

Chen Liao, Ph.D.

EDUCATION AND TRAINING

- University of Science and Technology of China**, Hefei, Anhui, China 2010
- BS in Optics and Optical Engineering, School of Physical Sciences
- University of Illinois at Urbana-Champaign**, Illinois, USA. 2018
- Ph.D. in Bioengineering (Thesis Advisor: Dr. Ting Lu), College of Engineering

PROFESSIONAL APPOINTMENTS

Graduate Research Assistant (2012-2018)

Advisor: Dr. Ting Lu

Department of Bioengineering, University of Illinois at Urbana-Champaign

Postdoctoral Scholar (2018-2021)

Advisors: Drs. Joao Xavier and Tobias Hohl

Computational & Systems Biology Program, Memorial Sloan Kettering Cancer Center

Research Associate (2022-present)

Advisors: Drs. Joao Xavier and Tobias Hohl

Computational & Systems Biology Program, Memorial Sloan Kettering Cancer Center

Incoming Assistant Professor (2025-)

Department of Microbiology and Immunology, Dartmouth College

HONORS & AWARDS

- The Anthony C. Brown Society Scholar, Memorial Sloan Kettering Cancer Center, 2020-2024
- Chinese Government Award for Outstanding Self-financed Students Abroad, Chinese Scholarship Council, 2017
- Yee Memorial Fund Fellowship, University of Illinois at Urbana-Champaign, 2015
- Gold Medal & Best Software Tool (team leader on behalf of University of Science and Technology of China), International Genetically Engineered Machine (iGEM) Competition, 2010
- Meritorious Winner, the Mathematical Contest in Modeling (MCM), 2010
- Outstanding Student Scholarship, University of Science and Technology of China, 2008, 2009

RESEARCH GRANTS

1. NIH-NIAID K99/R00 (PI: Chen Liao, Amount: \$745,661) 05/2024-04/2028
Project title: Unraveling the ecology of intestinal fungal expansion in immunocompromised patients through computational modeling and machine learning

PEER-REVIEWED PUBLICATIONS

First/Co-first (#) Author Publications

1. Liao, C.#, Priyanka, P.#, Lai, Y.-H.#, Rao, C.V., Lu, T. (2024) "How does *Escherichia coli* allocate proteome?". *ACS Synthetic Biology* 13(9):2718-2732.
2. Zhai, B.#, Liao, C.#, Jaggavarapu, S.#, Tang, Y.#, Rolling, T., Ning, Y., Sun, T., Bergin, S.A., Gjonbalaj M., Miranda, E., Babady, N.E., Bader, O., Taur, Y., Butler, G., Zhang, L., Xavier, J.B., Weiss, D.S., Hohl

T.M. (2024) “Antifungal heteroresistance causes prophylaxis failure and facilitates breakthrough *Candida parapsilosis* infections”. **Nature Medicine** 30:3163-3172

3. **Liao, C.#**, Rolling, T.#, Djukovic, A.#, Fei, T., Mishra, V., Liu, H.B., Lindberg, C., Dai, L., Zhai, B., Peled, J.U., van den Brink, M.R.M., Hohl, T.M., Xavier, J.B. (2024) “Oral bacteria relative abundance in faeces increases due to gut microbiota depletion and is linked with patient outcomes”. **Nature Microbiology** 9:1555-1565.
4. Chen, C.#, **Liao, C.#**, Liu, Y.-Y. (2023) “Teasing out missing reactions in genome-scale metabolic networks through hypergraph learning”. **Nature Communications** 14:2375.
5. Santamaria, G.#, **Liao, C.#**, Wang, Z., Rhee, K., Pinto F., Yan, J., Xavier, J.B. (2022) “Evolution and regulation of microbial secondary metabolism”. **eLife** 11: e76119.
6. Liu, H.#, **Liao, C.#**, Wu, L., Tang, J., Chen, J., Lei, C., Zheng, L., Zhang, C., Liu, Y.-Y., Xavier, J.B., Dai, L. (2022). “Ecological dynamics of the gut microbiome in response to dietary fiber”. **The ISME Journal** 16(8):2040-2055.
7. **Liao, C.**, Taylor, B.P., Ceccarani, C., Fontana, E., Amoretti, L.A., Wright, R.J., Gomes, A.L.C., Peled, J.U., Taur, Y., Perales, M.-A., van den Brink, M.R.M., Littmann, E., Pamer, E.G., Schluter, J., Xavier, J.B. (2021). “Compilation of longitudinal microbiota data and hospitalome from hematopoietic cell transplantation patients”. **Scientific Data** 8(1):71.
8. **Liao, C.**, Wang, T., Maslov, S., Xavier, J.B. (2020). “Modeling microbial cross-feeding at intermediate scale portrays community dynamics and species coexistence”. **PLoS Computational Biology** 16(8): e1008135.
9. **Liao, C.**, Xavier, J.B., Zhu, Z. (2020). “Enhanced inference of ecological networks by parameterizing ensembles of population dynamics models constrained with prior knowledge”. **BMC Ecology** 20(1):3.
10. **Liao, C.**, Blanchard, A.E., Lu, T. (2017) “An integrative circuit-host modelling framework for predicting synthetic gene network behaviours”. **Nature Microbiology** 2(12):1658.
11. **Liao, C.**, Seo, S.O., Lu, T. (2016) “System-level modeling of acetone-butanol-ethanol fermentation”. **FEMS Microbiology Letters** 393(9):fnw074.
12. **Liao, C.**, Seo, S.O., Celik, V., Liu, H., Kong, W., Wang, Y., Blaschek, H., Jin, Y.S., Lu, T. (2015) “An integrated, systems metabolic picture of the acetone-butanol-ethanol fermentation by *Clostridium acetobutylicum*”. **PNAS** 112(27):8505-8510.
13. **Liao, C.**, Lu, T. (2013) “A minimal transcriptional controlling network of regulatory T cell development”. **The Journal of Physical Chemistry B** 117(42):12995-13004.
14. **Liao, C.**, Cai, Y. (2014). “Towards Modeling Automation for Synthetic Biology”, In A Systems Theoretic Approach to Systems and Synthetic Biology II: Analysis and Design of Cellular Systems (pp. 201-217). Springer Netherlands.

Collaborative Publications

15. Mathur D., **Liao, C.**, Lin, W., La Ferlita, A., Alaimo S., Taylor, S., Zhong, Y., Iacobuzio-Donahue, C., Ferro, A., Xavier, J.B. (2023) “The ratio of key metabolic transcripts is a predictive biomarker of breast cancer metastasis to the lung”. **Cancer Research** 83(20):3478-3491.

16. Schluter, J., Djukovic, A., Taylor, B.P., Yan, J., Duan, C., Hussey, G.A., **Liao, C.**, Sharma, S., Fontana, E., Amoretti, L.A., Wright, R.J., Dai, A., Peled, J.U., Taur, Y., Perales, M.-A., Siranosian, B.A., Bhatt, A.S., van den Brink, M.R.M., Pamer, E.G., Xavier, J.B. (2023) "The TaxUMAP atlas: Efficient display of large clinical microbiome data reveals ecological competition in protection against bacteremia". **Cell Host & Microbe** 31(7):1126-1139.e6.
17. Nguyen, C., Markey, K., Miltiadous, O., Dai, A., Waters, N., Sadeghi K., Fei, T., Shouval, R., Taylor, B.P., **Liao, C.**, Slingerland, J.B., Slingerland, A.E., Clurman, A.G., Maloy, M.A., Bohannon, L., Giardina, P.A., Brereton, D.G., Armijo, G.K., Fontana, E., Gradissimo, A., Guyrkcoza, B., Sung, A.D., Chao, N.J., Devlin, S.M., Taur, Y., Giral, S.A., Perales, M.-A., Xavier, J.B., Pamer, E.G., Peled, J.U., Gomes, A.L.C., van den Brink, R.M. (2023) "High resolution analyses of associations between medications, microbiome and mortality in cancer patients". **Cell** 186(12):2705-2718.e17.
18. Li, L., Qiao, J., Yu, G., Wang, L., Li, H.-Y., **Liao, C.**, Zhu, Z. (2022). "Interpretable tree-based ensemble model for predicting beach water quality". **Water Research** 211:118078.
19. Xavier, J.B., Monk, J.M., Poudel, S., Norsigian, C.J., Sastry, A.V., **Liao, C.**, Bento, J., Suchard, M.A., Arrieta-Ortiz, M.L., Peterson, E.J., Baliga, N.S. (2022). "Mathematical models to study the biology of pathogens and the infectious diseases they cause". **iScience** 25(4):104079.
20. Yan, J., **Liao, C.**, Taylor, B.P., Fontana, E., Amoretti, L.A., Wright, R.J., Dai, A., Waters N., Peled, J.U., Taur, Y., Perales, M.-A., Siranosian B.A., Bhatt A.S., van den Brink, M.R.M., Pamer, E.G., Schluter, J., Xavier, J.B. (2022). "A compilation of fecal microbiome shotgun metagenomics from hospitalized patients undergoing hematopoietic cell transplantation". **Scientific Data** 9(1):219.
21. Wang, L., Zhu, Z., Sassoubre, L., Yu, G., **Liao, C.**, Hu, Q., Wang, Y. (2021). "Improving the Robustness of Beach Water Quality Modeling using an Ensemble Machine Learning Approach". **Science of The Total Environment** 765:142760.
22. Yan, J., Estanbouli, H., **Liao, C.**, Kim, W., Monk, J.M., Rahman, R., Kamboj, M., Palsson, B.O., Qiu, W., Xavier, J.B. (2019). "Systems-level analysis of NalD mutation, a recurrent driver of rapid drug resistance in acute *Pseudomonas aeruginosa* infection". **PLoS Computational Biology** 15(12):e1007562.
23. Pan, J., Ma, J., Wu, H., Chen, B., He, M., **Liao, C.**, Wei, C. (2018). "Application of metabolic division of labor in simultaneous removal of nitrogen and thiocyanate from wastewater". **Water Research** 150:216-224.
24. Blanchard, A.E., **Liao, C.**, Lu, T. (2018) "Circuit-host coupling induces multifaceted behavioral modulations of a gene switch". **Biophysical Journal** 114(3):737-746.
25. Kong, W., Blanchard, A.E., **Liao, C.**, Lu, T. (2017) "Engineering robust and tunable spatial structures with synthetic gene circuits". **Nucleic Acids Research** 45(2):1005-1014.
26. Blanchard, A.E., **Liao, C.**, Lu, T. (2016) "An ecological understanding of quorum sensing-controlled bacteriocin synthesis". **Cellular and Molecular Bioengineering** 9(3):443-454.
27. Kong, W., Celik, V., **Liao, C.**, Hua, Q., Lu, T. (2014) "Programming the group behaviors of bacterial communities with synthetic cellular communications". **Bioresources and Bioprocessing** 1(1):24.

SEMINAR/CONFERENCE TALKS

Seminar Talks

1. Unintended Consequences: Antimicrobial Collateral Damage in the Human Gut Microbiome. Department of Biological Sciences, Purdue University, West Lafayette, IN., USA., June 5, 2023.
2. Learning microbiome ecology from perturbations. Department of Microbial Infection and Immunity, The Ohio State University, Columbus, OH., USA., Mar. 30, 2023.
3. Learning microbiome ecology from perturbations. Department of Microbiology and Immunology, Dartmouth College, Hanover, NH., USA., Feb. 13, 2023.
4. Oral bacteria in feces reflect the loss of intestinal bacteria. *Channing Microbiome Seminar (Virtual)*, Channing Division of Network Medicine, Department of Medicine, Brigham and Women's Hospital, Boston, MA., USA., Nov. 19, 2021.
5. An integrative circuit-host modeling framework for synthetic biology. *Graduate Student Speaker Exchange Program*, University of Wisconsin-Madison, Madison, WI., USA., May 1, 2017.
6. Integrative modeling of acetone-butanol-ethanol (ABE) fermentation. *Bioengineering Graduate Student Seminar Series*, University of Illinois at Urbana-Champaign, Champaign, IL., USA., Oct. 12, 2015.
7. Understanding microbial metabolism through integrative modeling. Institute of Microbiology, Chinese Academy of Sciences, Beijing, China, Jun. 30, 2015.

Conference Talks

8. Making sense of gut microbiome dysbiosis. *Rust Belt Microbiome Conference 2022*, Nov. 3-4, 2022. **Invited talk.**
9. Machine learning-based diagnosis of antimicrobial drug heteroresistance. *SMBEeverywhere GS5 (Virtual)*. Oct. 20, 2022.
10. Modeling microbial cross-feeding at intermediate scale portrays community dynamics and species coexistence. *Microbial Ecology & Evolution (MEEVirtual)*, Aug. 12-14, 2020.
11. An integrative circuit-host modeling framework for predicting synthetic gene network behaviors. *The 4th Synthetic Biology Young Scholar Forum*, Shenzhen, China, Jul. 7, 2018.
12. An integrative circuit-host modeling framework for predicting synthetic gene networks. *Spring 2018 CPLC/CBQB Graduate Student and Postdoc Symposium*, University of Illinois at Urbana-Champaign, Champaign, IL., USA., Apr. 24, 2018.
13. An integrative circuit-host modeling framework for synthetic biology. *Bioengineering Graduate Student Symposium*, University of Illinois at Urbana-Champaign, Champaign, IL., USA., Apr. 29, 2017.
14. Rule-based modeling approach for synthetic biology. *Six-Academy Synthetic Biology Symposium*, Shanghai, China, Oct. 12-14, 2011. **Invited talk.**

PROFESSIONAL ACTIVITIES & SCIENTIFIC LEADERSHIP

- External Reviewer for *Nature Medicine*, *Nature Computational Science*, *Nature Communications*, *PNAS*, *Cell Reports Methods*, *Microbiome*, *elife*, *PLoS Computational Biology*, *Scientific Data*, *Gut Microbes*, etc.