1145-92-616 **Jana Gevertz*** (gevertz@tcnj.edu). *Robust optimization of cancer immunotherapy.*

Mathematical models of biological systems are often validated by fitting the model to the average of an often small 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 melanoma treated with two forms of immunotherapy. We have hierarchically developed a system of ordinary differential equations to describe the average of this experimental data, and optimized treatment subject to clinical constraints. Using a virtual population method, we explore the robustness of treatment response to the predicted optimal protocol; that is, we quantify the extent to which the optimal treatment protocol elicits the same qualitative response across virtual populations. We find that our predicted optimal is not robust and in fact is potentially a dangerous protocol for a fraction of the virtual populations. However, if we consider a different drug dose than used in the experiments, we are able to identify an optimal protocol that elicits a robust anti-tumor response across virtual populations. This is joint work with Eduardo Sontag (Northeastern University) and Michael Ochs (The College of New Jersey). (Received September 11, 2018)