

A Framework for Bayesian Network Mapping

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Abstract

This research is motivated by the need to support inference across multiple intelligence systems involving uncertainty. Our objective is to develop a theoretical framework and related inference methods to map semantically similar variables between separate Bayesian networks in a principled way. The work is to be conducted in two steps. In the first step, we investigate the problem of formalizing the mapping between variables in two separate BNs with different semantics and distributions as pair-wise linkages. In the second step, we aim to justify the mapping between networks as a set of selected variable linkages, and then conduct inference along it.

At present, a Bayesian network (BN) is used primarily as a standalone system. When the problem scope is large, a large network slows down inference process and is difficult to review or revise. When the problem itself is distributed, domain knowledge and evidence has to be centralized and unified before a single BN can be created for the problem. Alternatively, separate BNs describing related subdomains or different aspects of the same domain may be created, but it is difficult to combine them for problem solving — even if the interdependency relations are available. This issue has been investigated in several works, including most notably Multiply Sectioned Bayesian Network (MSBN) by Xiang (Xiang 2002) and Agent Encapsulated Bayesian Network (AEBN) by Valtorta *et al.* (Valtorta *et al.*, 2002). However, their results are still restricted in scalability, consistency and expressiveness. MSBN's pair-wise variable linkages are between identical variables with the same distributions, and, to ensure consistency, only one side of the linkage has a complete CPT. AEBN also requires a connection between identical variables, but allows these variables with different distributions. Here, identical variables are the same variables deployed into different BNs. In this paper, we propose a framework that supports inference across BNs through mappings between semantically similar variables.

Formalization of BN mapping

We modeled BN mapping as a set of four-layered concepts. The first layer is called *pair-wise probabilistic relations*,

which use joint probabilities to represent the dependency between the two variables. These variables have similar but not necessarily identical semantics and are in two BNs. In our framework we assume these joint probabilities are already available. Then *pair-wise variable linkages*, the second layer concept, are created from these probabilistic relations to provide channels for propagating probabilistic influences between the variables across the two BNs. The third layer is called *valid BN mapping*, a selected subset of all available linkages that ensures the *consistency of mapped networks*. The fourth layer, *Minimum valid BN mapping*, is obtained by *mapping reduction*, a process that minimizes the set of linkages while maintaining the consistency.

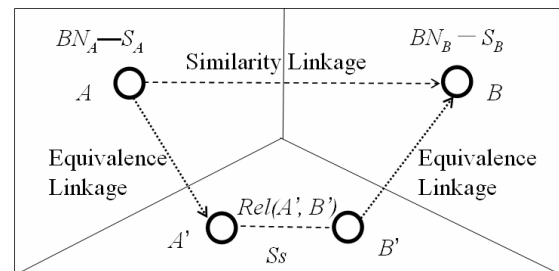


Figure 1. A Variable Linkage

A variable linkage starts from one variable (source variable) and ends at another variable (destination variable) in a different BN. The purpose of building linkages between variables in different Bayesian networks is to propagate the probability influences from one network to the other. Suppose variable A in BN_A and variable B in BN_B represent two identical concepts. An observation of A (and hence B since A and B are identical) is made in BN_A as $P(A)$. This observed distribution of variable B can then be used as soft evidence (denoted by se) to update the distributions of BN_B (see Valtorta, Kim, and Vomlel 2002) using $P(B|se) = P(A)$. All other variables V_B in BN_B are then updated by Jeffrey's rule (Pearl 1990):

$$P(V_B \setminus B | se) = \sum_i P(V_B \setminus B | B = b_i) P(B = b_i | se). (1)$$

If A and B are similar but not identical, the similarity between them can be represented by a probabilistic relation (e.g., joint distribution of A and B). However, in general the probabilistic relation is described in a probability space S_S which is different from S_A and S_B , the spaces for BN_A

and BN_B , respectively. As depicted in Figure 1, A' and B' in S_s represent the same concept as A in S_A and B in S_B and. Then we can propagate soft evidence $P(A'|se) = P(A)$ from S_A to S_B through conditional probability established in S_s , and update the belief on B as

$$P(B|se) = \sum_i P(B|A=a_i)P(A=a_i). \quad (2)$$

All other variables in BN_B are updated using equation (1).

This leads us to define a linkage from A in S_A and B in S_B as:

$$\langle A, B, BN_A, BN_B, Rel(A, B) \rangle,$$

where $Rel(A, B)$ is a probabilistic relation between A and B established in some other space. We say such a linkage is the mapping between from variable A to B .

Mapping reduction and Inference

A pair-wise linkage provides a channel to propagate belief from A in one BN to influence the belief of B in another BN. When the propagation is completed, (1) must hold between the distributions of A and B . If there are multiple such linkages, (1) must hold simultaneously for all pairs. And if this can be achieved to a set of linkages, we say these linkages are consistent. If all probabilistic relations in a set of consistent linkages S can be satisfied by a subset S' of S , we say S' is valid.

In theory, any pair of variables between two BNs can be linked, albeit with different degree of similarities. Fortunately, satisfying a given probabilistic relation between A and B does not require the utilization, or even the existence, of a linkage between A and B . Several probabilistic relations may be satisfied by one linkage. As shown in Figure 2(a), we have variables A and B in BN_1 , C and D in BN_2 , and probability relations between every pair as below:

$$P(C, A) = \begin{pmatrix} 0.3 & 0 \\ 0.1 & 0.6 \end{pmatrix}, P(D, A) = \begin{pmatrix} 0.33 & 0.18 \\ 0.07 & 0.42 \end{pmatrix},$$

$$P(D, B) = \begin{pmatrix} 0.348 & 0.162 \\ 0.112 & 0.378 \end{pmatrix}, \text{ and } P(C, B) = \begin{pmatrix} 0.3 & 0 \\ 0.16 & 0.54 \end{pmatrix}.$$

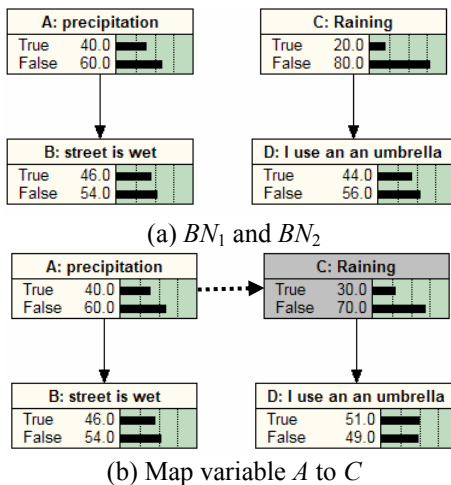


Figure 2. Mapping Reduction Example

However, we do not need to set up linkages for all these relations. As Figure 2(b) depicts, when we have a linkage from A to C , all these relations are satisfied. This is because not only beliefs on C , but also beliefs on D are properly updated by the mapping A to C .

A process called “Mapping Reduction” will be used to form a small valid set of linkages from all pair-wise relations. Our current focus is to develop reduction rules by exploring the network structure of BNs on both sides.

Suppose we already have BN_A and BN_B , and valid BN mappings as k linkages L_1, \dots, L_k between k pairs of nodes A_1, A_2, \dots, A_k in BN_A and B_1, \dots, B_k in BN_B . Note that more than one of these linkages may start from one node in BN_A and more than one may end at one node in BN_B . The inference process is outlined as below:

1. Apply the hard evidence in BN_A and then obtain the posterior distributions of the source nodes A_1, \dots, A_k of linkages $L_1, \dots, L_k: P(A_i | \text{hard_evidence})$.
2. For each linkage, compute the distributions of $B_i, Q(B_i)$, using equation (2).
3. Enter the hard evidence to BN_B , and update it using both hard and soft evidences $Q(B_1), \dots, Q(B_k)$.

Iterative proportional fitting procedure may be used to satisfy multiple soft evidences (Valtorta et al, 2002).

Conclusion and Future Work

Compared with previous works on distributed BN, our framework is more expressive in representing probabilistic relations and more applicable with the help of the mapping reduction process. A series of experiments have been conducted on synthetic BNs to validate our ideas of the formalization of BN mapping and inference methods. We had obtained encouraging results and now are focusing on mapping reduction. We are also working on the semantics of BN mapping and examine its scalability and applicability. A potential Application of this framework is to support ontology mapping, if the ontologies can be translated in BNs as suggested in (Ding et al, 2004).

References

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