Cleveland Clinic Innovations

PRODUCT
Prediction model

INDICATION
Drug discovery, development and repurposing

VALUE PROPOSITION
- Incorporates chemical, genomic, phenotypic, and cellular networks
- Self-learning capabilities to uncover, model, and capture underlying chemical structure and semantic relationships between multiple of drug or target nodes in the heterogeneous network

DEVELOPMENT STAGE
Computational model validated for drug repurposing for multiple sclerosis in vivo

INTELLECTUAL PROPERTY
Patent Pending

RELATED PUBLICATIONS
Zeng, Xiangxiang et al. "Target identification among known drugs by deep learning from heterogeneous networks." Chemical science vol. 11,7 1775-1797. 13 Jan. 2020.

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DeepDTnet: Prediction Model for Drug Discovery, Development, Repurposing

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UNMET NEED

Drug discovery and development is currently a long and expensive endeavor, with a high failure rate (an average of 12 years from preclinical testing to final approval, at an estimated cost of $3 billion, with an 80-90% failure rate). Disease complexity paired with lack of knowledge of the complete drug-target information is a significant challenge for new drug discovery and development strategies. Unintended therapeutic effects and/or multiple drug-target interactions can lead to off-target toxicities and/or suboptimal effectiveness, which contribute to high failure rates at the expensive and time-consuming clinical trial stage.

SOLUTION

Computational approaches offer novel, testable hypotheses for systematic, unbiased identification of molecular targets. DeepDTnet systematically embeds 15 types of chemical, genomic, phenotypic, and cellular networks and applies a deep neural network algorithm to learn a low-dimensional vector representation of the features for each node. After learning the feature matrix *X* and *Y* for drugs and targets DeepDTnet applies Positive-Unlabeled (PU)-matrix completion learning framework to find the best projection from the drug space onto the target (protein) space, such that the projected feature vectors of drugs are geometrically close to the feature vectors of their known interacting targets. DeepDTnet then infers new targets for a drug ranked by geometric proximity to the projected feature vector of the drug in the projected space to aid in the prediction of drug-target interactions (DTIs), drug repurposing and/or characterization and prediction of adverse effects. For example, DeepDTnet-predicted topotecan, drug approved for treatment of ovarian and small cell lung cancer, reverses experimental autoimmune encephalomyelitis (EAE), a mouse model of multiple sclerosis.