Iterata AG Medical Services
Industriestrasse 8
5722 Gränichen | Switzerland
www.iterata.ch

Iterata Health Platform – Next Avenues

Innovative Platform for Data Collection, Retrieval and Evaluation in Digital Diagnostics & Research

Project Transcription

Current issues with data

Prof. Paul Hasler, Kantonsspital Aarau: "Not much has moved in the last ten years, since Kohane and Mandl voiced their grievances on information technology (IT) in health care. Admittedly, some administrative functions, such as retrieval of imaging exams and laboratory results have improved. Likewise, electronic transfer of reports has been enabled. Yet, electronic systems that provide these advances have, in many instances, increased the time and resources on clinical tasks and documentation in patient care.

Amorphous sets of enormous amounts of data generated from different software applications are amassed in fragmented and increasingly indigestible compilations. Complex interfaces are needed to allow the exchange of data, which are shifted between systems in huge volumes. These overload hardware infrastructure capacity, driving costs while reducing usability. Often, "single solution" systems are adopted, which inherently are an amalgamation of subsystems, with many of the flaws of individual solutions connected by interfaces. Management of upgrades of systems entail considering adaptations to a host of associated components, while proprietary data storage limits access and transfer of data to new platforms. All the while, evaluation of the data is difficult and costly.

Attempts to develop and introduce direct structured data capture into clinical routine have largely petered out, after promising developments in the first decade of the millennium. A proliferation of apps and devices have improved many individual facets of care, but analysis of content across systems is rarely possible. The incorporation of genomics in the diagnostic process is tedious, slow and prohibitively expensive, with results of a mere handful of variants available after several days to weeks. "

Participating Organisations

- Kantonsspital Aarau (CH)
- Kantonsspital St. Gallen (CH)
- Universitair Medisch Centrum Utrecht (NL)
- Ludwig-Maximilians-Universität München (DE)
- Fachhochschule Zentralschweiz – Hochschule Luzern (CH)
- PharmGenetix GmbH (AT)
- Arpage AG (CH)
- Punkt International GmbH (CH)
- Forschungsstiftung für Informationstechnologie und Gesellschaft (CH)

External Expert Advisory Board Members

- Janet Cowell
- Prof. Dr. Joachim Möller
- Prof. Dr. med. Peter Taylor
- Prof. Russ Biagio Altman
- Dr. Zubin Dastoor
- Dr. Kai Grunwald

The Project

Experienced rheumatologists, genomics and imaging research experts in rheumatoid arthritis (RA) and specialists in data analysis and IT-technology have integrated extraordinary medical knowhow and knowledge in secure handling of sensitive patient data to develop an innovative Platform for Data Collection, Retrieval and Evaluation in Digital Diagnostics and Research (INCREASE) for RA.

The novel platform resolves the fundamental predicaments of canonical, narrative-based, clinical documentation, information analysis and reporting. The outdated format of clinical items is replaced with digital objects that are linked with attributes and properties following uniform, standardized nomenclature. Storage in a searchable database enables algorithms to identify items and events of interest for interoperable analysis with other digital data sets or numerical data, e.g. laboratory results. Thus, limited data integration from various internal and external sources, costly migration of programs and complex adaptations of interfaces are averted, whilst the data remain in their original policy space. Searchability and algorithmic evaluation across large data pools enables a detailed, real-time personalized health status assessment and fully digital clinical decision support. Besides, the creation of defined cohorts allows comparisons over time and against a benchmark of care to optimize outcomes and safety.

The novel platform provides a bottom-up, domain knowledge-driven, clinical decision support system. Expediting digital integration of clinical, laboratory and genomic data - using ultrafast enterprise search engine technology (ESET) and software solutions - saves time and resources. In this project, the usual clinical data are extended by investigating genomic variants for their utility to predict disease course, undesired effects and response to therapy. Inherently, these highly personalized diagnostic features are extendable to any clinical condition of choice.

Major aims of project

1. Providing a comprehensive basis for digital diagnostics:
- digitizing documents and using innovative enterprise search engine technology (ESET) to consolidate the digital clinical and routine laboratory datasets of individual patients. The main principle is that the whole process functions without copying or removing the data from their policy space, hence, guaranteeing security of patient data
- providing a structured data entry (SDE) tool to capture clinical data as discrete objects with references to defined properties, location and time

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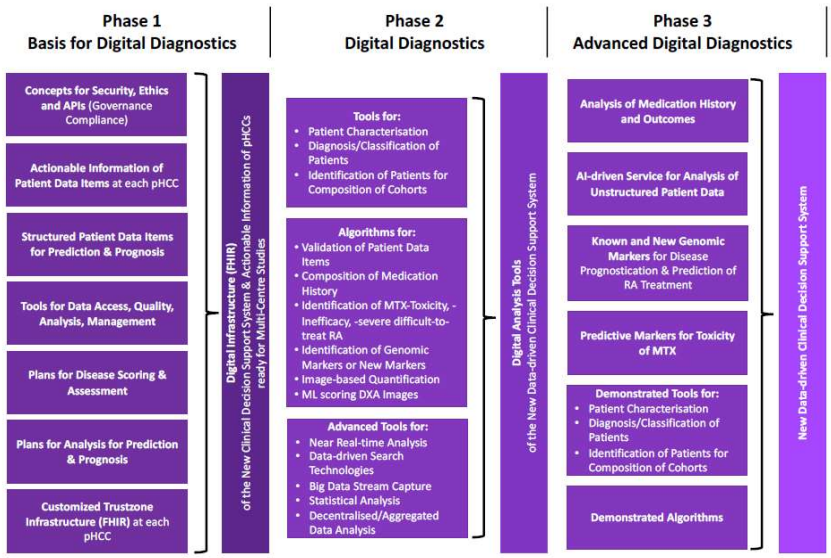
- developing advanced IT tools to access the consolidated data from different healthcare providers and decentralized sources, and to facilitate data aggregation and evaluation of large cohorts

2. Seamlessly integrating existing genomic and imaging data of large cohorts of patients with RA with all other modalities for health assessment and treatment in an easy to use clinical decision support system (CDSS):
- directly targeting the data stream of high-throughput, allelic level resolution whole genome sequencing (WGS)
- examining the prospect for image analysis in addition to routinely collected (unstructured) data in clinical care
- aggregating data to obtain data-driven diagnostic and prognostic information to support precise and fast clinical decision making and personalized medicine.



Introduction Iterata Health Platform
Keywords: Enterprise search engine technology, Structured data entry, Solr Integrated Wolfram Mathematica, Cryptography, Secure interoperability, Genomics, Imaging, Pharmacogenetics, Prognosis, Diagnosis, Response to treatment

Genomics and pharmacogenetics are conducted on **whole genome sequences** for allelic variants associated with intensity of inflammation, Methotrexate (MTX) toxicity, and in a second step, of the entire genomic sequences. **Search Engine Integrated Wolfram Mathematica** (SIMA) is uniquely proficient for counting, tabulating and statistically analyzing large sets of data. This capacity is used for **analysis of patients' medication data and for detection of features that predict outcome of rheumatoid arthritis (RA)**. Initial exploration has confirmed that SIMA can detect prespecified genomic targets that have a bearing on the inflammatory response. Subsequent analyses evaluate the association of other potential markers across the whole genome and perform comparisons between cohorts.

The **basis for full interoperability of information** is provided by a noSQL database system that is inherently fully addressable by **enterprise search engine technology (ESET)**. ESET **indexes** other data archiving systems to make them addressable, while **avoiding the need for interfaces**. This satisfies the prerequisites for data use across platforms in personalized medicine and systems medicine/biology without the need for interfaces. This solution integrates data held in different formats. ESET lays an index over the content and context and allows accessing data without copying or removing them from their policy spaces. The capacities of ESET has been potentiated by integrating a symbolic statistical program by project partner Iterata (Wolfram Mathematica, Wolfram Research, Champaigne IL, USA). **A search engine with integrated Wolfram Mathematica (SIMA)** delivers **high-speed and capacity for across-the-board exploration and analysis** of health data of individuals and patient populations.

In INCREASE, SIMA is implemented for the computation of genomic data. The advantages of this methodology are high data processing capacity and aptitude for counting and comparing events. Not only can pre-defined DNA sequences be sought and identified, but also alignment and haplotype analysis are possible. High-speed and high-throughput evaluations are supported, if necessary, on parallel devices. The possibility of capturing the raw data stream of the sequencing apparatus is evaluated and implemented. Equally, tabulations, complex cluster analysis and accessing existing gene databases are within the scope of the technology as well as seamless analysis with the clinical dataset and, thus, to incorporate the results of WGS into the routine CDSS. Likewise, other -omics data can be seamlessly integrated into the novel CDSS. More benefit can be expected from these modalities though, if they are measured longitudinally.

Please do not hesitate to contact us
Sincerely yours, Iterata Team
Phone +41 62 842 88 27 | info@iterata.ch