

## Editorial

# Networking Clinical Research

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## Introduction

Latest scientific and technological innovations in medicine and biology are increasing the demands on medical informatics and statistics in several research areas. The 51st annual conference of the German Society of Medical Informatics, Biometry and Epidemiology (GMDS), September 10-14, 2006 in Leipzig, focused on substantial contributions of medical informatics, biometry and epidemiology to progress in clinical research. These contributions have mostly been a result of 1) a tight cooperation between medical informatics, biometry and epidemiology as well as strong interactions with medicine and biology and of 2) the scientific commitment of many statisticians, computer scientists and medics on new research opportunities. The rising importance of “cross-over-disciplines” as bioinformatics, medical image computing or genetic statistics represent good examples for successful common efforts in recent fields of research [1-4]. An integration of these new subjects in medical departments of universities and in the GMDS is becoming pivotal.

The aim of the annual conference 2006 – expressed by the motto “Networking Clinical Research” – was to encourage further cooperation and to give an introduction into new scopes of research. Within the congress this motto was reflected by a series of “interdisciplinary sessions”. Computer scientists, statisticians, epidemiologists, biologists and clinicians discussed jointly current topics in medical research, e.g. computer-assisted surgery, heritable cancer disposition, malignant lymphomas or genome-wide association studies [5]. Bioinformatics was introduced as novel topic in the scientific program of a GMDS conference.

## Special Topic GMDS 2006: Overview of Selected Papers

Authors and organizers of high-quality presentations and sessions were invited to write a paper on their contributions for a possible publication in *Methods of Information in Medicine*. After the review process the following papers were selected for this special topic.

The first paper by Winter, Stausberg et al. [6] presents the results of an interdisciplinary session dealing with the integration of information infrastructures for research networks and information systems in patient care as the very basis for translational medicine. Since technical solutions to integrate even large medical information systems are at hand, medics and medical informatics from both the patient care and the clinical study side elaborated the need of a socio-technical rather than a mere technical approach. In particular organizational and economical regulations are needed to support translational medicine successfully.

Klein et al. [7] pick up the technical approaches and elucidate how collaborative acquisition, sharing and analysis of patient data in research and care networks can be maintained. They suggest using CDA not only as an interchange format for clinical documents but also as the basis for database design.

The following two papers address clinical processes and their management. Saboor et al. [8] introduce a method for not only modelling even complex clinical processes but also to, for example, automatically detect weak points as media cracks. They therefore combine concepts of structural modeling of information systems with concepts of business process modeling. Whereas Saboor et al. focused on syntactical aspects of clinical processes, Graeber

et al. [9] focus on the medical content. The authors discuss requirements for the successful implementation of clinical pathways and report on an evaluation study. Within that study they assessed whether clinical pathways actually have the promised positive effects on costs as well as on outcome quality of care.

The medical informatics part of this special topic section is closed by a paper dealing with medical image processing [10]. The histological examination of uterine cervix carcinoma, for example, leads to series of slices and corresponding microscopic images. Since slicing unavoidably causes severe artefacts like distortion, a 3D reconstruction of the specimen becomes a problem. To solve the problem Braumann et al. introduce a stepwise registration procedure which uses a nonparametric non-linear registration approach based on optical flow.

An interesting paper in medical biometry was selected for publication in this topic. Schumacher et al. [11] apply a multi-state model to data on mortality due to nosocomial infections. This useful method allows estimating various versions of attributable mortality taking temporal dynamics, competing events and potential censoring into account.

The paper by Kreuz et al. [12] details a bioinformatics tool for the analysis of array CGH data. The analysis pipeline supports

single and multi-chip analyses as well as combined analyses with paired mRNA gene expression data. For multi-chip analysis the tool provides a novel algorithm for automatic delineation and analysis of recurrent regions.

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#### References

1. Reipsilber U, Mansmann U, Brunner E, Ziegler A. Editorial: Tutorial on Microarray Gene Expression Experiments. *Methods Inf Med* 2005; 44: 392-399.
2. Mansmann U. Genomic Profiling Interplay between Clinical Epidemiology, Bioinformatics and Biostatistics. *Methods Inf Med* 2005; 44: 454-460.
3. Handels H, Horsch A, Meinzer HP. Advances in Medical Image Computing. *Methods Inf Med* 2007; 46: 251-253.
4. Wichmann HE. Genetic Epidemiology in Germany – From Biobanking to Genetic Statistics. *Methods Inf Med* 2005; 44: 584-589.
5. Loeffler M, Winter A (eds). Deutsche Gesellschaft für Medizinische Informatik, Biometrie und Epidemiologie e.V. 51. Jahrestagung. Programm- und Abstractband. pp 226-263.
6. Winter A, Funkat G, Haerber A, Mauz-Koerholz C, Pommerening K, Smers S, Stausberg J. Integrated Information Systems for Translational Medicine. *Methods Inf Med* 2007; 46: 601-607.
7. Klein A, Prokosch H-U, Ganslandt T. Experiences with an Interoperable Data Acquisition Platform for Multi-centric Research Networks Based on HL7 CDA. *Methods Inf Med* 2007; 46: 580-585.
8. Saboor S, Chimiak-Opoka J, Ammenwerth E. Supporting the Systematic Assessment of Clinical Processes: the MedFlow Method. *Methods Inf Med* 2007; 46: 586-594.
9. Graeber S, Richter S, Folz J, Pham PT, Jacob P, Schilling MK. Clinical Pathways in General Surgery: Development, Implementation, and Evaluation. *Methods Inf Med* 2007; 46: 574-579.
10. Braumann UD, Scherf N, Einenkel J, Horn LC, Wentzensen N, Loeffler M, Kuska JP. Large Histological Serial Sections for Computational Tissue Volume Reconstruction. *Methods Inf Med* 2007; 46: 614-622.
11. Schumacher M, Wangler M, Wolkewitz M, Beyersmann J. Attributable Mortality due to Nosocomial Infections: A Simple and Useful Application of Multistate Models. *Methods Inf Med* 2007; 46: 595-600.
12. Kreuz M, Rosolowski M, Berger H, Schwaenen C, Wessendorf S, Loeffler M, Hasenclever D. Development and Implementation of an Analysis Tool for Array-based Comparative Genomic Hybridization. *Methods Inf Med* 2007; 46: 608-613.

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