Biology and Medicine Through Mathematics Conference

2024

May 15th, 5:01 PM

A Random Differential Equation Model to Estimate Treatment Sensitivity in Synthetic and In Vitro Tumor Growth Data

Natalie Meacham
University of California, Merced, nmeacham@ucmerced.edu

https://scholarscompass.vcu.edu/bamm/2024/wed/19

A Random Differential Equation Model to Estimate Treatment Sensitivity in Synthetic and In Vitro Tumor Growth Data

Natalie Meacham

March 2024

Resistance to treatment, which comes from the heterogeneity of cell types within tumors, is a leading cause of poor treatment outcomes in cancer patients. Previous mathematical work modeling cancer over time has neither emphasized the relationship between cell heterogeneity and treatment resistance nor depicted heterogeneity with sufficient nuance. To respond to the need to depict a wide range of resistance levels, we develop a random differential equation model of tumor growth. Random differential equations are differential equations in which the parameters are random variables. In the inverse problem, we aim to recover the sensitivity to treatment as a probability mass function. This allows us to observe what proportions of cells exist at different sensitivity levels. After validating the method with synthetic data, we apply it to monoclonal and mixture cell population data of isogenic Ba/F3 murine cell lines to uncover each tumor's levels of sensitivity to treatment.