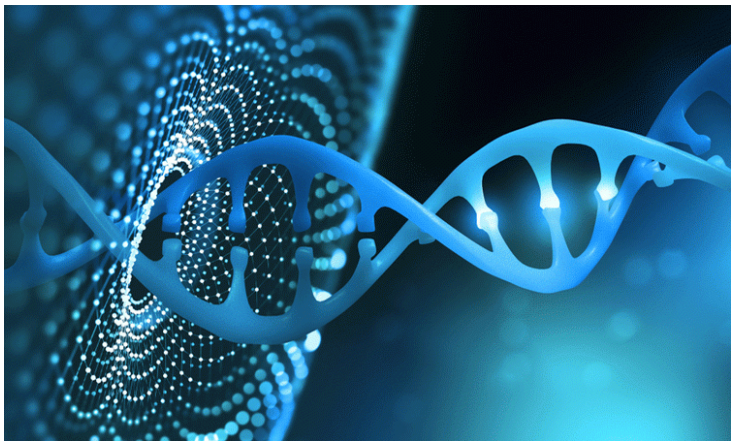
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Proteona and AI Singapore partner to improve cell therapies and IO treatments

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Innovative AI-driven genomic and proteomic analysis platform for improving cell therapy and immuno-oncology treatments through single-cell analysis of tumours and CAR T cells



Proteona Pte. Ltd., on 30 August 2019, announced its participation in AI Singapore's 100 Experiments (100E) programme to develop AI tools for single-cell multi-omics data analysis. The project is being conducted in collaboration with Prof Wong Limsoon, Kwan Im Thong Hood Cho Temple Chair Professor from the National University of Singapore (NUS) School of Computing, a leading expert in bioinformatics and computational biology. Together with Proteona bioinformaticians and data scientists, the team aims to solve key challenges in single-cell data analysis using artificial intelligence tools.

A key obstacle of single-cell data analysis is combining datasets from different sources such as different patient samples and obtaining robust cell clustering and cell-type annotation. Single-cell analysis often leads to the discovery of novel cell populations with features that had not been previously observed. Clinical samples, such as tumour biopsies, are known to be very heterogeneous, making cell type identification very challenging. Moreover, single-cell analysis is prone to noise and batch-effects that make comparisons across experiments difficult.

As a result of these challenges, cell clustering and cell annotation usually require extensive manual intervention. This is time-consuming, requires specialized knowledge and expertise, and is prone to human error and bias.

"Batch effects are prevalent in -omics data. This is particularly pronounced in single-cell measurements. Profiles from one batch are not directly compatible with that from another batch." says Prof Limsoon Wong, NUS School of Computing. "The AI-driven components here will facilitate a more convenient and explicit identification of the specific protein complexes and biological circuits relevant to cell-types and states."

With this collaboration, the team will further develop their robust computational workflows for knowledge-driven analysis, with an AI-based system trained using Proteona's in-house annotated datasets. Proteona's ESCAPE™ RNA-Seq technology and services simultaneously measure both proteomic and transcriptional expression at single-cell resolution. The developed AI-analysis will leverage this unique modality to enable deeper insights into single-cell biology.

“An immediate outcome of this collaboration will be a tool to improve the quality of results presented to our customers. It will save them time in annotating known cell types and correcting for batch effects. This platform is also used internally as a way for building our database of cell types and cell states which is then used for better annotating our customer’s data. We will also use these tools for our internal programs in biomarker discovery and diagnostic development,” says Dr Andreas Schmidt, CEO of Proteona.

“We see the merging of biotechnology and data-driven IT as one of the biggest value drivers in the health industry. With Proteona`s single-cell proteogenomic data platform the company is in a unique position to impact health decisions for therapy development and the clinic,” explains Chou Fang Soong, General Partner Pix Vine Capital, one of Proteona´s investors.

With founders Prof Gene Yeo of UCSD, Prof Jonathan Scolnick of NUS and Deputy Director of the Molecular Engineering Laboratory, A*STAR, Dr Shawn Hoon, Proteona has strong roots in cutting edge academic discoveries around the world. The Proteona - AI Singapore consortium actively seeks additional partners from the cell therapy and haematology-oncology communities to contribute to their international single-cell analysis initiative