pathCHEMO: An algorithm that identifies treatment-response biomarkers to chemotherapy across all cancer types

In the last decade, several computational methods have been successfully applied to understand cancer initiation and progression through integration of genomic and epigenomic data. However, despite recent advances in discovering a wide array of novel chemotherapy agents, identification of patients with poor and favorable response prior to treatment administration remains a major challenge in clinical oncology and cancer management.

Researchers at Rutgers University have developed a novel generalizable genome-wide computational framework that identifies biomarkers via integrative pathway enrichment analysis. The framework reveals an interplay between genomic and epigenomic mechanisms that explain the complexity of a cancer patient’s response to chemotherapy. This novel computational algorithm uses integrative approach, wherein, genomic (i.e. mRNA expression) and epigenomic (i.e. DNA methylation) patient profiles are used to uncover molecular pathways with significant (epi) genomic alterations that distinguish favorable from poor treatment response. To demonstrate generalizability of the approach, the Rutgers scientists have applied the algorithm across additional chemotherapy regimens and cancer types in order to demonstrate the tools ability to accurately predict the patients’ treatment response.

Applications

A novel integrative computational algorithm which can be utilized to identify (epi) genomically altered pathways implicated in primary chemo-response and effectively classify patients who would benefit from specific chemotherapy regimens or are at risk of resistance, which will significantly improve personalized therapeutic strategies and informed clinical decision making.

Advantages

1) Only computational approach that predicts whether a patient will be sensitive or resistant to chemotherapy.

2) Builds a strong foundation for improving personalized therapeutic options.

3) Potentially helps avoid harmful side effects and improve disease course for all cancer types.

Intellectual Property & Development Status

Patent Pending. Software available. Intellectual property available for licensing and/or research collaboration.
Inventors

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Dr. Mitrofanova is a pioneer in the emerging field of biomedical informatics. She is currently an Assistant Professor of Health Informatics at the Rutgers School of Health Professions, and a research member of the Rutgers Cancer Institute of New Jersey. Dr. Mitrofanova obtained her Ph.D in Computer Science at New York University and obtained post doctoral training in Computational Systems Biology at Columbia University Cancer Center.

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