BIOGRAPHICAL SKETCH

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NAME: Wang, Jinlian

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Research assistant professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE (if applicable)	END DATE MM/YYYY	FIELD OF STUDY
Beijing Univeristy of Technology, Beijing, Beijing	PHD	07/2008	Artificial intelligence

A. Personal Statement

I would like to provide a concise overview of my background and qualifications as a Ph.D with a research focus on the Artificial Intelligence (AI) and Bioinformatics. Through my academic journey and research experiences, I have developed a deep understanding of these fields and their potential to revolutionize biomedical research and healthcare.

From an early stage in my studies, I was captivated by the power of AI and its ability to process vast amounts of cancer gene expression data and derive meaningful insights. Simultaneously, I recognized the enormous potential of applying AI techniques to the vast amounts of biological data generated in the field of bioinformatics. This realization sparked my passion to bridge the gap between these disciplines and explore innovative solutions to complex biological problems.

During my Master's and PhD's studies, I actively sought opportunities to deepen my knowledge in both AI and bioinformatics. I immersed myself in coursework that encompassed machine learning, data mining, algorithms, genomics, and computational biology. Through hands-on projects and research collaborations, I gained valuable experience in applying AI methodologies to analyze and interpret biological data accommodated from genomics, transcriptomics and proteomics to pathway and network.

One significant research project involved developing a novel machine learning algorithm to predict biomarkers from large amount of cancer patient metabolic profile patterns, contributing to the field of liver cancer biomarker discovery . This experience honed my skills in feature selection, model optimization, and algorithm design. I also collaborated with a multidisciplinary team of biologists, statisticians, and computer scientists, fostering my ability to communicate across disciplines and work towards a common goal.

As I progressed in my academic journey, I realized the immense potential of AI and bioinformatics in addressing critical challenges in personalized medicine, drug discovery, and precision healthcare. My research interests have expanded to include leveraging AI techniques to uncover patterns in genomic data, identify disease biomarkers, and develop computational models for personalized medicine. I focused on rare disease and cancer genomic variants knowledge base research and implementation and provides retrieve, search functions both public and internally. Also I built the O-GlcNAcylated sites in protein databases OG proteins knowledge base.

Through my Ph.D. research, I aspire to develop innovative AI-based approaches that improve our understanding of complex biological systems and lead to actionable insights in precision medicine. By integrating AI algorithms with bioinformatics tools, I aim to unlock the potential of vast datasets, such as genomic sequences, gene expression profiles, and clinical data, to uncover hidden patterns and biomarkers that can revolutionize disease diagnosis and treatment.

I am excited about the opportunity to join UThealth Houston School of Biomedical Informatics and collaborate with esteemed faculty and researchers who share my research interests. The interdisciplinary environment, cutting-edge facilities, and collaborative culture present at UThealth Houston School of Biomedical Informatics are ideal for nurturing my ambitions and fostering innovative research.

In conclusion, my journey as a Ph.D specializing in Artificial Intelligence and Bioinformatics has equipped me with a solid foundation in both disciplines. I am committed to advancing our understanding of complex biological systems and improving healthcare outcomes through the application of AI techniques. I am confident that my skills, dedication, and enthusiasm make me an excellent fit for the research community at UThealth Houston School of Biomedical Informatics.

1. Qiao W, Wang J, Pullman BS, Chen R, Yang Y, Scott SA. The CYP2D6 VCF Translator. Pharmacogenomics J. 2017 Jul;17(4):301-303. PubMed Central PMCID: PMC5025353.

2. Wang J, Liao J, Zhang J, Cheng WY, Hakenberg J, Ma M, Webb BD, Ramasamudram-Chakravarthi R, Karger L, Mehta L, Kornreich R, Diaz GA, Li S, Edelmann L, Chen R. ClinLabGeneticist: a tool for clinical management of genetic variants from whole exome sequencing in clinical genetic laboratories. Genome Med. 2015 Jul 29;7:77. PubMed Central PMCID: PMC4558641.

3. Wang J, Zuo Y, Man YG, Avital I, Stojadinovic A, Liu M, Yang X, Varghese RS, Tadesse MG, Ressom HW. Pathway and network approaches for identification of cancer signature markers from omics data. J Cancer. 2015;6(1):54-65. PubMed Central PMCID: PMC4278915.

4. Wang J, Zuo Y, Liu L, Man Y, Tadesse MG, Ressom HW. Identification of functional modules by integration of multiple data sources using a Bayesian network classifier. Circ Cardiovasc Genet. 2014 Apr;7(2):206-17. PubMed Central PMCID: PMC4079061.

B. Positions, Scientific Appointments and Honors

Positions and Scientific Appointments

2023 - 2023	Research assistant professor, UThealth Houston School of Biomedical Informatics, Houston, TX
2017 - 2023	Senior bioinformatician/Manager, GeneDX, Stamford, CT
2014 - 2017	Bioinformatiican, Mount Sinai Department of Genomics and Genetic Science , New York, NY
2013 - 2014	Senior bioinformatician, City University of New York, Hunter College, New York, NY
2009 - 2013	Postdoc, Georgetown University, Washington DC, DC

C. Contribution to Science

1. As a cancer bioinformatician, I have made significant contributions to the field through my expertise in bioinformatics and data analysis. During the time when I was employed in GeneDX, I have contributed to the system analysis, design and development of novel computational tools specifically tailored for cancer genomics analysis including Vonc, VISta and VarSleuth. These tools integrate diverse omics data, such as genomic, transcriptomic, and expert knowledge base as well literature data, to identify genetic alterations, functional pathways, and potential therapeutic targets in cancer. These tools have been widely adopted daily by the GeneDX a

   a. Qiao W, Wang J, Pullman BS, Chen R, Yang Y, Scott SA. The CYP2D6 VCF Translator. Pharmacogenomics J. 2017 Jul;17(4):301-303. PubMed Central PMCID: PMC5025353.

   b. Wang J, Liao J, Zhang J, Cheng WY, Hakenberg J, Ma M, Webb BD, Ramasamudram-Chakravarthi R, Karger L, Mehta L, Kornreich R, Diaz GA, Li S, Edelmann L, Chen R. ClinLabGeneticist: a tool for clinical management of genetic variants from whole exome sequencing in clinical genetic laboratories. Genome Med. 2015 Jul 29;7:77. PubMed Central PMCID: PMC4558641.

c. Wang J, Zhang Y, Marian C, Ressom HW. Identification of aberrant pathways and network activities from high-throughput data. Brief Bioinform. 2012 Jul;13(4):406-19. PubMed Central PMCID: PMC3404398.

2. Integration of Multi-Omics Data: I have pioneered the integration of multi-omics data, including genomics, transcriptomics, proteomics, and clinical data, to provide a comprehensive view of cancer biology. By combining these diverse datasets, I have identified molecular subtypes, biomarkers, and signatures associated with cancer progression, prognosis, and response to therapy. This integrative approach has enabled a deeper understanding of the complex molecular mechanisms underlying cancer and has potential implications for precision medicine.

   a. Wang J, Zuo Y, Liu L, Man Y, Tadesse MG, Ressom HW. Identification of functional modules by integration of multiple data sources using a Bayesian network classifier. Circ Cardiovasc Genet. 2014 Apr;7(2):206-17. PubMed Central PMCID: PMC4079061.

   b. Wang J, Zhang Y, Marian C, Ressom HW. Identification of aberrant pathways and network activities from high-throughput data. Brief Bioinform. 2012 Jul;13(4):406-19. PubMed Central PMCID: PMC3404398.

3. Analysis of Large-Scale Cancer Genomics Data: I have played a key role in analyzing large-scale cancer genomics datasets, such as The Cancer Genome Atlas (TCGA) and International Cancer Genome Consortium (ICGC) projects. Through rigorous data mining, I have identified recurrent genetic alterations, driver mutations, and genomic rearrangements across different cancer types. My analyses have provided valuable insights into the landscape of genomic alterations in cancer and have helped identify potential therapeutic targets.

4. Development of Predictive Models and Biomarkers: Using machine learning and statistical modeling approaches, I have developed predictive models and biomarkers for cancer diagnosis, prognosis, and treatment response. By leveraging large-scale omics datasets and clinical information, I have identified molecular features that can accurately classify cancer subtypes, predict patient outcomes, and guide treatment decisions. These models and biomarkers hold

   a. Wang J, Zuo Y, Liu L, Man Y, Tadesse MG, Ressom HW. Identification of functional modules by integration of multiple data sources using a Bayesian network classifier. Circ Cardiovasc Genet. 2014 Apr;7(2):206-17. PubMed Central PMCID: PMC4079061.

   b. Xiao JF, Varghese RS, Zhou B, Nezami Ranjbar MR, Zhao Y, Tsai TH, Di Poto C, Wang J, Goerlitz D, Luo Y, Cheema AK, Sarhan N, Soliman H, Tadesse MG, Ziada DH, Ressom HW. LC-MS based serum metabolomics for identification of hepatocellular carcinoma biomarkers in Egyptian cohort. J Proteome Res. 2012 Dec 7;11(12):5914-23. PubMed Central PMCID: PMC3719870.

5. Collaborative Research and Data Sharing: I have actively collaborated with clinicians, biologists, and fellow bioinformaticians to facilitate interdisciplinary research and promote data sharing. By fostering collaborations, I have contributed to the translation of bioinformatics findings into clinically relevant applications. I have also been involved in initiatives aimed at enhancing data accessibility and standardization, ensuring that the broader scientific communi

   a. Chen E, Wang J. CNA Explorer and anaLyzer (CNAEL): an interactive web application and standard operating procedure enabling efficient clinical review and reporting of complex NGS-derived tumor copy number profiles. Bioinformatics. Forthcoming.

   b. Bin J, Wang J, Man Y. Differential lymphatic involvement in primary site of node positive and negative colorectal cancer. New Approaches combating Cancer & Aging. 2014; 1(1):29-45.