



EDUCATION

- Ph.D., Biostatistics, The Ohio State University, Columbus, OH, 2006.
- M.S., Statistics, The Ohio State University, Columbus, OH, 2005.
- M.S., Neuroscience, The Capital University of Medicine, Beijing, China, 2000.
- B.S., Clinical Medicine, Tianjin Medical University, Tianjin, China, 1995.

EXPERIENCE

- Associate Professor at University of Georgia (2016–present)
- Assistant Professor at University of Georgia (2011–2016)
- Assistant Professor at Delaware State University (2010-2011)
- Postdoctoral Fellow at Harvard University (2006-2009)
- Pediatrician at Tianjin Children’s Hospital (1995-1997).

PUBLICATIONS

Peer-reviewed journals

1. Chen, Y., Jiang, W., Liu, X., Du, Y., Liu, L., Ordovas, J., Lai, C., Shen, L. Curcumin Supplementation Improves Heat Stress Induced Cardiac Injury of Mice: Physiological and Molecular Mechanisms. *Journal of Nutritional Biochemistry* 2020
2. Jiang, X., Edwards, S.V., Liu, L. The Multispecies Coalescent Model Outperforms Concatenation across Diverse Phylogenomic Data Sets. *Syst Biol* 2020
3. Du, Y., Wu, S., Edwards, S.V., Liu, L. The Effect of Alignment Uncertainty, Substitution Models and Priors in Building and Dating the Mammal Tree of Life Uncertainty. *BMC Evol Biol* 2019, 19:203
4. Cai, L., Xi, Z., Amorim, A.M., Sugumaran, M., Rest, J., Liu, L., Davis, C.C. Widespread ancient whole genome duplications in Malpighiales coincide with Eocene global climatic upheaval. *New Phytologist* 2019, 221:565-576
5. Yu, L., Liu, L., Chen, D.G. A homoscedasticity test for the accelerated failure time model. *Computational Statistics* 2019, 34:433-446
6. Chen, Y., Liu, X., Jiang, C., Liu, L., Ordovas, J.M., Lai, C. Curcumin supplementation increases survival and lifespan in *Drosophila* under heat stress conditions. *BioFactors* 2018, 44:577-587
7. Wang, K., Lenstrab, J.A., Liu, L., Hu, Q., Ma, T., Liu, J. Incomplete lineage sorting rather than hybridization explains the inconsistent phylogeny of the wisent. *Communications Biology* 2018, 1:169

8. Wu, S., Edwards, S.V., Liu, L. Genome-scale DNA sequence data and the evolutionary history of placental mammals. *Data in Brief* 2018, 18:1971-1975.
9. He, M. Han, Z., Liu, L., Zheng, Y. Chemical biology approaches for investigating the functions of lysine acetyltransferases. *Angewandte Chemie* 2018, 57:1162-1184
10. Liu, L, Zhang, Jin, Rheindt, F.E., Lei, F., Qu, Y., Wang, Y., Sullivan, C., Ni, W., Wang, J., Yang, F., Chen, J., Edwards, S.V., Meng, J., and Wu, S. Reply to Gatesy and Springer: Claims of homology errors and zombie lineages do not compromise the dating of placental diversification. *Proceedings of the National Academy of Sciences (USA)* 2017,114(45):E9433-E9434.
11. Liu, L, Zhang, Jin, Rheindt, F.E., Lei, F., Qu, Y., Wang, Y., Sullivan, C., Ni, W., Wang, J., Yang, F., Chen, J., Edwards, S.V., Meng, J., and Wu, S. Genomic evidence reveals a radiation of placental mammals uninterrupted by the KPg boundary. *Proceedings of the National Academy of Sciences (USA)* 2017, 114(35):E7282-E7290.
12. Xin, X., Chen, Y., Chen, D., Xiao, F., Parnell, L., Zhao, J., Liu, L., Ordovas, J., Lai, C., Shen, L. Supplementation with Major Royal Jelly Proteins Increases Lifespan, Feeding and Fecundity in *Drosophila*. *Journal of Agricultural and Food Chemistry* 2016, 64(29):5803-5812.
13. Teufel, A., Liu, L., Liberles, L. Models for gene duplication when dosage balance works as a transition state to subsequent neo- or sub-functionalization. *BMC Evol Biol* 2016, 16:45.
14. Edwards, S.V., Xi, Z., Janke, A., Faircloth, B.C., McCormack, J.E., Glenn, T.C., Zhong, B., Wu, S., Lemmon, E.M., Lemmon, A.R., Leaché, A.D., **Liu, L.**, Davis, C.C. Implementing and testing the multispecies coalescent model: a valuable paradigm for phylogenomics. *Mol Phylogenet Evol* 2016, 94:447-462.
15. H. Lorenzi, A. Khan, M.S. Behnke, S. Namasivayam, L.S. Swapna, M. Hadjithomas, S. Karamycheval, D. Pinney, B. Brunk, J.W. Ajioka, D. Ajzenberg, J.C. Boothroyd, J.P. Boyle, M.L. Dardé, M.A. Diaz-Miranda, J.P. Dubey, H.M. Fritz, SM Gennari, B.D. Gregory, K. Kim, J. Saeij, C. Su, M.W. White, XQ Zhu, D.K. Howe, B M. Rosenthal, M.E. Grigg, J. Parkinson, **L. Liu**, J.C. Kissinger, D.S. Roos, L. D. Sibley. Local admixture of amplified and diversified secreted pathogenesis determinants shapes mosaic *Toxoplasma gondii* genomes. *Nature Comm* 2016, 7:10147.
16. Xi, Z., Liu, L., Davis, C.C. The impact of missing data on species tree estimation. *Mol Biol Evol* 2016, 33:838-860.
17. Zhao, J., Teufel, A.I., Liberles, D.A., **Liu, L.** A generalized birth and death process for modeling the fates of gene duplication. *BMC Evol Biol* 2015, 15:275.
18. Xi, Z., **Liu, L.**, Davis, C.C. Genes with minimal phylogenetic information are problematic for coalescent analyses when gene tree estimation is biased. *Mol Phylogenet Evol* 2015, 92:63-71.

19. **Liu, L.**, Wu, S., Xi, Z., Davis, C.C., S V. Edwards, S.V. Estimating phylogenetic trees from genome-scale data. *NY. Acad. Sci.* 2015, 1360:36-53.
20. **Liu, L.**, Edwards S.V. Comment on Statistical binning enables an accurate coalescent-based estimation of the avian tree. *Science* 2015, 350 (6257): 171.
21. **Liu, L.**, Wu, S., Yu, L. Coalescent methods for estimating species trees from phylogenomic data. *Journal of Systematic Evolution* 2015, 53(5):380-390.
22. Su, D., Zhou, X., Chen, Q., Jiang, Y., Yang, X., Zheng, W., Tao, K., Wu, J., Yan, Z., **Liu, L.**, Wu, S., Mao, W. Prognostic nomogram for thoracic esophageal squamous cell carcinoma after radical esophagectomy. *PLoS One* 2015, 10: e0124437.
23. **Liu, L.**, Xi, Z., Davis, C.C. Coalescent methods are robust to long-branch artifacts in species tree estimation. *Mol Biol Evol* 2015, 32(3): 791-805.
24. Jarvis ED, Mirarab S, Aberer AJ, Li B, Houde P, Li C, Ho SY, Faircloth BC, Nabholz B, Howard JT, Suh A, Weber CC, da Fonseca RR, Li J, Zhang F, Li H, Zhou L, Narula N, **Liu L**, Ganapathy G, Boussau B, Bayzid MS, Zavidovych V, Subramanian S, Gabaldón T, Capella-Gutiérrez S, Huerta-Cepas J, Rekepalli B, Munch K, Schierup M, Lindow B, Warren WC, Ray D, Green RE, Bruford MW, Zhan X, Dixon A, Li S, Li N, Huang Y, Derryberry EP, Bertelsen MF, Sheldon FH, Brumfield RT, Mello CV, Lovell PV, Wirthlin M, Schneider MP, Prosdocimi F, Samaniego JA, Vargas Velazquez AM, Alfaro-Núñez A, Campos PF, Petersen B, Sicheritz-Ponten T, Pas A, Bailey T, Scofield P, Bunce M, Lambert DM, Zhou Q, Perelman P, Driskell AC, Shapiro B, Xiong Z, Zeng Y, Liu S, Li Z, Liu B, Wu K, Xiao J, Yinqi X, Zheng Q, Zhang Y, Yang H, Wang J, Smeds L, Rheindt FE, Braun M, Fjeldsa J, Orlando L, Barker FK, Jønsson KA, Johnson W, Koepfli KP, O'Brien S, Haussler D, Ryder OA, Rahbek C, Willerslev E, Graves GR, Glenn TC, McCormack J, Burt D, Ellegren H, Alström P, Edwards SV, Stamatakis A, Mindell DP, Cracraft J, Braun EL, Warnow T, Jun W, Gilbert MT, Zhang G. Whole Genome Analyses Resolve Early Branches in the Tree of Life of Modern Birds. *Science* 2014, 346(6215):1320-1331.
25. Erich D. Jarvis, Siavash Mirarab, Andre J. Aberer, Bo Li, Peter Houde, Cai Li, Simon Y. W. Ho, Brant C. Faircloth, Benoit Nabholz, Jason T. Howard, Alexander Suh, Claudia C. Weber, Rute R. da Fonseca, Alonzo Alfaro-Núñez, Nitish Narula, **Liang Liu**, Dave Burt, Hans Ellegren, Scott V. Edwards, Alexandros Stamatakis, David P. Mindell, Joel Cracraft, Edward L. Braun, Tandy Warnow, Wang Jun, M Thomas P Gilbert, Guojie Zhang, and The Avian Phylogenomics Consortium. Phylogenomic analysis data of the Avian Phylogenomics Project. (Epub 2014; 2015) *GigaScience* 4:4.
26. Teufel, A., Zhao, J., O'Reilly, M.[§], **Liu, L.**[§], Liberles, D.A.[§] On Mechanistic Modeling of Gene Content Evolution: Birth-Death Models and Mechanisms of Gene Birth and Gene Retention. *Computation* 2014, 2(3):112-130.

27. Xi, Z., **Liu, L.**, Rest, J.S., Davis, C.C. Phylogenomics and Coalescent Analyses Resolve the Placement of Amborella as Sister to Water Lilies. *Syst. Biol.* 2014, 63 (6): 919-932.
28. Jhwueng, D., Huzurbazar, S., O'Meara, B.C., **Liu, L.**[§]. Investigating the performance of AIC in selecting phylogenetic models. *Stat Appl. Genetic. Mole Biol* 2014, 13(4):459-75.
29. Ma, Q., Reeves, J.H., Liberles, D.A., Yu, L., Chang, Z., Zhao, J., Cui, J., Xu, Y., **Liu, L.** A phylogenetic model for understanding the effect of gene duplication on cancer progression. *Nuclear Acid Research* 2013, 42(5):2870-8.
30. Liberles, D., Teufel, A., **Liu, L.**, Stadler, T. On the Need for Mechanistic Models in Computational Genomics and Metagenomics. *Genome Biology and Evolution* 2013, 5(10):2008-18.
31. Zhong, B., **Liu, L.**, Yan, Z., Penny, D. Origin of land plants using the multispecies coalescent model. *Trends in Plant Science* 2013, 18:492-495.
32. Shaw, T., Z. Ruan, T. Glenn, **Liu, L.** STRAW: a web server for species tree analysis. *Nucleic Acids Research* 2013, 41(Web Server issue):W238-41.
33. Wu, S., Song, S., **Liu, L.**, Edwards, S.V. Reply to Gatesy and Springer: The multispecies coalescent model can effectively handle recombination and gene tree heterogeneity. *Proceedings of the National Academy of Sciences (USA)* 2013, 110(13):E1180.
34. Fuchs, J., Pons, J., **Liu, L.**, Ericson, P.G.P, Couloux, A., Pasquet, E. A multi-loci phylogeny suggests an ancient hybridization event between Campephilus and melanerpine woodpeckers (Aves: Picidae). *Mol Phylogenet Evol.* 2013, S1055-7903(13)00071-7.
35. Yu, L., **Liu, L.**, Chen, D. Weighted least-squares method for right-censored data in accelerated failure time mode. *Biometrics* 2013, 69(2):358-65.
36. Shaw, T.I., Srivastava, A., Chou, W., **Liu, L.**, Hawkinson, A., Glenn, T.C., Rick Adams, R., Schountz, T. Transcriptome Sequencing and Annotation for the Jamaican Fruit Bat (*Artibeus jamaicensis*). *PLoS One* 2012, 7(11):e48472.
37. Song, S., **Liu, L.**, Edwards, S.V., Wu, S. Resolving Conflict in Placental Mammal Phylogeny Using Phylogenomics and the Multispecies Coalescent Model. *Proceedings of the National Academy of Sciences (USA)* 2012, 109:14942-14947.
38. Yu, L., **Liu, L.** Extended Quasi-Likelihood with Fractional Polynomials in the Frame of the ATF model. *Statistics in Medicine* 2012, 31:1369-1379.
39. Ronquist, F., Teslenko, M., Mark, P., Ayres, D.L., Darling, A., Höhna, S., Larget, B., **Liu, L.**, M.A. Suchard, M.A., Huelsenbeck, J.P. MrBayes 3.2: Efficient Bayesian Phylogenetic Inference and Model Choice Across a Large Model Space. *Syst Biol* 2012, 61:539-542.

40. Zhang, L., **Liu, L.**, Chen, L. A Multivariate Generalized Linear Regression Analysis for Golfer Perceived Value and Satisfaction. *International Journal of Sport Management* Volume 13 #2 April 2012.
41. **Liu, L.**, Yu, L., Kalavacharla, V., Liu, Z. A Bayesian model for gene family evolution. *BMC Bioinformatics* 2011, 12:426.
42. **Liu, L.**, Yu, L. Estimating species trees from unrooted gene trees. *Syst Biol* 2011, 60: 661-667.
43. **Liu, L.**, Yu, L., Edwards, S.V. A maximum pseudo-likelihood approach for estimating species trees under the coalescent model. *BMC Evol. Biol.* 2010, 10:302.
44. Shen, L, Zhang, W., Jin, F., Zhang, L., Chen, Z., **Liu, L.**, Li, D. Expression of Recombinant AccMRJP1 protein from Royal Jelly of Chinese honeybee in *Pichia pastoris* and its Proliferation Activity in Insect Cell Line. *J. Agric. Food Chem.* 2010, 58:9190–9197.
45. **Liu, L.**, Yu, L. Phybase: an R package for species tree analysis. *Bioinformatics* 2010, 26(7):962-963.
46. Shen, L., Ding, M., Zhang, L., Zhang, W., **Liu, L.**, Li, D. Expression of a Bee-Venom phospholipase A2 from *Apis cerana cerana* in the Baculovirus-insect cell. *J Zhejiang Univ Sci B.* 2010, 11(5): 342–349.
47. **Liu, L.**, Yu, L., Pearl, D.K., Edwards, S.V. Estimating species phylogenies using coalescence times among sequences. *Systematic Biology* 2009, 58(5):468-477.
48. **Liu, L.**, Yu, L., Kubatko, L., Pearl, D.K., Edwards, S.V. Coalescent methods for estimating multilocus phylogenetic trees. *Mol Phylog Evol* 2009, 53(1): 320-328.
49. **Liu, L.**, Edwards, S.V. Phylogenetic Analysis in the Anomaly Zone. *Syst Biol* 2009, 58(4):452-460.
50. Liu, L., Yu, L., D.K. Pearl, D.K. Maximum tree: a consistent estimator of the species tree. *Journal of Mathematical Biology* 2009, 60(1):95-106.
51. Yu, L., Yu, R., **Liu, L.** Quasi-likelihood for Right-Censored Data in the Generalized Linear Model. *Communications in Statistics - Theory and Methods* 2009, 38:2187-2200.
52. **Liu, L.** BEST: Bayesian estimation of species trees under the coalescent model. *Bioinformatics* 2008, 24(21):2542:2543.
53. Brumfield, R.T., **Liu, L.**, Lum, D., Edwards, S.V. Comparison of species tree methods for reconstructing the phylogeny of bearded manakins (Aves: Pipridae: *Manacus*) from multilocus sequence data. *Syst Biol* 2008, 57(5):719-731.

54. **Liu, L.**, Pearl, D.K., Brumfield, R.T., Edwards, S.V. Estimating species trees using multiple-allele DNA sequence data. *Evolution* 2008, 62(8):2080-2091.
55. Belfiore, N.M., **Liu, L.**, Moritz, C. Multilocus phylogenetics of a rapid radiation in the genus *Thomomys* (Rodentia: Geomyidae). *Syst Biol* 2008, 57:294-310.
56. **Liu, L.**, Pearl, D.K. Species trees from gene trees: reconstructing Bayesian posterior distributions of a species phylogeny using estimated gene tree distributions. *Syst Biol* 2007, 56:504-514.
57. Edwards, S.V., **Liu, L.**, Pearl, D.K. High resolution species trees without concatenation. *Proceedings of the National Academy of Sciences (USA)* 2007, 104:5936-5941.
58. Wolfe, A.D., Randle, C.P., **Liu, L.**, Steiner, K.E. Phylogeny and biogeography of orobanchaceae. *Folia Geobotanica* 2005, 40:115-125.
59. **Liu, L.**, Lu, G. Protective effect of protein-free supernatant of brain homogenate taken from hypoxia preconditioned mice on synaptosome membrane exposed to hypoxia. *Chinese Journal of Neuroscience* 2001, 17:373-375.

Submitted but not yet accepted

1. Xi, Z., Xiong, H., Liu, L., Wang, D., Shao, C., Yang, X., Ma, T., Davis, C., Liu, J. Species Tree Estimation and the Impact of Extensive Gene Loss Following Whole-Genome Duplication. *Syst Biol* 2019 (submitted)
2. Cai, L., Xi, Z., Lemmon, E.M., Lemmon, Mast, A., Buddenhagen, C.E., Liu, L., Davis, C.D. Gene Tree Estimation Error, Incomplete Lineage Sorting, and Ancient Gene Flow Explain the Most Recalcitrant Ancient Angiosperm Clade, Malpighiales. *Syst Biol* (in revision)
3. Tu, W., Wang, W., Ha, H., Liu, L. Investigating the association between the state-level household firearm ownership and the county-level suicide rates in the United States using spatial regression models, *Applied Geography* (in revision)

Conference papers

1. Weimin Mao, Xinming Zhou, Qixun Chen, Youhua Jiang, Xun Yang, Jie Wu, Kaiyi Tao, Weihui Zheng, Zhen Yan, **Liang Liu**, Shaoyuan Wu, Dan Su. Nomogram predicting long-term survival probability of thoracic esophageal squamous cell carcinoma after radical esophagectomy. *J Clin Oncol* 31, 2013 (suppl; abstr 4094)

Book chapters

1. Liu, L., Anderson, C., Pearl, D.K., Edwards, S.V. Modern phylogenomics: building phylogenetic trees using the multispecies coalescent model. In: *Evolutionary genomics: statistical and computational methods* 2018
2. Yohe, L.R., Liu, L., Dávalos, L.M., Liberles D.A. Protocols for the molecular evolutionary analysis of gene duplicates. In: *Computational Methods in Protein Evolution* 2018

3. Anderson, C., Liu, L., Pearl, D.K., Edwards, S.V. Tangled Trees: The challenge of inferring species trees from coalescent and non-coalescent genes. In: *Evolutionary genomics: statistical and computational methods*, 2012
4. Castillo, S., Liu, L., Pearl, D.K., Edwards, S.V. Bayesian estimation of species trees: a practical guide to optimal sampling and analysis. In: *Estimating species trees* (edited by Laura Kubatko and Lacey Knowles), 2010

Technical reports

1. Liu, L. and Pearl, D.K. 2006. Species trees from gene trees: Reconstructing Bayesian posterior distributions of a species phylogeny using estimated gene tree distributions. Mathematical Biosciences Institute Technical Report #53. The Ohio State University

AWARDS

- Publisher's Award for Excellence in Systematic Research from Society of Systematic Biologists 2008.
- Travel award for Joint Statistical Meeting, 2005.

GRANTS

- RAPID: finding virulence genes as therapeutic targets in Covid-19. (Co-PI, 33% effort). NSF DBI-2029595 (\$200,000), 2020 – 2021
- Stochastic models for the evolution of gene families. (Co-PI). Australian Research Council (ARC, Australia NSF, \$300,000), 2018 – 2021
- Community Transmission of Tuberculosis Urban Africa. (Co-PI, 10% effort). NIH/NIAID R01AI093856 (\$2,639,335), 2018 – 2022
- Developing a probabilistic model for gene family evolution. (PI). NSF DMS-1222745 (\$172,888), 2012-2015. This is part of a collaborative proposal with Dr. Liberles (NSF DMS-1222940, \$127,112)
- Maximum pseudo-likelihood estimates of species trees. (PI). Professional Development Fund (\$3000), Delaware State University, 2010

PUBLIC PRESENTATIONS

- “The coalescent model outperforms concatenation across diverse phylogenomic data sets”, Lanzhou University, 2019
- “R for bioinformatics”, short course, Jiangsu Normal University, 2019
- “A Bayesian model for gene family evolution”, invited talk, GSD, 2019
- “Statistical phylogenetics”, workshop, Jiangsu Normal University, 2019
- “Statistical phylogenetics”, workshop, Sichuan University, 2019
- “Bayesian coalescent model for epidemiological inference”, The Molecular Tree of Life: From Coalescence to Comparative Genomics, Xuzhou, 2018
- “Alignment uncertainty, substitution model misspecification, species tree estimation”, International conference on Phylogenomic data analysis and coalescent models, Organizer, Xuzhou, 2018
- “A Bayesian birth-death model for gene family evolution”, Seminar, Auburn University, November 2017
- “Building phylogenetic trees from phylogenomic data”, invited talk, Sichuan University, June 2017

- “Stochastic models in phylogenetics”, invited talk, Jiangsu Normal University, June 2017
- “Workshop on ecological functional genomics”, co-organizer, Lacawac Sanctuary, May 2017.
- “Phylogenomics”, Seminar, Jiangsu Normal University, 2016.
- “Species tree estimation”, Sichuan University, 2016.
- “Statistical Phylogenetics”, Session Organizer, ICSA 2016.
- “A probabilistic model for gene family evolution”, JSM 2015.
- “A birth-death process for modeling the mechanisms of gene retention”, ICSA 2015.
- “Gene family evolution”, The 4th Workshop on Biostatistics and Bioinformatics 2015.
- “Introduction to R programming”, 2014, Brown Bag Bioinformatics tutorials, University of Georgia.
- “Estimating phylogenetic trees”, 2014, Beijing Institute of Genomics, Chinese Academy of Science.
- “A probabilistic model for gene family evolution”, 2014, Gene family evolution workshop, New Mexico State University.
- “Phylogenetics and its applications”, 2013, Bioinformatics Seminar, Department of Biostatistics and Bioinformatics, Emory University.
- “A phylogenetic model for cancer evolution”, 2013, Mechanisms of Protein Evolution Meeting, University of Colorado.
- “Gene duplication and cancer progression”, 2012, NIMBioS, University of Tennessee.
- “Asymptotic properties of the median tree”, International symposium on Bioinformatics Research and Applications, May 2012, Dallas, Texas.
- “Estimating species trees”, invited talk at workshop “Estimating species trees: a phylogenetic paradigm for the 21st century”, January 2012, Columbus, OH.
- “Gene family data and phylogenetic trees”, 2011, NIMBioS, University of Tennessee.
- “Pseudo-likelihood estimation of species trees”, invited talk, 2011, University of Wyoming.
- “Implementing BEAGLE library in MrBayes”, 2010, Mathematical Biotechnology Institute, the Ohio State University.
- “Estimating species trees from multilocus sequences (STAR and STEAC)”, 2009. Department of Organismic and Evolutionary Biology, Harvard University.
- “Estimating species trees”, Invited talk, Workshop, January 2009, Department of Ecology and Evolutionary Biology, University of Michigan.
- “Species trees and gene trees”, Invited talk, Symposium, June 2008, Society of Systematic Biology.
- “Coalescence meets phylogenetics”, Invited talk, July 2007, Museum of Vertebrate Zoology at UC Berkeley.
- “Species tree estimation”, Invited talk, Symposium of “Bayesian Invasion”, February 2006, Yale University.
- “Reconstructing posterior distributions of a species phylogeny using estimated gene tree distributions”, July 2006, Joint Meeting of the American Statistical Society.
- “Reconstructing posterior distributions of a species phylogeny using estimated gene tree distributions”, Poster, June 2006, Society for the Study of Evolution.

PROFESSIONAL MEMBERSHIPS

- Society of Systematic Biology
- Institute of Chinese Statistical Association (ICSA)

EDITORIAL WORK

- Associate Editor: Journal of Molecular Evolution
- Editorial Board: Frontiers Ecology and Evolution, Journal of Systematics and Evolution, Jacob Journal of Biostatistics, AIMS Microbiology
- Referee: Systematic Biology, Bioinformatics, Journal of Mathematic Biology, Molecular Phylogenetics and Evolution, and International Journal of Knowledge Discovery in Bioinformatics, Molecular Ecology, Molecular Biology and Evolution, Heredity, Journal of Molecular Evolution, Theoretical Population Biology, BMC Evolutionary Biology, JASA, Mathematical Biosciences, National Science Foundation.
- NSF Panel.

TEACHING

- Statistics inference for bioinformatics (BINF8441, Spring 2020)
- Statistics inference for bioinformatics (BINF8441, Spring 2019)
- Statistics inference for bioinformatics (STAT8440, Fall 2018)
- Statistics inference for bioinformatics (BINF8441, Spring 2018)
- Computing techniques in statistics II (STAT8070, Spring 2018)
- Introduction to Grant Writing (BINF8600, Fall 2017)
- Stochastic Process (STAT4/6100, Spring 2017)
- Statistics inference for bioinformatics (STAT 8440, Spring 2017)
- Essential Computing Skills for Biologists (BINF4/6005, Fall 2016)
- Molecular Evolution and Phylogenetics (P BIO 8350, Spring 2016)
- Statistics inference for bioinformatics (STAT 8440, Spring 2016)
- Essential Computing Skills for Biologists (BINF4/6005, Fall 2015)
- Molecular Evolution and Phylogenetics (P BIO 8350, Spring 2015)
- Statistical Bioinformatics II (STAT4/6640 Spring 2015)
- Essential Computing Skills for Biologists (BINF4/6005 Fall 2014)
- STAT6220, Fall 2014
- Statistical Bioinformatics II (STAT4/6640, Spring 2012)
- Molecular Evolution and Phylogenetics (P BIO 8350, Spring 2014)
- Molecular Evolution and Phylogenetics (P BIO 8350, Spring 2013)
- Nonparametric Statistics (STAT 4/6290, Spring 2013)
- Introduction to Bioinformatics (BINF 4/6005, Fall 2012)
- Computing techniques in statistics II (STAT 8070, Spring 2012)
- Nonparametric Statistics (STAT 4/6290, Spring 2012)
- Advanced Statistics (Spring 2011, Delaware State University)
- Biometrics (Fall 2010, Delaware State University)

ADVISING STUDENTS (current students are highlighted)

- **Yan Du (PhD, advisor)**
- **Weifeng Wang (PhD, advisor)**
- **Huimin Hu (PhD, advisor)**
- **Kristen Knight (PhD, co-advising with Dr. Lazar)**
- **George Zheng (Master, advisor, graduated Spring 2020)**
- Xiaodong, Jiang (PhD, co-advising with Dr. Ji, graduated Spring 2019)
- Yipping Wang (Master, advisor, graduated Spring 2019)
- Shawn Joshua Queen (Master, advisor, IOB, graduated 2018)
- Jing Zhao (PhD, 2012 - 2016, advisor)

- Zhen Yan (Ph.D, 2012 - 2016, advisor)
- Chenghong Shen (Ph.D, 2012-2013 (withdraw from the program), advisor)
- Veronika Novoselsky (MS, 2012, advisor)
- Jiayang Liu (MS, 2013, co-advisor, advisor: Dr. Park)
- Yiwen Yang (MS, 2014, graduated, advisor)
- Spencer Hall (Undergraduate, STAT)
- Nevada Basdeo (Master, 2016-2017, advisor)

GRADUATE COMMITTEES (current students are highlighted)

- **Hanxia Li (PhD, advisor Jason Wallace)**
- **Michael Skaro (PhD, advisor Jonathan Arnold)**
- **Noah Legall (PhD, advisor Liliana Salvador)**
- **Zachary Petty (PhD, advisor Justin Bahl)**
- **Jiani Chen (PhD, advisor Justin Bahl)**
- **Wanxue Zou (PhD, advisor: Lynne Billard)**
- **Iluk Kang (PhD, advisor: Cheolwoo Park)**
- **Wenhao Pan (PhD, advisor: Lynne Billard)**
- **Tawanda Benesi (PhD, advisor Dan Hall)**
- **Shumeng Zhang (PhD, IOB, advisor Jeff Bennetzen)**
- **Yiran Li (PhD, IOB, advisor Jessie Kissinger)**
- **Cristian Caranica (PhD, advisor: Jonathan Arnold)**
- **Hongye Zhou (PhD, advisor Jeff Bennetzen)**
- **Shunhua Han (PhD, advisor Casey Bergman)**
- **Ziyang Ma (PhD, advisor Jeongyoun Ahn)**
- **Eduardo Scopel (PhD, advisor Douda Bensasson)**
- **Ashley Scrusse (PhD, advisor: Jonathan Arnold)**
- Ronald Galiwango (PhD, advisor Christopher Whalen, 2019)
- Yu Wang (Master, advisor: Cheolwoo Park, 2019)
- Tao Sheng (PhD, advisor: Dr. Ying Xu, 2019)
- Waleed Navarro (MS, advisor: Dr. Seymour, 2013)
- JungAe Lee (Ph.D, advisor: Dr. Ahn)
- Qianqian Tang (MS, advisor: Dr. Reeves, 2012)
- Tracy Kimethu (MS, advisor: Dr. Schliekelman, 2013)
- Xiao Cheng (MS, advisor: Dr. Ahn, 2012)
- Normal Hassell (MS, advisor: Dr. Elizabeth Ottesen)
- Yifan Dai (MS, advisor: Lynne Seymour)
- Chi Zhang (PhD, advisor: Ying Xu)
- Kemin Liu (Master, advisor: Dr. Ahn)
- Daniel McSkimming (Ph.D, IOB, advisor: Dr. Kannan)
- Stacy Cobb (PhD, advisor: Schliekelman)
- Wei Qi (Master, advisor: Pengsheng Ji)
- Vallery Flint (PhD, advisor: Dr. Schliekelman)
- Shubham Basu (PhD, advisor Jessie Kissinger)

SERVICE

- Graduate Advisor, 2018-2020, STAT
- Research Development Committee, 2019 – 2020, STAT
- Graduate committee, 2019 - 2020, STAT
- Personal Committee, 2019 – 2020, STAT

- Mentoring committee for Dr. Liliana Salvador (Assistant professor IOB)
- Faculty Affair Committee, 2019 – 2020, IOB
- Graduate committee, 2018-2019, STAT
- Graduate affair committee, 2018-2019, IOB
- Personal committee, 2017-2018, STAT
- Graduate affair committee, 2017-2018, IOB
- Graduate affair committee, 2016-2017, IOB
- Personal committee, Exam committee (data analysis), and Computing committee (Chair), 2016-2017, STAT
- Research Development Committee (chair), Spring 2016, STAT
- Computing committee, Spring 2016, STAT
- Faculty search committee, Spring 2016, STAT, UGA
- Graduate Committee, Spring 2015, IOB, UGA
- QEM committee, Spring 2015, STAT, UGA
- Seminar Committee (co-chairing with Gauri), Spring 2015, STAT, UGA
- QEM Committee, Fall 2014, STAT, UGA
- Maintaining the IOB server
- Graduate Committee, Fall 2014, IOB, UGA
- Graduate Committee, Spring 2014, IOB, UGA
- QEM Committee, Spring 2014, STAT, UGA
- Curriculum Committee, Fall 2013, IOB, UGA
- Faculty Search Committee, Spring 2013, IOB, UGA
- Faculty Search Committee, Fall 2012, IOB, UGA
- Curriculum Committee, Fall 2012, IOB, UGA
- Curriculum Committee, Spring 2013, IOB, UGA
- Seminar Committee, 2011-2012, IOB, UGA
- Computing Committee, Fall 2012 and Spring 2013, Statistics, UGA
- Infrastructure Committee, 2011-2012, Statistics, UGA
- Graduate Committee, 2010 – 2011, Delaware State University
- Curriculum Committee, 2010 – 2011, Delaware State University
- Faculty Senate, 2010 – 2011, Delaware State University
- Statistical Consulting Service, 2010 – 2011, Delaware State University