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## **Bayesian Networks and Influence Diagrams**

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### **Abstract**

Bayesian networks are graphical models that have been developed in the field of artificial intelligence as a framework to assist researchers and practitioners in applying probability theory to inference problems of substantive size as encountered in real-world applications. Influence diagrams (Bayesian decision networks) extend Bayesian networks to a modelling environment for coherent decision analysis under uncertainty. This chapter provides an overview of these methods and explains their contribution to the body of formal methods for the study, development, and implementation of probabilistic procedures for assessing the probative value of scientific evidence and the coherent analysis of related questions of decision-making.

### **Keywords**

Bayes' theorem

Bayesian network

Decision analysis

Decision theory

DNA evidence

Evidence evaluation and interpretation

Influence diagram

Probability theory

Uncertainty

## Key points

- Bayesian networks (BNs) are graphical probabilistic models that support scientists and lawyers in the evaluation of scientific evidence and in the coherent analysis of inference.
- BNs are particularly well-suited for the analysis of complex configurations of scientific evidence.
- Influence diagrams are a rigorous analytical framework for analysing questions of coherent decision-making.

## Introduction

Some 40 years ago, Bayesian networks (BNs) have been developed in the field of artificial intelligence as a framework to assist researchers and practitioners in applying probability theory to inference problems of substantive size as encountered in real-world applications. Since the late 1980s, Bayesian networks have also attracted the interest of researchers in forensic science. This tendency has considerably intensified throughout the last two decades. There is now a considerable body of scientific literature that reports on the use Bayesian networks for the study, understanding, development and implementation of probabilistic procedures for evaluating the probative value of particular items of scientific evidence in forensic science (Taroni et al., 2014; Dawid & Mortera, 2020), in particular DNA evidence (Taylor et al., 2018). Influence diagrams (IDs) are extensions of BNs, designed to deal with coherent decision analysis under uncertainty (Howard and Matheson, 1984). Originally developed in the context of intelligence research on political conflicts in the 1970s (Howard et al., 2006), IDs – also called Bayesian *decision* networks – became popular in artificial intelligence and statistics, with applications in business and medical decision-making and, more recently, forensic science (Taroni et al., 2014). This article presents an overview of BNs and IDs and their contribution to the body of analytical methods for the coherent analysis of problems of inference (e.g., inference of source) and decision (e.g., identification decisions) at the intersection between forensic science and the law (Biedermann et al., 2018).

## Bayesian Networks

### Preliminaries

Based on the elements of graph and probability theory, BNs can roughly be defined as a pictorial representation of the dependencies and influences (represented by arcs) among variables (represented by nodes) deemed to be relevant for a particular inference problem. Since the early 1980s, BNs have gained widespread acceptance in the field of expert system technology, a field that focuses on the study of knowledge bases associated to inference engines. Through their ability to coordinate probabilistic inference tasks, such as deduction and induction, BNs are now

considered a general representation scheme for uncertainty in knowledge. Although graphical approaches to represent probabilistic information have already been discussed in the first half of the nineteenth century, it is now generally agreed that the seminal works of Judea Pearl in the 1980s (Pearl, 1982) have initiated the development of the formalism known today as BNs. In the landscape of artificial intelligence (AI), BNs are a representative of the statistical AI approaches, covering the domains of reasoning, knowledge and planning (Floridi and Cowls, 2019).

The name ‘Bayesian networks’ is among the most frequently encountered designations. According to the field of application, a variety of other terms – some with possible nuances in definitional details – may be encountered. Among these other terms are ‘Bayes nets’, ‘Bayesian belief networks,’ ‘Bayesian expert systems,’ ‘graphical probabilistic networks,’ ‘probabilistic network models,’ or ‘causal networks.’ For example, the term ‘belief’ in ‘Bayesian belief networks’ emphasizes that the probabilistic assignments used in a given model reflect degrees of personal belief of the individual who conducts the modeling task. In yet other contexts, attention is drawn to the notion of causality. This stems from the fact that the arcs between the nodes of a BN can be interpreted as reflecting assumed causal relationships, even though the definition of BNs does not refer to causality and there is no requirement that the links represent causal impact. They only represent probabilistic relationships between variables.

### **Definition and Properties of BNs**

BNs are a combination of graph and probability theory. Graph theory used to specify the qualitative model structure and probability theory is used to characterize the nature and strength of the relationships between the variables of a model. More formally, a Bayesian network covers the following elements:

- A finite collection of random variables that are represented by nodes. Each of these nodes has a finite set of mutually exclusive states.
- A set of directed edges (arcs) that connect pairs of nodes. The set of variables and the set of directed edges are combined in such a way that a directed acyclic graph is obtained. An acyclic graph is one that contains no loops.
- Node probability tables are associated with each variable of a network. The probability table of a variable  $A$  that has entering edges from variables  $B_1, \dots, B_n$  contains conditional probabilities  $\Pr(A|B_1, \dots, B_n)$ . A variable  $A$  with no entering edges from other variables contains unconditional probabilities  $\Pr(A)$ . Here, the term ‘unconditional’ refers only to the absence of an explicit conditioning on other variables (nodes) in a network. Strictly speaking, a probability of the kind  $\Pr(A)$  is also considered to be conditional because there is always contextual (background) information, commonly denoted by  $I$ , which is used when assigning  $\Pr(A)$ . Thus, strictly speaking,  $\Pr(A)$  should be written as  $\Pr(A|I)$ . However, in forensic science literature, the conditioning on  $I$  is often omitted for simplicity.

The nodes of a BN represent propositional variables of interest. Broadly speaking, variables represent statements or assertions that such and such is the case. An example is the outcome or observation that the features of a given crime stain correspond to the features of control material. More generally, propositions are basic intellectual attributes formed by an individual during the course of a reasoning task. Thus, a proposition can also be thought of as referring to states of affairs (state of nature).

Most often, the actual state of nature is not known with certainty. For example, there may be uncertainty about the truth or otherwise of the proposition according to which a crime stain has

been left by the offender, or the proposition that a given person of interest, rather than an unknown person, is the source of the crime stain. In a BN, such propositions are conceptualized in terms of nodes with states representing, e.g. in case of a binary proposition, the truth and the falsity of the proposition of interest. The degree of belief attached to each state of a node is expressed numerically, i.e. in terms of probabilities representing – for example – personal degrees of belief. Probabilities are organized in node probability tables.

The mutually exclusive states of a variable are also referred to as the domain of the variable. The domain of a variable determines a variable’s subtype. Examples include {red, green, blue} for a labeled variable, {T, F} for a Boolean variable (with ‘T’ and ‘F’ denoting ‘true’ and ‘false,’ respectively), {-2, 1, 4, 5, 7.34, 8} for a numbered variable, and  $\{]-\infty; 0; ]0; 10], ]10; 100]\}$  for an interval node. Note that an interval node is usable for specifying the intervals over which a continuous quantity can be implemented in a discrete form.

The arrows in a BN represent probabilistic (relevance) relationships that correspond to a property that the analyst (modeler) assumes to hold within the context of a given inference problem. If a network is properly constructed, then a directed edge from a node  $A$  to a node  $B$  signifies that  $A$  has a direct influence on  $B$ .

A distinctive feature of BNs is their incorporation of probabilities in terms of tables associated with each node. This provides a probabilistic interpretation of the nature and the strengths of the relationships between the nodes of a network. The node tables can accommodate probabilities from a variety of different sources. Among the most common sources are personal probabilities from human experts and (statistical) data from, for example, databases or literature. Thus, node probability tables can be considered as a means to interface a model to data. Yet a further possibility to specify node probability tables is the use of mathematical expressions, exploiting various variable subtypes as described above.

An important property of BNs is the encoding of collections of conditional independence assumptions and the representation of probability distributions. For the purpose of illustration, consider a distribution  $\Pr$  defined on  $n$  discrete variables  $A_1, A_2, \dots, A_n$ , ordered arbitrarily. Using the product rule, the joint distribution  $\Pr(A_1, A_2, \dots, A_n)$  can be decomposed as follows, also known as the ‘chain rule’:

$$\Pr(A_1, A_2, \dots, A_n) = \left[ \prod_{i=2}^n \Pr(A_i | A_1, \dots, A_{i-1}) \right] \Pr(A_1)$$

A more economic representation of a joint probability distribution can be obtained if one can specify variables that are not ‘sensitive’ to (i.e., directly influenced by) all predecessors, but only to a certain subset of those predecessors. Stated otherwise, a variable  $A_i$  may be independent of all other predecessors once a selected group of predecessors of  $A_i$ , called parents ( $\text{par}$ ) of  $A_i$ , is known. In such a case, the product of the above equation can be rewritten in a shorter form:  $\Pr(A_i | \text{par}(A_i))$ . Now, if the conditional independencies in a BN hold for the collection of variables  $A_1, A_2, \dots, A_n$ , then the BN provides a representation of the joint probability distribution  $\Pr(A_1, A_2, \dots, A_n)$  in terms of the product of all specified potentials, that is,

$$\Pr(A_1, A_2, \dots, A_n) = \prod_{i=1}^n \Pr(A_i | \text{par}(A_i))$$

where  $\text{par}(A_i)$  represents the set of parental variables of  $A_i$ . This equation is called the ‘chain rule for Bayesian networks’ and formally defines what a BN means: a representation of the joint probability distribution for all the variables.

A key task operated by BNs is the processing of newly acquired information, i.e. calculating the conditional probabilities of the states of the nodes in the network given that the state of one or more variables has been observed (or becomes known). It is common to denote the latter as evidence variables and the former as query variables. Broadly speaking, the term evidence can be interpreted as information that is available to a particular individual and that is thought to be incorporated into the belief system maintained by that individual. In the context of forensic science, such information may take the form of one or more propositions whose actual state becomes known to the individual conducting the inference task (e.g., the scientist observes a given amount of similarities and differences between evidential and reference materials). Such newly acquired information provides the basis for reasoning about other propositions that are relevant to a given inference problem. There may also be situations in which information (evidence) is of a more technical nature, such as numerical data generated by an experimental procedure: for example, the number of glass fragments collected on a person’s clothing, detected alleles in the context of DNA evidence, or scores generated by an automatic forensic comparison system. Such results in numerical form may directly be used as input data that can be accommodated by a BN (e.g., by means of a numbered node). Thus, evidence on a variable corresponds to a statement of the certainties of that variable’s states. If it is known with certainty in which state a variable is, then the evidence is called ‘hard’ and the node is said to be ‘instantiated.’ An instantiated variable may also be referred to as an ‘observed’ variable. Generally, evidence that is not ‘hard’ is called ‘soft.’ One can also talk about evidence in terms of a function. For a variable with discrete states, for example, an evidence function that assigns a zero probability to all but one state may be said to provide hard evidence.

In BNs, evidence is processed according to Bayes’ theorem. This represents one of the main points of interest for the study of BNs for probabilistic inference in forensic science. A convenient illustration of this property amounts to a two-node network, involving the two binary variables  $H$  and  $E$ , in terms of the following representation:  $H \rightarrow E$ . A very common and general problem that can be represented in this way is the evaluation of a screening (or, diagnostic) test where  $E$  refers to the result of the test (which is known with certainty and may be either positive or negative), and  $H$  is the proposition about which one is uncertain. For example, one may be uncertain about whether or not a trace is human blood, or whether or not an unknown powder contains an illegal drug. On observing that  $E$  holds, e.g. a positive test outcome, one seeks to calculate  $\Pr(H|E,I)$ , where  $I$  denotes background information. To use Bayes’ theorem for this task, i.e.  $\Pr(H|E,I) = \Pr(H,E)/\Pr(E)$ , the following calculations are needed (omitting  $I$  for shortness of notation):  $\Pr(H,E) = \Pr(H)\Pr(E|H)$  and (ii)  $\Pr(E) = \Pr(E|H)\Pr(H) + \Pr(E|\bar{H})\Pr(\bar{H})$ . Notice that calculation (ii) invokes the so-called extension of the conversation rule.

In the above computation, evidence on the node  $E$  is ‘forwarded’ to the node  $H$  against the direction of the arc that holds between these two nodes. It is important to note that within BNs, propagation is also possible along the direction of the arcs. To continue the example introduced above, propagation along the direction of the arc  $H \rightarrow E$  means to “determine” the probability of  $E$  given  $H$ , or  $\Pr(E|H)$  for short. What happens during the passage from  $\Pr(E)$  to  $\Pr(E|H)$  can be seen in (ii). This relationship states that for assessing the uncertainty about  $E$ , uncertainty in relation to  $H$  needs to be taken into account. However, when  $H$  becomes ‘known,’ this means that  $\Pr(H) = 1$  and

$\Pr(\bar{H}) = 0$ . Consequently, (ii) reduces to  $\Pr(E|H)$ , and this is just the value that has been specified in the conditional probability table of the node  $E$ .

This is an informal description of probabilistic calculations that can be handled within BNs, based solely on a local network fragment. Since the beginning of the development of BNs, researchers and practitioners have sought ways to automate these calculations through computerized implementations, especially for large networks. This was considered to be an essential step to be achieved if the approach is to be of use for complex real-world applications. Several algorithms are now available to perform calculations in an efficient manner. These approaches have been implemented in academically and commercially available BN software packages.

Note, however, that the numerical specification of models may, at times, be challenging. In such situations, BNs may still be used, though at a more general level of detail, using qualitative abstractions and sensitivity analyses (e.g., Biedermann & Taroni, 2006).

## **Influence Diagrams**

Influence diagrams, also called Bayesian decision networks, extend probabilistic inference networks (BNs) to a framework for coherent decision analysis under uncertainty. Besides probabilistic nodes, representing uncertain events, influence diagrams contain two additional types of nodes: decision nodes and utility (loss) nodes. Decision nodes specify the available actions at a given decision point whereas utility (loss) nodes specify the decision-maker's preferences among various decision outcomes (e.g., Jensen & Nielsen, 2007; Kjaerulff & Madsen, 2008).

To set this into perspective, recall that BNs focus on reasoning under uncertainty, that is questions of the following kind: "Given knowledge of the occurrence of event(s)  $A$  ( $B$ ,  $C$ , etc.), e.g. the outcome of a diagnostic test, what is the probability of event(s)  $R$  ( $S$ ,  $T$ , etc.) occurring (or having occurred), e.g. the presence of a target substance in the examined item?"

Influence diagrams extend such inquiries to questions of decision analysis. For example, a BN for evaluating the result of a diagnostic test may contain a node to represent the decision to conduct a particular test or examination. See, for example, Taroni et al. (2005) for an application to the question of whether or not to conduct DNA analyses in disputed kinship cases, and Gittelsohn et al. (2013) in the context of fingerprint analysis.

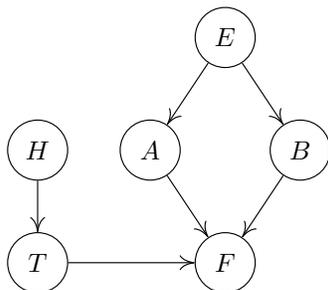
The key feature of influence diagrams is the computation of expected utilities (or, losses), a main criterion in decision theory to characterize and compare rival decisions. More specifically, in decision theory, the optimal decision is to select the decision that maximizes (minimizes) expected utility (loss).

## **Bayesian Networks and Influence Diagrams for Probabilistic Inference and Decision Analysis in Forensic Science**

### **Early Uses of Bayesian Networks for Particular Case Modeling**

One of the first studies, in print, on BNs applied to forensic case settings was published in the late 1980s in the Journal of the Forensic Science Society (Aitken & Gammerman, 1989). It focuses on a hypothetical murder case. The authors show how a network approach (see **Figure 1**) might be applied to cases involving several, possibly complicated, interrelated issues. They provide a

detailed discussion of how (i) to extract relevant propositions from a case description, (ii) qualitatively represent relationships between propositions in terms of a directed acyclic graph, and (iii) incorporate data-informed (personal) beliefs as probabilities and use them for inference. See Dawid & Evett IW (1997) for a further, early paper on the use of BNs for particular case modeling.



**Figure 1** Bayesian network for a hypothetical murder case. The nodes are defined as follows: *A*, ‘X’ committed the murder; *B*, ‘Y’ committed the murder; *E*, eyewitness evidence of a row between ‘X,’ ‘Y’ and the victim some time before the crime was committed; *F*, fibers from a jacket similar to one found in the possession of ‘X’ are found at the scene of the crime; *H*, ‘Y’ drives the car of ‘X’ regularly; *T*, ‘Y’ picks up fibers from jacket of ‘X’. (Reproduced from Aitken, C. & Gammerman, A. (1989). Probabilistic reasoning in evidential assessment. *Journal of the Forensic Science Society* **29**, 303–316; with permission from Elsevier).

### Bayesian Networks for Generic Patterns of Inference

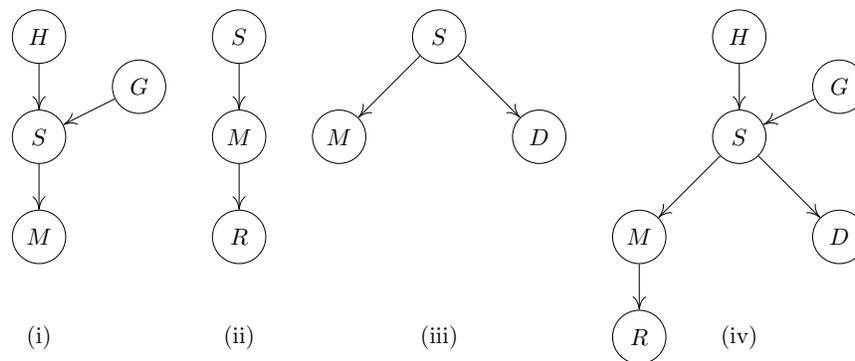
Rather than focusing on a particular case, as outlined in the previous section, one can construct BNs for recurrent patterns of inference concerning scientific evidence. This perspective places an emphasis on more generic and fundamental aspects that forensic scientists should account for when evaluating evidence with respect to propositions of judicial interest. Stated otherwise, the modeling concentrates on general case aspects (e.g., the relevance of trace material), irrespective of situational details. **Figure 2(i)** shows an example for such a BN, designed for evaluating one-trace cases involving transfer from the offender to the scene. It includes considerations such as

- the rarity of the analytical features among members of the relevant suspect population;
- the possibility that the stain was left by the person of interest, even though being innocent of the offense, and
- the relevance of the crime stain for the case (i.e., the probability that the stain has a true connection with the offender).

A more formal definition of the various nodes is given in **Table 1**.

**Table 1** Definition of the binary nodes used in the BNs shown in **Figure 2**

<i>Node</i>	<i>Definition</i>
<i>H</i>	The person of interest (POI) is the offender
<i>S</i>	The crime stain came from the POI
<i>G</i>	The crime stain came from the offender
<i>M</i>	The the POI and the crime stain have corresponding DNA profiles
<i>R</i>	Reported correspondence between DNA profile of the POI and the DNA profile of the crime stain
<i>D</i>	The other (N-1) profiles in the database do not correspond



**Figure 2** BN fragments for (i) one-trace one-offender cases (involving transfer from the criminal to crime scene), (ii) the problem of laboratory error, (iii) results of a database search. Model (iv) shows a combination of the network fragments (i), (ii), and (iii). The definition of the nodes is as given in **Table 1**. (Reproduced from Taroni, F., Biedermann, A., Garbolino, P. & Aitken C.G.G. (2004). A general approach to Bayesian networks for the interpretation of evidence. *Forensic Science International* **139**, 5–16; with permission from Elsevier).

**Figure 2(ii)** shows a more refined representation of a situation in which one seeks to draw an inference about *S*, the proposition according to which the person of interest is the source of a crime stain. A particular aspect of this model is a distinction between (a) a true, but actually unobserved, correspondence between the profiles of the crime stain and control material from the person of interest (node *M*) and (b) an observed (or reported) correspondence by the scientist. This distinction allows one to account for the probability of a false positive report (Thompson et al., 2003). A false positive occurs when a report states a correspondence when in fact the crime stain and the person of interest have different profiles.

**Figure 2(iii)** shows a further BN useable for inference about the proposition *S*, but including the additional item of information *D* that a certain number of profiles in a database were found to be different from that of the crime stain. This is a relevant item of information that provides distinct evidential value for the proposition that the POI is the source of the crime stain (rather than an unknown person), in the same way as learning about a correspondence *M* between the profiles of the POI and the crime stain.

All three BNs, Figures 2(i)–(iii), have probabilistic underpinnings that agree with published likelihood ratio formulae, designed to assess the probative value of DNA evidence in the respective type of case.<sup>1</sup> A further aspect worth mentioning is that these network fragments can be logically combined so as to lead to the model shown in **Figure 2(iv)**. This model allows one to jointly evaluate the various aspects considered in the separate local network fragments 2(i)–(iii). This illustrates that BNs play an important role in the coherent representation and analysis of complicated patterns of evidence. In particular, it is possible to approach inference problems on a more local level first, and then use the fragments thus constructed for reasoning about a problem of greater complexity, such as the joint evaluation of multiple items of evidence (e.g., Juchli, Biedermann & Taroni, 2012). It is important, however, to keep in mind that a model remains a probabilistic interpretation of a real phenomenon or, more generally, an inference problem, constructed at a given level of acceptable approximation. There is no claim that the result represents the ‘true model.’

## Contemporary uses of Bayesian Networks for Assessing Complex DNA Evidence

### *Representation of genotypes*

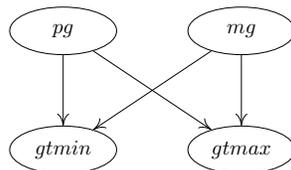
In the previous sections, a single discrete chance node was used for representing the outcome of the scientist’s analyses and examinations, such as the DNA profile of a biological trace or, more generally, the observed similarities and differences between questioned and known materials. In the simplest case, this perspective amounts to a two-node network fragment in which knowledge about the state of an observational variable, such as  $E$  (e.g., short for ‘corresponding DNA profiles’), is used for drawing an inference about propositions according to which the POI is (is not) the source of the crime stain. If the latter propositions are represented by the node  $H$ , the BN takes the structure  $H \rightarrow E$ .

Besides this formative and coarse modeling approach, considerable research has been devoted to the development of more sophisticated representational schemes for the outcomes of DNA profiling analyses, useable as repeatable submodules in similar situations (Dawid et al., 2002). These are generic network fragments, representing individual genes, rather than full genotypes or DNA profiles. As an example, consider the network fragment with the converging connection  $mg \rightarrow gt \leftarrow pg$ , where  $gt$  represents a genotype, modeled as a logical combination of the alleles inherited from the mother and father, represented by the nodes  $mg$  and  $pg$ , (short for, respectively, ‘maternal gene’ and ‘paternal gene’). A gene  $A$ , for instance, can take one of several different forms, also called alleles. Suppose there are  $n$  alleles at gene  $A$ , denoted  $A_1, A_2, \dots, A_n$ . In the BN  $mg \rightarrow gt \leftarrow pg$ , the states  $A_1, A_2$ , and  $A_x$  are specified for nodes  $mg$  and  $pg$ . The third state,  $A_x$ , accounts for all unobserved alleles  $A_3, \dots, A_n$ . The possible states of the genotype node  $gt$  can then be defined as  $A_1A_1, A_1A_2, A_1A_x, A_2A_2, A_2A_x$ , and  $A_xA_x$ , covering all the logical combinations of pairs of alleles. For a more general ready-to-use representation, one might want to specify, for each parental gene  $pg$  and  $mg$ , the full repertory of alleles at a given locus. However, this may lead to a rapid increase in the size of the probability table for the node  $gt$ . This can be avoided by replacing the node  $gt$  by two distinct nodes  $gtmin$  and  $gtmax$ , as shown in **Figure 3** (Dawid et al.,

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<sup>1</sup> For further examples of agreement between BN output and likelihood ratio formulae for value of evidence computations, see Garbolino & Taroni (2002).

2007). These two nodes represent, respectively, the minimum and the maximum allele number of the two parental gene nodes  $pg$  and  $mg$ .



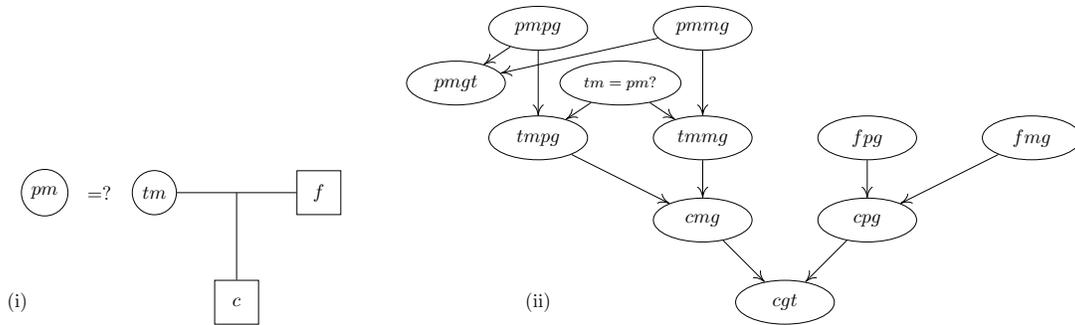
**Figure 3** Representation of an individual's genotype as the minimum ( $gtmin$ ) and maximum ( $gtmax$ ) of the two parental gene nodes  $pg$  and  $mg$ , inherited via the paternal and maternal line, respectively. (Adapted from Dawid, A.P., Mortera, J. & Vicard, P. (2007) Object-oriented Bayesian networks for complex forensic DNA profiling problems. *Forensic Science International* **169**, 195–205; with permission from Elsevier).

### ***Kinship analyses (disputed maternity)***

The application of the modeling approach for genotypes, outlined in the previous section, can be illustrated in the context of a case of disputed maternity. A certain woman, putative mother  $pm$ , is supposed to be the mother of a child  $c$ . DNA profiles are available for the putative mother  $pm$  and the child  $c$ . No (putative) father is available in this case. The purpose of the analysis is to derive the likelihood ratio for the proposition that the putative mother  $pm$ , rather than an unknown woman, is the true mother  $tm$ , noted  $tm = pm ?$ , given knowledge about the child's genotype  $cgt$  and the putative mother's genotype  $pmgt$ . The pedigree corresponding to this inference problem is shown in **Figure 4(i)**.

**Figure 4(ii)** shows a representation of this disputed maternity case in terms of a BN. A BN with this structure can be constructed for each genetic marker for which DNA profiling results are available. These networks can be analyzed separately and the resulting likelihood ratios combined subsequently. It is also possible to combine the single-locus networks to build a 'top-level' network, in the context also called 'supernetwork,' which can be implemented with the help of *object-oriented Bayesian networks* (OOBNs) (Dawid et al., 2006). OOBNs are BNs with various hierarchical levels of specification (Kjaerulff & Madsen, 2008), providing a framework for probabilistic modelling at different levels of abstraction and representation.

The BN shown in **Figure 4(ii)** allows one to obtain the same results as with classic arithmetic calculus of Essen-Möller under the Hardy-Weinberg assumption of independence. One might be tempted, thus, to conclude that working with BNs implies no real advantage, as there is no need to develop new methods for problems that can be solved by simple algebra. However, the purpose of using a graphical probabilistic model of the kind shown in **Figure 4(ii)** is different. Such a model provides a general rather than a case-specific representation: i.e. the same BN can be used to solve other cases involving individuals with *different* DNA profiles. Moreover, the model provides a solid basis for evaluating DNA results in more complex cases for which no simple, predefined formulae exist. Examples include extensions to deal with aspects such as missing data (i.e., when profiling data of some individuals are unavailable), additional data (e.g., from a related person, if available), mutation or DNA mixtures.



**Figure 4** Different representations of a case of disputed maternity: (i) pedigree (with squares representing males and circles females, *pm* denoting the putative mother, *tm* denoting the true mother, *f* denoting the father and *c* denoting the child) and (ii) a BN. For the BN, *tmpg*, *tmmg*, *fpg*, and *fmg* denote the maternal *m* (in second place for *fmg*, and in third place for *tmmg*) and paternal *p* genes of the true mother *tm* and the father *f*; *cpg* and *cmg* denote the child’s paternal and maternal genes, respectively; *pmpg* and *pmmg* denote the putative mother’s paternal and maternal genes, respectively; *pmgt* and *cgt* denote the genotypes of the putative mother and the child, respectively, and *tm = pm?* takes two values in answer: ‘yes’ or ‘no’ as to whether the true mother is the putative mother.

### ***Evaluating Complex DNA Evidence Given Activity Level Propositions***

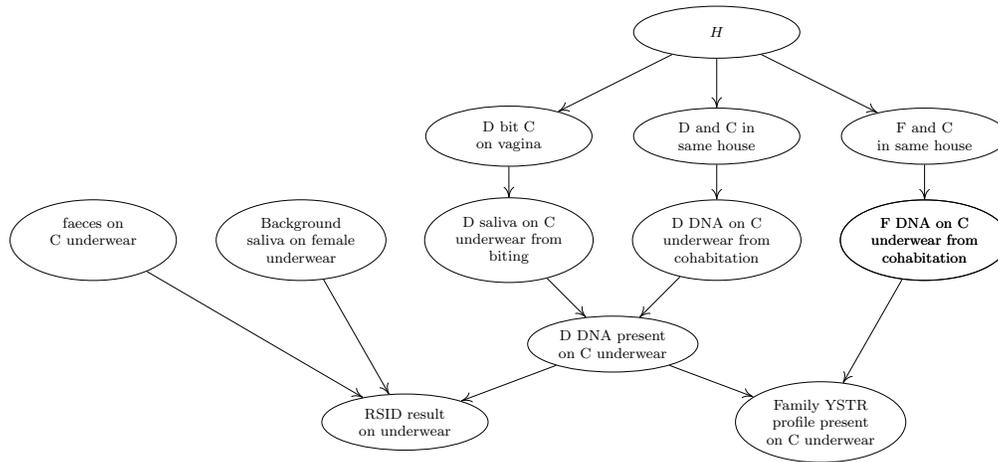
Forensic genetics laboratories encounter a considerable number of cases with biological traces containing only small quantities of DNA. Such traces pose interpretative challenges in the sense that, often times, the main question of interest for recipients of expert information is not ‘whose DNA is this?’, but a question of the kind ‘how did this DNA get there?’ (Taroni et al., 2013). DNA profiling results thus need to be interpreted with respect to so-called activity-level propositions. This requires the scientist to condition the evaluation on various intermediate propositions and case-specific allegations. It has long been recognized that BNs are well-suited to structure evaluative thinking that is required in such cases (Evetts et al., 2002).

For the purpose of illustration, consider the example presented in Taylor et al. (2018) regarding a case in which underwear from a complainant is examined. The case is described as follows: “A 24-year-old girl (*C*), who normally lives with her biological mother (*M*) and father (*F*) has stayed for a week at her older brother’s (*D*) house. A friend of the girl receives a phone call from the girl stating that her brother has bitten her on the vagina, over her underwear. The friend picks up the girl and they go immediately to the police, where the underwear is seized and a reference from the girl taken. The police then arrest the brother and take a reference DNA sample from him.” (at p. 138)

The challenge of constructing a BN for this case consists in, first of all, defining variables and their relationships. Taylor et al. (2018) propose a methodology that focuses on defining nodes for the main propositions, the findings (or, observations) as well as intermediate propositions regarding particular events. The nodes are connected in such a way that they logically define argumentative pathways that can account for the findings given the competing (main) propositions. Figure 5 shows an example of a BN that can be obtained when applying this methodology to the case described above. For the full numerical specification of this BN, see the supplementary materials in Taylor et al. (2018).<sup>2</sup>

<sup>2</sup> Freely available at: <http://dx.doi.org/10.1016/j.fsigen.2017.12.006>

A generalized model that extends previous works on evaluation given activity level propositions can be found in Taroni et al. (2021).

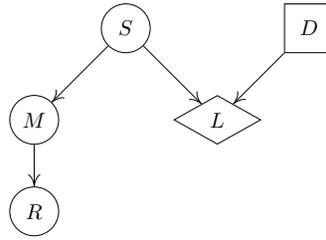


**Figure 5.** BN for a case of alleged sexual assault. The node  $H$  represents the propositions ‘D has bitten C on the vagina, over her underwear’ and ‘C has been staying at D’s home, but no biting occurred’. (Adapted from Taylor, D., Biedermann, A., Hicks, T. & Champod, C. (2018). A template for constructing Bayesian networks in forensic biology cases when considering activity level propositions. *Forensic Science International: Genetics* **33**, 136–146; with permission from Elsevier).

### Influence Diagrams for Modelling Forensic Identification Decisions

Influence diagrams are ideally suited to capture the conceptual relationship between inference and decision making. For the purpose of illustration, consider again **Figure 2(ii)**, representing a BN for inference about the proposition  $S$  according to which the POI, rather than an unknown person, is the source of a crime stain, based on the report  $R$  provided by the scientist. The report  $R$  states that the crime stain and reference material from the POI have corresponding analytical features. A decision-maker, however, may not only be interested in questions of the kind ‘What is the probability that the POI is the source of the crime stain, given the report  $R$  provided by the scientist, and the background information  $I$ ?’, i.e.  $\Pr(S|R,I)$ . The decision-maker may need to decide whether or not to consider (i.e., proceed as though) the POI is the source of the crime stain: this is commonly known as an identification (or, individualisation) decision. In this sense, identification is a question of decision-making for which  $\Pr(S|R,I)$  is an important, but not sufficient ingredient. Besides uncertainty about the proposition  $S$ , represented by the probability  $\Pr(S|R,I)$ , the decision-maker also needs to consider the relative (un-)desirability of the possible consequences of making a decision about identification. In decision-theoretic language, this amounts to introducing two elements that can be formally represented in terms of an influence diagram: the first is a node representing the available decisions, and the second is a node representing a utility (loss) function. Decision and utility nodes are commonly represented by square and diamond boxes, respectively. **Figure 6** illustrates how to use a decision node  $D$  and a loss node  $L$  for modelling the problem of forensic identification in our running example. The node  $L$  is specified as a direct descendant of the nodes  $S$  and  $D$ . This represents the understanding that the combination of a given decision (e.g., identification), together with a particular state of nature (e.g., the POI is the source of the crime

stain), leads to a well-defined outcome, the value (or, desirability) of which is expressed by the utility (loss) function at the node  $L$ .



**Figure 6** Influence diagram representing the problem of forensic identification. The definition of the nodes  $M$ ,  $R$  and  $S$  is as in Table 1. The node  $D$  is a decision node representing the possible decisions regarding identification whereas the node  $L$  implements the loss function.

For simplicity, consider only two possible decisions, identifying the POI as the source of the crime stain ( $d_1$ ) and not identifying the POI ( $d_2$ ) as the source of the crime stain (see Biedermann et al. (2008) for an extension to the conclusion “inconclusive”). Now make the following assumptions: (i) identifying (not identifying) the POI when the POI is (is not) the source of the crime stain represent desirable outcomes for which a zero loss is assigned; (ii) identifying the POI when in fact an unknown person is the source (i.e., an erroneous identification) is the overall worst consequence for which the maximum loss of  $l_1=1$  is assigned; (iii) not identifying the POI when the POI is in fact the source of the crime stain is an undesirable outcome, but less severe than a false identification, hence a loss value smaller than 1, i.e.  $l_2<1$ , is assigned. Based on these assignments, we can compute the *expected loss* (EL) of each decision, given the expert’s report  $R$  and information  $I$ . It can be shown that  $EL(d_1|R,I)$  reduces to  $1-\Pr(S|R,I)$  and  $EL(d_2|R,I)$  reduces to  $l_2\cdot\Pr(S|R,I)$ .

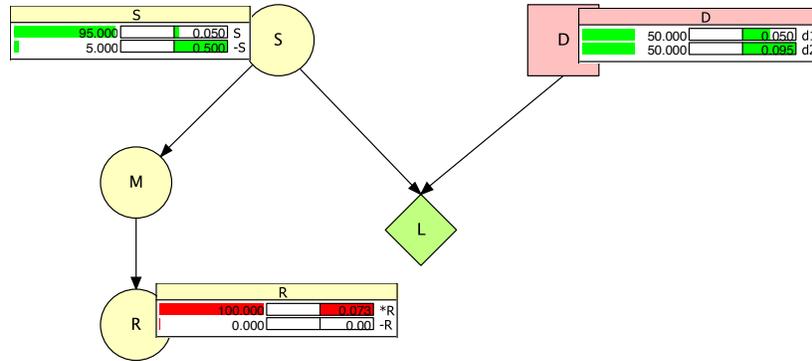
**Figure 7** illustrates the influence diagram defined in **Figure 6**, constructed with the program Hugin Researcher (vers. 9.0). Evidence on the node  $R$  is available and leads to posterior probability  $\Pr(S|R,I)=0.95$ , displayed as 95.00% in the monitor window associated with the node  $S$ . The loss  $l_2$  of a ‘missed’ identification is set to 0.1, i.e. ten times less than the loss  $l_1=1$  assigned to a false identification. The monitor window associated with the decision node  $D$  displays the expected losses for decisions  $d_1$  (identify the POI) and  $d_2$  (do not identify the POI). Following the formulae given above, we can see that

$$\begin{aligned} EL(d_1|R,I) &= 1-\Pr(S|R,I) \\ &= 1-0.95=0.05 \end{aligned}$$

and

$$\begin{aligned} EL(d_2|R,I) &= l_2\cdot\Pr(S|R,I) \\ &= 0.1\cdot0.95=0.095. \end{aligned}$$

Thus, in the case here,  $EL(d_1|R,I)< EL(d_2|R,I)$ , i.e. decision  $d_1$  is the optimal decision as it minimises the expected loss. More generally, it can be shown that  $d_1$  has a smaller expected loss than  $d_2$ , whenever the posterior odds  $\Pr(S|R,I) / \Pr(\bar{S}|R,I)$  exceeds the loss ratio  $l_1/l_2$ . More detailed decision-theoretic developments for forensic identification decisions can be found in Biedermann et al. (2008, 2016), Taroni et al. (2010, 2014) and Aitken et al. (2021).



**Figure 7** Implementation of the influence diagram shown in Figure 6, using the program Hugin Researcher (vers. 9.0). Evidence on the node *R*, the report of a scientist, is available (marked in red). This evidence leads to a posterior probability of 0.95 for the proposition that the POI is the source of the crime stain, displayed in the monitor window associated with the node *S*. The node *D* shows the expected losses of the two decisions *d*<sub>1</sub>, identify the POI as the source of the crime stain, and *d*<sub>2</sub>, do not identify the POI as the source of the crime stain.

## Conclusions

BNs and influence diagrams represent powerful graphical devices to support scientists and lawyers in assessing the value of scientific evidence and thinking logically about questions of decision-making (e.g., forensic identification). Compared to other graphical methods, BNs offers the additional advantage of incorporating probability theory as a coherent measure of uncertainty. In turn, influence diagrams allow one to operationalize decision-theoretic principles. Computerized systems currently exist that can perform calculations in BNs and influence diagrams over a number of variables with complex dependency structure. More recent developments, in particular, the extension to object orientation, have further increased the possibility to extend analyses to levels of complication that are commonly associated with real-world applications. BNs and influence diagrams thus represent a complementary contribution to the body of analytical techniques that are needed to approach inference and decision problems in accordance with probability and decision theory, both conceptually and practically.

## References

- Aitken, C. & Gammerman, A. (1989). Probabilistic reasoning in evidential assessment. *Journal of the Forensic Science Society* **29**, 303–316.
- Aitken, C., Taroni, F. & Bozza, S. (2021). *Statistics and the evaluation of evidence for forensic scientists* (3rd edn.). Chichester: John Wiley & Sons.
- Biedermann, A. & Taroni, F. (2006). Bayesian networks and probabilistic reasoning about scientific evidence when there is a lack of data. *Forensic Science International* **157**, 163–167.
- Biedermann, A., Bozza, S. & Taroni, F. (2008). Decision theoretic properties of forensic identification: underlying logic and argumentative implications. *Forensic Science International* **177**, 120–132.
- Biedermann, A., Bozza S. & Taroni F. (2016). The decisionalization of individualization. *Forensic Science International* **266**, 29-38,

- Biedermann, A., Bozza, S. & Taroni, F. (2018). Normative decision analysis in forensic science. *Artificial Intelligence and Law* **28**, 7–25.
- Dawid, A. P., & Evett, I.W. (1997). Using a graphical method to assist the evaluation of complicated patterns of evidence. *Journal of Forensic Sciences* **42**, 226–231.
- Dawid, A. P. & Mortera, J. (2020). Bayesian networks in forensic science. In Banks, D. L., Kafadar, K., Kaye, D.H. & Tackett, M. (eds) *Handbook of Forensic Statistics* (Chapman & Hall/CRC Handbooks of Modern Statistical Methods). 165–197. Boca Raton: CRC Press.
- Dawid, A. P., Mortera, J., Pascali V. & van Boxel, D. (2002). Probabilistic expert systems for forensic inference from genetic markers. *Scandinavian Journal of Statistics* **29**, 577–595.
- Dawid, A.P., Mortera, J. & Vicard, P. (2007) Object-oriented Bayesian networks for complex forensic DNA profiling problems. *Forensic Science International* **169**, 195–205.
- Evett, I. W., Gill, P. D., Jackson, G., Whitaker, J. & Champod, C. (2002). Interpreting small quantities of DNA: the hierarchy of propositions and the use of Bayesian networks. *Journal of Forensic Sciences*, **47**, 520–530.
- Floridi, L. & Cows, J. (2019). A unified framework of five principles for AI in society. *Harvard Data Science Review* **1**. <https://doi.org/10.1162/99608f92.8cd550d1>
- Garbolino, P. & Taroni, F. (2002). Evaluation of scientific evidence using Bayesian networks. *Forensic Science International* **125**, 149–155.
- Gittelsohn, S., Bozza, S., Biedermann, A. & Taroni, F. (2013). Decision-theoretic reflections on processing a fingerprint. *Forensic Science International* **226**, e42–e47.
- Howard, R. A., Matheson, J. E., Merkhofer, M. W., Miller, A. C., North, W. D. (2006), Comment on influence diagram retrospective. *Decision Analysis* **3**, 117–119.
- Howard, R. A. & Matheson, J. E. (1984). Influence diagrams. In Howard, R.A. & Matheson, J. E. (eds) *Readings on the Principles and Applications of Decision Analysis*, Volume 2. 719–762. Menlo Park: Strategic Decisions Group.
- Jensen, F. V. & Nielsen, T. D. (2007). *Bayesian networks and decision graphs*. New York: Springer.
- Juchli, P., Biedermann, A. & Taroni, F. (2012). Graphical probabilistic analysis of the combination of items of evidence. *Law, Probability & Risk* **11**, 51–84.
- Kjaerulff, U. B. & Madsen, A. L. (2008). *Bayesian networks and influence diagrams: a guide to construction and analysis*. New York: Springer.
- Pearl, J. (1982). Reverend Bayes on inference engines: A distributed hierarchical approach. In: American Association for Artificial Intelligence (Eds.) *Proceedings of the Second AAAI Conference on Artificial Intelligence* (AAAI'82). 133–136. Pittsburgh: AAAI Press.
- Taroni, F., Biedermann, A., Bozza S., Garbolino P. & Aitken C. (2014). *Bayesian networks for probabilistic inference and decision analysis in forensic science* (2nd edn.). Chichester: John Wiley & Sons.
- Taroni, F., Biedermann, A., Garbolino, P. & Aitken C.G.G. (2004). A general approach to Bayesian networks for the interpretation of evidence. *Forensic Science International* **139**, 5–16.

- Taroni F., Biedermann A., Vuille J., Morling N. (2013). Whose DNA is this? This is not the relevant question (a note for forensic scientists). *Forensic Science International: Genetics* **7**, 467–470.
- Taroni, F., Bozza, S. & Aitken, C. (2005). Decision analysis in forensic science. *Journal of Forensic Sciences* **50**, 894–905.
- Taroni, F., Bozza, S., Biedermann, A., Garbolino, P. & Aitken, C. (2010). Data analysis in forensic science: a Bayesian decision perspective. Chichester: John Wiley & Sons.
- Taroni, F., Garbolino, P. & Aitken, C. (2021). A generalised Bayes' factor formula for evidence evaluation under activity level propositions: Variations around a fibres scenario. *Forensic Science International* **322**, 110750.
- Thompson, W.C., Taroni, F. & Aitken, C. (2003). How the probability of a false positive affects the value of DNA evidence. *Journal of Forensic Sciences* **48**, 47–54.
- Taylor, D., Biedermann, A., Hicks, T. & Champod, C. (2018). A template for constructing Bayesian networks in forensic biology cases when considering activity level propositions. *Forensic Science International: Genetics* **33**, 136–146.
- Taylor, D., Kokshoorn, B., & Biedermann, A. (2018). Evaluation of forensic genetics findings given activity level propositions: A review. *Forensic Science International: Genetics* **36**, 34–49.