

## SUDHIR KUMAR, PH.D.

### RESEARCH STATEMENT

#### **Molecular Evolution and Phylomedicine**

We use integrative and comparative approaches to make fundamental discoveries in the fields of phylomedicine, molecular evolution and functional genomics. The common theme of our research is the use of comparative analysis to reveal genome differences that are outcomes of natural selection on novel mutations. The taxonomic breadth of our studies spans the tree of life and the timescale of mutation transmission ranges from generation to generation and cell division to cell division. The resulting patterns of evolutionary conservation and divergence form the basis of a Pattern-Process-Prediction-Product (P<sup>4</sup>) approach that enables us to conduct research investigations ranging from scaling the tree of life to time (Timetree of Life) to forecasting disruptive mutations found in personal germline and somatic genomes (Phylomedicine). In pursuit of these biological discoveries, we are developing new statistical methods and computer algorithms to quickly analyze large-scale datasets. We have also developed and disseminated many high-impact software tools (MEGA) and databases (TimeTree, FlyExpress, www.myPEG.info).

### CITATION PROFILE

#### **H-INDEX = 63 WITH >120,000 CITATIONS**

“Sudhir Kumar” on Google Scholar ([Click Here to Access](#))

More than 100,000 citations to software and databases

More than 15,000 citations to discoveries and methods

More than 5,000 citations to reviews and books

### EDUCATION

#### **(1990) B. ENGG. – ELECTRICAL & ELECTRONICS ENGINEERING (HONORS)**

Birla institute of Technology & Science, Pilani, Rajasthan, India, 1985–1990

#### **(1990) M. SC. – BIOLOGICAL SCIENCES (HONORS)**

Birla institute of Technology & Science, Rajasthan, India (\*concurrent with B. Engg.)

#### **(1996) PH. D. – GENETICS (ADVISOR: M. NEI)**

Pennsylvania State University, University Park, Pennsylvania, USA, 1991–1996

### APPOINTMENTS (ACADEMIC)

#### **(2014) LAURA H. CARNELL PROFESSOR**

Department of Biology, Temple University, 2014–present

#### **(2014) FULL PROFESSOR**

Department of Computer and Information Sciences, Temple University, 2014–present

#### **(2012) REGENTS’ PROFESSOR**

School of Life Sciences, Arizona State University (ASU), 2012–2014

#### **(2011) FOUNDATION PROFESSOR**

School of Life Science, ASU, 2011–2016

**(2006) FULL PROFESSOR**

School of Life Science, ASU, 2006–2011

**(2002) ASSOCIATE PROFESSOR, SOLS, ASU**

School of Life Science, ASU, 2002–2006

**(1998) ASSISTANT PROFESSOR**

Department of Biology, ASU, 1998–2002

**(1996) POSTDOCTORAL FELLOW (WITH M. NEI)**

Department of Biology, Pennsylvania State University (PSU), 1996–1998

**(1991) RESEARCH AND TEACHING ASSISTANT (WITH M. NEI)**

Department of Biology, PSU, 1991–1996

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**APPOINTMENTS  
(LEADERSHIP)**

**(2014) DIRECTOR ([HTTP://IGEM.TEMPLE.EDU](http://igem.temple.edu))**

Institute for Genomics and Evolutionary Medicine (iGEM), Temple University

**(2010) DIRECTOR, CENTER FOR EVOLUTIONARY MEDICINE & INFORMATICS**

Biodesign Institute, ASU, 2010–2014

**(2008) CHIEF SCIENTIFIC OFFICER**

Espis Vaccines, LLC, 2008–2010

**(2003) DIRECTOR, CENTER FOR EVOLUTIONARY FUNCTIONAL GENOMICS**

Biodesign Institute, ASU, 2003–2010

**(2003) FACULTY LEADER, GENOMICS, EVOLUTION, AND BIOINFORMATICS**

School of Life Science, ASU, 2003–2004

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**APPOINTMENTS  
(SCIENTIFIC  
SOCIETIES)**

**(2013) PRESIDENT (ELECTED)**

Society for Molecular Biology and Evolution, 2012–2014

**(2012) EDITOR-IN-CHIEF**

Molecular Biology and Evolution (2012–2022)

**(2004) SECRETARY (ELECTED)**

Society for Molecular Biology and Evolution, 2004–2006

**(2004) WEBMASTER**

Society for Molecular Biology and Evolution ([www.smbe.org](http://www.smbe.org)), 2004–2008

**(1999) WEBMASTER**

American Genetic Association ([www.theaga.org](http://www.theaga.org)), 1999–2007

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**APPOINTMENTS  
(ADJUNCT)**

**(2014) MEMBER, MOLECULAR THERAPEUTICS PROGRAM**

Fox Chase Cancer Center, Philadelphia, PA.

**(2013) ADJUNCT PROFESSOR**

Research Center for Genomics and Bioinformatics, Tokyo Metropolitan University, Tokyo, Japan

**(2013) ADJUNCT PROFESSOR**

Center of Excellence in Genomic Medicine Research (CEGMR), King Abdulaziz University, Jeddah, Saudi Arabia

**(2007) GUEST PROFESSOR**

Center for Computational and Evolutionary Biology (CCEB), Institute of Zoology @ Beijing, China

**(2005) AFFILIATE PROFESSOR**

Department of Biomedical Informatics, ASU, 2005–2007

**(2004) ADJUNCT SENIOR INVESTIGATOR**

Translational Genomics Research Institute (TGen), Phoenix, AZ, 2004–2007

**(2002) AFFILIATE PROFESSOR**

School of Computing, Informatics, and Decision Support Engineering, ASU

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**APPOINTMENTS  
(OTHER)**

**(2012) COORDINATOR, ACADEMIC EXCHANGE AND COLLABORATION**

Tokyo Metropolitan University, Japan and Arizona State University

**(2012) CO-DIRECTOR**

Biological Design Graduate (Ph.D.) Program, ASU, 2012–2013

**(2000) MEMBER, ASTROBIOLOGY/EVOLUTIONARY GENOMICS FOCUS GROUP**

National Aeronautics and Space Administration (NASA)

**(1998) ASSOCIATE MEMBER, ASTROBIOLOGY RESEARCH CENTER**

Pennsylvania State University, USA

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**AWARDS/HONORS**

**(2015) OUTSTANDING SCIENCE ALUMNI AWARD**

Pennsylvania State University, USA

**(2015) FACULTY OF THE GAME, TEMPLE VS. PENN STATE FOOTBALL**

Temple University Athletics, USA

**(2014) HIGHLY CITED RESEARCHER (COMPUTER SCIENCE)**

Thomson Reuters ScienceWatch, 2013, 2014

**(2014) MOST INFLUENTIAL MINDS**

Thomson Reuters ScienceWatch, 2014

**(2011) GOVERNOR'S CELEBRATION OF INNOVATION – ACADEMIA (FINALIST)**

State of Arizona, USA (also in 2009)

**(2009) AAAS FELLOW**

American Association for the Advancement of Science (AAAS)

**(2009) HONORARY PROFESSORSHIP**

School of Computing and Informatics, ASU

**(2007) LONG-TERM VISITING FELLOWSHIP AWARD**

Japanese Society for Promotion of Science (JSPS), 2007–2008

**(2006) EXEMPLAR FACULTY**

Arizona State University

**(2000) INNOVATION AWARD IN FUNCTIONAL GENOMICS**

Burroughs-Wellcome Fund

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**CITATION HONORS**

**(2014) TOP-100 CITED ARTICLES OF ALL TIME**

Nature (October 29, 2014) [Molecular Biology and Evolution 24:1596–1599]

**(2014) TOP CITED ARTICLE OF THE DECADE (2001-2011)**

SCOPUS (09/2014), Agriculture and Biological Sciences section

Molecular Biology and Evolution 24:1596–1599

**(2013, 2014) MBE CITATION CLASSICS**

Molecular Biology and Evolution 28:2731–2739 (RECENT CLASSIC; 2013, 2014)

Molecular Biology and Evolution 21:36–44 (EARLY CLASSIC; 2014)  
Molecular Biology and Evolution 24:1596–1599 (EARLY CLASSIC; 2013,2014)  
**(2013) ARTICLE OF SPECIAL SIGNIFICANCE BY FACULTY OF 1000 PRIME**  
Proceedings of the National Academy of Sciences, USA 109:19333–19338  
**(2010) CURRENT CLASSIC IN MULTIDISCIPLINARY SCIENCES, WEB OF SCIENCE (WOS)**  
Proceedings of the National Academy of Sciences, USA 101:11030–11035  
**(2010) CURRENT CLASSIC IN BIOLOGY & BIOCHEMISTRY, WOS**  
Molecular Biology & Evolution 24:1596–1599 (2010-2011)  
**(2007) CURRENT CLASSIC COMPUTER SCIENCE, WOS**  
Briefings in Bioinformatics 5: 150–163 (2007-2010)  
**(2009) HOT PAPER IN COMPUTER SCIENCE, WOS**  
Briefings in Bioinformatics 9:299–306  
**(2006) HOT PAPER IN COMPUTER SCIENCE, WOS**  
Briefings in Bioinformatics 5:150–163  
**(2006) SCIENCE, EDITOR’S CHOICE, AUGUST 25**  
Molecular Biology and Evolution 23:1946–1951  
**(2004) TOP-10 MOST-CITED AUTHOR, COMPUTER SCIENCE**  
Web of Science, 2004 –2009 (series discontinued)  
**(2004) HOT PAPER IN BIOLOGY & IN COMPUTER SCIENCE, WOS**  
Bioinformatics 17:1244–1245  
**(2000) HOT PAPER IN BIOLOGY, WOS**  
Nature 392: 917–920

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## EDITORIAL BOARDS

### EDITOR-IN-CHIEF

Molecular Biology and Evolution, 2012–present

### EDITORIAL BOARD

Biomolecules, 2010-2014

Bioinformatics and Biology Insights, 2009–2014

Molecular and Developmental Evolution (J. Exp. Zool.), 2004–2010

### ASSOCIATE EDITOR

Quarterly Review of Biology, 2010–2013

Evolutionary Bioinformatics Online, 2005–2014

Molecular Biology and Evolution, 2005–2012

Genome Research, 2005–2009

Gene: Functional Genomics, 2005–2006

Journal of Heredity, 1999–2005

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## GRANT SUPPORT

### CURRENT

### **(2016) EVOLUTIONARY BIOINFORMATICS OF TUMOR PROFILES**

National Institutes of Health (NLM) (PI), 2016–2019

### **(2016) eQTL MEGA-ANALYSIS FOR FUNCTIONAL ASSESSMENT OF MULTI-ENHANCER REGULATION**

National Institutes of Health (NHGRI; co-I), 2016–2019

### **(2016) INNOVATIVE MOLECULAR TIMING APPLICATIONS TO OBTAIN ACCURATE HISTORIES OF EARLY LIFE**

NASA Exobiology (co-PI), 2016–2019

**(2015) NRT-IGE: INNOVATING GRADUATE STEM EDUCATION THROUGH BIO-SOCIAL PARTNERSHIPS**

National Science Foundation (co-PI), 2015–2017

**(2015) TEMPLE GENOMICS AND ANALYTICS COLLABORATIVE (TGAC) RESEARCH INFRASTRUCTURE**

PA Commonwealth University Enhancement Program (PI), 2015–2018

**(2014) ABI INNOVATION: IDENTIFYING PHYLOGENETICALLY INFORMATIVE DATA FROM NEXT-GENERATION SEQUENCING**

National Science Foundation (ABI; co-I), 2014–2017

**(2014) COMPUTATIONAL DIAGNOSIS OF NON-SYNONYMOUS VARIATIONS USING STRUCTURAL DYNAMICS (R21)**

National Institutes of Health (NLM; co-I), 2014–2017

**(2013) METHODS FOR EVOLUTIONARY INFORMED NETWORK ANALYSIS TO DISCOVER DISEASE VARIATION (R01)**

National Institutes of Health (NIDDKS; co-PI), 2013–2017

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GRANT SUPPORT  
COMPLETED

PRINCIPAL INVESTIGATOR

**(2013) ENABLING DISCOVERY ACROSS DISCIPLINES THROUGH A SYNTHESIS OF TIME-CALIBRATED EVOLUTIONARY HISTORIES**

National Science Foundation (ABI; PI), 2013–2016

**(2012) IDENTIFYING DISEASE-ASSOCIATED GENOME VARIANTS THROUGH COMPUTATIONAL PREDICTION OF FUNCTIONAL SITES IN PROTEIN STRUCTURES**

ASU/Mayo Seed Grant, 2012–2013

**(2011) COMPARATIVE MOLECULAR SEQUENCE ANALYSIS (R01)**

National Institute of Health (NHGRI), 2011–2015

**(2011) COMPUTATIONAL ANALYSIS OF GENE EXPRESSION PATTERN IMAGES (R01)**

National Institutes of Health (NHGRI; PI), 2011–2016

**(2011) COMPUTATIONAL METHODS FOR EXPRESSION IMAGE ANALYSIS (R01)**

Multi-PI, National Institutes of Health (NLM), 2011–2015

**(2010) EVOLUTIONARY BIOINFORMATICS OF HUMAN MUTATIONS (R01)**

National Institutes of Health (NLM), 2010–2014

**(2007) COMPARATIVE MOLECULAR SEQUENCE ANALYSIS (R01)**

National Institutes of Health (NHGRI), 2007–2011

**(2007) COMPUTATIONAL ANALYSIS OF GENE EXPRESSION PATTERN IMAGES (R01)**

National Institutes of Health (NHGRI), 2007–2011

**(2007) BIOINFORMATICS OF ASSEMBLING THE TIMESCALE OF LIFE**

Science Foundation of Arizona, 2007–2008

**(2007) RE-ENGINEERING THE MEGA SOFTWARE PACKAGE (R01)**

National Institutes of Health (NIGMS/ARRA), 2007–2011

**(2004) COMPARATIVE MOLECULAR SEQUENCE ANALYSIS (R01)**

National Institutes of Health (NHGRI), 2004–2007

**(2003) COMPUTATIONAL GENOMIC ANALYSIS TO IDENTIFY AND DISSECT FUNCTIONALLY IMPORTANT MUTATIONS IN PROTEIN SEQUENCES**

Burroughs-Wellcome Fund, USA, 2003–2006

**(2003) COMPUTATIONAL ANALYSIS OF GENE EXPRESSION PATTERN IMAGES (R01)**

National Institutes of Health (NHGRI), 2003–2007

**(2000) COMPARATIVE MOLECULAR SEQUENCE ANALYSIS (R01),**

National Institutes of Health (NHGRI), 2000–2004

**(2000) DESIGN OF A BIOINFORMATIC DATABASE FOR FUNCTIONAL EVOLUTIONARY FOOTPRINTS IN MULTIGENE FAMILIES**

National Science Foundation (DBI), 2000–2004

**CO-PRINCIPAL OR CO-INVESTIGATOR**

**(2014) III: SMALL: LARGE-SCALE STRUCTURED SPARSE LEARNING**

National Science Foundation (co-PI), 2014–2016

**(2013) RATIONAL DESIGN AND TARGETED SELECTION OF EFFECTIVE DNA-SCAFFOLDED NICOTINE VACCINES (R01)**

National Institutes of Health (NIDA; co-I), 2013–2016

**(2011) A PHYLOGENETIC APPROACH TO METAGENOMIC ANALYSIS (R21)**

National Institutes of Health (NHGRI), 2011–2014

**(2010) CENTER FOR MEMBRANE PROTEINS IN INFECTIOUS DISEASES (MIPD, U54)**

National Institutes of Health (NIGMS), 2010–2015

**(2009) TEAM APPROACH TO TRANSLATE NOVEL BIOMARKERS FOR DIABETES**

National Institutes of Health (NIDDK), 2009–2010

**(2009) BIOINFORMATICS OF MOLECULAR TIMETREES**

National Science Foundation (DBI), 2009–2013

**(2008) DISCOVERING THE HIDDEN PROTEOME IN THE HUMAN GENOME (R01)**

National Institutes of Health (EUREKA), 2008–2012

**(2006) DEVELOPING A BIOINFORMATIC DATABASE FOR STOICHIOPROTEOMICS**

National Science Foundation (DBI), 2006–2010

**(2006) MACHINE LEARNING APPROACHES FOR BIOLOGICAL IMAGE INFORMATICS**

National Science Foundation, 2006–2010

**(2004) BIODESIGN BRIDGES TO THE DOCTORATE**

National Science Foundation (LSAMP), 2004–2006 (instructional)

**(2001) DEVELOPMENT OF AN EVOLUTIONARY TIMESCALE DATABASE**

National Science Foundation (DBI), 2001–2004

**(2001) A COMPUTATIONAL BIOSCIENCES PROFESSIONAL MASTER'S PROGRAM**

Sloan Foundation, 2001–2003 (instructional)

**(2000) EMERGING WILDLIFE DISEASES: THREATS TO AMPHIBIAN BIODIVERSITY**

National Science Foundation (IRCEB), 2000–2008

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**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

Society for Molecular Biology and Evolution

Society for the Study of Evolution

CONFERENCES AND  
ORGANIZED  
SYMPOSIA

**(2016) ORGANIZER, SYMPOSIUM ON NEXT GENERATION TOOLS**

Annual meeting of Society for Molecular Biology and Evolution, Gold Coast, Australia

**(2014) MEMBER, EXTERNAL ADVISORY BOARD**

Annual meeting of the Society for Molecular Biology and Evolution (SMBE), Puerto Rico

**(2012) SYMPOSIUM ON PHYLOMICINE @ ASU (3/23–3/24; 100 ATTENDEES)**

Awarded by Society for Molecular Biology and Evolution

**(2011) MEMBER, GLOBAL ORGANIZING COMMITTEE (GOC)**

Annual meeting of SMBE, Kyoto Japan (7/26–7/30)

**(2010) ORGANIZER, SYMPOSIUM ON EVOLUTIONARY BIOLOGY IN HEALTH AND MEDICINE**

Annual meeting of SMBE, Lyon France (7/4–7/8); co-organizers: J Dudley and A Butte

**(2010) CO-ORGANIZER, MOLECULAR PHYLOGENETICS SYMPOSIUM,**

Moscow State University, Russia (5/17–5/21)

**(2007) MEMBER, PROGRAM COMMITTEE**

International Conference on Computational Phylogenetics and Molecular Systematics,  
Moscow State University, Russia (12/16–12/19)

**(2006) LEAD ORGANIZER OF ANNUAL MEETING OF SMBE (750 ATTENDEES)**

Arizona State University, Tempe, Arizona (5/24–5/28)

**(2005) ORGANIZER, GENOME DATABASE WORKSHOP**

National Evolutionary Synthesis Center, Wilmington Beach, North Carolina, (5/31–6/3)

**(2004) SYMPOSIUM ON EVOLUTIONARY AND POPULATION GENOMICS**

Future of Statistics Conference at Indian School of Business, Hyderabad (12/29–1/1)

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MAJOR ADVISORY &  
REVIEW BOARDS

**(2016) ADVISORY BOARD, SICCS**

Northern Arizona University

**(2016) CHAIR, GENOME VARIATION AND EVOLUTION (GVE)**

Study Section, National Institutes of Health, 2016–2018

**(2015) INVITED MEMBER, THOUGHT LEADER SUMMIT**

American Heart Association

**(2013) STANDING MEMBER, GENOME VARIATION AND EVOLUTION (GVE)**

Study Section, National Institutes of Health, 2013–2018

**(2012) MEMBER, REVIEW COMMITTEE, GENOMIC SCIENCES PROGRAM**

NC State University, Raleigh, North Carolina

**(2011) ADVISORY BOARD MEMBER**

Münster Graduate School of Evolution (MGSE), Münster, Germany

**(2010) MEMBER, 10-YEAR REVIEW COMMITTEE**

Institute for Genomics and Bioinformatics @ University of California, Irvine

**(2007) FLYBASE ADVISORY GROUP**

2007-2008

**(2006) CONSULTANT, AMERIGENICS, INC., USA**

**(2006) MEMBER, ADVISORY COMMITTEE ON EVOLUTIONARY BIOINFORMATICS**

University of South Dakota, USA

**(2006) STANDING MEMBER, BIODATA MGMT. AND ANALYSIS (BDMA)**

Study Section, National Institutes of Health, 2006 – 2010

**(2006) MEMBER, INFORMATICS ADVISORY COMMITTEE**

National Center for Evolutionary Synthesis (NESCent), 2006–2009

**(2006) MEMBER, WORKING GROUP ON EVOLUTIONARY INFORMATICS**

Supporting Interoperability in Evolutionary Analysis, NESCent, 2006–2008

**(2005) MEMBER, FIVE-YEAR REVIEW COMMITTEE**

Institute for Genomics and Bioinformatics @ University of California, Irvine

**(2002) CONSULTANT, PHARMACIA CORPORATION, USA**

2002-2003

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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; >2500 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).

ARTICLES: 1992 – 1999

4. Hedges SB, **Kumar S**, Tamura K & Stoneking M (1992) Human origins and analysis of mitochondrial DNA sequences. *Science* 255:737–739.
5. **Kumar S**, Tamura K & Nei M (1994) MEGA: Molecular Evolutionary Genetics Analysis software for microcomputers. *Computer Applications in Biosciences* 10:189–191.
6. Rzhetsky A, **Kumar S** & Nei M (1995) Four-cluster analysis: A simple method to test phylogenetic hypotheses. *Molecular Biology & Evolution* 12:163–167.
7. Yang Z, **Kumar S** & Nei M (1995) A new method of inference of ancestral nucleotide and amino acid sequences. *Genetics* 141:1641–1650.
8. Winnepenninckx W, Backeljau T, Mackey LY, Brooks JM, De-Wachter R, **Kumar S** & Garey JR (1995) 18S rRNA data indicate that Aschelminthes are polyphyletic in origin and consist of at least three distinct clades. *Molecular Biology and Evolution* 12:1132–1137.
9. Hedges SB, Parker PH, Sibley CG & **Kumar S** (1996) Continental breakup and the ordinal diversification of birds and mammals. *Nature* 381:226–229.
10. **Kumar S** (1996) A stepwise algorithm for finding minimum evolution trees. *Molecular Biology and Evolution* 13:584–593.
11. **Kumar S** (1996) Patterns of nucleotide substitution in mitochondrial protein coding genes of vertebrates. *Genetics* 143:537–548.
12. **Kumar S**, Balczarek KA & Lai Z-C (1996) Evolution of the hedgehog gene family. *Genetics* 142:965–972.
13. **Kumar S** & Rzhetsky A (1996) Evolutionary relationships of eukaryotic kingdoms. *Journal of Molecular Evolution* 42:183–193.
14. 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.
15. Balczarek KA, Lai Z-C & **Kumar S** (1997) Evolution and functional diversification of the Paired box (Pax) DNA-binding domains. *Molecular Biology and Evolution* 14:829–842.
16. Zhang J & **Kumar S** (1997) Detection of convergent and parallel evolution at the amino acid sequence level. *Molecular Biology and Evolution* 14:527–536.
17. 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.



18. 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.
19. Leitner TL, **Kumar S** & Albert J (1997) Tempo and mode of nucleotide substitutions in gag and env gene fragments in Human Immunodeficiency Virus Type 1 populations with a known transmission history. *Journal of Virology* 71:4761–4770.
20. **Kumar S** & Hedges SB (1998) A molecular timescale for vertebrate evolution. *Nature* 392:917–920.
21. Nei M, **Kumar S** & Takahashi K (1998) The optimization principle in phylogenetic analysis tends to give incorrect topologies when the number of nucleotides or amino acids used is small. *Proceedings of the National Academy of Sciences (USA)* 95:12390–12397.
22. Hedges SB & **Kumar S** (1999) Divergence times of eutherian mammals. *Science* 285:2031a.
23. Newfeld SJ, Wisotzkey RG & **Kumar S** (1999) Molecular evolution of a development pathway: Phylogenetic analyses of transforming growth factor- $\beta$  family ligands, receptors, and Smad signal transducers. *Genetics* 152:783–795.
24. Wang Y-C, **Kumar S** & Hedges SB (1999) Divergence time estimates for the early history of animal phyla and the origin of plants, animals, and fungi. *Proceedings of the Royal Society, London. B* 266:163–171.

#### ARTICLES: 2000 – 2005

25. **Kumar S**, Mitnik C, Valente G & Floyd-Smith G (2000) Expansion and molecular evolution of the interferon-induced 2'-5' oligoadenylate synthetase gene family. *Molecular Biology and Evolution* 17:738–750.
26. **Kumar S**, Hedrick P, Dowling T & Stoneking M (2000) Questioning evidence for recombination in human mitochondrial DNA. *Science* 288:1931a.
27. **Kumar S** & Gadagkar SR (2000) Efficiency of the neighbor-joining method in reconstructing deep and shallow evolutionary relationships in large phylogenies. *Journal of Molecular Evolution* 51:544–553.
28. Purdom PW, Bradford PG, Tamura K & **Kumar S** (2000) Single column discrepancy and dynamic max-mini optimizations for quickly finding the most parsimonious evolutionary trees. *Bioinformatics* 16:140–151.
29. **Kumar S**, Tamura K, Jakobsen IB & Nei M (2001) MEGA2: Molecular Evolutionary Genetics Analysis software. *Bioinformatics* 17:1244–1245.
30. Gerber AS, Loggins R, **Kumar S** & Dowling TE (2001) Does non-neutral evolution shape observed patterns of DNA variation in animal mitochondrial genomes? *Annual Review of Genetics* 35:539–566.
31. **Kumar S**, Gadagkar SR, Filipowski A & Gu X (2001) Determination of the number of conserved chromosomal segments between species. *Genetics* 157:1387–1395.
32. **Kumar S** & Gadagkar SR (2001) Disparity Index: A simple statistic to measure and test the homogeneity of substitution patterns between molecular sequences. *Genetics* 158:1321–1327.
33. **Kumar S** & Panchanathan S (2001) Elucidating gene interaction networks based on gene expression pattern image analysis. *Proceedings of the International Conference on Biomedical Engineering* 5A:232–234.
34. Rosenberg MS & **Kumar S** (2001) Traditional phylogenetic reconstruction methods reconstruct shallow and deep evolutionary relationships equally well. *Molecular Biology and Evolution* 18:1823–1827.
35. Rosenberg MS & **Kumar S** (2001) Incomplete taxon sampling is not a problem for phylogenetic inference. *Proceedings of the National Academy of Sciences (USA)* 98:10751–10756.

36. Miller MP & **Kumar S** (2001) Understanding human disease mutations through the use of interspecific genetic variation. *Human Molecular Genetics* 10: 2319–2328.
37. Hedrick P & **Kumar S** (2001) Mutation and linkage disequilibrium in human mtDNA. *European Journal of Human Genetics* 9:969–972.
38. Hedges SB, Chen H, **Kumar S**, Wang DY-C, Thompson AS & Watanabe H (2001) A genomic timescale for the origin of eukaryotes. *BMC Evolutionary Biology* 1:4 (10 pp).
39. Jayaraman K, Panchanathan S & **Kumar S** (2001) Classification and indexing of gene expression images. *Proceedings of Society of Photo-optical Instrumentation Engineers* 4472:471–481.
40. Hedges SB & **Kumar S** (2002) Vertebrate genomes compared. *Science* 297:1283–1285.
41. **Kumar S** & Subramanian S (2002) Mutation rates in mammalian genomes. *Proceedings of the National Academy of Sciences (USA)* 99:803–808.
42. **Kumar S**, Jayaraman K, Panchanathan S, Gurunathan R, Marti-Subirana A & Newfield SJ (2002) BEST: A novel computational approach for comparing gene expression patterns from early stages of *Drosophila melanogaster* development. *Genetics* 162:2037–2047.
43. Tamura K & **Kumar S** (2002) Evolutionary distance estimation under heterogeneous substitution pattern among lineages. *Molecular Biology & Evolution* 19:1727–1736.
44. Jiang Z, Melville JS, Cao H, **Kumar S**, Filipski A & Verrinder Gibbins AM (2002) Measuring conservation of contiguous sets of autosomal markers on bovine and porcine genomes in relation to the map of the human genome. *Genome* 45:769–776.
45. Hedges SB & **Kumar S** (2003) Genomic clocks and evolutionary timescales. *Trends in Genetics* 19:200–206.
46. Subramanian S & **Kumar S** (2003) Neutral substitutions occur as a faster rate in exons than in noncoding DNA in primate genomes. *Genome Research* 13:838–844.
47. Rosenberg MS & **Kumar S** (2003) Taxon sampling, bioinformatics, and phylogenomics. *Systematic Biology* 52:119–124.
48. Rosenberg MS, Subramanian S & **Kumar S** (2003) Patterns of transitional mutation biases within and among mammalian genomes. *Molecular Biology and Evolution* 20:988–993.
49. Rosenberg MS & **Kumar S** (2003) Heterogeneity of nucleotide frequencies among evolutionary lineages and phylogenetic inference. *Molecular Biology and Evolution* 20:610–621.
50. Miller MP, Parker JD, Rissing SW, & **Kumar S** (2003) Quantifying the intragenic distribution of human disease mutations. *Annals of Human Genetics* 67:567–579.
51. Jancovich J, Mao J, Chinchar VG, Wyatt C, Case S, **Kumar S**, Valente G, Subramanian S, Davidson EW, Collins JP & Jacobs BL (2003) Genomic sequence of a ranavirus (family Iridoviridae) associated with salamander mortalities in North America. *Virology* 316:90–103.
52. **Kumar S**, Tamura K & Nei M (2004) MEGA3: Integrated software for Molecular Evolutionary Genetics Analysis and sequence alignment. *Briefings in Bioinformatics* 5:150–163.
53. Hedges SB & **Kumar S** (2004) Precision of molecular time estimates. *Trends in Genetics* 20:242–247.
54. Tamura K, Subramanian S & **Kumar S** (2004) Temporal patterns of fruit fly evolution revealed by mutation clocks. *Molecular Biology and Evolution* 21:36–44.
55. Briscoe A, Gaur C & **Kumar S** (2004) The spectrum of human rhodopsin disease mutations through the lens of interspecific variation. *Gene* 332:107–118.
56. Tamura K, Masatoshi Nei, & **Kumar S** (2004) Prospects for inferring very large phylogenies using the neighbor-joining method. *Proceedings of the National Academy of Sciences (USA)* 101:11030–11035.
57. Subramanian S & **Kumar S** (2004) Gene expression intensity shapes evolutionary rates of the proteins encoded by the vertebrate genome. *Genetics* 168:373–381.

58. Gurunathan R, Van Emden B, Panchanathan S & **Kumar S** (2004) Identifying spatially similar gene expression patterns in early stage fruit fly embryo images: Binary feature versus invariant moment digital representations. *BMC Bioinformatics* 5:202 (13 pp).
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MANUSCRIPTS IN  
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169. **Kumar S**, Patel R, Lanham TR, Sanderford MD, Tamura K, Glicksberg BS, Xu K, Dudley JT & Scheinfeldt LD (2017) Ancient Adaptive landscape of the human coding genome.
170. **Kumar S**, Konikoff C, Sanderford M, Liu L, Newfeld S, Ye J, & Kulathinal RJ (2017) FlyExpress 7: An integrated discovery platform to study co-expressed genes using in situ hybridization images in *Drosophila*.
171. Miura S, Gomez K, Murillo O & **Kumar S** (2017) Discovering clonal sequences and phylogenies from tumor variation profiles.
172. Tao Q, Mello B, Tamura K & **Kumar S** (2010) Molecular dating when clades evolve with different rate models.
173. Gomez K, Miura S, Spell BS & **Kumar S** (2017) Somatic evolutionary timings of driver mutations.
174. Xu K, ..., **Kumar S**, ..., Dudley JT (2017) Genome-wide analysis provides evidence of association between heterozygote advantage and healthy aging in humans.
175. Dubey B, ..., **Kumar S** & Ragin C (2017) Interactive effect of TLR SNPs and exposure to sexually transmitted infections on Prostate Cancer risk in Jamaican men.

EDITORIALS

Molecular Biology and Evolution (MBE) Editor's messages (2013, 2014)  
 MBE Citation Classics (2013-2017)  
 MBE Editor-in-Chief's annual reports (2013-2017)

INVITED  
PRESENTATIONS

**2016** • University of Pittsburgh • Symposium in the Annual meetings of Society for Molecular Biology and Evolution.

**2015** • 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** • 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

**2013** • 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** • 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

2011 • 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 Bioinformatic 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 SMBE, 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 SMBE, 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

## TEACHING

Average Rating in Parentheses (Scale: 1 = Best; 4 = Worst)

BIO 494	(1.2)	Advanced Evolution	(14 Students)	ASU	1999
BIO 594	(1.5)	Molecular Evolutionary Genetics	(10 Students)	ASU	1999
BIO 594	(1.3)	Molecular Evolutionary Genetics	(7 Students)	ASU	2000
BIO 445	(1.7)	Organic Evolution	(106 Students)	ASU	2000
BIO 494	(1.3)	Computational Genomics	(7 Students)	ASU	2001
BIO 445	(1.4)	Organic Evolution	(180 Students)	ASU	2001
BIO 494	(1.2)	Introduction to Comparative Genomics	(12 Students)	ASU	2003
BIO 345	(1.4)	Organic Evolution	(185 Students)	ASU	2003
BIO 494	(1.3)	Introduction to Comparative Genomics	(11 Students)	ASU	2004
BIO 345	(1.6)	Organic Evolution	(150 Students)	ASU	2005
BIO 345	(1.4)	Organic Evolution	(180 Students)	ASU	2006
BIO 494	(1.2)	Introduction to Comparative Genomics	(12 Students)	ASU	2007
BIO 455	(1.2)	Introduction to Comparative Genomics	(10 Students)	ASU	2008
BIO 455	(1.2)	Introduction to Comparative Genomics	(25 Students)	ASU	2009
BIO 494	(1.1)	Evolutionary Medicine	(30 Students)	ASU	2010
BIO 455	(1.2)	Introduction to Comparative Genomics	(41 Students)	ASU	2011
BIO 494	(1.5)	Evolutionary Medicine	(41 Students)	ASU	2012
BIO 189	(1.4)	Phylomedicine	(19 Students)	ASU	2013
BIO 591	(1.5)	Seminar: Evolution in Medicine	(12 Students)	ASU	2013
BIO 3112/5112		Genomic Evolutionary Medicine	(49 Students)	TU	2016
BIO 3112/5112		Genomic Evolutionary Medicine	(45 Students)	TU	2017

## STUDENTS MENTORED

### CURRENT DOCTORAL AND POSTDOCTORAL TRAINEES

**(2012) SAYAKA MIURA**

Project: Cancer Phylogenetics (Postdoctoral; Research Faculty)

**(2014) RAVI PATEL**

Project: Phylomedicine of complex diseases (Doctoral)

**(2014) QIQING TAO**

Project: Molecular Phylogenetics and Timetrees (Doctoral)

**(2016) CARYN BABAIAAN**

Project: Bridging Science with Art to communicate the Timetree of Life (Doctoral)

**CURRENT UNDERGRADUATE TRAINEES**

**HEATHER R. DEWALL**, Evolutionary Medicine of Complex Diseases

**KAREN GOMEZ**, Tumor Phylogenetics

**LOUISE A HUUKI**, Timetree of Life

**JESSICA PRIEST**, Timetree and Phylomedicine

**TAMERA R. LANHAM**, Population polymorphism and disease

**BRIANNA SPELL**, Analysis of tumor variation data

**HARRY HO**, MEGA software development

SUJAY RAJKUMAR, Bioinformatics data processing

**PAST POSTDOCTORAL TRAINEES**

**BEATRIZ MELLO** (2015-2016) Research Scientist, Brazil

**CHARLOTTE KONIKOFF** (2013-2015) Teacher, Arizona

**LI LIU** (2012-2015) Assistant Professor, Biomed Informatics, Arizona State U (M.D. China).

**ALAN FILIPSKI**, (1998-2014) Retired (Ph.D. Michigan state).

**LIFANG LIU**, (2012-2013) Associate Professor (China)

**NEVIN GEREK**, (2010-2013) Sr. Research Engineer, Schneider Electric, CA (Ph.D., University of Akron, OH).

**FABIA BATTISTUZZI**, (2008-2012) Assistant Professor, Oakland University, CA (Ph.D., Biology/Astrobiology, Penn State).

**CLAUDIA ACQUISTI**, (2006-2010) Junior Professor, Westfälische Wilhelms-Universität Münster (Ph.D., Molecular Evolution, Italy).

**ANTONIO MARCO-CASTILLO**, (2008-2009) Lecturer, University of Essex, UK (Ph.D., Genetics, Spain)

**BAO HONG SHEN**, (2005-2007) Software Engineer, Microsoft Inc., Seattle, WA (Ph.D., Computer Science, ASU).

**ANUP SOM**, (2005-2007) Assistant Professor, University of Allahabad, India (Ph.D., Bioinformatics, India).

**CHRISTINE KUSLICH**, (2003-2005) Chief Scientific Officer, Hologic, Inc. San Diego, CA (Ph.D., Biomedical Sciences, Hawaii).

**SANKAR SUBRAMANIAN**, (2000-2006) Research Fellow in Genomics, Griffith School of Environment, QLD, Australia (Ph.D., Microbiology, IARI, India).

**ARAXI URRUTIA**, (2003-2004) Lecturer in Genetics, University of Bath, UK (Ph.D., Evolutionary Genomics).

**MICHAEL S. ROSENBERG** (2000-2003) Associate Professor, Arizona State University (Ph.D., Stony Brook, NY).

**MARK P. MILLER**, (2000-2002) Statistician, USGS-FRESC, OR (Ph.D., Evol & Conservation Genetics).

**SUDHINDRA R. GADAGKAR** (1998–2003). Associate Professor, Midwestern University, Arizona (PHD, Dalhousie, Canada).

**PAST CHAIR/CO-CHAIR OF GRADUATE STUDENT COMMITTEES**

Charlotte Konikoff • Siddarth Selvaraj • Bindu Koshy • Vinod Swarna • Hector Ramos • Xiaofen Liu • Stephanie Rogers • Madhusudhana Gargasha • Rajalakshmi Gurunathan • Vinod Swarna • HoJoon Lee • Shubhra Gupta • Jian Yang • Sandhya Durvasala • Patrick Kolb • Rekha Iyer • Karthik Jayaraman

#### PAST UNDERGRADUATE/HIGH SCHOOL RESEARCH ASSISTANTS MENTORED (SORTED BY YEAR)

Anant Bhargava • Stephen McAleer • Anna Freydenzen • Oscar Murillo • Adam Orr • Stephanie Tate • Ivan Montiel • Pegah Biparvah • Diana Alarcon • Brandy Buck • Eric Thomas • Kristyn Gerold • Brandon Butler • Ronika Nirankari • Chikku Baiju • Natalia Santiago • Liz Garcia • Amber Ahmed • Alyza Villa • Greg McInnes • Paul Billing-Ross • Vanessa Gray • Alicia Varma • Aditya Paliwal • Glenn Markov • Kimberly Kukurba • Jenna Makis • Hariharan Mohanraj • Nate Sutton • Michael Suleski • Nicholas Peterson • Simon Lawrence • Adithya Rajan • Stephen Watson • Robert Adrian • Alexander Woodard • Elizabeth Villalba • Nicolas Feddern • Kailah Davis • Christopher Busick • Bryan Sexton • Veronica Shi • Asaria Jimenez • Melizabeth Santana • Yea Jin Ko • Ariana Rodriguez • Stephanie Negron • Thania Martinez • Wilda Rivera • Victor Correa • Liris Gonzalez • Jose Maldonado • German Velez • Cristina Rivera • Krizia Cabrera • Karen Canales • Carol Diaz • Raul Navedo • Rachel Sipes • Antoine Al-Foune • Jacob Reidhead • Veena Ganeshan • Emily Davenport • Diana Tlougan • Heather Wiemann • Candice White • Roman Johnson • Timothy Sweeney

#### MEMBER OF GRADUATE STUDENT COMMITTEES

Matthew Dunn • HoJoon Lee • Joel Dudley • Takahiro Maruki • Jianhui Chen • Hugo F. Gante • Shuiwang Ji • Michael Schwemm • Peter Unmack • Evan Carson • Carla Hurt • Daniel Garrigan

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#### TECHNICAL STAFF MANAGED

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