عنوان مقاله:

A Framework for Improving the Predictive Model of Breast Cancer Recurrence

محل انتشار:

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خلاصه مقاله:

Breast cancer recurrence (BCR) is therapeutically a giant difficulty that is principally not well implicit. To precisely predict prognosis and recognize patients who can take survival advantages from adjuvant therapies we need to identify biomarkers for the risk of BCR. Previous studies on prediction of BCR applied various feature selection algorithms to discover oncogenes from the gene expression microarray data. Whereas, the biomarkers introduced by different methods are inconsistent and have less predictive power in other independent breast cancer datasets, they are not reliable for biological interpretation [۱]. The inconsistency problem has been addressed with a mixture of causes including: the lack of sufficient and homogenous samples [۲], curse of dimensionality and different technological platforms in microarray data analysis, and independent analysis of genes [۳]. Recently, we proposed a feature-scoring criterion to select a stable gene set from microarray data with a good prediction power in independent datasets [۳]. In this paper, we attempt to draw a more organized picture of the BCR hallmarks to provide a systematic viewpoint of gene signature sets, which obtained by the mentioned in-house developed method. In our previous efforts, using protein-protein interaction (PPI) network led to increase the stability and repeatability of the introduced biomarkers. We believe that the proposed viewpoint of gene signature sets drawn here can be useful for constructing a framework that help us to redefine gene neighborhood concept in common pathways such as one used in PPI network in order to improve the previous predictive model.

کلمات کلیدی:

Breast cancer recurrence, prediction, cancer hallmarks, biological pathways

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