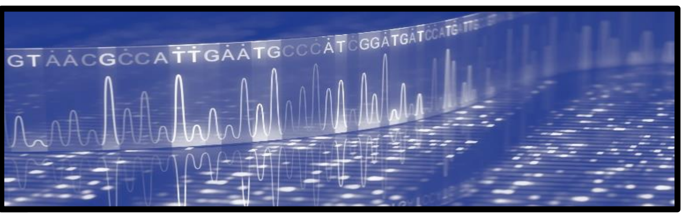
Yale Center for Biomedical Data Science



CBDS Seminar Series

"Molecular Evolution Informs Genomic Medicine"

Sudhir Kumar

Director, Institute for Genomics and Evolutionary Medicine
Carnell Professor, Biology, Temple University

Wednesday, November 4, 2020
4:00 to 5:00 p.m.
Zoom: https://yale.zoom.us/j/95068930828
Host: Jeffrey Townsend

Nature has been the greatest experimenter on Earth for millennia. New mutations continuously arise in genomes and subject to negative, positive, and neutral selection. Comparative sequence analysis at individual, population, and species levels yields a record of their outcomes in patterns of conservation and divergence of genomes in different species. These evolutionary patterns and their underlying causes are now the foundation of many approaches to forecasting adaptive and disruptive mutations found in our personal genomes. Predictive evolutionary techniques and the associated fundamental research investigations are encompassed by Phylomedicine, becoming a key discipline at the intersection of molecular evolution, genomics, and biomedicine. I will present highlights of our recent research in phylomedicine of Mendelian, cancer, and complex diseases. I will also show results from our big data analysis aimed at building an evolutionary portrait of SARS-CoV-2. Ultimately, this presentation will conclude that the molecular evolutionary studies are the key to detecting neutral, deleterious, and adaptive alleles in populations and pathogens.

Bio: Sudhir Kumar has been an early leader in exploring the theoretical and empirical intersection of evolutionary biology with computational biology. His group has made numerous contributions to phylogenetics' mathematical theory through advances in estimating evolutionary distances, inference of divergence times, and algorithms for constructing phylogenetic trees. Kumar and his laboratory continue to work actively on improving phylogenetic theory and applications to the growing field of phylomedicine, which explores disease via phylogenetic methods and makes predictions informed by evolutionary biology.

He has also led the development of widely accessible tools that allow researchers from diverse backgrounds to harness modern computational biology's analytical power. He developed Molecular Evolutionary Genetics Analysis (MEGA), a freely-accessible software package, which he and his colleagues have maintained and improved for more than 25 years. MEGA's enduring popularity results from Kumar's responsiveness to community needs and dedication to accessibility and scientific rigor.

His work has been cited more than 200,000 times (H-index = 75). One of his scientific articles was included in the Thomson Reuters Web of Science top-100 most-cited papers of all time and designated the top article of the decade by The Scopus database of peer-reviewed literature. He has published numerous citation classics and hot papers. He received an Innovation Award in Functional Genomics from the Burroughs-Wellcome Fund in 2000 and is a fellow of the American Association for the Advancement of Science.

Sudhir Kumar is currently the Laura H. Carnell Professor of Biology and the Director of the Institute for Genomics and Evolutionary Medicine at Temple University. He completed a Ph.D. and postdoctoral work in Genetics at Pennsylvania State University, after receiving a dual degree in Biological Sciences and Electrical & Electronics Engineering from the Birla Institute of Technology and Sciences (India).