Yanli Wang

M.D., Ph.D.

I am an aspiring physician scientist who hope to elucidate clinical genetic questions; with robust and extensive computational skills and through multidisciplinary collaborations with other researchers.

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CURRENT EXPERIENCE

Residency (PGY/PL-4), Combined Pediatric and Genetics, Children's Hospital of Philadelphia, 2020-

Co-leader, NERD (New Epic Resident Development) Squad, Children's Hospital of Philadelphia, 2021-2023

- Interfaces between residents, residency program and Epic (electronic health record) leadership
- Teaches Epic to new interns, helps current residents develop new Epic skills

RESEARCH HIGHLIGHTS

Constructing the 3D Genome Browser

- The 3D Genome Browser (http://3dgenome.org) is a web-based genome browser used to visualize the spatial organization of the vertebrate genome. It has several modes to illustrate interactions from cis-regulatory contacts, to topologically-associating domains (TADs), to interchromosomal interactions. Furthermore, the browser integrates tracks from well-known genome browsers such as the WashU Epigenome Browser and UCSC Genome Browser to facilitate the functional annotation of genomic elements, giving insight into the function of non-coding elements and effects of non-coding genetic variants.
- Role: Served as the original main architect, first-author
- The browser has over 1 million hits as of Oct 2020; the paper received **High Attention Score** by Altmetric.

Exploring the Epigenomics and 3D Genome Structure of Zebrafish

- We performed a variety of next-generation sequencing-based assays (RNA-seq, ATAC-seq, ChIP-seq, bisulfite sequencing, and Hi-C) on several adult and embryonic zebrafish (*Danio rerio*) tissues in an effort to functionally annotate its genome via transcriptomes, map of cis-regulatory elements, heterochromatin, methylome, 3D genomic structure and evolutionary analyses.
- Role: Served as supporting computational analyzer, original main analyser (graduated before project completion).

Utilizing Supervised Machine Learning to Identify Biomarkers in Asthma

- In this collaboration with my fellow MD/PhD student at Penn State College of Medicine, we sought to identify the role of circulating microRNAs in the pathogenesis of asthma. Utilizing supervised machine learning (random forest classification), we were able to identify six circulating microRNAs whose levels were highly predictive of having asthma and therefore could serve as viable biomarkers for the disease.
- Role: Applied supervised machine learning.

QUALITY IMPROVEMENT

POCUS in a Primary Care Setting

- Point-of-Care Ultrasound (POCUS) is currently widely utilized at the Emergency Room setting to obtain clinical imaging in a quick and safe (no radiation) manner. Together with a co-resident, we explored whether a role for POCUS training exists in a primary setting by investigating the types of ultrasound ordered by Primary Care Pediatricians.
- Role: Served as analyst, extracted data and provided analysis

EDUCATION

M.D./Ph.D. Bioinformatics and Genomics

🏛 Penn State College of Medicine   📅 2010-2019   📍 Hershey, PA

- MD completed in Dec 2019
- PhD Thesis: "Identification and Visualization of Regulatory Elements and 3D Genome Structure"
- Doctoral advisor: Feng Yue, PhD

B.Sc. Computer Science & Biological Sciences

🏛 University of Pittsburgh   📅 2006-2009   📍 Pittsburgh, PA

- Graduated *summa cum laude*

CERTIFICATION SKILLS

Epic - Physician Builder Advanced

🏛 Children's Hospital of Philadelphia 📅 2022- 📍 Philadelphia, PA

PEER-REVIEWED PUBLICATIONS

- Yang, H., Luan, Y., Liu, T., Lee, H.J., Fang, L., **Wang, Y.**, ...14 authors...Gerhard, G.S., Hardison, R.C., Wang, T., Cheng, K.C. & Yue, F. A map of cis-regulatory elements and 3D genome structures in zebrafish. <u>Nature</u>. 2020, Dec; 588(7837): 337-343.

- Zhang, J., Lee, D., Dhiman, V., Jiang, P., Xu, J....41 authors...**Wang, Y.**, ...6 authors...Cheng, C., Yue, F., Liu, X.S., White, K.P. & Gerstein, M. An integrative ENCODE resource for cancer genomics. <u>Nature Communications</u>. 2020, Jul; 11(1): 3696.

- **Wang, Y.**, Song, F., Zhang, B., Zhang, L., Xu, J., Kuang, D., Li, D., Choudhary M.N.K., Li, Y., Hu, M., Hardison, R., Wang, T., & Yue, F. The 3D Genome Browser: a web-based browser for visualizing 3D genome organization and long-range chromatin interactions. <u>Genome Biology</u>. 2018, Oct; 19(1): 151.

- Dixon, J.R., Xu, J., Dileep, V., Zhan, Y., Song, F....4 authors...**Wang, Y.**, ...22 authors...Ay, F., Noble, W.S., Dekker, J., Gilbert, D.M., & Yue, F. Integrative detection and analysis of structural variation in cancer genomes. <u>Nature Genetics</u>. 2018, Oct; 50(10): 1388-1398.

- Panganiban, R.P., **Wang, Y.**, Howrylak, J., Chinchilli, V.M., Craig, T.J., August, A., & Ishmael, F.T. Circulating MicroRNAs as Biomarkers in Allergic Rhinitis and Asthma. <u>Journal of Allergy and Clinical Immunology</u>. 2016, Mar; 137(5): 1423-32.

- Perez-Andreu, V., Roberts, K.G., Xu, H., Smith, C., Zhang, H., Yang, W., . . . 20 authors. . . Yue, F., **Wang, Y.**, Pui, C.H., Jeha, S., Relling, M.V., Evans, W.E., Gerhard, D.S., Loh, M.L., Willman, C.L., Hunger, S.P., Mullighan, C.G., & Yang, J.J. A genome-wide association study of susceptibility to acute lymphoblastic leukemia in adolescents and young adults. <u>Blood</u>. 2015, Jan; 125(4): 680-6.

- Pope, B.D., Ryba, T., Dileep, V., Yue, F., Wu, W., Denas, O., Vera, D.L., **Wang, Y.**, ...6 authors... Snyder, M., Stamatoyannopoulos, J.A., Taylor, J., Hardison, R.C., Kahveci, T., Ren B., & Gilbert, D.M. Topologically-associating domains are stable units of replication-timing regulation. <u>Nature</u>. 2014, Nov; 515(7527): 402-5.

- Yue, F., Cheng, Y., Breschi, A., Vierstra, J., Wu, W., Ryba, T., Sandstrom, R., Ma, Z., Davis, C., Pope, B.D., Shen, Y., ...103 authors. . ., **Wang, Y.**, . . . 20 authors. . . Gilbert, D.M., Hardison, R.C., Beer, A.M., Ren., B. A comparative encyclopedia of DNA elements in the mouse genome. <u>Nature</u>. 2014, Nov; 515(7527): 355-64.

- Ananda, G., Hile, S.E., Breski, A., **Wang, Y.**, Kelkar, Y., Makova, K.D., & Eckert, K.A. Microsatellite Interruptions Stabilize Primate Genomes and Exist as Population-Specific Single Nucleotide Polymorphisms within Individual Human Genomes. <u>PLoS Genetics</u>. 2014 Jul 17;10(7):e1004498.

- Kuppuswamy, U., Ananthasubramanian, S., **Wang, Y.**, Balakrishnan, N., & Ganapathiraju, M.K. Predicting gene ontology annotations of orphan GWAS genes using protein-protein interactions. <u>Algorithms for Molecular Biology</u>. 2014, 9(1):10.

CONFERENCES AND ABSTRACTS

- **Wang, Y.**, Zhang, B., Zhang, L., Wang, T. & Yue, F. Visualizing three-dimensional organization and long-range interactions of the mammalian genome with the 3D Genome Browser. <u>Oral Presentation</u>. RECOMB/ISCB RSG DREAM Conference 2015, Philadelphia, PA, USA.

- **Wang, Y.**, Zhang, B., Zhang, L., Wang, T. & Yue, F. Visualizing three-dimensional organization and long-range interactions of the mammalian genome with the 3D Genome Browser. <u>Poster Presentation</u>. ISMB/ECCB 2015, Dublin, Ireland.

- **Wang, Y.** & Yue, F. ENCODE element browser and the 3D genome browser. <u>Oral Presentation</u>. ENCODE 2015: Research Applications and Users Meeting, Potomac, MD, USA.

SKILLS

UNIX Environment	**CSS**	**Perl**	**C++**
LAMP Stack	**JavaScript/JQuery**	**Java**	**LaTeX**
HTML5	**Python/Matplotlib**	**C**	**R**