New visualization software uncovers cancer subtypes

by Stephanie Dutchen

October 3, 2014

A new tool helps researchers uncover patterns among cancer patient sets. Credit: Caleydo team

(Medical Xpress)—Much of biomedical research these days is about big data—collecting and analyzing vast, detailed repositories of information about health and disease. These data sets can be treasure troves for investigators, often uncovering genetic mutations that drive a particular kind of cancer, for example.

Trouble is, it's impossible for humans to browse that much data, let alone make any sense of it.

Computer algorithms and visualization tools help. Still, many biologists and clinicians find themselves having to guess which gene or other variable might be affecting their patients; they have to develop their own custom programs to find possible correlations, analyze the results and then test likely candidates with statistical software. It can be a long, tedious process requiring skills outside their expertise.

Seeing that the toolbox isn't yet complete, computational specialists in the lab of Peter Park at Harvard Medical School's Center for Biomedical Informatics and in the lab of Hanspeter Pfister at Harvard University's School of Engineering and Applied Sciences (SEAS) have teamed up with colleagues at Johannes Kepler University Linz and Graz University of Technology in Austria to produce software that makes it easier for nonspecialists to fish out clues from an ocean of numbers.

"It's a tool to help you make sense of the data you're collecting and find the right questions to ask," said Nils Gehlenborg, research associate in biomedical informatics at HMS and co-senior author of the correspondence in Nature Methods. "It gives you an unbiased view of patterns in the data. Then you can explore whether those patterns are meaningful."

"We meet a lot of biologists who want to test their hypotheses with available data but aren't trained in statistical analysis," said Peter Park, co-senior author and HMS associate professor of pediatrics at Boston Children's Hospital. "We want to give them tools to refine their ideas and come up with new ones without having to rely on a computational person and by reducing the time spent chasing false leads."

The software, called StratomeX, was developed to help researchers distinguish subtypes of cancer by crunching through the incredible amount of data gathered as part of The Cancer Genome Atlas, a National Institutes of Health-funded initiative. Identifying...
was collected from hundreds of patients and detects patterns that might indicate significant similarities or differences between groups of patients. The software presents those connections in an easy-to-grasp visual format.

"It helps you make meaningful distinctions," said co-first author Alexander Lex, a postdoctoral researcher in the Pfister group.

"You might see that a subset of patients seems to live longer. Then you can explore whether there's a genetic variant or deletion that affects survival. You don't have to have a suspect in mind when you start," said Gehlenborg.

"It's an iterative process," added co-first author Marc Streit, assistant professor at the Institute of Computer Graphics at Johannes Kepler University Linz and visiting professor at SEAS. "You can formulate a question, get ranked results and refine the question."

Researchers can then take their refined, informed hypotheses into the clinic for further testing.

StratomeX certainly isn't the only visualization tool out there, but it is the first specifically designed to ferret out cancer subtypes. However, its potential reaches beyond cancer. Researchers can input data sets gathered on any disease and run the same kind of analyses, said Lex.

The team has made StratomeX available for download. They plan to make it web-based and hope to enhance it so it can analyze finer differences between patient groups, such as where a particular mutation occurs in a gene rather than simply whether a mutation exists.

"We want it to pick up subtler details that might play an important role in disease," said Streit.

Explore further: What's behind a No. 1 ranking? Open-source LineUp software enables granular analysis of subjective ranking systems


Journal reference: Nature Methods

Provided by Harvard Medical School

5 /5 (7 votes)

Related Stories

What's behind a No. 1 ranking? Open-source LineUp software enables granular analysis of subjective ranking systems

Jan 31, 2014

Behind every "Top 100" list is a generous sprinkling of personal bias and subjective decisions. Lacking the tools to calculate how factors like median home prices and crime rates actually affect the "best ..."

Team develops tool to better visualize, analyze human genomic data

Aug 03, 2014

Scientists at the University of Maryland have developed a new, web-based tool that enables researchers to quickly and easily visualize and compare large amounts of genomic information resulting from high-throughput ...

Recommended for you

New approach could kill tumor cells in the brain more effectively and avoid side effects

1 hour ago

Every year, about 100,000 Americans are diagnosed with brain tumors that have spread from elsewhere in the body. These tumors, known as metastases, are usually treated with surgery followed by chemotherapy, ...

Most Internet sources on prostate cancer disagree with expert panel's recommendation

5 hours ago

Only 17 percent of top-ranked consumer health websites advise against screening for prostate cancer, a recommendation made more than two years ago by the U.S. Preventive Services Task Force (USPSTF), according to a study ...
MS drug candidate also shows promise for ulcerative colitis
Positive new clinical data were released today on a drug candidate for ulcerative colitis that was first discovered and synthesized at The Scripps Research Institute (TSRI).

Gene variation links to autistic-like traits
Researchers have confirmed an association between a genetic mutation and a higher level of autistic-like traits in individuals.

Lack of new drugs is being overcome by new ways of delivering old ones
Development of new drugs for treatment of disease is an expensive, time-consuming and labour-intensive effort for both pharmaceutical companies and academics. For the past 15 years, “cost per approval” of...

Five Halloween candies to avoid for the sake of your kids’ teeth
A big sack of candy is the top priority for most children on Halloween, but with some easy substitutions, adults can offers kids treats that preserve dental health and Halloween fun.

Ebola vaccine trials to start in Switzerland this week
Ebola vaccine trials are set to start in Switzerland this week after receiving the green light from the country’s authorities, the World Health Organization said Tuesday.

Nasal spray treats heroin overdose
“Every year, drug overdoses are responsible for roughly 1000 ambulance calls in Oslo,” says Arne Sluiberg, an anaesthesiologist, a PhD candidate at NTNU and the 2014 winner of Norway’s Researcher Grand Prix...

Finding out how the nation really feels about physical education
A nation-wide survey, launched today, will use our memories of PE at school to identify how our experiences of sports days, shared showers and plimsolls have influenced our relationship with physical activity...

DNA repair enzyme can worsen tissue damage caused by stroke and organ transplantation
When tissues are deprived of blood, as happens during a stroke or heart attack, the lack of oxygen can cause serious damage. After blood flow is restored, further damage occurs as the tissues become inflamed. ...

Researchers prove mathematical models can predict cellular processes
How does a normal cellular process derail and become unhealthy? A multi-institutional, international team led by Virginia Tech researchers studied cells found in breast and other types of connective tissue...

Don’t bet on stinginess to keep stress low
Is generosity less stressful than being stingy? QUT research, published in scientific journal PLOS ONE, examined the physiological reactions of participants in a financial bargaining game and found that n...