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The contribution of White Blood Cells' gene expression in prediction of gastrointestinal cancer

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Background: Gastrointestinal cancer (GI) remains one of the most deadly and common types of cancer worldwide. The early detection of GI cancer contributes in designing more efficient treatment algorithms and therefore reduction in mortality rates. The present study aimed to introduce and evaluate a non-invasive and sensitive technique, able to distinguish between normal and GI cancer samples. The recommended assay is based on the synergy of molecular biology with artificial neural networks.

Figure 1: Delta Ct qPCR Data among all samples. The higher the DeltaCt the lower the gene expression.

Methods: The data set included healthy samples as well as GI cancer patients from a variety of cancer types (colon, pancreatic, stomach etc.) at different stages. In particular, from 60 samples (in a ratio of healthy-cancer approximately 1:1), a small quantity of whole blood was removed, and white blood cells were further isolated. Then, total RNA extracted and qRT-PCR reactions for more than 50 different genes were performed. The chosen genes consist of common oncogenes, tumor suppressor genes, and/or genes associated with key cellular processes (metastasis, apoptosis, signaling pathways etc.). The calculated DeltaCt values were provided as input to a supervised pattern recognition model for the classification between healthy subjects and cancer patients. The model was an artificial neural network ensemble, designed and built deploying the Bagging (Bootstrap Aggregating) method, while its performance was evaluated by 10-fold cross validation.

Results: The average accuracy of the ensemble was 90.24% (±13.95), achieving a high rate of identification, namely the ensemble predicted the correct class (healthy or GI cancer) in almost all cases. The specificity and sensitivity of the method calculated at 87.5% and 90.63% respectively.

Conclusions: These preliminary results indicate that the proposed system, namely the exploitation of qPCR data by neural network ensembles, can be very helpful towards a more accurate and less time consumable prognostic method of GI cancer. The above system is not affected by the stage or particular type of cancer. Further studies in more samples and different types of cancer, are required for the verification of this method at clinical level.

Selected References:

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