

Developing computational models to evaluate biomarkers (w/ Video)

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To diagnose prostate cancer, urologists, such as John Wei, and pathologists, such as Scott Tomlins, at the University of Michigan Health System, use biomarkers, which are biochemical signatures in blood, urine and tissue that suggest the disease may be present. Some biomarkers are genetic.

With support from the National Science Foundation (NSF), University of Michigan engineer Brian Denton is working with a multidisciplinary team that includes Wei and Tomlins to develop a quicker and less expensive way to evaluate biomarkers, using computational models. The researchers sift through vast medical databases and then use Denton's engineering methods to assess the most effective predictors of prostate cancer.

"Research that transitions the power of [computational modeling](#) into the health care domain has the potential to significantly impact the delivery of health care service," notes Sheldon Jacobson, program director for Operations Research in the Division of Civil, Mechanical and Manufacturing Innovation within NSF's Directorate for Engineering.

Traditionally, doctors evaluate biomarkers in clinical trials. But, those are expensive, complicated and can take decades to complete. With new biomarkers being identified regularly, Denton says computational modeling is a quicker way to identify the most promising ones. These large data sets include information about patients' test results, biomarker test results, biopsy results, and whether or not the patients have had

treatment. Then the researchers use that information to help define data-driven assumptions in order to build the computer models.

"As a discoverer of one of the [prostate cancer](#) biomarkers being tested, the TMPRSS2-ERG gene fusion, it is especially gratifying for me to see it developed clinically," says Arul Chinnaiyan, director of the Michigan Center for Translational Pathology, which is dedicated to finding new diagnostics and therapeutics for cancer patients.

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