Developing a Unique Model to Predict the Efficacy of a Revolutionary Cancer Therapy

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HER2-positive breast cancer is characterized by an overexpression of HER2, a growth receptor protein, on the surface of the cancer cell, which increases the rate of cell growth and replication of the breast cancer. Pertuzumab is a chemical which targets and binds to HER2 proteins, resulting in an inhibition of cell signaling, eventually leading to the death of the cell. Ado-trastuzumab emtansine (T-DM1) is an antibody-drug conjugate that not only binds to the HER2 protein and inhibits signaling, but also injects emtansine, a derivative of chemotherapeutic agent maytansine, into the cell following the bonding of the compound to the HER2 protein, thus killing the cancer cell. Mathematical modeling of breast cancer tumors in response to various treatment regimens of T-DM1 and pertuzumab can provide a cost effective method of analyzing dosing regimens by decreasing the number of clinical trials necessary. This goal is achieved by modifying a previously created integrated model for predicting tumor growth in the presence of two drugs by developing parameter ranges, accounting for differing cell responses to the drugs, and incorporating a multiple dosing regimen. Obtaining exact parameter values and data is the next step in the process, which will allow for the confirmation of the accuracy of the model.

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