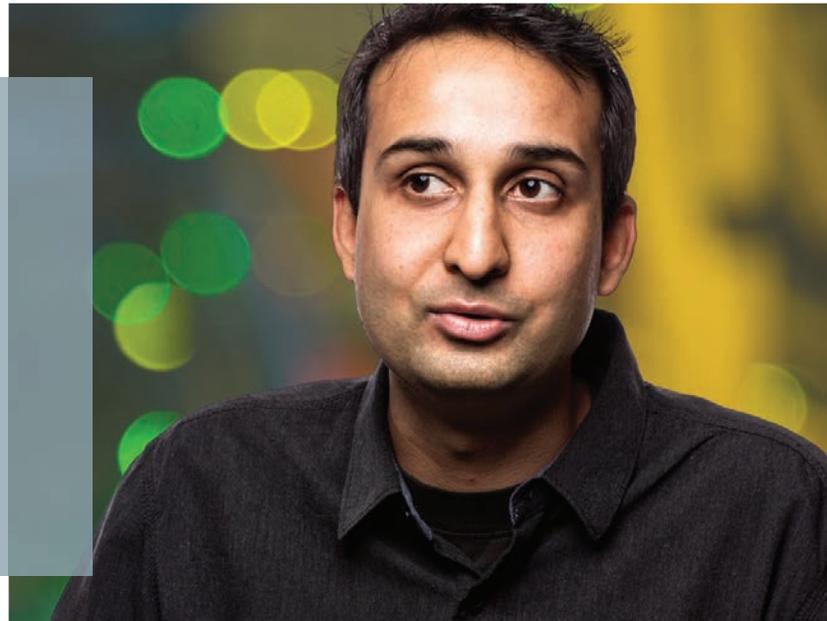


Saket Navlakha

Assistant Professor
Integrative Biology Laboratory



The Problem

Biological systems, from protein interactions to neural networks, are highly complex, and we still have only a basic understanding of how they work. With current and newly emerging technologies, biologists are producing massive amounts of data that could unveil the rules that govern complex biological processes and how these processes are disrupted by diseases. But new algorithmic and computational methods are needed to decipher this data to help inform future experiments and gain a better understanding of biology.

The Approach

Saket Navlakha develops new algorithms to understand the interactions, dynamics and evolution of large, noisy and complex biological networks. By mining massive amounts of data in new ways, he aims to reveal how molecular and cellular networks are organized and have evolved. Navlakha also studies “algorithms in nature”—for example, how groups of distributed molecules and cells communicate and process information to collectively solve computational problems. Discovering such shared principles can lead to the design of improved computing algorithms and can provide a way to understand, quantify and predict the behavior of large, distributed biological systems. To accomplish this,

Navlakha is bridging theoretical computer science and systems biology and developing collaborations with experimentalists to learn from biological data.

The Innovations and Discoveries

- Navlakha is uncovering new principles of neural circuit development in the brain to improve the design of communication networks and to understand why too many or too few synapses during critical periods may lead to neurodevelopmental disorders, such as autism and Rett syndrome.
- He is comparing strategies of how biological and engineered networks attempt to overcome environmental noise, failures and disturbances and is making predictions of how the networks perform in different conditions.
- Navlakha’s lab is developing new algorithms to: model ancestral molecular interactions in the cell to understand how networks evolved; extract critical modules embedded within networks to predict protein function and disease-causing genes; and identify missing edges in signaling pathways.

For more information, please visit:
www.salk.edu/scientist/saket-navlakha

Computational Biology, Immunology, Neurobiology,
Plant Biology and Agriculture, Systems Biology