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ASIA EDITION

Singapore scientists use AI to extract RNA modifications and functional variations

August 5, 2021 | News | By Hithaishi C Bhaskar

xPore, a software that extracts RNA modifications (an additional layer of the information above the genetic molecule RNA) from genomics data



A team of researchers from Singapore's Agency for Science, Technology and Research's (A*STAR) Genome Institute of Singapore (GIS) have developed xPore, a software that extracts RNA modifications (an additional layer of information above the genetic molecule RNA) from genomics data. Their research was published in *Nature Biotechnology* on 20 July 2021.

"RNAs have chemical molecules that may change the function of the same RNA. These RNA modifications are widespread, but because they do not change the letters of the RNA. They are very difficult to identify," said Dr Jonathan Göke, Group Leader of Laboratory of Computational Transcriptomics at GIS.

More than 100 RNA modifications are known to play different roles in cells. Some of these RNA modifications are associated with disease risk, while others are used in mRNA vaccines. In the past, identifying RNA modifications required labour- and time-intensive bench-experiment assays that only very few laboratories can perform.

To overcome these limitations, the team utilised Nanopore direct RNA-sequencing, a new transcriptomic technology that sequences native RNA molecule with its modifications retained. To extract the hidden layer of RNA modifications, they developed xPore, a machine learning-based method that re-purposes tools from AI research to precisely detect differences in RNA modifications. A property employed in the method is the consistent data of the unmodified sites, and the existence of modifications disrupts this consistency.

Dr Sho Goh, Assistant Prof from Shenzhen Bay Laboratory who co-led the study, said, "The ability to map new RNA modifications is vital for determining their functions. Since xPore does not require specific reagents that specialise in identifying only a single RNA modification type, it can potentially detect many RNA modifications. Therefore, xPore's flexibility can expedite our efforts to discover novel RNA modification functions."

Prof Patrick Tan, Executive Director of GIS, said, "This study introduces a computational method that enables the profiling of differential RNA modifications transcriptome wide, and provides a systematic resource of direct RNA-Seq data. It will be valuable as a benchmark data set for modification detection, with the potential to lead to better patient outcomes."