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# Zongliang Yue, Ph.D.

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709 Meagan Ln, Auburn, Alabama, 36832  
205-563-4481 | zzy0065@auburn.edu  
Webpage: <https://zongyue1010.github.io>

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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.

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## Experience

Mar 2023 - Now	<b>HORP, Harrison College of Pharmacy, Auburn University, UAB, AL, US</b> Postdoc employee. Advisor: Jake Chen, PhD
Dec 2020 - Feb 2023	<b>ALMED Lab, Informatics Institute in School of Medicine, UAB, AL, US</b> Postdoc employee. Advisor: Jake Chen, PhD
Jun 2016 - Oct 2020	<b>ALMED Lab, Informatics Institute in School of Medicine, UAB, AL, US</b> Research Assistant. Ph.D. thesis advisor: Jake Chen, PhD
Jun 2015 - Aug 2015	<b>Bioinformatics department, Covance, Greenfield, IN, US</b> Intern. Advisor: Walter Jessen, PhD
Jan 2014 - Jun 2016	<b>ALMED Lab, School of Informatics &amp; Computing, Indiana University, IN, US</b> Research Assistant. MS thesis advisor: Jake Chen, PhD
Nov 2012 - Dec 2013	<b>Bioinformatics department, Capital Normal University, China</b> Project leader
Apr 2011 - Jan 2012	<b>ZMBP Plant Biochemistry, Tübingen University, Germany</b> Exchange student, Bachelor's thesis advisor: Frédéric Brunner, PhD
Oct 2010 - Apr 2011	<b>Bioinformatics department, Capital Normal University, China</b> Project leader

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## Education

Jun. 2016 - Oct. 2020	<b>The University of Alabama at Birmingham, AL, USA</b> Doctor of Philosophy in Biomedical Science (Genetics, Genomics and Bioinformatics)
Jan. 2014 - Jun. 2016	<b>Indiana University Purdue University in Indianapolis, IN, USA</b> Master's degree in Bioinformatics
Sep. 2008 - Jun. 2013	<b>Capital Normal University, Beijing, China</b> Bachelor' degree in Life Science Minor: Bachelor' degree in Computer Application

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## Academic Service

2023 - Now	Associate editor in <b>JMIR Bioinformatics and Biotechnology</b>
2022 - Now	Topic editor in <b>Frontiers in Artificial Intelligence</b>
2020 - Now	Associate editor in <b>RE:GENOpen</b>
Mar 2023	Session chair in <b>MCBIOS Conference 2023</b>
Apr 2022	Session chair in <b>MCBIOS Conference 2022</b>

Apr 2021  
Jul 2019

Session chair in MCBIOS and MAQC Joint Conference 2021  
Session co-chair in MCBIOS 2019

### *Society Member*

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2015 – now                    **International Society for Computational Biology (ISCB)**  
Member  
2014 – now                    **Midsouth Computational Biology & Bioinformatics Society (MCBIOS)**  
Senior Member

### *Publication*

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1. **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>
2. Thanh Nguyen, **Zongliang Yue**, Radomir Slominski, Robert Welner, Jianyi Zhang, Jake Y. Chen\*. (2023) WINNER: a Network Biology Tool for Biomolecular Characterization and Prioritization, *Frontiers in Big Data*.
3. 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)
4. Zhenyu Weng<sup>#</sup>, **Zongliang Yue**<sup>#</sup>, 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)
5. **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)
6. Carlene L. Zindl<sup>#</sup>, Steven J. Witte<sup>#</sup>, Vincent A. Laufer<sup>#</sup>, 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)
7. **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*
8. 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
9. **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.
10. 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)
11. **Zongliang Yue**<sup>#</sup>, Eric Zhang<sup>#</sup>, 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)
12. 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

lncRNAs IN GBM RADIATION RESISTANCE AND TUMOR RECURRENCE, Neuro-Oncology. (Impact factor: 12.3)

13. 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.
14. 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.
15. 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)
16. **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)
17. **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)
18. **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)
19. **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)
20. **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)
21. 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).
22. 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)
23. 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)
24. **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)
25. Zongliang Yue, Ping Wan, Zhan Xie, and Jake Y. Chen\*, (2014) Computational Identification of Decentric Genetic Regulatory Relationships from Functional Genomic Data, [Bioinformatics Research and Applications Lecture Notes in Computer Science](#) Volume 8492, 2014, pp 224-235.
26. **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)
27. 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**

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11/01/2023-10/31/2024 Zongliang Yue (PI) PhRMA Foundation's Faculty Starter Grant in Drug Discovery  
scDRAGN: Single-cell Enabled Drug Repositioning Acting on Gene Network Modules  
Total direct: \$100,000

04/01/2024-03/31/2026 Zongliang Yue (Co-I) NIH/NHGRI  
Perturbation of the immune landscape by the pre-leukemic inflammatory environment  
Total direct: \$275,000

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**

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BMC bioinformatics  
IEEE/ACM Transactions on Computational Biology and Bioinformatics  
Frontiers  
AMIA - American Medical Informatics Association  
Conference on Biological Information and Biomedical Engineering  
Molecular Carcinogenesis

## **Teaching**

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<b>2021, 2022</b>	<b>UAB INFO 603-703 Database course</b> Co-instructor
<b>2017, 2018</b>	<b>UAB Special Topic-Biological Data Management</b> Teaching Assistant
<b>Jan 2015 - Mar 2015</b>	<b>MURI Project (Multidisciplinary Undergraduate Research Initiative)</b> Co-mentor

## **Tools and Applications**

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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)

### *Honors, Awards, and Fellowships*

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- 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 16<sup>th</sup> MCBIOS Travel Fellowship (\$500)  
2017 The Conference of Multi-Omics QC data workshop Travel Fellowship, Mount Sinai University, NY (\$1000)  
2017 14<sup>th</sup> MCBIOS Travel Fellowship (\$500)  
2016 13<sup>th</sup> MCBIOS Travel Fellowship (\$500)  
2014 11<sup>th</sup> MCBIOS Travel Fellowship (\$500)  
2014 **11<sup>th</sup> MCBIOS Best Paper Award**  
2013 **Biology teacher qualification certificate, China**  
2013 Outstanding Bachelor's Degree Thesis  
2011 The third prize, 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*

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- 2023 PAGER-scFGA: PAGER single-cell functional genomics analysis in revealing cell functions and molecular mechanisms in cell trajectories, March 15-17, 2023, University of Dallas  
2023 Cancer Patient Stratification and Molecular Mechanism Identification using Patient Clinotypes and Transcriptomic Embeddings, Oncological Data Science (ODSi), Feb 28<sup>th</sup>, 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  
2022 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  
2021 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.  
2020 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 16<sup>th</sup> 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), 1<sup>st</sup> Southern Genome Maintenance Conference, the Holiday Inn Conference Center in Mobile, Alabama, 36602

2018 Oral presentation of WIPER: Weighted in-path edge ranking for biomolecular association networks. The 15<sup>th</sup> 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 14<sup>th</sup> 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 13<sup>th</sup> 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

2014 Oral presentation of SLDR: A Method to Identify New Gene Regulatory Relationship Candidates, The 11<sup>th</sup> MCBIOS, Oklahoma State University, Stillwater, OK, USA

2013 Conference of International Bioinformatics Workshop, ShangHai, China