عنوان مقاله:

Colorectal cancer driver gene detection in human gene regulatory network using independent cascade diffusion model

محل انتشار:

اولین کنفرانس ملی سیستم های پیچیده با محوریت علم شبکه (سال: 1400)

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خلاصه مقاله:

one of the important topics in oncology for treatment and prevention is the identification of genes that initiate cancer in cells. These genes are known as cancer driver genes (CDG). Identifying driver genes is important both for a basic understanding of cancer and for helping to find new therapeutic goals or biomarkers. Several computational methods for finding cancer driver genes have been developed from genome data. However, most of these methods find key mutations in genomic data to predict cancer driver genes. These methods are dependent on mutation and genomic data and often have a high rate of false positives in the results. In this study, we proposed a network-based method, GeneIC, which can detect cancer driver genes without the need for mutation data. In this method, the concept of influence maximization and the independent cascade model is used. First, a cancer gene regulatory network was created using regulatory interactions and gene expression data. Then we implemented an independent cascade propagation algorithm on the network to calculate the coverage of each gene. Finally, the genes with the highest coverage were introduced as driver genes. The results of our proposed method were compared with ۱۹ previous computational and network methods based on F-measure metric and the number of detected drivers. The results showed that the proposed method has a better outcome than other methods. In addition, more than ۲۵.۴۹% of the driver genes reported by * Corresponding author. Room No. ۲۱۰, ۲nd Floor, Information Technology Engineering group, School of Systems and Industrial Engineering, Tarbiat Modares University (TMU) Chamran/Al-e-Ahmad Highways Intersection, Tehran, P.O. Box ۱۴۱۱۵-۱۱۱, Iran. GeneIC are new driver genes that have not been reported by any other .computational method

کلمات کلیدی:

;Gene regulatory network; Driver genes; Influence maximization; cancer; Independent Cascade

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