Global network of adverse drug effects

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Abstract

**Background:** Many clinical trials failed due to lack of drug efficacy and safety concerns. Therefore, there is a need to develop new methodologies in order to have a better understanding of the biological mode of action of drugs, to optimize therapeutic benefits and to avoid adverse effects. Among them, computational methods present a new opportunity in toxicity research in drug development, and allow as well to reduce the use of animal testing and drug development costs.\textsuperscript{1}

**Methods:** In order to describe the complex qualitative relationships between adverse drug effects and biological components, we have compiled information such as drug-side effect associations from public databases. The next step is to integrate these data to create a network-based model in order to determine potential adverse outcomes connections. To do it, we will take advantage of the protein-protein associations network methodology previously developed in the team, which has been validated.\textsuperscript{2,3}

**Results:** The computational model under development will statistically allow prediction of potential novel connections between adverse effects, the aim being to provide a global mapping of adverse drug effects relationships and to suggest the risk of adverse drug reactions for molecules before they reach the market.

Bibliography:

