

Li Liu, MD. MS.

Associate Professor

College of Health Solutions | Arizona State University
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<http://liliulab.org>**EDUCATION**

1999 – 2001	M.S.	Information System	New Jersey Institute of Technology Newark, NJ, USA
1995 – 1999	M.D.	Medicine	Peking Union Medical College Beijing, China
1991 – 1995	B.S.	Pre-medicine	Peking University Beijing, China

POSITIONS & EMPLOYMENT**Arizona State University**

2021 – present	Associate Professor	College of Health Solutions Scottsdale, AZ, USA
2015 – 2021	Assistant Professor	College of Health Solutions Scottsdale, AZ, USA
	Faculty	Center for Personalized Diagnostics Biodesign Institute Tempe, AZ, USA
2010 – 2015	Research Scientist	Center for Evolutionary Medicine & Informatics Biodesign Institute Tempe, AZ, USA

Mayo Clinic Arizona

2017 – present	Adjunct Assistant Professor	Department of Neurology College of Medicine and Science Scottsdale, AZ, USA
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University of Florida

2002 – 2010	Director, Associate Scientist	Bioinformatics Core Facility Interdisciplinary Center for Biotechnology Research Gainesville, FL, USA
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TripodSoft, Inc.

2001 – 2002	Bioinformatics Scientist	TripodSoft, Inc. Edison, NJ, USA
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RESEARCH & SCHOLARSHIP

AREAS OF RESEARCH INTEREST

- ❖ Develop computational methods to enable precision medicine
 - Knowledge-based data-driven biomarker discovery
 - Cancer molecular evolution
 - Precision population health
- ❖ Study the evolution of human genomes and the indications in diseases
 - Fine mapping pathogenic variants
 - Evolution of regulatory elements within and across species
 - Gene-environment interaction in complex diseases
- ❖ Translate informatics advances to biomedical discoveries
 - Experimental design and bioinformatics support to multi-omics studies
 - Integrative analysis of heterogeneous multimodal data

PROFESSIONAL MEMBERSHIPS

2014-Present	Member, International Society for Computational Biology
2018-Present	Member, Society for Molecular Biology and Evolution
2021-Present	Member, International Association for Intelligent Biology and Medicine
2024-Present	Member, American Society of Human Genetics
2005-2010	Member, the Association of Biomolecular Resource Facilities

HONORS & AWARDS

2024	Distinguished Service Award, International Association for Intelligent Biology and Medicine
2017	Nomination of Searle Scholar
2014	1 st place in the DREAM9 AML Challenge
1998	China-Switzerland Medical Student Scholarship

SPONSORED RESEARCH GRANTS (since 2015)

Overview of grants & proposals

	My Role		Sum
	PI/MPI	Co-I	
Total funding awarded	\$4.4M	\$20.6M (\$2.0M recognition)	\$25M
Total grants awarded	14	10	24
Total proposals submitted	30	84	114

List of funded research grants

As PI/MPI:

- | | | |
|---|--------------|-------------|
| 1. Discover and analyze germline-somatic interactions in cancer | | |
| NIH-R01 | \$1,016,895 | 2021 – 2026 |
| PI: Liu | | |
| 2. Interdisciplinary Systems-based Training for Precision Nutrition | | |
| NIH-T32 | \$ 1,808,715 | 2023 – 2028 |

PI: Whisner & Liu

3. Harnessing Artificial Intelligence with Community Engagement to Devise Precision Public Health Strategies to Reduce Vaccine Hesitancy among Pregnant and Lactating Refugee Women
Merck & Company Inc. \$348,563 2023 – 2026
PI: Koskan, Liu, Johnson
4. Early Avocado Exposure on Development and the Gut Microbiome in American Hispanic
Hass Avocado Board: Avocado Nutrition Science Advisory \$353,944 2025 – 2028
PI: Whisner, Liu, Peter
5. Targeting Whole-body Fatty Acid Metabolism in Alzheimer’s Disease, with Special Interest in Lauric acid
Florida International University \$64,940 2021 – 2023
PI: Liu.
I am the site PI of an NIH grant (R21, \$459K) awarded to Dr. Gu at Florida International University. I lead the bioinformatics analysis of multiomics data.
6. Effect of palmitoylethanolamide (PEA) compared to a placebo on symptoms of upper respiratory tract infection (URTI) in an adult population – a double blind, randomised controlled trial
Gencor Lifestage Solutions \$264,084 2020 – 2021
PI: Johnston, Chang, Liu
7. Annotate functional genetic variants
Mayo Clinic \$46,382 2019 – 2022
PI: Liu
8. Precision diagnosis of pathogenic noncoding variants in diabetes
Flinn Foundation \$100,000 2019 – 2021
PI: Liu
9. eQTL mega-analysis for functional assessment of multi-enhancer gene regulation
Georgia Institute of Technology \$120,303 2016 – 2020
PI: Liu.
I am the site PI of an NIH grant (R01, \$757K) awarded to Dr. Gibson at Georgia Institute of Technology.
10. Reduced genomic diversity as a risk factor for nonfamilial young onset Alzheimer’ disease
Mayo Clinic \$6,706 2018 – 2020
PI: Liu.
I am the site PI of a grant (\$1M) awarded to Dr. Caselli at Mayo Clinic.
11. Prioritize functional genetic variants in melanoma with network biology and evolution
Flinn Foundation \$100,000 2017 – 2019
PI: Liu
12. Discovering the roles of cellular adaptability in late-onset Alzheimer’s disease
Arizona Alzheimer’s Consortium \$30,000 2017 – 2018
PI: Liu
13. Subclonal diversity: prognostic role in acute myeloid leukemia patients with minimal residual disease

Mayo / ASU Health Alliance Seed Grant PI: Liu	\$39,588	2016 – 2017
14. Discovering immunosignatures of systemic lupus erythematosus Healthtell Inc. PI: Liu	\$55,000	2016 – 2017
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As Co-I		
15. Developing an Innovative and Scalable Model to Bolster Health Research Data Management & Science Capabilities in the Phoenix Bioscience Core Flinn Foundation PI: Woodbury Co-I: Liu (12% recognition). I co-lead the Doctoral Twinning program that pairs graduate students in the Biomedical Informatics program at ASU with clinicians at Valleywise Health to develop collaborative research projects.	\$998,712	2022 – 2025
16. Leveraging bio-cultural mechanisms to maximize the impact of multi-level preventable disease interventions with southwest populations NIH-U54 supplement PI: Marsiglia Co-I: Liu (10% recognition). I lead the analysis of COVID-19 surveillance data to identify high risk groups and evaluate the outcomes of community-based services.	\$4,707,512	2020 – 2022
17. Arizona Cancer and Evolution (ACE) Center NIH (U54) PI: Maley Co-I: Liu (6% recognition). I am responsible for developing computational methods to incorporate somatic selection to discover cancer drivers.	\$10,648,553	2018 – 2023
18. ACE: Administrative Supplement: Parameterizing multi-scale agent-based modeling	\$116,790	2018 – 2019
19. ACE: Administrative Supplement: Parameterizing multi-scale agent-based modeling	\$42,105	2019 – 2020
20. Investigating the influences of sleep-wake patterns and gut microbiome development in infancy on rapid weight gain, an early risk factor for obesity NIH (R01) PI: Petrov & Whisner Co-I: Liu (10% recognition). I lead the experimental design, integrative analysis of survey data and molecular data, and building and interpreting predictive models.	\$3,571,554	2020 – 2025
21. Genotype-phenotype associations in reading disorders NIH (F32) PI: Lancaster Co-mentor: Liu (10% recognition). I advised the trainee on incorporating population and family structure in genomic analysis.	\$186,222	2017-2019

22. Multiple genomics data to predict drug response
 Mayo Clinic \$12,118 2019
 PI: Runger
 Co-I: Liu (50% recognition). I am responsible to advise students on applying deep-learning techniques to integrate multi-omics data.
23. Rapid nanoplasmonic quantification of tumor-derived EVs for pancreatic cancer diagnosis
 Baylor Scott & White Health \$156,500 2017 – 2019
 PI: Hu
 Co-I: Liu (3% recognition). I am responsible for statistical analysis to select biomarkers and assess technology robustness.
24. Nanoplasmonic quantification of tumor-derived circulating extracellular vesicles
 Fred Hutchinson Cancer Research Center \$153,936 2017 – 2019
 PI: Fan
 Co-I: Liu (33% recognition). I am responsible for experimental design, statistical analysis and building machine-learning models to predict tumor metastasis.

PUBLICATIONS

Overview of peer-reviewed publications

	All	Since 2019
Citations [☆]	4525	1866
h-index [☆]	36	23
i10-index [☆]	61	43
Total peer-reviewed publications	86	36
Lead-author peer-reviewed publications [*]	26	15
Publications with student authors [§]	23	21
Publications in journals with impact factor (IF)>10 [♦]	15	6

[☆] google scholar statistics (<https://scholar.google.com/citations?user=J9WIecoAAAAJ&hl=en>)

^{*} lead-author includes first-, co-first-, last- and corresponding author

[§] students for whom I am a mentor/advisor

[♦] IF released by Journal Citation Reports

Peer-reviewed articles (in reverse-chronological order)

^{*} lead-author publication; [§] publication with student/trainee authors; [♦] IF>10

Journal articles:

- ^{*§} Cheng R[§], Shu J[§], Chen H[§], Li M, Cheng X, **Liu L** (2024) DNA Methylation in Aging and Alzheimer's Disease. *Human Brain* (in press)
- [§] Boby M[§], Oh H, Marsiglia F, **Liu L** (2024) Bridging social capital among Facebook users and COVID-19 cases growth in Arizona. *Social Science & Medicine* 360:117313. PMID: 39270574
- [§] Fessler SN[§], **Liu L**, Chang Y, Johnston C (2024) Body mass index is associated with post-acute elevations in biomarkers of platelet activation and inflammation in unvaccinated adults diagnosed with covid-19 in the previous 8 weeks. *Obes Facts*. 8:1-6. PMID: 39116840
- ^{*§♦} Chi J, Shu J[§], Li M, Mudappathi R[§], Jin Y, Lewis F, Boon A, Qian X, **Liu L**, Gu H (2024) Artificial intelligence in metabolomics: a current review. *Trends Analyt Chem*. 178:117852. PMID: 39071116

5. *§♦ Shu J[§], Jelinek J, Chen H, Zhang Y, Qin T, Li M, **Liu L**, Issa JJ. (2024) Genome-wide screening and functional validation of methylation barriers near promoters. *Nucleic Acids Res.* 52(9):4857-4871. PMID: 38647050
6. § Petrov ME, **Liu L**, Mudappathi R[§], Whisner CM. (2024) Actigraphic sleep patterns are associated with bone turnover and bone mineral density among university students. *J Sleep Res.* [Epub ahead of print] PMID: 38494335.
7. Wang J, Ye Q, **Liu L**, Guo NL, Hu G. (2024) Scientific figures interpreted by ChatGPT: strengths in plot recognition and limits in color perception. *NPJ Precis Oncol.* 5;8(1):84. PMID: 38580746
8. Hu G, **Liu L**, Xu D (2023) On the responsible use of chatbots in bioinformatics. *Genomics, Proteomics & Bioinformatics.* 22(1):qzae002. PMID: 38862428
9. *§ Chandrashekar P[§], Chen H[§], Lee M[§], Ahmadinejad N[§], **Liu L**. (2024) DeepCORE: An interpretable multi-view deep neural network model to detect co-operative regulatory elements. *Computational and Structural Biotechnology Journal.* 23:679-687. PMID: 38292477
10. *§ Chen H[§], Shu J[§], Maley CC, **Liu L**. (2023) A mouse-specific model to detect genes under selection in tumors. *Cancers* 15(21):5156. PMID: 37958330
11. *§ Ahmadinejad N[§], Chung Y, **Liu L**. (2023) J-score: a robust measure of clustering accuracy. *PeerJ Computer Science.* 9:e1545. PMID: 37705621
12. Wang L, Ge X, **Liu L**, Hu G. (2023) Code interpreter for bioinformatics: are we there yet? *Annals of Biomedical Engineering.* Online ahead of print. PMID: 37482573
13. Shue E, **Liu L**, Li B, Feng B, Li X, Hu G. (2023) Empowering beginners in bioinformatics with ChatGPT. *Quantitative Biology* 11(2):105-108. PMID: 36945641
14. *§ Shen FL[§], Shu J[§], Lee M[§], Oh H, Li M, Runger G, Marsiglia F, **Liu L**. (2023) Evolution of COVID-19 health disparities in Arizona. *Journal of Immigrant and Minority Health.* 25(4):862-869. PMID: 36757600
15. § Fessler SN[§], Chang Y, **Liu L**, Johnston C. (2022) Curcumin confers anti-inflammatory effects in adults who recovered from COVID-19 and were subsequently vaccinated: a randomized controlled trial. *Nutrients.* 15(7):1548. PMID: 37049389
16. *§ Morrison M[§], Nobles V[§], Johnson-Agbaksu C, Bailey C, **Liu L**. (2022) Classify refugee status using common features in EMR. *Chemistry and Biodiversity.* 19(10):e202200651. PMID: 36050919
17. *§♦ Ahmadinejad N[§], Troftgruben S[§], Wang J, Chandrashekar P[§], Dinu V, Maley C, **Liu L**. (2022) Accurate identification of subclones in tumor genomes. *Molecular Biology and Evolution.* 39(7):msac136. PMID: 35749590
18. § Fessler SN[§], **Liu L**, Chang Y, Yip T, Johnston C. (2022) Palmitoylethanolamide reduces proinflammatory markers in unvaccinated adults recently diagnosed with COVID-19: A Randomized Controlled Trial. *Journal of Nutrition.* 152(10):2218-2226. PMID: 36084236
19. *§ Lee M[§], Chang Y, Ahmadinejad N[§], Johnson-Agbaksu C, Bailey C, **Liu L**. (2022) COVID-19 mortality is associated with pre-existing impaired innate immunity in health condition. *PeerJ.* 10:e13227. PMID: 35547187
20. Whisner CM, Brown JC, Larson DM, Rodriguez LA, Peter B, Reifsnider E, Bever J, **Liu L**, Raczynski E, Chavez JR, Ojinnaka C, Berkel C, Bruening M. (2022) A new American university model for training the future MCH workforce through a translational research team. *Maternal and Child Health Journal.* 26(Suppl 1):10-19. PMID: 35060070

21. *§ **Liu L**, Chandrashekar P[§], Zeng B, Maxwell D, Kumar S Gibson G. (2021) TreeMap: A structured approach to fine mapping of eQTL variants. *Bioinformatics*. 23;37(8):1125-1134. PMID: 33135051
22. Jasbi P, Shi X, Chu P, Elliott N, Hudson H, Jones D, Serrano G, Chow B, Beach TG, **Liu L**, Jentarra G, Gu H (2021) Metabolic profiling of neocortical tissue discriminates Alzheimer's disease from mild cognitive impairment, high pathology controls, and normal controls. *Journal of Proteome Research*. 20(9): 4303-4317. PMID: 34355917
23. Wei Y, Jasbi P, Shi X, Turner C, Hrovat J, **Liu L**, Rabena Y, Porter P, Gu H (2021) Early Breast Cancer Detection Using Untargeted and Targeted Metabolomics. *Journal of Proteome Research*. 20(6):3124-3133. PMID: 34033488
24. Petrov ME, Jiao N, Panchanathan SS, Reifsnider E, Coonrod DV, **Liu L**, Krajmalnik-Brown R, Gu H, Davidson LA, Chapkin RS, Whisner CM. (2021) Protocol of the Snuggle Bug/Accurcadio Study: a longitudinal study investigating the influences of sleep-wake patterns and gut microbiome development in infancy on rapid weight gain, an early risk factor for obesity. *BMC pediatrics*. 21(1):374. PMID: 34465311
25. * **Liu L**, Caselli RJ. (2020) Unbalanced sample size introduces spurious correlations to genome-wide heterozygosity analyses. *Human Heredity*. 84(4-5):197-202. PMID: 32541150
26. ♦ Qi X, Liu X, Matiski L, Villa RRD, Yang T, Zhang F, Sokalingam S, Jiang S, **Liu L**, Yan H, Chang Y. (2020) RNA origami nanostructures for potent and safe anti-cancer immunotherapy. *ACS Nano*. 14(4):4727-4740. PMID: 32275389
27. §♦ Liu Y, Fan J, Xu T, Ahmadinejad N[§], Hess K, Lin S, Zhang J, **Liu L**, Ning B, Liao Z, Hu Y. (2020) Extracellular vesicle tetraspanin-8 expression predicts distant metastasis in non-small cell lung cancer after concurrent chemoradiation, *Science Advances*. 11;6(11):eaaz6162. PMID: 32195353
28. *§ Guan X[§], Runger G, **Liu L**. (2020) Dynamic incorporation of prior knowledge from multiple domains in biomarker discovery. *BMC Bioinformatics*. 21(Suppl 2):77 PMID: 32164534
29. *§ Chandrashekar P[§], Ahmadinejad N[§], Sekulic A, Wang J, Kumar S, Maley C, **Liu L**. (2019) Somatic selection distinguishes oncogenes and tumor suppressor genes. *Bioinformatics*. 36(6):1712-1717. PMID: 32176769
30. Jasbi P, Mitchell NM, Shi X, Grys TE, Wei Y, **Liu L**, Lake DF, Gu H. (2019) Coccidioidomycosis detection using targeted plasma and urine metabolic profiling. *Journal of Proteome Research*. 18(7):2791-2802. PMID: 31244214
31. Xu K, Kosoy R, Shameer K, Kumar S, **Liu L**, Readhead B, Belbin GM, Lee H, Chen R, Dudley JT. (2019) Genome-wide analysis indicates association between heterozygote advantage and healthy aging in humans. *BMC Genetics*. 20(1):52. PMID: 31266448
32. § Peter B, Dinu V, **Liu L**, Huentelman M, Naymik M, Lancaster H[§], Vose C[§], Schrauwen I. (2019) Exome sequencing of two siblings with sporadic autism spectrum disorder and severe speech sound disorder suggests pleiotropic and complex effects. *Behavior Genetics*. 49(4):399-414. PMID: 30949922
33. *§♦ **Liu L**, Maxwell D, Patel R, Chandrashekar P[§], Gibson G, Kumar S. (2019) Biological relevance of computationally predicted pathogenicity of noncoding variants. *Nature Communications*. 10:330. PMID: 30659175
34. Jasbi P, Wang D, Cheng SL, Fei Q, Cui JY, **Liu L**, Wei Y, Raftery D, Gu H. (2019) Breast cancer detection using targeted plasma metabolomics. *Journal of Chromatography B*. 1105:26-37. PMID: 30562627

35. * **Liu L**, Caselli RJ. (2018) Age stratification corrects bias in estimated hazards of APOE Genotype in Alzheimer's disease. *Alzheimer's & Dementia TRCI*. 4:602–608. PMID: 30450407
36. § Li C[§], **Liu L**, Dinu V. (2018) Pathways of topological rank analysis (potra): a novel method to detect pathways involved in cancer. *PeerJ*. 6:e4571 PMID: 29666752
37. Arutla V, Leal J, Liu X, Sokalingam S, Raleigh M, Adaralegbe A, **Liu L**, Pentel P, Hecht S, Chang Y. (2017) Prescreening of nicotine hapten linkers in vitro to select hapten-conjugate vaccine candidates for pharmacokinetic evaluation in vivo. *ACS Combinatorial Science*. 19(5):286-298. PMID: 28383252
38. Kumar S, Konikoff C, Sanderford M, **Liu L**, Newfeld S, Ye J, Kulathinal RJ (2017) FlyExpress 7: An integrated discovery platform to study coexpressed genes using in situ hybridization images in drosophila. *G3: Genes, Genomes, Genetics*. 8(8):2791-2797. PMID: 28667017
39. Xie G, Chastain-Gross R, Belanger M, Kumar D, Whitlock J, **Liu L**, Farmerie W, Zeng C, Daligault H, Han C., Brettin T, Progulske-Fox A. (2017) Genome sequence of Porphyromonas gingivalis Strain A7A1-28. *Genome Announcement*. 5(10): e00021-17. PMID: 28280013
40. Chastain-Gross RP, Xie G, Bélanger M, Kumar D, Whitlock JA, **Liu L**, Raines SM, Farmerie WG, Daligault HE, Han CS, Brettin TS, Progulske-Fox A (2017) Genome sequence of Porphyromonas gingivalis strain 381. *Genome Announcement*. 5(2): e01467-16. PMID: 28082501
41. * **Liu L**, Chang Y, Yang T, Noren DP, Amina Q, Kornblau S, Ye J. (2016) Evolution-informed modeling improves outcome prediction for cancers. *Evolutionary Applications*. 10(1):68-76. PMID: 28035236
42. *♦ **Liu L**, Tamura K, Sanderford M, Gray VE, Kumar S (2016) A molecular evolutionary reference for the human variome. *Molecular Biology and Evolution*. 33(1):245-54. PMID: 26464126
43. Szedlak A, Smith N, **Liu L**, Paternostro G, Piermarocchi C. (2016) Evolutionary and topological properties of genes and community structures in human gene regulatory network. *PLoS Computational Biology*. 12(6):e1005009. PMID: 27359334
44. Noren DP, Long B, Norel R, Rhrissorrakrai K, Hess K, Hu W, Bisberg A, Schultz A, Engquist E, **Liu L**, Lin E, Chen, G, Xie H, Hunter G, Stepanov O, Norman T, Friend SH, Stolovitzky G, Kornboau S, Qutub AA. (2016) A crowd sourcing approach to developing and assessing prediction algorithms for AML Prognosis. *PLoS Computational Biology*. 12(6):e1004890. PMID: 27351836
45. * Gerek ZN, **Liu L** (co-first author), Gerold K, Biparva P, Thomas ED, Kumar S. (2015) Evolutionary diagnosis of non-synonymous variants involved in differential drug response. *BMC Medical Genomics*. 8;Suppl 1:S6. PMID: 25952014
46. Chastain-Gross RP, Xie G, Belanger M, Kumar D, Whitlock JA, **Liu L**, Farmerie G, Daligault HE, Han CS, Brettin TS, Progulske-Fox A. (2015) Genome sequence of porphyromonas gingivalis strain A7436. *Genome Announcements*. 3(5).e00927. PMID: 26404590
47. Xie G, Chastain-Gross RP, Belanger M, Kumar D, Whitlock JA, **Liu L**, Farmerie G, Daligault HE, Han CS, Brettin TS, Progulske-Fox A. (2015) Genome sequence of porphyromonas gingivalis strain AJW4. *Genome Announcements*. 3(6).e01304. PMID: 26543127
48. *♦ Kumar S, **Liu L**. (2014) No positive selection for G-allele in a p53 response element in Europeans. *Cell*. 157(7):1497-1499. PMID: 24949959
49. *♦ Kumar S, Ye J, **Liu L** (2014) Reply to: “Proper reporting of predictor performance”. *Nature Methods*. 11(8):781-2. PMID: 25075901
50. *♦ Gray VE, **Liu L** (co-first author), Nirankari R, Hornbeck P, Kumar S (2014) Signatures of natural selection on mutations of residues with multiple posttranslational modifications. *Molecular Biology and Evolution*. 31(7):1641-5. PMID: 24739307

51. Stecher G, **Liu L**, Sanderford M, Peterson D, Tamura K, Kumar S. (2014) MEGA-MD: molecular evolutionary genetics analysis software with mutational diagnosis of amino acid variation. *Bioinformatics* 30(9):1305-7. PMID: 24413669
52. *♦ **Liu L**, Kumar S. (2013) Evolutionary balancing is critical for correctly forecasting disease associated amino acid variants. *Molecular Biology and Evolution*. 30(6):1252-7. PMID: 23462317
53. Wellensiek BP, Larsen AC, Stephens B, Kukurba K, Waern K, Briones N, **Liu L**, Snyder M, Jacobs BL, Kumar S, Chaput JC. (2013) Genome-wide profiling of human cap-independent translation-enhancing elements. *Nature Methods*. 10(8):747-50. PMID: 23770754
54. Yin L, Hou W, **Liu L**, Cai Y, Wallet MA, Gardner BP, Chang K, Lowe AC, Rodriguez CA, Sriaroon P, Farmerie WG, Sleasman JW, Goodenow MM (2013) IgM repertoire biodiversity is reduced in HIV-1 infection and systemic lupus erythematosus. *Frontiers in HIV and AIDS*. 4:373. PMID: 24298273
55. *♦ Kumar S, Sanderford M, Gray VE, Ye J, **Liu L** (2012) Evolutionary diagnosis method for variants in personal exomes. *Nature Methods*. 9(9):855-6. PMID: 22936163
56. ♦ Dudley JT, Kim Y, **Liu L**, Markov GJ, Gerold K, Chen R, Butte AJ, Kumar S (2011) Human genomic disease variants: a neutral evolutionary explanation. *Genome Research*. 22(8):1383-94. PMID: 22665443
57. * Kumar S, Dudley JT, Filipowski A, **Liu L** (2011) Phylomedicine: an evolutionary telescope to explore and diagnose the universe of disease mutations. *Trends in Genetics*. 27(9):377-86. PMID: 21764165. PMID: 21764165
58. Yin L, **Liu L**, Sun Y, Hou W, Lowe AC, Gardner BP, Salemi M, Williams WB, Farmerie WG, Sleasman JW, Goodenow MM (2012) High-resolution deep sequencing reveals biodiversity, population structure, and persistence of HIV-1 quasispecies within host ecosystems. *Retrovirology*. 9:108. PMID: 23244298
59. Aggelen GV, Ankley GT, Baldwin WS, Bearden DW, Benson WH, Chipman JK, Collette TW, Craft JA, Denslow ND, Embry MR, Falciani F, George SG, Helbing CC, Hoekstra PF, Iguchi T, Kagami Y, Katsiadaki I, Kille P, **Liu L**, Lord PG, McIntyre T, O'Neill A, Santos EM, Skirrow RC, Snape JR, Tyler CR, Versteeg D, Viant M, Volz DC, Williams TD, Yu L, (2010) Integrating omic technologies into aquatic ecological risk assessment and environmental monitoring: hurdles, achievements, and future outlook, *Environmental Health Perspectives*. 118(1):1-5. PMID: 20056575
60. Spade DJ, Griffith RJ, **Liu L**, Brown-Peterson NJ, Kroll KJ, Feswick a, Glazer RA, Barber DS, Denslow ND. (2010) Queen conch (*Strombus gigas*) testis regresses during the reproductive season at nearshore sites in the Florida Keys. *PloS One*. 5(9):e12737. PMID: 20856805
61. Paul A, **Liu L**, Laughner B, McClung S, Chen S, Ferl R. (2009) Comparative interactomics: analysis of Arabidopsis 14-3-3 complexes reveals highly conserved 14-3-3 interactions between humans and plants. *Journal of Proteome Research*. 8:1913-1924. PMID: 19714877
62. Rosser CJ, **Liu L**, Sun Y, Villicana P, McCullers M, Porvasnik S, Young PR, Parker AS, Goodison S. (2009) Bladder cancer-associated gene expression signatures identified by profiling of exfoliated urothelia. *Cancer Epidemiology, Biomarkers and Prevention*. 18(2):444-53. PMID: 19190164
63. Duan YP, Zhou LJ, Hall DG, Li WB, Doddapaneni H, Lin H, **Liu L**, Sun Y, Gabriel DW, Vahling CM, Williams K, Dickerman A, Gottwald T. (2009) Complete genome sequence of citrus huanglongbing bacterium, 'Candidatus Liberibacter asiaticus' obtained through metagenomics, *Molecular Plant-Microbe Interaction*. 22(8):1011-20 PMID: 19589076

64. Garcia-Reyero N, Kroll KJ, **Liu L**, Orlando EF, Watanabe KH, Sepúlveda MS, Villeneuve DL, Perkins EJ, Ankley GT, Denslow ND. (2009) Gene expression responses in male fathead minnows exposed to binary mixtures of an estrogen and antiestrogen. *BMC Genomics*. 10:308. PMID: 19594897
65. ♦ Sun Y, Cai YP, **Liu L**, Yu F, Farrell M, McKendree W, Farmerie WG. (2009) ESPRIT: estimating species richness using large collections of 16S rRNA shotgun sequences. *Nucleic Acid Research*. 37(10):e76 PMID: 19417062
66. Yu F, Sun Y, **Liu L**, Farmerie WG. (2009) GSTaxClassifier: a genomic signature based taxonomic classifier for metagenomics data analysis. *Bioinformatics*. 4(1):46-49. PMID: 20011152
67. Garcia-Reyero N, Adelman I, **Liu L**, Denslow N. (2008) Gene expression profiles of fathead minnows exposed to surface waters above and below a sewage treatment plant in Minnesota. *Marine Environmental Research*. 66(1):134-6. PMID: 18417205
68. Garcia-Reyero N, Griffitt RJ, **Liu L**, Kroll KJ, Farmerie WG, Barber DS, Denslow ND. (2008) Construction of a robust microarray from a non-model species (largemouth bass) using pyrosequencing technology. *Journal of Fish Biology*. 72(9):2354-2376. PMID: 19936325
69. Sun Y, Goodison S, Li J, **Liu L**, Farmerie WG. (2007) Improved breast cancer prognosis through the combination of clinical and genetic markers. *Bioinformatics*. 23(1):30-37. PMID: 17130137
70. Popp MP, **Liu L**, Timmers A, Esson DW, Shiroma L, Meyers C, Berceci S, Tao M, Wistow G, Schultz GS, Sherwood MB. (2007) Development of a microarray chip for rabbit ocular research. *Molecular Vision*. 13:164-73. PMID: 17293780
71. Luo X, Pan Q, **Liu L**, Chegini N. (2007) Genomic and proteomic profiling II: Comparative assessment of gene expression profiles in leiomyomas, keloids, and surgically-induced scars. *Reproductive Biology and Endocrinology*. 5(1):35. PMID: 17718906
72. Larkin P, Villeneuve DL, Knoebl I, Miracle AL, Carter BJ, **Liu L**, Denslow ND, Ankley GT. (2007) Development and validation of a 2,000-gene microarray for the fathead minnow (*Pimephales promelas*). *Environmental Toxicology and Chemistry*. 26(7):1497-506. PMID: 17665692
73. ♦ Moroz LL, Edwards JR, Puthanveetil SV, Kohn A, Ha T, Heyland A, Knudsen B, Sahni A, Yu F, **Liu L**, Jezzini S, Sadreyev R, Lovell P, et al. (2006) neuronal transcriptome of Aplysia: neuronal compartments and circuitry. *Cell*. 127(7):1453-1467. PMID: 17190607
74. Chao EM, **Liu L**, Farmerie WG, Keyhani NO (2006) EST analysis of cDNA libraries from the entomopathogenic fungus *Beauveria (Cordyceps) bassiana*. *Microbiology*. 152(Pt 9):2843-54. PMID: 16946278
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76. Farmerie WG, Hammer J, **Liu L**, Sahni A, Schneider M. (2005) Biological workflow with BlastQuest. *Data and Knowledge Engineering*. 53(1):75-97
77. Kornberg LJ, Villaret D, Popp MP, **Liu L**, McLaren R, Brown H, and McFadden M. (2005) Gene expression profiling in squamous cell carcinoma of the oral cavity shows abnormalities in several signaling pathways. *Laryngoscope*. 115(4):690-8. PMID: 15805883

78. Esson DW, Popp MP, **Liu L**, Schultz GS, Sherwood MB. (2004) Microarray analysis of the failure of filtering blebs in a rat model of glaucoma filtering surgery. *Investigative Ophthalmology and Visual Science*. 45(12):4450-62. PMID: 15557454
79. Cousins RJ, Blanchard RK, Popp MP, **Liu L**, Cao J, Moore JB and Green CL. (2003) A global view of the selectivity of zinc deprivation and excess on genes expressed in human THP-1 mononuclear cells. *Proceedings of the National Academy of Science*. 100:6952-6957. PMID: 12756304
80. Li YJ, **Liu L**, Zhang FC. (2003) The clinical significance of SSA antigen and its different positive expressions. *Zhonghua Nei Ke Za Zhi*. 42(3):165-8. PMID: 12816697

Conference proceedings: (full research articles)

81. *[§] Guan X[§], **Liu L**. (2018) Know-GRRF: Domain-knowledge informed biomarker discovery with random forests. *6th International Work-conference on Bioinformatics and Biomedical Engineering*. Granada, Spain.
82. Li Y, Wang J, Yang T, Chen J, **Liu L**, Zhan L, Hibar DP, Jahanshad N, Wang Y, Zhao S, Thompson PM, Ye J, (2016) Identification of Alzheimer's disease risk factors by tree-structured group lasso screening. *IEEE International Symposium on Biomedical Imaging*
83. Yang T, Wang J, Sun Q, Hibar DP, Jahanshad N, **Liu L**, Wang Y, Zhan L, Thompson PM, Ye J (2015) Detecting genetic risk factors for Alzheimer's disease in whole genome sequence data via lasso screening. *IEEE International Symposium on Biomedical Imaging*
84. Sun Y, **Liu L**, Popp M, Farmerie W. (2006) Estimation of cross-hybridization signals using support vector regression. *First International Multi-Symposiums on Computer and Computational Sciences (IMSCCS'06)*

Editorials:

85. * **Liu L**, Li F, Liu X, Wang K, Zhao Z (2025). Frontiers of Computational and Artificial Intelligence Models in Cancer Research. *Cancers*. (accepted)
86. Li F, **Liu L**, Wang K, Liu X, Zhao Z (2024). Intelligent biology and medicine: accelerating innovative computational approaches. *Computational and Structural Biotechnology Journal*. 27:32-34

Manuscripts submitted and under review:

- R1. *[§] Mudappathi R, Patton T, Chen H, Ping Y, Sun Z, Wang P, Shi C, Wang J, **Liu L**. reg-eQTL: Integrating transcription factor effects to unveil regulatory variants. *American Journal of Human Genetics* (revised and resubmitted).
- R2. * **Liu L**. Li F, Liu X, Wang K, Zhao Z. Frontiers of computational and artificial intelligence models in cancer research. *Cancers*
- R3. [§] Mudappathi R, Maguire A, Yi ES, Peng Y, Kachergus J, Khoor A, Tan K, Zaniletti I, Wampfler JA, Shi J, Lou Y, Santos PA, Cunha JD, Sun Z, **Liu L**, Jelinek DF, Wang J, Tazelaar HD, Thompson EA, Yang P. Spatially defined intratumoral immune response signatures in resected T1-2N0M0 non-small cell lung cancer predict recurrent versus second primary tumors. *Precision Clinical Medicine* (revised and resubmitted)
- R4. [§] Panwen Wang, **Liu L**, Wang J, Yang P, Sun Z. ceQTL: A co-expression QTL model to reveal mediators between variants and target genes. *RECOMB 2025*
- R5. Alexis's paper

Manuscripts under preparation:

- U1. *§ Mudappathi R, Nyarige V, **Liu L**. CITE-Traffick: Computational modeling of intracellular protein transportation using single-cell sequencing data.
- U2. *§ Mudappathi R, Nyarige V, **Liu L**. scGGC: guided clustering of single-cell multi-omics data.
- U3. *§ Chen H, **Liu L**. TEATIME: Multidimensional Analysis of Pan-Cancer Evolutionary Trajectories
- U4. *§ Chen H, **Liu L**. Domain under selection in tumors
- U5. *§ Patton T, **Liu L**. Effectiveness of culture health navigators in promoting COVID-19 vaccination among refugee pregnant and lactating women in Arizona

CONFERENCE ORAL PRESENTATIONS:

- O1. Shifting Focus from Gene-centric to Evolution-centric Analyses in Cancer Genomics. *Annual conference of the Society of Molecular Biology and Evolution*. Puerto Vallarta, Mexico. 2024
- O2. Discovering condition-specific cell populations via integrative clustering of single-cell data. *International Conference on Intelligent Biology and Medicine*. Houston, TX, USA. 2024 (presented by student).
- O3. DeepCORE: An interpretable multi-view deep neural network model to detect co-operative regulatory elements. *International Conference on Intelligent Biology and Medicine*. Tampa, FL, USA. 2023 (presented by student).
- O4. A mouse-specific model to detect genes under selection in tumors. *International Conference on Intelligent Biology and Medicine*. Tampa, FL, USA. 2023 (presented by student).
- O5. Evolution of COVID-19 health disparities in Arizona. *27th Annual Conference of the Society for Social Work and Research*. Phoenix, AZ, USA. 2023.
- O6. Classifying refugee status using common features in EMR. *International Conference on Intelligent Biology and Medicine*. Philadelphia, USA. 2022 (presented by student).
- O7. The role of multi-level genetic diversity in cancers. *Annual conference of the Society of Molecular Biology and Evolution*. Online. 2021
- O8. Discovering subclones in tumors sequenced at standard depths. *17th Annual Rocky Mountain Bioinformatics Conference, a meeting of the International Society for Computational Biology*. Aspen, Colorado, USA. 2019
- O9. Deep learning based multi-view model for deciphering gene regulatory networks. *17th Annual Rocky Mountain Bioinformatics Conference, a meeting of the International Society for Computational Biology*. Aspen, Colorado, USA. 2019 (presented by student).
- O10. Know-GRRF: domain-knowledge informed biomarker discovery with random forests. *6th International Work-conference on Bioinformatics and Biomedical Engineering*. Granada, Spain. 2018
- O11. Contextual selection of cancer drivers & clinical implications. *4th Annual Arizona Biomedical Research Centre Research Conference*. Phoenix, AZ, 2018
- O12. Biological adaptability as a biomarker for risk assessment. *Arizona Alzheimer's Consortium Annual Conference*. Sedona, AZ, 2018
- O13. Fast fine mapping of causal eQTL variants. *International Symposium on Molecular Evolution and Medicine*, Philadelphia, PA, 2017
- O14. Evolution-informed biomarker discovery for precision oncology, *6th International Conference on Bioinformatics & Systems Biology*, Philadelphia, PA, 2016
- O15. An evolutionary diagnosis method for variants in personal exomes. *Phylomedicine Symposium*, Tempe, AZ, 2012

CONFERENCE POSTERS:

- P1. COVID-19 Vaccination Rates Among Diverse Pregnant and Lactating Refugee Women. *North American Refugee Health Conference*. Minneapolis, MN. 2024
- P2. COVID-19 Vaccination Rates Among Diverse Pregnant and Lactating Refugee Women. *Biodesign FUSION Research Retreat*. Phoenix, AZ. 2024 – “Best Use of Big Data” Award
- P3. Spatially Defined Immune Response Signatures in 5µm Tumor Section of Resected T1-2N0M0 Lung Cancer Predict Clinical Outcome. *IASLC 2023 World Conference on Lung Cancer*. Singapore. 2023
- P4. Discovery of DNA methylation protector element in human genome. *International Conference on Intelligent Biology and Medicine*. Philadelphia, USA. 2022
- P5. DeepCore: Attention-based interpretable deep learning approach for detecting regulatory elements. *International Conference on Intelligent Biology and Medicine*. Philadelphia, USA. 2022
- P6. Discovering subclones in tumors sequenced at standard depths. *17th Annual Rocky Mountain Bioinformatics Conference*, a meeting of the International Society for Computational Biology. Aspen, Colorado, USA. 2019
- P7. Deep learning based multi-view model for deciphering gene regulatory keywords. *17th Annual Rocky Mountain Bioinformatics Conference*, a meeting of the International Society for Computational Biology. Aspen, Colorado, USA. 2019
- P8. Contextual selection of cancer driver genes & clinical implications. *Annual Conference of the Society for Molecular Biology and Evolution*, Manchester, UK. 2019
- P9. Know-GRRF: domain-knowledge informed biomarker discovery with random forests. *6th International Work-conference on Bioinformatics and Biomedical Engineering*. Granada, Spain. 2018
- P10. Decomposing cancer subclonal structures with model-based clustering. *International Symposium on Molecular Evolution and Medicine*, Philadelphia, PA. 2017
- P11. Discover eQTL with flexible LD structure and tree-guided group lasso, *Pacific Symposium on Bio-computing*, Hawaii, USA. 2016
- P12. Distinct evolutionary and mutational patterns in oncogenes and tumor suppressor genes, *AACR Annual Meeting*, Philadelphia, USA. 2015

INVITED TALKS

- T1. Genetic and epigenetic resilience during aging. *Neuro Conclave*. Online. 2024
- T2. Exploring ChatGPT's ability to generate novel algorithms in bioinformatics. *International Conference on Intelligent Biology and Medicine*. Tampa, USA. 2023
- T3. Biomedical informatics training in diverse environments. *International Conference on Intelligent Biology and Medicine*. Philadelphia, USA. 2022
- T4. Reduced genetic diversity as a risk factor of Alzheimer's disease. Mayo Clinic, Scottsdale, AZ. 2018.
- T5. Genomics for Alzheimer's disease. Phoenix Veterans Affairs Health Care System, Phoenix, AZ. 2018.
- T6. Shooting the moving target in cancer combat. Midwestern University, Glendale, AZ. 2017
- T7. Understanding the genetic basis of human diseases in an evolutionary framework. Mayo Clinic Arizona, Scottsdale, AZ. 2017
- T8. Computational genomics: identifying biomarkers for precision medicine. AZBio Expo, Phoenix, AZ. 2016.
- T9. Evolution-informed modeling. *RECOMB/ISCB Conference*, San Diego, CA, 2014
- T10. Having a BLAST with BlastQuest: Where do we go from here? *INFORMS Annual Meeting*, Denver, CO, 2004

PATENTS

- 2023 Inventor, DNA METHYLATION BARRIERS (provisional, US Patent Number 63/522,078).
 2017 Inventor, IMMUNOSIGNATURE MICROARRAY ANALYSIS AND IMMUNOSIGNATURES IN SYSTEMIC LUPUS ERYTHEMATOSUS (provisional, US Patent Number 62/547,748).

SOFTWARE

- ❖ DeepCORE: An interpretable multi-view deep neural network model to detect co-operative regulatory elements
<https://github.com/liliulab/DeepCORE>
- ❖ GUST: Genes under selection in tumors
<https://github.com/liliulab/gust>
- ❖ GUST-mouse: Genes under selection in tumors for mice
<https://github.com/liliulab/gust.mouse>
- ❖ Know-GRRF: Know-guided regularized random forests
<https://cran.r-project.org/web/packages/KnowGRRF>
- ❖ MAGOS: Model-based Adaptive Grouping of Subclones
<https://github.com/liliulab/magos>
- ❖ TreeMap: A Nested Machine- and Statistical-Learning Approach to Discover Causal Variant
<http://github.com/liliulab/treemap>
- ❖ TreeGuidedLasso: An R implementation of the tree-guided group lasso algorithm
<https://github.com/pbchandr/TreeGuidedLasso>
- ❖ RIS: Refugee identification system
<http://github.com/liliulab/ris>
- ❖ J-score: A metric of clustering accuracy
<https://cran.r-project.org/web/packages/jScore>
- ❖ address2geocoord: Conversion of home addresses to geographical coordinates with masking
<https://github.com/liliulab/address2geocoord>

TEACHING & MENTORING

Overview of teaching and mentoring activities

Courses taught at ASU	21
Curriculum developed	8
Mentor of postdoctoral scholars	4
Committee chair (co-chair)	
Doctoral students	9 (5 have graduated)
Master students	10 (9 have graduated)
Undergraduate students: Honor's thesis and Capstone project	10 (10 have graduated)
Committee member	
Doctoral students	10 (8 have graduated)
Training grant proposals developed	3 (1 funded)

COURSES TAUGHT AT ASU

Course	Semester	New curriculum development	Enrolled	Instructor Score (out of 5)	Note
BMI-101: Introduction to Biomedical Informatics (undergraduate level, 3 credits)					
	Fall 2015	✓	29	4.1	
BMI-201: Introduction to Clinical Informatics (undergraduate level, 3 credits)					
	Fall 2020		74	4.3	Online iCourse First time taught
BMI-311: Modeling Biomedical Knowledge (undergraduate level, 3 credits)					
	Fall 2016	✓	9	4.5	
	Fall 2017		18	4.4	
	Fall 2018		21	4.7	
	Fall 2019		20	4.6	
	Fall 2020		31	4.8	Taught remotely
	Fall 2021		18	4.6	
	Fall 2022		16	4.8	
	Fall 2023		16	4.8	
BMI-312: Modeling Biomedical Data (undergraduate level, 3 credits)					
	Spring 2019	✓	16	4.9	
	Spring 2020		18	4.8	
	Spring 2021		21	4.7	
	Spring 2022		18	4.5	
BMI-330: Topics in Translational Bioinformatics (undergraduate level, 3 credits)					
	Spring 2017	✓	15	4.8	
	Spring 2018		19	4.5	
	Spring 2019		20	4.9	
	Spring 2020		22	4.8	
	Spring 2021		26	4.9	
	Spring 2022		20	4.8	
	Spring 2023		27	4.9	
	Spring 2024		6	4.8	
BMI-550: Translational Bioinformatics * (graduate level, 3 credits)					
	Spring 2016	✓	13	4.4	
BMI-570: BMI Symposium (graduate level, 1 credit)					
	Fall 2016		23	4.8	
	Fall 2017		17	4.1	
BMI-110: Introduction to Python *					

(undergraduate level, 3 credits)

Spring 2022 ✓

NTR-598: Topic: AI & Precision Nutrition
(graduate level, 3 credits)

Spring 2025 ✓

* Course materials I developed are currently used by other instructors at ASU.

WORKSHOPS

Precision Nutrition & AI Introductory bootcamp Summer 2024, August 12 – 16
Developed the curriculum, delivered the lectures, and guided hands-on projects.

GUEST LECTURES

AT ASU

BMI-201: Introduction to Clinical Informatics	Fall 2017, Recorded videos on two topics for online courses
BMI-461: Advanced Topics in BMI I	Fall 2019, Fall 2020, Fall 2021, Fall 2022, Fall 2023, Fall 2024
BMI-540: Problem-solving in BMI	Fall 2019, Fall 2020, Fall 2021, Fall 2022, Fall 2023, Fall 2024
BMI-505: Foundations of BMI Methods II	Spring 2020

OUTSIDE ASU

Pre-clerkship MBLD block: The Molecular Basis of Life and Disease	Fall 2018
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MENTOR OF POSTDOCTORAL SCHOLARS

<i>Abdulkadir Elmas, Ph.D.</i>	2016-2017
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Dr. Elmas is now an assistant professor at Giresun University in Turkey, and currently works in the Icahn School of Medicine at Mount Sinai as a participant of an international exchange program.

<i>Hope Lancaster, Ph.D.</i>	2017-2020
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Dr. Lancaster is now a faculty and director of Etiologies of Language and Literacy Laboratory at Boys Town National Research Hospital

<i>Rekha Mudappathi, Ph.D.</i>	2024-
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Dr. Mudappathi studies multi-omics data integration in my lab at ASU.

<i>Alex Mohr, Ph.D.</i>	2024-
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Dr. Mohr studies AI and precision nutrition in Dr. Whisner's lab at ASU.

COMMITTEE CHAIR (CO-CHAIR)

Doctoral Students

1. <i>Xin Guan, Ph.D.</i>	2015-2017 (co-chair)
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Dissertation: Novel methods of biomarker discovery and predictive modeling using random forest

Publications: three peer-reviewed articles, two as the first author.

Dr. Guan is now a data scientist at the Intel Inc.

2. *Navid Ahmadinejad, Ph.D.* 2016-2019
 Dissertation: Discovering subclones and their driver genes in tumors sequenced at standard depths
 Publications: four peer-reviewed articles, two as the first author.
 Dr. Ahmadinejad is now a data scientist at the Illumina Inc.
3. *Pramod Chandrashekar, Ph.D.* 2016-2020
 Dissertation: Deep learning based multi-view model for deciphering genetic regulatory keywords
 Publications: five peer-reviewed articles, three as the first author.
 Dr. Chandrashekar is a postdoctoral research associate at University of Wisconsin-Madison.
4. *Verah Nyarige, Ph.D.* 2018-2022
 Dissertation: Novel bioinformatics methods for co-expression analysis of time series transcriptome data
 Dr. Nyarige is now a bioinformatics scientist at Bristol Myers Squibb.
5. *Rekha Mudappathi, Ph.D.* 2022-2023
 Dissertation: Unveiling cellular complexity, genetic regulation and protein trafficking dynamics through integration of multi-omics insights
 Dr. Mudappathi is now a postdoctoral research associate at ASU.
6. *Jingmin Shu* 2020-
 Dissertation: TBD
7. *Hai Chen* 2020-
 Dissertation: TBD
8. *Tatiana Patton* 2022-
 Dissertation: TBD
9. *Naif Ganadily* 2024-
 Dissertation: TBD

Master Students

10. *Brian Hanratty, M.S.* 2015-2016
 Applied project: An improved workflow for bisulfite sequencing analysis.
 Mr. Hanratty is now a bioinformatics scientist at the Fred Hutchinson Cancer Research Center.
11. *Margaret Linan, M.S.* 2015-2016
 Applied project: The best practice to pre-process amplicon reads
 Ms. Linan is now a research scientist at the Icahn School of Medicine at Mount Sinai.
12. *Ai-sawan Jonguksawas, M.S.* 2016
 Applied project: Exploring common autoantibodies derived from NAPPA screening studies in breast cancer, diabetes, and lung cancer populations

13. *Anna Freydenzon, M.S.* 2016-2017
Applied project: Evolution-informed biomarker discovery for staging ER+ breast carcinomas
Ms. Freydenzon is now a PhD candidate at the University of Queensland.
14. *Rabia Maqsood, M.S.* 2018
Applied project: Effects of microRNA-15b in breast cancer
Ms. Maqsood is now a bioinformatics scientist at the Biodesign Institute.
15. *Jingmin Shu, Ph.D., M.S.* 2020
Applied project: The role of transposable elements in tumorigenesis.
16. *Abdelrahman Younis, M.S.* 2021
Applied project: The Correlation between Education Level and Health Awareness (Vaccination rates for Flu, Pneumonia and Shigella)
17. *Frederick Chang, M.S.* 2022
Applied project: Examine American Indian Health Population's glycemic control using Medicaid AHCCCS claims data in conjunction with Arizona's Health Information Exchange
18. *Vanessa Nobles, M.S.* 2021-2023
Applied project: Classify refugee status using EMR data
19. *Tanner Soderblom* 2024-
- Barrett Honors Thesis***
20. *Richard Li, B.S.* 2018-2019
Thesis: A retrospective investigation to assess the potential application of predictive machine learning algorithms in oncology clinical trials
Mr. Li is now a medical student at the Carle Illinois College of Medicine
21. *Maria Bobby, B.S.* 2022-2023
Thesis: Examining the significance of economic connectedness as an indicator of disparities in COVID-19 infection risk in Arizona ZCTAs
- Undergraduate Capstone Projects***
22. *Shayna Troftgruben, B.S.* 2018-2019
Project: Order of mutations in cancer genomes
Ms. Troftgruben is now a software engineer at the Harris Corporation.
23. *Yara Hawwari, B.S.* 2018-2019
Project: Database and web application of genes driving oncogenesis
Ms. Hawwari is now a data analyst at the Banner Corporate Center.
24. *Matthew Lee* 2019-2020
Project: Discover regulatory elements using deep-learning models
25. *Ryan Pan* 2020-2021

- Project: Tissue-specific eQTL discovery in human brains
26. *Jason Reyes* 2020-2021
Project: Tissue-specific eQTL discovery in mouse brains
27. *Sarah Paul* 2020-2021
Project: Gene expression markers in extracellular vesicles in tumors
28. *Malia Morrison* 2020-2021
Project: Improve interoperability of clinical databases at Valleywise Clinics
29. *Savannah Graffin* 2021-2022
Project: Clonal hematopoiesis in multiple myeloma.

COMMITTEE MEMBER

Doctoral Students

30. *Chaoxing Li, Ph.D.*, 2016-2017
Molecular and Cell Biology, School of Life Sciences
Dissertation: Topological analysis of biological pathways: genes, microRNAs and pathways involved in hepatocellular carcinoma
31. *Caitlin Vose, Ph.D.* 2016-2018
Speech and Hearing Science, College of Health Solutions
Dissertation: Genetic Variations and associated electrophysiological and behavioral traits in children with childhood apraxia of speech
32. *Shobana Sekar, Ph.D.* , 2016-2018
Biomedical Informatics, College of Health Solutions
Dissertation: Circular RNA characterization and regulatory network prediction in human tissue
33. *Laurel Bruce* 2018-2020
Speech and Hearing Science, College of Health Solutions
Dissertation: Biomarkers of familial speech sound disorders: genes, perception, and motor control
34. *Matteo Vaiente* 2018-2020
Biomedical Informatics, College of Health Solution
Dissertation: Learning RNA viral disease dynamics from molecular sequence data
35. *Michelle Winerip, Ph.D.* 2016-2021
Biomedical Informatics, College of Health Solutions
Dissertation: Protein network informed feature selection of candidate proteomic biomarkers in the presence of disease heterogeneity
36. *Carmen Ortega Santos, Ph.D.* 2018-2021
School of Nutrition & Health Promotion, College of Health Solutions
Dissertation: Exercise, genistein, and the combined effect on gut microbiota and mitochondrial oxidative capacity after 12-week of a Western diet on C57BL/6J adult mice

37.

38. *Yookyung Kim* 2020-
Speech and Hearing Science, College of Health Solutions
Dissertation: TBD
39. *Courtney Grigsby* 2021-
Biology, School of Life Sciences
Dissertation: TBD

INTERNSHIP AND SCHOLARSHIPS AWARDED TO STUDENTS

- *Verah Nyarige*, Google Women Techmakers Scholar, American Association of University Women Scholar, Schlumberger Foundation Scholar, International Association of Intelligent Biology and Medicine Fellowship
- *Matthew Lee*, bioinformatics summer intern at Harvard Medical School
- *Megan Hiestand*, cancer bioinformatics summer intern at Memorial Sloan Kettering Cancer Center
- *Yaohan Ding*, bioinformatics iSURE fellow at University of Notre Dame, and
- *Austin Gutierrez, Komal Agrawal, Bryce Turner, Andrew Jarman, Matthew Lee, Richard Li, Bianca Argente, and Saahithi Mallapragada* – eight Helico Scholars at TGen.

TRAINING GRANT PROPOSALS

funded

NIH T32	MPI: Wu, Li, Co-I: Liu	\$1,808,715
Advance translational research on AD and AD-related dementias		

Submitted but not funded

NSF Research Traineeship	MPI: Sterner & Liu	\$2,999,916
Biodiversity data science from discovery to governance		
NIH T15	PI: Wang, Co-I: Liu	\$ 5,577,873
Integrated research training in biomedical informatics & data science (bmi x ds)		

COMMUNITY OUTREACH

PRESENTATIONS TO COMMUNITY GROUPS

- ❖ *Biotechnology industry*
 - In the AZBio Expo 2016, I presented to over 300 attendees of the “Arizona IT and Life Science Innovators” session to promote translational applications of biomedical informatics.
 - In 2018, I presented to 37 Chinese entrepreneurs who visited the Biodesign Institute at ASU to discuss the newest advances and future direction of artificial intelligence in precision medicine.
- ❖ *Clinicians*
 - In 2018, I gave a lecture on the genetic basis of Alzheimer’s disease. It was held on the Mayo Clinic Scottsdale campus and broadcast to four Mayo Clinic locations nationwide. More than 40 physicians and clinical staff attended my talk as a part of the graduate medical education accreditation (GME) program.
 - In 2018, I gave the same lecture on the genetic basis of Alzheimer’s at the Phoenix VA Hospital. About 20 physicians and clinical staff attended my talk and received GME credits.
- ❖ *Patients and families*

- In 2017, I was invited to present to the Valley Engineering, Science & Technology Club in Sun City West, Arizona. The audience was a group of more than 250 retirees, many of whom are cancer survivors or their family members. I discussed the latest advances in precision oncology and offered consultations.

WORKSHOPS

- ❖ *Cancer evolution and precision oncology.*
I was invited twice to give this workshop. The first time was at the Precision Medicine Leaders Summit, San Diego, CA in 2017. The second time was at the Peking Union Medical College, Beijing, China in 2017. A total of 60 people attended this workshop.
- ❖ *Bioinformatics and biostatics workshop at ASU.*
I was the advisor of 25 workshops that covered various topics of bioinformatics and biostatistics.

TRANSLATIONAL INITIATIVES

- ❖ *Behavioral Genomics Initiative*
In 2019, I joined the ASU Leadership Academy program. Working with six researchers at ASU in different fields, we built the Behavioral Genomics Initiative group. Our vision is to upend the management of behavioral, developmental, and mental health conditions in children and adolescents through research, education and community outreach. I lead the bioinformatics effort in this initiative to study genetic-environment interactions
- ❖ *Maternal-Child Health (MCH) Translational Team*
As a research co-lead, we kicked off the MCH team in February 2020. Our team involves community network, healthcare network, training, and research to address healthcare needs of children and mothers, focusing on behavioral health, opioid crisis, obesity prevention and social determinants of health.

SERVICES

COMMITTEES AT ASU

University level

2024-present	Member, Biodesign FUSION Retreat Planning Committee
2023-present	Advisor, ADHS Statewide Genomics Platform Initiative
2023-present	Advisor, Data and Data Science Core, ASU Research Computing
2018-present	Advisor, Bioinformatics Core, ASU Biosciences Research Facility
2016-present	Reviewer, ASU Limited Submission
2016-2018	Director, Founder, Bioinformatics Core, Biodesign Institute
2017-2019	Reviewer, Mayo/ASU Alliance for Health Care Collaborative Research Seed Grant

College level

2022-2023	Chair, CHS Metabolomics Faculty Search Council
2022	Member, CHS/Biodesign Microbiome Faculty Search Council
2020-present	Member, CHS Research Council
2022-present	Member, Committee on Committees
2022-present	Member, Personnel Committee (Ad Hoc Annual Review)
2022-present	Member, Grant Review Committee
2020-2021	Member, CHS Biostats Faculty Search Committee
2018-2020	Member, CHS Affinity Network Committee
2019	Reviewer, CHS JumpStart program

2015–2018 Member, CHS Standards & Grievance Committee
 2015 Member, CHS Student Engagement Committee

Program level

2023-present Member, BMI/BMD Admission Committee
 2020-2022 Chair, BMI/BMD Admission Committee
 2020-2022 Member, BMI/BMD Academic Program Committee
 2021-2022 Member, APR BMI/BMD Self-Study Committee
 2019-2020 Member, BMI/BMD Admission Committee
 2017–2019 Chair, BMI Recruitment Committee
 2018–2019 Member, BMI Academic Program Committee
 2016–2017 Member, BMI Recruitment Committee
 2016 Member, BMI Training Grant Planning Committee

NATIONAL & INTERNATIONAL LEVEL

Journal editor

- 2019–Present Associate Editor, *Molecular Biology and Evolution* (IF=14.8)
- 2024–Present Associate Editor, *Frontiers in Bioinformatics* (IF=2.8)
- 2024–Present Associate Editor, *Human Brain* (new journal)
- 2019–2021 Guest Editor, *Frontiers in Genetics* (IF=3.5)

Conference organizer

- 2024–present Member, Planning Committee
Biodesign FUSION Retreat (Tempe, AZ)
- 2022–2023 Co-chair, Program Committee
International Conference on Intelligent Biology and Medicine (ICIBM 2023, Tampa, FL)
- 2022 Session Chair, Informatics in team science: to lead, support, and educate
International Conference on Intelligent Biology and Medicine (ICIBM 2022, Philadelphia, PA)
- 2021 Co-chair, Symposium of Phylomedicine and Tumor Evolution
Annual Conference of the Society of Molecular Biology and Evolution (SMBE 2021, Virtual)

Ad hoc grant reviewer

- 2022–Present National Institutes of Health
- 2016–2019 Ireland Health Research Board
- 2020 Israel Science Foundation

Ad hoc manuscript reviewer

- Science
- Nature Communications
- Nature Genetics
- Molecular Biology and Evolution
- Nucleic Acid Research
- Bioinformatics
- BMC Bioinformatics
- BMC Medical Genomics
- BMC Evolutionary Biology

- Alzheimer's & Dementia
- Pacific Symposium on Biocomputing