

**Li Liu, MD. MS.**

Associate Professor

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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
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)

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#### As PI/MPI:

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1. Discover and analyze germline-somatic interactions in cancer  
NIH-R01 2021 – 2024  
PI: Liu
2. Interdisciplinary Systems-based Training for Precision Nutrition  
NIH-T32 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. 2023 – 2025  
PI: Koskan, Liu, Johnson
4. 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 R21 grant awarded to Dr. Gu at Florida International University. I lead the bioinformatics analysis of multiomics data.

5. 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
6. Annotate functional genetic variants  
Mayo Clinic 2019 – 2022  
PI: Liu
7. Precision diagnosis of pathogenic noncoding variants in diabetes  
Flinn Foundation 2019 – 2021  
PI: Liu
8. 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 R01 grant awarded to Dr. Gibson at Georgia Institute of Technology.
9. Reduced genomic diversity as a risk factor for nonfamilial young onset Alzheimer' disease  
Mayo Clinic 2018 – 2020  
PI: Liu.  
I am the site PI of a grant (\$1M) awarded to Dr. Caselli at Mayo Clinic.
10. Prioritize functional genetic variants in melanoma with network biology and evolution  
Flinn Foundation 2017 – 2019  
PI: Liu
11. Discovering the roles of cellular adaptability in late-onset Alzheimer's disease  
Arizona Alzheimer's Consortium 2017 – 2018  
PI: Liu
12. Subclonal diversity: prognostic role in acute myeloid leukemia patients with minimal residual disease  
Mayo / ASU Health Alliance Seed Grant 2016 – 2017  
PI: Liu
13. Discovering immunosignatures of systemic lupus erythematosus  
Healthtell Inc. 2016 – 2017  
PI: Liu

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 As Co-I
 

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14. Developing an Innovative and Scalable Model to Bolster Health Research Data Management & Science Capabilities in the Phoenix Bioscience Core  
Flinn Foundation 2022 – 2025  
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.

15. Leveraging bio-cultural mechanisms to maximize the impact of multi-level preventable disease interventions with southwest populations  
NIH-U54 supplement 2020 – 2022  
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.
16. Arizona Cancer and Evolution (ACE) Center  
NIH (U54) 2018 – 2023  
PI: Maley  
Co-I: Liu (6% recognition). I am responsible for developing computational methods to incorporate somatic selection to discover cancer drivers.
  17. ACE: Administrative Supplement: Parameterizing multi-scale agent-based modeling 2018 – 2019
  18. ACE: Administrative Supplement: Parameterizing multi-scale agent-based modeling 2019 – 2020
19. 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  
Co-I: Liu (10% recognition). I lead the experimental design, integrative analysis of survey data and molecular data, and building and interpreting predictive models.
20. Genotype-phenotype associations in reading disorders  
NIH (F32) 2017-2019  
PI: Lancaster  
Co-mentor: Liu (10% recognition). I advised the trainee on incorporating population and family structure in genomic analysis.
21. Multiple genomics data to predict drug response  
Mayo Clinic 2019  
PI: Runger  
Co-I: Liu (50% recognition). I am responsible to advise students on applying deep-learning techniques to integrate multi-omics data.
22. Rapid nanoplasmic quantification of tumor-derived EVs for pancreatic cancer diagnosis  
Baylor Scott & White Health 2017 – 2019  
PI: Hu  
Co-I: Liu (3% recognition). I am responsible for statistical analysis to select biomarkers and assess technology robustness.
23. Nanoplasmonic quantification of tumor-derived circulating extracellular vesicles  
Fred Hutchinson Cancer Research Center 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**

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

**Peer-reviewed articles (in reverse-chronological order)**

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

Journal articles:

1. \*§ Chandrashekar P<sup>§</sup>, Chen H<sup>§</sup>, Lee M<sup>§</sup>, Ahmadinejad N<sup>§</sup>, **Liu L.** (2024) DeepCORE: An interpretable multi-view deep neural network model to detect co-operative regulatory elements. *Computational and Structural Biotechnology Journal*. In press
2. Hu G, **Liu L.**, Xu D (2024) On the responsible use of chatbots in bioinformatics. *Genomics, Proteomics & Bioinformatics*. qzae002
3. \*§ Chen H<sup>§</sup>, Shu J<sup>§</sup>, Maley CC, **Liu L.** (2023) A mouse-specific model to detect genes under selection in tumors. *Cancers* 15(21):5156. PMID: 37958330
4. \*§ Ahmadinejad N<sup>§</sup>, Chung Y, **Liu L.** (2023) J-score: a robust measure of clustering accuracy. *PeerJ Computer Science*. 9:e1545. PMID: 37705621
5. 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
6. 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
7. \*§ Shen FL<sup>§</sup>, Shu J<sup>§</sup>, Lee M<sup>§</sup>, 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
8. § Fessler SN<sup>§</sup>, 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: 36084236
9. \*§ 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
10. \*§♦ 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
11. § 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*. 152(10):2218-2226. PMID: 36084236
12. \*§ 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. *PeerJ*. 10:e13227. PMID: 35547187
13. Whisner CM, Brown JC, Larson DM, Rodriguez LA, Peter B, Reifsnider E, Bever J, **Li Liu.**, 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
14. \*§ **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

15. 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
16. 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
17. 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
18. \* **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
19. ♦ 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
20. §♦ 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):eaaz6162. PMID: 32195353
21. \*§ 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
22. \*§ 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
23. Jasbi P, Mitchell NM, Shi X, Gryns 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
24. 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
25. § 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
26. \*§♦ **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
27. 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
28. \* **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
29. § 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

30. 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
31. 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
32. 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
33. 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
34. \* **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
35. \*♦ **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
36. 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
37. 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
38. \* 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
39. 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
40. 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
41. \*♦ 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
42. \*♦ Kumar S, Ye J, **Liu L** (2014) Reply to: “Proper reporting of predictor performance”. *Nature Methods*. 11(8):781-2. PMID: 25075901
43. \*♦ 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
44. 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

45. \*♦ **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
46. 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
47. 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
48. \*♦ 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
49. ♦ 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
50. \* 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
51. 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
52. 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
53. 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
54. 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
55. 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
56. 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
57. 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



58. ♦ 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
59. 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
60. 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
61. 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
62. 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
63. Popp MP, **Liu L**, Timmers A, Esson DW, Shiroma L, Meyers C, Berceli 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
64. 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
65. 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
66. ♦ 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
67. 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
68. 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
69. Farmerie WG, Hammer J, **Liu L**, Sahni A, Schneider M. (2005) Biological workflow with BlastQuest. *Data and Knowledge Engineering*. 53(1):75-97
70. 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
71. 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

72. 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
73. 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)

74. \*§ 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.
75. 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*
76. 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*
77. 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*

**CONFERENCE ORAL PRESENTATIONS:**

- O1. DeepCORE: An interpretable multi-view deep neural network model to detect co-operative regulatory elements. *International Conference on Intelligent Biology and Medicine*. Tampa, USA. 2023 (presented by student).
- O2. A mouse-specific model to detect genes under selection in tumors. *International Conference on Intelligent Biology and Medicine*. Tampa, USA. 2023 (presented by student).
- O3. 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.
- O4. Classifying refugee status using common features in EMR. *International Conference on Intelligent Biology and Medicine*. Philadelphia, USA. 2022 (presented by student).
- O5. The role of multi-level genetic diversity in cancers. *Annual conference of the Society of Molecular Biology and Evolution*. Online. 2021
- O6. 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
- O7. 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).
- O8. Know-GRRF: domain-knowledge informed biomarker discovery with random forests. *6th International Work-conference on Bioinformatics and Biomedical Engineering*. Granada, Spain. 2018
- O9. Contextual selection of cancer drivers & clinical implications. *4<sup>th</sup> Annual Arizona Biomedical Research Centre Research Conference*. Phoenix, AZ, 2018
- O10. Biological adaptability as a biomarker for risk assessment. *Arizona Alzheimer's Consortium Annual Conference*. Sedona, AZ, 2018
- O11. Fast fine mapping of causal eQTL variants. *International Symposium on Molecular Evolution and Medicine*, Philadelphia, PA, 2017

- O12. Evolution-informed biomarker discovery for precision oncology, *6th International Conference on Bioinformatics & Systems Biology*, Philadelphia, PA, 2016
- O13. An evolutionary diagnosis method for variants in personal exomes. *Phylomedicine Symposium*, Tempe, AZ, 2012

### INVITED TALKS

- T1. Exploring ChatGPT's ability to generate novel algorithms in bioinformatics. *International Conference on Intelligent Biology and Medicine*. Tampa, USA. 2023
- T2. Biomedical informatics training in diverse environments. *International Conference on Intelligent Biology and Medicine*. Philadelphia, USA. 2022
- T3. Reduced genetic diversity as a risk factor of Alzheimer's disease. Mayo Clinic, Scottsdale, AZ. 2018.
- T4. Genomics for Alzheimer's disease. Phoenix Veterans Affairs Health Care System, Phoenix, AZ. 2018.
- T5. Shooting the moving target in cancer combat. Midwestern University, Glendale, AZ. 2017
- T6. Understanding the genetic basis of human diseases in an evolutionary framework. Mayo Clinic Arizona, Scottsdale, AZ. 2017
- T7. Computational genomics: identifying biomarkers for precision medicine. AZBio Expo, Phoenix, AZ. 2016.
- T8. Evolution-informed modeling. *RECOMB/ISCB Conference*, San Diego, CA, 2014
- T9. 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>
- ❖ 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  
<https://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>

<b>TEACHING &amp; MENTORING</b>
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*Overview of teaching and mentoring activities*

<b>Courses taught at ASU</b>	21
<b>Curriculum developed</b>	6
<b>Mentor of postdoctoral scholars</b>	4
<b>Committee chair (co-chair)</b>	
Doctoral students	8 (5 have graduated)
Master students	9 (9 have graduated)
Undergraduate students: Honor's thesis and Capstone project	11 (11 have graduated)
<b>Committee member</b>	
Doctoral students	9 (7 have graduated)
<b>Training grant proposals developed</b>	4

### COURSES TAUGHT AT ASU

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

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

## MENTOR OF POSTDOCTORAL SCHOLARS

<i>Abdulkadir Elmas, Ph.D.</i>	2016-2017
<i>Rekha Mudappathi, Ph.D.</i>	2024-

## COMMITTEE CHAIR (CO-CHAIR)

### Doctoral Students

1. <i>Xin Guan, Ph.D.</i> Dissertation: Novel methods of biomarker discovery and predictive modeling using random forest	2015-2017 (co-chair)
2. <i>Navid Ahmadinejad, Ph.D.</i> Dissertation: Discovering subclones and their driver genes in tumors sequenced at standard depths	2016-2019
3. <i>Pramod Chandrashekar, Ph.D.</i> Dissertation: Deep learning based multi-view model for deciphering genetic regulatory keywords	2016-2020
4. <i>Verah Nyarige, Ph.D.</i> Dissertation: Novel bioinformatics methods for co-expression analysis of time series transcriptome data	2018-2022
5. <i>Rekha Mudappathi, Ph.D.</i> Dissertation: Unveiling cellular complexity, genetic regulation and protein trafficking dynamics through integration of multi-omics insights	2022-2023
6. <i>Jingmin Shu</i> Dissertation: TBD	2020-

7. *Hai Chen* 2020-  
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, M.S.* 2021-2023  
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
19. *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***

20. *Shayna Troftgruben, B.S.* 2018-2019  
Project: Order of mutations in cancer genomes

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|---|-----------|
| 21. <i>Yara Hawwari, B.S.</i>   | 2018-2019 |
| Project: Database and web application of genes driving oncogenesis            |           |
| 22. <i>Matthew Lee</i>  | 2019-2020 |
| Project: Discover regulatory elements using deep-learning models              |           |
| 23. <i>Ryan Pan</i>   | 2020-2021 |
| Project: Tissue-specific eQTL discovery in human brains                       |           |
| 24. <i>Jason Reyes</i>  | 2020-2021 |
| Project: Tissue-specific eQTL discovery in mouse brains                       |           |
| 25. <i>Sarah Paul</i>   | 2020-2021 |
| Project: Gene expression markers in extracellular vesicles in tumors          |           |
| 26. <i>Malia Morrison</i>   | 2020-2021 |
| Project: Improve interoperability of clinical databases at Valleywise Clinics |           |
| 27. <i>Savannah Graffin</i>   | 2021-2022 |
| Project: Clonal hematopoiesis in multiple myeloma.                            |           |

## COMMITTEE MEMBER

### *Doctoral Students*

- |   |           |
|---|-----------|
| 28. <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           |           |
| 29. <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 |           |
| 30. <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   |           |
| 31. <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                                       |           |
| 32. <i>Matteo Vaiente</i>   | 2018-2020 |
| Biomedical Informatics, College of Health Solution  |           |
| Dissertation: Learning RNA viral disease dynamics from molecular sequence data  |           |
| 33. <i>Michelle Winerip, Ph.D.</i>  | 2016-2021 |
| Biomedical Informatics, College of Health Solutions   |           |

Dissertation: Protein network informed feature selection of candidate proteomic biomarkers in the presence of disease heterogeneity

34. *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
35.  
 36. *Yookyung Kim* 2020-  
 Speech and Hearing Science, College of Health Solutions  
 Dissertation: TBD
37. *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.

### 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 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*

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
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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