

Title: Extrachromosomal and other mechanisms of oncogene amplification in cancer

Abstract:

Increase in the number of copies of tumor promoting (onco-) genes is a hallmark of many cancers, and cancers with copy number amplifications are often associated with poor outcomes. Despite their importance, the mechanisms causing these amplifications are incompletely understood. In this talk, we describe our recent results suggesting that a large fraction of amplification is due to formation of extrachromosomal DNA (ecDNA). EcDNA play a critical role in tumor heterogeneity, accelerated cancer evolution, and drug resistance through their unique mechanism of non-chromosomal inheritance. While predominant, ecDNA are not the only mechanism to cause amplification. We also describe recent algorithmic methods required to distinguish ecDNA from other mechanisms including Breakage Fusion Bridge formation, Chromothripsis, and simpler events such as tandem duplications and translocations. The talk is a mix of published and unpublished work, largely in collaboration with Paul Mischel's lab at UCSD. EcDNA was recently recognized as one of the grand challenges of cancer research by Cancer Research UK and the National Cancer Institute.

Reading

[Luebeck, 2020](#),
[Verhaak 2019](#)

Biography

Vineet Bafna, Ph.D., joined the Computer Science faculty at the University of California, San Diego in 2003, after seven years in the biosciences industry. He received his Ph.D. in computer science from The Pennsylvania State University in 1994 and was an NSF postdoctoral researcher at the Center for Discrete Mathematics and Theoretical Computer Science for two years. From 1996-99, Bafna was a senior investigator at SmithKline Beecham, conducting research on DNA signaling, target discovery and EST assembly. From 1999 to 2002, he worked at Celera Genomics, ultimately as director of Informatics Research, participating in the human genome project. He arrived at the Jacobs School from the Center for Advancement in Genomics, set up by Celera founder Craig Venter. Vineet Bafna's research incorporates algorithmic methods into the analysis of molecular biology data including complex structural variation in (tumor) genomes, genetic signals of adaptation, and proteogenomics. He has co-authored 150 research articles in the leading journals in the field. He served as co-Director of the Bioinformatics and Systems Biology Ph.D. program from 2013-19, and was founding faculty of the Halicoglou Data Science Institute at UCSD. In 2019, he was selected as a fellow of the International Society of Computational Biology.

Contact. 619-618-9126 (M), 858-538-9147 (H)