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INTERVAL CODED SCORING
TOWARDS DATA-DERIVED MEDICAL SCORING SYSTEMS

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ABSTRACT

In an expanding biomedical field, ever more data is made available to clinicians due to newly arising modalities or newly defined features on known signals. It allows to draw more powerful conclusions, but also complicates a clinician's task: he or she might easily be overwhelmed by the amount of information. As a result, many attempts have been made to create clinical decision support systems [1]. Several well-known machine learnings techniques allow for e.g. classification tasks. However, common techniques are mostly black boxes, whereas interpretability is a key requirement for acceptance in a clinical environment.

Already since decades ago, medical scoring systems have been used to summarize medical knowledge and serve as decision support. One example is Alvarado for appendicitis [2]. It indicates important variables and references values, attributing points if these have been exceeded. The total score relates to a risk of (in this case) appendicitis. However, such scoring systems are based on experience and rules of thumb rather than objective evidence. We propose a framework for semi-automatic extraction of such systems from measured data.

The system we propose, Interval Coded Scoring (ICS) [3], combines a specific data representation with sparse optimization. First, every variable is expanded to binary features corresponding to statistically-derived bins in its range. Every bin gets a separate weight. Finally, sparse total variation optimization techniques allow to both reject uninformative initial variables and to derive a simple model with as few ranges per variable as possible. The approach is semi-automatic in the sense that the user indicates the acceptable trade-off between model simplicity and performance by selecting a regularization parameter .

The ICS approach has been successfully tested to detect both main effects and interactions in a synthetic data set. The influence of noise and training set size have been quantified. Moreover the scaling of the execution time with both the set size and the number of variables has been determined. This sensitivity analysis presents evidence of the potential of the system for real biomedical applications. Moreover, its usefulness has been demonstrated on public data sets from the UCI Machine Learning database, with highly accurate results.

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