Institute of Medical Informatics, Biometry, and Epidemiology

Chair of Medical Informatics

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Research focus
- Process support through health information systems
- Medical ontologies and medical knowledge processing
- Evaluation of health information systems
- Analysis, assessment, and visualization of medical data
- IT-infrastructure applications for medical research
- Clinical bioinformatics

Structure of the Chair

Professorship: 1
Personnel: 20
- Doctor (of Medicine): 1
- Scientists: 16 (thereof funded externally: 12)
- Graduate students: 10

Research

Various working groups are concerned with the development and the introduction of electronic medical records, the integration of clinical decision support functions into hospital information systems (HIS), the modelling and optimization of clinical workflows, both data warehouse and data mining applications, the evaluation of the effect of health technology interventions on processes and persons involved in the health system, the development of IT infrastructures for research and teaching and with clinical bioinformatics. The integration of clinical and research data within hospitals and data sharing within large networks, e.g. in the context of the German Medical Informatics Initiative and the German Biobank Alliance, are a particular focus of our research activities.
Prof. Dr. H.-U. Prokosch is as Chief Information Officer also responsible for the strategic development of information processing at UK Erlangen.

Process support through health information systems
One of the major challenges in the design, establishment, and management of health information systems (HIS) is the intersectoral interoperability which is important to optimize the cooperation of the various health service providers across institutional boundaries in outpatient and inpatient care in order to deliver the best patient care. For an additional reduction of patient risks, we integrate clinical decision support functionalities into HIS. Clinical information flow and communication functionalities should ultimately involve and benefit patients, e.g. by the application of medication plans or by the use of a personal electronic health record. In addition to grant funded projects, the Chair also pursues and supports several innovative pilot projects embedded in the SOARIAN®/Meona® HIS environment of Erlangen University Hospital. The direct integration of the patient by means of an online-based capturing of follow-up information and the vision of a patient portal which is integrated into HIS, additionally supports a patient´s eConsent processes and provides transparent information about the use of his data in research projects completes the range of research in this field.

Medical ontologies and medical knowledge processing
In our projects, providing knowledge processing systems in medicine always comprises knowledge modeling and the implementation of standardized knowledge modules for example to support drug therapy and drug prescription or to reduce patient risks within intensive care units (ICU). Within the patient data management system of an ICU, a clinical decision support system has been integrated to monitor the exceedance of threshold values or to monitor critical trends of various laboratory values and, as a consequence, to have a direct feedback sent as a text message to the DECT telephone of the clinician on duty. Within the MIRACUM project one focus is the integration of molecular analysis results with clinical data and its efficient visualization for physician´s support in therapy decisions. Further research aims on the AI-based development of classification and prognosis algorithms, as well as the provision of medication dosage recommendations. In the context of those developments we are also concerned with all aspects of the use of software as a medicinal product.

Evaluation of health information systems
When introducing new information technologies, it is essential to evaluate their effect on user satisfaction, work processes, and process costs to avoid adverse effects of these technologies on medical care. Successful use of IT in medicine may be hindered by negative user attitudes, user-unfriendly interfaces, and insufficient usability in general. In numerous evaluation studies, we have applied methods, such as usability questionnaires, observations, thinking aloud, and cognitive walkthrough, to both optimize and evaluate the acceptance of different kinds of IT artefacts. In cooperation with the Department of Anesthesiology, as well as further German anesthesiologists and the foundation German anesthesiology (“Stiftung Deutsche Anästhesiologie”) we perform usability analysis of different levels of prototypes and mockups for a computerized emergency checklist. Further, we cooperate with the Department of Pediatrics and Adolescent Medicine in the stepwise development and usability analysis of a web-based medication information system to support drug therapy for children. In the context of developing user interfaces for searching biospecimens and for feasibility analyses, we cooperate very closely with the Institute for Medical Informatics and Biometry at the TU Dresden in conducting usability evaluations.

Analysis, assessment, and visualization of medical data
An increasing amount of data is documented electronically in clinical IT systems during routine patient care. To avoid information overload or overlooking of essential facts, appropriate and flexible visualization methods are required. We have been creating a learning health system by reusing such data for research projects. In cooperation with Harvard University Medical Center, the i2b2 (informatics for integrating biology and the bedside) platform has been integrated with UK Erlangen Clinical Data Warehouse and enhanced with semantic ontology annotations as well as timeline-based visualization methods. It has been established as a research integration platform for several projects at UK Erlangen, but also within national collaborations. Furthermore, we have provided the tranSMART platform for different research groups at our Faculty for the purpose of integrating genomic data into clinical data. Here we are also evaluating the use and the usability of the platform for its application in the fields of cohort identification and data exploration. In the MIRACUM consortium (Medical Informatics in Research and Care in University Medicine) we evaluate and enhance the translational platform cBioPortal (originally developed at the Memorial Sloan Kettering Cancer Center, New York, USA), which aims at integrating and visualizing clinical findings and genomic analysis data. The final goal is to provide an optimized information presentation for enhanced IT supported therapy decisions in molecular tumor boards.

IT-infrastructure applications for medical research
Today, medical research is often pursued within networked multi center structures, which require efficient and safe IT-infrastructures. Amongst others current activities comprise IT infrastructures to support biobanking and the development of biobank networks on a national (German Biobank Node, German Biobank Alliance) and international (BBMRI-EIRC Common Service IT) level. A further focus was laid on the single-source reuse of patient data for clinical and translational research. The Chair is member and active partner in many projects and working groups of the TMF (German technology and methods platform for networked medical

research). We lead the MIRACUM consortium, in which we design, develop, and implement an ecosystem of open source software tools (MIRACOLIX: e.g. ID-management, consent-management, federated authentication, several research data repositories and research data management based on the FAIR principles), which form the building blocks for the establishment of data integration centers at each of the MIRACUM university hospitals.

Clinical bioinformatics
Another research focus includes bioinformatics analysis and modeling of medical data. Our work focuses on high-dimensional omics and imaging data (bulk/single-cell transcriptomics, proteomics, metabolomics, interactomics, ATAC-Seq, FACS, CyTOF), which we systematically analyze using methods of integrative and comparative bioinformatics and machine learning. The goal is to gain a comprehensive understanding of molecules (e.g. non-coding RNAs, RNA-binding proteins) and signaling pathways in the pathogenesis and their pharmacological applications. The thematic focus of our work is in particular (auto)immune, fibrosis and tumor diseases. In this context, we have developed innovative methods and integrative analysis tools and successfully applied them in various collaborative projects and research alliances. For example, we have identified markers for various cardiac and lung diseases as well as novel mediators in fibroblast activation in systemic sclerosis, but also elucidated mechanism of immune cells in the pathogenesis. Another aspect of the work involves disease modeling. Here, we identified a blood-based metabolome signature for the diagnosis of adrenocortical tumors using machine learning approaches. In addition, we have developed computer models for various tumor diseases that reflect the underlying mutations and involved signaling pathways of a tumor and can be used, for example, for targeted therapy decisions in the context of molecular tumor boards.

Teaching

The Chair of Medical Informatics is involved in the education of students of Medicine, in the degree programs of informatics (minor subject: medical informatics) of the Faculty of Engineering as well as in the interdisciplinary degree program Medical Process Management and in the cross-faculty courses of the degree programs in medical engineering. In all these courses, the innovative laboratory for medical informatics and eHealth which is an established feature at the Chair of Medical Informatics is used as the Erlangen laboratory of medical informatics (“EMIL”) in the form of a Skills Lab and in the context of an innovative teaching concept.

Selected publications
Gruendner J, Wolf N, Tögel L, Haller F, Prokosch HU, Christoph J. Integrating Genomics and Clinical Data for Statistical Analysis by Using GEnome MINIng (GEMINI) and Fast Healthcare Interoperability Resources (FHIR): System Design and Implementation. JMIR 2020; 22:e19879.

Gulden C, Kirchner M, Schüttler C, Hinderer M, Kampf M, Prokosch HUP, Toddenroth D. Extractive summarization of clinical trial descriptions. Int J Med Inform. 2019;129:114-121.

Vey J, Kapsner LA, Fuchs M, Unberath P, Veronesi G, Kunz M. A toolbox for functional analysis and the systematic identification of diagnostic and prognostic gene expression signatures combining meta-analysis and machine learning. Cancers (Basel), 2019 Oct; 11(10). pii: E1606. doi: 10.3390/cancers11101606

Kunz M, Wolf B, Fuchs M, Christoph J, Xiao K, Thum T, Atlan D, Prokosch HU, Dandekar T. A comprehensive method protocol for annotation and integrated functional understanding of lncRNAs. Brief Bioinform., 2020; 21(4):1391-1396. doi: 10.1093/bib/bbz066

Fuchs M, Kreutzer FP, Kapsner LA, Mitzka S, Just A, Perbellini F, Terracciano CM, Xiao K, Geffers R, Bogdan C, Prokosch HU, Fiedler J, Thum T, Kunz M. Integrative Bioinformatic Analyses of Global Transcriptome Data Decipher Novel Molecular Insights into Cardiac Anti-Fibrotic Therapies. Int J Mol Sci., 2020; 21(13):4727. doi: 10.3390/ijms21134727

International cooperations
Prof. Dr. E. Ammenwerth, Private Universität für Medizinische Informatik und Technik (UMIT), Innsbruck: Österreich

Prof. Dr. T. Bürkle, Berner Fachhochschule, Biel: Schweiz

Prof. Dr. I. Kohane, National Center for Biomedical Computing, Boston: USA

Prof. Dr. C. Sawyers, Dr. A. Zehir, Memorial Sloan Kettering Cancer Center, New York: USA

Prof. Dr. George Hripcsak. Columbia University, New York: USA.