

The Nijmegen Health Care Computing Initiative

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Bayesian Decision Support in Medical Screening

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The availability of huge data sets (e.g., the digitisation of the Dutch breast cancer screening) may lead to important changes in health care by mining those data for the development of decision support systems.

Aims

The further development of CAD technology using Bayesian Networks to address the problem of interpretation failures by radiologists.

- Development of novel classification methods such that:
 - Medical background knowledge can be incorporated
 - Classifiers are faithful w.r.t. the data
- Develop new image representation techniques
- Extend mammographic breast cancer data sets
- Determine experimentally how to use CAD as a decision aid

References

- [1] M. Samulski, N. Karssemeijer, P. Lucas, and P. Groot. Classification of mammographic masses using support vector machines and Bayesian networks. In *SPIE Medical Imaging*, 2007.



Breast mammogram with visible mass

With the department of Radiology of



Background

The Nijmegen Health Care Computing Initiative is an NWO funded hefboom program. Health care is in a phase of transition. The role of basic biological sciences in health care for example has increased considerably. Furthermore, there is a mounting pressure on health care organisations to improve the efficacy and cost-effectiveness, without sacrificing the quality of care. Information Technology is and will be a major factor in steering these developments.

The aim of the project is to broaden the expertise within our department to the health care domain by setting up new research collaborations with other organisations (e.g., Radboud University Hospital, Nictiz, Philips, etc.). Some examples of research areas that we are interested in are:

- Bayesian networks
- Datamining, machine learning
- Medical guidelines (www.protocol.org)
- Security
- Telemedicine
- Information Architectures
- Software Quality (Laboratory for Quality Software (www.laquso.com))

Medical Guidelines

Health care is more and more based on scientific evidence, which has led to the development of medical guidelines, i.e., structured documents providing detailed steps for disease management.

Aims

Support guideline developers in the health-care profession in the construction and maintenance of high-quality and up-to-date living guidelines and protocols using formal techniques.

We are closely working together with a number of European partners:

- Universitat Jaume I - UJI, Castelln, Spain.
- Dutch Institute for Healthcare Improvement - CBO, Utrecht, Netherlands.
- Fundaci Biblioteca Josep Laporte - FBIL, Barcelona, Spain.
- Vienna University of Technology - TUW, Vienna, Austria.
- University of Augsburg - UA, Augsburg, Germany.
- Vrije Universiteit Amsterdam - VUA, Amsterdam, Netherlands.

References

- [1] P.J.F. Lucas. Quality checking of medical guidelines through logical abduction. In *Proceedings of AI-2003*, volume XX, pages 309–321. Springer, 2003.
- [2] A.J. Hommersom, P.J.F. Lucas, and M. Balsler. Meta-level verification of the quality of medical guidelines using interactive theorem proving. In *JELIA*, volume 3229 of LNCS, pages 654–666. Springer-Verlag, 2004.
- [3] A.J. Hommersom, P. Groot, P. Lucas, M. Balsler, and J. Schmitt, Combining Task Execution and Background Knowledge for the verification of Medical Guidelines. *KBS Journal*, 2007.
- [4] A. Hommersom, P. Groot, P. Lucas, M. Marcos, and B. Martinez-Salvador. A Constraint-based Approach to Medical Guidelines and Protocols. In *ECAI 2006 Workshop*, 2006.

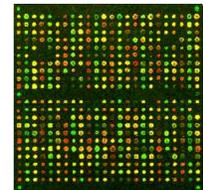
Bioinformatics

With the development of microarray technology the unravelling of the functioning of DNA has taken an enormous step forward. A problem that currently receives a lot of attention is the prediction of protein-to-protein interactions.

Aims

Recover gene regulatory networks from gene expression data involving

- Bayesian network technology
- Use of preprocessing techniques
- Development of significant features of gene expression
- Use of human genome data

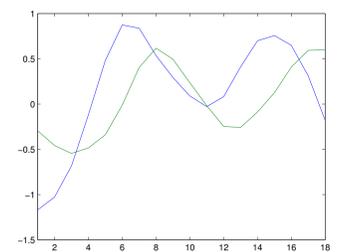


Microarray data

References

- [1] C. Gilissen, P. Groot, M. Egmont-Petersen, P. Lucas, et al. Prediction of protein-to-protein interactions from expression microarray time series. In preparation.

With the department of Human Genetics



Gene expression profiles time series

Future Work

New trends in health care offer many interesting opportunities. For example, moving health care to the home environment in telemedicine applications or the introduction of the electronic patient record in our society. Some of the next steps on our agenda are the following:

LaQuSo: The Nijmegen health care computing initiative is part of LaQuSo (Laboratory for Quality Software), which is a joint venture with the Technische Universiteit Eindhoven. LaQuSo works together with partners from industry, government and science and focuses on verification (formal) methods, techniques and tools; validation (empirical) methods, techniques and tools and software system certification. One goal is to broaden the expertise of formal verification with mCRL2 to quality checking medical guidelines.

Nictiz: With the choice of a national electronic patient record and a nationwide infrastructure for the exchange of health care information, a big step forward has been made. Together with Nictiz (Nationaal ICT Instituut in de Zorg), who leads the development of the new e-health infrastructure, we are interested in a close analysis of the security and representation issues involved in the proposed architecture.

Bioinformatics: Currently, we are closely collaborating with the Human Genetics department of the UMC St. Radboud. After a successful joint supervision of a master student, the aim is to use the acquired knowledge to expand the available manpower in this domain through writing a research proposal.

Master Students: Supervise students who are interested in the health care domain with their master thesis to further explore areas in the field of health care (<http://osiris.cs.kun.nl/~perry/hcc>).