Vineet Bafna, Ph.D.
Professor, Computer Science & Engineering
Director, Bioinformatics and Systems Biology
UC San Diego
9500 Gilman Drive La Jolla, CA 92093-0404

vbafna@cs.ucsd.edu
858-822-4978
www.cse.ucsd.edu/~vbafna

Education

- **B.Tech-** Computer Science and Engineering (1985-89), Indian Institute of Technology, New Delhi, India.
- **Ph.D.** - Computer Science (1994), The Pennsylvania State University.
- **Postdoctoral.** NSF Postdoctoral fellow at the Center for Discrete Mathematics and Theoretical Computer Science (DIMACS), Piscataway, NJ (1994-1996).

Affiliations

- 7/12- Director, Bioinformatics and Systems Biology PhD program.
- 7/09- Professor, Computer Science and Engineering, Univ. California, San Diego
- 7/07-7/09 Associate Professor, Computer Science and Engineering, Univ. California, San Diego
- 7/03-6/07 Assistant Professor, Computer Science and Engineering, Univ. California, San Diego
- 9/02-7/03 Senior Investigator, The Center for Advancement of Genomics.
- 1/01-9/02 Director, Informatics Research, Celera Genomics. 9/99-12/00 Principal Investigator, Informatics Research, Celera. 8/96-9/99 Senior Investigator, SmithKline Beecham.

Relevant Products

- Zhou, D., Udpa, N., Gersten, M., Visk, D. W., Bashir, A., Xue, J., Frazer, K. A., Posakony, J. W., Subramaniam, S., Bafna, V., and Haddad, G. G. Experimental selection of hypoxia-tolerant Drosophila melanogaster. *Proc. Natl. Acad. Sci.* U.S.A. 108 (Feb 2011), 2349–2354. (PMID:18563926, Free PMC article).
- Ronen, R., Udpa, N., Halperin, E., and Bafna, V. Learning natural selection from the site frequency spectrum. *Genetics* 195, 1 (Sep 2013), 181–193.
- Stobdan T, Akbari A, Azad P, Zhou D, Poulsen O, Appenzeller O, Gonzales GF, Telenti A, Wong EHM, Saini S, Kirkness EF, Venter JC, Bafna V, Haddad GG. New insights into the genetic basis of Monge's disease and adaptation to high-altitude. Mol Biol Evol. 2017.
- Ronen, R., Tesler, G., Akbari, A., Zakov, S., Rosenberg, N. A., and Bafna, V. Predicting Carriers of Ongoing Selective Sweeps without Knowledge of the Favored Allele. *PLoS Genet.* 11, 9 (Sep 2015), e1005527.
- Chu WK, Edge P, Lee HS, Bansal V, Bafna V, Huang X, Zhang K. Ultraaccurate genome sequencing and haplotyping of single human cells. *Proc Natl Acad Sci U S A.* 2017.

Significant Products

- Zakov, S., Kinsella, M., and Bafna, V.. An algorithmic approach for breakage-fusion-bridge detection in tumor genomes. *Proc. Natl. Acad. Sci.* U.S.A. 110, 14 (Apr 2013), 5546–5551. PMID: 23503850.
- Stobdan, T., Zhou, D., Ao-Ieong, E., Ortiz, D., Ronen, R., Hartley, I., Gan, Z., McCulloch, A. D., Bafna, V., Cabrales, P., and Haddad, G. G. Endothelin receptor B, a candidate gene from human studies at high altitude, improves cardiac tolerance to hypoxia in genetically engineered heterozygote mice. *Proc. Natl. Acad. Sci.* U.S.A. 112, 33 (Aug 2015), 10425–10430.
- Patel, A., Edge, P., Selvaraj, S., Bafna, V., and Bafna, V. InPhaDel: integrative shotgun and proximity-ligation sequencing to phase deletions with single nucleotide polymorphisms. *Nucleic Acids Res.* 44, 12 (Jul 2016), e111.
- Edge, P., Bafna, V., and Bansal, V. HapCUT2: robust and accurate haplotype assembly for diverse sequencing technologies. *Genome Res.* (Dec 2016).
- Turner, K. M., Deshpande, V., Beyter, D., Koga, T., Rusert, J., Lee, C., Li, B., Arden, K., Ren, B., Nathanson, D. A., Kornblum, H. I., Taylor, M. D., Kaushal, S., Cavenee, W. K., Wechsler-Reya, R., Furnari, F. B., Vandenberg, S. R., Rao, P. N., Wahl, G. M., Bafna, V., and Mischel, P. S. Extrachromosomal oncogene amplification drives tumour evolution and genetic heterogeneity. *Nature* (Feb 2017).

Synergistic Activities

- Conferences: Program Chair, RECOMB2011. Chair, Workshop in Computational Pro- teomics at Institute for Pure and Applied Mathematics, (Los Angeles, 2004), Institute for Mathematics and its Applications (Columbus, 2005), and RECOMB satellite conference on Computational Proteomics (San Diego, 2006). Program Committee for RECOMB2002, RECOMB2003, RECOMB2004, RECOMB2005, RECOMB2007, RECOMB2008, RE- COMB2016. RECOMB is the primary conference for Computational Biology with about 30 members selected for program committee.
- Editorial Board of Jnl. of Bioinformatics and Computational Biology, IEEE Transactions on Computational Biology and Bioinformatics, Biology Direct, Bioinformatics, Journal of Computational Biology, Molecular and Cellular Proteomics.
- Director, UCSD PhD Program in Bioinformatics and Systems Biology