Support for the Inclusion of Domain Knowledge in Prediction Models User Evaluations of a Tool for Generating Prediction Models for Serious Adverse Events in Oncology

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- Keywords: Clinical Decision Support Tools, Clinical Prediction Modeling, Inclusion of Domain Knowledge, User Interface Design, User Evaluation, Data Visualization.
- Abstract: As healthcare is becoming more personalized, prediction models have become an important tool for decision support. In order to create sensible, understandable and useful prediction models, it is often necessary to include domain knowledge. This requires multi-disciplinary communication which has proven to be difficult, as the different parties involved are not always aware of each other's information needs. This paper presents the design process of a tool which supports the communication between clinical experts and data mining experts. Interviews and user tests were executed on four different sites and with 14 different users from both domains. The results from these user tests confirm the need for support on the communication process and provide evidence that the tool presented here indeed provides support by helping both parties to understand each other's information needs. The tool provides a graphical user interface which guides the users through the steps required to create a prediction model. The graphical user interface helps the clinical expert to understand the choices to be made which rely on his/her expertise, while the fact that a 'quick-and-dirty' first version of a prediction model is generated in the process, helps the data mining expert to uncover all formal requirements for the model.

1 INTRODUCTION

As healthcare is becoming more and more personalized, prediction models have become an important tool for decision support. In order to create sensible, understandable and useful prediction models, it is often necessary to include domain knowledge. Clinical expertise is needed in order to clarify which outcome variable is of interest, which features should be included in the model, to uncover possible confounding factors, etc.

Inclusion of clinical domain knowledge requires two experts from different domains to communicate, namely a clinical expert who has knowledge of the data set and a data mining expert. Such interdisciplinary communication has proven to be difficult, as both parties are not always aware of each other's information needs. The process of creating prediction models is therefore often burdened with the need for multiple sessions where the data mining expert and the domain expert sit together and adapt their current perspective on the requirements for the model.

To facilitate the interdisciplinary communication process and to reduce the time and effort required for both parties to uncover the requirements for the envisioned model, we have developed a prototype tool aimed at users from both domains. The tool supports a discussion session where a data mining expert and a clinical domain expert generate a 'quickand-dirty' first version of a prediction model, to ensure that all requirements from the clinical domain have been made explicit. The tool instantly generates a model based on the given requirements, such that the clinical domain expert can review the model and has a concrete perspective on how the model could be applied in practice. The data mining expert can then continue to work on the model using his own domain knowledge to fine tune it.

The prototype is aimed at the oncology domain and specifically at prediction models for Serious Adverse Events (SAEs). However, the principles

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applied may be useful in other healthcare domains as well.

The development process of the SAE prediction tool is steered by evaluations with potential end users of both domains. This iterative development process helps us to obtain more fine-grained requirements regarding useful features and the design of the user interface in each cycle. The evaluations consist of interviews with users regarding their current way of working and issues they run into as well as a guided execution of a representative task. This paper presents the results of the first sets of user evaluations.

2 BACKGROUND

The work presented here is part of the EURECA project (www. http://eurecaproject.eu/) and builds on the framework developed within this project. The goal of the EURECA project is to integrate data from research and clinical practice such that the integrated data can be leveraged upon, among others, to derive new knowledge or to find support for existing hypotheses. The EURECA framework supports uniform and secure access to the data and tools have been built to query the data.

The SAE Prediction tool is the result of a scenario based on a concrete need of one of the clinical partners in the project, a university hospital's paediatric oncology department. The scenario asked for the analysis of relations between patient and treatment characteristics and the SAE Veno-Occlusive Disease (VOD). While discussing this scenario, it became clear that this sort of inquiries for data analysis were made more often, but it was difficult to find the resources to do the data analysis. The tools used for data analysis at this site were Excel, Access and SQL and SPSS. The obstacles that were encountered when doing data analysis using these tools ranged from difficulties in extracting the right data, in understanding the data model, to making sure that there were no mistakes in e.g. the SQL queries and that the right methods were applied in SPSS. The site has no dedicated data analysis experts.

3 THE SAE PREDICTION TOOL

The SAE prediction tool is a prototype supporting domain experts and data mining experts to clarify the requirements for a prediction model in one session, where they use the tool to generate a 'quick-anddirty' first version of a prediction model. This first version will ensure that the data mining experts is aware of all requirements for the model, allowing him/her to work alone to improve the model, without having to confer with the clinical expert.

The tool uses the EURECA framework (Medina et al., 2014) for uniform access to heterogeneous, multisource data. Due to the EURECA common data model and the uniform access tools, the SAE prediction tool can provide a set of generic operations on the data in order to obtain a prediction model for any SAE and any set of features recorded in the data.

The tool guides the user through the process of creating a prediction model in four steps: selection of

SAE Prediction	1			
My new model		Execut	Execute!	
Select Data				
Event Selection	Select a cohort	Maastro Lung Survival		
Feature Selection	UdS SIOP Maastro Lung Survival			
Analysis Settings		Number of patients:	5016	
D —	Logged in as	eureca-monique		



the data set (Figure 1), selection of the SAE (the outcome variable), feature selection and specific analysis settings.

For each included feature, the required preprocessing to be undertaken should be discussed with the domain expert. E.g. date of birth should be converted to age at time of treatment, continuous scale variables can be discretized, missing values may be imputed, etc. The tool provides a number of basic pre-processing options. These methods can be applied to the data set directly and a preview of the result is shown to the users (see Figure 2 and Figure 3).

Once all requirements for the prediction model are provided, the tool will generate a first version of the model, as shown in Figure 4. The model can be applied to different patients, in order to explore its applicability, as shown in Figure 5.

A detailed description of the tool is available in (Hendriks et al., 2014).

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Features	Feature name Body weight
	Original feature name: (Body weight measure (observable entity), value)
Transformation preview	 Missing value strategy
9.5 8.6 8.6 15.4 15.2 15.2	Casewise deletion Replace with O Closest match Add features Remove feature Weight Penalty for missing value
19.6 21 21 ~	• Formatting
Apply preprocessing Preview may not be up to date	Even F1 for help on preprocessing options

Figure 2: Screenshot of the SAE Prediction tool. Selection of a missing value strategy.

4 PROTOCOL AND PARTICIPANTS

Two different versions of the tool have been evaluated at four sites and with 14 potential end users from both domains (data mining experts as well as clinical experts). Table 1 lists the participants, their relevant domain knowledge and the site at which they are located. The first version of the tool has been discussed in informal, unstructured interviews with four potential end-users at three different sites. The second version has been evaluated in a think aloud protocol. This protocol consisted of a short description of a use case and a description of the steps to be taken in order to define a prediction model for this use case. The use case was based on a data set acquired during a trial testing the effectiveness of different treatment protocols for Wilm's tumor. The users were asked to use the tool to construct a prediction model for the adverse event Venoocclusive disease (VOD). The prediction model should include censors for premature end of treatment (lost to follow-up), relapse or death, as these may bias the results. The features to be included in the model were the patient's age and body weight, the location of the tumor, the location of radiation therapy and the dosages of chemotherapy drug Actinomycin D. If necessary, due to the lack of background knowledge regarding statistics or data mining or due to the lack of knowledge regarding this specific use case, the user was guided by the executer of the test. Reports were written on the way in which the users executed the test protocol as well as their comments on the usefulness and usability of the tool. The most important conclusions from these reports are summarized in the next section.

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Features	Feature name Original feature name	Body weight Body weight measur	e (observable entity	y), value)	
Transformation preview	• Missing value strate	ду			
9.5 8.6 8.6	 Formatting Date to age 	Comparison date:	Today	or select from data	- v
15.4 15.2 15.2 19.6	Select first	1	,	Granularity	days -
21 21 v Apply preprocessing	Select last Repeated measure	1 uresSelect reference field:		Comparison date: Granularity	• days •
Preview may not be up to date	Clustering	Cluster size Cluster method	0 average		uays
		Expression:			
	Quantiles	Number of quantiles	0	: III.	
	Ranges	Add range	Remove range		hai
	Categories	Add category	Remove category		Open histogram

Figure 3: Screenshot of the SAE Prediction tool. Selection of pre-processing options.

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Figure 4: Screenshot of the SAE Prediction tool. The resulting 'quick-and-dirty' prediction model.



Figure 5: Screenshot of the SAE Prediction tool. The resulting 'quick-and-dirty' prediction model applied to an individual patient.

5 RESULTS

Here, we present the most important conclusions from the informal interviews as well as the user tests conducted on the first and second version of the SAE prediction tool.

5.1 Informal Interviews

Initially, the tool was intended for use by clinicians

only, enabling them to define prediction models on their own, which could then be refined by data mining experts. From the first informal interviews, it was concluded that this task was too difficult for a nonexpert, even with a specialized graphical user interface. However, the difficulty of the communication across the domains of data mining and clinical knowledge was recognized. All users indicated that the process often involved a lot of back and forth between discussing and updating the model Support for the Inclusion of Domain Knowledge in Prediction Models - User Evaluations of a Tool for Generating Prediction Models for Serious Adverse Events in Oncology

Site	Participants	Participated in
University hospital's paediatric oncology department in Germany	- Oncologist	Informal unstructured interview
Radiation oncology clinic in The Netherlands	 Data mining expert Radiation oncologist 	Informal unstructured interview
University's oncology department in Great Brittain	- Data mining expert	Informal unstructured interview
University hospital's paediatric oncology department in Germany	 Two paediatric oncologists 1 Trial physician 3 participants involved in healthcare ICT related research projects with backgrounds in the medical domain 2 excluded due to insufficient domain knowledge 	Think aloud protocol
Institute for oncology in Italy	 Oncologist Statistician 1 excluded due to insufficient domain knowledge 	Think aloud protocol

Table 1: Overview of participants to the evaluations of the SAE Prediction Tool.

before arriving at the desired end result. Therefore, the focus of the development was shifted towards use of the tool by a clinical expert together with a data mining expert, the added value of the tool consisting of a reduction in time and effort required to obtain the exact formal requirements for a prediction model. The tool could support this interdisciplinary communication by allowing the data mining expert to immediately show the effect of certain choices on the data set and/or the resulting prediction model and how it can be applied to new patients.

The two oncologists both indicated that using this tool would result in an increased understanding of the model, and therefore in greater trust in the model. This would mean that use of the tool could increase the chances of adoption of a prediction model.

The two data mining experts both indicated a need for data inspection and visualization. If the distribution of certain features could be shown instantly, it is easier to discuss pre-processing details, e.g. strategies for dealing with missing values and outliers, for discretizing continuous variables, etc, and also to discuss the possibility of biasing conditions in the data.

The detailed results of the informal interviews can be found in EURECA deliverable 6.7 (Huang et al., 2015).

5.2 Test Protocol

The user tests at the university hospital and the institute for oncology showed that the tool forces users to go through all of the steps of defining a prediction model, including formally defining a goal variable (the SAE), specifying the predictors and formally defining the best method for dealing with missing values and the pre-processing operations

required to create meaningful predictors from features selected from the data.

The tests showed that the approach supported by the tool helped bring up the right questions; questions that would otherwise have been overlooked in a first discussion between a data mining expert and a clinical domain expert.

For example, one user with a medical background, who had some experience in statistics, indicated that in order to deal correctly with missing values, one would need to involve a domain expert to make sure that the reasons values may be missing are clear (i.e. if values for radiation therapy dosages are missing, this may also mean that no radiation therapy was received by the patient), but also someone with a background in statistics to make sure no bias is introduced.

Another user, who has a strong medical background and who was familiar with the data set, remarked that in this particular case, the value to be predicted, the occurrence of the SAE veno-occlusive disease (VOD), should be looked for not only as recorded VOD events, but also in a combination of recorded symptoms, because VOD can only be confirmed with autopsy, so it is not always recorded as a (suspected) VOD event). He suggested to also abdominal mark patients pain, with thrombocytopenia and elevated liver enzymes for possible VOD events, and even patients with treatment delay where the stated reason is a suspected VOD event.

Another user with strong medical background and familiarity with the data set indicated that if we wanted to include chemotherapy dosages, it would make sense to investigate dosages related to a subsequent VOD event within a time frame of two or three weeks, as VOD is an acute toxicity. Use of the tool also triggered this user to be more specific about his interest in the effect of radiotherapy on the risk for a VOD event. He was interested in finding out whether the risk would be increased if radiotherapy was applied on the right side compared to radiotherapy applied only to the left side. However, in order to find out on which side radiotherapy was applied, one would need to look up first on which side the tumor was located, because radiation site was only recorded in terms of whether it was applied only at the tumor site, at the lymph nodes or on the whole abdomen.

These results show that the tool was successful in helping to uncover a larger part of the formal requirements for a prediction model in a first discussion with a domain expert.

With respect to future development, it was noted that all seven users showed an explorative attitude towards the data. One oncologist indicated that even to explore his own data, he would currently need the help of a data mining expert and he found this very frustrating. The tool already supported him to some extent to start exploring the data on his own. This explorative attitude stresses the importance of investigating other data visualization options, besides providing histograms for each included feature, such as visualizations to help explore ranges and units as well as distributions, and interlinking of features (e.g. showing body weight and chemotherapy drug doses in the same graph/table).

It should also be noted that the user interface of the tool was still quite complicated. This seemed to be mainly related to the fact that the user interface does not show the effects of certain actions on the end result instantaneously; the resulting prediction model is only shown after filling in all the required information. Providing more immediate feedback would improve the usability to a great extent.

Furthermore, the user tests indicated that it is also very important to invest in a clear (annotated) data model, from which the meaning of the recorded values is immediately clear.

Detailed reports of the user tests at the university hospital and the institute for oncology can be found in EURECA deliverable 8.5 (Koumakis et al., 2015) and EURECA deliverable 8.6 (Gleave et al., 2015) respectively.

6 CONCLUSIONS AND FUTURE WORK

The first user tests reported here indicate a strong need for a tool such as the SAE prediction tool presented here, to help reduce the time and effort needed to uncover the formal requirements for a prediction model by supporting the communication between a data mining expert and a domain expert.

At all sites where the tool was discussed, it was mentioned that the tools used currently for building prediction models were too difficult to be used by non-experts, allowing non-experts only to use verbal communication with the data mining expert and to provide feedback on the models once they are complete.

These tools that are currently used are too complex for non-experts due to their genericity. Restricting to the domain of oncology and to prediction models for SAE's allowed us to simplify the process by standardizing the steps and presenting them in a graphical user interface, so that the domain expert can understand the process. The use of the EURECA common data model and the tools for uniform data access allowed us to create generic operations on the data, routinely used in data mining and to include these operations in the graphical user interface. Including a preview of the effect of an operation on the data furthers the understanding of the domain expert of the process involved in generating the prediction model and helps the data mining expert to obtain the formal requirements for the model more quickly.

The first user tests uncovered that future work should focus on supporting more explorative functionality as well as providing immediate feedback of any step in the definition of the prediction model on the end result.

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