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Researchers develop expert systems for identifying treatment targets for cancer and rare diseases

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In recent months, several national initiatives for personalized medicine have been announced, including the recently launched precision medicine initiative in the US, driven by rapid advances in genomic technologies and with the promise of cheaper and better healthcare. Significant challenges remain, however, in the management and analysis of genetic information and their integration with patient data. The sheer scale and complexity of this data, generated using cutting-edge technologies such as next generation DNA sequencing, requires the development of new computer algorithms and systems that can mine this data to get actionable knowledge.

Now, scientists at A*STAR's Genome Institute of Singapore (GIS) have reported another breakthrough in the development of expert systems that can trawl large datasets, integrating complex disease information to guide doctors in the diagnosis and treatment of diseases. The latest in this series is the development of a system called OncoIMPACT that combines cancer omics data and models learned from hundreds of patients to better sift through genetic mutations and pick potentially causal ones.

The lead investigator in this study, Dr Niranjan Nagarajan, Associate Director of Computational and Systems Biology at the GIS, noted, "We are particularly excited about OncoIMPACT's ability to take into account the unique genetic makeup of each patient to predict treatment

targets. It allows us to crunch massive cancer genome datasets in an integrative and model-driven fashion to distill them down to the few key driver mutations."

Assistant Professor Johannes Schumacher from the Institute of Human Genetics at the University of Bonn, added: "The integration of different 'omics' datasets for the identification of cancer driver genes is a challenge. OncoIMPACT fills a gap in integrative analyses and provides the opportunity to revisit large complex datasets for the identification of disease driving genes."

The team of researchers at A*STAR have applied OncoIMPACT to more than a thousand cancers such as melanomas, glioblastomas, prostate, bladder and ovarian cancers, and are in the process of building a complete map of driver mutations across cancers. They also demonstrated a proof-of-concept in this study for using driver mutation signatures to predict clinical outcomes for cancer patients. This is an exciting alternative to currently available tests based on RNA and protein levels as DNA can be more reliably assayed, and the team plans to develop this work further.

Dr Nagarajan remarked, "Our hope is to create a resource for cancer researchers and clinicians in Singapore and around the world. We envisage a future where expert systems such as OncoIMPACT can leverage genomic data generated worldwide and contribute to personalised and targeted medicine in Singapore."

Dr Gopal Iyer, Principal Investigator of the Cancer Therapeutics Research Laboratory at the National Cancer Centre of Singapore (NCCS) noted, "With the availability of large amounts of genetic data, it is difficult to focus our attention on the real cause and drivers in cancers. There are a number of algorithms that help narrow this search down in groups of cancers. OncoIMPACT, however, is different as it can focus

these analyses on a single patient. This is the first step for true treatment individualisation: if we can uncover the drivers behind a tumour in a specific patient, we can ask if this can then be treated with specific drugs."

OncoIMPACT is the latest in the series of expert systems from the GIS and follows the recent publication of Phen-Gen - the first such system to cross-reference patient's symptoms with genome sequence to detect causal genes for rare diseases. Both methods fall in the emerging area of integrative omics, where complex, multi-dimensional datasets are jointly analysed with sophisticated algorithms to reveal novel biological and medical insights.

The development of OncoIMPACT was recently published in the journal *Nucleic Acids Research*, while Phen-Gen's development was published in *Nature Methods* in August 2014.

More information: The research findings described in the media release can be found in the *Nucleic Acids Research* journal, under the title, "Patient-specific driver gene prediction and risk assessment through integrated network analysis of cancer omics profiles".

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