

Using AI to speed up vaccine development against Disease X

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Norway-based Coalition for Epidemic Preparedness Innovations (CEPI), and the Houston Methodist Research Institute (HMRI), US have announced a partnership to combine cutting-edge artificial intelligence (AI) technology with established laboratory techniques to speed up development of future vaccines against novel viral threats (also known as Disease X).

Disease X is a placeholder name that was adopted by the World Health Organisation in February 2018 on their shortlist of blueprint priority diseases to represent a hypothetical, unknown pathogen that could cause a future epidemic.

HMRI will lead a consortium including experts from Argonne National Laboratory (University of Chicago), J Craig Venter Institute, La Jolla Institute, The University of Texas Medical Branch, and The University of Texas, Austin.

CEPI will provide up to \$4.98 million to HMRI to advance the application of AI to analyse the structures of viruses from priority viral families from which the next Disease X is likely to emerge.

These AI approaches will be used to identify target pieces of protein in the virus that stimulate the immune system, known as epitopes. The HMRI-led consortium will initially focus their efforts on paramyxoviruses and arenaviruses, viral families which include the likes of Nipah virus and Lassa virus, respectively.

AI experts from the HMRI, University of Texas-Austin, La Jolla Institute, and Argonne National Laboratory (University of Chicago) will use machine-learning approaches to optimise the design of potential epitopes. The University of Texas Medical Branch will then validate the immunogenicity of these potential vaccine candidates using established preclinical models.

Should a new pathogen emerge in future, vaccine developers could quickly respond by selecting AI-identified epitopes that would have already been validated in preclinical tests, thereby enabling vaccine candidates to be moved quickly into clinical testing.