Article

Design of a common pathway drug for all types of cardiovascular diseases: A network biology approach

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Abstract

More than an era among all non-communicable diseases, cardiovascular diseases have become a major concern worldwide. Cardiovascular diseases have occurred around the world because of some common risk factors. Diseases have a genetic association indirectly or directly resulting from similar risk factors. A disease is caused when a gene misses out its normal activity and affects the body negatively. Several research works have revealed the ways of how a structure-based drug from key biomolecule or protein can be designed for diseases using modern bioinformatics techniques and tools in network biology. This study evaluates protein-protein interaction network and designs a common pathway drug for all types of cardiovascular diseases. The data mining application called knowledge discovery in database (KDD) has been applied and genes are filtered, pre-processed, transformed and mined to identify common cardiovascular disease genes. Cardiovascular disease genes are collected using R from the National Center for Biotechnology Information gene database. Unihi is used as a tool for achieving the goal.

Keywords cardiovascular disease; data mining; R; protein-protein interaction network; drug design.

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1 Introduction

Bioinformatics is the solicitation of information technology that analyzes living data and addresses biological problems. Integration of tools, databases and methods are endeavoring to solve biological problems (Zhang, 2016b). The invention and absorption of new drugs are the main concern in pharmaceutical and biomedical research (Rask-Andersen et al., 2011). Genomics, proteomics as well as drug design are the united working areas in bioinformatics to lead drug discovery (Anderson, 2003; Burbaum and Tobal, 2002; Iqbal et al., 2014). At present, network biology figures out new common pathways or interrelation mechanisms among various diseases affected by disease genes based on their sub-networks (Zhang, 2011, 2016a-b, 2018; Zhang and

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