

# XIAOTONG YAO

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