Automated Generation of Individual and Population Clinical Pathways with the OMOP Common Data Model

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Background

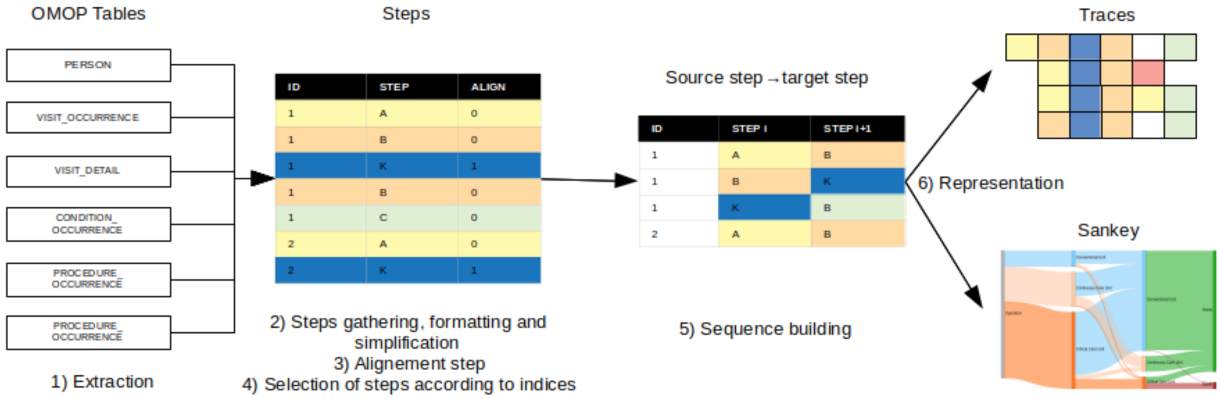
Clinical pathways represent the sequence of care events that patients experience during their encounters with health care facilities.[1, 2] They are used in two contexts. The first one is an individual-based context, where the objective is to visualize the global pathway of a single patient to synthetise its care, or to make a decision about the next stage of care. The second context is a population-based context that relates to a whole population and addresses research or decision-making objectives.

There are several complex issues which make it difficult to represent these pathways.[3] First, information is caracterized by different entities with different dimensions, with a number of events variable from one individual to another. Secondly, the high number of patients and events overloads the unprocessed representation of the clinical pathway. Third, each patient encounters the events at its own dates which complicates the alignment of pathways.

By proposing the selection of steps through different index lists, and by simplifying the heterogeneous labels, our tool helps to reduce the complexity of the patient's journey. We tested our tool with the representation of three clinical pathways.[4]

Methods

We developed a R library to query the OMOP CDM and generate automatically the patient pathway. The process is composed of 5 main steps represented in Figure 1.



ID	STEP	ALIGN
1	A	0
1	B	0
1	K	1
1	B	0
1	C	0
2	A	0
2	K	1

ID	STEP I	STEP I+1
1	A	B
1	B	K
1	K	B
2	A	B

Figure 1. Generation of individual traces and sankey diagram

In a first step, the user provides the concept_id of the events of interest. The domain of each concept is useful to query the appropriate OMOP table. Secondly, events extracted are gathered and homogenized in a table *step*, and are characterized by a start date, an end date, and a step label and concept_id. Labels complexity is reduced in combining multiple events of the same state into a single meta-event, based on *concept_relationship* table.

In order to address complexity and to avoid pattern explosion and information overload, we defined a *alignment step* and a *selection step.* In the alignment step, the user defines the event which will centre and harmonise the different steps of the pathway. Events are ranked according to their occurrence and priority.

According to the two lists of indices referencing the order of each step in the individual pathway (Figure 2, CH List and KS List), the user is able to select the final steps to represent, in accordance with their rank around the alignment step.

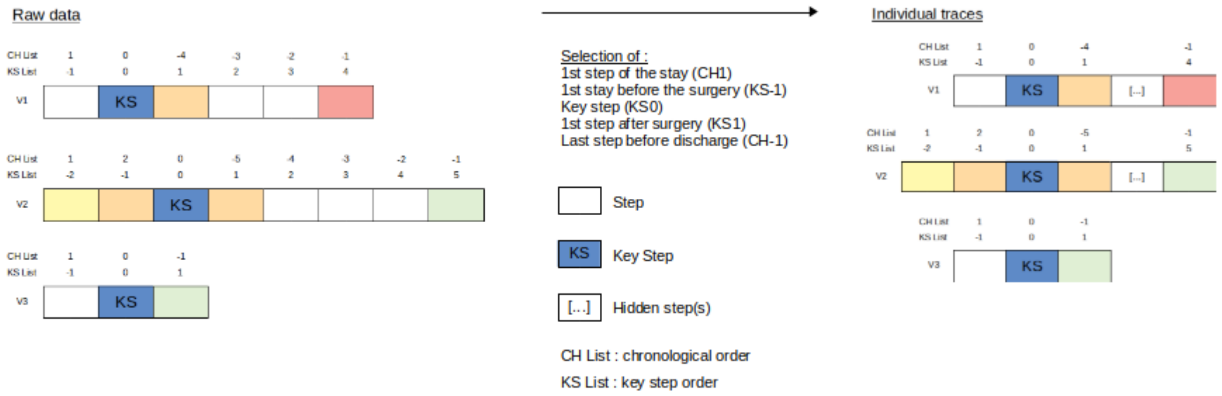


Figure 2. Alignment, simplification and selection of steps of interest

Fifthly, sequence are built to associate *step i* to step *i+1*. Lastly, individual traces and population flows are implemented.

Results

We tested our with three surgery procedures: the total hip replacement, the coronary bypass and the transcatheter aortic valve implantation.[4] The tool provided different ways of visualizing pathways depending on the question asked: the pathway before a surgery, the pathway of deceased patients or the complete pathway with different steps of interest. The algorithm developed to align, filter and select events of interest has reduce the complexity of the visualization.

Conclusion

We proposed a tool automating the representation of the clinical pathways, and reducing complexity of visualization. Representations may be detailed from an individual and population points of view. The tool functionalities will be extended to cover a greater number of use cases, in particular in allowing users to interact with the visualization.

References/Citations

1. Pryor TA, Gardner RM, Clayton RD, Warner HR. The HELP system. J Med Sys. 1983;7:87-101.
2. Gardner RM, Golubjatnikov OK, Laub RM, Jacobson JT, Evans RS. Computer-critiqued blood ordering using the HELP system. Comput Biomed Res 1990;23:514-28.
3. Huang CW, Lu R, Iqbal U, et al. A richly interactive exploratory data analysis and visualization tool using electronic medical records. *BMC Med Inform Decis Mak*. 2015;15:92.
4. Boudis F, Clement G, Bruandet A, Lamer A. Automated Generation of Individual and Population Clinical Pathways with the OMOP Common Data Model. Stud Health Technol Inform. 2021;281:218-222.