

## **A genomics-based method to identify candidates for cancer treatment**

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### **Unmet Need**

Metastatic cancer accounts for up to 90% of all cancer deaths in the United States. Treatment at advanced stages of various cancers include immune checkpoint blockade therapy, targeted tumor therapy, cytotoxic chemotherapy, and radiotherapy. Immune checkpoint blockade treatment is an exciting new course of action among advanced stage cancer patients. However, only a minority of patients respond to immune checkpoint blockade treatment – in the U.S. in 2018, the estimate percentage of patients with cancer eligible for checkpoint inhibitor drugs was 43.63%, but less than 1% responded to the drugs. Targeted tumor therapy also come with severe side effects and a need to identify patient subgroups. Chemotherapy and radiotherapy also can lead to cancer cell resistance, damage to surrounding tissue and require a method to determine favorable candidates. There exists an urgent need for clear identification of tumor mutations that will respond favorably to late-stage cancer therapies due to the various treatments' high cost and severe side effects.

### **Technology**

Duke inventors and colleagues have developed a new genomic-based method to identify a cancer patient's response to a particular therapy. The team created a method termed Genomic Treatment Index, which is an index based on sampling different genomic changes and assigns different weights to different genomic features. This approach will allow clinicians to assign a score to a patient and predict their response to a particular therapy, including but not limited to, immune checkpoint blockade therapy, targeted tumor therapy, cytotoxic chemotherapy, and radiotherapy. The team's



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#### Meet the Inventors

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#### Publication(s)

#### External Link(s)

- [From the lab of Dr. Chuan-Yuan Li, D.Sc.](#)

ability to generate a novel genomic-based diagnostic approach allows for an open system that can be based on any number of genes and treatment types.

### Advantages

- Can use genomic data derived from either fresh or archival tumor tissues
- Continuously improved by an increasing amount of clinical data
- An open system that can be based on different numbers of genes
- Applicable to various kinds of treatment that include immune checkpoint blockade therapy, targeted tumor therapy, cytotoxic chemotherapy, and radiotherapy.

