

Ken has always been a proponent of combining computational analysis and experiments to solve complex problems in biology. Ken did his graduate work in the laboratory of Dr. James Dennis at the Lunenfeld-Tanenbaum Research Institute in Toronto, working on how the N-glycan modification pathway regulates ensembles of cell surface signaling receptors using computational modeling. Ken was the first Ph.D. graduate (2008) from the program of Proteomics and Bioinformatics (now known as Genome Biology and Bioinformatics) at the University of Toronto, Canada. He then went on to do a joint postdoctoral fellowship in the laboratories of Kevin Haigis at Massachusetts General Hospital/Harvard Medical School and Douglas Lauffenburger at MIT. There, he combined mouse genetics with network modeling to decipher how combination of signaling activities synergistically control complex phenotypes in the gut. Ken started his laboratory in the Epithelial Biology Center at Vanderbilt in March of 2013, with a primary appointment in the Department of Cell and Developmental Biology. Ken's training is truly interdisciplinary, ranging from stochastic computational modeling to surgeries on small animals. His work has been published in *Cell*, *Science Signaling*, and *PLoS Biology* to name a few.

Ken is interested in how cells communicate with its environments (including neighboring cells, cells from different systems, microbial components, etc.), and how cells process environmental data to generate in behavioral and functional outputs. Furthermore, Ken is interested in understanding the basis of why and how cells behave differently from each other in tissue, and how these behaviorally distinct cells act together in a functional organ. He believes that these multicellular communication principles can shed light on complex diseases like cancer, where a tumor is aberrantly organized to function as its own organ. To address these challenges, Ken makes use of high-dimensional technology for conducting single cell signaling analysis in intact tissues (mouse and human), and generate mathematical models of how multicellular components process information as a network. His model system currently is the intestinal epithelium, which is an organ that interacts intimately with the microbiome and immune system. He hopes that by understanding complexities at the molecular, cellular and tissue levels, one can develop better and smarter means to combat complex diseases in the clinic.