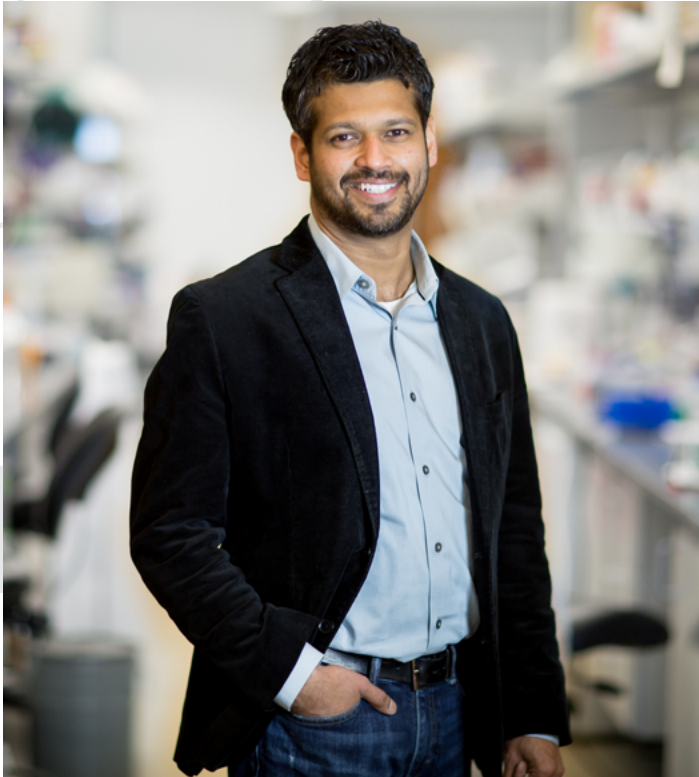


Nitin Baliga, PhD

Senior Vice President & Director



Nitin Baliga develops predictive models of biological networks that catalyze strategies for personalized medicine, and a sustainable environment. Dr. Baliga is also actively engaged in [HS education](#), bringing innovative inquiry-based curriculum on current science concepts [throughout the United States](#). His contributions to HS education have been recognized internationally and have won awards including the [Alvin J. Thompson award](#). As a Professor at the Institute for Systems Biology, he was one of the founding members, and currently serves as the Director and Senior Vice President. Dr. Baliga did his early schooling in Mumbai, India, where he received a B.Sc. in Microbiology (1992) from [Ruia College](#) within the [Mumbai University](#) system. In 1992, Dr. Baliga entered a national competition and won the highly coveted Central Government of India sponsored [Department of Biotechnology](#) studentship, which supported his graduate studies in Marine Biotechnology at [Goa University](#). After getting a M.Sc. in Marine Biotechnology in 1994, Dr. Baliga won the prestigious [Council for Scientific and Industrial Research](#) fellowship through another Central Government of India-sponsored national competition. After completing his Ph.D. in Microbiology in 2000 at the University of Massachusetts at Amherst, Dr. Baliga moved to Seattle for postdoctoral training with [Dr. Leroy Hood](#) at the [Institute for Systems Biology](#).

In 2007, Dr. Baliga published a landmark paper¹ that demonstrated for the first time that it is possible to accurately predict how an organism would respond to a new environment. This discovery was made possible by a suite of technologies²⁻⁵, experimental strategies⁶⁻¹¹ and computational tools¹²⁻¹⁹ that Dr. Baliga and his team developed to reverse engineer the complete regulatory network of a free living organism. This study uncovered the theory and fundamental principles that underlie the evolution and predictability of biological responses^{1,6,20,21}. Applying this approach to environmental issues, Dr. Baliga has discovered how some extremophiles might explore life in a new environment^{6,22,23}, revised a >5 decade old “operon” paradigm of gene regulation in prokaryotes^{24,25}, discovered diurnal anticipatory behavior in archaea²⁶, uncovered the role of programmed cell death in unicellular chlorophytes²⁷, elucidated how cells maintain copper ions at a safe concentration²⁸ and discovered the role of RNases in adaptation to rapid environmental changes. Together with collaborators at the University of Washington, and the Lawrence Berkeley Laboratories, he is now elucidating the biological networks underlying [social interactions](#) and [fuel production](#) by microbes.

Dr. Baliga has also expanded his research program to complex human disease to elucidate dysfunctional networks in cancer²⁹ and the basis for latency in TB infections³⁰. His work has identified a core set of miRNAs responsible for disease-characteristic oncogenic signatures across multiple cancers^{16,29,31}. The predictive and actionable network models of disease have important implications for drug target discovery, drug repositioning, and combinatorial therapeutics. Dr. Baliga’s work has been published in top international journals including Cell, Science and Nature, he has been invited to the [Google SciFoo Camp](#), and has been profiled by [The Scientist](#), [Genome Web](#), [Wired magazine](#), [Genetic Engineering News](#), [Ars Technica](#), [Xconomy](#), and [Nature Methods](#), among many others. Research in Dr. Baliga’s laboratory has been supported by the National Science Foundation, National Institutes of Health, NASA, Department of Energy, and the Department of Defense. He is the [Section Editor of BMC Systems Biology](#), and [Nature Scientific Data](#) serves on scientific advisory boards of numerous academic and industrial organizations, and been instrumental in research program planning for the NSF and DOE.

Dr. Baliga has also made transformative contributions to high school education. He founded the Systems Science Education Experiences program that has offered internship opportunities to dozens of high school students of disadvantaged backgrounds. This program has developed science curriculum modules to bring current science concepts and practices to high schools. Five modules developed in this program are in use across all 50 states in the US and across 144 countries worldwide.

Citations

1. Bonneau, R. et al., A predictive model for transcriptional control of physiology in a free living cell. *Cell* 131 (7), 1354-1365 (2007).
2. Bonneau, R., Baliga, N.S., Deutsch, E.W., Shannon, P., & Hood, L., Comprehensive de novo structure prediction in a systems-biology context for the archaea Halobacterium sp. NRC-1. *Genome Biol* 5 (8), R52 (2004).
3. Goo, Y.A. et al., Low-pass sequencing for microbial comparative genomics. *BMC Genomics* 5 (1), 3 (2004).
4. Goo, Y.A. et al., Proteomic Analysis of an Extreme Halophilic Archaeon, Halobacterium sp. NRC-1. *Mol Cell Proteomics* 2 (8), 506-524 (2003).
5. Van, P.T. et al., Halobacterium salinarum NRC-1 PeptideAtlas: toward strategies for targeted proteomics and improved proteome coverage. *J Proteome Res* 7 (9), 3755-3764 (2008).
6. Brooks, A.N., Turkarslan, S., Beer, K.D., Yin Lo, F., & Baliga, N.S., Adaptation of cells to new environments. *Wiley Interdiscip Rev Syst Biol Med* 3 (5), 544-561 (2011).
7. Facciotti, M.T., Bonneau, R., Hood, L., & Baliga, N.S., Systems Biology Experimental Design - Considerations for Building Predictive Gene Regulatory Network Models for Prokaryotic Systems. *Current Genomics* 5 (7), 527-544 (2004).
8. Facciotti, M.T. et al., Large scale physiological readjustment during growth enables rapid, comprehensive and inexpensive systems analysis. *BMC Syst Biol* 4, 64 (2010).
9. Koide, T., Lee Pang, W., & Baliga, N.S., The role of predictive modelling in rationally re-engineering biological systems. *Nat Rev Micro* 7 (4), 297-305 (2009).
10. Schmid, A. & Baliga, N., Prokaryotic Systems Biology in *Cell Engineering*, edited by Mohammed El-Rubeai (Springer, 2006), Vol. 5.
11. Weston, A.D., Baliga, N.S., Bonneau, R., & Hood, L., Systems approaches applied to the study of Saccharomyces cerevisiae and Halobacterium sp. *Cold Spring Harb Symp Quant Biol* 68, 345-357 (2003).
12. Bare, J.C., Koide, T., Reiss, D., Tenenbaum, D., & Baliga, N., Integration and visualization of systems biology data in context of the genome. *BMC Bioinformatics* 11 (1), 382 (2010).
13. Bare, J.C., Shannon, P.T., Schmid, A.K., & Baliga, N.S., The Firegoose: two-way integration of diverse data from different bioinformatics web resources with desktop applications. *BMC Bioinformatics* 8 (1), 456 (2007).
14. Bonneau, R. et al., The Inferelator: an algorithm for learning parsimonious regulatory networks from systems-biology data sets de novo. *Genome Biol* 7 (5), R36 (2006).
15. Gehlenborg, N. et al., Visualization of omics data for systems biology. *Nat Methods* 7 (3 Suppl), S56-68 (2010).
16. Plaisier, C.L., Bare, J.C., & Baliga, N.S., miRvestigator: web application to identify miRNAs responsible for co-regulated gene expression patterns discovered through transcriptome profiling. *Nucleic Acids Res* 39 Suppl 2, W125-131 (2011).
17. Reiss, D.J., Baliga, N.S., & Bonneau, R., Integrated biclustering of heterogeneous genome-wide datasets for the inference of global regulatory networks. *BMC Bioinformatics* 7 (1), 280 (2006).
18. Shannon, P. et al., Cytoscape: a software environment for integrated models of biomolecular interaction networks. *Genome Res* 13 (11), 2498-2504 (2003).
19. Shannon, P., Reiss, D.J., Bonneau, R., & Baliga, N.S., Gaggle: An open-source software system for integrating bioinformatics software and data sources. *BMC Bioinformatics* 7, 176 (2006).
20. Ashworth, J., Wurtmann, E.J., & Baliga, N.S., Reverse engineering systems models of regulation: discovery, prediction and mechanisms. *Current Opinion in Biotechnology* 23 (4), 598-603 (2012).
21. Baliga, N.S., The scale of prediction. *Science* 320 (5880), 1297-1298 (2008).
22. Facciotti, M.T. et al., General transcription factor specified global gene regulation in archaea. *Proc Natl Acad Sci U S A* 104 (11), 4630-4635 (2007).
23. Turkarslan, S. et al., Niche adaptation by expansion and reprogramming of general transcription factors. *Molecular systems biology* 7, 554 (2011).
24. Koide, T. et al., Prevalence of transcription promoters within archaeal operons and coding sequences. *Mol Syst Biol* 5, 285 (2009).
25. Yoon, S.H. et al., Parallel evolution of transcriptome architecture during genome reorganization. *Genome Research* 21 (11), 1892-1904 (2011).
26. Whitehead, K., Pan, M., Masumura, K., Bonneau, R., & Baliga, N.S., Diurnally entrained anticipatory behavior in archaea. *PLoS ONE* 4 (5), e5485 (2009).
27. Orellana, M.V., Pang, W.L., Durand, P.M., Whitehead, K., & Baliga, N.S., A role for programmed cell death in the microbial loop. *PLoS ONE* 8 (5), e62595 (2013).
28. Pang, W.L. et al., Metallochaperones regulate intracellular copper levels. *PLoS Computational Biology* 9 (1), e1002880 (2013).
29. Plaisier, C.L., Pan, M., & Baliga, N.S., A miRNA-regulatory network explains how dysregulated miRNAs perturb oncogenic processes across diverse cancers. *Genome Research* 22 (11), 2302-2314 (2012).
30. Rustad, T.R. et al., Global analysis of mRNA stability in Mycobacterium tuberculosis. *Nucleic acids research* 41 (1), 509-517 (2013).
31. Plaisier, C.L. & Baliga, N.S., Harnessing the power of human tumor-derived cell lines for the rational design of cancer therapies. *Pigment Cell Melanoma Res* 25 (4), 406-408 (2012).