

Genome databases, immunotherapy combination may be key in fighting cancer

Immunotherapy is being hailed as the future of cancer treatment. Harnessing the body's own immune system to attack and kill cancer cells, immunotherapy is a burgeoning field of medicine that offers a more nuanced way to treat cancer than traditional chemotherapy, which works by delivering a broad punch – often with severe side effects.

Some cancer immunotherapies have already shown standout results in clinical trials, including partial and complete responses in patients with advanced cancer. But while interest in immunotherapy is surging in the biotech and pharmaceutical space, the drugs don't work for every cancer patient. Researchers are trying to change that by identifying more high-performing immune cells that could be used to develop new immunotherapies.

Engineers from the [University of Houston](#), working with physicians from the University of Texas M.D. Anderson Cancer Center, have invented new software that can pinpoint tens of thousands – and even hundreds of thousands – of these cells. They're particularly interested in how various types of T-cells – white blood cells that play a key role in the immune system – can kill cancer cells.

The researchers have dubbed the software TIMING, which stands for Time-lapse Imaging Microscopy in Nanowell Grids, and detail the technology in [a new paper appearing in the Aug. 15 issue of the journal *Bioinformatics*](#). The field of bioinformatics combines elements of computer science and biology and has arisen from the flood of data being generated by newly available genomic sequencing tests.

The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion and analysis. Read full, original post: [How Bioinformatics Could Find The Next Breakthrough Cancer Drug](#)