Global network of adverse drug effects

Wu Q[1,2], Taboureau, O.[3], Audouze K.[2]

[1] qier.wu@etu.parisdescartes.fr
[2] *Université de Paris, Inserm UMR S-1124, T3S, MetaTox team, SysTox group, 75006 Paris, France*
[3] *Université de Paris, CMPLI (U1133), unité BFA (UMRS 8251), 75013 Paris, France*

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.[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.[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 :

[1] BARRATT, Michael J. et FRAIL, Donald E. (ed.). Drug repositioning: Bringing new life to shelved assets and existing drugs. John Wiley & Sons, 2012.
[2] TABOUREAU, Olivier et AUDOUZE, Karine. Human Environmental Disease Network: A computational model to assess toxicology of contaminants. ALTEX-Alternatives to animal experimentation, 2017, vol. 34, no 2, p. 289-300.
[3] AUDOUZE, Karine, JUNCKER, Agnieszka Sierakowska, ROQUE, Francisco JSSA, et al. Deciphering diseases and biological targets for environmental chemicals using toxicogenomics networks. PLoS computational biology, 2010, vol. 6, no 5, p. e1000788.