Bayesian Logic Programs

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There has been an increasing interest in integrating probability theory with first order logic within the last years.

Bayesian networks are elegant and efficient probabilistic frameworks, but they inherit disadvantages of propositional logic (see next slides).

Our presentation introduces Bayesian logic programs:

- They unify Bayesian networks with inductive logic programming and generalize both concepts.
  - Main goal: Inherit advantages and overcome limitations of both frameworks.

Key idea: One-to-one mapping between ground atoms (inductive logic programming) and random variables (Bayesian networks).
Agenda

1. Revisiting Bayesian Networks and Logic Programs

2. Bayesian Logic Programs

3. Learning Bayesian Logic Programs

4. Conclusion and Outlook
Agenda

1. Revisiting Bayesian Networks and Logic Programs
   1.1  Bayesian Networks
   1.2  Logic Programs

2. Bayesian Logic Programs

3. Learning Bayesian Logic Programs

4. Conclusion and Outlook
A person’s $X$ blood type $bt(X)$ is determined by a gene that is inherited. Each person $X$ has two copies of the chromosome containing this gene. $m_c(Y)$ inherited from the mother $m(Y, X)$ and $p_c(Z)$ inherited from the father $f(Z, X)$.

**The genetic model:**

- has a probabilistic part through the biological laws of inheritance, and
- requires the representation of the relational family structure
Bayesian Networks
Basics

- A Bayesian network is a directed acyclic graph
- Each node corresponds to a random variable $x_i$
- An edge from $x_1$ to $x_2$ indicates a direct influence from $x_1$ on $x_2$

\[ \Rightarrow \] The Bayesian network represents the joint probability distribution $P(x_1, ..., x_n)$ over the fixed, finite set \{ $x_1, ..., x_n$ \} of random variables
- The random variable $x_i$ possesses the finite set of possible states $S(x_i)$

Possible states:
- $S(bt\_dorothy) = \{a, b, ab, 0\}$
- $S(pc\_dorothy) = \{a, b, 0\}$
- $S(mc\_dorothy) = \{a, b, 0\}$
Bayesian Networks
Joint Probability Density

- The direct predecessors (parents) of a node $x$ are identified by $Pa(x)$
- For instance: $Pa(bt\_ann) = \{pc\_ann, mc\_ann\}$

**Independence Assumption of Bayesian Networks:** Each node $x_i$ in the graph is conditionally independent of any subset $A$ of nodes that are not descendants of $x_i$ given a joint state of $Pa(x_i)$

\[ P(x_i|A, Pa(x_i)) = P(x_i|Pa(x_i)) \]

Applying the independence assumption to the chain rule expression of the joint probability distribution we get the **joint probability density**:

\[ P(x_1, ..., x_n) = \prod_{i=1}^{n} P(x_i|Pa(x_i)) \]

And we associate every $x_i$ with a conditional probability distribution

\[ P(x_i|Pa(x_i)) \]
The conditional probability distribution for the blood type example could be:

<table>
<thead>
<tr>
<th>mc_dorothy</th>
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<th>P(bt_dorothy)</th>
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</thead>
<tbody>
<tr>
<td>a</td>
<td>a</td>
<td>(0.97,0.01,0.01,0.01)</td>
</tr>
<tr>
<td>b</td>
<td>a</td>
<td>(0.01,0.01,0.97,0.01)</td>
</tr>
<tr>
<td>...</td>
<td>...</td>
<td>(0.01,0.01,0.01,0.97)</td>
</tr>
<tr>
<td>0</td>
<td>0</td>
<td>(0.01,0.01,0.01,0.97)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>mc_ann</th>
<th>pc_ann</th>
<th>P(mc_dorothy)</th>
</tr>
</thead>
<tbody>
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<td>(0.98,0.01,0.01)</td>
</tr>
<tr>
<td>b</td>
<td>a</td>
<td>(0.01,0.98,0.01)</td>
</tr>
<tr>
<td>...</td>
<td>...</td>
<td>(0.01,0.01,0.98)</td>
</tr>
<tr>
<td>0</td>
<td>0</td>
<td>(0.01,0.01,0.98)</td>
</tr>
</tbody>
</table>

and for the apriori nodes (nodes having no parents):

<table>
<thead>
<tr>
<th>P(mc_ann)</th>
<th>P(pc_ann)</th>
<th>P(mc_brian)</th>
<th>P(pc_briany)</th>
</tr>
</thead>
<tbody>
<tr>
<td>(0.38,0.12,0.50)</td>
<td>(0.38,0.12,0.50)</td>
<td>(0.38,0.12,0.50)</td>
<td>(0.38,0.12,0.50)</td>
</tr>
</tbody>
</table>
Bayesian Networks
Pros and Cons

All Bayesian networks consist of two components:

- a qualitative or logical one, that represents the influences among the random variables using a directed acyclic graph
- a quantitative one that encodes the probability densities over these influences, represented by conditional probability tables

Therefore Bayesian networks provide a nice separation of the qualitative and the quantitative component. The major limitation of Bayesian networks is their propositional nature. It is not possible to formulate a general probabilistic rule like:

the localization $L$ of gene $G$ is influenced by the localization $L'$ of another gene $G'$ that interacts with $G'$
A Prolog program consists of **clauses**. There are two type of clauses: **facts** and **rules**. Facts describe attributes of an object or a relationship between multiple objects. Facts consist of a functor followed by the list of arguments. A predicate is a functor and its arity. Let’s have an example:

```prolog
male(jef).
pARENT(jef,paul).
pARENT(paul,ann).
grandparent(X,Y) :-
    pARENT(X,Z),parent(Z,Y).
```

**Existing terms:**
- `male / 1` and `parent / 2` are predicates
- `jef, paul and ann are constants`
- `X, Y and Z are variables`

**Rules** are logical statements like `grandparent(X,Y)`. This rule can be read as: X is the grandparent of Y if X is a parent of Z and Z is a parent of Y. Let us call this clause `c`. `grandparent(X,Y)` is called `head(c)` and `parent(X,Z),parent(Z,Y)` is `body(c)`.
Definitions:

- **Atoms** are predicates followed by the necessary number of terms e.g. `parent(jef,paul)`
- `Var(E)` are the variables occurring in a term, atom or clause: e.g. `Var(c) = X, Y, Z`
- If `Var(E) = ∅` (no variables occur in term, atom or clause `E`), `E` is called *ground*
- A substitution `θ = {V₁/t₁, ..., Vₙ/tₙ}`, e.g. `{X/ann}` is an assignment of terms `tᵢ` to variables `Vᵢ`
  ⇒ `cθ` is `grandparent(ann,Y) :- parent(ann,Z),parent(Z,Y)`
Logic Programs
Least Herbrand Model

- A Herbrand base $HB(T)$ of a logic program $T$ is the set of all ground atoms constructed with the symbols in $T$.
- E.g. $HB(grandparent) = \{\text{parent(ann,ann)}, \text{parent(jef,jef)}, \text{parent(paul,paul)}, \text{parent(ann,jef)}, \text{parent(jef,ann)}, \ldots, \text{grandparent(ann,ann)}, \text{grandparent(jef,jef)}, \ldots\}$
- A Herbrand interpretation is a subset of $HB(T)$.
- The least Herbrand model $LH(T)$ is the subset of $HB(T)$ containing all ground logical consequences (i.e. all relevant facts)
- There several methods to compute the least Herbrand model
- E.g. $LH(grandparent) = \{\text{male(jef)}, \text{parent(jef,paul)}, \text{parent(paul,ann)}, \text{grandparent(jef,ann)}\}$
Agenda

1. Revisiting Bayesian Networks and Logic Programs

2. Bayesian Logic Programs
   2.1 Representation Language and Semantics
   2.2 Graphical Representation
   2.3 Extension to the Basic Framework

3. Learning Bayesian Logic Programs

4. Conclusion and Outlook
Findings of the previous example:

- Random variables from the Bayesian network correspond to logical atoms
- The direct influence relation corresponds to the immediate consequence operator
- The logical component of Bayesian networks correspond to propositional logic (and inherit there limitations)

To overcome the limitations: Bayes logic programs have to upgrade the network structure of the Bayesian networks to first order clauses

⇒ Bayesian Clauses
**Definition: Bayesian Clauses** A Bayesian clause $c$ is an expression of the form $A | A_1, ..., A_n$ where $n \geq 0$, $A, A_1, ..., A_n$ are Bayesian atoms and all Bayesian atoms are universally quantified.

- A Bayesian predicate $p \ 1$ represents a set $S(p \ 1)$ of random variables.
- A Bayesian ground atom $g$ represents random variables over the states $S(g)$.
- ‘$|$’ is used instead of ‘:-’ to capture the idea of conditional probability distributions.
- Range assumption: All Bayesian clauses $c$ are range-restricted i.e. $\text{Var} (\text{head}(c)) \subseteq \text{Var} (\text{body}(c))$ to avoid the derivation of non-ground true facts.

**Example:** $bt(X) | mc(X), pc(X)$ is a Bayesian clause.
- E.g. $bt(ann)$ corresponds to a random variable over the states $S(bt(ann)) = \{a, b, ab, 0\}$.
**Probabilistic model**: Each Bayesian clause $c$ is associated with a conditional probability distribution $\text{cpd}(c) = P(\text{head}(c)|\text{body}(c))$

- There may be more than one clause. Considering the following clauses

\[
\begin{align*}
  c_1 : & \text{bt}(X) \mid \text{mc}(X) \\
  c_2 : & \text{bt}(X) \mid \text{pc}(X)
\end{align*}
\]

- Assume substitutions $\theta_i$ that ground the causes $c_1$ and $c_2$ so that they fulfill $\text{head}(c_1 \theta_1) = \text{head}(c_2 \theta_2)$. $\theta_i$ implies $\text{cpd}(c_1 \theta_1)$ and $\text{cpd}(c_2 \theta_2)$

- **Problem**: For probabilistic reasoning we need the distribution $P(\text{head}(c_1 \theta_1)|\text{body}(c_1) \cup \text{body}(c_2))$

- **Solution**: A **Combining Rule** $\text{cr}(p/l)$ is a function that maps finite sets of probability distributions onto one combined conditional probability distribution
A **Bayesian logic program** $B$ consists of a set of Bayesian clauses

- For each Bayesian clause $c$ there is exactly one $cpd(c)$
- For each Bayesian predicate $p/l$ there is exactly one $cr(p/l)$

**Example**: Bayesian logic program for the blood-type domain

$m(\text{ann, dorothy}).$
m(f(brian, dorothy)).
p(c(\text{ann}).$
p(c(brian)).
m(\text{mc(ann)}).$
m(c\text{brian}).$

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<td>a</td>
<td>(0.01,0.01,0.97,0.01)</td>
</tr>
<tr>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>0</td>
<td>0</td>
<td>(0.01,0.01,0.01,0.97)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>m(\text{ann, dorothy})</th>
<th>mc_ann</th>
<th>pc_ann</th>
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</thead>
<tbody>
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<td>a</td>
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</tr>
<tr>
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<tr>
<td>...</td>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>false</td>
<td>0</td>
<td>0</td>
<td>(0.33,0.33,0.33)</td>
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A Bayesian logic program $B$ can be visualized by a **dependency graph** $DG(B)$

- The **nodes** are the atoms in the least Herbrand model of the Bayesian logic program
- There is an **edge** between a node $x$ and a node $y$ if there exists a clause $c \in B$ and a substitution $\theta$, s.t. $y = head(c\theta)$, $x \in body(c\theta)$ and for all ground atoms $z$ in $c\theta$ : $z \in LH(B)$
- Application of the combining rule $cr(p/n)$ allows us to assign a **conditional probability distribution** to the nodes having parents

```
quality. attention | quality
sleep. attention | sleep
```
A Bayesian logic program $B$ that satisfies

1. $LH(B) \neq \emptyset$
2. $DG(B)$ is acyclic
3. each node in $DG(B)$ is influenced by a finite set of random variables

is called well-defined.

- Every well-defined Bayesian logic program specifies a unique joint distribution over $LH(B)$
- The joint distribution can be factored to

$$P(LH(B)) = \prod_{x \in LH(B)} P(x | Pa(x))$$
A **probabilistic query** to a Bayesian logic program $B$ can be defined as an expression of the form:

$$\text{?} - q_1, ..., q_n \mid e_1 = e_1, ..., e_m = e_m$$

where $n > 0$, $m \geq 0$. It asks for the conditional probability distribution

$$P(q_1, ..., q_n \mid e_1 = e_1, ..., e_m = e_m)$$

of the query variables $q_1, ..., q_n$ where $\{q_1, ..., q_n, e_1, ..., e_n\} \subseteq HB(B)$.

One naive approach would be to compute the whole least Herbrand model to answer queries.
In order to answer queries, one has not compute the whole least Herbrand model. One way to avoid complex network structures is to consider so-called support networks.

\[ N = \{x\} \cup \{y \mid y \in LH(B) \text{ and } y \text{ influences } x\} \]

The support network \( N \) of a random variable \( x \in LH(B) \) consists of \( x \) and all variables \( y \) that influence \( x \).

**Example:** Support Network for \( bt(dorothy) \)

- mc_dorothy
- pc_dorothy
- bt_dorothy
Extended representation for Bayesian networks:

- **Bipartite** directed acyclic graph
- Two disjoint sets of nodes in the bipartite graph:
  1. *light gray ovals* are random variables
  2. *black boxes* are local probability models
- The local probability models specify the conditional probability distribution $P(x_i|Pa(x_i))$
The local probability model for R9

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<tr>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>0</td>
<td>0</td>
<td>(0.01,0.01,0.01,0.97)</td>
</tr>
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</table>

R9 specifies the conditional probability distribution for $P(bt(dorothy)|mc(dorothy),pc(dorothy))$
Graphical Representation for Bayesian Logic Programs (1)

- Constants and functors such as `ann` are represented as white boxes.
- Bayesian atoms are represented as gray ovals containing the predicate: `pc`.
- Arguments are represented as white empty circles on the boundary of the ovals.
Arguments of atoms like \texttt{Person} are placeholders for terms.
Graphical Representation for Bayesian Logic Programs (3)

<table>
<thead>
<tr>
<th>f(Father,Person)</th>
<th>mc(Father)</th>
<th>pc(Father)</th>
<th>P(pc(Person))</th>
</tr>
</thead>
<tbody>
<tr>
<td>true</td>
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<tr>
<td>...</td>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
</tbody>
</table>
The `mother/2` and `father/2` relations are not really *random* variables, they are always in the same state. (*true* with probability 1) \( \Rightarrow \) `mother/2` and `father/2` are *logical* atoms

Logical atoms have no conditional probability distribution

\[ pc(X) | f(Y,X), mc(Y), pc(Y) \] is modified to \[ pc(X) | mc(Y), pc(Y) \] and it only applies for substitutions for which \( f(Y,X) \) is true (in the least Herbrand model)

*Bayesian* atoms are light gray ovals, *logical* atoms are dark gray ovals
The new `founder/1` relation is defined as:

```
founder(Person):- \
 \+(mother(\_,Person);father(\_,Person))
```

\+ is a negation, \_ represents a anonymous variable and ; stands for disjunction.

Essentially `founder(Person)` is true if `Person` has no parents (is an apriori node).
Graphical Representation for Bayesian Logic Programs
Logical Atoms (3)

<table>
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<td>...</td>
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<tr>
<td>0</td>
<td>0</td>
<td>(0.33, 0.33, 0.33)</td>
</tr>
<tr>
<td>...</td>
<td>...</td>
<td>...</td>
</tr>
</tbody>
</table>
Graphical Representation for Bayesian Logic Programs
Another example
Graphical Representation for Bayesian Logic Programs

Hidden Markov Models (1)

**left** General hidden Markov model

Parameters:
- $x$ states
- $y$ possible observations
- $a$ state transition probabilities
- $b$ output probabilities

**bottom** The graph of the Bayesian logic program on the previous slide directly encodes the Bayesian network structure of hidden Markov models.
Graphical Representation for Bayesian Logic Programs

Hidden Markov Models (2)
Agenda

1. Revisiting Bayesian Networks and Logic Programs

2. Bayesian Logic Programs

3. Learning Bayesian Logic Programs
   3.1 The Learning Setting
   3.2 Structural Learning of Bayesian Logic Programs
   3.3 Learning Probabilities in Bayesian Logic Programs
   3.4 Test Cases / Experiments

4. Conclusion and Outlook
Learning Bayesian Logic Programs

Previously:

- Assumption: There is an expert who designs the structure and also the conditional probability of the network
- Problem: Lack of persons with the necessary expertise or knowledge
- Solution: If there is access to data, there is a possibility learn Bayesian logic programs

Learning approach:

- Learning based on given data cases (*learning from interpretations*)
- Key idea: Rules that are valid on one interpretation are likely to be valid on other interpretations
A data case $D_i \in D$ consists of a

- Logical part: $\text{Var}(D_i) = LH(B \cup \text{Var}(D_i))$ (Herbrand interpretation) and a
- Probabilistic part: Assignment of values to some facts in $\text{Var}(D_i)$

Example of a data case:

$D_1 = \{ m(\text{cecily}, \text{fred}) = \text{true}, f(\text{henry}, \text{fred}) = ?, \text{pc}(\text{cecily}) = a, \text{pc}(\text{henry}) = b, \text{pc}(\text{fred}) = ?, \text{mc}(\text{cecily}) = b, \text{mc}(\text{henry}) = b, \text{mc}(\text{fred}) = ?, \text{bt}(\text{cecily}) = ab, \text{bt}(\text{henry}) = b, \text{bt}(\text{fred}) = ? \}$

- The logical part specifies the least Herbrand model of the target Bayesian program and highlights relevant random variables
- The probabilistic part induce a joint distribution over the random variables of the logical part
The **hypothesis space** consists of Bayesian logic programs, i.e.

- A finite set of Bayesian clauses
- Associated conditional probability distributions

Adequate **restrictions** have to be designed to define the hypothesis space, e.g.

- The clauses only contain constant and predicate symbols that occur in one of the data cases
- One clause is limited to only 3 atoms

Not every element of the hypothesis space is an adequate candidate. Possible candidates have to fulfill the following requirements:

- It has to be logically *valid* on the data
- The induced Bayesian network has to be *acyclic*
The Learning Setting
Formulation of the Learning Problem

Given:
- A set $D = \{D_1, ..., D_m\}$ of data cases
- A set $H$ of hypothesis
- Scoring function $score_D : H \mapsto \mathbb{R}$

Find: A hypothesis $H^* \in H$ such that
- For all $D_i \in D : Var(D_i) = LH(H^* \cup Var(D_i))$
- The Bayesian network implied by $H^*$ is acyclic
- $H^*$ maximizes $score_D : H \mapsto \mathbb{R}$

Assumption: An adequate score function is given that expresses how well a given candidate $H \in H$ fits the given Data. Example for a scoring function: Likelihood.
**Scooby**: Structural learning of intentional Bayesian logic programs

- performs a *heuristic search* through the hypothesis space
- uses the *refinement operators* $\rho_g$ and $\rho_s$ to traverse the hypotheses space
- Works for the special case of Bayesian networks only

**Example** of the use of the refinement operators:
Structural Learning of Bayesian Logic Programs
Scooby (2)

**Scooby**: Structural learning of intentional Bayesian logic programs

Let $H$ be an initial (valid) hypothesis; $S(H) := score_D(H)$; $ho_g$ and $\rho_s$ are generalization and specialization operators

repeat

$H' := H$; $S(H') := S(H)$;

for all $H'' \in \rho_g(H') \cup \rho_s(H')$ do

if $H''$ is (logically) valid on $D$ then

if the Bayesian networks induced by $H''$ on the data are acyclic then

if $score_D(H'') > S(H)$ then

$H := H''$

$S(H) := S(H'')$

end if

end if

end if

end for

until $S(H') = S(H)$

return $H$;

- $\rho_g$ deletes a Bayesian proposition from the body of a clause
- $\rho_s$ adds a Bayesian proposition to the body of a clause
In order to adapt Scooby to work in the case of Bayesian networks one has to consider:

1. Some Bayesian logic programs will be logically invalid
   ▶ Initialization of valid Bayesian logic programs
   ▶ Filtering out those Bayesian logic programs that are logically invalid

2. The traditional first order refinement operator must be used
   ▶ Instead of adding/deleting propositions, they add/delete constant-free atoms

Ideas to improve the algorithms performance:

▶ Lookahead: Allowing atoms to be chosen that do not result in a better score to avoid local optima of the score function
▶ Include Background Knowledge i.e. fixed regularities that are common to all examples
▶ Improve Scoring Function e.g. use of minimal description length principle
Previously we assumed that there is a given method to calculate the conditional probability distribution. Parameter Estimation:

- **Given:** A set $D = \{D_1, ..., D_n\}$ and a set $H$ of Bayesian clauses, a scoring function $score_D : H \rightarrow \mathbb{R}$
- **Find:** Parameters of $H$ maximizing $score_D$

**Maximum Likelihood** is used as the method for parameter estimation. As parameter estimation techniques
  - Gradient-based approaches and
  - Expectation-Maximization algorithm will be discussed.
Learning Probabilities
Maximum Likelihood Estimation

**Given:** Bayesian logic program $B$ consisting of Bayesian clauses $c_1, ..., c_n$, data cases $D = \{D_1, ..., D_n\}$

The **likelihood** $L(D|\lambda)$ is the probability of the data $D$ as a function of unknown parameters $\lambda$

$$L(D|\lambda) := P_B(D|\lambda)$$

**Task:** Find parameter values $\lambda^*$ that maximize the likelihood

$$\lambda^* = \max_{\lambda \in H} P_B(D|\lambda) = P_B(\lambda)(D)$$

Using the fact that it is sufficient to consider the support network $N$. Due to the monotonicity of the logarithm, we can formulate the problem like that:

$$\lambda^* = \max_{\lambda \in H} \log P_N(\lambda)(D)$$
According to the **Gradient-Based approach** the chain rule is applied and parameters $\lambda$ are fixed

$$\frac{\delta \log P_N(D)}{\delta \text{cpd}(c_i)_{jk}} = \sum_{\text{subst.}\theta\text{s.t.} sn(c_i\theta)} \frac{\delta \log P_N(D)}{\delta \text{cpd}(c_i\theta)_{jk}}$$

(1)

with grounding substitutions $\theta$ and $sn(c_i\theta)$ is true iff

$\{\text{head}(c_i\theta)_{jk}\} \cup \text{body}(c_i\theta) \subset N$ Equation (1) can be rearranged to:

$$\frac{\delta \log P_N(D)}{\delta \text{cpd}(c_i)_{jk}} = \frac{\text{en}(c_{ijk}|\theta, D)}{\text{cpd}(c_i\theta)_{jk}}$$

(2)

where $\text{en}(c_{ijk}|\theta, D) := \sum_{l=1}^m P_N(\text{head}(c_i\theta) = u_j, \text{body}(c_i\theta) = u_k| D_l)$ are the expected counts.
Learning Probabilities
Gradient-Based approach (Algorithm)

input: Bayesian logic program B, associated cpds parameterized by \( \lambda \), data cases D
output: Modified Bayesian logic program B

\( \lambda \leftarrow \text{INITIAL PARAMETERS} \)

\( N \leftarrow \text{SUPPORTNETWORK}(B, D) \)

repeat
  \( \Delta \lambda \leftarrow 0 \)
  set associated conditional probability distribution of \( N \) according to \( \lambda \)
  for all \( D_i \in D \) do
    set evidence in \( N \) from \( D_i \)
    for all Bayesian clause \( c \in B \) do
      for all ground instance \( c\theta \) s.t. \( \{ \text{head}(c\theta) \} \cup \text{body}(c\theta) \subset N \) do
        for all single parameter \( \text{cpd}(c\theta)_{jk} \) do
          \( \Delta \text{cpd}(c)_{jk} \leftarrow \text{cpd}(c)_{jk} + (\frac{\delta \log P_N(D_i)}{\delta \text{cpd}(c)_{jk}}) \)
        end for
      end for
    end for
  end for
  \( \Delta \lambda \leftarrow \text{PROJECTIONONTOCONSTRAINTSURFACE}(\Delta \lambda) \)
  \( \lambda \leftarrow \lambda + \alpha \ast \Delta \lambda \)
until \( \Delta \lambda \approx 0 \)
Return B
The algorithm is relatively simplified. There are two important points left out to keep it simple:

1. **Constraint satisfaction**
   - \( \lambda \) consists of probability values \( \Rightarrow \sum_j cpd(c_i)_{jk} = 1 \)
   - Way to enforce this: Re-parameterizing the problem i.e. design of parameters that automatically respect the constraint

2. **Decomposable combining rules** are assumed
   - Each group corresponds to a ground instance
   - The state of \( h \) is a deterministic function of the parents joint state
Learning Probabilities
Expectation-Maximization (EM)

Expectation-Maximization algorithm:
- Another approach to estimate parameters of the maximum likelihood function
- Used in the presence of missing values

If all values are available then the parameters corresponds to **frequency counting**:

\[
P(X = x \mid Pa(X) = u) = \frac{n(X = x, Pa(X) = u_k \mid D_l)}{n(Pa(X) = u_k \mid D_l)}
\]

where \( n(a \mid D) \) denotes the count of a state \( a \) given data \( D \).

If some values are missing the EM-algorithm performs two steps:

1. **E-Step**: Calculation of a distribution over all possible completions\(^1\) given \( \lambda \) and \( D \)
2. **M-Step**: Computes the parameters that maximize the log likelihood function

\(^1\)There is one completion for each partially observed data case. The completion are treated as weighted fully-observed data cases
Learning Probabilities
Gradient vs. EM

Both approaches:
- Rely on computing expected counts
- Perform a greedy local search

Key differences are:
- EM is easier to implement. Reason: EM does not have to enforce the constraint that the parameters are probabilities
- The EM converges faster to near by optimal solutions
- Gradient approaches are more flexible than EM as they allow to consider other scoring functions

Idea: Use of EM and then switch to gradient, since EM converges slowly when it is at a near by optimal solution
Test Cases and Experiments
Genetic Domain

Setting:
- Goal was to learn the *bloodtype* program that was used as example
- Two families with 12 respectively 15 members
- For each family 1000 data cases were given (total 2000)
- 40% of the given data was missing

Results:
- Fixing the definitions for $m/2$ and $f/2$ the hypotheses that scored best included: $bt(X) \mid mc(X), pc(X)$

⇒ The logical structure to generate the data cases was re-discovered
- The definitions of $mc/1$ and $pc/1$ considered the information from the grandparent to be important, the predicates $m/2$ and $f/2$ were not used
Test Cases and Experiments
Bongard Domain (1)

Setting 1:
- 20 positive and 20 negative examples of the concept ‘there is a triangle in a circle’
- \{ \text{class}(e_1) = \text{pos}, \text{obj}(e_1, o_1) = \text{triangle}, \text{obj}(e_1, o_2) = \text{circle}, \text{class}(e_2) = \text{false}, \text{obj}(e_2, o_1) = \text{triangle}, ... \}
- Given background knowledge \text{in}(e_1, o_1, o_2)
- 20% missing values in the dataset

Results:
- With \text{obj}(Ex, o_2) as lookahead for \text{in}(Ex, o_1, o_2) the best scored hypothesis is: \text{class}(Ex) | \text{obj}(Ex, o_1), \text{in}(Ex, o_1, o_2), \text{obj}(Ex, o_2)
- Without the lookahead the correct hypothesis was not considered
Setting 2 was based on the structure of the program learned in setting 1

- Goal: Estimating the parameters
- 20 positive and 20 negative examples of the disjunctive concept ‘there is a (triangle or a circle) in a circle’
- The probability for the object $o_1$ to be triangle or a circle was equal (no significant difference)

In Setting 3 background knowledge about $in(e_1, o_1, o_2)$ was not given
- The algorithm did not discover the correct rule

Setting 4 was a clustering experiment

- 20 positive and 20 negative examples of the concept ‘there is a triangle’
- The examples had 2 to 8 triangles, circles or squares
- 20% of the class labels were missing
- The algorithm learned $class(X) \mid obj(X,Y)$ which separated the classes perfectly
Test Cases and Experiments
KDD Cup 2001

- **Task**: Predict the localization of a given gene in a cell among 15 distinct positions
- **Data**: Relation table with six categorical attributes *Essential, Class, Complex, Phenotype, Motif, Chromosome Number*
- Training set has 862 genes and the test set 381 genes
  - The naive Prolog representation (4,400 random variables with over 60,000 parameters) broke cause of memory limits in Sicstus Prolog
- Due to this limitation, the logical structure was based on naive Bayes and only the parameters were estimated
- Estimating the parameters took 12 iterations (about 30 min.)
  - The learned Bayesian logic Program achieved an accuracy of 0.57 (top 50% of the submitted models was 0.61, best submission was 0.72)
- The correct localization of a gene was among the top 3 classifications in 77% of the test cases
Agenda

1. Revisiting Bayesian Networks and Logic Programs
2. Bayesian Logic Programs
3. Learning Bayesian Logic Programs
4. Conclusion and Outlook
Conclusion and Outlook (1)

- Bayesian logic programs link up Bayesian networks with inductive logic programming
- Any type of Bayesian network and all types of ’pure’ Prolog programs can be both represented with Bayesian logic networks. Possible implementations for the blood type example and hidden Markov models were introduced
- They combine the advantages of both Bayesian networks and definite clause logic, including the nice separation into
  - a qualitative part: logical structure of the domain
  - and a quantitative part: conditional probability distributions between the objects of the domain
- Along with strict separation comes the graphical representation
Conclusion and Outlook (2)

- A framework for learning Bayesian network was introduced
  - SCOOBY is used to learn the structure of Bayesian logic program
  - To learn the probabilities Maximum Likelihood approach was used. To estimate the parameters for the Maximum Likelihood two techniques were considered
    - Gradient based approach
    - Expectation Maximization algorithm
- In the experiments the principle of the algorithm is shown and some of the test cases brought good results
- For a general use, the framework has to be improved. This could be done with:
  - An enhanced scoring function for SCOOBY
  - Intensified research on the refinement operator to add or delete atoms
  - Also data cases that do not represent the complete logical structure should be considered respectively
References