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Prototypical Visualization of Patient Similarities in cBioPortal to Enhance Decision-Making in Molecular Tumor Boards

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Abstract. *Background*: Patient similarity analysis is pivotal in cancer research and clinical oncology, aiding in identifying patterns among patients with similar clinical

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and molecular profiles to guide therapeutic decisions, particularly in Molecular Tumor Boards (MTB), where therapy decisions are frequently informed by the treatment experiences of previously treated similar patients. However, the lack of standardized tools for automation and visualization limits efficiency here, especially in individualized MTB decisions. *Objective*: This study aims to develop a graphical user interface that aligns with clinician preferences to enhance patient similarity assessments and support decision-making in MTBs. *Methods*: Visualization concepts were developed through iterative design and evaluation cycles involving clinical experts. Mock-ups were created to represent various approaches for displaying patient similarities, focusing on molecular data relevant to MTB decisions. *Results*: Various designs were developed for visualizing patient similarity in cBioPortal. These include tabular views, network representations, and radar plots. *Conclusions*: These visualizations offer promise in enhancing decision-making in MTBs by making patient similarity assessments more accessible. Future development will focus on additional functionalities and better integration into clinical workflows.

Keywords. Patient Similarity, Precision Medicine, Molecular Tumor Board, Visualization Tools, cBioPortal

1. Introduction

With the increasing availability of sequencing technologies, Molecular Tumor Boards (MTB) are becoming increasingly relevant in clinical practice. These multidisciplinary boards provide personalized treatment recommendations based on patients' genetic profiles. Recent studies suggest that MTBs have the potential to improve therapeutic strategies, particularly for patients who do not respond to standard treatments or present with rare tumor types [1]. As MTBs are progressively integrated into routine clinical workflows [1], the amount of data from patients previously evaluated in such boards is also expanding. This growing dataset increases the likelihood of identifying patients with mutational profiles similar to those currently under review in the MTB. The inclusion of treatment recommendations and possibly treatment responses of similar patients could speed up subsequent treatment decisions and also potentially increase the quality of the recommendations. Büchner et al. (2020) [2] have already identified the need for a "Search Tool for Similar Patients" in a cBioPortal-based platform for MTBs. The basic expandability of cBioPortal [3] has already been proven several times [4].

The present study introduces design concepts for a user interface aimed at facilitating the comparison of molecular data from similar patients. The proposed designs extend the patient-centric view in cBioPortal and were developed in close collaboration with potential end-users like clinicians involved in MTBs to ensure alignment with clinical requirements and to optimize the interface for practical application. The designs integrated into cBioPortal could be utilized during MTBs or in preparation for such meetings.

2. Methods

The work builds on an ongoing scoping review of 154 publications (protocol published [5]) that examines different dimensions of patient similarity in cancer research. This focuses on developing visualization concepts for patient similarity to enhance clinical decision-making in MTBs. In this context, various mock-ups to extend the user interface of cBioPortal were created in an iterative feedback process with senior physicians and

pathologists of the University Hospital Halle (Saale) (UKH). The participants themselves are an essential part of the MTBs at the UKH and thus represented potential end users of the extension. These mock-ups were developed based on the assumption that a similarity score generated by a given algorithm could quantify the similarity between two patients. The score relies on molecular data, which is critical for decision-making in MTBs. Some mock-ups incorporated differentiated similarity scores across various data types, while others focused exclusively on molecular profiles. The usability of the mock-ups was evaluated through interviews with five experts, including heads of MTBs from the UKH, the University Medical Center Freiburg, and the University Medical Center Schleswig-Holstein. An exploratory testing approach [6] was used, where experts were asked to describe how they would interact with the static mock-ups. The designs were then evaluated by both open-ended questions and 5-point Likert scale ratings (1 = "strongly disagree", 5 = "strongly agree") [7] of various design aspects.

3. Results

3.1. Visualization Concepts

The proposed extension for cBioPortal may be integrated into a new tab within the patient-centered view called "Similar Patients". This tab would display patients with the highest similarity to the reference patient in a overview table, sorted by descending Similarity Scores. These currently hypothetical scores are designed to quantify patient similarity on a scale from 0 to 100. Since the score is currently theoretical, an alternative approach, as proposed by Büchner et al. (2020) [2], could be employed, allowing clinicians to manually adjust weighting factors to prioritize the data they consider most relevant for similarity calculations. Regardless of whether the table relies on similarity scores or manual settings, clinicians can navigate from it to a comparative view between the reference patient and the chosen similar patient (Figure 1), where shared and distinct molecular alterations are visualized. Additionally, therapy recommendations for the previously treated patient will be displayed, aiding clinicians in making informed therapeutic decisions.

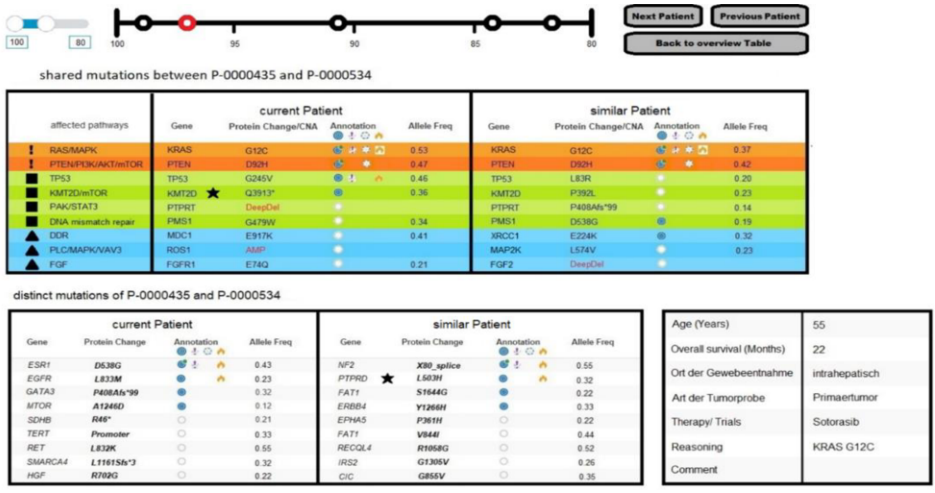

Figure 1. Mock-up of the comparison table between the reference patient and the selected patient

The network diagram in Figure 2a visualizes similarities across different data types, such as mutations and DNA methylation, with the thickness and color of the connections indicating the degree and type of similarity. A selection menu allows users to toggle between data types. The radar plot offers a graph view, where each node represents a patient, and the distance to the center reflects the degree of similarity to the reference patient. Different data types are color-coded, and hovering over a patient provides additional clinical patient data. These different visualizations aim to accommodate the preferences of a broad range of users.

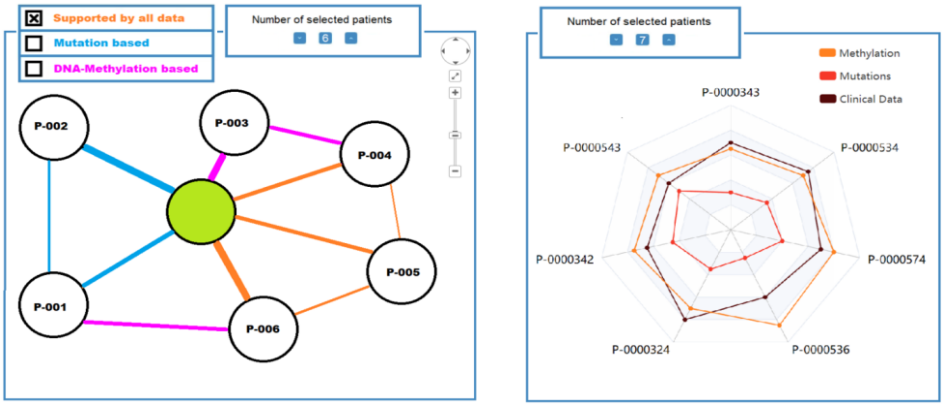

Figure 2. Mock-ups for the graphical representation of patient similarity: left (a) - as a network diagram, right (b) - as a radar plot [8].

3.2. Expert Evaluation and Findings

Evaluation sessions with clinicians, along with discussions with experts, provided valuable insights into the strengths and limitations of each visualization concept. The results indicated a preference for tabular representations in clinical decision-making due to their straightforward and data-driven format. The tabular overview received high average ratings for comprehensibility (4.2/5), usability (4.0/5), and transparency (3.8/5), underscoring its clarity and relevance. Experts particularly appreciated features such as the structured presentation of molecular alterations and the ability to directly compare similar patients without relying on complex visual representations. In contrast, graph-based visualizations were recognized as valuable tools for initial data exploration but were considered less intuitive for routine clinical use. This approach received ratings of 3.8/5 for transparency and comprehensibility, slightly lower than the tabular format. The radar plot was praised for its effectiveness in displaying multidimensional data, earning high scores for transparency (4.5/5), comprehensibility (4.2/5), and usability (4.7/5). However, its readability and practical application were seen as limited, particularly for clinicians unfamiliar with the format. In general, the experts emphasized the importance of transparency in calculating the similarity score. They noted that insights into specific factors and their weighting that resulted in the score could provide significant benefits.

4. Discussion

Key findings revealed that clinicians showed a strong preference for tabular representations in clinical decision-making due to their clarity, with high ratings for comprehensibility, usability, and transparency. While graph-based visualizations and radar plots were praised for their ability to explore data and represent multidimensional information, respectively, they were considered less intuitive and practical for routine clinical use, particularly for less experienced users.

Efforts to integrate the proposed visualization designs into an extended version of the cBioPortal front end are already in progress. The current implementation is available in the patient_similarity branch of https://github.com/buschlab/cbioportal-frontend. Future work will focus on further development and enhancement of this approach.

5. Conclusions

While the current implementation is still under development, the visualizations created in this study show clear potential to advance precision oncology by making patient similarity assessments more accessible and actionable for clinicians.

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