A METHOD FOR EXTRACTING IMAGING CORRELATIONS WITH ALTERATIONS IN GLOBAL GENE EXPRESSION

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PURPOSE

The high parallelism of data produced by cDNA microarrays requires the use of automated techniques to allow portable applications of the algorithms created to answer a wide range of clinical questions. We implement here an algorithm to evaluate the correlation of imaging features with global gene expression and their significance.

METHOD AND MATERIALS

An imaging dataset obtained from evaluation of 20 magnetic resonance (MR) scans of 20 solid tumors across 9 pre-defined variables was first evaluated and then coded into a categorical imaging scoring schema (binary or tertiary values) without knowledge of the underlying genomics. Next, cDNA microarray data representing 23,000 clones performed on the 20 corresponding tumors was filtered to a set of well measured clones based on data distribution. A stand alone script was then generated to correlate each independent imaging variable against every gene in this set, and significance measured using a conservative cut-off criterion.

RESULTS

Categorical coding of the imaging data was achieved in all 20 samples across all imaging parameters. Gene set reduction of the 23,000 cDNA microarray data resulted in a set of ~2300 clones whose expression varied most significantly across all tumor samples. Four of 9 imaging parameters showed statistically significant correlation ($p<0.05$) with gene expression using our method. Interestingly, we were not only able to capture well measured significant genes correlating to our imaging parameters but the algorithm also appeared to maintain the natural functional organization of gene expression into gene clusters (e.g. hypoxia, proliferation, immune etc). It also allowed for concurrent visualization of the entire data set to determine how each imaging parameter correlated longitudinally across the entire gene set and enabled us to identify the directionality of gene regulation relative to each significant imaging parameter.