Yujie (Jeffrey) Jiang

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Education

Rice University   **Houston, TX**
Ph.D. in Statistics, GPA: 3.92/4.0   *Aug 2018 – Present*
- American Statistical Association (ASA) Student Paper Award (2021)
- Ken Kennedy Institute Computational Science and Engineering Fellowship (2018)
- Advisor: Dr. Wenyi Wang

Wake Forest University   **Winston-Salem, NC**
B.S. in Computer Science and B.S in Mathematical Statistics, with honor   *Aug 2014 – May 2018*
- Graduation Honor: Magna Cum Laude
- Advisors: Dr. Robert Plemmons & Dr. Grey Ballard
- Atlantic Coast Conference Inter-Institutional Academic Collaborative (ACCIAC) Fellowship (2017)
- Pi Mu Epsilon honorary society & Upsilon Pi Epsilon honorary society (2017)
- Wake Forest Research Fellowship (2016)
- Honorable Mention of Mathematical Contest in Modeling (2016)
- Dean's List every semester

Professional Skills

Languages: Python, R, MATLAB, C/C++, SQL, JAVA, LaTeX, JavaScript, HTML

Software: Git, Vim, Ubuntu

Reseach Interest: Computational Cancer Biology, Tensor Decomposition, Multivariate Analysis, Machine Learning

Professional Experience

Quantlab Financial, LLC   **Houston, TX**
Quantitative Research Intern   *June 2020 – August 2020*
- Built core functions which extract insights from trading records with proprietary programming language.
- Implemented machine learning models in alpha research utilizing large data sets.
- Performed exploratory research on pairs trade, model development, and back-testing of strategies.

Wake Forest Demon Deacons Women's Basketball   **Winston-Salem, NC**
Basketball Statistical Analyst   *2016 – 2017*
- Implemented a scraper for team and player data on *NCAA.com*, constructed data analysis and calculated advanced metrics.
- Assisted in developing data strategy and supporting in-game analysis as well as player development.
- Restructured and maintained the statistical database for the team.
- Developed a scouting report to help game preparation and presented statistical analysis before each game.

Research Experience

Statistical Bioinformatics Lab, University of Texas MD Anderson Cancer Center   **Houston, TX**
Research Assistant   *2020 – present*
- Developing and applying computational methods to study the evolution of the human genome as well as the cancer genome.
- Proposing new methodologies and corresponding algorithms for large-scale complex data analysis on subclonal reconstruction.
- Advancing methodology ideas and efficient software that accurately analyze high-throughput genomic data.

Genevera Allen's Statistical Learning Group, Rice University   **Houston, TX**
Research Assistant   *2018 – 2019*
- Developed a new extension of the decomposition model that is specifically focused on modeling semi-symmetric tensors, and have them implemented to MRI & neuroimaging studies.

Ballard Research Group on Tensor Analysis, Wake Forest University   **Winston-Salem, NC**
Research Assistant   *2016 – 2018*
- Performed exploratory research on high-performance tensor computations and gave weekly presentations which specifically focused on low-rank approximation related topics.
- Developed new, efficient algorithms for dense canonical polyadic tensor decomposition, and implemented the codes in both C

and MATLAB.

Department of Mathematics & Statistics, Wake Forest University **Winston-Salem, NC**
Independent Researcher *2016 Summer*
- Studied propagation of values in recursive binary sequences in the context of feedback shift registers and generalizations of Schur's Theorem.
- Investigated latest discoveries and conjectures on convergence (and periodicities) of sequences in terms of number-theoretic properties of elements in underlying delay sets.
- Coded an efficient algorithm in C++, with parallel acceleration to boost the speed of generating and testing new conjectures.

Other Projects

Tensor Analysis: Supervised Tensor Decomposition for Semi-symmetric Tensors *2019 Summer*
- Explored the underlying relationship among PCA, CCA, and PLS, especially on high order spaces.
- Proposed general optimization formulation that expresses both tensor CCA and tensor PLS methods.
- Present one algorithm for tensor CCA and two algorithms for tensor PLS that are better suited for modeling semi-symmetric tensors in real-world problems.

Web Development: Bike Sharing at Wake Forest University *2017 Spring*
- Collaborated with group members to developed a full-stack web service for the university's Bike Sharing program, and aimed to change the current Google-Form-based system.
- Coded in JavaScript, HTML, and SQL to build the functionality which includes user registration, database management, and bike reservation & return.
- Developed under Agile test-driven methodologies, and kept regular communication with clients to ensure user requirements were fulfilled.

Publications

[1] A. Maniakas, Y. C. Henderson, H. Hei, S. Peng, Y. Chen, **Jiang, Yujie**, S. Ji, M. Cardenas *et al.*, "Novel anaplastic thyroid cancer pdxs and cell lines: Expanding preclinical models of genetic diversity," *The Journal of Clinical Endocrinology & Metabolism*, 2021.

[2] **Jiang, Yujie**, K. Yu, S. Ji, S. J. Shin, S. Cao, M. D. Montierth, L. Huang, S. Kopetz, P. Msaouel, J. R. Wang *et al.*, "CliP: subclonal architecture reconstruction of cancer cells in dna sequencing data using a penalized likelihood model," *bioRxiv*, 2021.

[3] K. Hayashi, G. Ballard, **Jiang, Yujie**, and M. J. Tobia, "Shared-memory parallelization of MTTKRP for dense tensors," in *Proceedings of the 23rd ACM SIGPLAN Symposium on Principles and Practice of Parallel Programming*, 2018, pp. 393–394.

[4] **Yujie Jiang** and R. Plemmons, "Blind hyperspectral unmixing through low-rank matrix and tensor approximation," *Submitted as the honor thesis to the Department of Mathematics & Statistics, Wake Forest University*, 2018.

Poster Presentations

- Tracking cancer evolution with whole-genome and whole-exome sequencing using reconstructed subclonal architecture, 26th International Conference on Research in Computational Molecular Biology (RECOMB), 2022
- CliP: A model-based method for subclonal architecture reconstruction using regularized maximum likelihood estimation, 25th International Conference on Research in Computational Molecular Biology (RECOMB), 2021
- CliP: A model-based method for subclonal architecture reconstruction using regularized maximum likelihood estimation, Joint Statistical Meeting (JSM), 2021
- CliP: A model-based method for subclonal architecture reconstruction using regularized maximum likelihood estimation, American Association for Cancer Research (AACR) Virtual Special Conference, 2020
- CliP: A model-based method for subclonal architecture reconstruction using regularized maximum likelihood estimation, American Society of Human Genetics (ASHG) Annual Meeting, 2020
- Algorithmic Optimization for Dense Tensor Decomposition, Wake Forest Undergraduate Research Day, 2017
- Binary Sequences with Structural Delays, Wake Forest Undergraduate Research Day, 2016
- Binary Sequences with Structural Delays, Mathematical Association of America MathFest Annual Conference, 2016

Extracurricular Activities

Second Violin, Wake Forest University Orchestra *2015 – 2017, Winston-Salem, NC*
- Rehearsed 4 hours every week and held two performances every semester.