Abstract:

Mathematical models are increasingly being used to better understand biological systems. These models are often validated by fitting the mathematical predictions to the average behavior observed in an experimental dataset. Here we ask the question of whether predictions made from a model fit to the average of a dataset are actually applicable in samples that deviate from the average. We will explore this in the context of a mouse model of cancer treated with two immunotherapeutic drugs. The talk will demonstrate how a mathematically optimal protocol for treating the average mouse can lack robustness, meaning the “best for the average” protocol can fail to be optimal (and in fact, can be far from optimal) in mice that differ from the average. We also show how mathematics can be used to identify an optimal treatment protocol that is robust to perturbations from the average. Time permitting, we will also explore how robustness influences the personalization of treatment protocols for individual mice.