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GeNIe: A Development Environment for Graphical Decision-analytic Models

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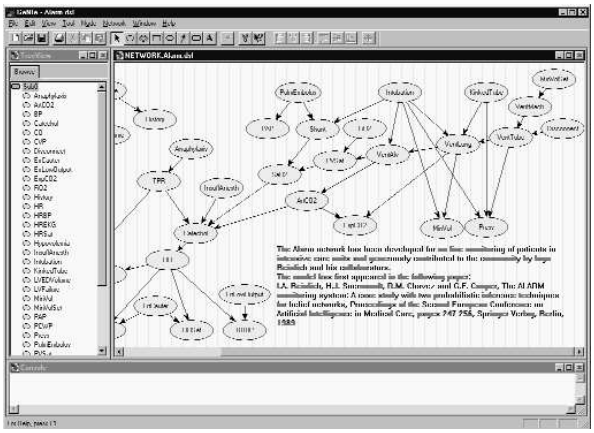
Decision-analytic modeling tools, such as Bayesian networks and influence diagrams, are increasingly finding successful applications in medical informatics. Their major strengths are sound theoretical foundations, ability to combine existing data with expert knowledge, and the intuitive framework of directed graphs. **GeNIe** is a general-purpose development environment for graphical decision-analytic models. Its reasoning engine, **SMILE**☺ (***S**tructural **M**odeling, **I**nference, and **L**earning **E**ngine*) is a fully portable library of C++ classes implementing graphical decision-analytic methods and directly amenable to inclusion in intelligent information systems. **SmileX**, an Active-X Windows version of **SMILE**☺, allows the library to be accessed from any Windows programming environment, including direct access from WWW pages. We have made all three modules available free of charge for non-commercial research, teaching, and personal use at the following address: http://www2.sis.pitt.edu/~genie since July 1998. As of March 1999, there are over 1,300 users from over 50 countries. While current applications of **GeNIe** and **SMILE**☺ cover a range of fields, a growing number of users apply **GeNIe** and **SMILE**☺ in medical informatics training and in building medical informatics systems, for example in medical diagnosis and therapy planning.

GeNIe and **SMILE**☺ are equipped with a pleasant and reliable user interface both in terms of the model development environment (**GeNIe**) and the programmer's interface to the library classes (**SMILE**☺). Their modeling capabilities include hierarchical sub-models, Noisy-OR nodes, deterministic nodes, multiple decision nodes, multiple utility nodes, and linearly additive multi-attribute utility nodes. They implement several exact and approximate algorithms to choose from, value of information computation, and relevance reasoning, which supports sequential information processing in practical systems. The development environment includes a graphical interface with several modules that aid in model navigation, such as hierarchical sub-models, a Windows-style tree view, and on-screen comments. (See **GeNIe** screen snapshot included on this page.) **GeNIe** is Decision Systems Laboratory's primary research and teaching vehicle, so naturally it will evolve with time. A version currently under development is capable of learning probabilistic models (both their structure and their numerical parameters) from data, if these are available. We are also working on graphical tools for both model building and presentation of results. **GeNIe**'s comprehensive HTML-based help system includes many documents, tutorials, and useful links to Internet resources and is fully integrated with the WWW. It is, to a degree, a standalone guide to decision- analytic modeling techniques.



The architecture of the system is flexible: **SMILE**☺ allows for building dedicated interfaces to models developed using **GeNIe**. Such dedicated interfaces can match user's expectations and expertise, screening off the details of decision- analytic modeling, if needed. **GeNIe** and **SMILE**☺ are able to read and write several popular Bayesian network and influence diagram file formats, including the most recent version of the Bayesian network interchange format. It can thus be used as a conversion program and a tool for exchanging models and research results among various research groups. During the AMIA conference demonstration, I will show a model development session and several medical models built using **GeNIe**.

Acknowledgments

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