Virtual review of cancer clinical trial treatment options quicker than conventional method

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Using virtual, cloud-based, interconnected computing techniques applied to 51,000 variables, researchers at Georgetown University Medical Center and colleagues reduced the time needed to assess a cancer patient's tumor profile and suitability for clinical trials from 14 to 4 days. This method also increased two-fold, over a four-year period, the number of cases that could be assessed compared to conventional methods.

That is the finding of a new study based on tumors from more than 1,700 people that was published online October 9, 2019, in the *Journal of the American Medical Informatics Association (JAMIA)*.

"Our platform is unique in that it integrates patient-specific data with genomic knowledge bases to provide a comprehensive report on potential trial enrollment opportunities," said corresponding author Subha Madhavan, Ph.D., FACMI, Chief Data Scientist and Director of the Innovation Center for Biomedical Informatics at Georgetown University Medical Center. "While the majority of the cases we examined were in pancreatic cancer, our platform was designed to be applicable to any type of advanced cancer." Madhavan is also a member of Georgetown Lombardi Comprehensive Cancer Center.

A conventional tumor board is comprised of oncologists, pathologists, and patient advocates, among others. They meet in person to review

cancer gene sequencing reports to determine if a patient's tumor has gene alterations that point to drugs that could act against those alterations. This approach is burdensome and typically does not allow tumor board review for all cases.

In their study, the researchers modeled virtual molecular tumor boards (VMTB) to assess the genetic makeup, previous treatment history and other factors for 1,725 cancer patients. They also compared VMTB outcomes with reviews by five gastrointestinal oncologists who performed tumor board duties in a conventional manner. The time spent assessing appropriate trials was noted and the results were compared to the virtual method.

Over a four-year period, the investigators found that virtual boards could make assessments based on patient tumors for over 2,000 clinical trials, more than 1,000 cancer drugs, and nearly 200 genetic biomarkers associated with targets known to be amenable to treatment. From 2014 to 2017, the number of cases assessed virtually increased from 46 to 622 compared to conventional board assessments going from 3 cases to 14.

Additionally, the virtual board process integrated comprehensive information about the distance between a patient and a potential treatment center, providing practical resources for a patient looking for a clinical trial. Notably, fewer than 5% of pancreatic cancer patients currently enroll in clinical trials, but 22% of such patients whose cases were reviewed by a virtual board enrolled in a clinical trial.

"As cancer diagnoses and treatment become more data driven and complex, a VTMB allows for deep discussions and insight into many aspects of a person's unique cancer profile," said Michael J. Pishvaian, MD, Ph.D., Associate Professor, Department of Gastrointestinal Medical Oncology, The University of Texas, MD Anderson Cancer Center, Houston, co-first author who conducted this research while at

Georgetown. "Additionally, while there are just a few immunotherapy-related biomarkers currently known for all types of cancer, VTMBs have tremendous potential, when new biomarkers are discovered, to assist in finding patients the best possible clinical trials for their treatment."

Provided by Georgetown University Medical Center

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