



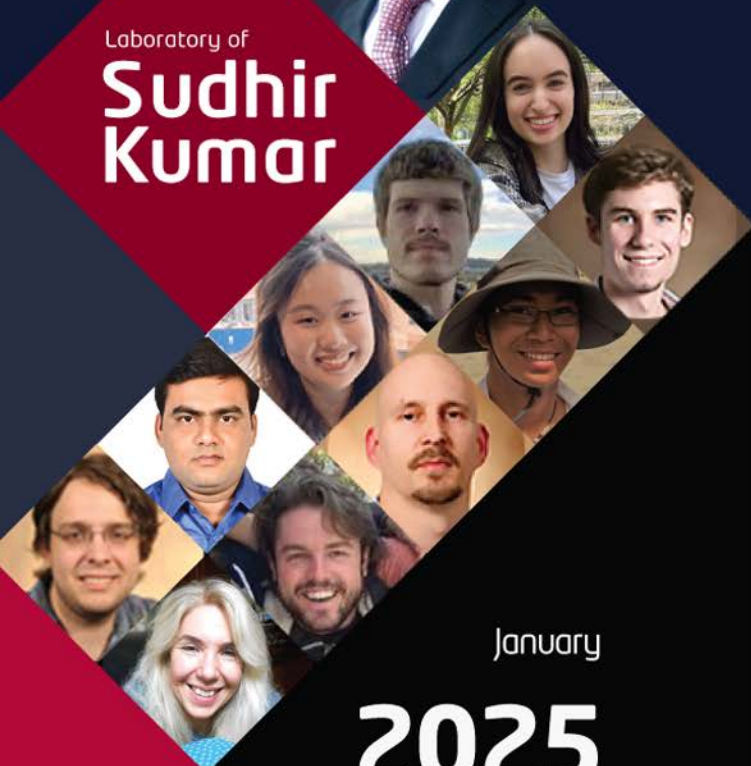
TEMPLE
UNIVERSITY

College of Science
and Technology



Laboratory of

**Sudhir
Kumar**



January

2025

kumarlab.net



Sudhir Kumar
623-225-5230
s.kumar@temple.edu



SERC 602
1925 N. 12th Street
Philadelphia, PA 19122



www.timetree.org

Timetree

A public knowledge-base of the
evolutionary timescales of the tree of life.



Download on the
App Store



Timetree of life

YEAR TIMETREE RESOURCE PUBLICATIONS

'22

TimeTree 5: An expanded resource for species divergence times
MBE 39:msac174

'17

TimeTree: A resource for timelines, timetrees, and divergence times
MBE 34:1812

'11

TimeTree2: Species divergence times on the iphone
Bioinformatics 27:2023

'06

TimeTree: A public knowledge-base of divergence times among
organisms *Bioinformatics 22:2971*



Flyexpress

www.flyexpress.net

An integrated discovery
platform to study
coexpressed genes using in
situ hybridization images in
Drosophila.



myPEG

www.mypeg.info

An integrated platform of
evolutionary tools for
phylomedicine.

YEAR PHYLOGENETIC METHODS

- '25 Integrating phylogenies with chronology to assemble the tree of life *Bioinformatics (in revision)*
- '23 Computational reproducibility of molecular phylogenies *MBE40:msad165*
- '23 Molecular timetrees using relaxed clocks and uncertain phylogenies *Frontiers in Bioinformatics 3:1225807*
- '22 Taming the selection of optimal substitution models in phylogenomics by site subsampling and upsampling *MBE 39:msac236*
- '22 TopHap: Rapid inference of key phylogenetic structures from common haplotypes in large genome collections with limited diversity *Bioinformatics 38:2719*
- '21 Fast and accurate bootstrap confidence limits on genome-scale phylogenies using little bootstraps *Nature Comput Sci 1:573*
- '20 A new method for inferring timetrees from temporally sampled molecular sequences *PLoS Comput Biology 16:e1007046*
- '18 Theoretical foundation of the RelTime method for estimating divergence times *MBE 35:1770*
- '12 Estimating divergence times in large molecular phylogenies *PNAS 109:19333*
- '04 Prospects for inferring very large phylogenies by using the neighbor-joining method *PNAS 101:11030*
- '01 Disparity index: A simple statistic to measure and test the homogeneity of substitution patterns between molecular sequences *Genetics 158:1321*
- '01 Incomplete taxon sampling is not a problem for phylogenetic inference *PNAS 98:10751*
- '96 Stepwise algorithm for finding minimum evolution trees *MBE 13:584*
- '95 A new method of inference of ancestral nucleotide and amino-acid-sequences *Genetics 141:1641*

YEAR TIMETREES AND SPECIATION

- '25 Completing a molecular timetree of primates *Frontiers in Bioinformatics 4:1495417*
- '23 The origin of eukaryotes and rise in complexity were synchronous with the rise in oxygen *Frontiers in Bioinformatics 3:1233281*
- '22 TimeTree 5: An expanded resource for species divergence times *MBE 39:msac174*
- '22 Limitations of phylogenomic data can drive inferred speciation rate shifts *MBE 39:msac0383*
- '15 Tree of life reveals clock-like speciation and diversification *MBE 32:835*
- '05 Placing confidence limits on the molecular age of the human-chimpanzee divergence *PNAS 102:18842*
- '04 Temporal patterns of fruit fly (*Drosophila*) evolution revealed by mutation clocks *MBE 21:36*
- '98 A molecular timescale for vertebrate evolution *Nature 392:917*
- '96 Continental breakup and the ordinal diversification of birds and mammals *Nature 381:226*

YEAR MACHINE LEARNING

- '25 Evolutionary sparse learning reveals the shared genetic basis of convergent traits *Nature Communications (in revision)*
- '25 STICI: Split-transformer with integrated convolutions for imputation *Nature Communications (in revision)*
- '24 Discovering fragile clades and causal sequences in phylogenomics by evolutionary sparse learning *MBE 41:msae131*
- '22 Discovering research articles containing evolutionary timetrees by machine learning *Bioinformatics 39:btad035*
- '21 Evolutionary sparse learning for phylogenomics *MBE 38:4674*
- '21 TreeMap: A structured approach to fine mapping of eQTL variants *Bioinformatics 37:1125*
- '20 Deep model based transfer and multi-task learning for biological image analysis *IEEE Transactions on Big Data 6:322*
- '19 A machine learning method for detecting autocorrelation of evolutionary rates in large phylogenies *MBE 36:811*
- '12 Learning sparse representations for fruit-fly gene expression pattern image annotation and retrieval *BMC Bioinformatics 13:107*

YEAR GENOMIC MEDICINE

- '24 Methods for estimating personal disease risk and phylogenetic diversity of hematopoietic stem cells *MBE 41:msad279*
- '22 Clone phylogenetics reveals metastatic tumor migrations, maps, and models *Cancers 14:4326*
- '21 The durability of immunity against reinfection by SARS-CoV-2: A comparative evolutionary study *The Lancet Microbe 12:e666*
- '20 An evolutionary portrait of the progenitor SARS-CoV-2 and its dominant offshoots in COVID-19 pandemic *MBE 38:3046*
- '20 PathFinder: Bayesian inference of clone migration histories in cancer *Bioinformatics 36:i675*
- '19 Biological relevance of computationally predicted pathogenicity of noncoding variants *Nature Communications 10:330*
- '18 Computational enhancement of single-cell sequences for inferring tumor evolution *Bioinformatics 34:i917*
- '18 Predicting clone genotypes from tumor bulk sequencing of multiple samples *Bioinformatics 34:4017*
- '15 Evolutionary diagnosis of non-synonymous variants involved in differential drug response *BMC Medical Genomics 8:S6*
- '13 Genome-wide profiling of human cap-independent translation-enhancing elements *Nature Methods 10:747*
- '12 Evolutionary diagnosis method for variants in personal exomes *Nature Methods 9:855*
- '12 Performance of computational tools in evaluating the functional impact of laboratory-induced amino acid mutations *Bioinformatics 28:2093*
- '01 Understanding human disease mutations through the use of interspecific genetic variation *Human Molecular Genetics 10:2319*

YEAR GENOME EVOLUTION

- '23 Analyses of allele age and fitness impact reveal human beneficial alleles to be older than neutral controls *eLife* **13:RP93258**
- '19 On estimating evolutionary probabilities of population variants *BMC Evolutionary Biology* **19:133**
- '18 Adaptive landscape of protein variation in human exomes *MBE* **35:2015**
- '16 A molecular evolutionary reference for the human variome *MBE* **33:245**
- '14 Signatures of natural selection on mutations of residues with multiple posttranslational modifications *MBE* **31:1641**
- '12 Comparison of embryonic expression within multigene families using the FlyExpress discovery platform reveals more spatial than temporal divergence *Developmental Dynamics* **241:150**
- '11 Rampant purifying selection conserves positions with posttranslational modifications in human proteins *MBE* **28:1565**
- '09 Signatures of nitrogen limitation in the elemental composition of the proteins involved in the metabolic apparatus *Proceedings of the Royal Society B-Biological Sciences* **276:2605**
- '06 Signatures of ecological resource availability in the animal and plant proteomes *MBE* **23:1946**
- '04 Gene expression intensity shapes evolutionary rates of the proteins encoded by the vertebrate genome *Genetics* **168:373**
- '03 Neutral substitutions occur at a faster rate in exons than in noncoding DNA in primate genomes *Genome Research* **13:838**
- '02 Mutation rates in mammalian genomes *Proceedings of the National Academy of Sciences (USA)* **99:803**
- '02 BEST: A novel computational approach for comparing gene expression patterns from early stages of *Drosophila melanogaster* development *Genetics* **162:2037**

YEAR PROTEIN DYNAMICS

- '23 Some mechanistic underpinnings of molecular adaptations of SARS-COV-2 spike protein by integrating candidate adaptive polymorphisms with protein dynamics *eLife*.**92063.1**
- '22 Epistasis creates invariant sites and modulates the rate of molecular evolution *MBE* **39:msac106**
 Dynamic coupling of residues within proteins as a mechanistic foundation of many enigmatic pathogenic missense variants *PLoS Comput Biology* **18:e1010006**
- '21 Epistasis produces an excess of invariant sites in neutral molecular evolution *PNAS* **118:e2018767118**
- '15 Conformational dynamics of nonsynonymous variants at protein interfaces reveals disease association *Proteins* **83:428**
- '14 Signatures of natural selection on mutations of residues with multiple posttranslational modifications *MBE* **31:1641**
- '13 Structural dynamics flexibility informs function and evolution at a proteome scale *Evolutionary Applications* **6:423**

Reviews & Perspectives

- YEAR '22 Embracing green computing in molecular phylogenetics *MBE* **39:msac043**
- '21 Tumors are evolutionary island-like ecosystems *Genome Biology and Evolution* **13:evab276**
- '20 The bits and bytes of biology: Digitalization fuels an emerging generative platform for biological innovation *Handbook of Digital Innovation* **253**
 The role of conformational dynamics and allostery in modulating protein evolution *Annual Review of Biophysics* **49:267**
 Efficient methods for dating evolutionary divergences in *The Molecular Evolutionary Clock* Springer **197**
- '18 Neutral theory, disease mutations, and personal exomes *MBE* **35:1297**
- '16 Advances in time estimation methods for molecular data *MBE* **33:863**
- '12 Human genomic disease variants: A neutral evolutionary explanation *Genome Research* **22:1383**
 Statistics and truth in phylogenomics *MBE* **29:457**
- '11 Stoichiogenomics: The evolutionary ecology of macromolecular elemental composition *Trends in Ecology & Evolution* **26:38**
 Phylomedicine: An evolutionary telescope to explore and diagnose the universe of disease mutations *Trends in Genetics* **27:377**
- '07 Multiple sequence alignment: In pursuit of homologous DNA positions *Genome Research* **17:127**
- '05 Molecular clocks: Four decades of evolution *Nature Reviews Genetics* **6:654**
- '03 Genomic clocks and evolutionary timescales *Trends in Genetics* **19:200**

CITATIONS

Top-100 platinum h-index
 h-index = 86 (>300,000 citations)
 Google Scholar

HOT PAPERS

Among the top 0.1% of all the papers published in two years following their release

<i>Bioinformatics</i> 17:1244	<i>Nature</i> 392:917
<i>Briefings in Bioinformatics</i> 9:299	<i>MBE</i> 39:msac174; 38:3022;
<i>Briefings in Bioinformatics</i> 5:150	35:1547 and 34:1812

HIGHLY CITED

Citation count in the 1% of all articles in a 10-year period

<i>PNAS, USA</i> 101:11030	<i>Nature</i> 450:203
<i>Briefings in Bioinformatics</i> 9:299	<i>MBE</i> 39:msac174; 38:3022;
<i>Briefings in Bioinformatics</i> 5:150	37:1237; 35:1547; 34:1812;
<i>Bioinformatics</i> 28:2685	33:1870; 32:835; 30:2725;
<i>The Lancet Microbe</i> 12:e666	28:2731 and 24:1596

TOP CITED

In Nature's top-100 articles of all time in the published literature
MBE **24:1596** (see *Nature* [2014] 514:550-553)

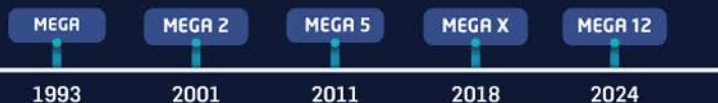


www.megasoftware.net

User-friendly software suite for analyzing DNA and protein sequence data from species and populations.

Timeline

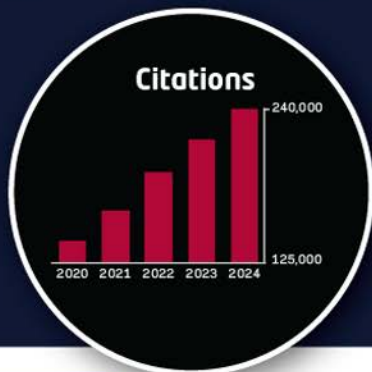
of major MEGA software releases



Available on



GUI & Command Line



MEGA SOFTWARE PUBLICATIONS

- '24 MEGA12: Molecular Evolutionary Genetics Analysis version 12 for adaptive and green computing *MBE (in review)*
- '21 MEGA11: Molecular Evolutionary Genetics Analysis version 11 *MBE 38:3022*
- '20 Molecular Evolutionary Genetics Analysis (MEGA) for macOS *MBE 37:1237*
- '18 MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms *MBE 35:1547*
- '16 MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets *MBE 33:1870*
- '14 MEGA-MD: Molecular Evolutionary Genetics Analysis Software with mutational diagnosis of amino acid variation *Bioinformatics 30:1305*
- '12 MEGA-CC: Computing core of Molecular Evolutionary Genetics Analysis program for automated and iterative data analysis *Bioinformatics 28:2685*
- '01 MEGA2: Molecular Evolutionary Genetics Analysis software *Bioinformatics 17:1244*
- '94 MEGA: Molecular Evolutionary Genetics Analysis software for microcomputers *Bioinformatics 10:189*

Education

Our research laboratory hosts students pursuing doctoral dissertations, masters' projects, and undergraduate interns. They receive one-on-one research and development mentoring. We have developed degree and certificate programs for all the undergraduate students at Temple University, which are:

- B.S. degree in Genomic Medicine
- B.S. degree in Data Science (Genomics and Bioinformatics)
- B.S. certificate in Genomic Medicine

YEAR EDUCATION

- '24 Visualizing genomic medicine: An introduction to general biology *The American Biology Teacher 86:265*
Of phylogenies and tumors: Cancer as a model system to teach evolution *The American Biology Teacher 86:62*
- '22 Storyboarding for biology: An authentic STEAM experience *The American Biology Teacher 82:328*
- '21 How to build a super predator: From genotype to phenotype *The American Biology Teacher 83:138*
- '20 Molecular memories of a cambrian fossil *The American Biology Teacher 82:586*
- '19 Adventures in evolution: The narrative of tardigrada, trundlers in time *The American Biology Teacher 81:543*

Lab Members

Postdoctoral, Doctoral, MS

Rohan Alibutud
John Allard
Sarah Chung
Jack Craig
Lisa Schmelkin
Sudip Sharma

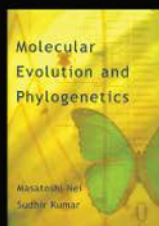
Undergraduate & Intern

Kelly Abramowitz
Louise Dupont
Sid Jaggi
Hardik Sharma
Brandon Khoa Son
Deyana Tabatabaei
Anushka Tejeswi

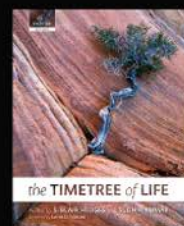
Technologist

Maxwell Sanderford
Glen Stecher
Michael Suleski

Books



Masatoshi Nei & Sudhir Kumar



S. Blair Hedges & Sudhir Kumar

