

Searching for side effects

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Extracting relevant information from the scientific literature about side effects and adverse drug reactions to pharmaceutical products is an important part of data mining in this area. Writing in the *International Journal of Data Mining and Bioinformatics*, a team from China has developed a new search strategy that offers the optimal trade-off



between retrieving pertinent abstracts and coping with the vast amounts of information available.

The team's "corpus-oriented perspective on terminologies" of side effect and ADRs could be, they suggest, an important tool in a thriving area of pharmaceutical research and development – drug repurposing.

Alex Chengyu Fang of the Department of Linguistics and Translation, at City University of Hong Kong, Yemao Liu, Yaping Lu, and Jingbo Xia of the College of Informatics at Huazhong Agricultural University, Jing Cao of Zhongnan University of Economics and Law, Wuhan, China, describe their approach as offering a useful compromise between the relevance of the content retrieved given a large body of work. The terms "side effects" and "adverse drug reactions" are commonly used interchangeably and the latter might in some sense be considered a euphemism of the former term used by members of the public.

Indeed, side effects and ADRs are synonyms. The two, of course, have many hyponyms, terms that are essentially related to examples of both side effects and ADRs, which by definition are the hypernyms to those hyponyms. These terms too must be retrievable by any data mining algorithm that analyses a body of work and is intent on seeking relevant abstracts discussing the "hypernyms. Phrases such as "adverse drug event", "drug toxicity", "undesirable effects", and others all fall into the same clade and so must be involved in the retrieval.

More information: Alex Chengyu Fang et al. A corpus-oriented perspective on terminologies of side effect and adverse reaction in support of text retrieval for drug repurposing, *International Journal of Data Mining and Bioinformatics* (2019). DOI: 10.1504/IJDMB.2018.097684



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