

Jiazhen LIU

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EDUCATION

Columbia University

Master of Public Health in Biostatistics (GPA: 3.97)

New York, NY

May 2024

Coursework: Epidemiology | Public Health Determinants | Applied Biostatistics | Categorical Data Analysis | Survival Analysis | Molecular Epidemiology | Occupational Health | Applied Regression

Boston University

Bachelor of Science in Biomedical Engineering (Cum Laude) (Dean's List)

Boston, MA

May 2022

Coursework: Molecular & Cellular Biology | Biomolecular Architecture | Biomaterial | Nanotechnology | Microbiology | Thermodynamics | System Physiology

Honor & Awards: The Nelson and Vicky Fong Scholarship (Received a \$20,000 scholarship for 4 consecutive years)

RESEARCH EXPERIENCE

Genetic Circuits for Early Cancer Detection

Feb 2020 – May 2022

Research Assistant, Wilson Wong Lab, Boston University

Advisor: Prof. Wilson Wong, Biological Design Center, Boston University

- Led a project focused on engineering genetic circuits to improve synthetic biological signaling in mammalian cells, including complex gene constructs designed for programmable responses to cancer-related signals
- Developed modular DNA constructs and simulated gene circuit behavior on Benchling, incorporating elements like recombinases, synthetic transcription factors, and inducible promoters to test programmable signal pathways
- Designed and optimized primers for various genetic constructs, performing lab techniques such as ligation, Gibson assembly, and restriction digestion to assemble DNA sequences aimed at precise gene activation in response to synthetic inputs
- Employed sequencing validation techniques to confirm construct integrity, ensuring each assembled circuit aligned with the intended modular design for specific activation and repression patterns within mammalian cell
- Integrated synthetic biology tools, such as CRISPR and recombinase-mediated logic gates, to establish complex analog and Boolean processing circuits, creating constructs capable of responding to multiple input signals with distinct outputs
- Contributed to research goals of bridging analog and digital signal processing in living cells, laying groundwork for advanced diagnostic tools by enabling sensitive and specific responses to early cancer biomarkers in cellular environment

Predictive Modeling for Lung Cancer Risk Assessment

June 2023 – May 2024

Columbia University Irving Medical Center

Advisor: Prof. Martina Pavlicova, Mailman School of Public Health, Columbia University Irving Medical Center

- Implemented advanced predictive models based on Lasso regression and Random Forest algorithms to assess lung cancer risk and achieved accuracies of 93.95% and 94.14%, respectively, with an AUC of 0.887 for Random Forest, reflecting strong model performance despite dataset imbalance with caret.
- Enhanced model robustness through meticulous preprocessing of large-scale datasets from 2010–2019 federal censuses and surveys by performing data cleaning, factorization, and downsampling to balance class representation
- Optimized computational efficiency and model performance by leveraging parallel computing with the doParallel package and employing cross-validation strategies, then utilized ROC and AUC metrics to rigorously evaluate and improve model sensitivity and specificity
- Identified avenues for model improvement, underscoring the potential impact of enhanced sensitivity on early lung cancer detection and risk assessment

Implementation of Machine Learning Models for COVID-19 Severity Risk Prediction

Sept 2023 – May 2024

Columbia University Irving Medical Center

- Implemented and evaluated multiple predictive models including General Linear Models, Penalized Logistic Regression, Classification Trees, Random Forest, and Gradient Boosting Machine (GBM), to assess COVID-19 severity risk, focusing on key predictors like vaccination status, blood pressure, and age ()
- Optimized model performance through rigorous hyperparameter tuning using grid searches for parameters (e.g., lambda and alpha in PLR, complexity parameter for trees, and interaction depth for GBM), implemented 10-fold cross-validation and enhanced computational efficiency through parallel processing
- with the GBM model, which attained an AUC of that effectively distinguished between severe and non-severe cases
- Conducted comprehensive variable importance analysis, revealing vaccination status as the most influential predictor, followed by systolic blood pressure (SBP) and age, guiding insights into demographic and health factors that contribute to COVID-19 severity risk

Complete Workflow Analysis System for RNA-seq Data

May 2023 – Sept 2023

Bioinformatics Associate, National Laboratory of Protein and Peptide Drugs, Chinese Academy of Science

- Pioneered the design and implementation of a comprehensive RNA-seq data analysis workflow to investigate potassium ion imbalances in the tumor microenvironment and executed rigorous data quality control and preprocessing, utilizing FastQC for quality assessment, STAR for high-precision sequence alignment against the GRCh38.p14 genome, and featureCounts for

- accurate gene quantification and achieved high Q30 scores and consistency across sample %GC content
- Applied stringent criteria for differential gene expression analysis by integrating q-values and fold changes ($|\log_2(\text{Fold Change})| > 1$ and $q < 0.05$) for rigorous selection, and visualized findings using heat maps, volcano plots, and Pearson correlation matrices
- Developed an intuitive, user-friendly interface, making the workflow accessible to non-programmers and streamlined the analysis process, facilitating the effective application of this robust workflow to future RNA-seq projects.

Cloud-based Framework for Organizing and Analysis of fNIRS Datasets

Sept 2021 – May 2022

Advisor: Prof. David Boas, Department of Biomedical Engineering, Boston University

- Engineered a cloud-based framework to convert functional Near-Infrared Spectroscopy (fNIRS) data from SNIRF (Shared Near-Infrared Spectroscopy Format) to BIDS (Brain Imaging Data Structure) format and facilitated standardized data storage and sharing, enabling seamless cross-laboratory collaboration in brain imaging research
- Developed a robust dataset validator to check SNIRF files for completeness, standardize metadata with BIDS, and streamline data organization, improving accessibility for researchers without programming experience
- Created an advanced quality check module that assesses datasets based on metrics such as motion artifacts and connection quality and provides real-time feedback on data reliability and generated comprehensive quality reports to enhance data integrity
- Collaborated with Boston University's Software & Application Innovation Lab (SAIL) to design a user-friendly interface using Figma, ensuring fNIRS datasets are readily usable for researchers, reinforcing data sharing and reproducibility within the neuroscience community

WORK EXPERIENCE

Teaching Assistant, BE755: Molecular System and Synthetic Biology Lab

Jan 2022 – May 2022

Instructor: Wilson Wong, College of Engineering, Boston University

- Led instructional sessions on molecular techniques, including transfection, RNA purification, cDNA synthesis, and rt-PCR, equipping students with hands-on experience in critical steps of synthetic biology experimentation
- Designed and authored detailed lab protocols for procedures such as HEK293FT transfection, RNA purification, and cDNA synthesis, ensuring high standards for sterile technique and accuracy in experimental workflows
- Developed and assembled materials for each lab, including quality control setups and step-by-step guides, enhancing students' understanding of complex techniques like plasmid transfections and gene expression validation
- Monitored and validated student lab work, identifying areas needing additional guidance and troubleshooting experimental issues to ensure rigorous and consistent results in synthetic biology applications

Front-end Developer, Department of Analytical Instruments, Autobio Diagnostics

Jul 2020 – Sept 2021

- Developed the front-end interface for a microbial database used in antibiotic susceptibility testing, employing HTML5, JavaScript, and Vue CLI to create a responsive, user-friendly search platform
- Implemented dynamic features, including real-time search and filtering functions, to streamline data retrieval for over 12,000 microorganisms, improving efficiency for diagnostic use
- Worked with database management protocols to translate and populate microbial data, ensuring accuracy and completeness in the representation of antibiotic susceptibility profiles
- Enhanced user experience by designing intuitive navigation and data visualization elements, advancing the functionality of diagnostic tools for clinical environments

PUBLICATION

- Li, Guilin, **Jiazhen Liu**, Zhenzhen Guan, Sujuan Wang, Songrui Li, Yanna Dong, et al. "CHO-S Expression of a Novel Human Recombinant IgG1 of Anti-ALD Antibody Isolated by Phage Mutation Display." [Preprint]

SKILLS

Synthetic/ Molecular Biology: ELISA | rt-PCR | Plasmid Ligation | Primer Design | Gel Extraction | qPCR | Transfection | Protein Extraction | CRISPR | Flow Cytometry | Western Blot | Synthetic Biology Platforms: Benchling, SnapGene

Data Analysis: Python (pandas, scikit-learn, NumPy, Pytorch, TensorFlow, OpenCV) | R (caret, ggplot2, survival, DEseq2) | SAS | SQL | Machine Learning Techniques: Penalized Logistic Regression, Random Forest, Gradient Boosting, K-Means Clustering | Statistical Analysis: Survival Analysis, PCA, Risk Analysis

Web Development: JavaScript | HTML5 | Vue CLI | Front-End Frameworks: Bootstrap, Vue.js | Data Visualization: D3.js, Plotly

Graphics: Adobe Premiere (Pr) | Adobe Photoshop (Ps) | Adobe Illustrator (Ai) | Adobe Aftereffect (Ae) | DaVinci Resolve

Language Abilities: Chinese (Native), English (Fluent), Japanese (Elementary)