1135-VF-3037 **Qing Wang*** (qwang@shepherd.edu), Dept. of Computer Science, Math & Engineering, Shepherd University, Shepherdstown, WV 25443, **Zhijun Wang** (zwang@shepherd.edu), Dept. of Computer Science, Math & Engineering, Shepherd University, Shepherdstown, WV 25443, and **David J Klinke** (david.klinke@mail.wvu.edu), Dept. of Chemical Engineering, West Virginia University, Morgantown, WV 25606. *A Multi-Scale Model of Tumor Growth in Response to an Anti-Nodal Antibody Therapy Combined with a Chemotherapy.*

Nodal, a member of the transforming growth factor-beta superfamily, is not typically observed in most normal adult tissues but is reactivated in various advanced-stage cancers. Recent research reported that some front-line therapies such as BRAF inhibitors as well as chemotherapy agents Dacarbazine (DTIC) and Doxorubicin (DOX) failed to affect Nodal levels in aggressive cancers such as melanoma and breast cancer tissues. Based on the in vitro work presented by Dr. Hendrix and colleagues, a mathematical model was developed to describe the effect of a combination therapy involving an anti-Nodal antibody and DOX on triple-negative breast cancer (TNBC) cell growth. Model parameters were calibrated to published experimental data using a genetic algorithm. Stability analysis and sensitivity analysis were discussed with biological relevance. This research was supported by the NIGMS of the NIH grant as part of the WV-INBRE (P20GM103434). (Received September 26, 2017)