Advancing Usability and Decision Support for Molecular Tumor Boards: Insights from PM4Onco's Visual Analytics Workshop

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Abstract. The PM4Onco project aims to optimize cBioPortal for use in Molecular Tumor Boards (MTBs), enhancing its usability in the clinical setting and integration of clinical and genomic data. A visual analytics workshop at the PM4Onco Symposium 2024, organized in a co-creative and participatory manner, using a user-centered design (UCD) approach, identified key improvements through discussion among involved stakeholders and exchange of perspectives. These improvements included customizable workflows, role-based access controls, and advanced visualization tools like time-series plots and patient similarity metrics. Participants also highlighted the need to address media silos and ensure seamless data integration from external sources like electronic health records (EHRs). Decision support systems, especially those leveraging annotation sources, were emphasized to improve the interpretation of molecular findings and provide therapy recommendations. The workshop ensured that new features would be practical, user-friendly, and aligned with the specific needs of MTB users, facilitating more efficient clinical decision-making and enhancing the platform's functionality in personalized oncology.

Keywords. Molecular Tumor Boards, cBioPortal, User-Centered Design, Data Integration, Decision Support

1. Introduction

Molecular Tumor Boards (MTBs) serve as critical forums for discussing personalized cancer treatments based on a patient's clinical and high-throughput molecular data. However, preparing these cases can be a resource-intensive process, requiring clinicians

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to collect and interpret data from various systems, including local databases and external resources such as OncoKB [1]. This manual collection and review process introduces inefficiencies, limiting the number of cases that can be discussed and may affect the quality of decision-making in MTBs [2].

The PM4Onco [2] project seeks to address these challenges by developing and improving infrastructure for the exchange and integration of clinical and genomic data. An important part of this project is cBioPortal [3], a widely used platform for visualizing cancer genome data originally developed by the Memorial Sloan Kettering Cancer Center, which is being used in MTBs but still requires further customization to meet user needs. A user-centered design (UCD) approach is key, ensuring that only necessary, feasible features are implemented to enhance the platform's practical utility [4].

This paper outlines the findings from the visual analytics workshop conducted at the PM4Onco Symposium 2024. The workshop aimed to identify user-driven needs and ensure the prioritization of requirements that improve workflows and support decision-making in MTBs without adding unnecessary complexity.

2. Methods

2.1. Workshop and User-Centered Design

The visual analytics workshop was conducted on September 23, 2024, during the PM4Onco Symposium. A total of 17 participants from nine sites, including clinicians, bioinformaticians, software developers, and one patient representative contributed to the workshop. The workshop's objectives were to refine the requirements for visualizing heterogeneous data types in MTBs, which were collected at the start of the project as part of a requirements analysis, identify usability challenges, and propose solutions for improving MTB-cBioPortal's [3] interface and workflow integration, based on UCD method [5]. The workshop was planned and conducted by the three research associates from the site responsible for the workshop.

The UCD process consists of four phases (see figure 1): Context of Use Analysis identifies stakeholders and gathers requirements, followed by Requirement Specification through interviews and surveys. Then, in the Design and Development phase, visual mockups and software are created, and the final phase, Evaluation, uses usability testing to ensure the software meets user needs. Requirements are progressively specified, evaluated, and implemented, with a summative evaluation conducted at the end to assess the software's effectiveness in MTB-cBioPortal.

Surveys and interviews with stakeholders at the beginning of the project provided the basis for discussions [6]. Participants were divided into groups based on their roles to ensure a thorough analysis from clinical and technical perspectives. The workshop included interactive reviews, where live feedback on workflow customization, data integration, and visualizations was collected, using the live demo of cBioPortal. Quick surveys were used to refine requirements in real time, and post-workshop analyses consolidated feedback into a prioritized list of actionable improvements.

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[2] https://pm4onco.de/

[3] The MTB-cBioPortal, an extension of cBioPortal, was developed within the MIRACUM consortium's use case 3 project to support personalized medicine.

2.2. Focus area

The workshop focused on three key areas for improvement, including:

- Improving Efficiency & Usability (1)
- Additional (Advanced) Visualizations (2)
- Decision Support & Enriched Annotation (3)

(1) Customizable workflows, role-based access controls, and personalized preferences are essential for improving the efficiency of MTBs, supported by a scalable architecture and a user-friendly interface to reduce navigation burdens. (2) Advanced visualization tools like time-series plots and animations are crucial for tracking tumor progression and therapy outcomes, with high demand for effective molecular data interpretation. (3) Additionally, decision support systems and algorithms are needed to interpret molecular results and provide therapy recommendations. Integrating databases on mutations, drug interactions, and clinical data is key to MTB decision-making.

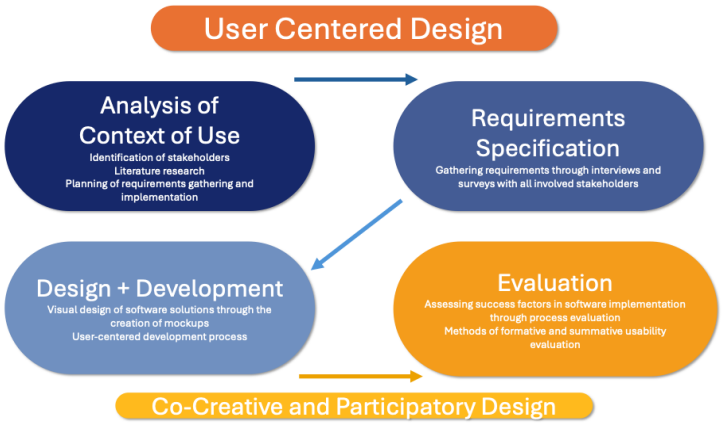

Figure 1. Iterative Steps of User Centered Design Integrating Utility and Usability.

3. Results

3.1. Improving Usability & Efficiency

The evaluation prioritized addressing media silos, followed by customizable interfaces and filter options. Key challenges included integrating external patient data and seamless PDF exports for MTBs. Existing tools like CBPManager[4] are useful but require site-specific expertise. Concerns about data validity, unstructured external data, and licensing limitations for databases like OncoKB hinder efficient use. Although cBioPortal is valuable as a case archive, its lack of PDF exports, automatic integration, and fine-grained access controls limits broad clinical adoption [5].

[4] https://arsenij-ust.github.io/cbpManager/index.html

3.2. Additional (Advanced) Visualization

The workshop emphasized advanced visualization tools for better interpretation of molecular data and tracking therapy responses. Proposed solutions included time-series plots, dynamic tumor evolution models, and enhancements like color-coding in timelines to monitor tumor changes and therapy effectiveness in real-time. Additionally, patient similarity metrics were suggested to compare molecular profiles, enabling clinicians to identify therapy response patterns and apply insights from similar cases to future patients, improving personalized treatment approaches.[7,8]

3.3. Decision Support & Enriched Annotation

There is a critical need for decision support systems to annotate molecular findings and recommend therapies based on clinical guidelines and trial data, with OncoKB as a leading option. Major challenges include integrating mutation, drug interaction, and clinical trial databases with electronic health records, molecular tests, and imaging. Comprehensive data annotations, such as drug interactions and mutation impact, are crucial. Key concerns include harmonizing evidence levels, improving patient similarity metrics, and simplifying data visualization for effective use in MTBs. Furthermore, the question arises whether to use simple data display or complex algorithmic analysis. These approaches can be combined to maximize the potential of the available data.[8,9]

3.4. Key Findings

The workshop identified key areas for improvement:

- Prioritization of User-Requested Features
- Feasibility-Driven Development
- Minimizing Data Silos
- Cognitive Load through Visual Simplicity
- Balancing Innovation and Practicality

In more detail, it emphasized addressing specific clinician-driven needs, focusing on customizable workflows and role-based access controls with higher granularity to avoid creating duplicate data when it needs to be used in multiple contexts. By following a UCD framework, only features that could be easily implemented without major system changes were prioritized, such as customizable data filters and views. This practical focus minimized complexity while addressing critical user pain points.

One of the major pain points identified was the existence of data silos, especially concerning manual data transfers between systems, which result in inefficiencies and errors. A critical proposal was the automation of data integration, particularly from EHRs to cBioPortal. Participants also stressed the need for seamless integration with molecular databases like OncoKB to streamline data flow. Simplified timelines, color-coded annotations, and intuitive visualizations were deemed essential to minimize cognitive load and help users interpret complex molecular data (e.g. biomarkers).

The workshop highlighted balancing innovative features with clinical workflow constraints, prioritizing immediate improvements like real-time data integration and patient-matching algorithms. This approach ensures that new features are practical and directly usable within current clinical infrastructure.

4. Discussion and Conclusions

The visual analytics workshop emphasized the value of UCD in enhancing MTB cBioPortal for MTBs. The goal was to consolidate feedback from clinicians and developers to define practical and feasible data visualization methods for development and integration into cBioPortal's user interface. A major development challenge is providing long-term support for features like flexible workflows and role-based access, ensuring platform evolution without user overwhelm. A significant and challenging task due to site-specific differences (e.g., data flows and hospital information systems) will be to eliminate data silos. Thus, automating integration into systems like electronic health records is crucial. Advanced visualizations are appropriate when it comes to improving data interpretation using time series plots and similarity measures for patients. While real-time data integration and decision support algorithms were prioritized, aligning these innovations with clinical workflows is key to ensuring adoption. The right balance between creating value and gaining acceptance should be sought, but also, 'He who thinks too much will achieve little' - Johann Wolfgang von Goethe.

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References

[1] Chakravarty D, Gao J, Phillips S, Kundra R, Zhang H, Wang J, et al. OncoKB: A precision oncology knowledge base. JCO Precis Oncol. 2017;(1):1–16. https://doi.org/10.1200/PO.17.00011

[2] Kato S, Kim KH, Lim HJ, Boichard A, Nikanjam M, Weihe E, et al. Real-world data from a molecular tumor board demonstrates improved outcomes with a precision N-of-One strategy. Nat Commun. 2020 Oct 2;11(1):4965. https://doi.org/10.1038/s41467-020-18613-3

[3] Gao J, Aksoy BA, Dogrusoz U, Dresdner G, Gross B, Sumer SO, et al. Integrative analysis of complex cancer genomics and clinical profiles using the cBioPortal. Sci Signal. 2013;6:pl1. doi:10.1126/scisignal.2004088

[4] Dopp AR, Parisi KE, Munson SA, Lyon AR. A glossary of user-centered design strategies for implementation experts. Transl Behav Med. 2019 Dec;9(6):1057–64. https://doi.org/10.1093/tbm/iby119

[5] Reimer N, et al. Challenges and experiences extending the cBioPortal for cancer genomics to a molecular tumor board platform. Stud Health Technol Inform. 2021;287:139–43. doi:10.3233/SHTI210833

[6] Strantz C, Boehm D, Ganslandt T, Börries M, Metzger P, Pauli T, et al. Empowering oncologists: the evolution of digital support and visualization tools for molecular tumor boards. BMC Med Inform Decis Mak. (In review).

[7] Boehm D, Strantz C, Christoph J, Busch H, Ganslandt T, Unberath P. Data visualization support for tumor boards and clinical oncology: protocol for a scoping review. JMIR Res Protoc. 2024 Mar 5;13:e53627. doi:10.2196/53627

[8] Manuilova I, Bossenz J, Weise AB, Boehm D, Strantz C, Unberath P, et al. Identifications of similarity metrics for patients with cancer: protocol for a scoping review. JMIR Res Protoc. 2024;13:e58705. doi:10.2196/58705

[9] Renner C, Reimer N, Christoph J, Busch H, Metzger P, Boerries M, et al. Extending cBioPortal for therapy recommendation documentation in molecular tumor boards: development and usability study. JMIR Med Inform. 2023 Dec 11;11:e50017. doi:10.2196/50017.