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Feasibility of Representing a Danish Microbiology Model Using FHIR

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Abstract. Achieving interoperability in health is a challenge and requires standardization. The newly developed HL7 standard: Fast Healthcare Interoperability Resources (FHIR) promises both flexibility and interoperability. This study investigates the feasibility of expressing a Danish microbiology message model content in FHIR to explore whether complex in-use legacy models can be migrated and what challenges this may pose. The Danish microbiology message model (the DMM) is used as a case to illustrate challenges and opportunities associated with applying the FHIR standard. Mapping of content from DMM to FHIR was done as close as possible to the DMM to minimize migration costs except when the structure of the content did not fit into FHIR. From the DMM a total of 183 elements were mapped to FHIR. 75 (40.9%) elements were modeled as existing FHIR elements and 96 (52.5%) elements were modeled as extensions and 12 (6.6%) elements were deemed unnecessary because of build-in FHIR characteristics. In this study, it was possible to represent the content of a Danish message model using HL7 FHIR.

Keywords. Health Level Seven, Medical Informatics, Standards, FHIR, eHealth

1. Introduction

During the last decades, an on-going digitalization of hospitals and healthcare organizations has led to the modularized implementation of a landscape of heterogeneous Healthcare IT (HIT) systems [1]. As a consequence, the HIT systems have become islands of clinical information that exists in silos [2]. The increasing demand for seamless and coherent treatment of patients across hospitals, practitioners and laboratories require that clinicians have access to the most recent patient information. These information-access requirements have led to the need for integrated HIT systems that are able to share and reuse the information of other HIT systems, i.e. obtain more than technical interoperability [3]. When aiming for interoperable HIT systems, health information standardization is a core part of the solution [4].

In the Danish healthcare sector, a great variety of HIT systems have been developed on an ad hoc basis to address local needs. To overcome heterogeneity and to ensure technical interoperability, national messaging standards (MedCom messages) are used to support communication across the healthcare sector [2, 5]. However, new Danish health strategies have prioritized international standardization [6].

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Recently, these strategies resulted in Denmark joining HL7 [7]. HL7 has initiated the development of a next generation standards framework; FHIR - Fast Health Interoperability Resources [8]. FHIR has flexible modeling opportunities and supports structural and semantic interoperability. FHIR models can be used across multiple infrastructures and architectures e.g. REST and SOA, and FHIR models are claimed to be highly reusable [9]. For example, if a laboratory message is developed, the underlying models (called resources) can be reused when developing a new laboratory information system, the same underlying models will still be usable and ensure the semantic consistency of the laboratory domain when migrating from a message-based to a SOA-based architecture. An important characteristic of FHIR resources is that they only contain elements that are implemented in 80 % or more of existing HIT systems. Focus is therefore retained on the most common elements, whereas more specific and local elements must be handled through the use of extensions i.e. the 80/20 guideline [10]. Another important aspect of FHIR is the use of profiles. Profiles are developed to customize resources to specific use cases. In FHIR profiles, restrictions can be enforced on resources, and data types can be specified (including terminology binding). In addition, profiles are the extendable parts of the FHIR standard. The extendibility means that elements needed to meet a use case can be inserted in a profile of a relevant resource, even though the element is not specified or foreseen in the original resource.

In the scientific literature, the first FHIR related research has already been published [4-5, 11-13]. However, evidence is still scarce, and to our knowledge, none of the existing studies report in depth about the modeling challenges, associated with applying the FHIR specification for real life use cases.

The aim of this study is to evaluate the feasibility of expressing a Danish MedCom message model in FHIR and analyze areas requiring significantly structural design changes. We have chosen to take our point of departure in one specific Danish message model, the Danish microbiology model (DMM) [14]. The purpose of the DMM is to exchange lab results. This model contains rather complex interrelated findings, which makes it possible to investigate design challenges. Using a simple model could potentially lead to an underestimation in design challenges.

2. Methods

To investigate representation of content of a DMM using FHIR the information content was modeled as close to the DMM as possible, i.e. mapping each attribute in the DMM to a FHIR attribute. However, we identified cases where DMM excerpts were structured in a way that did not fit into FHIRs way of modeling in an obvious way. These were identified as incompatibilities and alternative ways of modelling these were identified.

To evaluate feasibility, each attribute in the DMM was modeled to a corresponding FHIR attribute in a relevant resource. Exceptions were if the characteristics of the FHIR standard made attributes unnecessary, or if a FHIR attribute that accurately covered the content of the Danish attribute could not be found. In the latter case, the FHIR profile was extended with an extra attribute in a relevant resource. In the end of the modeling experiment the number of existing FHIR attributes used, the number of extended attributes, and the number of attributes not relevant in the FHIR framework were calculated. In addition, when a matched attribute contained a predefined FHIR

value set, we evaluated whether this value set covered the content of the Danish value set. The result is a model that represents the content of the DMM using FHIR attributes.

Authors 1-4 were responsible for the modelling of the DMM to a FHIR profile. Authors 1-4 have received training by an expert in the FHIR standard. Authors 5-6 evaluated the modeling, based on their experience in health terminology and models research.

3. Results

In Figure 1, an overview is provided that shows the FHIR resources used to represent the content of the DMM. The model is simplified, so that it does not show all the ten linked observations needed to represent the complex microbiology content. The model shows that eight different resources are utilized. The message header e.g. contains information about date and receiver and sender. The clinical data carried in the message is defined by the data-attribute that links to a diagnostic report. The diagnostic report contains information about the patient, the sample and what kind of analysis that has to be performed. In addition, it has its result defined by the ten linked observations mentioned earlier. These observations hold information about e.g. microscopic and culture findings.

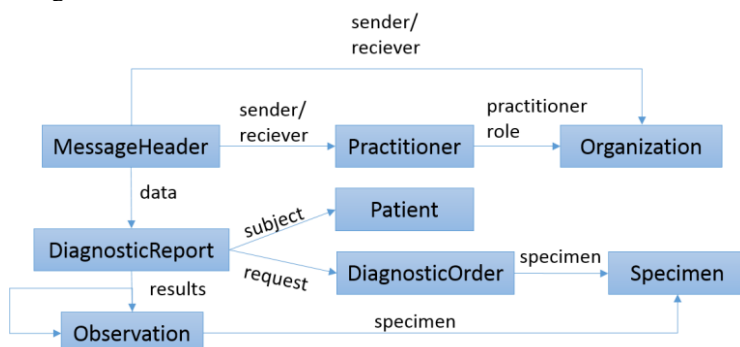


Figure 1. FHIR resources used in the representation of the Danish microbiology model. Arrows are representing references from one resource to another.

The type of information from the DMM controlled whether an element was modeled with an existing FHIR element or whether it was necessary to use an extension. The characteristics of the information that can be modeled directly to an existing FHIR element is information of general character i.e. information which is expected to be used in clinical information systems internationally. The characteristics of the information that needs to be modeled as extensions is information of local or national character. The number of elements from the DMM that is modeled as an existing FHIR element and the number of elements that is modeled as an extension is shown in Table 1.

Table 1. Overview of the distribution of the modeled elements.

Elements modeled as existing FHIR attributes	75 (40.9%)
Elements modeled as extensions	96 (52.5%)
Elements not modeled in FHIR	12 (6.6%)
Total	183 (100%)

Besides from minor design challenges, two major incompatibilities between the DMM and the FHIR model were identified. One was the representation of a table containing the results of a culture analysis, where the antibiotic resistance of bacteria is measured. The other was grouping of microscopic findings. Each of these cases is characterized by linking together a number of findings. Modeling these cases too close to the DMM created an overflow of linked observations with almost no content. Staying more true to the ideas of FHIR modeling allowed us to represent the content much simpler.

4. Discussion

Our results showed that it was possible to represent the content of a Danish microbiology message model using HL7 FHIR with approximately half of the attributes being native for FHIR, and the other half being extensions.

4.1. Extendability

Whenever representing clinical content using standardized models, the extent to which localization is needed should be scrutinized. Extensions means content, and later on patient data, that other systems cannot interpret without access to the local profiles. Given this consideration, the results of this study with half of the attributes represented with extensions, is not very encouraging. However, the percentage of extended clinical content is comparable to other studies representing clinical content using standardized frameworks. For example, Buck et al. (2009) [15] modeled a neonatology electronic patient record using openEHR archetypes and identified 1818 items from the electronic patient record and 1175 items from the paper-based record which were modeled into a total of 132 archetypes. 43.9% (58/132) were reused from available archetypes. Of these 40 archetypes reused as is, 13 were specialized and 12 were extended. 50.8% (67/132) were developed as new archetypes. Even though Buck et al. count per archetype whereas we count per attribute, the additional local content needed is higher or at least comparable to that of our study. While we acknowledge that the complexity of Buck et al.'s study is higher than ours, it shows that getting high re-use percentages is a challenge. To support this, one of our earlier studies also shows that the content overlap between clinical templates in routine use is quite low [16].

Whereas one size fits all would be desirable from a technical viewpoint, it is one of the basic claims of clinical information system research that this is seldom the case e.g. Garde and Knaup (2006) [17]. Consequently, it is very important what kind of content we put in our extensions and what kind of support the standard framework suggests for handling localization of content. In our study, the type of attributes which could not be modeled, were typically content that is only relevant in a local or national context.

4.2. Modeling Approach

In our study, we modeled as close to the original model as possible, because this would allow for the easiest migration. However, the alternative could have been to model as a "close to FHIR" approach where meaning is modeled instead of attributes. Actively choosing a modeling approach would be an essential part of any infrastructure project where existing models have to be migrated to HL7 FHIR. Our study has the limitation

of not considering the use of standardized terminologies, since standardized terminologies and information models are both a prerequisite in achieving semantic interoperability (e.g. Semantic health report [18]). In our model, local value sets could be replaced with value sets using international classifications or terminologies e.g. SNOMED CT [19]. Using international standards in value sets improve the transfer of meaning, and thus the possibilities of a receiving organization to interpret the transferred patient information correctly.

In conclusion, it was possible to represent the content of a Danish message model using HL7 FHIR. Further investigations are needed to get an overview of implications of adopting HL7 FHIR in a Danish context e.g. getting an overview of design and migration cost given different modeling approaches and decisions about where and how to publish national HL7 FHIR profiles.

References

- [1] Smits, M., et al., *A comparison of two Detailed Clinical Model representations: FHIR and CDA*. European Journal for Biomedical Informatics, 2015. **11**(2).
- [2] Dalsgaard, E., K. Kjelström, and J. Riis. *A federation of web services for Danish health care*. in *Proceedings of the 7th symposium on Identity and trust on the Internet*. 2008. ACM.
- [3] HIMSS. *Definition of interoperability*. 2013; Available from: <http://www.himss.org/files/FileDownloads/HIMSS%20Interoperability%20Definition%20FINAL.pdf>.
- [4] Bender, D. and K. Sartipi. *HL7 FHIR: An Agile and RESTful approach to healthcare information exchange*. in *Proceedings of the 26th IEEE International Symposium on Computer-Based Medical Systems*. 2013. IEEE.
- [5] Pape-Haugaard, L. *Higher level of interoperability through an architectural paradigm shift: A study of shared medication record*. in *2011 4th International Conference on Biomedical Engineering and Informatics (BMEI)*. 2011. IEEE.
- [6] Sundhed, D., *National strategi for digitalisering af sundhedsvæsenet 2008–2012*. 2008.
- [7] HL7. *Denmark joining HL7*. 2013; Available from: http://www.hl7.org/implement/standards/product_brief.cfm?product_id=92.
- [8] FHIR. *FHIR Overview*. 2014; Available from: <https://www.hl7.org/fhir/overview.html>.
- [9] FHIR. *HL7 FHIR introduction*. 2014; Available from: <http://www.hl7.org/implement/standards/fhir/summary.html>.
- [10] Grieve, G., #*FHIR and confusion about the 80/20 rule*, in *HealthIntersections*. 2014.
- [11] Alterovitz, G., et al., *SMART on FHIR Genomics: facilitating standardized clinico-genomic apps*. Journal of the American Medical Informatics Association, 2015: p. ocv045.
- [12] Lamprinakos, G.C., et al. *Using FHIR to develop a healthcare mobile application*. in *Wireless Mobile Communication and Healthcare (Mobihealth), 2014 EAI 4th International Conference on*. 2014. IEEE.
- [13] Kasthurirathne, S., et al., *Towards Standardized Patient Data Exchange: Integrating a FHIR Based API for the Open Medical Record System*. Studies in health technology and informatics, 2014. **216**: p. 932-932.
- [14] MedCom, *Det nye gode XML mikrobiologisvar*. 2011.
- [15] Buck, J., et al., *Towards a comprehensive electronic patient record to support an innovative individual care concept for premature infants using the openEHR approach*. International journal of medical informatics, 2009. **78**(8): p. 521-531.
- [16] Goeg, K.R., et al., *Content analysis of physical examination templates in electronic health records using SNOMED CT*. International journal of medical informatics, 2014. **83**(10): p. 736-749.
- [17] Garde, S. and P. Knaup, *Requirements engineering in health care: the example of chemotherapy planning in paediatric oncology*. Requirements Engineering, 2006. **11**(4): p. 265-278.
- [18] Society, E.C.D.-G.f.t.I. and Media, *Semantic Interoperability for Better Health and Safer Healthcare: Research and Deployment Roadmap for Europe. Semantic Health Report January 2009*. 2009: EUR-OP.
- [19] FHIR. *Using SNOMED CT with FHIR*. 2014; Available from: <http://hl7.org/fhir/snomedct.html>.