

Jeet Sukumaran

CONTACT INFORMATION

Current Position: Assistant Professor
Institutional Address: Biology Department, SLS 260
San Diego State University
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ONLINE

Lab Website: <https://sukumaranlab.org>
Google Scholar: <https://scholar.google.com/citations?user=-Amj93IAAAAJ>
ResearchGate: https://www.researchgate.net/profile/Jeet_Sukumaran
Twitter: <https://twitter.com/jeetsukumaran>
Personal Website: <http://jeetblogs.org/>
Photography Website: <https://www.flickr.com/jeetsukumaran>

DATE OF BIRTH April 2nd, 1972

EDUCATION

PhD, Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, USA (2012). “Geographies and genealogies: phylogeographic simulation and Bayesian approaches to statistical phylogeographic model selection.” Advisors: Dr. Mark T. Holder and Dr. Rafe M. Brown.

MSc, Institute of Biological Sciences, University of Malaya, Kuala Lumpur, Malaysia (2005): “Habitat structure and organization of montane stream anuran assemblages.”

BSc (Biology: Ecology, Evolution and Conservation), Section of Integrative Biology, University of Texas, Austin, USA (1998).

POST-DOCTORAL TRAINING

Feb 2014 – Aug 2018 University of Michigan, Ann Arbor (with Dr. L. Lacey Knowles)
Oct 2015 – Aug 2018 University of Kansas, Lawrence (with Dr. Mark T. Holder)
Feb 2012 – Feb 2014 Duke University (with Dr. Allen Rodrigo)

REFEREED PUBLICATIONS

1. Knowles, L Lacey, Huateng Huang, **Jeet Sukumaran** and Stephen A Smith (2018) “A matter of phylogenetic scale: Distinguishing incomplete lineage sorting from lateral gene transfer as the cause of gene tree discord in recent versus deep diversification histories”. *American Journal of Botany* 105.3, pp. 376–384. URL: <https://doi.org/10.1002/ajb2.1064>.
2. Li, Jingchun, Jen-Pen Huang, **Jeet Sukumaran** and L Lacey Knowles (2018) “Microevolutionary processes impact macroevolutionary patterns”. *BMC evolu-*

- tionary biology* 18.1, p. 123. URL: <https://bmcevolbiol.biomedcentral.com/articles/10.1186/s12862-018-1236-8>.
3. **Sukumaran, Jeet** and L Lacey Knowles (2018) “Trait-Dependent Biogeography:(Re) Integrating Biology into Probabilistic Historical Biogeographical Models”. *Trends in Ecology & Evolution*. URL: <https://doi.org/10.1016/j.tree.2018.03.010>.
 4. Huang, Huateng, **Jeet Sukumaran**, Stephen A Smith and L Lacey Knowles (2017) “Cause of gene tree discord? Distinguishing incomplete lineage sorting and lateral gene transfer in phylogenetics”. *PeerJ PrePrints*, 5:e3489v1. URL: <https://doi.org/10.7287/peerj.preprints.3489v1>.
 5. **Sukumaran, Jeet** and L. Lacey Knowles (2017) “Multispecies coalescent delimits structure, not species”. *Proceedings of the National Academy of Sciences* 114.7, pp. 1607–1612. eprint: <http://www.pnas.org/content/early/2017/01/25/1607921114.full.pdf>. URL: <http://www.pnas.org/content/early/2017/01/25/1607921114.abstract>.
 6. Zeng, Qinglong, Steven Wu, **Jeet Sukumaran** and Allen Rodrigo (Sept. 2017) “Models of microbiome evolution incorporating host and microbial selection”. *Microbiome* 5.1, p. 127. URL: <https://doi.org/10.1186/s40168-017-0343-x>.
 7. **Sukumaran, Jeet**, Evan P. Economo and L. Lacey Knowles (2016) “Machine-learning biogeographic processes from biotic patterns: a new trait-dependent dispersal and diversification model with model-choice by simulation-trained discriminant analysis”. *Systematic Biology* 65.3, pp. 525–545. URL: <http://sysbio.oxfordjournals.org/content/65/3/525>.
 8. Zeng, Qinglong, **Jeet Sukumaran**, Steven Wu and Allen Rodrigo (2015) “Neutral models of microbiome evolution”. *PLOS Computational Biology* 11.7, e1004365. URL: <http://www.ncbi.nlm.nih.gov/pubmed/26200800>.
 9. Oaks, Jamie R, Charles W Linkem and **Jeet Sukumaran** (Dec. 2014) “Implications of uniformly distributed, empirically informed priors for phylogeographical model selection: a reply to Hickerson et al.” *Evolution* 68.12, pp. 3607–3617. URL: <http://www.ncbi.nlm.nih.gov/pubmed/25213163>.
 10. Oaks, Jamie R., **Jeet Sukumaran**, Jacob A. Esselstyn, Charles W. Linkem, Cameron D. Siler, Mark T. Holder and Rafe M. Brown (2013) “Evidence for climate-driven diversification? A caution for interpreting ABC inferences of simultaneous historical events”. *Evolution* 67.4, pp. 991–1010. URL: <http://www.ncbi.nlm.nih.gov/pubmed/23550751>.
 11. Stoltzfus, Arlin, Hilmar Lapp, Naim Matasci, Helena Deus, Brian Sidlauskas, Christian M Zmasek, Gaurav Vaidya, Enrico Pontelli, Karen Cranston, Rutger Vos, Campbell O Webb, Luke J Harmon, Megan Pirrung, Brian O’Meara, Matthew W Pennell, Siavash Mirarab, Michael S Rosenberg, James P Balhoff, Holly M Bik, Tracy A Heath, Peter E Midford, Joseph W Brown, Emily Jane McTavish, **Jeet Sukumaran**, Mark Westneat, Michael E Alfaro, Aaron Steele and Greg Jordan (2013) “Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient”. *BMC Bioinformatics* 14.1, p. 158. URL: <http://www.ncbi.nlm.nih.gov/pubmed/23668630>.
 12. Vos, Rutger A., James P. Balhoff, Jason A. Caravas, Mark T. Holder, Hilmar Lapp, Wayne P. Maddison, Peter E. Midford, Anurag Priyam, **Jeet Sukumaran**, Xuhua Xia and Arlin Stoltzfus (2012) “NeXML: Rich, extensible, and verifiable representation of comparative data and metadata”. *Systematic Biology* 61.4, pp. 675–689. URL: <http://www.ncbi.nlm.nih.gov/pubmed/22357728>.
 13. Jiménez-Valverde, Alberto, Narayani Barve, Andrés Lira-Noriega, Sean P. Maher, Yoshinori Nakazawa, Monica Papes, Jorge Soberón, **Jeet Sukumaran** and A. Townsend Peterson (2011) “Dominant climate influences on North American bird distributions”. *Global Ecology and Biogeography* 20.1, pp. 114–118. URL: <http://www.ncbi.nlm.nih.gov/pubmed/21411118>.

[//onlinelibrary.wiley.com/doi/10.1111/j.1466-8238.2010.00574.x/abstract](http://onlinelibrary.wiley.com/doi/10.1111/j.1466-8238.2010.00574.x/abstract).

14. **Sukumaran, Jeet** and Mark T. Holder (2011) “Ginkgo: spatially-explicit simulator of complex phylogeographic histories”. *Molecular Ecology Resources* 11.2, pp. 364–369. URL: <http://www.ncbi.nlm.nih.gov/pubmed/21429145>.
15. Brown, Rafe M., Charles W. Linkem, Cameron D. Siler, **Jeet Sukumaran**, Jacob A. Esselstyn, Arvin C. Diesmos, Djoko T. Iskandar, David Bickford, Ben J. Evans, Jimmy A. McGuire, Lee Grismer, Jatna Supriatna and Noviar Andayani (2010) “Phylogeography and historical demography of *Polypedates leucomystax* in the islands of Indonesia and the Philippines: Evidence for recent human-mediated range expansion?” *Molecular Phylogenetics and Evolution* 57.2, pp. 598–619. URL: <http://www.ncbi.nlm.nih.gov/pubmed/20601009>.
16. Holder, Mark T., **Jeet Sukumaran** and Rafe M. Brown (2010) “Recent developments in Bayesian phylogenetics”. In: *Bayesian Modeling in Bioinformatics*. Ed. by Dipak K. Dey, Samiran Ghosh and Bani K. Mallick. Chapman & Hall/CRC, pp. 193–221. URL: <https://www.crcpress.com/Bayesian-Modeling-in-Bioinformatics/Dey-Ghosh-Mallick/9781420070170>.
17. Matsui, Masafumi, Atsushi Tominaga, Wanzhao Liu, Wichase Khonsue, Lee L. Grismer, Arvin C. Diesmos, Indraneil Das, Ahmad Sudin, Paul Yambun, Hoisen Yong, **Jeet Sukumaran** and Rafe M. Brown (2010) “Phylogenetic relationships of *Ansonia* from Southeast Asia inferred from mitochondrial DNA sequences: Systematic and biogeographic implications (Anura: Bufonidae)”. *Molecular Phylogenetics and Evolution* 54.2, pp. 561–570. URL: <http://www.ncbi.nlm.nih.gov/pubmed/19679193>.
18. **Sukumaran, Jeet** and Mark T. Holder (2010) “DendroPy: a Python library for phylogenetic computing”. *Bioinformatics* 26, pp. 1569–1571. URL: <http://www.ncbi.nlm.nih.gov/pubmed/20421198>.
19. **Sukumaran, Jeet** and Charles W. Linkem (2009) “Choice of topology estimators in Bayesian phylogenetic analysis”. *Molecular Biology and Evolution* 26.1, pp. 1–3. URL: <http://www.ncbi.nlm.nih.gov/pubmed/18984901>.
20. Wiens, John, **Jeet Sukumaran**, Alex Pyron and Rafe Brown (2009) “Evolutionary and biogeographic origins of high tropical diversity in Old World frogs (Ranidae)”. *Evolution* 63, pp. 1217–1231. URL: <http://www.ncbi.nlm.nih.gov/pubmed/19154386>.
21. Holder, Mark T., **Jeet Sukumaran** and Paul Lewis (2008) “A justification for reporting the majority-rule consensus tree in Bayesian phylogenetics”. *Systematic Biology* 57.5, pp. 814–8221. URL: <http://www.ncbi.nlm.nih.gov/pubmed/18853367>.
22. Das, Indraneil, Norsham Yaakob and **Jeet Sukumaran** (2007) “A new species of *Microhyla* (Anura: Microhylidae) from the Malay Peninsula”. *Hamadryad* 31.2, pp. 304–314.
23. Brown, Rafe M., S. Richards, **Jeet Sukumaran** and J. Fougopoulos (2006) “A new morphologically cryptic species of forest frog (genus *Platymantis*) from New Britain Island, Bismarck Archipelago”. *Zootaxa* 1334, pp. 45–68. URL: <https://bit.ly/2NYnse0>.
24. **Sukumaran, Jeet**, Indraneil Das and Alexander Haas (2006) “A synopsis of bioacoustic studies of Anuran amphibians of Borneo”. *Herpetological Review* 37.3, pp. 288–293.
25. **Sukumaran, Jeet**, Norshaam Yaakob and Dennis Yong (2006) “The herpetofauna of the Southeast Pahang peat-swamp forests”. *Hamadryad* 30.1&2, pp. 75–91.
26. Yaakob, Norsham and **Jeet Sukumaran** (2006) “An inventory of the amphibians of Pasoh Forest Reserve, Negeri Sembilan, Peninsular Malaysia”. *Hamadryad* 30.1&2, pp. 102–107.

27. Grismer, Lee, **Jeet Sukumaran**, Jesse Grismer, Tim Youmans, Perry Wood and Renee Johnson (2005) “Report on the herpetofauna from the Temengor Forest Reserve, Perak, West Malaysia”. *Hamadryad* 29.1, pp. 15–35.
28. **Sukumaran, Jeet** (2002) “The amphibian fauna of a forested area in Temengor, Northern Peninsular Malaysia”. *Hamadryad* 27.1, pp. 1–10.

NON-REFEREED
TECHNICAL
PUBLICATIONS

1. Das, Indraneil, Norsham Yaakob, **Jeet Sukumaran** and Tzi Ming Leong (2014) “Conservation status of the amphibians of Malaysia and Singapore”. In: *Conservation Biology of Amphibians of Asia (Status of Conservation and Decline of Amphibians: Eastern Hemisphere)*. Ed. by Harold Heatwole and Indraneil Das. Kota Kinabalu: Natural History Publications (Borneo), pp. 281–299. URL: http://www.nhpborneo.com/book/amphibians-asia/#.Vfg1_mRVhBc.
2. Shepherd, C.R., **Jeet Sukumaran** and S. A. Wich (2004) *Open Season: an analysis of the pet trade in Medan, Sumatra 1997–2001*. Tech. rep. Petaling Jaya: TRAFFIC Southeast Asia. URL: http://www.traffic.org/general-reports/traffic_pub_trade5.pdf.
3. Azmi, Reza and **Jeet Sukumaran** (2002) *Biodiversity assessments and conservation planning for sustainable production forestry in high-conservation value forests: a preliminary biodiversity assessment*. Tech. rep. Petaling Jaya: WWF Malaysia. URL: <http://bit.ly/1KcZ9AE>.
4. **Sukumaran, Jeet** (1999) *Tiger parts in traditional Chinese medicine: a survey of traditional Chinese medicine shops in Peninsular Malaysia*. Tech. rep. Petaling Jaya: WWF Malaysia.

ORAL
PRESENTATIONS

1. **Sukumaran, Jeet** and L. Lacey Knowles (2017) *Multispecies Coalescent Species Delimitation: Conflating Populations with Species in the Grey Zone*. Joint Annual Meeting of the Society for the Study of Evolution (SSE), the Society of Systematic Biologists (SSB), and the American Society of Naturalists (ASN): Portland, Oregon. URL: <https://www.youtube.com/watch?v=PDhHJJdPpNA>.
2. Knowles, L. Lacey, Huateng Huang, **Jeet Sukumaran** and Stephen Smith (2016) *Interrogating transcriptomes to characterize the different causes of gene tree discord in empirical data*. Joint Annual Meeting of the Society for the Study of Evolution (SSE), the Society of Systematic Biologists (SSB), and the American Society of Naturalists (ASN): Austin, Texas.
3. **Sukumaran, Jeet** and Mark T. Holder (2016) *A Simulation-Based Approach to Learning About Host-Parasite Biogeography: Distinguishing Between Phylogenetic and Geographic Processes*. Joint Annual Meeting of the Society for the Study of Evolution (SSE), the Society of Systematic Biologists (SSB), and the American Society of Naturalists (ASN): Austin, Texas. URL: https://figshare.com/articles/A_Simulation-Based_Approach_to_Learning_About_Host-Parasite_Biogeography_Distinguishing_Between_Phylogenetic_and_Geographic_Processes/3471557.
4. **Sukumaran, Jeet**, Evan P. Economo and L. Lacey Knowles (2015) *Machine learning biogeographic processes from biotic patterns: a new trait-dependent dispersal and diversification model, with model-choice by simulation-trained discriminant analysis*. Joint Annual Meeting of the Society for the Study of Evolution (SSE), the Society of Systematic Biologists (SSB), and the American Society of Naturalists (ASN): São Paulo, Brazil. URL: http://figshare.com/articles/Machine_Learning_Biogeographic_Processes_from_Biotic_Patterns_A_New_Trait_

- Dependent_Dispersal_and_Diversification_Model_with_Model_Choice_By_Simulation_Trained_Discriminant_Analysis/1466748.
5. Blackburn, David C., David C. Cannatella, **Jeet Sukumaran** and David B. Wake (2013) *The impact of taxonomic progress on knowing the Tree of Life: an example from amphibians*. Society for Integrative and Comparative Biology Annual Meeting: San Francisco, CA, USA. URL: <http://www.sicb.org/meetings/2013/schedule/abstractdetails.php?id=1410>.
 6. **Sukumaran, Jeet**, Steven Wu and Allen Rodrigo (2013) *A general approach to measuring distance between phylogenetic structures: comparisons between unlabeled phylogenetic structures of varying sizes*. Joint Annual Meeting of the Society for the Study of Evolution (SSE), the Society of Systematic Biologists (SSB), and the American Society of Naturalists (ASN): Snowbird, Utah, USA. URL: http://figshare.com/articles/A_general_approach_to_measuring_distance_between_phylogenetic_structures_comparisons_between_unlabeled_phylogenetic_structures_of_varying_sizes/1544581.
 7. **Sukumaran, Jeet** and Allen Rodrigo (2012) *A posteriori tests of phylogeographic hypotheses*. Joint Annual Meeting of the Society for the Study of Evolution (SSE), the Society of Systematic Biologists (SSB), and the American Society of Naturalists (ASN): Toronto, Canada. URL: http://figshare.com/articles/A_posteriori_tests_of_phylogeographic_hypotheses/1544582.
 8. **Sukumaran, Jeet** and Mark T. Holder (2010a) *Performance and robustness of phylogeographic statistics under complex simulations*. Joint Annual Meeting of the Society for the Study of Evolution (SSE), the Society of Systematic Biologists (SSB), and the American Society of Naturalists (ASN): Portland, Oregon, USA. URL: http://figshare.com/articles/Performance_and_robustness_of_phylogeographic_statistics_under_complex_simulations/1544578.
 9. **Sukumaran, Jeet** and Mark T. Holder (2010b) *Phylogenetic operations in Python with DendroPy*. Informatics for Phylogenetics, Evolution, and Biodiversity Conference: Portland, Oregon, USA.
 10. **Sukumaran, Jeet** and Mark T. Holder (2009) *Performance of phylogeographic test statistics using complex simulations*. Joint Annual Meeting of the Society for the Study of Evolution (SSE), the Society of Systematic Biologists (SSB), and the American Society of Naturalists (ASN): Moscow, Idaho, USA. URL: http://figshare.com/articles/Performance_of_phylogeographic_test_statistics_using_complex_simulations/1544584.
 11. **Sukumaran, Jeet**, Brian Stuart, L. Lee Grismer and Rafe Brown (2007) *Phylogeography of Microhyla: testing biogeographic hypotheses using relative divergence time estimation (preliminary results)*. Joint Meeting of Ichthyologists and Herpetologists: St. Louis, Missouri, USA. URL: http://figshare.com/articles/Phylogeography_of_Microhyla_testing_biogeographic_hypotheses_using_relative_divergence_time_estimation_preliminary_results_/1544579.

INVITED TALKS

1. **Sukumaran, Jeet** (2015) *Model-based Biogeographical Analyses: Principles and Practice*. Society of Systematic Biologists (SSB) Workshop: Ann Arbor, Michigan. URL: <https://github.com/jeetsukumaran/2015-SSB-AnnArbor-Biogeography>.
2. **Sukumaran, Jeet** (2013) *Approximate Bayesian computation and phylogeographic model selection*. Society of Systematic Biologists (SSB) Workshop: Snowbird, Utah, USA. URL: http://figshare.com/articles/_Approximate_Bayesian_Computation_and_Phylogeographic_Model_Selection/1544576.

3. **Sukumaran, Jeet** (2011) *Geographies and genealogies: performance of phylogeographic summary statistics under complex forward-time simulations*. Symposium and Workshop on Bayesian Inference of Phylogeny: University of California at Berkeley, Berkeley, USA. URL: http://figshare.com/articles/Geographies_and_genealogies_performance_of_phylogeographic_summary_statistics_under_complex_forward_time_simulations/1544577.

WORKSHOP
TEACHING
EXPERIENCE

- Society of Systematic Biologists Standalone Meeting, Baton Rouge, Jan 8-10, 2017: “Phylogenetic Computing with *DendroPy*”. (Materials available here: <https://github.com/ssb2017/dendropy>).
- NESCENT Ambassadorship Program, Ecuador 2013: “Statistical Phylogenetic Methods, Theory, and Practice”.
- Workshop on Molecular Evolution, Woods Hole (teaching assistant).
- NESCENT Ambassadorship Program, Bali 2012: “Statistical Phylogenetic Methods, Theory, and Practice”.

NSF/NESCENT
WORKING GROUPS

- Evolutionary Informatics Working Group (“Database Interoperability” Hackathon)
- Hackathons, Interoperability, Phylogenies (“Phylotastic!” Hackathon)
- Open Tree of Life (“Tree for All” Hackathon)

GRANTS

- National Science Foundation DEB 1655607 Collaborative Proposal: A Bayesian statistical approach to determine whether genetic data delimits species versus populations – \$656,849 (Co-PI; 2016)
- KU EEB Special Summer Funding – \$4000 (2010)
- KU EEB Graduate Student Travel Fund – \$300 (2009)
- KUNHM/EEB Special Request – \$1300 (2005)
- KUNHM Panorama – \$600 (2005)

PENDING GRANTS

- National Science Foundation DBI 1759728 ABI Innovation: GENOSPATIAL: A Geospatial Metadata Information Service for GENBANK Genetic Sequences – \$508,304 (PI; pending; 2017)
- National Science Foundation CSBR: Natural History: Database CROSSTALK: a digital resource on species interactions – \$308,996 (Co-PI; pending; 2017)

DECLINED GRANTS

- National Science Foundation DEB 1732259 Preliminary Proposal: Development of a phylogenetic method to test the incumbent species advantage concept – (PI; not invited; 2017)
- National Science Foundation DEB 1732412 Preliminary Proposal: A quaternary-sensitive model of island biogeography: testing hypotheses through model selection in endemic insects – (Co-PI; not invited; 2017)
- National Science Foundation DBI 1661328 ABI Innovation: GENOSPATIAL: A Geospatial Metadata Information Service for GENBANK Genetic Sequences – \$504,275 (PI; declined; 2016)

PEER-REVIEW
SERVICES

- *BMC Bioinformatics* (3)
- *Biodiversity Informatics* (1)
- *Copeia* (1)
- *Evolution* (3)
- *Journal of Biogeography* (1)
- *Molecular Ecology* (2)
- *PeerJ* (1)
- *Systematic Biology* (6)

OTHER SERVICES

- IUCN/SSC Amphibian Specialist Group (ASG) Working Group Chair for Malaysia (2007-2011).
- Managed multiple HPC clusters for phylogenetic and evolutionary analyses for multiple labs in the department (KU EEB).
- Training, direct assistance and other forms of facilitation of analysis on HPC clusters for various researchers, faculty as well as graduate students, across the department (KU EEB).

PROGRAMS,
APPLICATIONS,
AND SOFTWARE

DendroPy A Python library for phylogenetic computing: simulation, processing, and manipulation of phylogenetic trees and character matrices, as well as the reading and writing of phylogenetic data in a range of formats, such as NEXUS, NEWICK, NeXML, Phylip, FASTA, etc. Available at: <http://dendropy.org>.

SumTrees Summarizations of collections of trees: MCMC samples from a posterior distribution, non-parametric bootstrap replicates. Mapping of posterior probability, support, or frequency that splits/clades are found in the source set of trees onto a target tree. More information at: <http://dendropy.org/programs/sumtrees.html>

Ginkgo Forward-time spatially-explicit agent-based simulations of phylogeographic history over dynamic landscapes and environments. Available at: <http://github.com/jeetsukumaran/Ginkgo>.

archipelago Trait-dependent historical biogeographical analysis using machine-learning for model classification. Available at: <https://github.com/jeetsukumaran/archipelago>.

Distriscopeia A JavaScript application to visualize multiple common parameteric distributions simultaneously for teaching or learning purposes. Demo available at: <http://jeetworks.org/distriscopeia/>.

FULL
EMPLOYMENT
HISTORY

Aug 2018 – Current	Assistant Professor San Diego State University, San Diego.
Feb 2015 – Aug 2018	Assistant Research Scientist University of Michigan, Ann Arbor.
Feb 2014 – Aug 2018	Post-doctoral research associate with Dr. L. Lacey Knowles, University of Michigan, Ann Arbor.
Oct 2015 – Current	Post-doctoral research associate with Dr. Mark T. Holder University of Kansas, Lawrence.
Feb 2012 – Feb 2014	Post-doctoral research associate with Dr. Allen Rodrigo, Duke University.
Jun 2011 – Jan 2012	Support Programmer, Simultaneous Alignment and Tree Inference (SATé), Dept. of Ecology and Evolutionary Biology, University of Kansas.
Jan 2010 – May 2010	Teaching Assistant, Introduction to Organismal Biology Labs, Dept. of Ecology and Evolutionary Biology, University of Kansas (Instructor: Dr. Julie Brown).
Aug 2009 – Dec 2009	Teaching Assistant, Biometry, Dept. of Ecology and Evolutionary Biology, University of Kansas (Instructor: Dr. John Kelly).
Jan 2009 – July 2009	Programmer and Systems Administration for CIPRES (Cyberinfrastructure for Phylogenetic Research), Dept. of Ecology and Evolutionary Biology, University of Kansas.

Aug 2008 – Dec 2008	Teaching Assistant, Herpetology Lab, Dept. of Ecology and Evolutionary Biology, University of Kansas (Instructor: Dr. Rafe Brown).
May 2008 – Aug 2008	Programmer for Jorge Soberon, Dept. of Ecology and Evolutionary Biology, University of Kansas (simulation and analysis).
Aug 2007 – May 2008	Programmer for CIPRES (Cyberinfrastructure for Phylogenetic Research), Dept. of Ecology and Evolutionary Biology, University of Kansas .
Aug 2005 – Aug 2007	HerpNet Georeferencer, Dept. of Ecology and Evolutionary Biology, University of Kansas .
Feb 2005 – Aug 2005	Research Assistant, University of Malaysia, Sarawak (anuran bioacoustics recording and analysis).
Nov 2004 – Dec 2004	Research Assistant, University of Malaya (multivariate statistical analysis and correlation of phytoplankton biodiversity and physico-chemical data).
Oct 2004 – Nov 2004	Consultant Database Developer, TRAFFIC Southeast Asia (continued development on an informant and specimen tracking database for the investigation of illegal wildlife trade in Southeast Asia).
Jun 2003 – Nov 2003	Consultant Herpetologist, Wetlands International (herpetological assessment of the Southeast Pahang peat-swamp forests).
Apr 2000 – Oct 2002	Scientific Officer, World Wide Fund for Nature, Malaysia (UNDP-GEF Project to protect the marine biodiversity of the Marine Park Islands of Malaysia; Conservation planning in production forests; Nature tourism in Ulu Muda).
Feb 2000 – Apr 2000	Research Assistant, World Wide Fund for Nature, Malaysia .
Jun 1999 – Aug 1999	Research Assistant, TRAFFIC Southeast Asia (field survey and analysis of use of tiger parts in traditional Chinese medicine in Malaysia).
May 1999 – Jun 1999	Research Assistant, World Wide Fund for Nature, Malaysia (ecoregional approach to identification of high-conservation value habitats).
Mar 1999 – May 1999	Research Assistant, World Wide Fund for Nature, Malaysia (planning and preparation for the Johore State Workshop on implementing the Convention of Biological Diversity and the National Biodiversity Policy).
Jun 1998 – Dec 1998	Environmental Technical Officer, Malaysian Wetlands Foundation .

TECHNICAL SKILLS

- Programming/scripting languages: Python, C/C++, R, Java, SQL, JavaScript, shell scripting.
- Mathematical and statistical packages: R, Mathematica, SPSS, MiniTab.
- Databases: Advanced relational database design, development, front-end/back-end programming, management, and support, using SQL (PostgreSQL/MySQL).
- Web: Design, development and maintenance of websites using static (HTML and CSS-only), dynamic database-driven (e.g. Python CGI, Apache/PHP/SQL).

stack), CMS (Drupal, WordPress, MediaWiki, etc.), or custom application server framework (e.g. web2py) technologies.

- GIS: Training and experience in using the ESRI ArcGIS family of products.
- Systems administration: Linux HPC cluster (for phylogenetic, bioinformatics, and scientific computing).
- Operating Systems: Linux, BSD, Mac OS X, Microsoft Windows XP/2000.
- Various build systems (autotools, CMake, etc.) and version control systems (Git, Mercurial, SVN, CVS).