

Sudhir Kumar

Founding Director, Institute for Genomics and Evolutionary Medicine (iGEM)
Laura H. Carnell Professor, Department of Biology
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EDUCATION

- Ph.D. *Genetics*** 1991 – 1996
Pennsylvania State University
University Park, Pennsylvania, USA
Thesis: Molecular Evolutionary Analysis
New Phylogeny Reconstruction Algorithm, Computer Application, and Data Analysis
Mentor: Masatoshi Nei
- M.Sc. *Biological Sciences**** (Hons.) 1985 – 1990
Birla Institute of Technology and Sciences, BITS
Pilani, Rajasthan, India
Thesis: Computer Simulation in Population Genetics
Mentor: Sandhya Mitra
- B.Eng. *Electrical & Electronics engineering**** (Hons.) 1985 – 1990
Birla Institute of Technology and Sciences, BITS
Pilani, Rajasthan, India
- *M.Sc. and B.Eng. were completed simultaneously in a visionary dual degree program.

PROFESSIONAL APPOINTMENTS

- Temple University, Philadelphia, Pennsylvania, USA
Founding Director, Institute for Genomics and Evolutionary Medicine 2014 – Present
Laura H. Carnell Professor, Department of Biology 2014 – Present
Full Professor, Department of Computer Information & Sciences 2014 – Present
- Arizona State University, Tempe, Arizona, USA
Regents' Professor, School of Life Sciences 2012 – 2014
Foundation Professor, School of Life Sciences 2011 – 2014
Director, Center for Evolutionary Medicine and Informatics, Biodesign Institute 2010 – 2014
Full Professor, School of Life Sciences 2006 – 2011
Director, Center for Evolutionary Functional Genomics, Biodesign Institute 2003 – 2010
Faculty Leader, Genomics, Evolution & Bioinformatics, School of Life Sciences 2003 – 2004
Associate Professor, School of Life Sciences 2002 – 2006
Assistant Professor, Department of Biology 1998 – 2002
- Pennsylvania State University, University Park, USA (Mentor: Masatoshi Nei)
Postdoctoral Fellow, Department of Biology 1996 – 1998
Research Assistant, Department of Biology 1991 – 1996

ADVISOR AND CONSULTANT

- Scientific Advisory Board Member*, Discovery Bio Inc., USA 2021 – Present
Scientific Advisory Board Member, Eloxx Pharmaceuticals, USA 2018 – Present
Chief Scientific Officer, Espis Vaccines, USA, 2008 – 2010
Consultant, Amerigenics, Inc., USA 2006
Advisory Committee Member, National Center for Evolutionary Synthesis 2006 – 2009
Consultant, Pharmacia Corporation, USA 2002 – 2003
Member, Astrobiology/Evolutionary Genomics Focus Group, NASA 2000

<i>Advisory Board, SICCS</i> , Northern Arizona University, USA	2016 – 2019
<i>Member</i> , Thought Leader Summit, American Heart Association, USA	2015
<i>Member</i> , Review Committee, Genomic Sciences Program, NC State U.	2015
<i>Advisory Board</i> , Münster Graduate School of Evolution, Münster, Germany	2011
<i>Member</i> , Review Committee, Inst. Genomics & Bioinfo. U. California, Irvine	2010 & 2005
<i>Advisory Board, FlyBase</i> , Harvard University, USA	2007 – 2008
<i>Advisory Member</i> , Committee on Evolutionary Bioinfo. U. South Dakota	2006
<i>Member</i> , NESCent group on Evolutionary Informatics (Interoperability)	2006 – 2008

AWARDS AND HONORS

Societies, Associations, and Academic

<i>Dean's Distinguished Excellence in Research Award</i> , Temple University	2021
<i>Community Service Award</i> , Society for Molecular Evolution and Biology	2017
<i>Fellow</i> (elected), American Association for the Advancement of Science <i>Citation</i> : Exemplary contributions in evolutionary bioinformatics, particularly in developing high-impact comparative analysis software for biologists and in illuminating the evolutionary dynamics of mutations and species through comparative genomics	2009
<i>Outstanding Science Alumni Award</i> , Pennsylvania State University	2015
<i>Faculty of the Game</i> , Temple Vs. Penn State Football, Temple Athletics	2015
<i>Fellow of F1000</i> , Faculty of 1000, Ltd.	2017
<i>Visiting Fellowship Award</i> , Japanese Society for Promotion of Science	2020 & 2008
<i>Governor's Celebration of Innovation – Academia</i> (Finalist), State of Arizona	2011 & 2009
<i>Honorary Professorship</i> , School of Computing and Informatics, ASU	2009
<i>Exemplar Faculty</i> , Arizona State University	2006
<i>Innovation Award in Functional Genomics</i> , Burroughs Wellcome Fund	2000

Citations

225,000+ citations (Google Scholar) 2021

<https://tinyurl.com/KumarScholar>

H-index = 78; i10-index = 156

- 190,000+ citations to software and databases
- 20,000+ citations to new methods and discoveries
- 10,000+ citations to books and reviews

Top-100 article of all time 2014

One article describing the MEGA software (Molecular Biology and Evolution, 2007, 24:1596-1599) was among the top-100 most-cited papers of all time (*Nature*, Oct 29/2014).

Top-cited article of the decade 2014

MEGA software article (Molecular Biology and Evolution, 2007, 24:1596-1599) was the most-cited article of the decade in the SCOPUS Agriculture and Biological Sciences section.

Top-100 Scientist by Platinum H-Index 2015

Archives of Environmental/Occupational Health (2015) 70:69-67

Top-10 most-cited scientist in Computer Sciences (Web of Science) 2004

Highly-Cited Researcher, Thomson-Reuter Web of Science 2014

Most Influential Minds, Thomson Reuters ScienceWatch 2014

Hot Papers/Citation Classics¹

Biology & Biochemistry section

Molecular Biology and Evolution 37:1237–1239 2019 – Present

¹ Essential Science Indicators (Web of Science) gives a HOT paper designation to articles in the top 0.1% of all articles published in the past two years. It assigns a Citation classic/Highly Cited designation to an article if the citation count is in the 1% of all articles in the last 10 years.

Molecular Biology and Evolution 35:1547–1549	2018 – Present
Molecular Biology and Evolution 34:1812–1819	2017 – Present
Molecular Biology and Evolution 33:1870–1874	2016 – Present
Molecular Biology and Evolution 32:835–845	2015 – Present
Molecular Biology and Evolution 30:2725–2729	2013 – Present
Molecular Biology and Evolution 28:2731–2739	2011 – Present
Molecular Biology and Evolution 24:1596–1599	2007
Computer Science section	
Briefings in Bioinformatics 9:299–306	2008
Briefings in Bioinformatics 5:150–163	2004
Bioinformatics 17:1244–1245	2001
Multidisciplinary Sciences section	
PNAS 101:11030–11035	2004
Biology section	
Bioinformatics 17:1244–1245	2001
Nature 392:917-920	1998
Faculty of 1000 Prime	
PNAS (2012) 109:19333-1933	2013
SCIENCE editor's choice	
Molecular Biology and Evolution (2006) 23:1946–1951	2006

PROFESSIONAL SERVICE

Societies

<i>President</i> (elected), Society for Molecular Biology and Evolution	2013
<i>Councilor</i> , Society for Molecular Biology and Evolution	2012 – Present
<i>Secretary</i> (elected), Society for Molecular Biology and Evolution	2004 – 2006
<i>Webmaster</i> , Society for Molecular Biology and Evolution	2004 – 2008
<i>Webmaster</i> , American Genetic Association	1999 – 2007

Editorial

<i>Editor-in-Chief</i> , Molecular Biology and Evolution; <i>Impact Factor</i> = 16	2012 – Present
<i>Editorial Board</i> , Genome Research	2005 – 2009
<i>Editorial Board</i> , Molecular and Developmental Evolution	2004 – 2010
<i>Associate Editor</i> , Gene: Functional Genomics	2005 – 2006
<i>Associate Editor</i> , Journal of Heredity	1999 – 2005
<i>Associate Editor</i> , Molecular Biology and Evolution	2005 – 2012
<i>Associate Editor</i> , Quarterly Reviews of Biology	2010 – 2014
<i>Associate Editor</i> , Evolutionary Bioinformatics	2005 – 2014
<i>Editorial Board</i> , Biomolecules	2010 – 2014
<i>Editorial Board</i> , Bioinformatics and Biology Insights	2009 – 2014

National Institutes of Health (NIH)

<i>Co-Chair</i> , Information Technology in Cancer Research Section	2018
<i>Chair</i> , Genome Variation, and Evolution Study Section	2016 – 2018
<i>Member</i> , Genome Variation and Evolution Study Section	2014 – 2016
<i>Member</i> , BioData Management and Analysis Study Section	2006 – 2010

National Science Foundation

<i>Member</i> , Information Technology Research-Medium Panel	2003
<i>Member</i> , Information Technology Research-Small Panel	2002

PROFESSIONAL AFFILIATIONS

Academic faculty and membership

<i>Affiliated Faculty</i> , Center for Sustainable Communities, Temple University	2019 – Present
<i>Member</i> , Molecular Therapeutics Program, Fox Chase Cancer Center, USA	2014 – Present
<i>Adjunct Professor</i> , Research Center for Genomics and Bioinformatics Tokyo Metropolitan University, Tokyo, Japan	2013 – Present
<i>Adjunct Professor</i> , Center of Excellence in Genomic Medicine Research King Abdulaziz University, Jeddah, Saudi Arabia	2013 – Present
<i>Guest Professor</i> , Center for Computational and Evolutionary Biology Institute of Zoology @ Beijing, China	2007
<i>Affiliate Professor</i> , Department of Biomedical Informatics, Arizona State	2005 – 2007
<i>Adjunct Senior Investigator</i> , Translational Genomics Research Institute, USA	2004 – 2007
<i>Affiliate Professor</i> , School of Computing, Informatics, and Decision Support Engineering, Arizona State University, Tempe, AZ, USA	2002
<i>Associate Member</i> , Astrobiology Research Center, Penn State University	1998

MEMBERSHIPS IN SCIENTIFIC & PROFESSIONAL ORGANIZATIONS

American Association for the Advancement of Science
American Association for Cancer Research
American Genetic Association
The Genetics Society of America
Human Genome Variation Society
International Society of Computational Biologists (lifetime)
National Association of Biology Teachers
Society for Molecular Biology and Evolution (lifetime)
Society for the Study of Evolution (lifetime)

LEADERSHIP OF INSTITUTIONAL AND GLOBAL ORGANIZATIONS

<i>Center for Evolutionary Functional Genomics @ Arizona State University</i> I was invited to lead a university-wide initiative in Genome Informatics in collaboration with the Computer Science department leaders in 2000. This initiative's success was the precursor to establishing a new Center for Evolutionary Functional Genomics (EFG) in the newly formed Biodesign Institute. I collaborated with leaders of Life Sciences, Anthropology, Computer Sciences, and Biomedical Informatics to recruit and mentor many outstanding faculty members in evolutionary biology, functional genomics, infectious diseases, and big data informatics. EFG became an intellectual hub of well-funded interdisciplinary research and graduate training.	2002 – 2010
<i>Center for Evolutionary Medicine and Informatics @ Arizona State University</i> Recognizing the emerging importance of evolution and medicine's interface, I led the evolution of EFG into the Center for Evolutionary Medicine and Informatics (CEMI). CEMI was featured in <i>Nature Medicine</i> (12/2010, 16:1346) as the premier evolutionary medicine center globally, with four major themes: Personal Genomics, Disease Origins, Functional Proteomics, and Discovery Bioinformatics. CEMI developed world leaders in evolutionary medicine, synthetic genetics, epidemiology, and machine learning. High scholarly impact, considerable extramural funding, and training of many interdisciplinary graduates were highlights of CEMI.	2010 – 2014

Institute for Genomics and Evolutionary Medicine @ Temple University

2014 – Present

A Temple-wide institute with a mission to harness molecular evolutionary rules of life to make breakthroughs in genome medicine and biodiversity, develop innovative computational methods for big data, and train young minds to pursue the next generation of challenges. We have developed research and teaching excellence at the convergence of genomics, evolution, and medicine, with a strong focus on machine learning, somatic evolution of tumors, malaria epidemiology, and infectious and complex diseases. The Institute has already made a positive impact through outstanding scholarship and software and database product developments and has a solid record of extramural funding and teaching. The Institute has also successfully developed a high-performance computing environment collaboratively through extramural funding from local (PA Commonwealth University Enhancement program) and national agencies (National Science Foundation).

Molecular Biology and Evolution (MBE)

2012 – Present

I am serving the scientific community as the Editor-in-Chief of MBE. Every year, I receive ~1,500 manuscripts and handle them editorially in close collaboration with 60 eminent scientists and four staff members. We have made MBE the top specialist journal in molecular evolution that publishes fundamental discoveries, methods, and tools. During my term, I have modernized the MBE website, made the editorial system more efficient and transparent, established a press office for outreach, and developed mechanisms to celebrate authors. Consequently, we have a high-impact, fast turn-around journal. I also manage some production, the press office, website updates, and budgets (\$1M annually). We are proud to return a large income to the Society for Molecular Biology and Evolution that supports scientific conferences, initiatives, and young investigators.

LEADERSHIP OF MAJOR RESEARCH RESOURCES

MEGA: Molecular Evolutionary Genetics Analysis software

1993 – Present

megasoftware.net

This is user-friendly software to analyze molecular sequences. First published in 1993, it is currently in its 11th major release and fully cross-platform. It is downloaded over 350,000 times each year (2.5 million downloads to date) and cited in over 24,000 publications annually (> 190,000-lifetime citations). It continues to be developed actively.²

TimeTree: The Timescale of Life knowledge-base

2004 – Present

timetree.org

TimeTree is a knowledge-base for scientists and the general public to access divergence times estimated from molecular dates and published in peer-reviewed scientific journals. It currently contains a global evolutionary synthesis of the evolutionary tree of ~100,000 species based on published dates from ~4000 articles. More than 250,000 queries are launched annually on this web resource and the associated iPhone app. It continues to be expanded actively.

FlyExpress: Co-expressed Developmental Genes by Image Analysis

2003 – Present

flyexpress.net

FlyExpress database contains 100,000+ images of expression from ~5,000 genes derived from high-throughput in situ hybridization studies and more than 30,000 images extracted and curated from peer-reviewed articles. It provides unique tools to search the library of in situ embryonic images through image matching. This database was last updated in 2016.

² MEGA's 25-year history is chronicled in a news story in *Molecular Biology and Evolution* (2018) 35:1558–1560.

TRAINING AND CURRICULUM DEVELOPMENT

Temple University, Philadelphia, Pennsylvania, USA

<i>Developer</i> and <i>Coordinator</i> , Bachelor of Science (BS) in Genomic Medicine	2020 – Present
<i>Developer</i> , Genomics and Bioinformatics concentration in Data Science (BS)	2017
<i>Developer</i> and <i>Coordinator</i> , Undergraduate certificate in Genomic Medicine	2016 – Present
<i>Co-Principal Investigator</i> , Innovating Graduate Stem Education through Bio-Social Partnerships, National Science Foundation	2015 – 2020

Arizona State University, Tempe, Arizona, USA

<i>Co-Director</i> , Biological Design Doctoral Program,	2012 – 2013
<i>Coordinator</i> , Academic exchange/Collaboration, Tokyo Metropolitan Univ.	2012
<i>Investigator</i> , Computational Biosciences Professional Master's Sloan Foundation	2001 – 2003
<i>Investigator</i> , Biodesigned Bridges to the Doctorate, National Science Foundation	2004 – 2006

RESEARCH GRANTS

National Institutes of Health (NIH)

Principal Investigator

Methods for Evolutionary Genomics Analysis <i>Comparative genomics, sparse learning, molecular evolution</i>	2021 – Present
Bioinformatics of metastatic migration histories <i>Bayesian methods, tumor phylogenetics, somatic variation</i>	2020 – Present
Inferring Molecular Evolutionary Rates and Divergence Dates <i>Relative rates, divergence times, software development</i>	2017 – 2021
Evolutionary Bioinformatics of Tumor profiles <i>Bulk-sequencing, clone deconvolution, multi-tumor analytics</i>	2016 – 2020
Evolutionary Bioinformatics of Human Mutations <i>Mendelian mutation diagnosis, machine learning, mypeg.info</i>	2010 – 2014
Re-Engineering the MEGA Software Package <i>Refactoring and hardening MEGA, testing and debugging</i>	2007 – 2011
Computational Analysis of Gene Expression Pattern Images (12 years) <i>Drosophila, embryogenesis, image analysis, flyexpress.net</i>	2003 – 2015
Comparative Molecular Sequence Analysis (15 years) <i>Statistical Methods, MEGA, molecular phylogenetics</i>	2000 – 2015

Co-Principal Investigator or Major Contributor

Bayesian Evolution-Aware Methods for Tumor Single Cell Sequences <i>Single-cell sequencing, imputation, statistical methods, phylogeny</i>	2017 – 2021
eQTL Mega-analysis for... Multi-enhancer Gene Regulation <i>GWAS, evolutionary probabilities, CRISPR, polymorphisms</i>	2016 – 2020
Computational Diagnosis of Non-syn Variations using Structural Dynamics <i>Disease mutation diagnosis, protein structures, phylomedicine</i>	2014 – 2017
Methods for Evol. Informed Network Analysis to Discover Disease Variation <i>GWAS, evolutionary probabilities, diabetes, polymorphisms</i>	2013 – 2017
Rational Design... of Effective DNA-Scaffolded Nicotine Vaccines <i>Evolutionary vaccinology, smoking, drug discovery, polymorphisms</i>	2013 – 2016
A Phylogenetic Approach to Metagenomic Analysis <i>Minimum evolution, phylogenetic placement, rRNA sequencing</i>	2011 – 2014
Center for Membrane Proteins in Infectious Diseases <i>Protein structure, evolutionary optimization, crystallization</i>	2010 – 2015
Team Approach to Translate Novel Biomarkers for Diabetes <i>Proteomics, polymorphisms, disease markers</i>	2009 – 2010
Discovering The Hidden Proteome in The Human Genome <i>mRNA display, cap-independent translation-enhancing elements</i>	2008 – 2012

National Science Foundation

Principal Investigator

Understanding Epistasis: The Key for Genotype to Phenotype Mapping <i>The convergence of many disciplines to discover epistasis</i>	2019 – Present
Open-source, Extensible, and Cross-platform MEGA <i>MEGA software, multi-platform, plug-in architecture</i>	2017 – 2021
Reconstructing the contemporary history and progenitor of SARS-CoV-2 strains causing COVID-19 <i>Pathogen genomics, COVID-19, phylogenetics</i>	2020 – 2021
Design of a Bioinformatic Database for Functional Evolutionary Footprints <i>Gene duplications, divergent substitutions, functional genomics</i>	2000 – 2004

Co-Principal Investigator or Major Contributor

Accelerating the Discovery and utility of the timescale of life <i>timetree of life, synthesis, open-source, expansion, TimeTree.org</i>	2020 – Present
Identifying phylogenetically informative data from next-gen sequencing <i>Molecular phylogenies, big data, signal and noise</i>	2014 – 2018
Large-Scale Structured Sparse Learning <i>Machine learning, image analysis, embryogenesis</i>	2014 – 2017
Enabling Discovery... through a Synthesis of... Evolutionary Histories <i>Timetree of life, synthesis, speciation process, TimeTree.org</i>	2013 – 2016
Computational Methods for Expression Image Analysis <i>Machine learning, image analysis, Drosophila embryogenesis</i>	2011 – 2015
Bioinformatics of Molecular TimeTrees <i>Timetree of life, synthesis, speciation process, TimeTree.org</i>	2009 – 2013
Developing a Bioinformatic Database for Stoichioproteomics <i>The convergence of proteomics and ecological stoichiometry</i>	2006 – 2010
Machine Learning Approaches for Biological Image Informatics <i>Machine learning, image analysis, gene expression</i>	2006 – 2010
Development of an Evolutionary Timescale Database <i>The timescale of life, synthesis of evolutionary timetrees, TimeTree.org</i>	2001 – 2004
Threats to Amphibian Biodiversity (8 years) <i>Emerging wildlife diseases, fungal pathogenesis, databases</i>	2000 – 2008

NASA Astrobiology

Innovative Molecular Timing... to obtain Accurate Histories of Early Life <i>Deep time, rocks vs. clocks, molecular dating</i>	2016 – 2020
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Science Foundation of Arizona

Bioinformatics of Assembling the Timescale of Life <i>TimeTree database, literature curation, phylogeny</i>	2007 – 2008
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Burroughs-Wellcome Fund

Computationally... Dissect Functionally Important Mutations... <i>Multigene families, Gene duplications, functional divergence</i>	2003 – 2006
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PUBLICATIONS

Books and guides

1. Kumar S, Tamura K & Nei M (1993) A Guide to Molecular Evolutionary Genetics Analysis Program for Microcomputers, Institute of Molecular Evolutionary Genetics, Pennsylvania State University, University Park, PA (140 pp; >2,500 printed manuals distributed).
2. Nei M & Kumar S (2000) Molecular Evolution and Phylogenetics. Oxford University Press, New York (333 pp). (*Translated in Chinese, Japanese, and Russian.*)
3. Hedges SB & Kumar S (2009) The Timetree of Life. Oxford University Press, New York (550 pp; edited volume with 81 contributions).

Submitted

4. Amendola A, Canuti M, Bianchi S, Kumar S, Fappani C, Gori M, Colzani D, Pond SLK, Miura S, Baggeri M, Marchi A, Borghi E, Zuccotti GV, Raviglione MC, Magurano F, Tanzi E (2021) Molecular evidence for SARS-CoV-2 in samples collected from patients with morbilliform eruptions since late summer 2019 in Lombardy, Northern Italy. (*In preparation*)
5. Miura S, Vu T, Choi J, Townsend JP & Kumar S (2021) Evolution of somatic mutational processes in cancer. (*Submitted*)

Revision invited

6. Barba-Montoya J, Tao Q & Kumar S (2021) Assessing rapid methods for phylogenomic dating. *Genome Biology and Evolution* (in revision).
7. Chroni A & Kumar S (2021) Tumors are evolutionary islands. *Genome Biology and Evolution* (revision invited).

Manuscripts accepted and in Press

8. Townsend JP, Hassler Hayley B., Wang Z, Miura S, Singh J, Kumar S, Ruddle N, Galvani AP & Dornburg A (2021) Durability of immunity against reinfection by SARS-CoV-2. *Lancet Microbe* (accepted).
9. Dasari K, Somarelli JA, Kumar S & Townsend JP (2021) The somatic molecular evolution of cancer: mutation, selection, and epistasis. *Progress in Biophysics and Molecular Biology* (in press).
10. Cai L, Wang Z, Kulathinal R, Kumar S, Ji S (2021) Deep low-shot learning for biological image classification and visualization from limited training samples. *IEEE Transactions on Neural Networks and Learning Systems* (accepted).
11. Sharma S & Kumar S (2021) Fast and accurate bootstrap confidence limits on genome-scale phylogenies using little bootstraps. *Nature Computational Science* (in press).
12. Chroni A & Kumar S (2021) Migrations of cancer cells through the lens of phylogenetic biogeography. *Scientific Reports* 11:17184.
13. Kumar S & Sharma S (2021) Evolutionary sparse learning for phylogenomics. *Molecular Biology and Evolution* 38 (in press).

Published in 2021

14. Kumar S, Tao Q, Weaver S, Sanderford M, Caraballo-Ortiz MA, Sharma S, Pond SLK & Miura S (2021) An evolutionary portrait of the progenitor SARS-CoV-2 and its dominant offshoots in COVID-19 pandemic. *Molecular Biology and Evolution* 38:3046-3059.
15. Patel R & Kumar S (2021) Epistasis Produces an Excess of Invariant Sites in Neutral Molecular Evolution. *Proceedings of the National Academy of Sciences (USA)* 118:e2018767118.
16. Tamura K, Stecher G & Kumar S (2021) MEGA11: Molecular Evolutionary Genetics Analysis version 11. *Molecular Biology and Evolution* 38:3022-3027.
17. Tao Q, Barba-Montoya J & Kumar S (2021) Data-driven Speciation Tree Prior for Better Species Divergence Times in Calibration-poor Molecular Phylogenies. *Bioinformatics* 37:i102-i110.
18. Liu L, Chandrashekar P, Zeng B, Sanderford MD, Kumar S & Gibson G (2021) TreeMap: A structured approach to fine mapping of eQTL variants. *Bioinformatics* 37:1125-1134.
19. Barba-Montoya J, Tao Q & Kumar S (2021) Molecular and morphological clocks for estimating evolutionary divergence times. *BMC Ecology and Evolution* 21:83 (15 pp).
20. Babaian C & Kumar S (2021) How to build a super predator: From genotype to phenotype. *American Biology Teacher* 83:138-146.

21. Scheinfeldt LB, Brangan A, Kusic DM, Kumar S & Gharani N (2021) Common treatment, common variant: Evolutionary prediction of functional pharmacogenomic variants. *Journal of Personalized Medicine* 11:131.
22. Tao Q, Tamura K & Kumar S (2021) Rapid and reliable methods for molecular dating in *The Molecular Evolutionary Clock: Theory and Practice*, edited by Simon YW Ho (Springer, NY), pp 197-219.
23. Mello B, Tao Q, Barba-Montoya J & Kumar S (2021) Molecular dating for phylogenies containing a mix of populations and species by using Bayesian and RelTime approaches. *Molecular Ecology Resources* 21:122-136.

Published in 2020

24. Kumar S, Chroni A, Tamura K, Sanderford M, Oladeinde O, Aly V, Vu T & Miura S (2021) PathFinder: Bayesian inference of clone migration histories in cancer. *Bioinformatics* 36 (S2): i675–i683.
25. Barba-Montoya J, Tao Q & Kumar S (2021) Using a GTR+ Γ substitution model for dating sequence divergence when stationarity and time-reversibility assumptions are violated. *Bioinformatics* 36 (S2): i884–i894.
26. Tao Q, Barba-Montoya J, Huuki L, Durnan MK & Kumar S (2020) Relative efficiencies of simple and complex substitution models in estimating divergence times in phylogenomics. *Molecular Biology and Evolution* 37:1819–1831.
27. Leitner T & Kumar S (2020) Where did SARS-CoV-2 come from? *Molecular Biology and Evolution* 37:2463:2464.
28. Kulathinal R, Yoo Y & Kumar S (2020) The bits and bytes of biology: Digitalization fuels an emerging generative platform for biological innovation. Pp. 253-265 in *Handbook of Digital Innovation*, edited by Satish Nambisan (Edward Elgar Publishers, UK).
29. Miura S, Tamura K, Pond S, Huuki LA, Priest J, Deng J & Kumar S (2020) A new method for inferring timetrees from temporally sampled molecular sequences. *PLoS Computational Biology* 16 (24 pp).
30. Miura S, Vu T, Deng J, Buturla T, Oladeinde O, Choi J & Kumar S (2020) Power and pitfalls of computational methods for inferring clone phylogenies and mutation orders from bulk sequencing data. *Scientific Reports* 10:3498 (21 pp).
31. Tao Q, Tamura K, Mello B & Kumar S (2020) Reliable confidence intervals for RelTime estimates of evolutionary divergence times. *Molecular Biology and Evolution* 37:280-290.
32. Stetcher G, Tamura K & Kumar S (2020) Molecular Evolutionary Genetics Analysis (MEGA) for macOS. *Molecular Biology and Evolution* 37:1237-1239.
33. Babaian C & Kumar S (2020) Molecular memories of a Cambrian fossil. *American Biology Teacher* 83:586–595.
34. Campitelli P, Modi T, Kumar S, Ozkan SB (2020) The Role of conformational dynamics and allostery in modulating protein evolution. *Annual Review of Biophysics* 49:269-290
35. Somarelli J, ..., Kumar S, ... (2020) Molecular biology and evolution of cancer: from discovery to action. *Molecular Biology and Evolution* 37:320-326.
36. Chandrashekar P, ..., Kumar S, ... (2020) Somatic selection distinguishes oncogenes and tumor suppressor genes. *Bioinformatics* 36:1712-1717.
37. Zhou X, ..., Sanderford M, ..., S. Kumar, ... (2020) Beaver and Naked Mole Rat Genomes Reveal Common Paths to Longevity. *Cells Reports* 32:(13 pp)
38. Pyott SJ, ..., Sanderford M, Kumar S, ... (2020) Human hearing loss mutations are adaptive for subterranean hearing in African mole-rats. *Current Biology* 30:1-13.

39. Dubey B, ... , Kumar S, ... (2020) Interactive effect of TLR SNPs and exposure to sexually transmitted infections on Prostate cancer risk in Jamaican men. *The Prostate* 80: 1365- 1372.

Published in 2019

40. Liu L, Sanderford MD, Patel R, Chandrashekar PB, Gibson G & Kumar S (2019) Biological relevance of computationally predicted pathogenicity of noncoding variants. *Nature Communications* 10:330 (11 pp).
41. Tao Q, Tamura K, Battistuzzi F & Kumar S (2019) A machine learning method for detecting autocorrelation of evolutionary rates in large phylogenies. *Molecular Biology and Evolution* 36:811-824.
42. Chroni A, Vu T, Miura S & Kumar S (2019) Delineation of tumor migration paths by using a Bayesian biogeographic approach. *Cancers* 11:1880.
43. Babaian C & Kumar S (2019) Adventures in evolution: the narrative of Tardigrada, Trundlers in time. *American Biology Teacher* 81:543-552.
44. Patel R & Kumar S (2019) On estimating evolutionary probabilities of population variants. *BMC Evolutionary Biology* 19:133 (14 pp).
45. Xu K, Kosoy R, Shameer K, Kumar S, Liu L, Readhead B, Belbin GM, Lee HC, Chen R & Dudley JT (2019) Genome-wide analysis indicates association between heterozygote advantage and healthy aging in humans. *BMC Genetics* 20:52 (14 pp).

Published in 2018

46. Kumar S & Patel R (2018) Neutral theory, disease mutations, and personal exomes. *Molecular Biology and Evolution* 35:1297-1303.
47. Kumar S, Stecher G, Li M, Knyaz C & Tamura K (2018) MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. *Molecular Biology and Evolution* 35:1547-1549.
48. Tamura K, Tao Q & Kumar S (2018) Theoretical foundation of the RelTime method for estimating divergence times from variable evolutionary rates. *Molecular Biology and Evolution* 35:1770-1782.
49. Battistuzzi FU, Tao Q, Jones L, Tamura K & Kumar S (2018) RelTime relaxes the strict molecular clock throughout the phylogeny. *Genome Biology and Evolution* 10:1631-1636.
50. Patel R, Scheinfeldt LB, Sanderford MD, Lanham TR, Tamura K, Platt A, Glicksberg BS, Xu K, Dudley JT & Kumar S (2018) Adaptive landscape of protein variation in human exomes. *Molecular Biology and Evolution* 35:2015-2025.
51. Miura S, Gomez K, Murillo O, Huuki LA, Vu T, Buturla T & Kumar S (2018) Predicting clone genotypes from tumor bulk sequencing of multiple samples. *Bioinformatics* 34:4017-4026.
52. Miura S, Huuki LA, Buturla T, Vu T, Gomez K & Kumar S (2018) Computational enhancement of single-cell sequences for inferring tumor evolution. *Bioinformatics* 34:i917-i926.
53. Hedges SB, Tao Q, Walker M & Kumar S (2018) Accurate timetrees require accurate calibrations. *Proceedings of the National Academy of Sciences (USA)* 115:E9510-E9511.
54. Gomez K, Miura S, Spell BS & Kumar S (2018) Somatic evolutionary timings of driver mutations. *BMC Cancer* 18:85 (10 pp).

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207. Hedges SB, Kumar S, Tamura K & Stoneking M (1992) Human origins and analysis of mitochondrial DNA sequences. *Science* 255:737–739.

Book reviews and other publications

208. Kumar S (2000) A review of the book *Genomes* by TA Brown. *The Quarterly Review of Biology* 75:316–317.
209. Kumar S & Filipski A (2001 and 2008) Molecular Phylogeny Reconstruction. *Encyclopedia of Life Sciences Macmillan Reference Ltd*, Oxford, UK. (www.els.net).
210. Kumar S & Filipski A (2001) Molecular Clock Testing. *Encyclopedia of Life Sciences, Macmillan Reference Ltd*, Oxford, UK. (www.els.net).
211. Kumar S & Newfeld SJ (2002) A review of the book *Modern Genetic Analysis: Integrating Genes and Genomes* (second edition) by Griffiths AJF, Gelbart WM, Lewontin RC & Miller JH. *The Quarterly Review of Biology* 77:456–457.
212. Rawls A & Kumar S (2002) A review of the book *Genomic Regulatory Systems: Development and Evolution* by E. H. Davidson. *The Quarterly Review of Biology* 77:456.
213. Lorson C & Kumar S (2003) A review of the book *Genomes* (second edition) by T.A. Brown. *The Quarterly Review of Biology* 78:225.
214. Kumar S (2003) MacTrees made easy, a review of the book *Phylogenetic trees made easy: a how-to-manual for molecular biologists* by Hall BG. *Molecular Evolution and Phylogenetics* 27:165–167.
215. Kumar S & Filipski A (2004) Bayesian Phylogenetic Analysis. *Dictionary of Bioinformatics and Computational Biology* edited by Hancock J & Zvelebil M, Wiley-Liss, New York.
216. Kumar S & Filipski A (2005) Reconstructing Vertebrate Phylogeny. *Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics* edited by Subramaniam S. John Wiley & Sons, New York.
217. Kumar S and other authors (2007) Sequence Assembly and Alignment Tech Guide. In *Genome Technology* (10 pp).
218. Battistuzzi FU, Filipski A & Kumar S (2011) Molecular clock: testing (version 2.0). *Encyclopedia of Life Sciences*. John Wiley & Sons, Ltd, Chichester, UK (7pp) (www.els.net).
219. Kumar S (2013) Foreword for the book *Molecular Genetics: Concepts and Development* by S Mitra. MacMillan India Limited.
220. Kumar S (2017) F1000Prime Recommendation of Shen et al., *Nat Ecol Evol* 2017, 1(5):126 [in](#) F1000Prime (DOI: 10.3410/f.727814781.793536165).
221. Kumar S (2017) F1000Prime Recommendation of Warnock RCM et al., *Proc Biol Sci* 2017, 284(1857) (DOI: 10.3410/f.727752709.793536398).

RESEARCH MENTORING

Postdoctoral scholars

Current Antonia Chroni (2018–) • Caryn Babaian (2021–) • Jack Craig (2020–) • Jose Barba-Montoya (2018–) • Marcos Caraballo-Ortiz (2020–) • Qiqing Tao (2020–) • Ravi Patel (2021–)

Past Alan Filipiski (1998–2014) • Antonio Marco-Castillo (2008–2009) • Anup Som (2005–2007) • Araxi Urrutia (2003–2004) • Bao Hong Shen (2005–2007) • Beatriz Mello (2015–2016) • Christine Kuslich (2003–2005) • Claudia Acquisti (2006–2010) • Fabia Battistuzzi (2008–2012) • Li Liu (2012–2015) • Lifang Liu (2012–2013) • Mark P. Miller (2000–2002) • Michael S. Rosenberg (2000–2003) • Nevin Gerek (2010–2013) • Sankar Subramanian (2000–2006) • Sayaka Miura (2012–2016) • Sudhindra R. Gadagkar (1998–2003)

Doctoral and graduate students

Current Lisa Schmelkin (2019–) • Sudip Sharma (2018–)

Past Bindu Koshy • Caryn Babamaian • Charlotte Konikoff • Hector Ramos • HoJoon Lee • Jian Yang • Karthik Jayaraman • Louise Huuki • Madhusudhana Gargasha • Michael Suleski • Patrick Kolb • Qiqing Tao • Rajalakshmi Gurunathan • Ravi Patel • Rekha Iyer • Sandhya Durvasala • Shubhra Gupta • Siddarth Selvaraj • Stephanie Rogers • Vinod Swarna • Xiaofen Liu

Undergraduate and graduate research interns

Current Hasnat Hasib • Jared Huzar • Julia Davis • Maansi Suvarna • Nisarg Patel • Sara Vahdatshoar • Tenzin Dolker • Tracy Vu • Tyler Ebinger • Vivian Aly

Past Adam Orr • Adithya Rajan • Aditya Paliwal • Alexander Woodard • Alicia Varma • Alyza Villa • Amber Ahmed • Anant Bhargava • Anna Freydenzen • Antoine Al-Foune • April Merdon • Ariana Rodriguez • Asaria Jimenez • Brandon Butler • Brandy Buck • Brianna Spell • Bryan Sexton • Candice White • Carol Diaz • Chikku Baiju • Christopher Busick • Cristina Rivera • Diana Alarcon • Diana Tlougan • Elizabeth Santana • Elizabeth Villalba • Emily Davenport • Eric Thomas • Erika Garcia • German Velez • Glenn Markov • Greg McInnes • Hanna Pronina • Hariharan Mohanraj • Harry Ho • Heather R. DeWall • Heather Wiemann • Ivan Montiel • Jacob Reidhead Jenna Makis • Jessica Priest Jiamen Deng • Jiyeong Choi • Jonathan Falciani Jose Maldonado • Joy Wenslas • Kailah Davis • Karen Canales • Karen Gomez • Kari Strauss • Kimberly Kukurba • Kristyn Gerold • Krizia Cabrera • Kruti Patel • Lauren Hamilton • Liris Gonzalez • Liz Garcia • Louise Huuki • Mary Kate Durnan • Michael Suleski • Morgan Day • Natalia Santiago • Nate Sutton • Nicholas Peterson • Nicolas Feddern • Olumide Oladeinde • Oscar Murillo • Paul Billing-Ross • Pegah Biparvah • Rachel Sipes • Raul Navedo • Robert Adrian • Roman Johnson • Ronika Nirankari • Simon Lawrence • Stephanie Negron • Stephanie Tate • Stephen McAleer • Stephen Watson • Sujay Rajkumar • Tamera Lanham • Thania Martinez • Tiffany Buturla • Timothy Sweeney • Tina To • Vanessa Gray • Veena Ganeshan • Veronica Shi • Victor Correa • Viriya Keo • Wilda Rivera • Yea Jin Ko

Visiting Scholars/Tech Staff

Ade Banjoko • Aditya Rajan • Annirudha Kadne • Ashini Bolia • Ashly Ruttman • Ben Timmerick • Bernard Van Emden • Bremen Braun • Dana Desonie • Daniel Peterson • David Fisher • David Schwartz • Dishant Patel • Eric Thomas • Glen Stecher • Graziela Valente • Jana McAlpin • Jason Wulf • Jered Knoblock • Joel Dudley • Joseph Svitak • Keith Davis • Kelly Boccia • Lakshmi Viswanathan • Lin-Wei Wu • Mahesh Sundara Raman • Maxwell Sanderford • Melinda Caballero • Mia Champion • Michael Li • Michael *McCutchan* • Michael Suleski • Natalia Briones • Nicholas Harras • Nicholas Peterson • Nimit Johri • Quan Nguyen • Raj Bayapu • Renee Grothe • Revak Raj Tyagi • Roman Fuentes Ruttman • Sean Dudley • Siddarth Selvaraj • Suganthi Cidambaram • Vesna Djinicovic • Wayne Parkhurst • Zach Hanson-Hart

CLASSROOM TEACHING

Temple University

Genomic Evolutionary Medicine

2016 – 2020

*Introduces evolutionary principles and perspectives in Genomic Medicine
Designed for junior and senior undergraduate students (BIOL 3112/5112)
Interactive and discovery-based; taught five times
Enrollment has increased steadily from 49 to 146
Class satisfaction rating: Exceptional 4.5 (range 1 – 5)*

Seminar in Molecular Phylogenetics

2017 – 2019

Discusses early research articles in molecular phylogenetics (BIOL 8201)

*Intended for graduate students; taught two times
 Attended by many students and senior scientists
 Class satisfaction rating: Maximum 5.0 (range 1 – 5)*

Arizona State University

Evolutionary Medicine	2010 – 2013
<i>Introduces molecular evolution through examples from medicine Special topics designed for undergraduate to graduate students Attended by 12 – 41 students; taught four times (BIO 189/494) Class satisfaction rating: Exceptional 1.4 (range 1 - 4)</i>	
Introduction to Comparative Genomics	2001 – 2011
<i>Introduces fundamentals of evolutionary genomics Designed for senior undergrads and grad students Increasing enrollment from 10 to 41; taught seven times (BIO 494) Class satisfaction rating: Exceptional 1.2 (1 – 5)</i>	
Organic Evolution	2000 – 2006
<i>Basic course in evolutionary biology Designed for junior undergraduate Attended by 106 – 185 students; taught five times Class satisfaction rating: Exceptional 1.5 (range 1 – 4)</i>	
Molecular Evolutionary Genetics	1999 – 2000
<i>An advanced course on molecular evolution and phylogenetics Designed for graduate students (BIO 594/494) Attended by 7 – 14 students; taught three times Class satisfaction rating: Exceptional 1.3 (range 1 – 4)</i>	
CONFERENCE AND SYMPOSIA ORGANIZED	
Organizer, Growing Convergence Research Workshop on Epistasis (4/7)	2021
<i>Temple University, Philadelphia, Pennsylvania, virtual workshop</i>	
Organizer, MEGA 25th Anniversary Workshop (7/8-7/12)	2018
<i>The annual meeting of Society for Molecular Biology and Evolution (SMBE), Yokohama, Japan</i>	
Coordinator, Workshop in Biogenomics & Nanobiology (4/23-4/24)	2018
<i>International Collaboration Conference, Riyadh, Saudi Arabia</i>	
Organizer, Molecular Evolution and Medicine (9/16-9/17)	2017
<i>Temple University, Philadelphia, USA (100 attendees)</i>	
Organizer, Symposium on Next-Generation Tools	2016
<i>The annual meeting of SMBE, Gold Coast, Australia</i>	
Member, External Advisory Board	2014
<i>The annual meeting of SMBE, Puerto Rico, USA</i>	
Organizer, SMBE Symposium on Phylomedicine	2012
<i>Arizona State University, SU, Tempe, AZ, USA (75 attendees) (03/23-24)</i>	
Member, Global Organizing Committee	2011
<i>The annual meeting of SMBE, Kyoto Japan (7/26–7/30)</i>	
Organizer, Symposium on Evolutionary Biology in Health and Medicine	2010
<i>The annual meeting of SMBE, Lyon France (7/4–7/8) co-organizers: J Dudley and A Butte</i>	
Co-organizer, Molecular Phylogenetics Symposium	2010
<i>Moscow State University, Russia (5/17–5/21)</i>	
Member, Committee, International Conference on... Molecular Systematics	2007
<i>Moscow State University, Russia (12/16–12/19)</i>	
Organizer, Annual Meeting of Society for Molecular Biology and Evolution	2006
<i>Arizona State University, Tempe, Arizona (5/24–5/28) 750 participants</i>	
Organizer, Genome Database Workshop	2005
<i>National Evolutionary Synthesis Center, North Carolina (5/31– 6/3)</i>	
Organizer, Symposium on Evolutionary and Population Genomics	2004

INVITED PRESENTATION

2021 – 2015

Yale University • Duke University • Plenary speaker, 4th Chinese Systematics Conference, Beijing • Nangiang Lecture, Xiamen University, China • Plenary Speaker, NSF China, Xiamen • Peking University • Chinese Academy of Sciences, Beijing • Headlining speaker, Symposium on Molecular Biology and Evolution of Cancer, Yale University, New Haven, CT • U North Texas, Denton • Digital Innovation Workshop, Case Western Reserve, Cleveland • Silver Jubilee Workshop for MEGA, Yokohama, Japan • Selected Talk, Annual meetings of Society for Molecular Biology and Evolution. Manchester, UK • Silver Jubilee Workshop for MEGA, Yokohama, Japan. • Keynote Presentation, Symposium, Tokyo Metropolitan University, Japan • King Abdullah University of Science and Technology (KAUST) Selected Talk, Annual meetings of Society for Molecular Biology and Evolution • University of California (Los Angeles) • Keynote Presentation, King Abdullah University of Science and Technology (KAUST) • University of Pittsburgh • Symposium in the Annual meetings of Society for Molecular Biology and Evolution • Arizona State U • Northern Arizona U • Keynote, International Symposium ISEGB, Kaohsiung, Taiwan • Biodiversity Workshop, Temple Univ., Philadelphia • Fox Chase Cancer Center, Philadelphia, PA • University of Maryland, College Park, MD • Plenary Speaker, Center of Excellence in Genomic Medicine Research at King Abdulaziz University, KSA.

2014 - 2013

Chancellor's Distinguished Visitor/Speaker, University of Missouri, Columbia, MO • Keynote Address, Temple University, Philadelphia, PA • Speaker at two symposia, Society for Molecular Biology and Evolution Annual Conference, Puerto Rico • Presenter, Research Center for Genomics and Bioinformatics International symposium, Tokyo Metropolitan University, Japan • Speaker, Population Genetics Group, University of Bath, England • Plenary Speaker, Center of Excellence in Genomic Medicine Research at King Abdulaziz University, KSA • VWR Distinguished Speaker, Georgia Tech School of Biology • Keynote Address, Molecular Medicine: Next-Gen Sequencing for the Clinic, Frankfurt • Nei Lecture, SMBE Annual Meeting @ Chicago, Illinois • Chinese Academy of Sciences (CAS), Beijing, China • Nanjing Normal University, China • Center of Excellence in Genomic Medicine Research at King Abdulaziz University, KSA • Quantitative Biology Colloquium, University of Arizona, Tucson, AZ • Mount Sinai School of Medicine CME Seminar Series, New York, NY • National Cancer Institute Conference of Physical Sciences-Oncology, Scottsdale, Arizona • Temple University, Department of Biology, Philadelphia, Pennsylvania • Keynote Speaker, Sigma Xi, Oakland University, Rochester, Michigan

2012 – 2011

Plenary Speaker, Society for Evolutionary Studies Annual Meetings @ Tokyo Metropolitan University • SMBE Annual Meeting (The animal tree of life and its application) @ Dublin, Ireland • Biomedicine: Big Data and New Paths to Personalized Medicine, ASU • International Conference on Bioinformatics & Computational Biology @ BKK, Thailand • SMBE Satellite Meeting on Phylomedicine @ Arizona State University • ORSP Research Seminar Series @ Midwestern University, Phoenix, Arizona • Molecular Biosciences Seminar Presentation on Phylomedicine at Montana State • Keynote Speaker, Young Scientists' Workshop on Evolutionary Genomics @ Tokyo, Japan • SMBE Annual Meeting (Methods for multiple alignment and phylogenetic tree) @ Kyoto, Japan • International Society for Molecular Biology/ECCB (SNPSigs Selection) @ Vienna, Austria • Workshop on Bioinformatics Software for Comparative Genomics and Metagenomics. The Smithsonian Institution (SI), American Museum of Natural History (AMNH) and the Food and Drug Administration (FDA) • Department of Biomedical Informatics, ASU • Barrett Honors College, ASU • SMBE Symposium on Molecular and Genomic Evolution @ Penn State University •

Keynote, Mini-symposium on Data Mining for Biomedical Informatics @ SIAM International Conference on Data Mining, Mesa, Arizona • Keynote, Interdisciplinary Graduate Student's Symposium on Evolution Across Fields @ Institute for Evolution and Biodiversity, Muenster, Germany

2010 – 2008

Plenary Speaker, Molecular Phylogenetics Symposium, Russia • Stanford University, California, USA • Symphogen Corporation (Copenhagen) • Chalk Talk, Physics Department, ASU • Spirit of Senses Group, Phoenix, Arizona • University of Cologne, Germany • Quantitative Expression Analysis workshop @ Drosophila Research Conference, Chicago, Illinois • University of North Carolina, Charlotte, NC • Washington University, St. Louis, MO • Keynote, Symposium on Evolutionary Bioinformatics, Lava Springs, Idaho State University • Japan Biological Information Research Center (JBIRC), Tokyo, Japan • Symposium on New Insight of Genome Evolution into Fundamental Activities of Life, National Institute of Genetics (NIG) and the Tokyo Institute of Technology (TIT), Japan • Global Center for Excellence, Hokkaido University, Sapporo, Japan • Discussion leader, Computational and Statistical Advances, Gordon Conference in Molecular Evolution @ Ventura, California

2007 – 2005

SOLUR Program, Arizona State University • Department of Biomedical Informatics, Arizona State University • FlyBase Advisory Group @ Harvard University, Boston, MA • Keynote Speaker, Ohio Collaborative Conference on Bioinformatics (OCCBIO) @ Miami University, Oxford, Ohio, • EMBO workshop on "Human Evolution and Disease" @ Center for Cellular and Molecular Biology, Hyderabad, India • Department of Biological Sciences, University of Idaho, Moscow, ID • Microbiology Department, Montana State University, Bozeman, MT • ASU Emeritus Faculty Association, Tempe, Arizona • Symposium on Molecular Evolution @ Moscow Conference on Computational Molecular Biology, Moscow State University, Russia • Symposium on Systems Biology @ Moscow Conference on Computational Molecular Biology, Moscow State University, Russia • Special presentation to the Panel on Chemical Imaging, National Academies (USA), Washington DC

2004 – 2002

Symposium on Evolutionary and Population Genomics @ Future of Statistics Conference, Hyderabad, India • Symposium on Advances in Methods for Estimating Species Divergence Dates using Molecular Data @ International Congress of Zoology, Beijing, China • Symposium on Molecular Phylogeny and Molecular Clocks @ Annual Meeting of SMCB, Penn State University, University Park, PA • Hexapodium, Center for Insect Research, University of Arizona • Techniques Workshop @ 44th Annual Drosophila Research Conference, Chicago, IL • Comparative and Functional Genomics Workshop, Wellcome Trust and Dept. of Energy, Hinxton, Cambridgeshire, UK • Annual Meeting of SMCB, Newport Beach, CA • Department of Biology, Duke University, Durham, NC • Bioinformatics Research Center, North Carolina State University, Raleigh, NC • Symposium on Evolutionary Genetics @ Annual meeting of the American Genetic Association, Arizona State University, Tempe, Arizona • The 12th International Workshop on Beyond the Identification of Transcribed Sequences: Functional, Evolutionary, and Expression Analysis sponsored by Department of Energy, Washington, DC • The 18th International Symposium in Conjunction with Award of the International Prize for Biology, Tokyo, Japan • Department of Biology, Indiana University, Bloomington, Indiana • Department of Computer Science, Arizona State University, Tempe, AZ • Department of Biology, University of Michigan, Ann Arbor, Michigan

2001 – 1995

International Workshop on Population Genetics @ University of Montreal, Montreal, Canada • ASU President's Community Enrichment Program, Phoenix, Arizona • Department of Biology, Ohio State University, Columbus, Ohio • Department of Biology, Hong Kong University, Hong

Kong, China (2 lectures) • Department of Biology, Syracuse University, Syracuse, New York • Program in Ecology and Evolutionary Biology, University of Illinois, Urbana Champaign, Illinois • Department of Biology, Grand Canyon University, Phoenix, Arizona • Ecology & Evolutionary Biology Program/IGERT, Indiana University, Bloomington, Indiana • Department of Biology, Tokyo Metropolitan University, Tokyo, Japan • Biomedical Engineering, Indian Institute of Science, Bangalore, India • Department of Biology, Tokyo Metropolitan University, Tokyo, Japan • Graduate University for Advanced Studies, Hayama, Japan • Genetics Program, University of Arizona, Tucson, Arizona • Birla Institute of Technology & Sciences, Pilani, India • University of South Carolina, Columbia, South Carolina • Symposium on Genomic Diversity @ Annual meeting of the American Genetic Association, Pennsylvania State University, University Park, PA • Department of Biology, Arizona State University-West, Phoenix, Arizona • Department of Zoology and Genetics, Iowa State University, Ames, Iowa • Symposium on Large Phylogenies @ Annual meeting of the Society for the Study of Systematic Biology, University of Colorado, Boulder, Colorado • National Cancer Institute, Frederick, Maryland • Department of Biology, Arizona State University, Tempe, Arizona