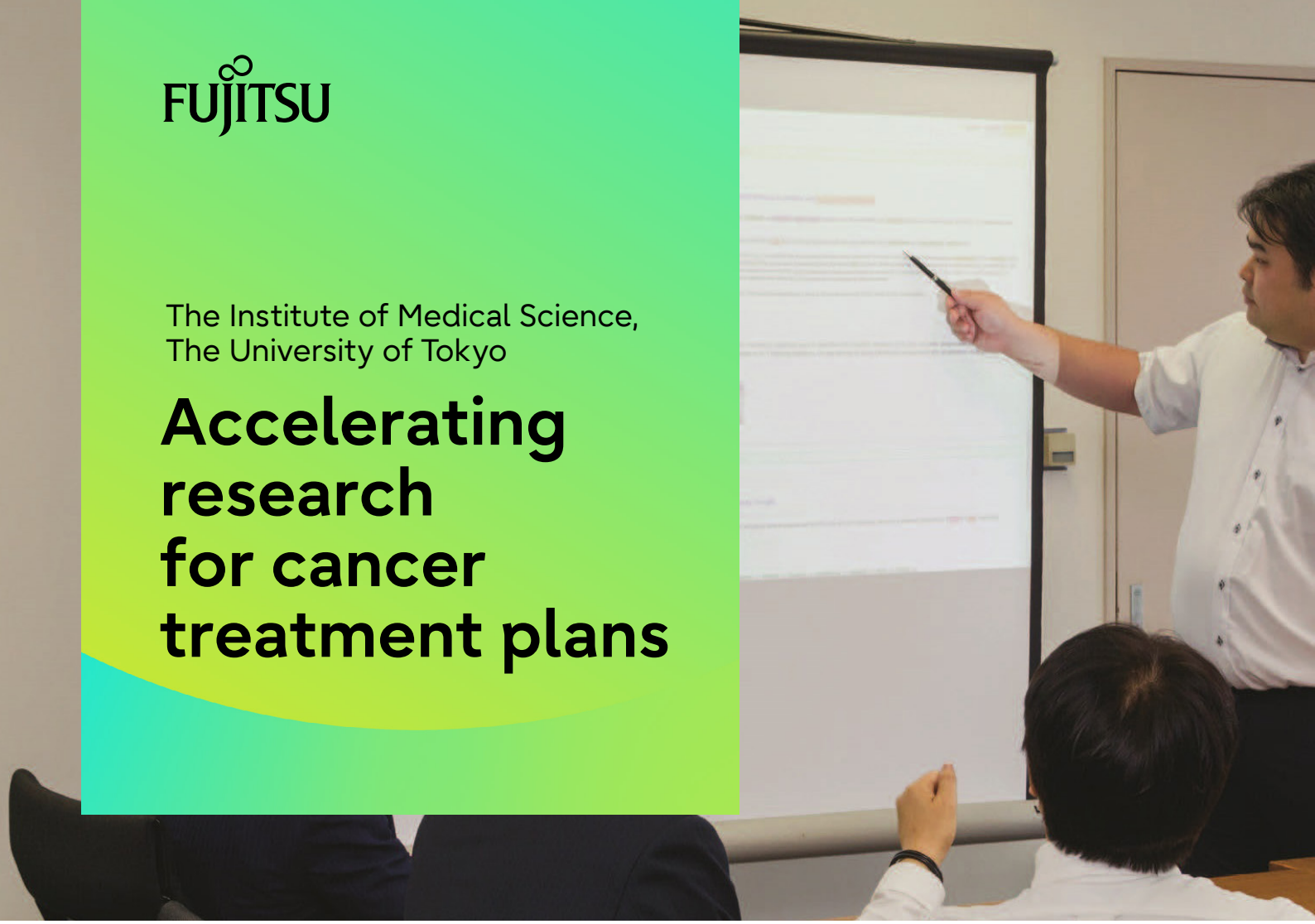
FUJITSU



The Institute of Medical Science,
The University of Tokyo

Accelerating research for cancer treatment plans

AI – halving the time spent investigating treatment plans in cancer genomic medicine.

Challenge

To make effective use of analyzed genomic information, treatment plans currently require research across multiple sources of information on mutated genomes. It takes doctors a huge amount of time to sift through the research documentation and to determine specific treatment plans, even in situations where they use only some of the genomic information available.

Solution

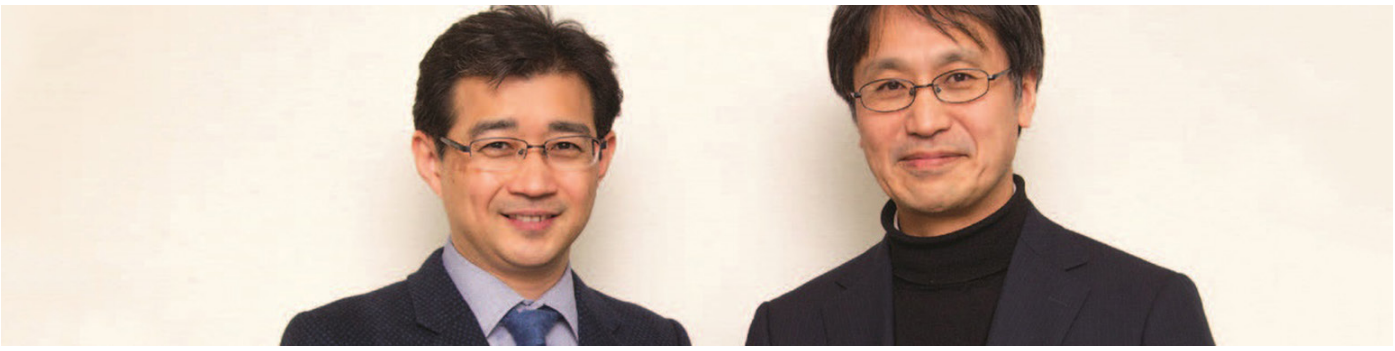
AI technology is used to discover and extract literature relating to the specific genomic data required. Relevant text is highlighted to make it easy for doctors to use. Prognostic information is also selected from graphs and tables and linked to the relevant text.

Outcomes

- The AI technology displays the key knowledge extracted from each paper, thereby reducing the time required to process the overall content
- The AI technology filters the documentation to highlight relevant papers only, more than halving the time required to review each gene variation
- The technology has the potential to overcome bottlenecks in the future when whole-genome information is used.

"This successful project was the result of applying the AI technology expertise of Fujitsu Laboratories to the needs of the medical world. The Proof of Concept demonstrated that doctors could more than halve the time to access key research which can provide the validity of treatment plans for blood tumor."

Professor Seiya Imoto, Division of Health Medical Intelligence Human Genome Center, The Institute of Medical Science, The University of Tokyo (IMSUT)



Professor Seiya Imoto - Division of Health Medical Intelligence Human Genome Center, The Institute of Medical Science, The University of Tokyo

Masaru Fuji - Research Manager AI Frontier Project Artificial Intelligence Laboratory, Fujitsu Laboratories Ltd.

50%
reduction in review times

Using AI to support the use of whole-genome information in genomic medicine

Research carried out by IMSUT's Human Genome Center includes Whole-Genome Analysis (WGA), an exhaustive study of genetic information and genomics. In the United States, WGA has already enabled a previously unmanageable disease to be cured.

There are about 22,000 human genes, but they represent only 2% of the whole genome. Furthermore, only a few hundred of these genes have been properly studied in the context of cancer-related treatments. The remaining 98% could hold the key to fighting diseases for which there is currently no cure. Professor Seiya Imoto, who leads health medicine intelligence at IMSUT's Human Genome Center, states "I believe that whole-genome research must be undertaken if we are to fight cancer."

However, implementing genomic medicine in a way that fully exploits genomic information presents a major challenge. For each mutated genome, matches with past pathologies need to be investigated in order to identify the most appropriate anti-cancer drugs. Searching for the most relevant clinical papers from a database of over 30 million documents is clearly a very time-consuming exercise.

Professor Seiya Imoto comments, "Using the data from whole-genome analysis would obviously be a massive undertaking. On top of that, the number of cancer-related academic papers is increasing at a rate of more than 200,000 every year. Solving this challenge is a vital first step to enable whole-genome analysis to contribute to medicine. We therefore decided to implement a joint research project into using AI, working with Fujitsu Laboratories, given their expertise in natural language processing."

Joint research that leverages AI to automate the investigation of treatment plans

IMSUT launched their joint research project with Fujitsu Laboratories in April 2018. The goal was to exploit AI in order to shorten the time required to investigate treatment plans. First, experts in natural language processing at Fujitsu Laboratories developed a technology to build a graph-structured database, known as a knowledge graph. Using the knowledge and expertise of IMSUT, they created a dedicated dictionary by extracting knowledge from medical literature.

As Professor Seiya Imoto explains, "We developed a mechanism to identify prognostic information. Prognostic information is often provided in graphs and tables, and is essential to determining treatment plans. However, this prognostic information is often overlooked in conventional text searches. So, we ensured this system could also identify prognostic information in graphs and tables." Masaru Fuji, Research Manager heading the AI Frontier Project at the Artificial Intelligence Laboratory at Fujitsu Laboratories, adds "We considered the ease of viewing information by highlighting the most relevant parts of papers and articles, and linking prognostic information, including graphs and tables, to the clinical papers from which they were extracted."

Industry:
Medicine

Founded:
1892

Location:
Japan

Website:
www.ims.u-tokyo.ac.jp/imsut/en/

About the customer

The Institute of Medical Science, The University of Tokyo is an affiliated institute specializing in medical research. Human Genome Center is a university research center established within IMSUT with a mission to promote human genome research and to practice genomic medicine. In the area of health and medical intelligence, research covers a wide range of fields, including human genome and symbiotic metagenomic data analysis, health and medical big data analysis and technology development, and the use of IoT devices.

Products and Services

- **Explainable AI technology (knowledge graph)**

The next step was to implement a Proof of Concept to verify effectiveness. The technology was used to mine over 860,000 medical papers and create the knowledge graph. Four physicians from the Department of Hematology and Oncology at the University of Tokyo were then asked to retrieve specific information using the knowledge graphs. This was then compared with the time it would have taken them using conventional methods. This research uses a database developed by Fujitsu Limited in cooperation with Kyoto University, as part of the "Program for an Integrated Database of Clinical and Genomic Information" (*1)(*2) under the Japan Agency for Medical Research and Development as part of the knowledge graph.

The results were impressive. Whereas it previously took an average of 30 minutes to review each gene mutation case, the new approach successfully reduced the time required to less than half that time.

Expanding the scope by trialing the technology in a medical environment

Professor Seiya Imoto believes the technology holds great promise. "If we can shape it so that it can be used in a medical environment in accordance with guidelines, it will enable genomic information to be returned to patients without delay, increasing the practical application of genomic medicine." The costs associated with genome analysis are starting to reduce, with some tests already covered by health insurance. "The time will come when all cancer patients will be able to obtain a whole-genome sequence. We must prepare for that eventuality, and this paves the way" says Professor Seiya Imoto, expressing his high regard for the results of the joint research project.

Based on the success of this project, Fujitsu believes that knowledge graphs can be extended to target a wide range of cancer types. Indeed, trials are already planned with frontline medical teams to see how this technology can contribute further.

(*1) A program based on the interim report of the Council for Promotion of Genomic Medicine Implementation, to verify the relationship between genome information and disease specificity and clinical characteristics, to develop a database that handles clinical and genomic information for clinical and research purposes, and to promote advanced research and development based on the database

(*2) AMED Grant Number: JP20kk0205013

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AskFujitsu@uk.fujitsu.com