Award ID:
RP170387

Project Title:
Development and Validation of a Network-guided, Multi-objective Optimization Model for Cancer Data Analysis.

Award Mechanism:
Individual Investigator Research Awards for Computational Biology

Principal Investigator:
Liu, Zhandong

Entity:
Baylor College of Medicine

Lay Summary:

Chemotherapy is the most frequently used treatment in cancer. Although it has been shown to be effective in treating some cancers, a great spectrum of variation has been observed in the ability of chemotherapy to treat solid human cancers. Identifying key pathways that determine not only response to treatment but also survival is a critical step toward developing effective personalized cancer treatments.

Massive amounts of genomic, molecular, and clinical data has been generated in recent years with the goal of comprehensively characterizing human cancers. However, integration and analysis of this data is currently limited by its sheer size and complexity. To address this challenge, we have begun to develop a unique bioinformatic algorithm, known as MPA, that allows us to integrate multiple types of clinical outcome measures with patterns of gene expression. Here, we propose to further develop MPA with the goal of combing through massive data with the goal of identifying key cancer drivers that can be effectively used for therapeutic development. As part of the proposal, we intend to biologically validate the MPA using a series of primary and established ovarian cancer cell lines and patient-derived xenograft models in vivo. Our initial application of the MPA algorithm to 483 ovarian cancer profiles has identified a unique expression module that contains 9 distinct gene products. This module organized around a gene known as anaplastic lymphoma kinase (ALK) that has never before been identified as important for determining the response of ovarian cancer to chemotherapy and/or survival. We plan examine the role of ALK module in determining the response of ovarian cancer as well as at least one other genetic module identified by MPA with CPRIT support.

Long-term, we anticipate that MPA will be broadly useful for understanding the molecular basis of many different human cancers and developing more effective strategies for their prevention and treatment.