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iATC-mISF: a multi-label classifier for predicting the classes of anatomical therapeutic chemicals

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A correction has been published: Bioinformatics btx387.

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Abstract

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Motivation: Given a compound, can we predict which anatomical therapeutic chemical (ATC) class/classes it belongs to? It is a challenging problem since the information thus obtained can be used to deduce its possible active ingredients, as well as its therapeutic, pharmacological and chemical properties. And hence the pace of drug development could be substantially expedited. But this problem is by no means an easy one. Particularly, some drugs or compounds may belong to two or more ATC classes.

Results: To address it, a multi-label classifier, called **iATC-mISF**, was developed by incorporating the information of chemical–chemical interaction, the information of

the structural similarity, and the information of the fingerprintal similarity. Rigorous cross-validations showed that the proposed predictor achieved remarkably higher prediction quality than its cohorts for the same purpose, particularly in the absolute true rate, the most important and harsh metrics for the multi-label systems. **Availability and Implementation:** The web-server for **iATC-mISF** is accessible at http://www.jci-bioinfo.cn/iATC-mISF. Furthermore, to maximize the convenience for most experimental scientists, a step-by-step guide was provided, by which users can easily get their desired results without needing to go through the complicated mathematical equations. Their inclusion in this article is just for the integrity of the new method and stimulating more powerful methods to deal with various multi-label systems in biology.

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Supplementary information:Supplementary data are available at *Bioinformatics* online.

Issue Section: Sequence analysis

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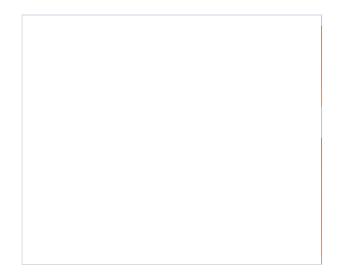
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