

Michael R. Berthold
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Preface

We are proud to present the proceedings of the seventh biennial conference in the Intelligent Data Analysis series. The conference took place in Ljubljana, Slovenia, September 6-8, 2007. IDA continues to expand its scope, quality and size. It started as a small side-symposium as part of a larger conference in 1995 in Baden-Baden (Germany). It quickly attracted more interest in both submissions and attendance as it moved to London (1997) and then Amsterdam (1999). The next three meetings were held in Lisbon (2001), Berlin (2003) and then Madrid in 2005. The improving quality of the submissions has enabled the organizers to assemble programs of ever-increasing consistency and quality. This year we made a rigorous selection of 33 papers out of almost 100 submissions. The resulting oral presentations were then scheduled in a single-track, two-and-a-half-day conference program, summarized in the book that you have before you.

In accordance with the stated IDA goal of “bringing together researchers from diverse disciplines,” we believe we have achieved an excellent balance of presentations from the more theoretical – both statistical and machine learning – to the more application-oriented areas that illustrate how these techniques can be used in practice. For example, the proceedings include papers with theoretical contributions dealing with statistical approaches to sequence alignment as well as papers addressing practical problems in the areas of text classification and medical data analysis. It is reassuring to see that IDA continues to bring such diverse areas together, thus helping to cross-fertilize these fields.

Organizing a conference such as IDA is not possible without the assistance and support of many individuals. We are particularly grateful to Tina Anžič and Heather Fyson, who worked tirelessly behind the scenes. Ingrid Fischer worked with Richard van de Stadt to make sure the proceedings were finished flawlessly in time for the meeting. But, crucially, putting together a program of assured quality was only possible through the detailed refereeing of the members of the Program Committee, many of whom also submitted papers and attended the conference.

September 2007

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Compact and Understandable Descriptions of Mixtures of Bernoulli Distributions

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Abstract. Finite mixture models can be used in estimating complex, unknown probability distributions and also in clustering data. The parameters of the models form a complex representation and are not suitable for interpretation purposes as such. In this paper, we present a methodology to describe the finite mixture of multivariate Bernoulli distributions with a compact and understandable description. First, we cluster the data with the mixture model and subsequently extract the maximal frequent itemsets from the cluster-specific data sets. The mixture model is used to model the data set globally and the frequent itemsets model the marginal distributions of the partitioned data locally. We present the results in understandable terms that reflect the domain properties of the data. In our application of analyzing DNA copy number amplifications, the descriptions of amplification patterns are represented in nomenclature used in literature to report amplification patterns and generally used by domain experts in biology and medicine.

1 Introduction

In data analysis, the model should absorb the essentials about the data measured from a phenomenon and abstract away the irrelevant details about a particular data set. Parsimonious representations aim at particularly compact and simplified models. These kind of models offer an appealing basis for understanding and describing a phenomenon of interest. Previously, we have investigated parsimonious model representations in ecology [12], where we predicted nutrient concentrations in coniferous trees with a sparse regression methodology. In a time series prediction context, we have proposed a fast input selection method for long-term prediction [14] using a filter strategy. This strategy selects a possibly non-contiguous set of autoregressive variables with linear techniques and builds more complex non-linear prediction models using only the selected variables. In our experience, the parsimonious models are highly desired by domain experts, for instance, in biology, medicine, and ecology. In the models mentioned above, we have included roughly ten percent of the variables (in fact, parameters) compared to the models represented by all the parameters (full models). The sparse models still produce as accurate predictions as the full models. Another line of

research where an attempt is made to concisely describe a data set is reported in [15]. We have presented a tool for automatically generating data survey reports for the modeler to be aware of the properties of the data set. While technically slightly different, the spirit still remains the same as in the current work: the focus is on describing the cluster structure and the contents of the clusters. The aim of the current paper is to present a way to summarize a finite mixture model for 0-1 data concisely and with a simple, domain-compatible representation.

Our research has been motivated by work in analyzing DNA copy number amplifications represented as 0-1 data by profiling [9] and by mixture modeling [13]. The mixture modeling approach offers an elegant way to model DNA amplification patterns in a probabilistic framework. However, the mixture models are summarized by arrays of numerical probability values that are hard to grasp. Therefore, we investigate how to describe the essential properties of the mixture models through the parameters of the models, or alternatively through the clustered data sets. Our proposed solution is based on the maximal frequent itemsets which are extracted from the clustered data sets. The descriptions are represented in the style of the descriptions used in literature to report amplification patterns and generally used by domain experts.

The rest of the paper is organized as follows: Sect. 2 describes the DNA copy number amplification data and our previous research in this context. Sect. 3 describes mixture models in the analysis of 0-1 data and the partitioning scheme for dividing the data in to cluster-specific data sets. The main topic of the paper — how to describe the mixture model for 0-1 data in a compact and understandable fashion — is explained in Sect. 4. Experiments are reported in Sect. 5 and the paper is summarized in Sect. 6. The nomenclature for the chromosome regions, which is used in the experimental part of the paper, is described in Appendix A.

2 DNA Copy Number Amplification Database

We have analyzed the database of DNA copy number amplifications collected with a bibliomics survey from 838 journal articles covering a publication period of ten years from 1992 until 2002 (for details, see [9]). DNA copy number amplifications are localized chromosomal aberrations that increase the number of copies of a chromosomal region from two to at least five. In the database, the DNA copy number amplifications are recorded for $N = 4590$ cancer patients in $d = 393$ chromosomal regions covering the whole human genome, and the observed data are the presence ($x_{ij} = 1$) or the absence ($x_{ij} = 0$) of DNA copy number amplifications for the patient i in the chromosomal region j , where $i = 1, \dots, 4590$ and $j = 1, \dots, 393$. For the case including only chromosome 1 presented later in the paper, the dimensions of the data are $N = 446$ and $d = 28$. The nomenclature for the chromosome regions used later in this paper is briefly described in Appendix A. In our previous work, we have analyzed a large 0-1 database of DNA copy number amplification patterns in human neoplasms [9]. We characterized the genome-wide data with cancer-specific amplification profiles with a probabilistic interpretation and