Voice disorders affect one in ten children and adults at some point over their lifetime. Vocal fold scars commonly appear after surgical injury to the vocal folds, triggering a highly complex acute inflammation and healing response. Such a response involves immune and repair cells (e.g., neutrophils, macrophages, fibroblasts) and molecules (e.g., inflammatory cytokines, damage-associated molecular pattern molecules [DAMPs]) that locate damaged tissue, eliminate the necrotic cells and debris, and produce extracellular matrix substances for eventual tissue repair.

My project focuses on the development of a computational platform that can guide surgeons and speech pathologists in the best methods to repair voices that have been lost. This project is to develop patient-specific computational models that will ultimately predict treatment responses of patients with vocal diseases. The models will help clinicians tailor their care for individual patients with enhanced voice outcomes. So far, relevant cellular data has been collected and analyzed from rats following vocal fold surgery. In particular, multi-parametric flow cytometry using up to 11 parameters were used to identify and enumerate neutrophils, macrophages, endothelial cells and fibroblasts in surgically injured rat vocal folds up to 4 weeks post injury. Time-varying dynamics for cell populations were analyzed with bivariate gating and mixed effects statistical models. The flow cytometry data will be used to expand, calibrate and validate the existing computational model of surgical vocal fold injury and repair.

The proposed project represents a crucial step for large scale systems biology modeling to improve our understanding of vocal fold injury, and enable its translation to clinical applications to predict patient-specific therapy outcomes.