Cornell Medicine** Jul 2015 - Present
Graduate Research Assistant
New York, NY
• Discovered three new patterns of complex structural variations from thousands of cancer genomes
• Designed *Junction Balance Analysis* to reconstruct genome graphs
• Conceptualized and developed *gGnome* for genome graph data structure
• Contributed to large cancer sequencing consortiums including TCGA and PCAWG
- New York University** December 2013 - May 2015
Graduate Research Assistant
New York, NY
• Trained predictive models for post-translational modification from protein function databases
- New York University** Feb 2014 - May 2015
Teaching Adjunct
New York, NY
• Taught R statistical programming for Introduction to Biostatistics
• Tutored techniques for Biological Databases and Data Mining
- 3E Bioenergy** Jun 2014 - May 2015
Bioinformatics Intern
New Brunswick, NJ
• Compared crop genomes for candidate genes linked to drought resistance in sweet sorghum

SELECTED PUBLICATIONS

- Hadi K, **Yao X**, Behr JM, ..., Imielinski M. *Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs*. *Cell*. 2020;183: 197–210.e32.
- (In review) Dewhurst SM, **Yao X**, ..., de Lange T, Imielinski M. *Structural Variant Evolution after Telomere Crisis*. *BioRxiv*. 2020. p. 2020.09.29.318436. doi:10.1101/2020.09.29.318436
- (In review) Carrot-Zhang J, **Yao X**, Devarakonda S, et al. *Whole-genome Characterization of lung Adenocarcinomas Lacking Alterations in RTK/RAS/RAF/MAPK Pathway*. *Cancer Res*. 2020;80: 5895–5895.

SKILLS

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| Biology | Cancer Genomics, Computational Biology, Systems Biology |
| Sequencing Informatics | Illumina, Oxford Nanopore |
| Statistics & Machine Learning | Generalized Linear Models, Random Forests |
| Computer Languages | R, Shell, Python, Java |
| Optimization | CPLEX, Gurobi |
| Data Visualization | ggplot, shiny, plotly |
| Scientific Communication | LaTeX, Adobe Illustrator, (R)markdown |
| Databases | SQLite, MySQL |
| Other Tools | Bioconductor, Git, Emacs, Docker, Nextflow, Hugo |