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Fujitsu, TMDU leverage world's fastest supercomputer to perform cancer gene network analysis

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Tokyo Medical and Dental University (TMDU) and Fujitsu Laboratories Limited have recently completed, in less than a day, an estimation of the network that represents the influence relationship between genes and prediction of their relationship with infiltration and metastasis based on genes highly likely to be involved in cancer development.

TMDU and Fujitsu achieved this leveraging Fujitsu Laboratories' explainable AI technology Deep Tensor with the world's fastest supercomputer, Fugaku, which was jointly developed by RIKEN and Fujitsu.

The project was conceived under the theme of "elucidation of the cause and diversity of cancer using large-scale data analysis and AI technology" as part of the supercomputer Fugaku achievement acceleration program being promoted by Japan's Ministry of Education, Culture, Sports, Science and Technology from May 2020 to March 2023.

Even with supercomputers available at universities, it previously took several months to extract network structures representing the behavior of genes likely related to the disease state of cancer from genetic data and to predict the disease state. This presented difficulties to researchers working to discover new mechanisms of cancer that could not be understood at the individual gene level and incorporate these findings into research.

Harnessing the power of the world's fastest supercomputer, Fugaku, Fujitsu and TMDU were able to extract a network representing the regulatory relationships among genes in epithelial cancer cells from the analysis of data with 20,000 genes, predict their relationship with infiltration and metastasis using deep tensor technology developed by Fujitsu Laboratories, and present prediction models.