

Virtual Reality for the visualization of high-dimensional relationships in bioinformatics

Subtitle

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Introduction

1.1 Background

Technological advancement has revolutionized the field of genomics, which has led to a cost-effective generation of big amounts of sequence data. The sequencing of the first human genome (2002) took around 13 years and cost over \$3 million to complete. Nowadays we can resequence a human genome for \$1000 and can generate more than 320 genomes per week[6]. This technological innovation leads to the accumulation of vast quantities of genomic data, posing a tremendous challenge to scientists for effective mining of data to explain a phenomenon of interest. New ways of analysing the produced data have been therefore necessary in order to discover interesting patterns and make the most out of it. No matter how much resources we use into extracting the data if we don't get anything interesting out of it[12].

Some of the main problems that researchers face when analysing genomic data are information overload, data interconnectivity and high dimensionality. Visualization is one way of facing this problems. For this reason it is very important to implement efficient visualization technologies that can lead to find new patterns and the extraction of good conclusions of the data. In the field of system biology there are usually network representations where the nodes or bioentities are connected to each other, where these edges represent associations. Because of the improvements in technology, these networks can increase dramatically in size and complexity. We need therefore better visualization systems and more efficient algorithms for the analysis of the data.

In 1.1 we can see a representation of the evolution for visualization of networks in system biology. From simple graphs in 2 dimensions, to 3D representations and nowadays also visualizations in virtual reality where we can interact directly with the data itself.

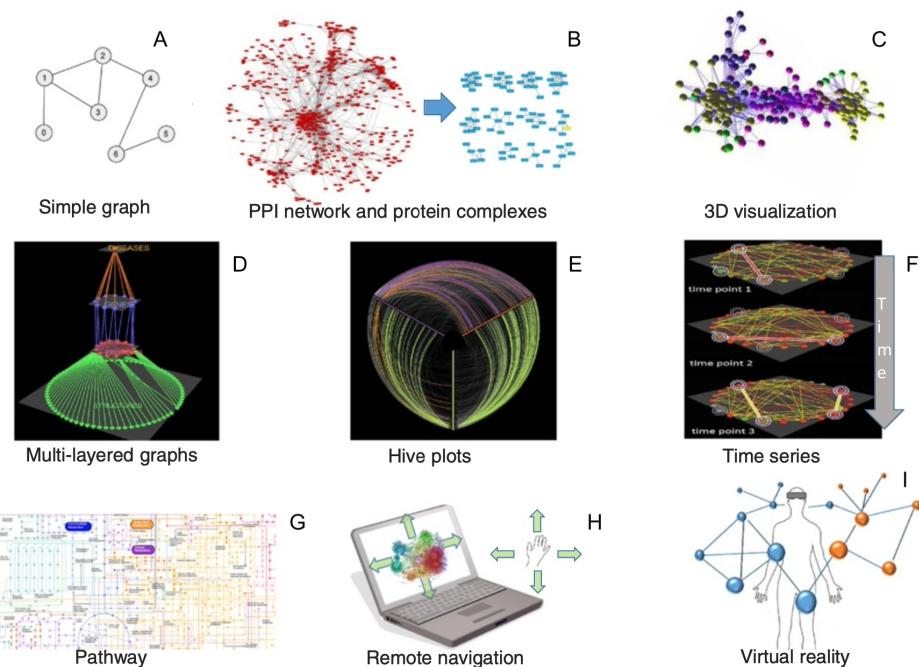


Figure 1.1: Visualization for network biology. a A simple drawing of an undirected unweighted graph. b A 2D representation of a yeast protein-protein interaction network visualized in Cytoscape (left) and potential protein complexes 3D identified by the MCL algorithm from that network (right). c A 3D view of a protein-protein interaction network visualized by BiolayoutExpress. d A multilayered network integrating different types of data visualized by Arena3D. e A hive plot view of a network in which nodes are mapped to and positioned on radially distributed linear axes. f Visualization of network changes over time. g Part of lung cancer pathway visualized by iPath. h Remote navigation and control of networks by hand gestures. i Integration and control of 3D networks using VR devices. Figure adapted[8].

Virtual reality (VR) is still a field under exploration and that can be of great help in network analysis. VR can be very powerful because it takes advantage of the way the human being perceives and analysis things. We as human beings have a great ability to discover patterns, however we are biologically optimized to see the world and the patterns in 3 dimensions. VR is one of the best ways then for better discovery in spatial dimensions. It has been demonstrated that VR help scientists work more effectively in fields like medicine [5][10][2], biology[11][9] and neuroscience[1][7], to cite some examples.

1.2 Challenges and research problem

This project focus mainly on solving the problem of visualization of high dimensional data from the MIxT project by using virtual reality. Furthermore the application allows the user to interact with the network created from the data in the virtual environment. It also allows the user compare the blood and biopsy networks at the same time in order to find relationship, which wasn't possible in the MIxT web application as this only allows the user to visualize one network at a time.

MIxT[4] is a web application for bioinformaticians. Among other tools, it offers a network visualization of genes which are represented as nodes in the network and where the edges represent statistically significant correlation in expression between two nodes. This tool was used in a study[3] that identifies genes and pathways in the primary tumor that are tightly linked to genes and pathways in the systemic response of a patient with breast cancer. When exploring a network in MIxT, it can be hard to understand the data and its relationships because there is too much data. This problem is easy to occur when there are too many node and edges. In figure 1.2 we can see an example of the network visualization from MIxT. As we can see in Figure 1.2a, there are many nodes and relationships among them and when we zoom in in the network, it becomes very difficult to understand the data and the relationships as shown in Figure 1.2b.

The network is also in 2-dimensions and what we propose in this project is to use a virtual reality 3d visualization in order to cope better with this problem.

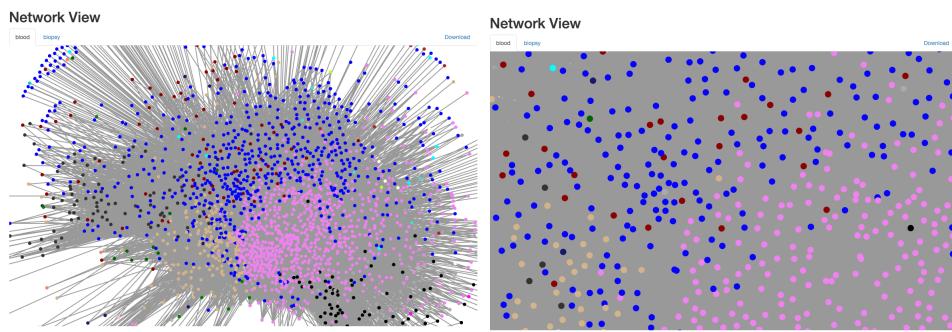


Figure 1.2: Network view of the MIxT application where nodes represent genes and the modules are represented by colors. Relationships are represented by grey lines that connect a gene with another one.

1.3 Proposed solution

1.4 Significance and contribution

This project contributes in the exploration of the possibilities that Virtual Reality offers for visualization of big data in bioinformatics.

1.5 Outline

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MIxT VR

MIxT VR is a virtual reality application for the interactive visualization of large-scale networks in a 3D space. The networks are represented using nodes and connections between them. In order to explore the data, the user can walk around, scale the network, move it around, filter the nodes using a 2D interface and also interact with the nodes to get more information about them. In Figure 2.1 we can see an example of the application running.

MIxT VR works with a dataset that contains the information of the nodes and relationships of the network. This dataset needs to be obtained from an external source or application. Once we have our dataset we can load it to the application and then run MIxT VR using a Head Mounted Display or HMD for VR. Finally we can explore the network and interact with it to visualize the dataset in a VR experience.

The implementation of MIxT VR is done in Unity, a cross-platform game engine. This engine is used for a wide range of applications, especially for the development of videogames in 3D and 2D, VR applications and engineering solutions. The programming language used to develop the application inside Unity is C#. As for the VR hardware used in the development, we used an Oculus Quest headset. This type of headset is an all-in-one HMD, which means that it doesn't need to be connected to a PC to run an application, it can be run inside the hardware of the headset itself. However during the development process, the headset needs to be connected to the PC and the application can be run directly from Unity.

For this chapter we will use dataset examples from MiXT to illustrate the concepts in this chapter. MiXT is a web application that is used for the visualization of bioinformatic data[4][3] and the datasets used here contain genetic information about a woman with breast cancer. There are in total 2 datasets, the first one is from a blood sample and the second one is from the tumor sample. In Figure 2.1 we can see an example of the application running using the blood dataset from MiXT.

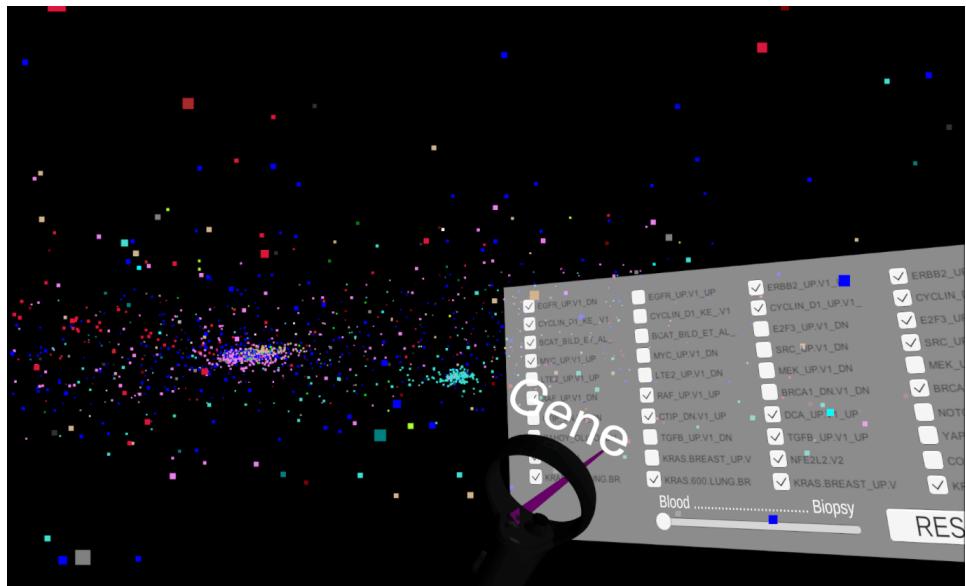


Figure 2.1: MiXT VR. Example of the application running on a Oculus Quest.

2.1 Visualization and interaction of the network

In this section I will write about the VR techniques used to visualize the network in a good way.

2.1.1 Locomotion

How the player can move around the environment.

2.1.2 Network manipulation

Translation and scaling of the network for better visualization.

2.2 Creation of the network in a 3D space

category	genes
brown	ARHGAP30 FERMT3 ARHGAP25 CD53 PLEK IRF8 DOCK2
cyan	SAFB MOB3A RAB35 ABR ASCC2 CDC37 ANKFY1 GLTSCR1
darkgrey	RAB40C ZNF213 ZNF263 PIGQ RHDF1 RAB11FIP3
darkorange	TCEB1 MRPL13 ENY2 MTERF3 UBE2W WDYHV1

Table 2.1: Fragment of the dataset with the categories and the genes belonging to each category from the biopsy sample.

source	target	weight	id
AAMP	ARGLU1	0.102486209330144	AAMP-ARGLU1
ACADM	FOXN2	0.107506881676173	ACADM-FOXN2
ACADM	MBNL1	0.12269622045714	ACADM-MBNL1
ACADM	PPM1B	0.103496640767895	ACADM-PPM1B

Table 2.2: Fragment of the dataset used to build the network relationships of the blood sample.

2.3 Filtering information in the network

How the network is filtered.

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Related work

I will focus in this chapter on VR applications found in the literature for the visualization of bioinformatic data.

3.1 BioVR

3.2 CellexaVR

3.3 BigTop

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Evaluation and discussion

Questions to answer in the evaluation chapter:

1. How big can the graph be so that it is comfortable visualizing the network?
What is comfortable? Number of FPS? How can we scale the graph? By adding nodes and spread them around, by adding more interconnexions? Should the experiment split in several parts? Scaling, filtering, moving around, etc. What is the performance by using Oculus Link and the performance using just the Quest hardware? -We can use the Unity GPU Profiler for Oculus Quest and Go in order to see the performance.
See: Getting Started w/ The Unity GPU Profiler for Oculus Quest and Go
2. How is this way of visualizing the graph better by using VR?
We are researchging the technology and the test with actual users is for future work.
3. In what way can the application and the visualization of the graph be improved?
Argue in the discussion part.

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Conclusion and future work

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