Sudhir Kumar

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

Efforts of individual laboratories to international consortia are producing data of vast breadth, depth, and complexity. These massive datasets are affording unprecedented understanding of basic to translational biomedicine, personal to population genomics, and gut to global biodiversity. Yet perceptive analyses of these data await scalable and efficient computational methods that can extract and harness the knowledge embedded in expanding databases of genome sequences, images, and phenotype annotations. At the nexus of machine learning, statistical analysis, and bioinformatics, data science is now practiced by individual investigators and large consortia alike, whose contributions enable fundamental insights, mechanistic understandings, and transformative solutions for science, medicine, technology, and public policy.

My research focuses on data science and analytics as the major challenge facing our field is to innovate methods that analyze, integrate, synthesize, and transform voluminous data into knowledge. My research is at the theoretical and empirical intersection of evolutionary and functional genomics with computational biology. I have pursued a biology-anchored research program, referred to as a Pattern-Process-Prediction-Product (P^4) paradigm. In P^4, we begin by discovering evolutionary and genomic *patterns* through comparative analyses of big data. These datasets include variation across populations, tumors, strains, and species. The patterns of sequence variation reveal the underlying biological *processes*. We harness evolutionary knowledge to develop *predictive* models that translate fundamental knowledge into actionable information. Ultimately, we make our innovations, along with those contributed by others, widely accessible by developing industrial-strength and user-friendly *products* such as software and databases.

My research group has developed new computational methods and algorithms for scalable and efficient analysis of big data through integrative approaches to research in molecular evolution, functional genomics, and biomedicine. Highlights include Bayesian methods, machine learning algorithms, and statistical approaches for inferring molecular phylogenies, divergence times, ancestral sequences, evolutionary distances, pathogenic mutations, tumor clone types, and adaptations. We have made several major discoveries through big data analytics and developed high-impact tools used by scientists, students, and the general public. Some recent efforts promote the application of molecular evolution to the growing fields of phylomedicine and tumor biology. We have democratized computational science throughout my career by making tools accessible to researchers regardless of research discipline or financial resources. In the future, we will continue to make big data analytics more widely accessible and advance the synthesis of evolutionary knowledge in the scientific literature.

We have championed interdisciplinary initiatives that converge disciplines through the founding and direction of a major research center at the interface of evolution, functional genomics, medicine, and data science. I currently lead a large research institute with a mission to make fundamental discoveries, develop informatics resources, and train the next generation of young scientists in the genomics of health, disease dynamics, and biological complexity. We have also developed three undergraduate programs that integrate genomics, evolution, and bioinformatics. Through the leadership of a top scientific journal and a premier professional society, I have contributed to the scientific community's growth in my profession at local, national, and international levels.

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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.Engg 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, Ciscovery 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
Advisory Board, SICCS, Northern Arizona University, USA	2016 – 2019

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

AWARDS AND HONORS

Societies, Associations, and Academic

Dean's Distinguished Excellence in Research Award, Temple University   2021
Highly-Cited Researcher[1], Clarivate Web of Science   2021
Community Service Award, Society for Molecular Evolution and Biology   2017
Fellow (elected), American Association for the Advancement of Science   2009
> *Citation:* 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

Outstanding Science Alumni Award, Pennsylvania State University   2015
Top-100 Scientist by Platinum H-Index   2015
> Archives of Environmental/Occupational Health (2015) 70:69-67

Faculty of the Game, Temple Vs. Penn State Football, Temple Athletics   2015
Highly-Cited Researcher, Thomson-Reuter Web of Science   2014
Most Influential Minds, Thomson Reuters ScienceWatch   2014
Fellow of F1000, Faculty of 1000, Ltd.   2017
Visiting Fellowship Award, Japanese Society for Promotion of Science   2020 & 2008
Governor's Celebration of Innovation – Academia (Finalist), State of Arizona   2011 & 2009
Honorary Professorship, School of Computing and Informatics, ASU   2009
Exemplar Faculty, Arizona State University   2006
Top-10 most-cited scientist in Computer Sciences (Web of Science)   2004
Innovation Award in Functional Genomics, Burroughs Wellcome Fund   2000

Citations

236,000+ citations (Google Scholar)   2022
> *https://tinyurl.com/KumarScholar*
> H-index = 80; i10-index = 161
> ➢ 200,000+ 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.

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[1] Highly Cited Researchers™ have demonstrated significant and broad influence reflected in their publication of multiple highly cited papers over the last decade. These highly cited papers rank in the top 1% by citations for a field or fields and publication year in the Web of Science™. Of the world's population of scientists and social scientists, Highly Cited Researchers are 1 in 1,000. https://recognition.webofscience.com/awards/highly-cited/2021/

Hot Papers/Citation Classics/Emerging Classics[2]

Biology & Biochemistry

Molecular Biology and Evolution 35:1770–1782	2018 – Present
Molecular Biology and Evolution 35:1547–1549	2018 – Present
Molecular Biology and Evolution 38:3022–3027	2021 – 2022
Molecular Biology and Evolution 37:1237–1239	2020 – 2022
Molecular Biology and Evolution 34:1812–1819	2017 – 2021
Molecular Biology and Evolution 33:1870–1874	2016 – 2021
Molecular Biology and Evolution 32:835–845	2015 – 2021
Molecular Biology and Evolution 30:2725–2729	2013 – 2021
Molecular Biology and Evolution 28:2731–2739	2011 – 2021
Molecular Biology and Evolution 24:1596–1599	2007

Computer Science

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

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

Editorial

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

National Institutes of Health (NIH)

Co-Chair, Information Technology in Cancer Research Section	2018
Chair, Genome Variation, and Evolution Study Section	2016 – 2018

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[2] 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.

Member, Genome Variation and Evolution Study Section	2014 – 2016
Member, BioData Management and Analysis Study Section	2006 – 2010

<u>*National Science Foundation*</u>

Member, Information Technology Research-Medium Panel	2003
Member, Information Technology Research-Small Panel	2002

PROFESSIONAL AFFILIATIONS

<u>*Academic faculty and membership*</u>

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

Center for Evolutionary Functional Genomics at Arizona State University	2002 – 2010

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.

Center for Evolutionary Medicine and Informatics at Arizona State University	2010 – 2014

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 *Nature Medicine* (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.

Institute for Genomics and Evolutionary Medicine at 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 21,000 publications annually (> 200,000-lifetime citations). It continues to be developed actively.[3]

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 >140,000 species based on published dates from >4,000 articles. Over 250,000 queries are launched annually on this web resource and the associated iPhone app. It continues to be expanded actively.

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

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.

TRAINING AND CURRICULUM DEVELOPMENT

Temple University, Philadelphia, Pennsylvania, USA

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

Arizona State University, Tempe, Arizona, USA

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

RESEARCH GRANTS

National Institutes of Health (NIH)

Principal Investigator

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

Co-Principal Investigator or Major Contributor

Bayesian Evolution-Aware Methods for Tumor Single Cell Sequences	2017 – 2021
Single-cell sequencing, imputation, statistical methods, phylogeny	
eQTL Mega-analysis for… Multi-enhancer Gene Regulation	2016 – 2020
GWAS, evolutionary probabilities, CRISPR, polymorphisms	
Computational Diagnosis of Non-syn Variations using Structural Dynamics	2014 – 2017
Disease mutation diagnosis, protein structures, phylomedicine	
Methods for Evol. Informed Network Analysis to Discover Disease Variation	2013 – 2017
GWAS, evolutionary probabilities, diabetes, polymorphisms	
Rational Design… of Effective DNA-Scaffolded Nicotine Vaccines	2013 – 2016
Evolutionary vaccinology, smoking, drug discovery, polymorphisms	

A Phylogenetic Approach to Metagenomic Analysis	2011 – 2014
Minimum evolution, phylogenetic placement, rRNA sequencing	
Center for Membrane Proteins in Infectious Diseases	2010 – 2015
Protein structure, evolutionary optimization, crystallization	
Team Approach to Translate Novel Biomarkers for Diabetes	2009 – 2010
Proteomics, polymorphisms, disease markers	
Discovering The Hidden Proteome in The Human Genome	2008 – 2012
mRNA display, cap-independent translation-enhancing elements	

National Science Foundation

Principal Investigator

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

Co-Principal Investigator or Major Contributor

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

NASA Astrobiology

Innovative Molecular Timing… to obtain Accurate Histories of Early Life	2016 – 2020
Deep time, rocks vs. clocks, molecular dating	

Science Foundation of Arizona

Bioinformatics of Assembling the Timescale of Life	2007 – 2008
TimeTree database, literature curation, phylogeny	

Burroughs-Wellcome Fund

Computationally… Dissect Functionally Important Mutations…	2003 – 2006
Multigene families, Gene duplications, functional divergence	

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).

Revisions/In review

4. Patel R, Carnevale V & Kumar S (2022) Epistasis creates invariant sites and modulates the rate of molecular evolution. *Molecular Biology and Evolution* (in revision/review).

5. Caraballo-Ortiz M, Miura S, Sanderford M, Dolker T, Tao Q, Weaver S, Pond SLK & Kumar S (2022) TopHap: Rapid inference of key phylogenetic structures from common haplotypes in large genome collections with limited diversity. *Bioinformatics* (in revision/review).

6. Miura S, Vu T, Choi J, Townsend JP, Karim S & Kumar S (2022) Evolution of somatic mutational processes in cancer. *Communications Biology* (in revision/review*).*

7. Huzar J, Kim H, Kumar S & Miura S (2022) MOCA for integrated analysis of gene expression and genetic variation in single cells. *Frontiers in Genetics* (in revision/review).

8. Ose NJ, Butler BM, Kumar A, Sanderford M, Kumar S & Ozkan SB (2022) Dynamic coupling of residues within proteins as a mechanistic foundation of many enigmatic pathogenic missense variants. *PLoS Computational Biology* (in revision/review).

9. Tao Q, Sharma S & Kumar S (2022) RRF: An R package for evolutionary dates, rates, and priors using relative rate framework. *bioRxiv*

10. 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 (2022) Molecular evidence for SARS-CoV-2 in samples collected from patients with morbilliform eruptions since late summer 2019 in Lombardy, Northern Italy. *Preprints with The Lancet*. (Submitted to Viruses)

Manuscripts accepted and in Press

11. Kumar S (2022) Embracing green computing in molecular phylogenetics. *Molecular Biology and Evolution* (In press).

12. Babaian C & Kumar S (2022) Storyboarding for biology: An authentic STEAM experience. *The American Biology Teacher* (In press).

13. Craig JM, Kumar S & Hedges SB (2022) Limitations of phylogenomic data can drive inferred speciation rate shifts. *Molecular Biology and Evolution* (In press).

    https://doi.org/10.1093/molbev/msac038

Published in 2022

14. Karim S, Al-Kharraz M, Mirza Z, Noureldin H, Abusamara H, Alganmi N, Merdad A, Jastanlah S, Kumar S, Rasool M, Abuzenadah A & Al-Qahtani M (2022) Development of "Biosearch System" for Biobank Management and Storage of Disease Associated Genetic Information. *Journal of King Saud University – Science* 34:101760 (10pp)*.*

Published in 2021

15. Kumar S & Sharma S (2021) Evolutionary sparse learning for phylogenomics. *Molecular Biology and Evolution* 38:4674-4682.

16. Sharma S & Kumar S (2021) Fast and accurate bootstrap confidence limits on genome-scale phylogenies using little bootstraps. *Nature Computational Science* 1:573-577.

17. 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.

18. 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.

19. Chroni A & Kumar S (2021) Tumors are evolutionary island-like ecosystems. *Genome Biology and Evolution* 13:evab276 (11pp).

20. Barba-Montoya J, Tao Q & Kumar S (2021) Assessing rapid relaxed-clock methods for phylogenomic dating. *Genome Biology and Evolution* 13:evab251 (14pp).

21. 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* 165:56-65.

22. 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*.

    https://ieeexplore.ieee.org/stamp/stamp.jsp?arnumber=9530249.

23. Townsend JP, Hassler HB, Wang Z, Miura S, Singh J, Kumar S, Ruddle N, Galvani AP & Dornburg A (2021) The durability of immunity against reinfection by SARS-CoV-2: A comparative evolutionary study. *The Lancet Microbe* 12:e666-e675.

24. Chroni A, Miura S, Oladeinde O, Aly V & Kumar S (2021) Migrations of cancer cells through the lens of phylogenetic biogeography. *Scientific Reports* 11:17184(13pp).

25. Tamura K, Stecher G & Kumar S (2021) MEGA11: Molecular Evolutionary Genetics Analysis version 11. *Molecular Biology and Evolution* 38:3022-3027.

26. 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.

27. 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.

28. 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).

29. Babaian C & Kumar S (2021) How to build a super predator: From genotype to phenotype. *American Biology Teacher* 83:138-146.

30. 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(13pp).

31. 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.

32. 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

33. 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.

34. 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.

35. 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.

36. Leitner T & Kumar S (2020) Where did SARS-CoV-2 come from? *Molecular Biology and Evolution 37:*2463:2464.

37. 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 <u>in</u> *Handbook of Digital Innovation*, edited by Satish Nambisan (Edward Elgar Publishers, UK).

38. 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).

39. 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).

40. 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.

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201. Zhang J & Kumar S (1997) Detection of convergent and parallel evolution at the amino acid sequence level. *Molecular Biology and Evolution* 14:527–536.

202. Zhang J, Kumar S & Nei M (1997) Small-sample tests of episodic adaptive evolution: A case study of primate lysozymes. *Molecular Biology and Evolution* 14:1335–1338.

203. Yeager M, Kumar S & Hughes AL (1997) Sequence convergence in the peptide-binding region of primate and rodent MHC class Ib molecules. *Molecular Biology and Evolution* 14:1035–1041.

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206. Kumar S (1996) Patterns of nucleotide substitution in mitochondrial protein-coding genes of vertebrates. *Genetics* 143:537–548.

207. Kumar S, Balczarek KA & Lai Z-C (1996) Evolution of the hedgehog gene family. *Genetics* 142:965–972.

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209. Hedges SB, Parker PH, Sibley CG & Kumar S (1996) Continental breakup and the ordinal diversification of birds and mammals. *Nature* 381:226–229.

210. Yang Z & Kumar S (1996) Approximate methods for estimating the pattern of nucleotide substitution and the variation of substitution rates among sites. *Molecular Biology and Evolution* 13:650–659.

Published in 1995

211. Kumar S (1995) PhylTest: A Program for Testing Phylogenetic Hypotheses. Pennsylvania State University, University Park.

212. Rzhetsky A, Kumar S & Nei M (1995) Four-cluster analysis: A simple method to test phylogenetic hypotheses. *Molecular Biology & Evolution* 12:163–167.

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Published in 1994 and earlier

215. Kumar S, Tamura K & Nei M (1994) MEGA: Molecular Evolutionary Genetics Analysis software for microcomputers. *Computer Applications in Biosciences* 10:189–191.

216. 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

217. Kumar S (2000) A review of the book Genomes by TA Brown. *The Quarterly Review of Biology* 75:316–317.

218. Kumar S & Filipski A (2001 and 2008) Molecular Phylogeny Reconstruction. *Encyclopedia of Life Sciences Macmillan Reference Ltd*, Oxford, UK. (www.els.net).

219. Kumar S & Filipski A (2001) Molecular Clock Testing. *Encyclopedia of Life Sciences, Macmillan Reference Ltd*, Oxford, UK. (www.els.net).

220. 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.

221. 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.

222. Lorson C & Kumar S (2003) A review of the book *Genomes* (second edition) by T.A. Brown. The Quarterly Review of Biology 78:225.

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225. Kumar S & Filipski A (2005) Reconstructing Vertebrate Phylogeny. *Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics* edited by Subramaniam S. John Wiley & Sons, New York.

226. Kumar S and other authors (2007) Sequence Assembly and Alignment Tech Guide. In *Genome Technology* (10 pp).

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229. Kumar S (2017) F1000Prime Recommendation of *Shen et al., Nat Ecol Evol 2017, 1(5):126* in F1000Prime (DOI: 10.3410/f.727814781.793536165).

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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–)

Past *Alan Filipski (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) • Ravi Patel (2021) • Sankar Subramanian (2000–2006) • Sayaka Miura (2012–2016) • Sudhindra R. Gadagkar (1998–2003)*

Doctoral and graduate students

Current John Allard (2021–) • Lisa Schmelkin (2019–) • Sudip Sharma (2018–)

Past Bindu Koshy • Caryn Babaian • Charlotte Konikoff • Hector Ramos • HoJoon Lee • Jian Yang • Karthik Jayaraman • Louise Huuki • Madhusudhana Gargesha • 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 • Madelyn Shenoy • Nandita Nagendra • Nisarg Patel • Tenzin Dolker • 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 • Julia Davis • Kailah Davis • Karen Canales • Karen Gomez • Kari Strauss • Kimberly Kukurba • Kristyn Gerold • Krizia Cabrera • Kruti Patel • Lauren Hamilton • Liris Gonzalez • Liz Garcia • Louise Huuki • Maansi Suvarna • 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 • Sara Vahdatshoar ▪ Simon Lawrence • Stephanie Negron • Stephanie Tate • Stephen McAleer • Stephen Watson • Sujay Rajkumar • Tamera Lanham • Thania Martinez • Tiffany Buturla • Timothy Sweeney • Tina To • Tracy Vu ▪ Tyler Ebinger • 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 • Jared Knobloch • Joel Dudley • Joseph Svitak • Keith Davis • Kelly Boccia • Lakshmie 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 Djinovic • 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

    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)

Introduction to Comparative Genomics	2001 – 2011

    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)

Organic Evolution	2000 – 2006

    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)

Molecular Evolutionary Genetics	1999 – 2000

    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)

CONFERENCE AND SYMPOSIA ORGANIZED

Organizer, Green Computing in Molecular Phylogenetics (7/10-14)   2022
        SMBE Everywhere; Kick-off annual meeting of the
        Society for Molecular Biology and Evolution (SMBE)

Organizer, Growing Convergence Research Workshop on Epistasis (4/7)   2021
        Temple University, Philadelphia, Pennsylvania, virtual workshop

Organizer, MEGA 25th Anniversary Workshop (7/8-7/12)   2018
        The annual meeting of the Society for Molecular Biology and Evolution (SMBE),
        Yokohama, Japan

Coordinator, Workshop in Biogenomics & Nanobiology (4/23-4/24)   2018
        International Collaboration Conference, Riyadh, Saudi Arabia

Organizer, Molecular Evolution and Medicine (9/16-9/17)   2017
        Temple University, Philadelphia, USA (100 attendees)

Organizer, Symposium on Next-Generation Tools   2016
        The annual meeting of SMBE, Gold Coast, Australia

Member, External Advisory Board   2014
        The annual meeting of SMBE, Puerto Rico, USA

Organizer, SMBE Symposium on Phylomedicine   2012
        Arizona State University, SU, Tempe, AZ, USA (75 attendees) (03/23-24)

Member, Global Organizing Committee   2011
        The annual meeting of SMBE, Kyoto Japan (7/26–7/30)

Organizer, Symposium on Evolutionary Biology in Health and Medicine   2010
        The annual meeting of SMBE, Lyon France (7/4–7/8)
        co-organizers: J Dudley and A Butte

Co-organizer, Molecular Phylogenetics Symposium   2010
        Moscow State University, Russia (5/17–5/21)

Member, Committee, International Conference on… Molecular Systematics   2007
        Moscow State University, Russia (12/16–12/19)

Organizer, Annual Meeting of Society for Molecular Biology and Evolution   2006
        Arizona State University, Tempe, Arizona (5/24–5/28) 750 participants

Organizer, Genome Database Workshop   2005
        National Evolutionary Synthesis Center, North Carolina (5/31– 6/3)

Organizer, Symposium on Evolutionary and Population Genomics   2004
        Future of Statistics, Indian School of Business, Hyderabad (12/29–1/1)

INVITED PRESENTATION

2022 – 2019

Keynote, Center for Computational and Integrative Biology (CCIB), Rutgers University, Camden Campus • *Keynote*, Second International Symposium on Genetics, Federal University of Rio de Janeiro • *Keynote* Presentation, Zakir Husain Delhi College, New Delhi • Symposium on the Origin of the COVID-19 Pandemic, Universite de Paris, France• *Distinguished Speaker Invitation*, Yale University • *Invited Talk*, Duke University • *Plenary*, 4th Chinese Systematics Conference, Beijing • *Nanqiang Lecture*, Xiamen University, China • *Plenary*, NSF China, Xiamen • *Invited Talk,* Peking University • *Invited Talk,* Chinese Academy of Sciences, Beijing • *Headliner*, Symposium on Molecular Biology and Evolution of Cancer, Yale University • *Invited Talk*, University of North Texas, Denton.

2018 – 2015

Invited Presenter, Digital Innovation Workshop, Case Western Reserve University, Cleveland • *Invited Presenter,* Silver Jubilee Workshop for MEGA, Yokohama, Japan • *Invited Talk,* Annual meetings of Society for Molecular Biology and Evolution, Manchester, UK • *Keynote,* Symposium, Tokyo Metropolitan University, Japan • *Invited Talk,* King Abdullah University of Science and Technology (KAUST) • *Invited Talk,* Annual meetings of Society for Molecular Biology and Evolution • *Invited Talk,* University of California (Los Angeles) • *Keynote,* King Abdullah University of Science and Technology (KAUST), Saudi Arabia • *Invited Talk,* University of Pittsburgh • *Invited*

Presenter, Symposium in the Annual meetings of Society for Molecular Biology and Evolution • *Invited Talk,* Arizona State University • *Invited Talk,* Northern Arizona University • *Keynote*, International Symposium ISEGB, Kaohsiung, Taiwan • *Invited Presenter,* Biodiversity Workshop, Temple University, Philadelphia • *Invited Talk,* Fox Chase Cancer Center, Philadelphia, PA • *Invited Talk,* University of Maryland, College Park, MD • *Plenary*, Center of Excellence in Genomic Medicine Research at King Abdulaziz University, KSA.

2014 - 2013

Chancellor's Distinguished Speaker, University of Missouri, Columbia, MO • *Keynote Address,* Temple University, Philadelphia, PA • *Invited Speaker* at two symposia, Society for Molecular Biology and Evolution Annual Conference, Puerto Rico • *Invited Presenter,* Research Center for Genomics and Bioinformatics International symposium, Tokyo Metropolitan University, Japan • *Invited Speaker,* Population Genetics Group, University of Bath, England • *Plenary,* 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 at Chicago, Illinois • *Invited Speaker,* Chinese Academy of Sciences (CAS), Beijing, China • *Invited Speaker,* Nanjing Normal University, China • *Invited Speaker,* Center of Excellence in Genomic Medicine Research at King Abdulaziz University, KSA • *Invited Presenter,* Quantitative Biology Colloquium, University of Arizona, Tucson, AZ • *Invited Speaker,* Mount Sinai School of Medicine CME Seminar Series, New York, NY • *Invited Speaker,* National Cancer Institute Conference of Physical Sciences-Oncology, Scottsdale, Arizona • *Invited Speaker,* 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 at Tokyo Metropolitan University • SMBE Annual Meeting (The animal tree of life and its application) at Dublin, Ireland • Biomedicine: Big Data and New Paths to Personalized Medicine, ASU • International Conference on Bioinformatics & Computational Biology at BKK, Thailand • SMBE Satellite Meeting on Phylomedicine at Arizona State University • ORSP Research Seminar Series at Midwestern University, Phoenix, Arizona • Molecular Biosciences Seminar Presentation on Phylomedicine at Montana State • *Keynote Speaker,* Young Scientists' Workshop on Evolutionary Genomics at Tokyo, Japan • SMBE Annual Meeting (Methods for multiple alignment and phylogenetic tree) at Kyoto, Japan • International Society for Molecular Biology/ECCB (SNPSigs Selection) at 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 at Penn State University • Keynote, Mini-symposium on Data Mining for Biomedical Informatics at SIAM International Conference on Data Mining, Mesa, Arizona • *Keynote,* Interdisciplinary Graduate Student's Symposium on Evolution Across Fields at 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 at 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 at Ventura, California

2007 – 2005

SOLUR Program, Arizona State University • Department of Biomedical Informatics, Arizona State University • FlyBase Advisory Group at Harvard University, Boston, MA • Keynote Speaker, Ohio Collaborative Conference on Bioinformatics (OCCBIO) at Miami University, Oxford, Ohio, • EMBO workshop on "Human Evolution and Disease" at 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 at Moscow Conference on Computational Molecular Biology, Moscow State University, Russia • Symposium on Systems Biology at 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 at Future of Statistics Conference, Hyderabad, India • Symposium on Advances in Methods for Estimating Species Divergence Dates using Molecular Data at International Congress of Zoology, Beijing, China • Symposium on Molecular Phylogeny and Molecular Clocks at Annual Meeting of SMBE, Penn State University, University Park, PA • Hexapodium, Center for Insect Research, University of Arizona • Techniques Workshop at 44th Annual Drosophila Research Conference, Chicago, IL • Comparative and Functional Genomics Workshop, Wellcome Trust and Dept. of Energy, Hinxton, Camridgeshire, UK • Annual Meeting of SMBE, Newport Beach, CA • Department of Biology, Duke University, Durham, NC • Bioinformatics Research Center, North Carolina State University, Raleigh, NC • Symposium on Evolutionary Genetics at 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 at 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 at 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 at 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