Network propagation models predicts cancer drug responsiveness

Technology #cu15136

The varied genetic pathways that result in different cancers can be difficult to distinguish, complicating diagnosis and treatment. There is a need for sound predictive models that can identify different cancers and their potential treatments by their genotypes, but to date most models cannot reliably predict drug responsiveness that is consistent with known biological pathways. This technology is a predictive model for cancer diagnosis that yields improved drug responsiveness data. It can accurately predict the drug responsiveness of different cancers, leading to more effective treatments and patient outcomes.

Integrated method prioritizes gene expression features that predict drug response

The predictive model described by this technology incorporates tumor genetic information, pharmaceutical data, and knowledge of protein-protein and drug-protein interactions. This helps to ensure that drug responsiveness data is related to specific gene expression signatures that respond eliminating hits caused by random chance or that are counter to understood biological mechanisms of cancer growth.

As a proof of concept, this technology has been used to more accurately predict the responsiveness of cancers to the drug BMS-754807 based on their gene expression levels. Studies of other pharmaceutical agents are ongoing.

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Applications:

- Development of personalized cancer treatment plans
- Research tool for identifying cancer drug targets
- Research tool for identifying known drugs as potential cancer treatments
- Research tool for predicting treatments for drug-resistant cancers
Advantages:

- Improved predictive power over other models
- Drug responsiveness data is correlated with known biological mechanisms
- Allows for screening of drugs for drug-resistant strains of cancer

Patent Information:

Patent Pending

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