

SUDHIR KUMAR

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www.azbio.org/efg/

CITIZENSHIP: Permanent U.S. Resident
(US Citizenship on July 9, 2004).

<u>EDUCATION</u>	<u>DEGREE</u>	<u>YEAR</u>	<u>DISCIPLINE</u>
Birla Institute of Tech. & Sci. (India)	B.Engg.	1990	Electrical/Electronics Engineering*
Birla Institute of Tech. & Sci. (India)	M.S.	1990	Biological Sciences*
Pennsylvania State University (USA)	Ph.D.	1996	Genetics

*Concurrent degrees

DOCTORAL AND POSTDOCTORAL RESEARCH MENTOR

Dr. Masatoshi Nei, Institute of Molecular Evolutionary Genetics,
Pennsylvania State University, University Park, PA 16802.

PROFESSIONAL APPOINTMENTS

2003 – present Leader, Faculty of Genomics, Evolution, and Bioinformatics,
School of Life Sciences (SoLS), Arizona State Univ (ASU)

2002 – present Director, Center for Evolutionary Functional Genomics, The Biodesign
Institute, ASU

2002 – present Associate Professor, SoLS, ASU

1998 – 2002 Assistant Professor, Department of Biology, ASU

1996 – 1998 Postdoctoral Fellow, Department of Biology, Penn State University

1991 – 1996 Research Assistant, Department of Biology, Penn State University

PROFESSIONAL AFFILIATIONS

2002 – present Affiliate Professor, Computer Science & Engineering, ASU

2000 – present Research Scientist, Arizona Research Laboratories

2000 – present Member, NASA Astrobiology/Evolutionary Genomics Focus Group

1998 – present Associate Member, Penn State Astrobiology Research Center

AWARDS & HONORS

Specific Articles

2004 (June) Top 10 (second) most highly cited paper in Computer Science in the last
10 years by *ISI Essential Science Indicators* (ESI). (*Bioinformatics* [2001]
Volume 17; pp 1244-1245).

2004 (Mar) ISI Hot Paper in Biology, Science Citation Index, Philadelphia
(*Bioinformatics* [2001] Volume 17; pp 1244-1245).

2000 (May) ISI Hot Paper in Biology, Science Citation Index, Philadelphia (*Nature*
[1998] Volume 392; pp 917-920)

Personal

2004 (June) Top 10 most highly cited researcher in Computer Science in the last
decade (*ISI Essential Science Indicators*)

2002 – 2004 EARS-Faculty Designation, ASU (selection based on size and complexity
of extramurally-funded research projects)

2000 (Aug) Innovation Award in Functional Genomics, Burroughs-Wellcome Fund

JOURNAL EDITORIAL BOARDS

2004 – present Editorial Board, *Molecular and Developmental Evolution*
1999 – present Associate Editor, *Journal of Heredity*

PROFESSIONAL SOCIETY ACTIVITIES

2004 – present Secretary (Elected), *Society for Molecular Biology and Evolution*
2004 – present Webmaster, *Society for Molecular Biology and Evolution*
1999 – 2003 Webmaster, *American Genetic Association*

MEMBERSHIP IN SCIENTIFIC AND PROFESSIONAL ORGANIZATIONS

American Association for the Advancement of Science
American Genetic Association
Society for Molecular Biology and Evolution
Society for the Study of Evolution
The Genetics Society of America

SCIENTIFIC AND PROFESSIONAL COMMITTEES (NATIONAL/INTERNATIONAL)

2003 Committee on Membership Enhancement in the *Society for Molecular Biology and Evolution*
2003 Tucson *Drosophila* Committee for generating a White paper for Fruit Fly genome sequencing projects

AD HOC REVIEWER

Journals

Bioinformatics, Development Genes & Evolution, Evolution, Gene, Genetics, Genome Research, Journal of Molecular Evolution, Molecular Biology & Evolution, Nature, Nucleic Acids Research, Proceedings of the National Academy of Sciences (USA), Proceedings of the Royal Society (UK), Science, Trends in Ecology & Evolution.

National Institutes/Foundations

*National Institutes of Health (2004; Development; Biodefense/Bioterror; Software)
National Science Foundation (2002; Information Technology Research-Small)
National Science Foundation (2003; Information Technology Research-Medium)*

RESEARCH INTERESTS

My computational and evolutionary functional genomics research is focused on (a) elucidating nature and complexity of gene interactions that lead to formation of an adult from a single celled embryo and (b) studying how the developmental complexity in animals has evolved over time by the processes of gene duplication and functional divergence in multigene families comprising metazoan genomes. To address these questions, we are (a) developing statistical methods and computational algorithms for data analysis and mining, (b) constructing integrated dynamic knowledge bases of genetic information, (c) testing biological hypotheses, and (d) building user-friendly tools and web-based resources for general purpose use in order to accelerate biological discovery.

CURRENT RESEARCH GRANT SUPPORT

Comparative Molecular Sequence Analysis

Principal Investigator (1/2000 – 1/2007)

National Human Genome Research Institute (NIH/NHGRI; R01)

Computational Analysis of Gene Expression Pattern Images

Principal Investigator (1/2003 – 6/2006)

National Human Genome Research Institute (NIH/NHGRI; R01)

Emerging Wildlife Diseases: Threats to Amphibian Biodiversity

Co-Principal Investigator (3/2001 – 2/2006)
National Science Foundation (NSF/IRCEB; PI: J. Collins).

Development of an Evolutionary Timescale Database

Co-Principal Investigator (8/2001 – 6/2004)
National Science Foundation (NSF/DBI, PI: S. B. Hedges)

Computational Genomic Analysis to Identify and Dissect Functionally Important Mutations ...

Principal Investigator (8/2000 – 7/2004)
Burroughs-Wellcome Fund (\$200,000)

Design of a Bioinformatic Database for Functional Evolutionary Footprints in Multigene Families

Principal Investigator (6/2000 – 5/2004)
National Science Foundation (NSF/DBI)

CURRENT TEACHING/TRAINING GRANT PARTICIPATION

LSAMP Biotransformed Bridges to the Doctorate

Co-Principal Investigator (2001-2006)
National Science Foundation (HRD-Alliances – Minority; PI: Antonio Garcia)

Evolutionary, Computational, and Molecular Approaches to Genome Structure and Function

Participating Investigator (2002-2005)
National Science Foundation (IGERT; PI: M. Nachman, Biology, Univ. of Arizona)

Phase III: Western Alliance to Expand Student Opportunities

Co-Principal Investigator (2001 – 2006)
Directorate for Education & Human Resources (NSF/EHR; \$878,422)

TEACHING/TRAINING

A Computational Biosciences Professional Master's Program

Participating Investigator (2001-2003)
Sloan Foundation (PI: R. Renaut, Mathematics, ASU)

WORKSHOPS ATTENDED FOR PROFESSIONAL ENHANCEMENT

2001 (Nov) National Human Genome Research Institute Grantee's Workshop on
Minority participation, Bethesda, Maryland
1999 (Summer) Attended workshop in teaching excellence sponsored by Howard Hughes
Medical Institute Undergraduate Research Program at Arizona State
University

RESEARCH VISITS TO OTHER INSTITUTIONS

Jan. 17 – Feb. 2, 2000 Tokyo Metropolitan University, Biology (Dr. Koichiro Tamura)
Jun. 5 – Jun. 12, 2001 Hong Kong University, Biology (Dr. Xuhua Xia)
Nov. 5 – Nov. 6, 2003 University College London, Biology (Dr. Ziheng Yang)

GRADUATE STUDENTS (COMMITTEE CHAIR/CO-CHAIR)

Current: R. Gurunathan (2000–), Ph.D., Computer Science & Engg.; J. Yang (2003–),
Ph.D., Biology. S. Durvasala (2003–), MS, Computer Science & Engg.
Past: R. Iyer (1999–2002), MS, Molecular & Cell Biology; P. Kolb (2001–2003), MNS,
Biology; K. Jayaraman (1999–2001), MS, Electrical Engineering.

COMPUTATIONAL BIOSCIENCE INTERNS (MS)

Current: S. Rogers (2004–), C. Prasanna (2004–), C. Gaur (2003–), S. Moturu (2003–), V.
Swarna (2003–), H. Lee (2003–)
Past: B. Fergusson (2002)

POSTDOCTORAL FELLOW

- Current:** A. Urrutia (2003–), C. Greenwood (2003–), C. Kuslich (2003–), A. Filipski (2001–), S. Subramanian (2000–)
- Past:** S. R. Gadagkar (1998–2002), M. S. Rosenberg (2000–2002), M. P. Miller (2000–2001), R. Friedman (2002)

OTHER RESEARCH/DEVELOPMENT LAB PERSONNEL

Faculty Research Associates

- Current:** B. Van Emden (2003–), D. Desonie (2003–), Joel Dudley (2002–), G. Valente (1999–), A. Marti-Subirana (2000–)

Graduate:

- Current:** V. Kalyanaraman (2004–), S. Gupta (2004–), S. Durvasula (2003–2004)
- Past:** K. Srinivasan (2001–2002), K. P. Reddy (2001–2002), B. Ramanujam (2002–2003)

Undergraduate:

- Past:** H. Wiemann (1998–2000), C. White (1998), R. Johnson (1999), V. Ganeshan (2000–2001), E. Davenport (2000), D. Tloutan (2000), J. Reidhead (2001–2003)

Technical

- Current:** D. Schwartz (2000–), R. Grothe (2002–), J. Dudley (2001–), Q. Nguyen (2003–), W. Parkhurst (2003–)
- Past:** C. Bevers (1998–1999), L. Casler (1999–2001), A. Rowsey (1999–2000), B. Timmerick (2001–2002)

VISITING SCHOLARS SPONSORED

1998. Dr. Paul Purdom, Indiana University (Sept. 7–14)
2000. Dr. Koichiro Tamura, Tokyo Metropolitan University, Japan (Jun. 1–30)
2000. Dr. S. Blair Hedges, Penn State University, University Park (Jul. 30–Aug. 3; Oct. 7–15)
2000. Dr. Joaquin Dopazo, Glaxo-Wellcome, Madrid, Spain (Dec. 5–8)
2001. Dr. Koichiro Tamura, Tokyo Metropolitan University, Japan (Jun. 18–Aug. 20)
2002. Dr. Ziheng Yang, University College, London (Mar. 22–29)
2002. Dr. Tom Brody, National Institute of Health, Bethesda, MD (May 7–10)
2002. Dr. Koichiro Tamura, Tokyo Metropolitan University, Japan (Jun. 21–Aug. 19)
2002. Dr. Paul Purdom, Indiana University (Aug. 11–12)
2002. Dr. Shozo Yokoyama, Syracuse University (Sept. 10–13)
2002. Dr. Mark Stoneking, University of Leipzig (Nov. 3–7)
2002. Dr. Blair Hedges, Penn State University (Nov. 7–9)
2002. Carla Ann Hass, Penn State University (Nov. 7–9)
2003. Dr. Bernt Walthers, University of Bergen, Norway and Princeton University (Feb. 2–4)
2003. Dr. Jianzhi George Zhang, University of Michigan (Feb. 23–25)
2003. Dr. Ross Hardison, Penn State University (Mar. 9–11)
2003. Dr. Koichiro Tamura, Tokyo Metropolitan University, Japan (Jul. 1–Aug. 17)
2003. Dr. Steve Sherry, National Center for Biotechnology Information (Oct. 2–4)
2003. Dr. Adriana Briscoe, University of California Irvine (Nov. 13–16)
2004. Dr. Stephen Schaeffer, Pennsylvania State University (Jan. 10–17)
2004. Dr. Kimberly Nelson, Mitotyping Technologies (Jan. 10–17)

PUBLICATIONS

1. Hedges SB, Kumar S, Tamura K & Stoneking M (1992) Human origins and analysis of mitochondrial DNA sequences. **Science** 255:737-739.
2. 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, Pennsylvania (140 pp; >2000 distributed).
3. Kumar S, Tamura K & Nei M (1994) MEGA: Molecular Evolutionary Genetics Analysis software for microcomputers. **Computer Applications in Biosciences** 10:189-191.
4. Yang Z, Kumar S & Nei M (1995) A new method of inference of ancestral nucleotide and amino acid sequences. **Genetics** 141:1641-1650.
5. Rzhetsky A, Kumar S & Nei M (1995) Four-cluster analysis: a simple method to test phylogenetic hypotheses. **Molecular Biology & Evolution** 12:163-167.
6. 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 & Evolution** 12:1132-1137.
7. Hedges SB, Parker PH, Sibley CG & Kumar S (1996) Continental breakup and the ordinal diversification of birds and mammals. **Nature** 381:226-229.
8. Kumar S (1996) A stepwise algorithm for finding minimum evolution trees. **Molecular Biology & Evolution** 13:584-593.
9. Kumar S (1996) Patterns of nucleotide substitution in mitochondrial protein coding genes of vertebrates. **Genetics** 143:537-548.
10. Kumar S, Balczarek KA & Lai Z-C (1996) Evolution of the *hedgehog* gene family. **Genetics** 142:965-972.
11. Kumar S & Rzhetsky A (1996) Evolutionary relationships of eukaryotic kingdoms. **Journal of Molecular Evolution** 42:183-193.
12. Kumar S (1996) *PHYLTEST: Phylogenetic Hypothesis Testing Software*. Version 2.0. Pennsylvania State University, University Park, Pennsylvania.
13. Yang Z & Kumar S (1996) Approximate methods for estimating the pattern of nucleotide substitution and the variation of substitution rates among sites. **Molecular Biology & Evolution** 13: 650-659.
14. Zhang J, Kumar S & Nei M (1997) Small-sample tests of episodic adaptive evolution: A case study of primate lysozymes. **Molecular Biology & Evolution** 14:1335-1338.
15. Yeager M, Kumar S & Hughes AL (1997) Sequence convergence in the peptide-binding region of primate and rodent MHC class Ib molecules. **Molecular Biology & Evolution** 14:1035-1041.
16. Balczarek KA, Lai Z-C & Kumar S (1997) Evolution and functional diversification of the Paired-box (*Pax*) DNA-binding domains. **Molecular Biology & Evolution** 14: 829-842.
17. Zhang J & Kumar S (1997) Detection of convergent and parallel evolution at the amino acid sequence level. **Molecular Biology & Evolution** 14:527-536.
18. 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.

19. ¹Kumar S & Hedges SB (1998) A molecular timescale for vertebrate evolution. **Nature** 392:917-920.
20. 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.
21. 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.
22. Newfeld SJ, Wisotzkey RG & Kumar S (1999) Molecular evolution of a development pathway: Phylogenetic analyses of transforming growth factor- β family ligands, receptors, and Smad signal transducers. **Genetics** 152:783-795.
23. Hedges SB & Kumar S (1999) Divergence times of eutherian mammals. **Science** 285:2031.
24. O'Brien S, Eisenberg JF, Miyamoto M, Hedges SB, Kumar S, & Wilson DE (1999) Comparative Genomics: Mammalian radiation. *Genome Maps* 10 (phylogenetic tree). **Science** 286:463-478.
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 & 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. ²Nei M & Kumar S (2000) *Molecular Evolution and Phylogenetics*. Oxford University Press, New York. (333 pp).
30. Kumar S (2000) *LDA: Linkage Disequilibrium Analysis of Bi-allelic Sites in Molecular Sequence Data*. Version 1.0. Arizona State University, Tempe, Arizona.
31. Kumar S, Gadagkar SR, Filipinski A, & Gu X (2001) Determination of the number of conserved chromosomal segments between species. **Genetics** 157:1387-1395.
32. Kumar S and Gadagkar SR (2001) Disparity Index: A simple statistic to measure and test the homogeneity of substitution pattern 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 & 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.

¹ ISI Hot Paper in Biology, Science Citation Index, Philadelphia (May 2000).

² Translated in Chinese and Japanese.

36. ³Kumar S, Tamura K, Jakobsen IB, & Nei M (2001) *MEGA2: Molecular Evolutionary Genetics Analysis software*. **Bioinformatics** 17:1244-1245.
37. ⁴Hedges 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).
38. Miller MP & Kumar S (2001) Understanding human disease mutations through the use of interspecific genetic variation. **Human Molecular Genetics** 10: 2319-2328.
39. Hedrick P & Kumar S (2001) Mutation and linkage disequilibrium in human mtDNA. **European Journal of Human Genetics** 9: 969-972.
40. 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.
41. 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.
42. Kumar S & Subramanian S (2002) Mutation rates in mammalian genomes. **Proceedings of the National Academy of Sciences (USA)** 99:803-808.
43. Jiang Z, Melville JS, Cao H, Kumar S, Filipowski A & Verrinder Gibbins A.M. (2002) Measuring conservation of contiguous sets of autosomal markers on bovine and porcine genomes in relation to the human genome map. **Genome** 45:769-776.
44. Tamura K & Kumar S (2002) Evolutionary distance estimation under heterogeneous substitution pattern among lineages. **Molecular Biology Evolution** 19:1727-1736.
45. Hedges SB & Kumar S (2002) Vertebrate genomes compared. **Science** 297: 1283-1285.
46. Kumar S, Jayaraman K, Panchanathan S, Gurunathan R, Marti-Subirana A & Newfeld SJ (2002) BEST: A novel computational approach for comparing gene expression patterns from early stages of *Drosophila melanogaster* development. **Genetics** 162: 2037-2047.
47. Rosenberg MS & Kumar S (2003) Taxon sampling, bioinformatics, and phylogenomics. **Systematic Biology** 52:119-124.
48. 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.
49. 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.
50. Rosenberg MS & Kumar S (2003) Patterns of transitional mutation biases within and among mammalian genomes. **Molecular Biology and Evolution** 20:988-993.
51. Rosenberg MS & Kumar S (2003) Heterogeneity of nucleotide frequencies among evolutionary lineages and phylogenetic inference. **Molecular Biology and Evolution** 20:610-621.
52. Hedges SB & Kumar S (2003) Genomic clocks and evolutionary timescales. **Trends in Genetics** 19:200-206.
53. Miller MP, Parker JD, Rissing SW, & Kumar S (2003) Quantifying the intragenic distribution of disease mutations. **Annals of Human Genetics** 67:567-579.
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.

³ ISI Hot Paper in Biology, Science Citation Index, Philadelphia (Mar 2004). Also 2nd most cited paper in Computer Science in the last 10 years (June 2004, *ISI Essential Science Indicators*)

⁴ One of the most viewed articles in BioMed Central (Nov 2002).

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. Hedges SB & Kumar S (2004) Precision of molecular time estimates. **Trends in Genetics** 20:242-247.
57. Filipski A & Kumar S (In press) Comparative genomics of Eukaryotes. **The Evolution of the Genome** edited by Ryan TG. Academic Press.
58. Kumar S, Tamura K, & Nei M (In press) MEGA3: Integrated software for Molecular Evolutionary Genetics Analysis and Sequence Alignment. **Briefings in Bioinformatics**. In press.
59. Gargesha M, Antin P, Van Emden B, Panchanathan S & Kumar S (In press) Image registration and similarity computation for chicken gene expression patterns. Workshop on **Genomic Signal Processing and Statistics** (GENSIPS), IEEE Signal Processing Society.
60. Tamura K, Masatoshi Nei, & Kumar S (In press) Prospects for inferring very large phylogenies using neighbor-joining method. **Proceedings of the National Academy of Sciences (USA)**.
61. Subramanian S & Kumar S (In press) Gene expression intensity shapes evolutionary rates of the vertebrate proteins. **Genetics**.

Encyclopedia/Dictionaries

62. Kumar S & Filipski A (2001) Molecular Phylogeny Reconstruction. **Encyclopedia of Life Sciences**, Macmillan Reference Ltd, Oxford, UK. (www.els.net).
63. Kumar S & Filipski A (2001) Molecular Clock Testing. Encyclopedia of Life Sciences, Macmillan Reference Ltd, Oxford, UK. (www.els.net).
64. Kumar S & Filipski A (In press) Phylogenetic Analysis. **Dictionary of Bioinformatics and Computational Biology** edited by Hancock J & Zvelebil M, John Wiley & Sons, Inc., New York, in press.

Book Reviews

65. Kumar S (2000) A review of the book Genomes by TA Brown. **The Quarterly Review of Biology** 75:316-317.
66. Kumar S (2002) MacTrees made easy, a review of the book Phylogenetic trees made easy: a how-to-manual for molecular biologists by Hall BG. **Molecular Evolution and Phylogenetics** 27:165-167.
67. Kumar S & Newfeld SJ (2002) A review of the book Molecular 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.
68. 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.
69. Lorson C & Kumar S (2003) A review of the book Genomes (second edition) by T.A. Brown. **The Quarterly Review of Biology**. 78:225.

Manuscripts submitted or in advanced stages of completion

70. Gurunathan R, Van Emden B, & Kumar S (Submitted) Effectiveness of methods based on binary feature and moment invariant representations in identifying spatially similar gene expression patterns in Fruit Fly embryo images. **BMC Bioinformatics**.
71. Kumar S & Filipski A (In press) Reconstructing Vertebrate Phylogeny. **Encyclopedia of Genetics, Genomics, Proteomics, and Bioinformatics** edited by Subramaniam S. John Wiley & Sons, New York.
72. Gadagkar S, Rosenberg M, & Kumar S (in prep) Effects of Gene Concatenation on the Accuracy of Inferring the Evolutionary History of Species. **BMC Bioinformatics**.

73. Purdom P, Rosenberg MS, & Kumar S (submitted) Fast weighted parsimony by recoding DNA sequences. *SIAM Journal of Computing*.

INVITATIONS TO SYMPOSIA/WORKSHOPS

- 2003 (Mar.) Techniques Workshop at the 44th Annual *Drosophila Research Conference*, Chicago, IL
Title: Basic Expression Search Tool (BEST): Computational framework for in silico analysis of in situ hybridization data
- 2003 (Nov) Comparative and Functional Genomics Workshop. Sponsored by the *Wellcome Trust and Department of Energy*, Hinxton, Cambridgeshire, UK
Title: Patterns of point mutation and protein substitution rates revealed by comparative mammalian genomics
- 2002 (Mar) Symposium on Evolutionary Genetics at the annual meeting of the *American Genetics Association Symposium*, Arizona State University, Tempe, Arizona.
Title: Rates of Point Mutation in Mammals
- 2002 (Nov) The 12th International Workshop on 'Beyond the Identification of Transcribed Sequences: Functional, Evolutionary, and Expression Analysis.' Sponsored by *Department of Energy*, Washington DC
Title: Building Fruit fly Developmental Networks: in silico approaches for analyzing in situ gene expression patterns
- 2002 (Dec) The Eighteenth International Symposium in Conjunction with Award of the *International Prize for Biology*, Tokyo, Japan
Title: Building Fruit fly Developmental Networks: in silico approaches for analyzing in situ gene expression patterns
- 2001 (Oct) International Workshop on Population Genetics, *University of Montreal*, Montreal, Canada
Title: Estimating Neutral Evolutionary Rates in Mammals
- 1999 (Aug) Symposium on Genomic Diversity at the annual meeting of the *American Genetic Association*, Pennsylvania State University, University Park, PA
Title: Genomic divergence between species in terms of the number of chromosomal rearrangements
- 1997 (June) Symposium on Large Phylogenies at the annual meeting of the *Society for the Study of Systematic Biology*, University of Colorado, Boulder, Colorado
Title: Inferring Large Phylogenies

OTHER INVITED PRESENTATIONS

- 1) National Cancer Institute, Frederick, Maryland (1997)
- 2) Department of Biology, Arizona State University, Tempe, Arizona (1997)
- 3) Department of Zoology and Genetics, Iowa State University, Ames, Iowa (1998)
- 4) Department of Biology, Arizona State University-West, Phoenix, Arizona (1999)
- 5) Department of Biology, Tokyo Metropolitan University, Tokyo, Japan (2000)
- 6) Graduate University for Advanced Studies, Hayama, Japan (2000)
- 7) Genetics Program, University of Arizona, Tucson, Arizona (2000)
- 8) Birla Institute of Technology & Sciences, Pilani, India (2000)
- 9) University of South Carolina, Columbia, South Carolina (2000)
- 10) ASU President's Community Enrichment Program, Phoenix, Arizona (2001)
- 11) Department of Biology, Ohio State University, Columbus, Ohio (2001)
- 12) Department of Biology, Hong Kong University, Hong Kong, China (2001) (2 lectures)
- 13) Department of Biology, Syracuse University, Syracuse, New York (2001)
- 14) Program in Ecology and Evolutionary Biology, University of Illinois, Urbana Champaign, Illinois (2001)

- 15) Department of Biology, Grand Canyon University, Phoenix, Arizona (2001).
- 16) Ecology & Evolutionary Biology Program/IGERT, Indiana University, Bloomington, Indiana (2001).
- 17) Department of Biology, Tokyo Metropolitan University, Tokyo, Japan (2001).
- 18) Biomedical Engg., Indian Institute of Science, Bangalore, India (2001).
- 19) Department of Biology, Indiana University, Bloomington, Indiana (2002).
- 20) Department of Computer Science, Arizona State University, Tempe, AZ (2002).
- 21) Department of Biology, University of Michigan, Ann Arbor, MI (2002).
- 22) National Ecological Observatory Network (NEON), NSF, Santa Barbara, CA (2002).
Invitation declined due to scheduling conflict.
- 23) Society of Molecular Biology and Evolution 2003 Annual Conference, Newport Beach, CA (2003).
- 24) Department of Biology, Duke University, Durham, NC (2003).
- 25) Bioinformatics Research Center, North Carolina State University, Raleigh, NC (2003).
- 26) Hexapodium, Center for Insect Research, University of Arizona (2004).