

Early detection of infection chains & outbreaks: Use Case Infection Control

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Abstract. Within the HiGHmed Project there are three medical use cases. The use cases include the scopes cardiology, oncology and infection. They serve to specify the requirements for the development and implementation of a local and federated platform, with the result that data from medical care and research should be retrievable, reusable and interchangeable. The Use Case Infection Control aims to establish an early detection of transmission events as well as clusters and outbreaks of various pathogens. Therefore the use case wants to establish the smart infection control system (SmICS).

Keywords. HiGHmed, Use Case, Infection, Outbreaks, Detection

1. Introduction

The HiGHmed-Project is funded by the Federal Ministry of Education and Research (BMBF) under the “Medical Informatics” funding scheme. HiGHmed aims to develop and use innovative information infrastructures to increase the efficiency of clinical research and to swiftly translate research results into validated improvements of patient care. These aims are connected with challenges to integrate and further develop solutions of innovative, internationally interoperable data integration and methods, targeting to demonstrate added value for health research and patient care. The concepts must be designed in a way that will help to develop sustainable structures and with the perspective for an easy roll-out to other hospitals. To ensure semantic interoperability and traceability, HiGHmed follows the openEHR (electronic health records) approach for clinical information modelling. [2]

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2. Use Case Infection and the smart infection control system (SmICS)

Outbreaks of infections are rare events and present a major health challenge today. To determine the source or location of the outbreak, the Use Case Infection Control was initiated as part of the HiGHmed project. Therefore the use case wants to establish the smart infection control system (SmICS).

The overall goal is to develop SmICS as an open source solution, providing the tool to the public. SmICS also aims to achieve the following goals for researchers:

- Facilitating the tracking of transmission dynamics.
- Gaining new insights into risk factors, sources and species-/clonal-specific differences allowing to define needed evidence for prevention measures.
- Identification of pathogen specific contact events and transmission pathways, incubation periods and date of infection.
- Generation of hypotheses about clusters and outbreaks.
- Application of algorithms to detect patient cluster and pathogen outbreaks.
- Interactive visualization of available patient movement data and pathogens

Furthermore, SMICS wants to achieve the following goals for the hospitals:

- Reduction of outbreaks by an effective and efficient infection control.
- Improvement of patient care quality.
- Shortening of stays and save costs by lean processes.

In order to develop SmICS, a minimal data record was created in cooperation with the domain experts. This includes patient and case data, as well as patient microbiological data and movement data. The data will be transmitted anonymously to the visualization partner TU-Darmstadt, so that a conclusion on the respective patient is excluded.

The SmICS will be implemented as a HiGHmed application. Therefore the data stewards of all project partners will create archetypes and terminology bindings. From a technical point of view, SmICS will be designed as a distributed system. It consists of local nodes, which are used at each clinical site. The visualization will be a dashboard-like component with a reporting function.

Further steps will be design extension such as presentation of longer periods, longer patient length of stay and connection between time, contact, location and movement. Also the modulation of Archetypes for the data collection, data integration in local repositories and establishment of interfaces to SmICS will be performed. Furthermore the evaluation regarding to contact points and transmission routes of pathogen- or patient-specific incubation and infection times will be carried out.

References

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