

Showcasing design study methodology through simpler design challenges: An application to a microbial genomics clinical report design

Anamaria Crisan*

Computer Science
University of British Columbia

Geoffrey McKee†

Population and Public Health
University of British Columbia

Tamara Munzner‡

Computer Science
University of British Columbia

Jennifer L. Gardy §

Population and Public Health
University of British Columbia
BC Centre for Disease Control

ABSTRACT

Design study methodologies developed by infovis researchers are not adopted beyond this community despite a growing repertoire of visualization tools created by domain specialists. While better knowledge translation between infovis and domain specialists is needed, it is also arguable that visualization tools, which can have many complex interacting parts, can make it challenging to demonstrate design study methodology in action. Here, we present our application of a design study methodology to a simpler problem of information design in a tuberculosis (TB) clinical report that presents results derived from TB whole genome sequencing (WGS). Clinical reports are a common and foundational element of medical and public health practice and as such are a good, and relatively simple, application context in which to demonstrate the value of applying design study methodology. Using an existing TB clinical WGS report as a base, we collected relevant tasks and data, linked those to alternative report designs, and finally compared those alternatives to the original report with stakeholders. The evidence gathered through our project demonstrated how the original, *ad hoc*, report design contained elements that were unnecessary, difficult to interpret, or insufficient. We also demonstrated how a number of procedural constraints around current reporting practices, such as how stakeholders received reports and how much time they had to review them, affected the reports design. Taking into consideration the evidence gathered and regulatory guidelines, we produced a new TB WGS clinical report that is currently under more detailed assessment and awaiting deployment. By using a simple and relatable design challenge, providing a concrete framework for data gathering and analysis, and through participatory engagement of the relevant domain specialist community, our work aimed to introduce infovis evidence-based design methodologies to the health sciences community.

Index Terms: J.3 [Life and Medical Science]: Biology and genetics—; D.2.10 [Design]: Methodologies—

1 INTRODUCTION

Technological changes have enabled healthcare researchers to collect and store more data of different types, including whole genome data derived either from human subjects or from microbes that live in or on humans, including harmful microbes known as pathogens. Considerable effort is being put toward the standardization of laboratory and bioinformatics methods in order to realistically apply genomic data to clinical and public health practice. However, the reporting of these data are currently developed *ad hoc*, a practice

that is increasingly viewed as inadequate by stakeholders required to interpret data. Thus, there are a number of opportunities for infovis researchers to influence the reporting of complex heterogeneous health data, including WGS data, from simple static reports to more intricate and interactive data visualization tools.

1.1 Application and Collaboration context

We collaborated with members of the COMPASS-TB team, affiliated with Oxford University and Public Health England, to help them redesign an existing TB WGS clinical report. COMPASS-TB is helping to transition TB management and monitoring in England from traditional laboratory techniques toward whole genome based methods [5]. Their work, and that of others, has shown that WGS can diagnose infections as accurately as, and in some cases better than, current protocols [4], [3], can predict antimicrobial resistance phenotypes with high concordance to current testing methods for certain drugs [2], [7], can be used to investigate disease transmission in an outbreak[6], and finally has a much faster turn-around time compared to existing methods [5].

We were presented with design constraints to conform to regulatory requirements of ISO15189:2012, limiting ourselves to available data, and producing a static report deliverable by existing electronic health record systems, the mail, or fax.

2 APPLYING DESIGN STUDY METHODOLOGY

We used a design study methodology [6] to form the basis of our TB WGS report redesign effort. The *precondition phase* of the design study methodology comprised the establishment of our collaboration with the COMPASS-TB group, a gathering of their expectations and requirements, and presenting them with a proposal for our approach. The COMPASS-TB team were the project gatekeepers with whom we interacted, but they were a subset of the broader stakeholder group, which included TB clinicians, nurses, epidemiologists, and researchers, that participated in our project.

In the *core analysis* phase, we applied study designs from mixed methods research to structure data gathering and analysis. The *Discover* stage executed an exploratory sequential model design [1], which gathers initial qualitative evidence to establish relevant themes, tasks, and data, and subsequently evaluates those findings using quantitative methods. To gather qualitative data, we conducted semi-structured interviews with 7 TB and infectious disease experts across different stakeholder roles, including two clinicians. We established tasks pertaining to TB diagnosis, treatment, and monitoring, which we refer to as the TB workflow. The workflow was transformed into a quantitative survey (Task and Data questionnaire) that recruited 17 participants (7 clinicians) to assess the extent to which individual tasks and data were associated and when WGS, or other genomic-derived (i.e. genotyping) data could be used in decision making. The findings from the *Discover* stage served as input to the *Design* stage and the design sprint, a half day interactive workshop conducted with four infovis research students at the University of British Columbia. The design sprint established four alternative report designs, which were broken down

*e-mail: acrisan@cs.ubc.ca

†e-mail:gwmckee@alumni.ubc.ca

‡e-mail:tmm@cs.ubc.ca

§e-mail:jennifer.gardy@bccdc.ca

into isolated (from the whole report) design elements to establish wording alternatives and design alternatives. The whole report and isolated design elements were prepared into a Design Choice questionnaire that compared the alternatives developed in the design sprint against the existing COMPASS-TB report using an embedded model design [1] that gathered primarily quantitative data with optional qualitative data to allow participants to justify their preferences. A total of 52 participants (13 clinicians) were recruited for the Design Choice questionnaire. Using the findings from the Design stage, regulatory requirements, and our own infovis design knowledge we implemented the final design. Currently we are awaiting deployment of the report in the COMPASS-TB reporting pipeline, and are submitting our work for publication in a health sciences venue.

3 KEY FINDINGS

Expert consultations showed that the amount of time to review the data, especially by clinicians, and data being reported over multiple time-delayed reports were the largest constraints to existing reporting practices and where WGS could have the most immediate impact. The Task and Data questionnaire corroborated this finding by showing that while many stakeholders felt that WGS data were useful there was not good consensus for which specific tasks, especially for TB monitoring tasks where stakeholders were very uncertain as to what data could be used. Clinician and non-clinician stakeholders also differed in the level of detail they wanted in the report, with clinicians emphasizing more actionable data that was clearly interpretable at-a-glance.

The design sprint took these findings into consideration, and established a visual hierarchy through various design techniques (applying gestalt principles, bolding, shading) to emphasize important and actionable information that was structured around a TB workflow narrative; the original COMPASS-TB report had a rough narrative structure, but lacked a clear visual hierarchy. When stakeholders were queried for their preferences we found that they had clearer design preferences when asked to compare isolated design elements, and had no clear preferences when asked to compare whole reports. In the isolated design elements comparison, participants favored the existing report design in only 2 of a total 14 instances. Overall, preferences were consistent between clinicians and non-clinicians. The preferred alternative designs were those that supported specific ways for conveying important information through a narratively structured visual hierarchy (in essence, supporting the design decisions of the infovis researchers). Furthermore, by allowing participants to provide us with qualitative data during survey taking we could identify themes that were of greatest participant concern (clearly showing what treatments will work; reducing potential to misinterpret data), instances where our questions were not clearly articulated or confusing, and instances where none of the design options were particularly good. The redesigned clinical report incorporates these findings and is currently under additional assessment by the COMPASS-TB team.

We are now in the process of presenting our findings to the broader TB and molecular biology communities, highlighting the benefits of applying design study methodology to improve reporting of microbial WGS data. Importantly, our project demonstrates how it possible to apply design study methodology by concretely linking the data gathered and analyzed in different stages to TB workflows, design decisions, and participant preferences. Our approach can thus serve as a template for future work not just for report design, but also domain specialist created data visualization tools.

4 REFLECTION

We developed three experimental and five design guidelines to transfer some of the knowledge from our project to others. The experimental guidelines concerned ways to set-up experiments comparing

alternative designs. These guidelines recommended: designing around tasks (evident in infovis, but not in other domains); comparing isolated elements in addition to complete reports; and comparing against a control whenever possible, whether that be an existing report or an informal but widely used convention. The design guidelines were aimed at the layout and aesthetics elements and included: exploiting visual hierarchy; carefully using emphasis to highlight important information; the precise use of wording, namely terms have multiple interpretations; densely pack information with caution; and only use images judiciously and when they pertain to a specific task. Our recommendations may also apply to more complex visualization tools, but we have not assessed them in such capacity.

ACKNOWLEDGMENTS

The authors wish to thank all of the participants within various phases during the project.

REFERENCES

- [1] J. W. Creswell. *Research Design: Qualitative, Quantitative, and Mixed Methods Approaches*. 2014. doi: 10.1007/s13398-014-0173-7.2
- [2] X. Didelot, A. S. Walker, T. E. Peto, D. W. Crook, and D. J. Wilson. Within-host evolution of bacterial pathogens. *Nature Reviews Microbiology*, 2016. doi: 10.1038/nrmicro.2015.13
- [3] Y. Fukui, K. Aoki, S. Okuma, T. Sato, Y. Ishii, and K. Tateda. Metagenomic analysis for detecting pathogens in culture-negative infective endocarditis. *Journal of Infection and Chemotherapy*, 21(12):882–884, 2015. doi: 10.1016/j.jiac.2015.08.007
- [4] N. J. Loman, C. Constantinidou, M. Christner, H. Rohde, J. Z.-M. Chan, J. Quick, J. C. Weir, C. Quince, G. P. Smith, J. R. Betley, M. Aepfelbacher, and M. J. Pallen. A Culture-Independent Sequence-Based Metagenomics Approach to the Investigation of an Outbreak of Shiga-Toxigenic *Escherichia coli* O104:H4. *Jama*, 309(14):1502, 2013. doi: 10.1001/jama.2013.3231
- [5] L. J. Pankhurst, C. del Ojo Elias, A. A. Votintseva, T. M. Walker, K. Cole, J. Davies, J. M. Fermont, D. M. Gascoyne-Binzi, T. A. Kohl, C. Kong, N. Lemaitre, S. Niemann, J. Paul, T. R. Rogers, E. Roycroft, E. G. Smith, P. Supply, P. Tang, M. H. Wilcox, S. Wordworth, D. Wyllie, L. Xu, and D. W. Crook. Rapid, comprehensive, and affordable mycobacterial diagnosis with whole-genome sequencing: A prospective study. *The Lancet Respiratory Medicine*, 4(1):49–58, 2016. doi: 10.1016/S2213-2600(15)00466-X
- [6] M. Sedlmair, M. Meyer, and T. Munzner. Design Study Methodology: Reflections from the Trenches and the Stacks. *IEEE Transactions on Visualization and Computer Graphics*, 18(12):2431–2440, dec 2012. doi: 10.1109/TVCG.2012.213
- [7] T. M. Walker, T. A. Kohl, S. V. Omar, J. Hedge, C. Del Ojo Elias, P. Bradley, Z. Iqbal, S. Feuerriegel, K. E. Niehaus, D. J. Wilson, D. A. Clifton, G. Kapatai, C. L. C. Ip, R. Bowden, F. A. Drobniowski, C. Allix-Bguec, C. Gaudin, J. Parkhill, R. Diel, P. Supply, D. W. Crook, E. G. Smith, A. S. Walker, N. Ismail, S. Niemann, T. E. A. Peto, J. Davies, C. Crichton, M. Acharya, L. Madrid-Marquez, D. Eyre, D. Wyllie, T. Golubchik, and M. Munang. Whole-genome sequencing for prediction of *Mycobacterium tuberculosis* drug susceptibility and resistance: A retrospective cohort study. *The Lancet Infectious Diseases*, 15(10):1193–1202, 2015. doi: 10.1016/S1473-3099(15)00062-6