

User-Driven Development of a Novel Molecular Tumor Board Support Tool^{*}

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Abstract. Nowadays personalized medicine is of increasing importance, especially in the field of cancer therapy. More and more hospitals are conducting molecular tumor boards (MTBs) bringing together experts from various fields with different expertise to discuss patient cases taking into account genetic information from sequencing data. Yet, there is still a lack of tools to support collaborative exploration and decision making. To fill this gap, we developed a novel user interface to support MTBs. A task analysis of MTBs currently held at German hospitals showed, that there is less collaborative exploration during the meeting as expected, with a large part of the information search being done during the MTB preparation. Thus we designed our interface to support both situations, a single user preparing the MTB and the presentation of information and group discussion during the meeting.

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1 Introduction

Personalized Medicine is a rapidly growing area in healthcare which fundamentally changes the way patients are treated. This is especially true for cancer therapy where more and more hospitals conduct molecular tumor boards (MTBs) bringing together experts from various clinical fields to jointly discuss individual patient cases [1]. Yet the exploration and discussion of the relevant data and information poses a tremendous challenge in this setting: Because of the experts distinct background expertise and time constraints, all data and information need to be presented in a concise form that is easy to grasp and supports the consensual elaboration of sound treatment recommendations.

We approach this need by developing a software solution which focuses on a novel, intuitive graphical user interface that integrates and visualizes patient data from several clinical information, laboratory and imaging systems,

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etc., together with additional external information from cancer-research systems (e.g. cBioPortal), genomic and pathway databases (e.g. KEGG), as well as (bio)medical literature (e.g. PubMed). A task analysis of MTBs was conducted and clinical experts were repeatedly shown a current version of a prototypical interface to integrate their feedback into the development process.

2 Methods

To detect the actual needs towards such a software, we initially visited five German MTBs where we used a questionnaire and interviews to gather information about specific requirements of each MTB, management and workflows, perceived weaknesses and room for improvements, as well as ideas on what functionalities an ideal software tool should provide (for comparison see [2]).

The interviews were conducted with the MTB organizers to gain insight into their workflow during preparation of the board, the resources they use for research and the overall procedure of the meeting itself. In the the questionnaires³ we first asked about personal information, like the participant's role in the MTB or his/her expertise and then about the procedure of the MTB and included questions, like whether therapy successes/failures and comparable cases are discussed or if there is a demand for online research during the MTB. Participants could answer on a scale ranging from *not at all* or *never* to *yes* or *always*.

The resulting requirement analysis formed the basis of our development process which is now accompanied by regular visits to our local MTB to discuss whether our software indeed reflects the experts specific needs and wishes. This allowed us to evaluate our interface design from the very beginning of the development and to adjust it to the actual needs of the MTB.

Our initial (naive) belief at project start was that during the MTB a group of experts would come together to jointly discuss and evaluate and data patient cases in depth on the spot. Hence our first prototype employed a large (84 inch) multi-touch screen table allowing the MTB participants to collaboratively and interactively explore all information sources and arrange the different kinds of documents, like clinical/patient data, radiologic images, research papers, etc. on the screen [3,4]. Our initial thought was that such a table would greatly improve collaborative decision making and reduce the cognitive load for the participants.

We implemented an initial prototype prior to completing the task analysis to show the capabilities of such an interface to some clinical experts. This was important, as based on their daily routine using standard clinical software solutions, they might lack the knowledge about the possibilities of novel multi-user interfaces. This also gave us important feedback of the actual needs for a MTB application. It is important to note, that clinical experts who were given the questionnaire were not shown the prototype prior to answering the questions.

³ Questionnaire: <https://bit.ly/persons-questionnaire>

3 Results

The interviews and our participation in the MTBs revealed that the given time constraints only allow for a relatively short discussion of the individual patient cases. As a consequence, there is no room for any interactive, collaborative research or data exploration and so basically all research needs to be done before.

We collected questionnaires from 23 participants. Although this seems a rather small number, it is important to note that at the time of our analysis only 5 hospitals in Germany were conducting MTBs with 15 to 25 participants per MTB. Thus our questionnaire was handed out to about 100 MTB participants making up for a feedback of almost 25%. After assigning each verbal scale numerical values from 1 = *never/not at all* to 4 = *yes/always*, our results showed that participants see only little demand for online research during the MTB ($\mu = 2.304$) which is mostly due to the mentioned time constraints. Also therapy successes/failures ($\mu = 2.047$) or comparable cases ($\mu = 2.273$) are rather seldom discussed yet participants mentioned this as highly desirable ($\mu = 3.667$).

Based on these findings, i.e. time constraints during the MTB and large amount of work to be done in the preparation, we changed our initial idea of having one tool, that only supports the group situation in the MTB and we thus divided the interface into two parts: One for the clinical experts to use on their usual computers to perform their explorative research when preparing a MTB and for the MTB moderator to then integrate and (visually) condense the results into a succinct presentation, and the second one to provide the means to present this during the MTB on any touch-enabled screen dynamically.

The user interface focuses on the presentation layer, performs no data processing at all and is realized in HTML and JavaScript using Electron. The advantage of electron is not only its platform independence and high portability, it also features a very important element: webviews. One of the key aspects of our interface, as described in detail below, is the possibility to display different sources of information (webpages, documents, visualizations) for free arrangement and comparison, in a single- or multi-user scenario. While this is not achievable with pure HTML and javascript using iframes, electron webviews offer all the functionality needed for such an interface.

The interface is then securely connected by an encrypted REST interface with the back-end services located within the secured hospital network. Those services – implemented in Java with Spring Boot and its sub-frameworks – perform the actual data fetching, processing and integration from the source systems and provide further means for data protection and pseudonymization.

Fig. 1 shows an example screenshot of the whole interface together with close-ups of the important elements. The development of the layout was guided by the following design principles derived from our task analysis: 1) Minimize the number of actions and interface elements to improve speed and simplicity of the workflow, 2) support memory offloading and information interpretation (e.g., by free arrangements and annotations of resources, simultaneous visibility of all information, near-hand processing of information [5]), and 3) use space in an optimal way to leave as much space as possible for visual data exploration.

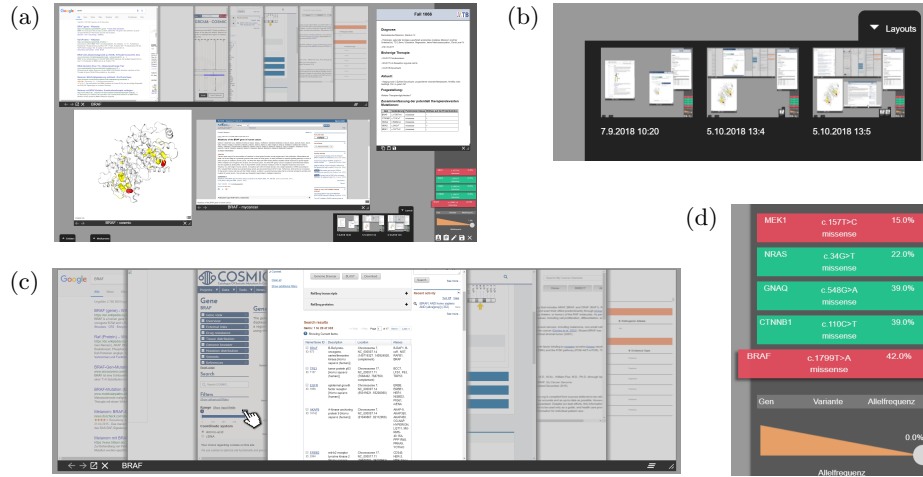


Fig. 1. Example screenshots of the prototypical interface: a) complete interface, b) collection of saved layout configurations with respective date, c) webview containing multiple resources for comparison, d) close-up of the gene sequencing data visualization (with activating and inactivating variants depicted in green and red respectively). For a more detailed overview of the interface see 4

When opening a new case for the first time the user is shown a summary of the patient's clinical history including diagnosis, previous therapy, questions for the MTB and the potentially therapy relevant genetic variants. This summary is generated automatically and replaces the PowerPoint slides that were manually created by the MTB organizer in a time consuming process of copying text from the clinical information system or typing in by hand.

The interface itself is divided into three different areas. In the first area on the right side there is an overview of the therapy relevant variants (Fig. 1d), that can be filtered by allele frequency and sorted by various criteria. A color code indicates activating or inactivating variants. To get information for each variant, the current workflow requires the user to open up multiple browser tabs and manually search within the respective databases. To compare different sources of information for a single variant or even between multiple variants the user has to constantly switch between different tabs or applications. Our interface allows to open multiple sources of information (Fig. 1c) for one variant with a single click in the second area of the interface, the large exploration area that takes up most of the screen-space (Fig. 1a). From this overview single information sources can be opened in separate floating windows and which can be arranged and resized freely for exploration and comparison within that area. The user can also open information sources for different variants in parallel to compare them.

Creating the presentation for the MTB in the current preparation workflow requires the user to copy and paste all relevant information manually into a separate power point slide. In contrast, our interface allows to save an arrangement of information sources as a fixed layout without having to switch the applica-

tion. Such a layout can later be restored for presentation during the meeting and due to the interactive properties of the HTML content these restored information sources can be used for further research and exploration as needed. Saved layouts are shown as thumbnails in a third area at the bottom (Fig. 1b).⁴

4 Conclusion and Outlook

We analyzed the workflow of MTBs currently held at German hospitals and developed a novel interface to support the preparation and the presentation for the meeting. In a next step, this interface will be evaluated in a clinical working environment and usability studies will be conducted. Also, additional features, deemed as valuable by clinical experts will be implemented as well, like the possibility to search for comparable local cases or the possibility for annotating documents and data to better document the decision making process.

References

1. van der Velden, D., van Herpen, C., van Laarhoven, H., Smit, E., Groen, H., Willems, S., Nederlof, P., Langenberg, M., Cuppen, E., Sleijfer, S., Steeghs, N., et al.: Molecular Tumor Boards: current practice and future needs. *Annals of Oncology* 28 2017
2. Hinderer, M., Boerries, M., Haller, F., Wagner, S., et al.: Supporting Molecular Tumor Boards in Molecular-Guided Decision-Making - The Current Status of Five German University Hospitals. *Stud Health Technol Inform.* 2017;236:48-54
3. Morris, M., Huang, A., Paepcke, A., Winograd, T.: Cooperative Gestures: Multi-User Gestural Interactions for Co-located Groupware. *Proc SIGCHI Hum Fact Comput Syst.* 2006;1201-1210
4. Streit, M., Schulz, H., Schmalstieg, D., Schumann, H.: Towards Multi-User Multi-Level Interaction. *Proc Work on Collab Visual on Interact Surf.* 2009;5-8
5. Brucker, B., Brömme, R., Weber, S., Gerjets, P.: Learning on multi-touch devices: Is directly touching dynamic visualizations helpful? 17th Biennial Conference of the European Association for Research on Learning and Instruction (EARLI).” Special Interest Group (SIG) 2. Tampere, Finland 2017

⁴ Interface Prototype Demo: <https://bit.ly/persons-interface-prototype-demo>