

Gene regulatory network construction of ovarian cancer based on passing attributes between network for data assimilation

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ABSTRACT

In the field of cancer informatics, there are computational methods or approach exists to share the same goal, which is to unravel the interactions between genes through the effort of gene regulatory network (GRN) inference and construction. Even now, such a complex task has always been challenging and at the same time, this challenge becomes a motivation for new methods to be invented. Hence, the development of PYPANDA, which is a new method for applying the assimilation of several different datasets input for the construction of the gene regulatory network. Moreover, this integration model is capable of redeeming information that was lost when using other methods that only utilize a single dataset, thus having an innate capacity of predicting a more accurate interaction between genes. The proposed improvement of PYPANDA in this article has been able to filter and determine the most informative or significant genes for the construction of the GRN. With this, the differences between the prior network and the improved PYPANDA network can be specified. As such, two new relationships between the highly informative genes that have not been identified before were successfully identified.

KEYWORDS

Ovarian cancer; Gene regulatory network; Python; Informative genes; Machine learning

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