ABSTRACT

A METHOD FOR IDENTIFICATION, PREDICTION AND PROGNOSIS OF CANCER AGGRESSIVENESS

A survival model, for each of one or more pairs of genes, includes a function of a corresponding measure of the ratio of expression levels of the pairs of genes. For each pair of genes, there is a corresponding a cut-off value, such that patients are classified according to whether the corresponding measure is above or below the cut- off value. It is proposed (in an algorithm called "DDgR") that the cut-off value should be selected so as to maximise the separation of the respective survival curves of the two groups of patients. It is further proposed that, for each of a number of genes or gene pairs, a selection is made from multiple survival models. The selection is according to whether a proportionality assumption is obeyed and/or according to a measure of data fit, such as the Baysian Information Criterion (BIC). Specific gene pairs identified by the methods are named.

Fig. 3