

**Li Liu, MD. MS.**

Associate Professor

College of Health Solutions | Arizona State University  
6161 E Mayo Blvd, Phoenix, AZ 85054[liliu@asu.edu](mailto:liliu@asu.edu)

480.727.9813

<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
----------------	-----------------------------	---

**University of Florida**

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

**TripodSoft, Inc.**

2001 – 2002	Bioinformatics Scientist	TripodSoft, Inc. Edison, NJ, USA
-------------	--------------------------	-------------------------------------

## 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
2005-2010	Member, the Association of Biomolecular Resource Facilities

### HONORS & AWARDS

2017	Nomination of Searle Scholar
2014	1 <sup>st</sup> place in the DREAM9 AML Challenge
1998	China-Switzerland Medical Student Scholarship

### SPONSORED RESEARCH GRANTS (since 2015)

#### *List of funded research grants*

---

As PI/MPI:

---

1. Discover and analyze germline-somatic interactions in cancer  
NIH-R01 2021 – 2024  
PI: Liu
2. 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. 2023 – 2025  
PI: Koskan, Liu, Johnson  
MPI: Liu. I lead the research of building an Artificial Intelligence system to identify risk factors and susceptible individuals.
3. Targeting Whole-body Fatty Acid Metabolism in Alzheimer's Disease, with Special Interest in Lauric acid  
Florida International University 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.
4. 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 2020 – 2021  
 PI: Johnston, Chang, Liu  
 MPI: Liu. I lead statistical analysis of clinical trial data and immunological data, and data mining efforts.
5. Annotate functional genetic variants  
 Mayo Clinic 2019 – 2022  
 PI: Liu
6. Precision diagnosis of pathogenic noncoding variants in diabetes  
 Flinn Foundation 2019 – 2021  
 PI: Liu
7. eQTL mega-analysis for functional assessment of multi-enhancer gene regulation  
 Georgia Institute of Technology 2016 – 2020  
 PI: Liu. I am the site PI of an NIH grant (R01, \$757K) awarded to Dr. Gibson at Georgia Institute of Technology.
8. Reduced genomic diversity as a risk factor for nonfamilial young onset Alzheimer' disease  
 Mayo Clinic 2018 – 2020  
 PI: Liu. I am a site PI of a philanthropic grant (\$1M) awarded to Dr. Caselli at Mayo Clinic.
9. Prioritize functional genetic variants in melanoma with network biology and evolution  
 Flinn Foundation 2017 – 2019  
 PI: Liu
10. Discovering the roles of cellular adaptability in late-onset Alzheimer's disease  
 Arizona Alzheimer's Consortium 2017 – 2018  
 PI: Liu
11. Subclonal diversity: prognostic role in acute myeloid leukemia patients with minimal residual disease  
 Mayo / ASU Health Alliance Seed Grant 2016 – 2017  
 PI: Liu. This is an intramural grant.
12. Discovering immunosignatures of systemic lupus erythematosus  
 Healthtell Inc. 2016 – 2017  
 PI: Liu

---

 As Co-I
 

---

13. Leveraging bio-cultural mechanisms to maximize the impact of multi-level preventable disease interventions with southwest populations  
 NIH-U54 supplement 2020 – 2022  
 PI: Marsiglia
14. Arizona Cancer and Evolution (ACE) Center  
 NIH (U54) 2018 – 2023  
 PI: Maley
15. 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) 2020 – 2025

PI: Petrov & Whisner

16. Genotype-phenotype associations in reading disorders  
NIH (F32) 2017-2019  
PI: Lancaster
17. Multiple genomics data to predict drug response  
Mayo Clinic 2019  
PI: Runger
18. Rapid nanoplasmonic quantification of tumor-derived EVs for pancreatic cancer diagnosis  
Baylor Scott & White Health 2017 – 2019  
PI: Hu
19. Nanoplasmonic quantification of tumor-derived circulating extracellular vesicles  
Fred Hutchinson Cancer Research Center 2017 – 2019  
PI: Fan

## PUBLICATIONS

*Journal articles: (peer reviewed, in reverse-chronological order)*

\* lead-author publication; § publication with student/trainee authors; ♦ IF>10

1. \*§ Shen FL<sup>§</sup>, Shu J<sup>§</sup>, Lee M<sup>§</sup>, Oh H, Li M, Runger G, Marsiglia F, **Liu L**. (2022) Evolution of COVID-19 health disparities in Arizona. *Journal of Immigrant and Minority Health*. In press
2. \*§ Morrison M<sup>§</sup>, Nobles V<sup>§</sup>, Johnson-Agbaksu C, Bailey C, **Liu L**. (2022) Classify refugee status using common features in EMR. *Chemistry and Biodiversity*. 19(10):e202200651. PMID: 36050919
3. \*§♦ Ahmadinejad N<sup>§</sup>, Troftgruben S<sup>§</sup>, Wang J, Chandrashekar P<sup>§</sup>, Dinu V, Maley C, **Liu L**. (2022) Accurate identification of subclones in tumor genomes. *Molecular Biology and Evolution*. 39(7):msac136. PMID: 35749590
4. § Fessler SN<sup>§</sup>, **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*. (Online ahead of print). PMID: 36084236
5. \*§ Lee M<sup>§</sup>, Chang Y, Ahmadinejad N<sup>§</sup>, Johnson-Agbaksu C, Bailey C, **Liu L**. (2022) COVID-19 mortality is associated with pre-existing impaired innate immunity in health condition. *PeeJ*. 10: e13227. PMID: 35547187
6. \*§ **Liu L**, Chandrashekar P<sup>§</sup>, 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
7. 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
8. 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

9. 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/Acurrucadito 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
10. \* **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
11. ♦ 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
12. §♦ Liu Y, Fan J, Xu T, Ahmadinejad N<sup>§</sup>, 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):eaz6162. PMID: 32195353
13. \*§ Guan X<sup>§</sup>, Runger G, **Liu L**. (2020) Dynamic incorporation of prior knowledge from multiple domains in biomarker discovery. *BMC Bioinformatics*. 21(Suppl 2):77 PMID: 32164534
14. \*§ Chandrashekar P<sup>§</sup>, Ahmadinejad N (co-first-author)<sup>§</sup>, 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
15. 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
16. 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
17. § Peter B, Dinu V, **Liu L**, Huentelman M, Naymik M, Lancaster H<sup>§</sup>, Vose C<sup>§</sup>, 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
18. \*§♦ **Liu L**, Maxwell D, Patel R, Chandrashekar P<sup>§</sup>, Gibson G, Kumar S. (2019) Biological relevance of computationally predicted pathogenicity of noncoding variants. *Nature Communications*. 10:330. PMID: 30659175
19. 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
20. \* **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
21. § Li C<sup>§</sup>, **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
22. 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
23. 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

24. 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
25. 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
26. \* **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
27. \*♦ **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
28. 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
29. 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
30. \* 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
31. 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
32. 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
33. \*♦ 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
34. \*♦ Kumar S, Ye J, **Liu L** (2014) Reply to: “Proper reporting of predictor performance”. *Nature Methods*. 11(8):781-2. PMID: 25075901
35. \*♦ 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
36. 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
37. \*♦ **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
38. 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
39. 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
40. \*♦ 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
  41. ♦ 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
  42. \* Kumar S, Dudley JT, Filipski 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
  43. 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
  44. 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
  45. Spade DJ, Griffitt 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
  46. 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
  47. 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
  48. 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
  49. 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
  50. ♦ 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
  51. 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

52. 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
53. 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
54. 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
55. 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
56. 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
57. 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
58. ♦ 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
59. 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
60. Gabriel DW, Allen C, Schell M, Denny TP, Greenberg JT, Duan Y, Flores-Cruz Z, Huang Q, Clifford JM, Presting G, Gonzalez ET, Reddy J, Elphinstone J, Swanson J, Yao J, Mulholland V, **Liu L**, Farmerie WG, Patnaikuni M, Balogh B, Norman D, Alvarez A, Walunas T, Zhukov A, Mikhailova N (2006) Identification of open reading frames unique to a select agent: *Ralstonia solanacearum* race 3 biovar 2. *Molecular Plant-Microbe Interaction*. 19(1):69-79. PMID: 16404955
61. Farmerie WG, Hammer J, **Liu L**, Sahni A, Schneider M. (2005) Biological workflow with BlastQuest. *Data and Knowledge Engineering*. 53(1):75-97
62. 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
63. 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
64. 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
65. 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)



66. \*§ Guan X<sup>§</sup>, **Liu L.** (2018) Know-GRRF: Domain-knowledge informed biomarker discovery with random forests. *6th International Work-conference on Bioinformatics and Biomedical Engineering. Granada, Spain.*
67. 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*
68. 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*
69. Sun Y, **Liu L.**, Popp M, Farmerie W. (2006) Estimation of cross-hybridization signals using support vector regression. *Proc. IEEE Symp. of Computations in Bioinformatics and Bioscience*

Manuscripts submitted and under review:

- R1. \*§ Ahmadinejad N, **Liu L.** J-Score: A Robust Measure of Clustering Accuracy. *Computational Statistics & Data Analysis* (preprint <https://arxiv.org/abs/2109.01306>)
- R2. \*§ Fessler SN, **L Liu.** Chang Y, Johnston CS. Associations between BMI and Inflammatory Biomarkers in Adults Recently Diagnosed with COVID-19: Secondary Analysis of an RCT. *Obesity Research & Clinical Practice*

Manuscripts under preparation:

- U1. \*§ Chen H, Chandrashekar P<sup>§</sup>, Matthew Lee<sup>§</sup>, Wang P, **Liu L.** EpiAttention: Decipher tissue-specificity of gene regulatory elements.
- U2. \*§ Shu J, Ming L, Issa JP, **Liu L.** Methylation spreading from repetitive elements dysregulates cancer genes.

**CONFERENCE ORAL PRESENTATIONS:**

- O1. Evolution of COVID-19 Health Disparities in Arizona. *27<sup>th</sup> Annual Conference of the Society for Social Work and Research.* Phoenix, USA. 2023.
- O2. Classifying refugee status using common features in EMR. *International Conference on Intelligent Biology and Medicine.* Philadelphia, USA. 2022 (presented by student).
- O3. The role of multi-level genetic diversity in cancers. *Annual conference of the Society of Molecular Biology and Evolution.* Online. 2021
- O4. Discovering subclones in tumors sequenced at standard depths. *17<sup>th</sup> Annual Rocky Mountain Bioinformatics Conference, a meeting of the International Society for Computational Biology.* Aspen, Colorado, USA. 2019
- O5. Deep learning based multi-view model for deciphering gene regulatory networks. *17<sup>th</sup> Annual Rocky Mountain Bioinformatics Conference, a meeting of the International Society for Computational Biology.* Aspen, Colorado, USA. 2019 (presented by student).
- O6. Know-GRRF: domain-knowledge informed biomarker discovery with random forests. *6th International Work-conference on Bioinformatics and Biomedical Engineering. Granada, Spain.* 2018
- O7. Contextual selection of cancer drivers & clinical implications. *4<sup>th</sup> Annual Arizona Biomedical Research Centre Research Conference.* Phoenix, AZ, 2018
- O8. Biological adaptability as a biomarker for risk assessment. *Arizona Alzheimer's Consortium Annual Conference.* Sedona, AZ, 2018
- O9. Fast fine mapping of causal eQTL variants. *International Symposium on Molecular Evolution and Medicine,* Philadelphia, PA, 2017

- O10. Evolution-informed biomarker discovery for precision oncology, *6th International Conference on Bioinformatics & Systems Biology*, Philadelphia, PA, 2016
- O11. Evolution-informed modeling. *RECOMB/ISCB Conference*, San Diego, CA, 2014
- O12. An evolutionary diagnosis method for variants in personal exomes. *Phylomedicine Symposium*, Tempe, AZ, 2012
- O13. Having a BLAST with BlastQuest: Where do we go from here? *INFORMS Annual Meeting*, Denver, CO, 2004

### CONFERENCE POSTERS:

- P1. Discoveray of DNA methylation protector element in human genome. *International Conference on Intelligent Biology and Medicine*. Philadelphia, USA. 2022
- P2. DeepCore: Attention-based interpretable deep learning approach for detecting regulatory elements. *International Conference on Intelligent Biology and Medicine*. Philadelphia, USA. 2022
- P3. Discovering subclones in tumors sequenced at standard depths. *17<sup>th</sup> Annual Rocky Mountain Bioinformatics Conference*, a meeting of the International Society for Computational Biology. Aspen, Colorado, USA. 2019
- P4. Deep learning based multi-view model for deciphering gene regulatory keywords. *17<sup>th</sup> Annual Rocky Mountain Bioinformatics Conference*, a meeting of the International Society for Computational Biology. Aspen, Colorado, USA. 2019
- P5. Contextual selection of cancer driver genes & clinical implications. *Annual Conference of the Society for Molecular Biology and Evolution*, Manchester, UK. 2019
- P6. Know-GRRF: domain-knowledge informed biomarker discovery with random forests. *6<sup>th</sup> International Work-conference on Bioinformatics and Biomedical Engineering*. Granada, Spain. 2018
- P7. Decomposing cancer subclonal structures with model-based clustering. *International Symposium on Molecular Evolution and Medicine*, Philadelphia, PA. 2017
- P8. Discover eQTL with flexible LD structure and tree-guided group lasso, *Pacific Symposium on Bio-computing*, Hawaii, USA. 2016
- P9. Distinct evolutionary and mutational patterns in oncogenes and tumor suppressor genes, *AACR Annual Meeting*, Philadelphia, USA. 2015

### INVITED TALKS

- T1. Biomedical informatics training in diverse environments. *International Conference on Intelligent Biology and Medicine*. Philadelphia, USA. 2022
- T2. Computational genomics: identifying biomarkers for precision medicine. AZBio Expo, Phoenix, AZ. 2016.
- T3. Shooting the moving target in cancer combat. Midwestern University, Glendale, AZ. 2017
- T4. Understanding the genetic basis of human diseases in an evolutionary framework. Mayo Clinic Arizona, Scottsdale, AZ. 2017
- T5. Reduced genetic diversity as a risk factor of Alzheimer's disease. Mayo Clinic, Scottsdale, AZ. 2018.
- T6. Genomics for Alzheimer's disease. Phoenix Veterans Affairs Health Care System, Phoenix, AZ. 2018.

### SOFTWARE

- ❖ *GUST*: Genes under selection in tumors  
<https://github.com/liliulab/gust>
- ❖ *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>

## PATENTS

2017 Inventor, Immunosignature microarray analysis and immunosignatures in systemic lupus erythematosus (provisional, US Patent Number 62/547,748).

## TEACHING & MENTORING

### 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	
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
<hr/>			
BMI-550: Translational Bioinformatics * (graduate level, 3 credits)			
Spring 2016	✓	13	4.4
<hr/>			
BMI-570: BMI Symposium (graduate level, 1 credit)			
Fall 2016		23	4.8
Fall 2017		17	4.1
<hr/>			
BMI-110: Introduction to Python * (undergraduate level, 3 credits)			
Spring 2022			

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

## 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
BMI-540: Problem-solving in BMI	Fall 2019, Fall 2020, Fall 2021, Fall 2022
BMI-505: Foundations of BMI Methods II	Spring 2020

### OUTSIDE ASU

Pre-clerkship MBLD block: The Molecular Basis of Life and Disease	Fall 2018
---	-----------

## MENTOR OF POSTDOCTORAL SCHOLARS

<i>Abdulkadir Elmas, Ph.D.</i>	2016-2017
--------------------------------	-----------

## COMMITTEE CHAIR (CO-CHAIR)

### Doctoral Students

1. *Xin Guan, Ph.D.* 2015-2017 (co-chair)  
Dissertation: Novel methods of biomarker discovery and predictive modeling using random forest
2. *Navid Ahmadinejad, Ph.D.* 2016-2019  
Dissertation: Discovering subclones and their driver genes in tumors sequenced at standard depths
3. *Pramod Chandrashekar, Ph.D.* 2016-2020  
Dissertation: Deep learning based multi-view model for deciphering genetic regulatory keywords

4. *Verah Nyarige, Ph.D. candidate* 2018-2022  
Dissertation: Novel bioinformatics methods for co-expression analysis of time series transcriptome data
5. *Jingmin Shu* 2020-  
Dissertation: TBD
6. *Hai Chen* 2020-  
Dissertation: TBD
7. *Rekha Mudappathi* 2022-  
Dissertation: TBD
8. *Tatiana Patton* 2022-  
Dissertation: TBD

### **Master Students**

9. *Brian Hanratty, M.S.* 2015-2016  
Applied project: An improved workflow for bisulfite sequencing analysis.
10. *Margaret Linan, M.S.* 2015-2016  
Applied project: The best practice to pre-process amplicon reads
11. *Ai-sawan Jonguksawas, M.S.* 2016  
Applied project: Exploring common autoantibodies derived from NAPPA screening studies in breast cancer, diabetes, and lung cancer populations
12. *Anna Freydenzon, M.S.* 2016-2017  
Applied project: Evolution-informed biomarker discovery for staging ER+ breast carcinomas
13. *Rabia Maqsood, M.S.* 2018  
Applied project: Effects of microRNA-15b in breast cancer
14. *Jingmin Shu, Ph.D., M.S.* 2020  
Applied project: The role of transposable elements in tumorigenesis.
15. *Abdelrahman Younis, M.S.* 2021  
Applied project: The Correlation between Education Level and Health Awareness (Vaccination rates for Flu, Pneumonia and Shigella)
16. *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
17. *Vanessa Nobles.* 2021 -  
Applied project: Classify refugee status using EMR data

### **Barrett Honors Thesis**

18. *Richard Li, B.S.* 2018-2019  
Thesis: A retrospective investigation to assess the potential application of predictive machine learning algorithms in oncology clinical trials

**Undergraduate Capstone Projects**

- |   |           |
|---|-----------|
| 19. <i>Shayna Troftgruben, B.S.</i>   | 2018-2019 |
| Project: Order of mutations in cancer genomes                                 |           |
| 20. <i>Yara Hawwari, B.S.</i>   | 2018-2019 |
| Project: Database and web application of genes driving oncogenesis            |           |
| 21. <i>Matthew Lee</i>  | 2019-2020 |
| Project: Discover regulatory elements using deep-learning models              |           |
| 22. <i>Ryan Pan</i>   | 2020-2021 |
| Project: Tissue-specific eQTL discovery in human brains                       |           |
| 23. <i>Jason Reyes</i>  | 2020-2021 |
| Project: Tissue-specific eQTL discovery in mouse brains                       |           |
| 24. <i>Sarah Paul</i>   | 2020-2021 |
| Project: Gene expression markers in extracellular vesicles in tumors          |           |
| 25. <i>Malia Morrison</i>   | 2020-2021 |
| Project: Improve interoperability of clinical databases at Valleywise Clinics |           |
| 26. <i>Savannah Graffin</i>   | 2021-2022 |
| Project: Clonal hematopoiesis in multiple myeloma.                            |           |

**COMMITTEE MEMBER****Doctoral Students**

- |   |           |
|---|-----------|
| 27. <i>Chaoxing Li, Ph.D.</i> ,   | 2016-2017 |
| Molecular and Cell Biology, School of Life Sciences   |           |
| Dissertation: Topological analysis of biological pathways: genes, microRNAs and pathways involved in hepatocellular carcinoma           |           |
| 28. <i>Caitlin Vose, Ph.D.</i>  | 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 |           |
| 29. <i>Shobana Sekar, Ph.D.</i>   | 2016-2018 |
| Biomedical Informatics, College of Health Solutions   |           |
| Dissertation: Circular RNA characterization and regulatory network prediction in human tissue   |           |
| 30. <i>Laurel Bruce</i>   | 2018-2020 |
| Speech and Hearing Science, College of Health Solutions   |           |
| Dissertation: Biomarkers of familial speech sound disorders: genes, perception, and motor control                                       |           |
| 31. <i>Matteo Vaiente</i>   | 2018-2020 |
| Biomedical Informatics, College of Health Solution  |           |
| Dissertation: Learning RNA viral disease dynamics from molecular sequence data  |           |

32. *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
33. *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
34. *Yookyung Kim* 2020-  
Speech and Hearing Science, College of Health Solutions  
Dissertation: TBD
35. *Hongseok Shim* 2021-  
Biomedical Informatics, College of Health Solutions  
Dissertation: TBD
36. *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

##### Submitted, pending review

NIH T32 MPI: Liu, Whisner \$1,956,879  
Advanced training in artificial intelligence for precision nutrition science research

NIH T32 MPI: Wu, Li, Co-I: Liu  
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 biostatistics workshop at ASU.*

I am the advisor of 25 workshops that cover 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*

- |              |   |
|--------------|---|
| 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-present 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)
- 2019–2021 Guest Editor, *Frontiers in Genetics* (IF=3.5)

### **Conference organizer**

- 2022–Present 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