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Tracing COVID-19 Infection Chains Within Healthcare Institutions - Another Brick in the Wall Against SARS-CoV-2

Antje Wulff[a], Pascal Biermann[a], Tatiana von Landesberger[b], Tom Baumgartl[b], Christoph Schmidt[c], Alan Yussef Alhaji[a,c], Kristina Schick[a], Paul Waldstein[a,d], Yufei Zhu[d], HiGHmed Infection Control Study Group*, Dagmar Krefting[d], Simone Scheithauer[e], Michael Marschollek[a]

[a] Peter L. Reichertz Institute for Medical Informatics of TU Braunschweig and Hannover Medical School, Hannover, Germany
[b] Technical University Darmstadt, Darmstadt, Germany
[c] University of Rostock, Rostock
[d] Institute of Medical Informatics, University Medical Center Göttingen (UMG), Georg-August University Göttingen, Göttingen, Germany
[e] Institute of Infection Control and Infectious Diseases, University Medical Center Göttingen (UMG), Georg-August University Göttingen, Germany
** List of study group can be found at the end of the article*

Abstract

Early anticipation of COVID-19 infection chains within hospitals is of high importance for initiating suitable measures at the right time. Infection control specialists can be supported by application systems able of consolidating and analyzing heterogeneous, up-to-now non-standardized and distributed data needed for tracking COVID-19 infections and infected patients' hospital contacts. We developed a system, Co-Surv-SmICS, assisting in infection chain detection, in an open and standards-based way to ensure reusability of the system across institutions. Data is modelled in alignment to various national modelling initiatives and consensus data definitions, queried in a standardized way by the use of OpenEHR as information modelling standard and its associated model-based query language, analyzed and interactively visualized in the application. A first version has been published and will be enhanced with further features and evaluated in detail with regard to its potentials to support specialists during their work against SARS-CoV-2.

Keywords:

COVID-19; Medical Informatics Applications; Health Information Interoperability

Introduction

The COVID-19 pandemic gives our health systems a reality check with regard to means to control the spread of a highly contagious virus. From this situation, a high demand for identifying contacts and thus potential transmission events arises, along with the need to be able to trace infection chains. At present, in many healthcare institutions, networks and beyond, there is still a lack of proper communication between different application systems, which hold invaluable data about patients, patients' movement or location within the institutions or lab findings about infectious agents [1]. Standardizing, harmonizing and using these precious data sets offer a realistic chance to support in detecting COVID-19 infection chains within healthcare institutions. Ideally, such a dataset prospectively used for infection control tasks would also include personnel data, as a potential entry point. Furthermore, this data should emanate from routine care application systems, with no additional manual extraction processes. On the application development side, an infection tracking system should provide an intuitive, easy-to-use user interface for local infection control specialists, teams or task forces. Furthermore, such a system should be based on standardized data representations and interfaces, thus, interoperable, to be sharable across institutions and networks. The aim of our research work for this paper is to demonstrate the feasibility of a standards-based, interoperable application system that is able to trace COVID-19 infection chains in hospitals.

Methods

Setting

Our development is based on previous work within the German HiGHmed consortium [2], aiming to provide an open platform approach for sharing data among eight university hospitals and other healthcare provider institutions and for developing Open Source, interoperable clinical applications on the basis of this platform, using openEHR archetypes as information models and open application programming interfaces [3]. In particular, this research work builds on the HiGHmed use case 'infection control' and the prototype of the HiGHmed Smart Infection Control System (SmICS), which aims to detect bacterial colonization clusters and potential outbreaks in hospitals [4].

Semantic interoperability

To ensure semantic interoperability, all data models are based on openEHR as information modelling standard [5]. Consequently, SmICS' development towards COVID-19, the 'COVID-19 Surveillance Smart Infection Control System' (Co-Surv-SmICS) required modeling a new OpenEHR template for virology lab findings in close cooperation with domain experts from all participating sites. Therefore, the clinical knowledge governance framework and defined modelling processes of HiGHmed have been followed [6]. All models are available at the Clinical Knowledge Manager (CKM)[1].

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[1] https://ckm.highmed.org/ckm/

Conceptual design and techniques

Co-Surv-SmICS is a .NET 5.0 Blazor Server Side web application with different modules resp. microservices (Figure 1). The core component 'SmICS Core' connects via HTTP to an openEHR server and uses standardized, open queries (*Archetype Query Language*, AQL[2]) to the server for retrieving data. It provides a RESTful API for communicating with other micro services such as 'SmICS Visualization' and 'SmICS Algorithms', implementing an interactive visualization interface and analytics. The further development of SmICS towards Co-Surv-SmICS necessitated the definition of new AQL queries to retrieve data from the newly composed data models such as the virology report. Additionally, all participating sites needed to enhance their data repository with these further data sets needed for tracing infections. Here, new institution-specific *extraction, load, and transformation* (ETL) processes for identifying data from the primary source systems and loading data to the openEHR based data repositories are required. Finally, new *interactive visualization interfaces* have been created by using Node.js as Open Source JavaScript runtime environment to envision both data and analyses results from the 'SmICS Algorithm' micro service.

Results

OpenEHR data models

As explained in the methods, a new complex OpenEHR template for representing virology findings was needed. The standardized OpenEHR based representation of a virology report can be found in the CKM (in German)[3]. To ensure reusability of the model but also the aspired application system, internationally consented and published archetypes have been reused for template modelling rather than creating new models (e.g. the archetype OBSERVATION.laboratory_test_result.v1). Furthermore, data is coded in terminologies such as SNOMED-CT and LOINC. For example, for storing results of a SARS-CoV-2 RNA test result in a quantitative manner (cycle threshold #), the LOINC code 94745-7 is deposited. The same is true for the value sets for the attributes *specimen type*, *anatomical location* the specimen has been taken from and the *qualitative result*. For tracing COVID-19 infections, data on the patients' encounters and specific locations during their entire stay is needed, also represented through OpenEHR templates. All OpenEHR based templates that will be used in Co-Surv-SmICS are available at the CKM project 'SmICS'[4].

AQL interface

To be able to incorporate new data for virology findings in Co-Surv-SmICS, new AQL queries and further processing of the AQL results, i.e. to make them usable by the visualization micro service, are needed. Figure 2 presents the initial query used for retrieving crucial information (e.g., patient identifier, specimen taken, pathogen result) from virology findings stored as OpenEHR template 'Virology Report' in an OpenEHR data repository. The CONTAINS statements represent the hierarchy structure of the OpenEHR template: it contains a *report result* composition as root, itself containing an archetype for *case* identification and the actual *laboratory test result*. The *specimen* archetype, the *laboratory test panel* archetype and the *laboratory test analyte* archetype, representing the result for each specific analyte, are parts of the overall test result archetype. Since different result report compositions might exist in the data repository, the specific report ('Virology Report') searched for is specified in the WHERE clause. Furthermore, this query is restricted to a specific list of patients, retrieved by other requests before.

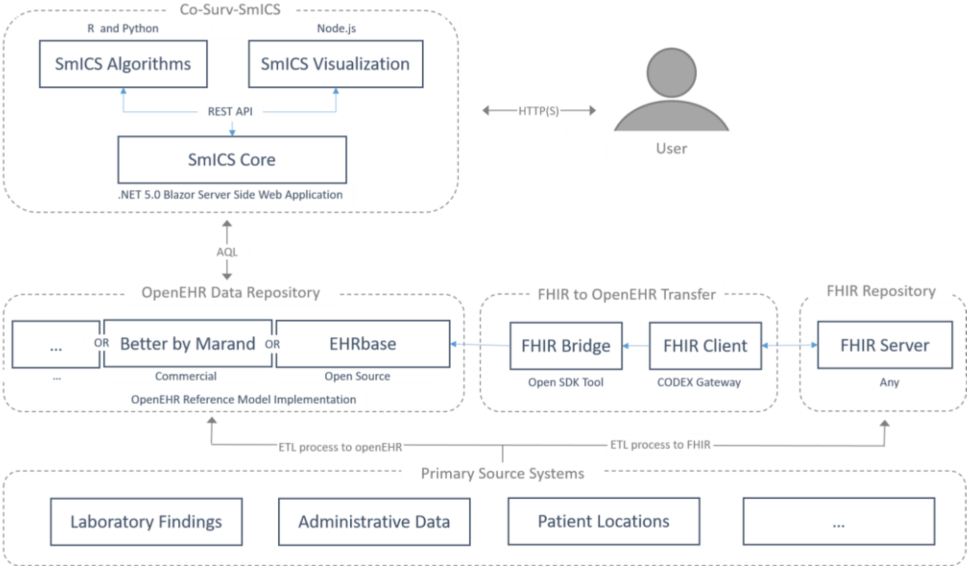

Figure 1 – Co-Surv-SmICS architecture

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[2] https://specifications.openehr.org/releases/QUERY/latest/AQL.html

[3] https://ckm.highmed.org/ckm/templates/1246.169.636

[4] https://ckm.highmed.org/ckm/projects/1246.152.34

```
SELECT
e/ehr_id/value as patientID,
c/context/start_time/value as reportTime,
y/items[at0001]/value/value as caseID,
a/items[at0001]/value/id as laboratoryDataID,
a/items[at0029]/value/defining_code/code_string as SpecimenID,
a/items[at0029]/value/value as specimenText,
a/items[at0015]/value/value as specimenCollectionTime,
a/items[at0034]/value/value as specimenReceivedTime,
d/items[at0024]/value/value as pathogenText,
d/items[at0024]/value/defining_code/code_string as pathogenID,
d/items[at0001,'Nachweis']/value/value as resultText,
d/items[at0001,'Nachweis']/value/defining_code/code_string as resultCode,
d/items[at0001,'Quantitatives Ergebnis']/value/magnitude as viralLoad,
l/data[at0001]/events[at0002]/data[at0003]/items[at0101]/value/value as comment

FROM EHR e
CONTAINS
COMPOSITION c[openEHR-EHR-COMPOSITION.report-result.v1]
      CONTAINS
      (CLUSTER y[openEHR-EHR-CLUSTER.case_identification.v0]
      AND OBSERVATION l[openEHR-EHR-OBSERVATION.laboratory_test_result.v1]
            CONTAINS
            (CLUSTER a[openEHR-EHR-CLUSTER.specimen.v1]
            AND CLUSTER b[openEHR-EHR-CLUSTER.laboratory_test_panel.v0]
                  CONTAINS
                  (CLUSTER d[openEHR-EHR-CLUSTER.laboratory_test_analyte.v1])))

WHERE
c/name/value = 'Virologischer Befund'
AND e/ehr_id/value MATCHES { patientList.ToAQLMatchString() }

ORDER BY
a/items[at0015]/value/value ASC
```

Figure 2 – Exemplary AQL used in SmICSCore to retrieve data from OpenEHR template 'Virology Report'

Co-Surv-SmICS modules

Co-Surv-SmICS has been published on March 31, 2021 and is available on GitHub [7,8] along with test data and an enhanced user manual. Test data comprise 18 patients with virology findings, encounter information and exemplary movements and stays within the hospital. Additionally, an open demonstrator is available[5]. The first release is able to visualize patients' movements on different levels (hospital – ward – service units – rooms) and associated virology findings in an ostensive way, so that spatiotemporal associations can be explored (*'Patient History'* module). Furthermore, it shows statistical views on new or retrospective COVID-19 cases in a user-specified time interval (*'Epidemiology Curve'* module). Furthermore, Co-Surv-SmICS can derive contact networks from data, thus supporting tracing of potential transmission contacts of infected patients with other patients (*'Contact Network'* module). Finally, it includes a statistics module representing the reported COVID-19 cases in Germany or in a specific region (*'Statistics'* module) and many other interactive features to explore data in a user-guided way. Figure 2 shows the Co-Surv-SmICS with three modules *'Patient History'*, *'Epidemiology Curve'*, *'Contact Network'*. At the top of the screen, there are four input fields that can be used by the end users to specify the period to be viewed and the patients to be displayed (as OpenEHR *ehr-ids*).

Discussion

Co-Surv-SmICS – as its sibling SmICS – is developed as an interoperable application. This means that these applications only use standardized, open source information models, which have been published. Queries are based on a standardized query language (AQL). Thus, these applications can run on any commercial or non-commercial repository implementation of the openEHR reference model (see Figure 1). The Co-Surv-SmICS already has been tested with a commercial repository (Better by Marand) and an Open Source platform (EHRbase). Therefore, these applications can be shared across institutions, who still have to extract their data from institutional applications, but can skip application development completely, thus avoiding continuously re-inventing the wheel.

As the German Medical Informatics Initiative has agreed to use HL7 FHIR as the minimum requirement for representing data to be shared on a national level, we currently integrate the necessary consensus data set FHIR profiles in the FHIR-bridge component of the Open Source openEHR repository 'EHRbase' (see Figure 1). Once this is achieved, Co-Surv-SmICS and EHRbase can be delivered as a bundle, implementing a FHIR façade. Furthermore, all data models align with the data and communication standards of the German Medical Informatics Initiative and the German Corona consensus data set6.

The 'SmICS Algorithm' micro service shortly will be expanded with an R algorithm, primarily developed by one of our partners (Robert Koch institute (RKI) which is the government's central scientific institution in the field of biomedicine). This algorithm will be able of detecting epidemic situations and clusters in a specific region, hospital or ward. There are also plans to include further modules and visualizations. The next releases and additional functionalities will be published in August and November 2021.e – as others [9] – have not yet been able to conduct a large-scale evaluation of the application, which has however been developed in close cooperation with numerous domain experts. A similar approach has been reported by Ho et al., however using a location system for healthcare workers to trace contacts over a two-day period, integrating location data with EHR data [10]. Venkataraman et al. have implemented a system similar to ours and report significant (> 60 %) time saving when identifying potential transmission contacts [11]. Finally, we firmly believe that our approach has the potential to support infection control specialists in hospitals and healthcare provider networks in identifying infection chains, especially for nosocomial infections with COVID-19, and in taking timely measures to contain the disease. The authors invite all parties interested to collaborate in this effort.

Conclusions

The authors present an interoperable, standards-based application system for supporting COVID-19 infection control within hospitals and healthcare provider networks. It is based on an open system architecture, open information models and an open programming interface. It can be used by infection control specialists to visualize patient data, virology lab data and movement data to identify potential transmission points and infection clusters or even sources by tracing back patients.

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[5] https://bfast.num.umg.eu:9787

[6] https://simplifier.net/ForschungsnetzCovid-19

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Index Patient c74f6215-4fc2-42a5-a3ad-l

Patients for History c74f6215-4fc2-42a5-a3ad-l

Figure 3 – Co-Surv-SmICS Visualization

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Address for correspondence

Dr. Antje Wulff,
Peter L. Reichertz Institute for Medical Informatics of
TU Braunschweig and Hannover Medical School,
Karl-Wiechert-Allee 3, 30625 Hannover, Germany.
E-Mail address: antje.wulff@plri.de (A.Wulff).
Phone: +49 531 / 391 – 9510
Fax: +49 531 / 391 - 9502
URL: http://www.plri.de (A. Wulff)

*Infection Control Study Group members

Simone Scheithauer[3]; Martin Kaase[3]; Patrick Fehling[3]; Sabine Rey[4]; Markus Suhr[4]; Vanessa M. Eichel[6]; Nico T. Mutters[6,7]; Klaus Heeg[8]; Dirk Schlüter[2]; Claas Baier[2]; Michael Marschollek[1]; Antje Wulff[1]; Sarah Ballout[1]; Petra Gastmeier[9]; Michael Behnke[9]; Luis Alberto Peña Diaz[9]; Sylvia Thun[10,11,12]; Roland Eils[10]; Alexander Mellmann[13]; Hauke Tönnies[13]; Cora Drenkhahn[5]; Benedikt Zacher[14]; Tim Eckmanns[14]; Timo Sztyler[15]; Brandon Malone[15]; Angela Merzweiler[16], Martin Dugas[17]; Michael Storck[17]; Marcel Wunderlich[18]; Tatiana von Landesberger[18]; Benjamin Gebel[19]; Thorsten Klingen[20]; Stephan Glöckner[20]

[1] *Peter L. Reichertz Institute for Medical Informatics of TU Braunschweig and Hannover Medical School, Hannover, Germany*

[2] *Institute for Medical Microbiology and Hospital Epidemiology, Hannover Medical School, Hannover, Germany*

[3] *Institute of Infection Control and Infectious Diseases, University Medical Center Göttingen (UMG), Georg-August University Göttingen, Göttingen, Germany.*

[4] *Institute of Medical Informatics, University Medical Center Göttingen (UMG), Georg-August University Göttingen, Göttingen, Germany*

[5] *IT Center for Clinical Research (ITCR-L) and Institute of Medical Informatics (IMI), University of Lübeck, Lübeck, Germany*

[6] *Section for Hospital Hygiene and Environmental Health, Centre of Infectious Diseases, Heidelberg University Hospital, Heidelberg, Germany*

[7] *Institute for Hygiene and Public Health, University Hospital Bonn, Bonn, Germany.*

[8] *Medical Microbiology and Hygiene, Department of Infectious Diseases, Heidelberg University Hospital, Heidelberg, Germany*

[9] *Charité-Universitätsmedizin Berlin, corporate member of Freie Universität Berlin, Humboldt-Universität zu Berlin, and Berlin Institute of Health, Institute of Hygiene and Environmental Medicine, Germany; National Reference Centre for Surveillance of Nosocomial Infections*

[10] *Berlin Institute of Health (BIH), Berlin, Germany*

[11] *Charité - Universitätsmedizin Berlin*

[12] *Hochschule Niederrhein - University of Applied Sciences, Krefeld, Germany*

[13] *Institute of Hygiene, University Hospital Muenster, Muenster, Germany*

[14] *Robert Koch Institute, Berlin, Germany.*

[15] *NEC Laboratories Europe GmbH, Heidelberg, Germany.*

[16] *Department MIS, Heidelberg University Hospital, Heidelberg, Germany.*

[17] *Institute of Medical Informatics, University of Muenster, Muenster, Germany.*

[18] *Technical University of Darmstadt, Darmstadt, Germany.*

[19] *Department of Infectious Diseases and Microbiology, University Medical Center Schleswig-Holstein, Luebeck, Germany.*

[20] *Helmholtz Centre for Infection Research (HZI), Braunschweig, Germany.*