Cancer Therapy Design Based on Pathway Logic

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Lecture Hall 143

Light lunch will be served

Cancer encompasses various diseases associated with loss of cell-cycle control, leading to uncontrolled cell proliferation and/or reduced apoptosis. Cancer is usually caused by malfunction(s) in the cellular signaling pathways. Malfunctions occur in different ways and at different locations in a pathway. Consequently, therapy design should first identify the location and type of malfunction and then arrive at a suitable drug combination.

We consider the growth factor (GF) signaling pathways, widely studied in the context of cancer. Interactions between different pathway components are modeled using Boolean logic gates. All possible single malfunctions in the resulting circuit are enumerated and responses of the different malfunctioning circuits to a ‘test’ input are used to group the malfunctions into classes. Effects of different drugs, targeting different parts of the Boolean circuit, are taken into account in deciding drug efficacy, thereby mapping each malfunction to an appropriate set of drugs.

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Aniruddha Datta received the B. Tech degree in Electrical Engineering from the Indian Institute of Technology, Kharagpur in 1985, the M.S.E.E. degree from Southern Illinois University, Carbondale in 1987 and the M.S. (Applied Mathematics) and Ph.D. degrees from the University of Southern California in 1991. In August 1991, he joined the Department of Electrical and Computer Engineering at Texas A&M University where he is currently a Professor and holder of the J. W. Runyon, Jr. ’35 Professorship II. His areas of interest include adaptive control, robust control, PID control and Genomic Signal Processing. He has co-authored 5 books and over 100 journal and conference papers on these topics. He is a Fellow of IEEE, has served as an Associate Editor of the IEEE Transactions on Automatic Control from 2001 to 2003, the IEEE Transactions on Systems, Man and Cybernetics-Part B from 2005-2006 and is currently serving as an Associate Editor of the EURASIP Journal on Bioinformatics and Systems Biology.