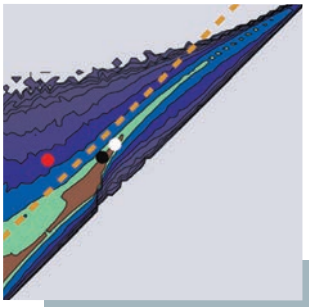

salk
Where cures begin.

# Edward Stites

Assistant Professor
Integrative Biology Laboratory

**The Problem**

Multiple checks and balances in our cellular programming mean that cancer develops only after a number of processes go awry. This is why understanding cancer at a systems level, how multiple cellular factors interact, may be able to uncover new ideas for how to treat cancer. Faulty cell signaling networks, which usher signals into the nucleus from outside the cell to change gene expression, have been implicated in cancer. Multiple drugs that target these networks have been developed and are benefitting cancer patients. A better understanding of the behavior of these networks and their component proteins may facilitate the development of treatments that benefit more patients, and that provide more benefit to each patient.

**The Approach**

Edward Stites uses mathematical and computational models to study the behaviors of signaling networks implicated in cancer. Signaling proteins operate within large, complex networks and even when the roles of individual proteins are well understood, the behavior of the network of proteins can be difficult to predict. Stites uses his methods to reveal how these networks promote cancer and respond to treatment. Mathematical models help illuminate the unknowns. They help formulate new hypotheses for experimental testing. The incorporation of data-driven models into cancer research should enable quicker and more efficient progress.

**The Innovations and Discoveries**

- Stites developed a mathematical model of the RAS signaling pathway that revealed multiple unexpected behaviors by the most common activating mutations in human cancer. This work also demonstrated how mathematical models can be used to study cancer-promoting mutations.
- It has become clear that not all mutations to the same gene behave similarly. Stites' models are capable of predicting the behaviors of different mutations to the same gene, including different responses to treatment. This suggests a role for these computational approaches in personalized cancer medicine.
- Stites' modeling found that certain mutations (such as mutations in the NF1 tumor suppressor gene) amplified the effects of other gene mutations, suggesting that certain combinations of mutations work together to drive cancer. These results were borne out with experiments using cancer cells and were observed in sequenced cancer genomes.

**For more information, please visit:**
**www.salk.edu/scientist/edward-stites**

## Cancer, Cellular Biology, Computational Biology, Therapeutics