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International Conference on ALZHEIMER AND DEMENTIA

July 12, 2021 | Webinar

Artificial intelligence-based drug repositioning method and its application for alzheimer's disease

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In this study, we developed a deep learning-based computational framework that can identify potential novel therapeutic targets. Our method utilizes protein-protein interaction networks to prioritize the targets. The key technology of the method is to extract low-dimensional representations (latent features) of high-dimensional protein-protein interaction data. The framework also includes state-of-the-art machine learning techniques to infer potential drug target genes.

We applied our method to obtain novel putative target genes for Alzheimer's disease and successfully identified key genes that may serve as novel therapeutic targets (e.g., DLG4, EGFR, RAC1, SYK, PTK2B, SOCS1). Furthermore, based on these putative targets, we could infer repositionable candidate-compounds for the disease (e.g., Tamoxifen, Bosutinib, and Dasatinib).

Our deep learning-based computational framework could be a powerful tool to efficiently prioritize new therapeutic targets and enhance the drug repositioning strategy.

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