

Jacqueline Chyr, Ph.D.

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I am an enthusiastic data scientist who is seeking a career at the Cancer Genomics Research Laboratory. I have 12 years of training in both wet labs and dry labs, with expertise in Cancer Biology, Genetics, Bioinformatics, and Computational Biology. I have years of experience managing lab members, attaining grants for NIH-funded research projects, and collaborating with multidisciplinary fields. I believe my educational background, work experience, and interpersonal skills will make me a great asset to your team.

Dry Lab Skills: Machine learning, deep learning, computational biology, bioinformatics, data analysis, genetics and genomics, next generation sequencing analysis, GWAS, mathematics, statistics, and systems biology.

Wet Lab Skills: DNA mutagenesis, RT-PCR, DNA/RNA sequencing, methylation profiling, cell culture, etc.

Languages: R (highly proficient), Python (proficient), SQL, MATLAB, TensorFlow, Java, and more.

EDUCATION

Doctor of Philosophy in Cancer Biology, Wake Forest School of Medicine

Aug 2013 – May 2020

Dissertation: Bioinformatics Analysis and Computational Biology Modeling of Genetic and Epigenetic Elements Dictating Chromatin Organization, Transcription Regulation, and Disease State in Cancer Genomes.

Bachelor of Science in Microbiology and Immunology, University of Miami

Aug 2010 – Dec 2012

Chemistry Minor, Graduated Magna Cum Laude, Honors, Dean's list every semester

WORK AND RESEARCH EXPERIENCE

Assistant Professor – Center for Computational Systems Medicine

Mar 2021 – Present

University of Texas Health Science Center, Houston, TX

Skills: AI models, personalized medicine, systems biology, bioinformatics, computational biology

- Developing pipelines to identify cancer neoantigens (cancer neopeptides arising from somatic mutations or fusion genes and are presented on HLA molecules).
- Modeling tumor evolution, immunogenicity, and immunotherapy efficacy in cancer patients.
- Developing drug repositioning tools to repurpose drugs for AD/ADRD.
- Designing AI tools to develop individualized dietary and behavioral interventions for Nutrition for Precision Health.
- Managing multiple NIH-funded research teams, research projects, databases, and pipelines.
- Fostering collaborations between UTHHealth Schools of Public Health, Dentistry, and Biomedical Informatics.
- Organizing and managing weekly and monthly seminars, progress report meetings, and project discussions.
- Mentoring research assistants, graduate students, and postdoctoral fellows.
- Promoting strong communication between lab members, our institute, and the broader biomedical community.

Ongoing Funding:

- NIH R01CA241930 PI: Zhou, X. 08/01/19-07/31/24
Multiscale Resolution and Deep Network Approaches for Deconvolving Different Cell Types in Bulk Tumor using Single-cell Sequencing Data (scDEC)
Role: co-investigator
- NIH R01GM123037 PI: Zhou, X. 09/01/17-07/31/22
Integrative approach to studying LncRNA functions
Role: co-investigator

WORK AND RESEARCH EXPERIENCE (continued)

Postdoctoral Research Fellow – School of Biomedical Informatics

May 2020 – Feb 2021

University of Texas Health Science Center, Houston, TX

Skills: Machine learning, deep learning, bioinformatics, computational biology, R, Python

- Identified miRNA-gene interactions using Weighted Gene Coexpression Network Analysis.
- Developed predTAD, a machine learning model to predict 3D chromatin organization alterations in breast cancer.
- Predicted knee osteoarthritis progression using Attention-Long Short-Term Memory.
- Functional analysis of alternative splicing on survival prognosis of triple-negative breast cancer.

Ph.D. Research Assistant – Center for Bioinformatics and Systems Biology

Aug 2013 – May 2020

Wake Forest University School of Medicine, Winston-Salem, NC

Skills: R, data analysis, cancer biology, genetics, bioinformatics, computational biology, machine learning, survival analysis

- Developed immune-based cascade propagation approach to stratify head & neck squamous cell carcinoma patients.
- Developed a new bioinformatics approach in studying associations between genetic variants and gene expression.
- Computationally modeled enhancer-promoter interactions using deep learning models.
- Modeled alterations in chromatin organization in cancer genomes using genetic and epigenetic elements.
- Genome-wide association studies (GWAS) in breast cancer, Alzheimer's disease, and knee osteoarthritis.
- Additional data analysis – differential gene expression, progression-free survival curves, biostatistical analysis, etc.

Undergraduate Research Assistant – Microbiology and Immunology

Aug 2012 – Dec 2012

Univ. of Miami's Miller Medical Campus, Miami, FL

Skills: Flow cytometry, ELISA, clinical study

- Studied the effects of aging on B cells immune response against influenza vaccine.
- Established biomarkers that predict vaccine effectiveness in elderly individuals.

Summer Research Assistant – Biochemistry and Biophysics

Summer 2012

UNC Chapel Hill, Chapel Hill, NC

Skills: Mutagenesis, DNA manipulation, cloning, electrophoresis

- Characterized Polymerase Q's role in double strand break repair.
- Poster Presentation – 1st Place award (Jul 2012)

Undergraduate Research Assistant – Chemistry

Jan 2011 – May 2012

University of Miami, Coral Gables, FL

Skills: Electrochemistry, fluorescence assays, western blot

- Analyzed poly(vinyl chloride)-based cation-selective electrode selectivity with different molar ratios of ionophores.
- Characterized aequorin's bioluminescence properties by strategically truncating the protein at different locations.

Research Intern – Biochemistry

Aug 2009 – May 2010

St. Thomas University, Miami Gardens, FL

Skills: Zebrafish spinal cord dissection, RT-PCR, neuron cell culture

- Developed novel primary culture system to study zebrafish neuron regeneration after spinal cord injury.

Summer Research Intern - Biochemistry and Molecular Biology

Summer 2009

Univ. of Miami's Miller Medical Campus, Miami, FL

Skills: DNA repair analysis, transfection, mutagenesis

- Genetically altered SynExo protein in *E. coli* to test its efficiency in homologous recombination.

MEDICAL EXPERIENCE

Emergency Room Intern, Aventura Hospital and Medical Center
Pharmacist Assistant, Pharmacy Department, Palmetto General Hospital

2009 – 2010 school years
Summer of 2007 and 2008

PUBLICATIONS

Chyr J, Zhang Z, Chen X, Zhou X. *PredTAD: A machine learning framework that models 3D chromatin organization alterations leading to oncogene dysregulation in breast cancer cell lines*. Comput Struct Biotechnol J. 2021; 19:2870-2880. PMID: 34093993.

Wu S, Wang J, Zhu X, **Chyr J**, Zhou X, Wu X, Huang L. *The Functional Impact of Alternative Splicing on the Survival Prognosis of Triple-Negative Breast Cancer*. Front Genet. 2021; 11:604262. PMID: 33519909.

Wang Y, You L, **Chyr J**, Lan L, Zhao W, Zhou Y, Xu H, Noble P, Zhou X. *Causal Discovery in Radiographic Markers of Knee Osteoarthritis and Prediction for Knee Osteoarthritis Severity with Attention-Long Short-Term Memory*. Front Public Health. 2020; 8:604654. PMID: 33409263.

Li Z, **Chyr J**, Jia Z, Wang L, Hu X, Wu X, Song C. *Identification of Hub Genes Associated with Hypertension and their Interaction with miRNA Based on Weighted Gene Coexpression Network Analysis (WGCNA) Analysis*. Med Sci Monit. 2020; 26:e923514. PMID: 32888289.

Peak TC, Panigrahi GK, Praharaj PP, Su Y, Shi L, **Chyr J**, Rivera-Chávez J, Flores-Bocanegra L, Singh R, Vander Griend DJ, Oberlies NH, Kerr BA, Hemal A, Bitting RL, Deep G. *Syntaxin 6 - mediated exosome secretion regulates enzalutamide resistance in prostate cancer*. Mol Carcinog. 2019; 59(1):62-72. PMID: 31674708.

Peak TC, Su Y, Chapple AG, **Chyr J**, Deep G. *Syntaxin 6: A novel predictive and prognostic biomarker in papillary renal cell carcinoma*. Sci Rep. 2019; 9(1):3146. PMID: 30816681.

Liu C, **Chyr J**, Zhao W, Xu Y, Ji Z, Tan H, Soto C, Zhou X. *Genome-Wide Association and Mechanistic Studies Indicate That Immune Response Contributes to Alzheimer's Disease Development*. Front Genet. 2018. 9:410. PMID: 30319691.

Chyr J, Guo D, Zhou X. *LSCC SNP variant regulates SOX2 modulation of VDAC3*. Oncotarget. 2018. 9(32):22340-52. PMID: 29854282.

Liu K., **Chyr J**, Zhao W, Zhou X. *Immune signaling-based Cascade Propagation approach re-stratifies HNSCC patients*. Methods. 2016; 111:72-9. PMID: 27339942.