A Network-Based Drug Repositioning Approach

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Abstract: The high cost and the long time required to bring drugs into market is to repurpose FDA approved drugs to find new uses for which they weren't intended, and it cause to reduce the overall cost of commercialization, and shorten the delay between drug discovery and availability [1][2]. In comparison to traditional drug repositioning, which relies on clinical discoveries, computational methods can simplify the drug development timeline even further [3]. In this study we propose a novel network-based approach to drug repositioning. Our method integrate various heterogeneous biological networks to obtain new drug candidates for a given disease. These networks include: protein-protein interaction network; gene-disease network; drug-target interaction network; drug-gene network; gene-gene network; drug-disease network suggest new drug candidates for treating breast, prostate and colorectal cancers. Our method showed an acceptable performance on a new published benchmark dataset from the CTD, Drugbank, Disgenet, Uniprot, Dailymed, database than the Predict report, and with the merge obtained from data from drug data, proteins and genes, we were able to make new drugs for breast and prostate and colorectal cancer [1][3]. The method appears to recommended promise for the identification of multi-target of drug candidates that can improve other disease. Particularly the computational performance exceeded that of existing computational method [4]. The suggested approach has the possibility to provide a more efficient drug combination pipeline.

Keywords: drug repositioning [1], network [2], computational method[3], drug-disease[4]

References

[1] A. Gottlieb, G. Y. Stein, E. Ruppin, and R. Sharan, "PREDICT : a method for inferring novel drug indications with application to personalized medicine," Mol. Syst. Biol., vol. 7, no. 496, pp. 1–9, 2011.
[2] J. Li, S. Zheng, B. Chen, A. J. Butte, S. J. Swamidass, and Z. Lu, "A survey of current trends in computational drug repositioning," vol. 17, no. March 2015, pp. 2–12, 2016.
[3] L. Yang, Q. Xie, D. K. Rajpal, P. Sanseau, and P. Agarwal, "Computational Drug Repositioning : From Data to Therapeutics," no. November 2012, 2013.
[4] A. S. Brown, S. W. Kong, I. S. Kohane, and C. J. Patel, "ksRepo : a generalized platform for computational drug repositioning," BMC Bioinformatics, pp. 1–5, 2016.