

David Lowe:

The Impact of Uncertainty on Gene Prognostic Indicators in Automated Cancer Prognosis

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Data uncertainty in information processing support environments can be a major factor affecting life-critical decisions.

The use of gene expression values extracted from high dimensional DNA microarrays for patient-specific cancer prognosis has recently led to the proposal that a small subset of special “Prognostic Genes” are capable of discriminating good from poor cancer prognosis. This prognosis is at a patientspecific level and has generated much international and media interest. These studies have now been transferred to clinical use for predicting the likely recovery of breast cancer patients, and commercial companies have been established to provide such analysis of patients’ gene expression profiles.

However, by incorporating knowledge of uncertainty, this claim of a unique low-dimensional “Prognostic Gene List” is very probably false, and likely to be the result of a naive approach to assisted decision support.

In this talk I discuss how the existence of a Prognostic Gene List is at first plausible, given the evidence of discriminative models, but that a careful consideration of incorporating uncertainty knowledge explicitly in automated machine learning approaches can disrupt this naive view. I will discuss how the use of uncertainty modifies the decision making process in supervised classification, and how unsupervised topographic visualisation algorithms can be modified to incorporate uncertainty. These modifications produce alternative descriptions of patient-specific data rendering the use of PGL’s useless.

The thesis of this talk is that in life-critical areas such as medical applications of cancer prognosis, it is misleading or dangerous to ignore potentially vital knowledge of uncertainty.

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