

## CURRICULUM VITAE

### Michael Samuel Rosenberg

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### EDUCATION

Ph.D., State University of New York at Stony Brook, Department of Ecology & Evolution, 2000.  
B.A., Northwestern University, Majors in Biology, Geology, and Anthropology, 1994.

### RESEARCH POSITIONS AND EMPLOYMENT

Associate Professor, School of Life Sciences, Arizona State University, 2008 – *present*.  
Assistant Professor, School of Life Sciences, Arizona State University, 2003 – 2008.  
Note: 7/2003 – 6/2008: School of Life Sciences  
1/2003 – 6/2003: Department of Biology  
Member, Center for Evolutionary Functional Genomics, The Biodesign Institute, Arizona State University, 2003 – *present*.  
Faculty Research Associate (to Dr. Sudhir Kumar), Department of Biology, Arizona State University, 2000 – 2002.  
Graduate Research Assistant (to Dr. Robert R. Sokal), Department of Ecology & Evolution, State University of New York at Stony Brook, 1995 – 1999.  
Graduate Research Assistant (to Dr. Manuel Lerchau), Department of Ecology & Evolution, State University of New York at Stony Brook, 1998.  
Graduate Teaching Assistant, Department of Ecology & Evolution, State University of New York at Stony Brook, 1994 – 1995, 1998 – 2000.  
Short Term Fellow, Smithsonian Tropical Research Institute, 1997.  
Intern, Vertebrate Fossils Department, Carnegie Museum of Natural History, 1991.  
Computing Consultant, Northwestern University Information Technology, 1991 – 1994.

### RESEARCH INTERESTS

Computational evolutionary biology and ecology; bioinformatics; sequence alignment; phylogenetics; spatial analysis and statistics; genomics; fiddler crab biology and evolution; meta-analysis; geometric morphometrics

### PUBLICATIONS († = *Sponsored PostDoc*)

#### *In Refereed Journals*

30. Ogden, T. H.†, and M. S. Rosenberg. 2007. Alignment and topological accuracy of the direct optimization approach via POY and traditional phylogenetics via ClustalW + PAUP\*. *Systematic Biology* 56:182–193.
29. Ogden, T. H.†, and M. S. Rosenberg. 2007. How should gaps be treated in parsimony? A comparison of approaches using simulation. *Molecular Phylogenetics and Evolution* 42:817–826. (Erratum: 2008, 46:807–808)

28. Ogden, T. H.<sup>†</sup>, and M. S. Rosenberg. 2006. Multiple sequence alignment accuracy and phylogenetic inference. *Systematic Biology* 55:314–328.
27. Rosenberg, M. S. 2005. Multiple sequence alignment accuracy and evolutionary distance estimation. *BMC Bioinformatics* 6:278. [10 pages]
26. Rosenberg, M. S. 2005. *MySSP*: Non-stationary evolutionary sequence simulation, including indels. *Evolutionary Bioinformatics Online* 1:81–83.
25. Rosenberg, M. S. 2005. Evolutionary distance estimation and fidelity of pair wise sequence alignment. *BMC Bioinformatics* 6:102. [9 pages]
24. Rosenberg, M. S. 2005. The file-drawer problem revisited: A general weighted method for calculating fail-safe numbers in meta-analysis. *Evolution* 59:464–468.
23. Gadagkar, S. R., M. S. Rosenberg, and S. Kumar. 2005. Inferring species phylogenies from multiple genes: Concatenated sequence tree versus consensus gene tree. *Journal of Experimental Zoology. B. Molecular and Developmental Evolution* 304B:64–74.
22. Rosenberg, M. S., K. A. Garrett, Z. Su, and R. L. Bowden. 2004. Meta-analysis in plant pathology: Synthesizing research results. *Phytopathology* 94:1013–1017.
21. Rosenberg, M. S. 2004. Wavelet analysis for detecting anisotropy in point patterns. *Journal of Vegetation Science* 15:277–284.
20. Sokal, R. R., N. L. Oden, M. S. Rosenberg, and B. A. Thomson. 2004. A new protocol for evaluating putative causes for multiple variables in a spatial setting, illustrated by its application to European cancer rates. *American Journal of Human Biology* 16:1–16.
19. Hyatt, L. A., M. S. Rosenberg, T. G. Howard, G. Bole, W. Fang, J. Anastasia, K. Brown, R. Grella, K. Hinman, J. P. Kurdziel, and J. Gurevitch. 2003. The distance dependence prediction of the Janzen-Connell hypothesis: A meta-analysis. *Oikos* 103:590–602.
18. Rosenberg, M. S., S. Subramanian, and S. Kumar. 2003. Patterns of transitional mutation biases within and among mammalian genomes. *Molecular Biology and Evolution* 20:988–993. [50% credit as assistant professor at ASU]
17. Rosenberg, M. S., and S. Kumar. 2003. Heterogeneity of nucleotide frequencies among evolutionary lineages and phylogenetic inference. *Molecular Biology and Evolution* 20:610–621. [50% credit as assistant professor at ASU]
16. Rosenberg, M. S., and S. Kumar. 2003. Taxon sampling, bioinformatics, and phylogenomics. *Systematic Biology* 52:119–124.
15. Dungan, J. L., J. Perry, M. Dale, S. Citron-Pousty, M.-J. Fortin, A. Jakomulska, P. Legendre, M. Miriti, and M. S. Rosenberg. 2002. A balanced view of scaling in spatial statistical analysis. *Ecography* 25:626–640.
14. Perry, J. N., A. Liebhold, M. S. Rosenberg, J. Dungan, M. Miriti, A. Jakomulska, and S. Citron-Pousty. 2002. Illustration and guidelines for selecting statistical methods for quantifying spatial patterns in ecological data. *Ecography* 25:578–600.
13. Dale, M. R. T., P. Dixon, M.-J. Fortin, P. Legendre, D. E. Myers, and M. S. Rosenberg. 2002. Conceptual and mathematical relationships among methods for spatial analysis. *Ecography* 25:558–577.
12. Rosenberg, M. S. 2002. Fiddler crab claw shape variation: A geometric morphometric analysis across the genus *Uca*. *Biological Journal of the Linnean Society* 75:147–162.

11. Rosenberg, M. S., and S. Kumar. 2001. Incomplete taxon sampling is not a problem for phylogenetic inference. *Proceedings of the National Academy of Sciences USA* 98:10751–10756.
10. Rosenberg, M. S., and S. Kumar. 2001. Traditional phylogenetic reconstruction methods reconstruct shallow and deep evolutionary relationships equally well. *Molecular Biology and Evolution* 18:1823–1827.
9. Rosenberg, M. S. 2001. The systematics and taxonomy of fiddler crabs: A phylogeny of the genus *Uca*. *Journal of Crustacean Biology* 21:839–869.
8. Rosenberg, M. S. 2000. The bearing correlogram: A new method of analyzing directional spatial autocorrelation. *Geographical Analysis* 32:267–278.
7. Sokal, R. R., N. L. Oden, M. S. Rosenberg, and B. A. Thomson. 2000. Cancer incidences in Europe related to mortalities, and ethnohistoric, genetic, and geographic distances. *Proceedings of the National Academy of Sciences USA* 97:6067–6072.
6. Rosenberg, M. S., R. R. Sokal, N. L. Oden, and D. DiGiovanni. 1999. Spatial autocorrelation of cancer in Europe. *European Journal of Epidemiology* 15:15–22.
5. Adams, D. C., and M. S. Rosenberg. 1998. Partial-warps, phylogeny, and ontogeny: A comment on Fink and Zelditch (1995). *Systematic Biology* 47:168–173.
4. Sokal, R. R., N. L. Oden, M. S. Rosenberg, and D. DiGiovanni. 1997. Ethnohistory, genetics and cancer mortality in Europeans. *Proceedings of the National Academy of Sciences USA* 94:12728–12731.
3. Sokal, R. R., N. L. Oden, M. S. Rosenberg, and D. DiGiovanni. 1997. The patterns of historical population movements in Europe and some of their genetic consequences. *American Journal of Human Biology* 9:391–404.
2. Adams, D. C., J. Gurevitch, and M. S. Rosenberg. 1997. Resampling tests for meta-analysis of ecological data. *Ecology* 78:1277–1283.
1. Rosenberg, M. S. 1997. Evolution of shape differences between the major and minor chelipeds of *Uca pugnax* (Decapoda: Ocypodidae). *Journal of Crustacean Biology* 17:52–59.

#### *Software*

5. Rosenberg, M. S. 2005. *MySSP*. Non-stationary evolutionary sequence simulation, including indels. Version 1.
4. Rosenberg, M. S. 2005. *Fail-Safe Number Calculator*. Version 1.
3. Rosenberg, M. S. 2001. *PASSAGE*. Pattern analysis, spatial statistics and geographic exegesis. Version 1. <http://www.passagesoftware.net>. [Since Oct 2002: downloaded > 4200 times, by > 2100 distinct, voluntarily provided email addresses (> 1000 additional anonymous), from at least 149 U.S. universities and 60 countries]
2. Rosenberg, M. S., D. C. Adams, and J. Gurevitch. 2000. *MetaWin*. Statistical software for meta-analysis. Version 2. Sinauer Associates, Sunderland, Massachusetts.
1. Rosenberg, M. S., D. C. Adams, and J. Gurevitch. 1997. *MetaWin*. Statistical software for meta-analysis with resampling tests. Version 1. Sinauer Associates, Sunderland, Massachusetts.

#### *Edited Books*

1. Rosenberg, M. S. 2009. *Sequence Alignment: Methods, Models, Concepts, and Strategies*. University of California Press: Berkeley, CA.

### *Book Chapters*

2. Rosenberg, M. S., and T. H. Ogden. 2009. Simulation approaches to evaluating alignment error and methods for comparing alternate alignments. Pp. 179–207 in *Sequence Alignment: Methods, Models, Concepts, and Strategies*, M. S. Rosenberg, ed. University of California Press: Berkeley, CA.
1. Rosenberg, M. S. 2009. Sequence alignment: Concepts and history. Pp. 1–22 in *Sequence Alignment: Methods, Models, Concepts, and Strategies*, M. S. Rosenberg, ed. University of California Press: Berkeley, CA.

### *Reports*

1. Dowling, T. E., P. C. Marsh, C. D. Anderson, M. S. Rosenberg, and A. T. Kelsen. 2008. Population structure in the roundtail chub (*Gila robusta* complex) of the Gila River basin as determined by microsatellites. Report to Arizona Game and Fish Department.

### *Other Publications*

2. E. A. Ainsworth, M. S. Rosenberg, and X. Wang. 2007. Meta-analysis: The past, present and future. *New Phytologist* 176:742–745. [commissioned meeting report]
1. Rosenberg, M. S. 2005. Why lectures seem to last forever. *Journal of Irreproducible Results* 49:16. [humor]

### *Book Reviews*

2. Rosenberg, M. S. 1998. (Book Review) Modeling Dynamic Biological Systems. *Quarterly Review of Biology* 73:340.
1. Rosenberg, M. S. 1997. (Software Review) Minitab for Windows. *Quarterly Review of Biology* 72:240–241.

### *Abstracts*

1. Sokal, R. R., N. L. Oden, M. S. Rosenberg, and B. A. Thomson. 2000. Cancer incidences in Europe related to ethnohistoric and genetic distances. *American Journal of Physical Anthropology* 111(S30):286–287.

### *Theses*

1. Rosenberg, M. S. 2000. The Comparative Claw Morphology, Phylogeny, and Behavior of Fiddler Crabs (Genus *Uca*). Ph.D. Thesis. Department of Ecology and Evolution, State University of New York at Stony Brook, Stony Brook, NY.

## **GRANTS AND RESEARCH SUPPORT**

### *Extramural Received*

- National Science Foundation, grant #DMS-0714949, “Collaborative research: Statistical methods and algorithms for genomic data.” PI: S.-C. Chen, Co-PI: M. S. Rosenberg (30% rec.) (8/15/2007 – 7/31/2011), \$624,592.
- National Science Foundation, grant #DBI-0542599, “Spatial analysis across biological disciplines.” PI: M. S. Rosenberg (7/1/2006 – 6/30/2010), \$642,862.

National Institutes of Health, grant #R03 LM008637, “Effect of sequence alignment fidelity on genome research.” PI: M. S. Rosenberg (7/1/2005 – 6/30/2007), \$142,453.

Sigma Xi, Grant-in-Aid of Research, “The study of combat and morphology in fiddler crabs (genus *Uca*).” PI: M. S. Rosenberg (1998), \$600.

Smithsonian Tropical Research Institute, Short Term Fellowship, “The study of combat and morphology in fiddler crabs.” PI: M. S. Rosenberg (9/15/1997 – 12/15/1997), \$2,800.

#### **AWARDS AND HONORS**

Nominated by the School of Life Sciences, Arizona State University, for “Sloan Research Fellowship in Computational and Evolutionary Molecular Biology” (2003).

Outstanding Graduate Student Presentation Award in Ecology & Evolution, State University of New York at Stony Brook (1996).

Robert R. Sokal Travel Award, State University of New York at Stony Brook (1996).

#### **LABORATORY AWARDS AND HONORS**

T. Heath Ogden (Postdoctoral Associate), 2005 finalist for Ernst Mayr Award (Society of Systematic Biologists) for “The use of simulation to study the role of alignment accuracy in phylogenetic inference” (T. H. Ogden and M. S. Rosenberg).

#### **INVITED PAPERS (\*Indicates presenter)**

Rosenberg, M. S.\* 2007. Plenary address: Methods for comparing alignments and the dissociation between primary and functional performance of alignment algorithms in phylogenetics and bioinformatics. Computational Phylogenetics and Molecular Systematics conference, Moscow, Russia.

Rosenberg, M. S.\* 2007. Keynote address: The bioinformatic approach to exploring the evolutionary history of infectious disease causing agents: A case study of tuberculosis and leprosy. Symposium on Biomedical Bioinformatics. Idaho State University Practical Bioinformatics Workshop, Lava Hot Springs, ID.

Rosenberg, M. S.\* 2007. What are ecological meta-analysts missing out on? *In* Synthesizing Ecological Studies in a Changing World Using Meta-Analysis. Ecological Society of America and Society for Ecological Restoration, joint meeting, San Jose, CA.

Ogden, T. H.\*, and M. S. Rosenberg. 2006. Direct optimization vs. traditional phylogenetics: Alignment and topological accuracy. *In* Phylogenetic Analysis and Alignment, Society for Molecular Biology and Evolution annual meeting, Tempe, AZ.

Rosenberg, M. S.\*, and T. H. Ogden. 2006. How should gaps be treated in parsimony? A comparison of approaches using simulation. *In* Phylogenetic Analysis and Alignment, Society for Molecular Biology and Evolution annual meeting, Tempe, AZ.

Rosenberg, M. S.\* 2002. Fiddler crab evolution: Systematics and geometric morphometric analysis of claw shape. *In* Patterns and Processes in Crustacean Evolution, Sixth International Congress of Systematic and Evolutionary Biology, Patras, Greece.

Rosenberg, M. S.\* 2002. Reasons and methods for directional spatial analysis of ecological data. *In* Spatial Ecology and Statistics, American Society of Naturalists annual meeting, Banff, Canada.

Perry, J. N.\* , A. Liebhold, M. S. Rosenberg, J. Dungan, M. Miriti, A. Jakomulska, S. Citron-Pousty, and P. Dixon. 2002. Selecting statistical methods for spatial patterns. *In* Spatial Ecology and Statistics, American Society of Naturalists annual meeting, Banff, Canada.

**RECENT CONTRIBUTED PAPERS (\*Indicates presenter)**

Pfister, L.-A.\* , M. S. Rosenberg, and A. C. Stone. 2008. How do we estimate bacterial mutation rates? Society for Molecular Biology and Evolution annual meeting, Barcelona, Spain.

Pfister, L.-A.\* , M. S. Rosenberg, and A. C. Stone. 2008. Full genome comparisons of Mycobacterium: Insight into the origin of tuberculosis and leprosy. American Association of Physical Anthropology annual meeting, Columbus, OH.

Rosenberg, M. S.\* , and C. D. Anderson. 2007. *PASSaGE: Pattern Analysis, Spatial Statistics, and Geographic Exegesis*. Version 2. Ecological Society of America and Society for Ecological Restoration, joint meeting, San Jose, CA.

Rosenberg, M. S., and C. D. Anderson\*. 2007. *PASSaGE: Pattern Analysis, Spatial Statistics, and Geographic Exegesis*. Version 2. Joint meeting of Ichthyologists and Herpetologists, St. Louis, MO.

Pfister, L.-A.\* , M. S. Rosenberg, and A. C. Stone. 2007. Full genome comparisons of mycobacteria: Insights into the origin of tuberculosis. Society for Molecular Biology and Evolution annual meeting, Halifax, Canada.

Rosenberg, M. S.\* , L.-A. Pfister, and A. C. Stone. 2007. Full genome comparisons of mycobacteria: Insights into the origin of tuberculosis. Society for the Study of Evolution, Society of Systematic Biologists, and American Society of Naturalists, joint meeting, Christchurch, New Zealand.

Rosenberg, M. S.\* , and C. D. Anderson. 2007. *PASSaGE: Pattern Analysis, Spatial Statistics, and Geographic Exegesis*. Version 2. Society for the Study of Evolution, Society of Systematic Biologists, and American Society of Naturalists, joint meeting, Christchurch, New Zealand.

Rosenberg, M. S.\* , and C. D. Anderson. 2007. *PASSaGE: Pattern Analysis, Spatial Statistics, and Geographic Exegesis*. Version 2. United States Regional Association of the International Association for Landscape Ecology meeting, Tucson, AZ.

Rosenberg, M. S.\* , and T. H. Ogden. 2006. Alignment, gaps, and parsimony. Society for the Study of Evolution, Society of Systematic Biologists, and American Society of Naturalists, joint meeting, Stony Brook, NY.

Goldberg, L. G.\* , and M. S. Rosenberg. 2006. Extending gene families via predicted ancestral sequences. Society for Molecular Biology and Evolution annual meeting, Tempe, AZ.

Kurdoglu, A. A.\* , T. H. Ogden, and M. S. Rosenberg. 2006. A comparative study of multiple alignment programs and evolutionary distance estimation. Society for Molecular Biology and Evolution annual meeting, Tempe, AZ.

Rosenberg, M. S.\* 2005. Multiple alignment can bias evolutionary distance estimation. Society for the Study of Evolution, Society of Systematic Biologists, and American Society of Naturalists, joint meeting, Fairbanks, AK.

Ogden, T. H.\* , and M. S. Rosenberg. 2005. The use of simulation to study the role of alignment accuracy in phylogenetic inference. Society for the Study of Evolution,

Society of Systematic Biologists, and American Society of Naturalists, joint meeting, Fairbanks, AK.

#### **PROFESSIONAL SOCIETIES (PAST\* AND PRESENT)**

American Association for the Advancement of Science, American Society of Naturalists\*, Animal Behavior Society\*, Scientific Research Society of North America (Sigma Xi), Society for Integrative and Comparative Biology\*, Society for Molecular Biology and Evolution, Society of Systematic Biologists, Society for the Study of Evolution

#### **FIELD RESEARCH**

Fiddler crab biology in Long Island, New York (1995 – 2000), Republic of Panama (1997).

#### **WORKING GROUPS/WORKSHOPS**

SEED: Proposal to develop a novel journal concept for evolutionary meta-analyses (Invited Working Group Member), National Evolutionary Synthesis Center, Durham, NC, 2006 – 2007.

Meta-analysis in ecology: Lessons, challenges and future (Invited Working Group Member), National Center for Ecological Analysis and Synthesis, Santa Barbara, CA, 2006 – 2007.

MARC Winter Institute (Participant), National Academies Summer Institutes on Undergraduate Education in Biology, Santa Cruz, CA, 2005.

Meta-Analysis: Synthesis across studies in plant pathology (Invited Workshop Instructor), American Phytopathological Society annual meeting, Milwaukee, WI, 2002.

Integrating the statistical modeling of spatial data in ecology (Invited Working Group Member), National Center for Ecological Analysis and Synthesis, Santa Barbara, CA, 1999 – 2000.

#### **COURSES TAUGHT**

*Arizona State University*

Instructor:

BIO/MAT 294 – Quantitative and Reasoning Skills in the Life Sciences (S05)

BIO 345 – Organic Evolution (F03, S04, F05, F06, F07, F08)

BIO/MAT/MBB 355 – Introduction to Computational Molecular Biology (S07<sup>†</sup>, S08, S09) [<sup>†</sup>*previously BIO/MAT/MBB 394*]

BIO 494/591 – Bioinformatics (F04); Molecular Evolution and Bioinformatics (S05)

BIO 591 – Seminar: Phylogenetics Discussion Group (S06)

BIO 591 – Seminar: Spatial Analysis for Ecology and Evolution (F08)

CBS 584 – Internship (SumI07)

CBS 590 – Readings & Conference (SumI07)

CBS 591 – Seminar: Computational Methods for Determining Functional Elements from Sequence Data (S04)

*State University of New York at Stony Brook*

Graduate Teaching Assistant:

BIO 150 – The Living World (S00)  
BIO 151 – Principles of Biology I: Organisms to Ecosystems (F94, F98)  
BIO 152 – Principles of Biology II: Molecules to Organisms (S95)  
BEE 552 – Biometry (S99, F99)  
BEE 585 – Introduction to Ecological Research (S98)

## **STUDENT SUPERVISION**

### *Sponsored Postdoctoral Associates*

Corey D. Anderson (2006 – present)  
T. Heath Ogden (2005 – 2006)

### *Dissertation Advisor*

Crystal Hepp, Ph.D. Molecular and Cellular Biology (2007 – present)

### *Thesis Advisor*

Virginia Earl-Mirowski, M.S. Computational Biosciences “Compare and contrast the effects of using less stringent criteria in BLASTCLUST to a novel iterative method for identifying gene families” (2007)  
Meraj Aziz, M.S. Computational Biosciences, “Estimating *ClustalW* pairwise alignment parameters for non-coding DNA sequences” (2007)  
Loretta Goldberg, M.S. Computational Biosciences, “Extending gene families via predicted ancestral sequences” (2006)

### *Graduate Student Research Supervisor*

Amy Harris, M.S. Computational Biosciences (2006 – 2007)  
Ahmet Kurdoglu, M.S. Computational Biosciences (2005 – 2006)  
Shruti Lal, M.S. Computational Biosciences (2004)

### *Graduate Committee Membership*

Committee member, Luz-Andrea Pfister, Ph.D. Anthropology (*in progress*)  
Committee member, Takahiro Maruki, Ph.D. Biology (*in progress*)  
Committee member, WangJuh Chen, Ph.D. Mathematics (*in progress*)  
Committee member, Daryn Stover, Ph.D. Biology (*in progress*)  
Committee member, Vinod Swarna, M.S. Biology (2007)  
Committee member, Ahmet Kurdoglu, M.S. Computational Biosciences (2006)  
Committee member, Shruti Lal, M.S. Computational Biosciences (2005)  
Committee member, Xiaofen Liu, M.S. Computational Biosciences (2005)  
Committee member, Kaushal Parekh, M.S. Computational Biosciences (2005)  
Committee member, Stephanie Rogers, M.S. Computational Biosciences (2005)  
Committee member, Vinod Swarna, M.S. Computational Biosciences (2005)  
Committee member, Patrick Kolb, M.N.S. Biology (2003)

### *Undergraduate Mentoring*

Footnote 18, Rebecca Oehler (BIO 345: Fall 2006)  
Reader for Barrett Honors College undergraduate thesis: Joseph Maranville (2007),  
Nicole Garber (2003)

*Other*

Volunteer post-baccalaureate research assistant, Nasser Hamdan (2005)

**SERVICE**

*Professional*

Principal co-organizer, 2006 annual meeting of the Society for Molecular Biology and Evolution, Tempe, AZ.

External manuscript reviewer for 46 journals: *Acta Oecologica*; *American Naturalist*; *Animal Behaviour*, *Behavioral Ecology and Sociobiology*; *Bioinformatics*; *Biological Reviews*; *Biology Letters*; *BMC Bioinformatics*; *BMC Evolutionary Biology*; *BMC Genomics*; *Bulletin of Environmental Contamination and Toxicology*; *Canadian Journal of Zoology*; *Cladistics*; *Ecography*; *Ecology Letters*; *Écoscience*; *Evolution*; *Evolutionary Bioinformatics Online*; *Genetics*; *Geographical Analysis*; *Global Ecology and Biogeography*; *Gulf and Caribbean Research*; *Heredity*; *Hydrobiologia*; *IEEE/ACM Transactions on Computational Biology and Bioinformatics*; *Image Analysis & Stereology*; *Insect Science*; *Journal of Crustacean Biology*; *Journal of Ecology*; *Journal of Experimental Marine Biology and Ecology*; *Journal of Heredity*; *Journal of Natural History*; *Journal of the Marine Biological Association of the United Kingdom*; *Journal of the Royal Society Interface*; *Journal of Vegetation Science*; *Journal of Zoology*; *Molecular Biology and Evolution*; *Molecular Phylogenetics and Evolution*; *Nauplius*; *Pacific Symposium on Biocomputing*; *PLoS Computational Biology*; *Quarterly Review of Biology*; *Rangifer*; *Revista Brasileira de Zoologia*; *Systematic Biology*; *Wetlands*; and *Zootaxa*.

External grant reviewer for the *National Science Foundation*.

External book proposal reviewer for *Blackwell Publishing*, *John Wiley & Sons*, *Pearson Education*, *Roberts & Company Publishers*, *Taylor and Francis*, and *W.W. Norton & Company*.

*Departmental/Center*

SCHOOL OF LIFE SCIENCES, ARIZONA STATE UNIVERSITY

Member/Liaison, Informatics Certificate Committee (School of Computing and Informatics) (S07 – *present*)

Undergraduate Program Committee (F05 – *present*).

IT Resources Committee (F05 – *present*).

Personnel Committee: Genomics, Evolution, and Bioinformatics (F03 – *present*).

Leader, Computational Biosciences iGELS (S06 – S08)

Search Committee, Evolutionary Bioinformatics (F04 – S05).

Adjunct/Affiliate Membership Committee (F04 – S05).

Search Committee, Computational Biology (F03 – S04).

Search Committee, Evolutionary Bioinformatics (F03 – S04).

*Ad hoc* Committee on Visualization Laboratory/Information Technology (F03).

DEPARTMENT OF BIOLOGY, ARIZONA STATE UNIVERSITY

Search Committee, Center for Evolutionary Functional Genomics (S03).