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Abstract

Code synthesis is routinely used in industry to generate GUIs and for database support. In this paper we consider whether code synthesis could also be applied as a rapid prototyping method to the data mining phase of knowledge discovery. Rapid prototyping of statistical data analysis algorithms would allow experienced analysts to experiment with different statistical models before choosing one, but without requiring prohibitively expensive programming efforts. It would also smooth the steep learning curve often faced by novice users of data mining tools and libraries. Finally, it would accelerate dissemination of essential research results. For the synthesis task, we use a specification language that generalizes Bayesian networks, a dependency model on variables. Using decomposition methods and algorithm templates, our system transforms the network through several levels of representation into pseudo-code which can be translated into the implementation language of choice. Here, we explain the framework on a mixture of Gaussians model used in some commercial clustering tools. We show the effectiveness of our framework by generating pseudo-code for some more sophisticated algorithms from recent literature.

1 Introduction

A key component of the data mining task within knowledge discovery is statistical data analysis. Applied and computational statisticians who perform this task on smaller data sets use experimentation with different statistical models and development of specialized algorithms to achieve reliable and useful results, especially in situations where the data cannot be cast into a form suitable for one of the standard algorithms. This capability is not practically available to the knowledge

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discovery community.

An alternative approach to algorithm prototyping from the statistics community is implemented in the BUGS system [14]. A probability model is simulated directly from its specification using Gibb's sampling. However, BUGS cannot make use of more efficient special-purpose algorithms because of its underlying simulation kernel. This restricts its applicability under real-world data mining conditions, e.g., scaling up to large data sets. We see the popularity of BUGS as an existence proof that rapid prototyping provides a needed capability for data mining.

In this paper we develop an alternative approach to rapid prototyping of data mining tools based on *program synthesis*, the automatic derivation of a program that meets a given specification. We apply these methods to synthesize data analysis programs from Bayesian network specifications using a library of efficient algorithm templates together with core special-purpose algorithms and general purpose solvers, as suggested in [3]. We show that this approach can address non-trivial data analysis problems.

Our approach is motivated by three observations. First, the success of BUGS demonstrates the need for data analysis tools suitable for reliable rapid prototyping. Second, Bayesian networks provide a ready, unifying specification language, as seen by their widespread use in communities such as applied Bayesian statistics and neural information processing [15, 7]; their role for the data mining community is to provide a flexible data modeling language [4]. Finally, program synthesis has been proven to be competitive in other domains. It offers:

- Rapid turn-around: even for large tasks mature synthesis systems usually require less than a few minutes to produce code [10, 2].
- *Reliability*: synthesized code is used in production systems to schedule military logistics [2] or to price stock options [13].
- Efficiency: synthesized code can be an order of magnitude faster than hand-crafted code [2].

^{*}Funded by NASA Universities Grant 05106 & Ultimode Inc.

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However, to the best of our knowledge, program synthesis has not previously been applied to data analysis algorithms; an edited discussion on its relevance appears in [5]. Specific advantages for data analysis, other than rapid prototyping, are that generated code should be time and space efficient; to achieve this we would rely on high-performance optimizing compiler techniques [1] coupled to our pseudo-code, as discussed in Section 3.2.

2 Preliminaries

2.1 A simple problem

As a simple running example to illustrate our concepts we will use mixture of Gaussians (cf. Fig. 1) which is covered in detail in many statistical texts. It is a model for the measured data vector \vec{x} based on parameter vectors $\vec{\rho}, \vec{\mu}, \vec{\sigma}$ that are to be estimated. Figure 1(left)



Figure 1: A mixture of Gaussians: data and model

shows a two dimensional version of the problem where each Gaussian can be fully covariate. Here, example data is represented with a scatter plot; projections of the component Gaussians that make up the distribution are shown on both axes. The dots are roughly clustered in four blobs: top left, bottom right, bottom left, and a diagonal blob. Hence, C, the number of Gaussians being "mixed", is four. An intuitive interpretation of this mixture model is that we first generate data from four individual Gaussians, mix these up according to some proportions, and throw away the information of the original Gaussian source.

The Bayesian network¹ for the model is given in Fig. 1(right). Bayesian networks are acyclic directed graphs that define probabilistic dependencies between variables; the shaded variables are supplied in the data and the remaining are to be inferred. The box around the variables c and x indicates that they are data vectors where each of the 200 components is independently and identically distributed. The vector \vec{c} (the "hidden variable" of the model which captures the assignment of the dots to the blobs) is discrete, with each entry taking a value $\{1, 2, ..., C\}$, and the vector \vec{x} is real-valued. The full joint probability for this model is

$$Pr(\rho) Pr(\sigma) Pr(\mu \mid \sigma) \prod_{i=1}^{200} Pr(c_i \mid \rho) Pr(x_i \mid \mu[c_i], \sigma[c_i]) ,$$

where ρ parameterizes the discrete distribution over each discrete value c_i for $i = 1, \ldots, 200$, and $(\mu[j], \sigma[j])$ are the Gaussian parameters for each of $j = 1, \ldots, C$ Gaussian peaks in the data. The precise form of the prior distributions for ρ, μ, σ is left unspecified here; they could be considered as variables for a maximum likelihood analysis, or be fully specified for a Bayesian analysis.

This kind of problem is traditionally handled using an algorithm known as Expectation-Maximization (EM); our presentation follows [11]. In the mixture of Gaussian problem, one common interpretation of the learning task is to seek to maximize $\sum_{i=1}^{N} \log Pr(x_i \mid \vec{\rho}, \vec{\mu}, \vec{\sigma})$. The problem here is that the inner probabilities are themselves a sum over c_i , $Pr(x_i \mid \vec{\rho}, \vec{\mu}, \vec{\sigma}) = \sum_{j=1}^{C} Pr(x_i, c_i \mid \vec{\rho}, \vec{\mu}, \vec{\sigma})$, and the combination with the log makes the formula intractable. To overcome this, a new set of parameters is introduced and a cyclic "reestimation" method is used as follows:

- 1. Set $q_{i,j} = Pr(c_i = j | x_i, \vec{\rho}, \vec{\mu}, \vec{\sigma})$ for i = 1, ..., N and j = 1, ..., C. Thus \vec{q} is a discrete distribution on \vec{c} .
- 2. Maximize $\mathcal{E}_{\vec{c} \sim \vec{q}} [\log Pr(\vec{x}, \vec{c} | \vec{\rho}, \vec{\mu}, \vec{\sigma})]$ for $\vec{\rho}, \vec{\mu}, \vec{\sigma}$ given \vec{q} above. Here, the log probability is evaluated according to the correct model, and then \vec{c} is quantified out by averaging using \vec{q} .

This EM algorithm applies for these general probability forms, and not just the mixture of Gaussians.

2.2 Indexed variables, Bayesian networks

In data analysis, indexed variables as vectors are ubiquitous: data $\vec{x} = \{x_1, \ldots, x_N\}$ with independent and identical distributions, and vectors of parameters $\vec{\theta} =$ $\{\theta_1,\ldots,\theta_C\}$ that behave similarly (e.g., different nodes in a neural net). The representation must allow full vectors, \vec{x} , generic single components, x_i , and particular single components, x_5 . During synthesis, the system needs to determine dependencies between these different combinations of variables, and the Bayesian network performs the role of a data-flow graph used in compilers [1]. In Bayesian networks, vector variables should not be "unfolded" (i.e., represented fully) because that obscures the model's regularities and increases the network's size. Instead, the network contains the most general representation and is unfolded only by demand and only locally.

Our system uses Prolog-terms; a theory of indexed Bayesian networks, where indices are represented as Prolog variables is developed in [6]. We have extended these results using difference sets² to work with nonground probability queries since we seek to determine

¹Tutorials and references are available at www.auai.org.

²Difference sets are substitutions representing equalities and inequalities to define a set of variables with inclusion/exclusion.

probabilities over indexed vectors. Tests for independence on these indexed Bayesian networks are easily developed in Lauritzen's framework which uses ancestral sets and set separation [8].

2.3 Expressions for probabilities

During synthesis, probability expressions are repeatedly evaluated and converted into mathematical formula for analysis or insertion into code. Some probabilities can easily be extracted from a Bayesian network by enumerating the component probabilities at each node:

Lemma 1 Let U, V be sets of variables over a Bayesian network with $U \cap V = \emptyset$. Then $V \cap descendants(U) = \emptyset$ and parents $(U) \subseteq V$ hold in the corresponding dependency graph iff the following probability statement holds:

$$Pr(U|V) = Pr(U|parents(U)) = \prod_{u \in U} Pr(u|parents(u))$$

How can probabilities not satisfying these conditions be converted to symbolic expressions? Symbolic probabilistic inference [9], for instance extracts an efficient expression for a particular probability, p(U|V). We have developed another result that lets us extract probabilities on a large class of mixed discrete and real, potentially indexed variables, where no integrals are needed and all marginalization is done by summing out discrete variables. We give the non-indexed case below; this is readily extended to indexed variables, and our proofs are constructive. Lemma 2 lets us evaluate a probability by a summation: $Pr(U|V) = \sum_{u' \in Dom(U')} Pr(U' =$ u', U|V). Lemma 3 lets us evaluate a probability by a summation and a ratio:

$$Pr(U|V) = \frac{q(u)}{\sum_{u \in Dom(U)} q(u)} ,$$

where $q(u) = \sum_{u' \in \text{Dom}(U')} Pr(U' = u', U, V/V' | V')$. Since the lemmas also show minimality of the sets U' and V/V', they also give the minimal conditions under which a probability can be evaluated by discrete summation without integration.

Lemma 2 $V \cap descendants(U) = \emptyset$ holds and ancestors(V) is independent of U given V iff there exists a set of variables U' such that Lemma 1 holds if we replace U by $U \cup U'$. Moreover, the unique minimal set U' satisfying these conditions is given by ancestors(U) / (ancestors(V) $\cup V$)

Lemma 3 Let V' be a subset of V/descendants(U) such that ancestors(V') is independent of $(U \cup V)/(V' \cup ancestors(V'))$ given V'. Then Lemma 2 holds if we replace U by $U \cup V/V'$ and V by V'. Moreover, there is a unique maximal set V' satisfying these conditions.

3 The Framework

3.1 Specification language PN

Our specification language PN (Probabilistic Networks) is a simple textual notation to describe networks as in Fig. 1(right) and to specify the distributions and equations at each node. The following small specification is already sufficient to model the Mixture of Gaussians.

The first three lines define the model constants N and C and declares the parameter vectors $\vec{\mu}, \vec{\sigma}$ and $\vec{\rho}$ with their respective types and dimensions; all types are builtin. Since the parameter vectors are to be estimated using a maximum likelihood analysis, no probability distributions are specified.

The next two lines define the hidden variable \vec{c} and the observed data vector \vec{x} which will ultimately become the only input to the synthesized program. Both vectors are independently and identically distributed, as the for-construct mirrors the box-notation of Figure 1(right).

The Bayesian network for the distribution is extracted from the specification dynamically and processed extensively with graph operations to determine applicability of different transformations. The above model is thus represented by the following small database, where each literal represents all arcs into a single node:

```
depends(sigma,[]). depends(rho,[]).
depends(mu,[sigma]). depends(c(I),[rho]).
depends(x(I),[mu,sigma,c(I)]).
```

The last lines of the specification contain the *optimization statement*. It specifies the variables to be optimized together with the initial probability expression; the trailing clause given $\{x\}$ identifies \vec{x} as the initial data vector. A different analysis, e.g., a Bayesian version, can be specified simply by changing the optimization statement.

3.2 Pseudo-code

For two reasons, our system generates an intermediatelevel pseudo-code and not any particular target language. First, pseudo-code is easier to translate into a variety of languages. Second, and more important, it is easier to optimize. Standard implementation languages, such as C++ and C, allow programming constructs that defeat good optimization, and the array languages often result in a programming style that defeats good optimization as well, as programmers attempt to avoid explicit iteration "at all costs." Thus program synthesis has the added advantage that it can probably make better use of modern code optimization capabilities [1] than most programmers.

3.3 Outline of the implementation

The system implementation comprises 9000 lines of Prolog, including a package for term rewriting. A number of procedures are specifically designed for manipulating indexed sums and products, and probabilities over independently and identically distributed array variables as in Section 2.2. We also have a database of distributions, and a term rewrite system for simplifying formula and probabilities in various ways: simplifying the log of a formula, moving a summation inwards, splitting a formula into its linear components, symbolically deriving a derivative, testing for positivity, and testing for nonzero.

Internally, our system uses three conceptually different levels of representation. Probabilities (including logarithmic and conditional probabilities) are the most abstract level. They are processed via methods for Bayesian network decomposition or matches with core algorithms such as EM. Formulae are introduced when probabilities of the form $Pr(U \mid \text{parents}(U))$, where parents(U) is the set of variables appearing in the definition for U, are detected, either in the initial network, or after the application of network decompositions. Atomic probabilities (i.e., U is a single variable) are directly replaced by formulae based on the given distribution and its parameters. General probabilities are decomposed into sums and products of the respective atomic probabilities. Pseudo-code programs are the lowest level of representation. They contain no probabilities and are ready for immediate optimization using symbolic or numeric methods but they can still be decomposed into independent subproblems. Each of the program transformations we apply operates on or between these levels.

3.4 Transformations for optimization

Our current list of transformations is as follows. Decomposition of a problem into independent sub-problems is always done. Decomposition of probabilities is driven by the Bayesian network. We also have a separate system for handling decomposition of formulae. A formula can be decomposed along a loop, e.g., the problem "optimize $\vec{\theta}$ for $\prod_i f(\theta_i)$ " is transformed into a for-loop over subproblems "optimize θ_i for $f(\theta_i)$ ". More commonly, "optimize θ, ϕ for $f(\theta) + g(\phi)$ " is transformed into the two subprograms "optimize θ for $f(\theta)$ " and "optimize ϕ for $g(\phi)$ ". The lemmas in Section 2.3 are applied to change the level of representation and thus for *simplification of probabilities*.

The statistical algorithm schema currently implemented is EM; others that can be encoded with the current primitives are mean-field methods for exponential family, iterative proportional fitting, and iterative reweighted least-squares [15, 7]. Usually, the schemas require a particular form of the probabilities involved; they are thus tightly coupled to the decomposition and simplification transformations. E.g., EM is a way of dealing with situation where Lemma 2 applies to vectors of data.

Likelihoods of the exponential family (i.e., sub-expressions of the form $\log \prod_i Pr(x_i | \theta)$) are identified in the initial specification or in intermediate representations and simplified into linear expression with terms such as $mean(x_i)$ and $mean(x_i^2)$.

As final resort, we pass formulae which cannot be handled symbolically off to a general purpose package for *numerical optimization*.

4 Some Examples

4.1 Mixture of Gaussians

Here, we show how our system derives pseudo-code for the mixture of Gaussians example as specified in Section 2.1.

The probability in the initial optimization statement matches the conditions of Lemma 2; moreover, U' is just $\{\vec{c}\}$ which has the same dimensions as the given data vector \vec{x} . This condition triggers the EM algorithm as described in Section 2.1, and instantiates its schema, resulting in the partial program: while (converging (μ, σ, ρ))

for ((i,j), ([1,200],[1,4]))

$$q_{i,j} = Pr(c_i = j | x_i = j, \mu, \sigma);$$

optimize $\{\mu, \sigma, \rho\}$
for $LogPr(x_i, c_i | \mu_{c_i}, \sigma_{c_i}, \rho)$
given $\{c_i \sim q_{i,*}, x\}$

In this, converging is a generic convergence criterion imposed over the variables $\vec{\mu}, \vec{\sigma}, \vec{\rho}$. Given $c_i \sim q_{i,*}$ implies we quantify c_i out of the objective by averaging; the for-loop bounds were easily extracted from the specification. The instantiated schema also contains two recursive calls to the synthesis system. The first is hidden in the the evaluation of $q_{i,j}$ using Lemma 3; the pseudo-code resulting from this call consists only of the symbolic expression representing the value of the probability. The second is represented explicitly by the optimization statement. Here, c_i is averaged out with the discrete distribution with parameters $q_{i,*}$, and the log probability is evaluated using Lemma 1. The Bayesian (sub-) network to evaluate this reduced problem reveals that $\vec{\rho}$ is independent of $\vec{\sigma}, \vec{\mu}$ thus the optimization problem can be decomposed. The second half of this decomposition contains the optimization goal log $Pr(x_i \mid \mu_{c_i}, \sigma_{c_i})$ which (under the given distribution for c_i) is simplified into $\sum_{j=1}^{4} q_{i,j} \log Pr(x_i \mid \mu_j, \sigma_j)$. This formula is then decomposed along the index j, leaving

while(converging(μ, σ, ρ)) for((i,j), ([1,200],[1,4])) $q_{i,j} = Pr(x_i | c_i = j, \mu, \sigma);$ optimize($\rho : \sum_j \rho_j = 1$, $\sum_{j=1}^4 (\sum_{i=1}^{200} q_{i,j}) \rho_j$); for(j, [1,4])

optimize({ μ_j, σ_j }, $\sum_{i=1}^{200} q_{i,j} \log Pr(x_i | \mu_j, \sigma_j))))$

The first optimization statement here is solved exactly to yield that $\vec{\rho}$ is set to \vec{q} -weighted frequencies. The second optimize statement is matched with a weighted log probability of a Gaussian, and thus turned into an expression for each μ_j , σ_j involving \vec{q} -weighted means of \vec{x} and $\vec{x^2}$. This is then solved exactly for μ_j , σ_j . Divide by zero is detected to occur here when $\sum_{i=1}^{200} q_{i,j} = 0$ for some j. Thus, the usual EM algorithm for mixture of Gaussians is derived.

4.2 Additional examples

We have tested our system on a variety of different problems. These include the simple Bayes classifier, linear regression on non-linear basis functions with Bayesian smoothing, and a "curve clustering" model suggested by Smyth which attempts to fit multiple curves at once. Our system yielded correct pseudo-code in all cases. We also modelled the distributional clustering framework of [12] but without introducing their "temperature" parameter. This method is the basis of techniques for featurizing documents by generating clusters of related words, and versions of it are used in text mining.

5 Conclusions

The one aspect of our framework not demonstrated is the generation of target code from pseudo-code, and thus a final empirical evaluation of the algorithms generated. We are developing a back-end for Lisp and Matlab. We have demonstrated the general feasibility of our approach, but also raised issues for future work. Necessary research to make this method suitable for data mining at a commercial level is to adequately address numerical issues such as divide by zero and ill-conditioned matrices, and to have the algorithms scale on large data-sets. We note that many divide by zero and ill-conditioning problems are actually due to modeling (e.g., too many basis functions are being used) and need to be addressed at the level of the statistical model. While scaling to large data sets is beyond the scope of our current research, we believe our demonstration here is an important first step towards a reliable prototyping system for data mining programs while scaling technology itself matures.

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