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G-KnowMe collaborates with researchers in UK to automate clinical interpretation of whole genome sequencing in cancer

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Genome sequencing has significantly advanced our understanding of cancer at an individual level



Bengaluru-based informatics startup G-KnowMe has entered into a partnership with researchers at the University of Cambridge and the Cambridge University Hospitals NHS Foundation Trust (CUH), United Kingdom (UK) to develop an automated workflow for interpreting data from sequencing the entire genome of cancers.

“Whole genome sequencing (WGS) of cancers is emerging as the new paradigm in cancer management as Next Generation Sequencing (NGS) technology scales and the cost of sequencing drops. But timely interpretation of the data to make informed clinical decisions is the challenge. Clinical interpretation of WGS data for the breast cancer patient management will be developed under this collaboration’’, commented Professor Jean Abraham, Director of the Precision Breast Cancer Institute at the University of Cambridge. “To achieve this at scale,” she added, “we need to rely on cutting-edge automation and natural language processing tools powered by artificial intelligence."

Tumour profiles carry information that can personalise treatment plans, predict response or resistance to approved therapies, suggest off-label therapies or relevant clinical trials for a patient, and at the same time identify any inherited basis for the cancer.

“G-KnowMe is leveraging its combined expertise in AI and cancer biology to develop solutions that enable adoption of large panels in clinical management of cancer. While our platform G-KnowMiner is already in use by large diagnostics labs the Indian market to interpret data from NGS panels used for cancer diagnostics, expanding its scope to interpreting WGS data, within a clinically relevant time frame is what we aim to achieve through this partnership”, commented Nimisha Gupta’’, Founder, G-KnowMe.