Quantification of Pathological Bias in the Signalome Level Analyzing the Transcriptome-Wide Data

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Recently, we have proposed a method for aggregation of gene expression data into special subsets that may be used for characterization and quantification of pathological changes for individual patients at the level of virtually every known cell signaling pathway. The quantitative measure of relative pathological changes, whether it is over-activation or inhibition, of each signaling pathway, which we have suggested in our software packages OncoFinder [1] and GeroScope [2], accumulates the transcriotomic data on gene expression for the normal an pathological cases. The results obtained shows that the aggregation of the transcriptomic data on the pool of genes into higher-level sets that correspond to distinct signaling pathways can restore the correlation between the mirroarray and RNA sequencing data, thus extracting the meaningful signal from the transcriptome-wide noise. We also apply our method for pathway perturbation analysis to the search for markers of cancer types with different morphology and localization. For each of eight nosologic forms that we have found the specific pathway markers, as well as discriminators of one cancer type from another.

References

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