Zongliang Yue, Ph.D.

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Summary

Motives: My past research focuses on biological data mining, systems biology, network biology, artificial intelligence, visual analytics and translational informatics to improve human health. I've constructed several webservers and applications for functional genomics downstream analysis and drug repositioning. My current research involves characterizing driver genes and underlying molecular mechanisms using multi-omics data and single-cell data.

Experience ———	
Mar 2023 - Now	HORP, Harrison College of Pharmacy, Auburn University, UAB, AL, US Assistant Research Professor
Dec 2020 - Feb 2023	AI.MED Lab, Informatics Institute in School of Medicine, UAB, AL, US Postdoc employee. Advisor: Jake Chen, PhD
Jun 2016 - Oct 2020	AI.MED Lab, Informatics Institute in School of Medicine, UAB, AL, US Research Assistant. Ph.D. thesis advisor: Jake Chen, PhD
Jun 2015 - Aug 2015	Bioinformatics department, Covance, Greenfield, IN, US Intern. Advisor: Walter Jessen, PhD
Jan 2014 - Jun 2016	AI.MED Lab, School of Informatics & Computing, Indiana University, IN, US Research Assistant. MS thesis advisor: Jake Chen, PhD
Nov 2012 - Dec 2013	Bioinformatics department, Capital Normal University, China Project leader
Apr 2011 - Jan 2012	ZMBP Plant Biochemistry, Tübingen University, Germany Exchange student, Bachelor's thesis advisor: Frédéric Brunner, PhD
Oct 2010 - Apr 2011	Bioinformatics department, Capital Normal University, China Project leader
Education ———	
Jun. 2016 - Oct. 2020	The University of Alabama at Birmingham, AL, USA Doctor of Philosophy in Biomedical Science (Genetics, Genomics and Bioinformatics)
Jan. 2014 - Jun. 2016	Indiana University Purdue University in Indianapolis, IN, USA Master's degree in Bioinformatics
Sep. 2008 - Jun. 2013	Capital Normal University, Beijing, China Bachelor' degree in Life Science
	Minor: Bachelor' degree in Computer Application
Academic Service -	
2023 - Now 2022 - Now	Editorial board in <i>JMIR Bioinformatics and Biotechnology</i> Topic editor in <i>Frontiers in Artificial Intelligence</i>
2022 - Now 2020 - Now 2019 - Now	Editorial board in DNA and Cell Biology Reports Session chair in MCBIOS Conference

Society Member

2015 – now International Society for Computational Biology (ISCB)

Member

2014 – now Midsouth Computational Biology & Bioinformatics Society (MCBIOS)

Senior Member

Publication

1. Qi Li, Cody Nichols, Robert S Welner, Jake Y Chen, Wei-Shinn Ku, **Zongliang Yue**. (under review) Toden-E: Topology-Based and Density-Based Ensembled Clustering for the Development of Super-PAG in Functional Genomics using PAG Network and LLM. Bioinformatics. (Impact factor: 4.4)

- 2. **Yue Z**, Zhou L, Huang F, Chen P. (under review) S2Map: An Online Interactive Platform for Signal Analysis in Cell Secretion-Signal Map. Bioinformatics Advances. (Impact factor: 2.4)
- 3. Nikitas Gerolimos, Vasileios Alevizos, Sabrina Edralin, Clark Xu, Akebu Simasiku, Georgios Priniotakis, George A. Papakostas, **Zongliang Yue**. (2024) Systematic Review of Swarm Intelligence for Autonomous Radiotherapy Planning Decision-Making. CICN 2024
- 4. Vasileios Alevizos, Akebu Simasiku, Dimitra Malliarou, Antonis Messinis, Sabrina Edralin, Clark Xu, **Zongliang Yue**, and George A. Papakostas. (2024) Integrating Artificial Open Generative Artificial Intelligence into Software Supply Chain Security, Proc. of the 5th International Conference on Data Analytics for Business and Industry (ICDABI).
- 5. Vasileios Alevizos, Sabrina Edralin, Akebu Simasiku, Dimitra Malliarou, Antonis Messinis, George A. Papakostas, Clark Xu, and **Zongliang Yue**, (2024) Handwriting Anomalies and Learning Disabilities through Recurrent Neural Networks and Geometric Pattern Analysis, ICECCE
- 6. **Yue Z**, McCormick NP, Ezeala OM, Durham SH, Westrick SC. (2024) EMSIG: Uncovering Factors Influencing COVID-19 Vaccination Across Different Subgroups Charactered by Embedding-based Spatial Information Gain Vaccines. (Impact factor: 5.2)
- 7. **Yue Z**, Jaradat S, Qian J. (2024) Prediction of cognitive impairment among Medicare beneficiaries using a machine learning approach. Arch Gerontol Geriatr. doi: 10.1016/j.archger.2024.105623. Epub ahead of print. PMID: 39260118. (Impact factor: 3.5)
- 8. Kang X, Mita N, Zhou L, Wu S, **Yue Z**, Babu RJ, Chen P. (2024) Nanotechnology in Advancing Chimeric Antigen Receptor T Cell Therapy for Cancer Treatment. Pharmaceutics. doi: 10.3390/pharmaceutics16091228. PMID: 39339264; PMCID: PMC11435308. (Impact factor: 4.9)
- 9. **Yue Z**, Xue X, Qian J. (2024) The association between polypharmacy and health-related quality of life among older adults with prostate cancer. J Geriatr Oncol. doi: 10.1016/j.jgo.2024.101772. Epub Apr 26. PMID: 38676976. (Impact factor: 3.0)
- 10. Jinquan Chao, Yan Li,Shuguang Yang, Xingming Chen, Yilin He, Jianan Zhang, **Zongliang Yue**, Qiang Gao, Weimin Tian. (2024) Design and application of the HbGBTS80K liquid chip in rubber tree. Tropical Plants. DOI=10.48130/tp-0024-0020
- 11. Huang F, Welner RS, Chen JY, Yue Z. (2024) PAGER-scFGA: unveiling cell functions and molecular mechanisms in cell trajectories through single-cell functional genomics analysis. Front Bioinform. doi: 10.3389/fbinf.2024.1336135. PMID: 38690527; PMCID: PMC11058213. (Impact factor: 2.8)
- 12. Huang F, Xu P, Yue Z, Song Y, Hu K, Zhao X, Gao M, Chong Z. (2024) Body Weight Correlates with Molecular Variances in Patients with Cancer. Cancer Res. Mar 4;84(5):757-770. doi: 10.1158/0008-5472.CAN-23-1463. PMID: 38190709; PMCID: PMC10911806. (Impact factor: 12.5)
- 13. Kang X, Huang Y, Wang H, Jadhav S, **Yue Z**, Tiwari AK, Babu RJ. (2023) Tumor-Associated Macrophage Targeting of Nanomedicines in Cancer Therapy. Pharmaceutics.16(1):61. (Impact factor: 5.4)
- 14. **Zongliang Yue**, Da Yan, Guimu Guo, Jake Chen. (2023) Biological Network Mining. Biostatistics Research. 1(1):31-59. Available from: https://ojs.wiserpub.com/index.php/BSR/article/view/1921

- 15. Thanh Nguyen, **Zongliang Yue**, Radomir Slominski, Robert Welner, Jianyi Zhang, Jake Y. Chen*. (2022) WINNER: a Network Biology Tool for Biomolecular Characterization and Prioritization, Frontiers in Big Data. (Impact factor: 2.4)
- 16. Christian T. Stackhouse, Joshua C Anderson, Zongliang Yue, Thanh Nguyen, Nicholas J Eustace, Lara Ianov, Catherine P. Langford, Jelai Wang, James R Rowland, Chuan Xing, Fady M. Mikhail, Eddy S Yang, Anita Hjelmeland, C. Ryan Miller, Jake Chen, G. Yancey Gillespie, and Christopher D Willey, (2022) A novel in vivo model of Glioblastoma radiation resistance identifies long non-coding RNAs and targetable kinases, JCI Insight. (Impact factor: 9.4)
- 17. Zhenyu Weng[#], **Zongliang Yue**[#], Yuesheng Zhu*, Jake Yue Chen*, (2022) DEMA: a distance-bounded energy-field minimization algorithm to model and layout bio-molecular networks with quantitative features, Bioinformatics. (Impact factor: 6.9)
- 18. **Zongliang Yue**, Radomir Slominski, Samuel Bharti and Jake Y. Chen*, (2022) PAGER Web APP: An interactive, online gene set and network interpretation tool for functional genomics, Front. in Genetics. (Impact factor: 4.2)
- 19. Carlene L. Zindl#, Steven J. Witte#, Vincent A. Laufer#, Min Gao, **Zongliang Yue**, Karen M. Janowski, Baiyi Cai, Blake F. Frey, Daniel J. Silberger, Stacey N. Harbour, Jeffrey R. Singer, Henrietta Turner, Frances E. Lund, Bruce A. Vallance, Alexander F. Rosenberg, Trenton R. Schoeb, Jake Y. Chen, Robin D. Hatton, and Casey T. Weaver, (2022) A nonredundant role for T cell-derived interleukin 22 in antibacterial defense of colonic crypts, Immunity. (Impact factor: 31.7)
- 20. **Zongliang Yue**, Nishant Batra, Hui-Chen Hsu, John Mountz, Jake Y Chen, PAGER-CoV-Run: An online interactive analytical platform for COVID-19 functional genomic downstream analysis. (2021) AMIA
- 21. Thanh M. Nguyen, Samuel Bharti, **Zongliang Yue**, Christopher D. Willey and Jake Y. Chen*, (2021) Statistical Enrichment Analysis of Samples (SEAS): a general-purpose tool to annotate metadata neighborhoods of biological samples, Front. Big Data | doi: 10.3389/fdata.2021.725276
- 22. **Zongliang Yue**, Da Yan, Guimu Guo, and Jake Y. Chen, (2021) Biological Network Mining. In: MUKHTAR S. (eds) Modeling Transcriptional Regulation. Methods in Molecular Biology, vol 2328.
- 23. Sweta B. Patel, Travis Nemkov, Davide Stefanoni, Gloria A. Benavides, Mahmoud A. Bassal, Brittany L. Crown, Victoria R. Matkins, Virginia Camacho, Valeriya Kuznetsova, Ashley T. Hoang, Danielle E. Tenen, Samuel L. Wolock, Jihye Park, Li Ying, **Zongliang Yue**, Jake Y. Chen, Henry Yang, Daniel G. Tenen, Paul Brent Ferrell, Rui Lu, Victor Darley-Usmar, Angelo D'Alessandro, Ravi Bhatia & Robert S. Welner, (2021) Metabolic alterations mediated by STAT3 promotes drug persistence in CML, Leukemia. (Impact factor: 11.5)
- 24. **Zongliang Yue#**, Eric Zhang#, Clark Xu, Sunny Khurana, Nishant Batra, Son Dang, and Jake Y. Chen*, (2021) PAGER-CoV: A Pathway, Annotated-list and Gene-signature Electronic Repository for Coronavirus Diseases Studies, Nucleic Acids Research. (Impact factor: 16.9)
- 25. Christian Stackhouse, James Rowland, Joshua Anderson, Jelai Wang, Thanh Nguyen, **Zongliang Yue**, Jake Chen, Lara Ianov, Yancey Gillespie, Christopher Willey, (2020) CBIO-12. THE ROLES OF IncRNAs IN GBM RADIATION RESISTANCE AND TUMOR RECURRENCE, Neuro-Oncology. (Impact factor: 12.3)
- 26. CD Willey, CT Stackhouse, JR Rowland, CP Langford, JC Anderson, L Ianov, **Z Yue**, T Nguyen, AB Hjelmeland, JY Chen, GY Gillespie, (2020) Multi-omic Exploration of Inherent and Acquired Radiation Resistance of Glioblastoma Patient-Derived Xenografts, International Journal of Radiation Oncology, Biology, Physics.
- 27. Christian Tyler Stackhouse; James R. Rowland; Jelai Wang; Thanh Nguyen; **Zongliang Yue**; Jake Y. Chen; Lara Ianov; G. Yancey Gillespie; Christopher D. Willey, (2020) Long non-coding RNAs in glioblastoma tumor recurrence and therapy resistance, Cancer Res, 80 (16 Supplement): 279.
- 28. Xiaowen Liu#, **Zongliang Yue#**, Yimou Cao#, Lauren Taylor, Qing Zhang, Sung W. Choi, Samir Hanash, Sawa Ito*, Jake Y. Chen*, Huanmei Wu*, and Sophie Paczesny*&, (2019) Graft-Versus-Host Disease–Free Antitumoral Signature After Allogeneic Donor Lymphocyte Injection Identified by Proteomics and Systems Biology, JCO personalized oncology. (Impact factor: 4.8)
- 29. **Zongliang Yue**, Thanh Nguyen, Eric Zhang, Jianyi Zhang, Jake Y Chen, (2019) WIPER: Weighted in-Path Edge Ranking for biomolecular association networks, Quantitative Biology. (Impact factor: 1.8)

- 30. **Zongliang Yue**, Christopher D. Willey, Anita B Hjelmeland, and Jake Y. Chen*, (2019) BEERE: a Web Server for Biomedical Entity Expansion, Ranking, and Explorations. Nucleic Acids Research. (Impact factor: 16.9)
- 31. **Zongliang Yue**, Michael T. Neylon, Thanh Nguyen, Timothy Ratliff, and Jake Y. Chen*, (2018) "Super gene set" causal relationship discovery from functional genomics data, IEEE Transactions on Computational Biology and Bioinformatics. (Impact factor: 3.0)
- 32. **Zongliang Yue**, Qi Zheng, Michael T. Neylon, Minjae Yoo, Jimin Shin, Zhiying Zhao, Aik Choon Tan, and Jake Y. Chen*, (2018) PAGER 2.0: an update to the pathway, annotated-list and gene-signature electronic repository for Human Network Biology. Nucleic Acids Research. (Impact factor: 16.9)
- 33. **Zongliang Yue**, Itika Arora, Eric Y. Zhang, Vincent Laufer, S. Louis Bridges, and Jake Y. Chen§, (2017) Repositioning drugs by targeting network modules: a Parkinson's disease case study, BMC bioinformatics. (Impact factor: 3.1)
- 34. Jake Y. Chen*, **Zongliang Yue**, Michael T. Neylon, Thanh Nguyen, Nafisa Bulsara, Itika Arora, and Timothy Ratliff, (2016) "Towards constructing 'Super Gene Sets' regulatory networks", IEEE International Conference on Bioinformatics and Biomedicine (BIBM).
- 35. Xiaowen Liu*, **Zongliang Yue**, Jeffrey Yu, Etienne Daguindau, Qing Zhang, Yuko Ogata, Philip R. Gafken, Yoshihiro Inamoto, Adam Gracon, David Wilkes, John A. Hansen, Stephanie J. Lee, Jake Y. Chen§, and Sophie Paczesny§, (2016) Proteomic characterization reveals that MMP-3 correlates with bronchiolitis obliterans syndrome following allogeneic hematopoietic cell and lung transplantation, American Journal of Transplantation. (Impact factor: 8.0)
- 36. Hui Huang, Thanh Nguyen, Sara Ibrahim, Sandeep Shantharam, **Zongliang Yue**, and Jake Y. Chen*, (2015) DMAP: a Connectivity Map Database to Enable Identification of Novel Drug Repositioning Candidates, BMC bioinformatics. (Impact factor: 3.1)
- 37. **Zongliang Yue**, Madhura Kshirsagar, Thanh Nguyen, Chayaporn Suphavilai, Michael Neylon, Liugen Zhu, Timothy Ratliff and Jake Y Chen*, (2015) PAGER: constructing PAGs and new PAG–PAG relationships for network biology, Bioinformatics. (Impact factor: 6.9)
- 38. Zongliang Yue, Ping Wan, Zhan Xie, and Jake Y. Chen*, (2014) Computational Identification of Decentric Genetic Regulatory Relationships from Functional Genomic Data, <u>Bioinformatics Research and Applications Lecture Notes in Computer Science</u> Volume 8492, 2014, pp 224-235.
- 39. **Zongliang Yue**, Ping Wan, Zhan Xie, and Jake Y. Chen*, (2014) SLDR: a computational technique to identify novel genetic regulatory relationships, BMC Bioinformatics (best paper) (Impact factor: 3.1)
- 40. Ping Wan*, #, **Zongliang Yue**#, Zhan Xie#, Qiang Gao, Mengyao Yu, Zhiwei Yang, and Jinsong Huang§, (2013) Mechanisms of Radiation Resistance in Deinococcus Radiodurans R1 by the Reconstruction of Gene Regulatory Network Using Bayesian Network Approach, Journal of Proteomics & Bioinformatics (JPB)

indicates the co-first authors.

Grant

05/01/2023-04/30/2024 Zongliang Yue (Co-PI) CCTS/NCAT internal grant

Super-PAGs: Mapping Multi-tier Network Modules to Characterize Genomics Data of Polygenic Diseases

Total direct: \$60,000

Ad-hoc Peer Review Activity

BMC bioinformatics
IEEE/ACM Transactions on Computational Biology and Bioinformatics
Frontiers
Scientific Report
AMIA - American Medical Informatics Association

Conference on Biological Information and Biomedical Engineering Molecular Carcinogenesis

Teaching

2021, 2022 **UAB INFO 603-703 Database course**

Co-instructor

2017, 2018 UAB Special Topic-Biological Data Management

Teaching Assistant

Jan 2015 - Mar 2015 MURI Project (Multidisciplinary Undergraduate Research Initiative)

Co-mentor

Tools and Applications -

1. GBM-TCGA RNA-seq Data Analysis Using Multi-Level GeneTerrain (streamlit application)

- 2. DEMA: a distance-bounded energy-field minimization algorithm to model and layout bio-molecular networks with quantitative features (Java)
- 3. PAGER Web APP: An interactive, online gene set and network interpretation tool for functional genomics (Rshiny application)
- 4. PAGER-CoV-Run: An online interactive analytical platform for COVID-19 functional genomic downstream analysis (streamlit application)
- 5. Statistical Enrichment Analysis of Samples (SEAS): a general-purpose tool to annotate metadata neighborhoods of biological samples (streamlit application)
- 6. PAGER-CoV: A Pathway, Annotated-list and Gene-signature Electronic Repository for Coronavirus Diseases Studies (web server)
- 7. WIPER: Weighted in-path edge ranking for biomolecular association networks (Django application)
- 8. BEERE: a Web Server for Biomedical Entity Expansion, Ranking, and Explorations (web server)
- 9. PAGER 2.0: an update to the pathway, annotated-list and gene-signature electronic repository for Human Network Biology (web server)
- 10. PAGER: constructing PAGs and new PAG-PAG relationships for network biology (web server)
- 11. DMAP: a Connectivity Map Database to Enable Identification of Novel Drug Repositioning Candidates (APEX)

- 2024 ACHE AI Conference Travel Grant (\$300), Auburn University
- 2022 Scientific Excellence Award (\$300), UAB Center for Clinical and Translational Science
- 2022 The third place, the Omics Hackathon, the University of Alabama at Birmingham
- **2021** MCBIOS Interdisciplinary Team Science Award, the AI Against Cancer Data Science Hackathon, the University of Alabama at Birmingham
- 2020 The Second place, the COVID-19 Data Science Hackathon, the University of Alabama at Birmingham
- 2019 Data Blitz Award, the UAB Aging Symposium
- 2019 The 4th place oral presentation, MCBIOS 2019
- 2018 16th MCBIOS Travel Fellowship (\$500)
- The Conference of Multi-Omics QC data workshop Travel Fellowship, Mount Sinai University, NY (\$1000)
- 2017 14th MCBIOS Travel Fellowship (\$500)
- 2016 13th MCBIOS Travel Fellowship (\$500)
- 2014 11th MCBIOS Travel Fellowship (\$500)
- 2014 11th MCBIOS Best Paper Award
- 2013 Biology teacher qualification certificate, China
- 2013 Outstanding Bachelor's Degree Thesis

- 2011 The third price, the 5th Knowledge Competition of Life Science, Beijing
- 2009 The second prize, HP graphical calculator competition in school
- 2010 The second prize, School Scholarship
- 2009 The second prize, School Scholarship
- 2008 The third prize, Maths Olympics, China

Invited Lectures and Seminars

- 2024 Yue Z, AI-Driven Paradigm for Uncovering New Insights in Biomedical Research, DDD department seminar talk, Aug 19th, 2024, Auburn, AL
- Huang F., McLeod M.C., Irwin R.K., Smithson M., Yue Z., Gao M., Hardiman K.M. and Chong Z., Poster Presentation: Molecular differentiation between complete and incomplete responders to neoadjuvant therapy in rectal cancer, AACR 2024, May 10th, 2024, San Diego, CA
- 2024 Yue Z., Zhou L., Huang F. and Chen P., Poster Presentation: S2Map: An Online Interactive Analytical Platform for Quantitative Signal Measurement of Cell Secretion Signal Map, AACR 2024, May 8th, 2024, San Diego, CA
- 2024 Li Q., Nichols C., Chen J.Y., Ku W.S. and Yue Z, Oral Presentation: TodenE: Topology-Based and Density-Based Ensembled Clustering for the Development of Super-PAG in Functional Genomics using PAG Network and LLM, MCBIOS 2024, March 24, Atlanta, GA
- 2024 Yue Z., Xue X. and Qian J., Poster Presentation: Benzodiazepines and Adrenergic Beta2-agonists: A Synergistic Impact on Health-related Quality of Life among Older Adults with Prostate Cancer, ISPOR 2024, May 8, 2024, Atlanta, GA
- 2023 Cancer Patient Stratification and Molecular Mechanism Identification using Patient Clinotypes and Transcriptomic Embeddings, Oncological Data Science (ODSi), Feb 28th, 2023, Utah University
- 2022 Patient stratification and molecular mechanism identification using patient clinotypes and transcriptomics embeddings, the Brain Tumor Research in Progress Meetings, 07/22/2022, UAB
- Application track, "Cancer patient stratification and molecular mechanism identification using patient clinotypes and transcriptomics embeddings", 21st European Conference on Computational Biology (ECCB)
- 2022 Functional Genomics Downstream Analysis and Common Informatics Tools, PowerTalk Seminar, February 11, UAB
- Functional genomics analysis using pathways, annotated gene lists and gene signatures electronic repository (PAGER), O'Neal Young Investigator Seminar, November 18, UAB
- 2021 Podium presentation of PAGER-CoV-Run: An online interactive analytical platform for COVID-19 functional genomic downstream analysis, AMIA 2021 Annual Symposium, Hilton San Diego Bayfront, San Diego, CA 92101
- 2021 Podium presentation of A Bioinformatics Approach to Finding Novel Drug Repositioning Candidates in Glioblastoma, MidSouth Computational Biology and Bioinformatics Society 2021 virtual conference.
- Workshops speaker, Bioinformatics Analysis of Single Cell Sequencing Data, Annual Translational and Transformative Informatics Symposium (ATTIS) 2020 virtual conference.
- 2019 Poster presentation of A Bioinformatics Approach to Finding Novel Drug Repositioning Candidates in Glioblastoma, O'Neal Comprehensive Cancer Center 21st Annual Research Retreat, The Club, Inc. 1 Robert S Smith Drive, Birmingham, AL 35209
- 2019 Poster presentation of A Bioinformatics Approach to Finding Novel Drug Repositioning Candidates Associated with Aging, The UAB Aging Symposium, the University of Alabama at Birmingham, AL, 35233
- 2019 Oral presentation of GS-rank: disease gene prioritization based on network and gene sets, and an Alzheimer's disease study, The 16th MCBIOS, Informatics for Precision Medicine, the University of Alabama at Birmingham, AL, 35233
- 2018 Poster presentation of Multi-scale Genomics Data Annotation with GOALS (Gene Ontology Analysis using Layered Shells), 1st Southern Genome Maintenance Conference, the Holiday Inn Conference Center in Mobile, Alabama, 36602
- Oral presentation of WIPER: Weighted in-path edge ranking for biomolecular association networks. The 15th MCBIOS, Genomics and Big Data, The Mill at MSU, Starkville, MS, 39759

2018 Poster presentation, Multi-omics Approach to Predict Radiographic Damage in Rheumatoid Arthritis. UAB 2018 Annual Translational and Transformative Informatics Symposium, Bevill Biomedical Research Building, Room 170, 845 19th Street South, Birmingham, Alabama, 35233

2018 Oral+Poster presentation of WIPER: Weighted in-path edge ranking for biomolecular association networks. UAB 2018 Annual Translational and Transformative Informatics Symposium, Bevill Biomedical Research Building, Room 170, 845 19th Street South, Birmingham, Alabama, 35233

2017 Oral presentation of Construct Parkinson's Disease-specific Gene Co-expression Modules for Drug Repositioning. The 14th MCBIOS, 11301 Financial Center Parkway, Little Rock, Arkansas, 72211

2017 Poster presentation of PAGER: The Pathway, Annotated-list, and Gene-signature electronic repository for Human Network Biology. 2017 Comprehensive Cancer center Poster Abstracts and 2017 Annual Scientific Retreat - UAB

2016 Poster presentation of Terrain Mapping as A Novel Disease Classification Tool: An Leukemia Case Study, The XI Annual Scientific Retreat, Lake Guntersville State Park, Guntersville, AL

2016 Poster presentation of Terrain Mapping as A Novel Disease Classification Tool: An Alzheimer Case Study, The 13th MCBIOS Conference, Memphis, TN, USA

2015 Poster of Proteomics to identify post-transplantation lung complication towards precision medicine in topic "Regulatory Pathways for Regenerative Medicine: Cell and Biological Therapeutics", Indiana Health Industry Forum, IN, USA

2015 Poster of GeneTerrain: a visual analytic platform to interpret high-throughput Omics data for clinical genomics applications in HiSeq15 conference, ECCB&ISMB, July 10-14th, Dublin, Ireland

2015 Extract Transform and Load (ETL) Citeline data into a database and Clinical Trial Intelligence (CTI) web interface design: node.js Denodo platform and angular.js, Covance Corp, Greenfield, IN, USA

Oral presentation of SLDR: A Method to Identify New Gene Regulatory Relationship Candidates, The 11th MCBIOS, Oklahoma State University, Stillwater, OK, USA

2013 Conference of International Bioinformatics Workshop, ShangHai, China

Mentored students

PhD student

Ongoing:

Liangliang Xu, Computer Science Department, Samuel Ginn College of Engineering, AU; 4th year. Sabina Tiwari, College of Forestry, Wildlife and Environment, AU; 1st year. Zeru Zhang, Computer Science Department, Samuel Ginn College of Engineering, AU; 4th year.

Graduated:

Qi Li, Computer Science Department, Samuel Ginn College of Engineering, AU; graduated in 2024.

Master student

Ongoing:

Angela Carver, Samuel Ginn College of Engineering
Aasrith Satya Matta, Samuel Ginn College of Engineering
Sri Lakshmi Manaswini Mudivarti, Samuel Ginn College of Engineering
Darahaas Nallagatla, Samuel Ginn College of Engineering
Tingjun Zhao, Samuel Ginn College of Engineering

Thesis Committee

Liangliang Xu, Computer Science Department, Samuel Ginn College of Engineering, AU; 4th year. Nicholas P. McCormick, Health Outcomes Research and Policy, Harrison College of Pharmacy, AU; 3rd year.