

# LIANG LIU

DEPARTMENT OF STATISTICS  
UNIVERSITY OF GEORGIA  
EMAIL: LLIU@UGA.EDU

---

## 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

- Assistant Professor at Delaware State University (2010-present)
- Postdoctoral Fellow at Harvard University (2006 -2009)
- Research Assistant at the Ohio State University (2003-2006)
- Teaching Assistant at the Ohio State University (2001-2003)
- Pediatrician at Tianjin Children's Hospital (1995-1997).

## PROGRAMS:

- BEST: Bayesian Estimation of Species Trees. [www.stat.osu.edu/~dkp/BEST](http://www.stat.osu.edu/~dkp/BEST)
- Phybase: an R package for simulating, manipulating, estimating phylogenetic trees. <http://code.google.com/p/phybase/>
- MP-EST: Maximum Pseudo-Likelihood estimation of species trees. <http://code.google.com/p/mp-est/>

## PUBLICATIONS:

Zhang, L., **L. Liu**, L. Chen. A Multivariate Generalized Linear Regression Analysis for Golfer Perceived Value and Satisfaction. International Journal of Sport Management. (in press)

**Liu, L.**, and L. Yu. Estimating species trees from unrooted gene trees. Syst. Biol. 2011, doi: 10.1093/sysbio/syr027

**Liu, L.**, L. Yu, S.V. Edwards. A maximum pseudo-likelihood approach for estimating species trees under the coalescent model. BMC Evol. Biol. 2010, 10:302.

Shen, L, W. Zhang, F. Jin, L. Zhang, Z. Chen, **L. Liu**, D. Li. 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.

**Liu, L.**, and L. Yu. Phybase: an R package for species tree analysis. Bioinformatics. 2010 26(7):962-963.

Shen, L., M. Ding, L. Zhang, W. Zhang, **L. Liu**, D. Li. Expression of a Bee-Venom phospholipase A2 from *Apis cerana cerana* in the Baculovirus-insect cell. *J Zhejiang Univ Sci B*. 2010 May; 11(5): 342–349.

Castillo, S., **L. Liu**, D.K. Pearl, S.V. Edwards, Bayesian estimation of species trees: a practical guide to optimal sampling and analysis, in book "Estimating species trees" (edited by Laura Kubatko and Lacey Knowles), 2010.

**Liu, L.**, L. Yu, D.K. Pearl, and S.V. Edwards. Estimating species phylogenies using coalescence times among sequences. *Systematic Biology* 2009, 58(5):468-477.

**Liu, L.**, L. Yu, L. Kubatko, D.K. Pearl, and S.V. Edwards. Coalescent methods for estimating multilocus phylogenetic trees. *Molecular Phylogenetics and Evolution* 2009, 53(1): 320-328.

**Liu, L.**, and S.V. Edwards. Phylogenetic Analysis in the Anomaly Zone. *Systematic Biology* 2009, 58(4):452-460.

**Liu, L.**, L. Yu, and D.K. Pearl. Maximum tree: a consistent estimator of the species tree. *Journal of Mathematical Biology* 2009, 60(1):95-106.

Yu, L., R. Yu, **L. Liu**. Quasi-likelihood for Right-Censored Data in the Generalized Linear Model. *Communications in Statistics - Theory and Methods* 2009, 38:2187-2200.

**Liu, L.** BEST: Bayesian estimation of species trees under the coalescent model. *Bioinformatics* 2008, 24(21):2542:2543.

Brumfield, R.T., **L. Liu**, D. Lum, and S.V. Edwards. Comparison of species tree methods for reconstructing the phylogeny of bearded manakins (Aves: Pipridae: *Manacus*) from multilocus sequence data. *Systematic Biology* 2008, 57(5):719-731.

**Liu, L.**, D.K. Pearl, R.T. Brumfield, and S.V. Edwards. Estimating species trees using multiple-allele DNA sequence data. *Evolution* 2008, 62(8):2080-2091.

Belfiore, N.M., **L. Liu**, and C. Moritz. Multilocus phylogenetics of a rapid radiation in the genus *Thomomys* (Rodentia: Geomyidae). *Systematic Biology* 2008, 57:294-310.

**Liu, L.** and D.K. Pearl. Species trees from gene trees: reconstructing Bayesian posterior distributions of a species phylogeny using estimated gene tree distributions. *Systematic Biology* 2007, 56:504-514.

Edwards, S.V., **L. Liu**, and D.K. Pearl. High resolution species trees without concatenation. *Proceedings of the National Academy of Sciences (USA)*, 2007, 104:5936-5941.

**Liu, L.**, and D.K. Pearl. 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

Wolfe, A.D., C. P. Randle, **L. Liu** and K.E. Steiner. Phylogeny and biogeography of orobanchaceae. *Folia Geobotanica*, 2005, 40:115-125.

**Liu, L.** and G. Lu. 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

## AWARDS

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

## GRANTS

- Estimating Species Trees from Multilocus DNA Sequence Data. NSF DEB 0743616 (\$450,000). S. Edwards, PI, D. Pearl, Co-PI. L. Liu, Senior Personnel - Assisted with writing and preliminary data analysis
- A Bayesian model for estimating gene family evolution. A NSF seed grant (pending).
- Maximum pseudo-likelihood estimate of the species tree, Professional Development Fund (\$3000), Delaware State University, 2011.

## PUBLIC PRESENTATIONS

- “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.
- “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 “Bayesian Invasion”. February 2006. Yale University.
- “Reconstructing posterior distributions of a species phylogeny using estimated gene tree distributions”, presentation. 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
- American Statistical Association

## EDITORIAL WORK

- Referee: Systematic Biology, Bioinformatics, Journal of Mathematical Biology, Molecular Phylogenetics and Evolution, and International Journal of Knowledge Discovery in Bioinformatics, Molecular Ecology, Molecular Biology and Evolution, Heredity.
- Referee: National Science Foundation.