Medical Xpress

Researchers develop algorithm to find precise cancer treatments

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Gordon Okimoto. Credit: UH Cancer Center

University of Hawai'i Cancer Center researchers developed a computational algorithm to analyze "Big Data" obtained from tumor samples to better understand and treat cancer.

"A growing problem in cancer research is figuring out how to analyze the many kinds of big genomic data for different cancers. The overwhelming quantity and complexity of the data has created an analysis bottleneck that has slowed the translation of the knowledge within the data to the clinic," said Gordon Okimoto, Co-Director of Biostatistics and Informatics Shared Resource at the UH Cancer Center.

"We have figured out a way to mine these data for the benefit of cancer patients."

Okimoto and collaborators developed a computational algorithm called the Joint Analysis of Many Matrices by ITeration (JAMMIT). JAMMIT uses advanced mathematics to identify different patterns across multiple molecular data types such as gene expression and genetic mutations that when taken together accurately predicts what treatments would be best for a given cancer patient.

"The algorithm could accelerate the approval of powerful treatments for many cancers, improve clinical outcomes, and reduce costs for treating cancer. I believe this discovery can open a path to more precision medicine clinical trials that could be initated and run locally in Hawai'i," said Randall Holcombe, incoming Director of the UH Cancer Center.

Algorithm use on liver and ovarian cancer

The findings published in Biodata Mining highlight JAMMIT analysis of ovarian and liver cancer data pulled from private research labs and public databases such as The Cancer Genome Atlas (TCGA), a National Cancer Institute data archive. The analysis identified small sets of genes that accurately predict which patients would benefit most from chemotherapy. These same signatures also suggest that many of the ovarian and liver cancer patients studied would benefit from combining chemotherapy with immunotherapy.

Okimoto plans on analyzing the data for dozens of more cancers.

TeamLiver data

The liver cancer results were based in part on tissue samples collected locally by the liver cancer working group (TeamLiver). TeamLiver includes about 15 researchers and physicians from the Cancer Center and local hospitals that make up the Hawai'i Cancer Consortium collaborating on liver cancer research for more than 4 years. Hawai'i has one of the highest rates of liver cancer in the nation and the second highest liver cancer mortality rate in the U.S. (Hawaii Cancer Facts & Figures).

Startup based on JAMMIT technology

Okimoto and Thomas Wenska started SNR Analytics, Inc. The start-up is focused on securing the IP and funding for the development of a computational pipeline based on the JAMMIT algorithm for the discovery of predictive gene signatures for cancer and other complex diseases.

More information: Gordon Okimoto et al, Joint analysis of multiple high-dimensional data types using sparse matrix approximations of rank-1 with applications to ovarian and liver cancer, *BioData Mining* (2016). DOI: 10.1186/s13040-016-0103-7

Provided by University of Hawaii Cancer Center

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