Google Cloud

Saving Lives by Bringing Precision Medicine to Patients

Precision medicine appears to be exactly what cancer patients need. The results of the NCI (National Cancer Institute) – MATCH (molecular analysis for therapy choice) precision medicine trial, which were presented at the 2019 American Society of Clinical Oncology Annual Meeting, showed that a drug combination designed to target cancers with certain BRAF gene mutations was effective in in 35 patients with 17 distinct tumor types.[1]

Therefore, it would stand to reason that patients would opt for the precision medicine route. However, here's the problem: Because the gene sequencing required to implement precision medicine treatments is such a complicated endeavor, patients typically need to wait up to six weeks to get such treatments started – and this delay brings tremendous risk.

> So, if you or a family member is diagnosed with cancer, do you choose immediate conventional therapy, or wait three to six weeks to receive precision medicine?" asked Takayuki Yoshino, Director for the Department of Gastroenterology and Gastrointestinal Oncology and Head of the Clinical Research Coordinating Division at National Center Hospital East in Japan.

That's a difficult question to answer "as waiting three to six weeks is a very long time if you have cancer." The decision, however, needs to be balanced with the fact that survival rates are significantly better with precision medicine, and "some patients might even be cured, even those diagnosed with advanced stage cancer," Yoshino said.

The current routine

Currently, in order to initiate precision medicine cancer treatments, healthcare providers must conduct a patient visit, obtain tissue through a biopsy, and then render a pathological diagnosis, all of which takes one to two weeks. However, the creation of additional tissue slides and next generation sequencing (NGS) — a non-Sanger-based, high-throughput DNA sequencing method used to determine a portion of nucleotide sequence of an individual's genome — does add another two to four weeks into the process. While NGS is much faster than the previously used Sanger method, which required more than a decade to sequence a single gene, it still "takes too much time," Yoshino said. "It takes two to four weeks to simultaneously manage the more than 100 genes needed for each patient."

The SCRUM-Japan GENESIS Virtual Sequencing Project is addressing this challenge. Through this nationwide cancer screening initiative, more than 270 hospitals, 17 pharma companies, and 50 clinical trials are joining together to create a large-scale database composed of patient history — including clinical, medication, chemotherapy, and treatment history — as well as specimen history, adverse-event details, inspection results, medical images, and genetic information.

[1] Salama AKS, Li S, Macrae ER, et al. Dabrafenib and trametinib in patients with tumors with BRAF V600E/K mutations: results from the molecular analysis for therapy choice (MATCH) Arm H. Presented at: 2019 American Society of Clinical Oncology Annual Meeting; May 31-June 4, 2019; Chicago, IL. Abstract 3002

Google Cloud

Developing a virtual sequencing method

The project's researchers are relying upon artificial intelligence algorithms to support a virtual sequencing method identifying and categorizing cancer genome alterations based on pathology images. To create these algorithms, FFPE (Formalin-Fixed, Paraffin-Embedded) section-image and genome-analysis results are collected. Data is then used to train and verify the accuracy of the algorithm. With these virtual sequencing algorithms, it is possible to sequence genes in a matter of minutes or seconds. As a result, two to four weeks is shaved off from the current precision medicine clinical course by eliminating NGS sequencing. In addition, virtual sequencing cuts the thousands of dollars associated with NGS for each patient out of the equation.

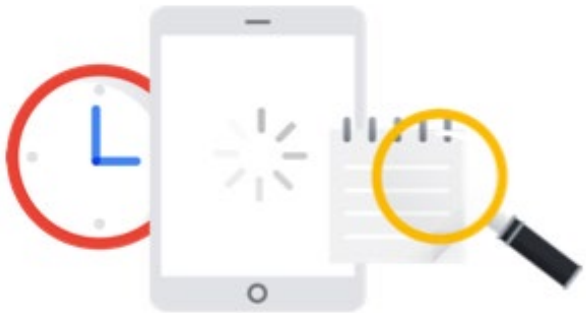
Confidence in the accuracy of the virtual sequencing is high. "Preliminary results show AUC .94, which means near perfect concordance between the NGS sequencing and the virtual sequencing," Yoshino said.

Turning to the cloud

Because of the significant volume of medical images and genome information, the project requires large storage capacity as well as "GPU intensive calculation." According to Ayatoshi Yoshizumi, Cloud Ace Chairman, the Google Cloud Platform makes this "mission-impossible" project possible by offering:

- ready-to-use servers, available at any time;
- a large number of graphics processing unit (GPU) nodes worldwide;
- a high level of security, capable of protecting medical information; and
- an excellent cost-performance balance compared to other cloud services.

In essence, the core infrastructure of the Google Cloud Platform makes it possible to securely access data, while the cloud services and application layers enable "providers and researchers to ask and answer new questions using the information they have," said Arie Meir, Google Cloud Product Manager. As such, the Japan SCRUM team is able to "essentially use data from the medical and pathology images that is equivalent to genetic information," which in turn is helping to "save time and help reduce anxiety for cancer patients" as they seek to undergo personalized medicine treatments. In the final analysis, the clinical value of virtual sequencing will be experienced by patients as the path to precision medicine treatments becomes much easier to traverse.



For more information visit the healthcare website:
https://cloud.google.com/solutions/healthcare/