Virtual Reality for the Observation of Oncology Models (VROOM): Immersive Analytics for Oncology Patient Cohorts

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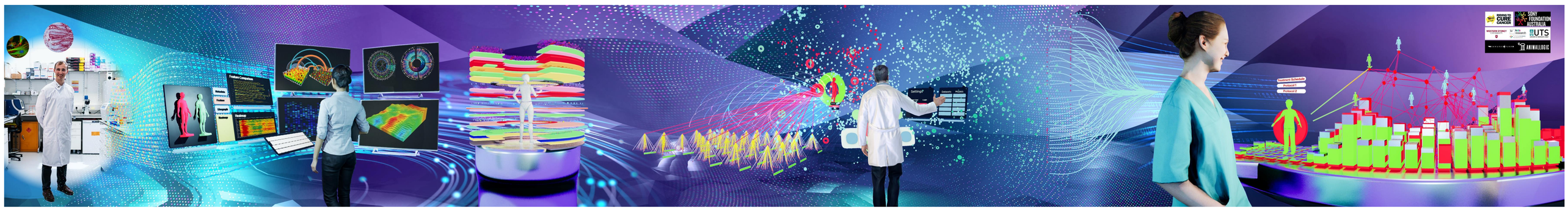
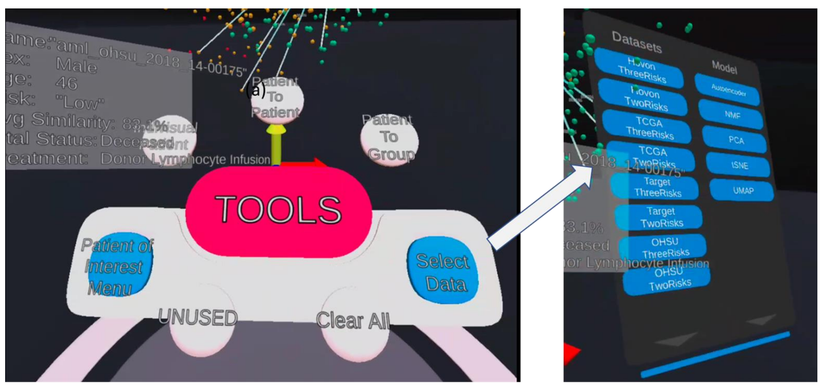


Background

The human genome is complex. It is within this complex data that information will be found that identify patients as individuals, the very basis of 'precision medicine'. Functionally, this complex genome underpins the biological mechanisms of an individual patient's cancer.

This project proposes a novel application of an immersive visual analytics framework with supporting visual design, environment optimisation, machine learning algorithms, and immersive analytics that enables the discovery of patterns from known biomarkers and their relationship with patient cohort and history. :

- An immersive visualisation for patients' cohort based on the similarity of the genomic changes that characterise their tumours, which also accounts for patient treatment histories and clinical indicators.
- A novel and effective visual design of an immersive environment that is built on our usability study of exocentric and egocentric visualisation through optimisation of audio and visual design principles.
- An intuitive user interface and visual analytics environment that implements similarity space for patient cohorts displayed in well-known 2D genomic charts and graphics with meaning to the biomedicine field, such as box plot, dendrogram and heatmap to ensure the information is easily perceivable by clinicians and oncologists in their patient assessment.
- To achieve targeted medicine, cancer biomarkers matched to patients' clinical history and analysed as a whole to maximise the chance of getting the right therapy for the incoming patients (Nguyen et al. 2016).
- The use of immersive visualisation and artificial intelligence could further enhance and improve the analysis of such empirical studies. Multisensory input of Immersive technologies has distinct advantages over traditional display (Moloney *et al*. 2018).



A. B.

Figure 1: . Our user interface mimics the real-world object as suggested by Pangilinan (2019) in the form of a virtual desk and dorm, which the users can intuitively know how to use (A) Our user interfaces with the options to interrogate the data (B) The four primary datasets categorised into two and three risk factors with Autoencoder, NMF, PCA, tSNE, and UMAP dimensional reduction algorithm

Project Aim

Build a novel application of the immersive visual analytics with supporting visual design, environment optimisation, machine learning algorithms, and visual analytics that enables the discovery of cancer patient-specific patterns of known genetic markers and their relationship within a patient cohort.

Results

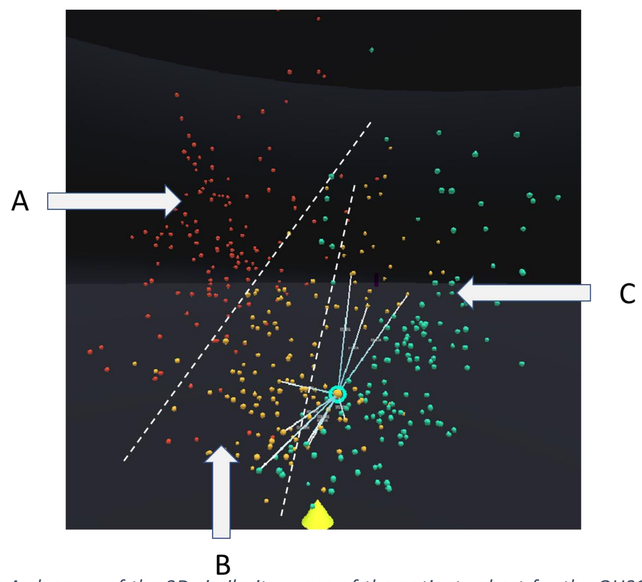


Figure 4: *A close-up of the 3D similarity space of the patient cohort for the OHSC three risk dataset. Colours are used to indicate the risk level. The cohort can roughly be divided into three regions, A, B and C.*

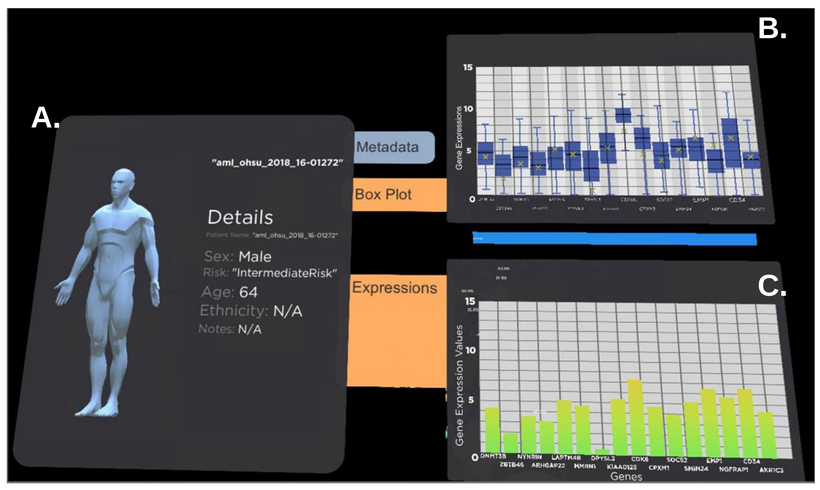


Figure 5: Patient of Interest (POI) is selected from Figure 4 and drag into (A) Patient of Interest panel. The panel shows the metadata for the patient, such as age, gender and ethnicity. The tablet also contains (B) the box plot of the patient gene data compared to the whole population. The patient gene expression value is clearly marked as an "x" (yellow) in the box plot.(C) a bar chart of the gene expression value.

Discussion and Summary

- Our design study aligned well with the recent study which indicated that both exocentric and egocentric references significantly impact usability; egocentric references reduce the mental load needed while exocentric leads to better performance (Wagner, Stuerzlinger, and Nedel 2021). Both modes were included in the system.
- VROOM is built on strong design principles and practical needs that allow analysts to move into the 3D environment to explore within the cohort for individual patients of interest. Tested on models involving gene expression data derived from 400 acute myeloid leukaemia patients, users can select individuals to compare within the 3D virtual genomic world. The system allows for the extraction of patient specific gene expression values which are then transferred to a virtual 2D working board that displays patient-specific information as well as different graphical representations, teasing out all user-defined data comparisons for the individuals in question. Stakeholder usability studies highlight ease of use and the unique merits of the application.

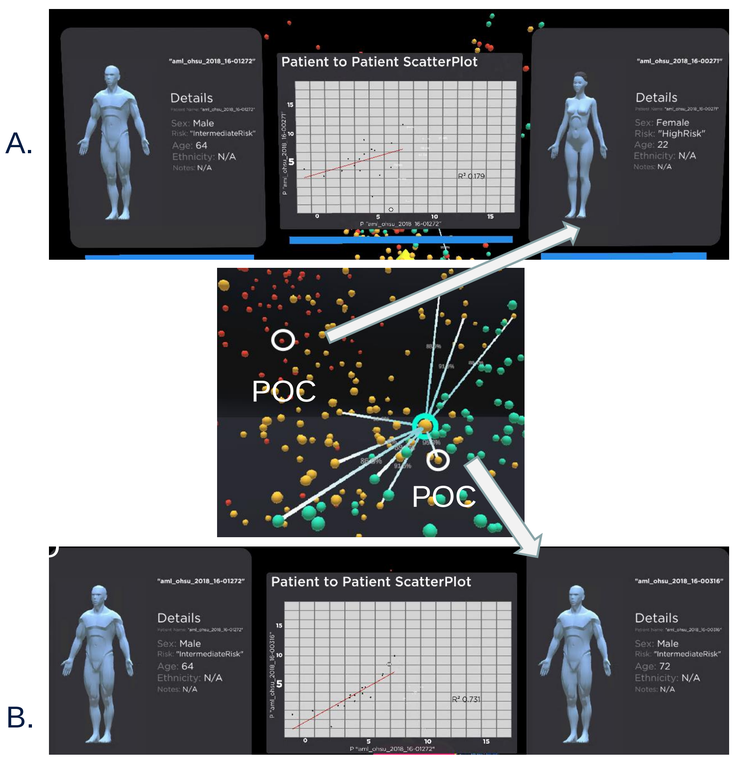


Figure 6: Patient-to-Patient Comparison panel. (A) The POI, is circled with green, while the Patient Of Comparisons, are circled with white. (A) is used to show the dissimilarity of the gene expression of the POC from POI. The scatter plot is used to analyze the similarity between the patient in term of their gene expression. When regression was carried out on the data, the model does not fit well, with only 0.179 R-square value. (B) In contrast, this POC is very similar to POI at 91.5%. Regression model fit well with R-square value of 0.731.

Method

1. Egocentric vs Exocentric Informed Study

A design exploration was made by investigating the use of egocentric and exocentric views to visualise the patient cohort displayed in a 3D graphical representation. Similarity space representation to assess the best approach to visualise and look at the impacts of visual analytics in a VR environment。Given that VR features need to be perceived as valuable and meaningful to achieve cognitive benefits, the construct of usability measures VR interaction experience and self-efficacy of effectiveness, including time and accuracy (Merchant et al. 2012)

Figure 2: An example of (A) exocentric view and (B) egocentric view of the patient population in the similarity space in our study

2. Immersive Analytics Framework

Machine learning analysis of complex genomic data embed the high dimensional features into low dimensional (3D) space to visualise the interrelationships between patients (eg PCA, tSNE, UMAP). Here we present VROOM (Virtual Reality to Observe Oncology Models), a novel VR prototype that allows the complete immersion of the user within the data 3D model for a cohort of patients which allows for comparative data analysis, visualisation and clinical interpretation of individual patients.

Immersive analytics framework consists of multiple components that reflect a complete analytic cycle by integrating the immersive technologies and introducing game theory to power the Decision Support System (Figure 3).

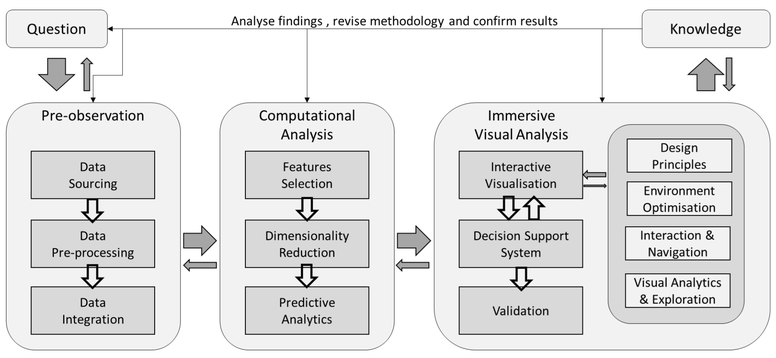


Figure 3 Immersive visual analytics of genomic data for cancer patients extends Nguyen et al. (2016)

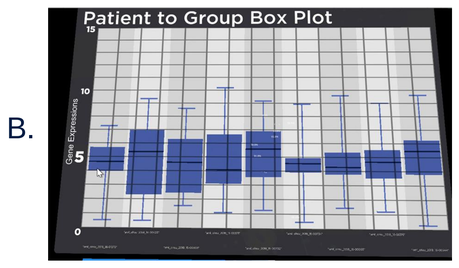


Figure 7: The Patient-to-Group comparison panel has four tools, hierarchical clustering heatmap, box plot, patient table and 3D heatmap. (A) The gene expression of the POI and the POCs are visualised in the heatmap. (B) POI to POCs box plot comparison. It shows the gene's median and IQR for the POI and the POCS. (C) 3D visualisation of the heatmap with the gene expression value determines the height of the mountain and the valley. (D) Patients clinical history in tabular format.

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NET3524/0218