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

Subtitle

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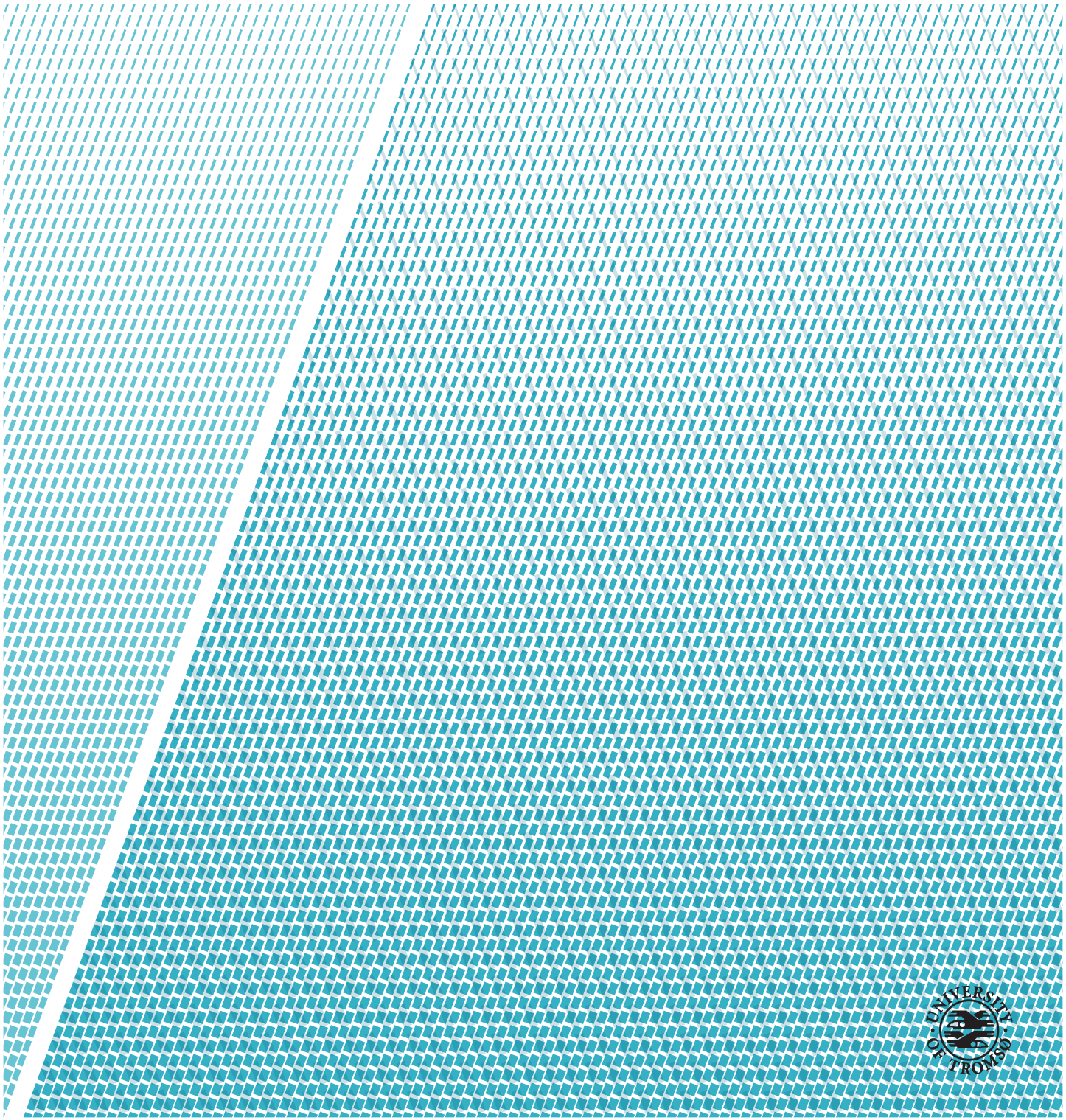

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Introduction

It is very cheap nowadays to produce data and many people are doing it due to technological advancement. Just as an example, in the field of genomics, the sequencing of the first human genome (2002) took around 13 years and cost over $3 million to complete. Now we can sequence hundreds of genomes in a few days[12]. This leads to the accumulation of vast quantities of genomic data, which can be used for new scientific discoveries, diagnose of rare diseases, etc. However we still need a human expert to visually inspect the data to find new signals and discover interesting patterns or to set a diagnosis. No matter how much resources we use into extracting the data if we don't get anything interesting out of it[31]. Therefore there is a great need for new and better tools to support this task.

Some of the main problems that researchers face when analysing genomic data are information overload, data interconnectivity and high dimensionality. One way to deal with all this data is to invent novel analysis. However we still need visual inspection of the data, so the information overload still remains as an important challenge and this is what we attempt to solve. 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. Networks can increase dramatically in size and complexity and this is due to computational power to create very large networks, scientific knowledge about large networks and the big amounts of data that we have to

analyze. We need therefore better visualization systems for the analysis and inspection of these networks.

In Figure 1.1 we can see a representation of the evolution for visualization of networks in system biology. Before the computers, networks were represented in 2 dimensions and they were static representations that lacked interactivity, see Figure 1.1 A. With the computer era and the advancement in computer graphics, 3D representations were possible, with the addition of interactivity with the network (See Figure 1.1 C). As computer science progressed, there was a big improvement in visualization and also new technologies emerged like virtual reality, which has a huge potential with regards to the interactivity (Figure 1.1 I).

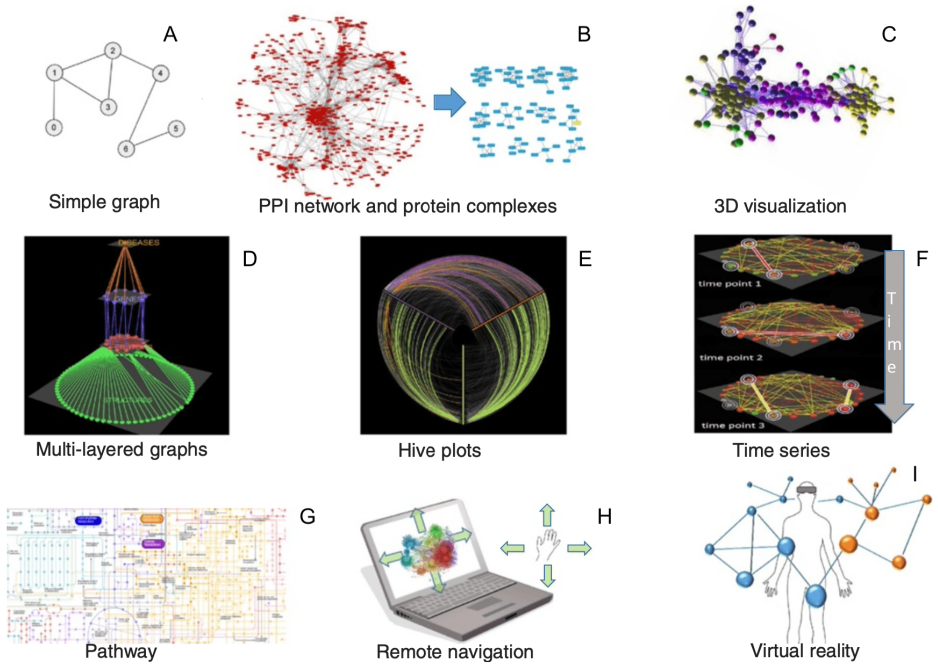


Figure 1.1: Visualization for network biology. a Undirected unweighted graph showing co-expression relationship between genes. b A 2D representation of a yeast protein-protein interaction network visualized in Cytoscape (left) and potential protein complexes 3D identified by the MCL algorithm from that network (right). c A 3D network of genes showing co-expression relationships. d A multilayered network integrating different types of data visualized by Arena3D. e A hive plot view of a network where nodes are mapped to and positioned on radially distributed linear axes. f Visualization of network changes over time. g Static picture showing part of lung cancer pathway. h Navigation of networks using hand gestures. i Integration and control of 3D networks using VR devices. Figure adapted[16].

We believe that virtual reality (VR) can offer new possibilities for visual inspec-

tion in large networks. Even though VR is still a field under exploration, it has been demonstrated that it help scientists work more effectively in fields like medicine [10][28][3], biology[29][23] and neuroscience[1][13], to cite some examples. VR can be very powerful because it takes advantage of the way the human being perceives and analysis things. We have a great ability to discover patterns, however we are biologically optimized to see the world and the patterns in 3 dimensions. Some of the advantages that VR has over non-VR approaches are the following:

1. Visualization of the network in a 3D space.

2. Possibility to move around the virtual environment and visualize the network from different perspectives as in real life.

3. Interaction with the the environment by using controllers and our virtual hands in the virtual world.

We have implemented a virtual reality application for the visualization of 3-dimensional networks of data. We have used up-to-date virtual reality techniques that we think it improves the visualization of this type of data structures. The techniques that we have used consist in: the exploration of the network by moving around the virtual space, making it easier for the user to see the network from different angles; interaction with the network and nodes to comprehend better the data that is being visualized; and the use of 2-dimensional user interfaces to filter and have more control of the data.

What did we learn... [Write when the evaluation is finished].

Thesis statment: *Virtual reality techniques can improve the visualization and interactivity of data networks.*

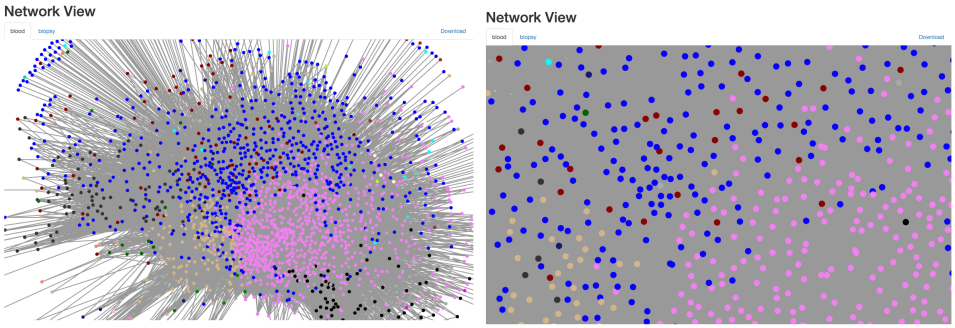
1.1 Challenges and research problem

This project focus mainly on solving the problem of visualization of high dimenasional 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 finde relationship, which wasn't possible in the MIxT web application as this only allows the user to visualize one network at a time.

MIxT[8] 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[7] 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 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.



(a) Network with several modules. **(b)** Zoom in the network.

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

1.2 Proposed solution

1.3 Significance and contribution

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

1.4 Outline

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GeneNet VR

GeneNet VR is a virtual reality application for the interactive visualization of gene networks in a 3D space. The network is represented using nodes and edges between them. In order to explore and visualize the data in GeneNet VR, the user can for example walk around the 3D environment, zoom in the network, translate it to other places, filter the nodes using a user interface, morph the network from one dataset to another and also obtain detailed information about the nodes.

GeneNet VR loads the data from local files with the information about the nodes and relationships. Then the network is built using the data and clustered using an algorithm. Finally, the user can explore it and interact with it using the VR headset and controllers.

We implemented GeneNet VR in Unity, a cross-platform game engine. This software is used for a wide range of applications, especially for the development of videogames in 3D and 2D, VR applications and engineering solutions. We used C# as the main programming language to develop the application in Unity. We also used VRTK, a VR toolkit to build VR solutions in Unity. As for the VR hardware, 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 has its own hardware to run the applications although this can be more limited than the hardware from a PC. Also, during the development process I used a cable and Oculus Link, a software to connect Oculus Quest to the PC, to run the application and test it directly from Unity

on the Oculus Quest, without having to load it to the headset. This was from great help during the development process.

We have chosen two datasets from MIxT to develop GeneNet VR. MIxT is a web application that is used for exploring and comparing bioinformatic data [8] [7]; and the data visualization is an important part of the process. The datasets used here contain genetic information about a woman with breast cancer. There are in total 2 tissues; the first one is from a blood sample and the second one is from tumor tissue. In Figure 2.1 we can see an example of GeneNet VR running using the blood dataset from MIxT. We will now go in deep with how we implemented GeneNet VR.

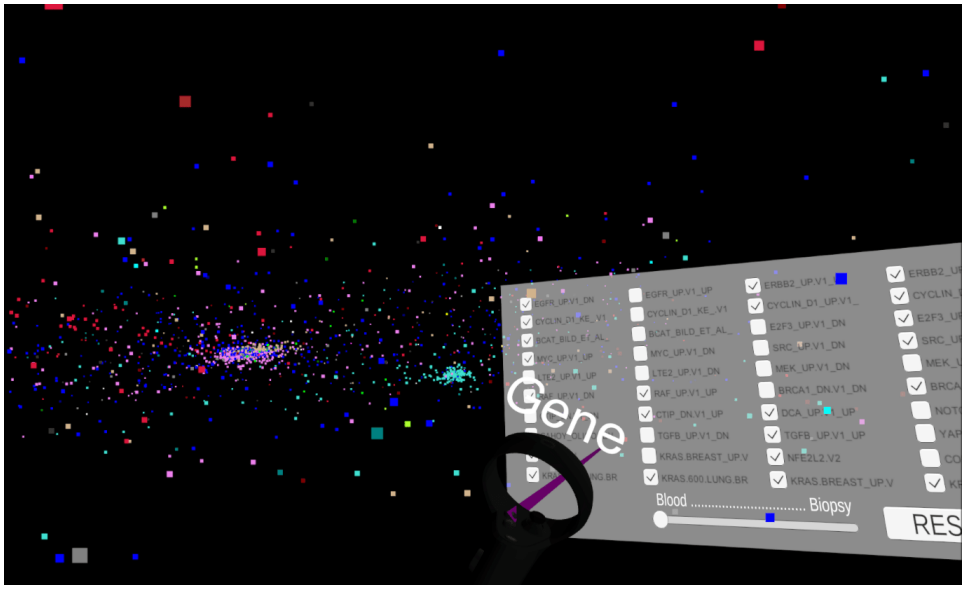


Figure 2.1: GeneNet VR. Example of the application running on a Oculus Quest.

2.1 Interaction with the network

Virtual reality headsets offer a rich inmmersive experience. It's not only about immersing the user into a 3D environment, but also giving the user the possibility to interact with the environment itself. This makes it possible to build complex VR applications where the user can do almost anything in a virtual world. Some examples of what it is possible to do in virtual reality is for example moving around, grabbing objects, interact with the environment using your hands or virtual tools, like pushing a button, 2D interfaces and menus, etc. In this section we will explain the techniques that we have implemented to visualize and interact with the network and make the most of VR.

The interaction and the visualization also depends on the VR technology used. We use Oculus Quest in this project, an all-in-one VR headset that doesn't need a PC nor wires to run the applications. Apart from the headset, it comes with 2 controllers; one for each hand. These controllers have inputs as buttons, thumbsticks and triggers that can be used to activate actions in the VR application. We have used some of these inputs available in the controllers in GeneNet VR and mapped them to different actions that allow the user interact with the network and the environment.

In Figure 2.2 we can see which actions correspond to each input from the controllers. We will briefly explain now what these actions consist of: 1. Snap rotation: It allows the user to instantly rotate to the right or to the left 45°; 2. Filter menu: The user can filter the nodes of the network according to a filtering algorithm used in GeneNet VR; 3. Translate network: The network can be translated or moved to other positions in the scene; 4. Scale network: The network can be scaled or "zoomed"; 5. Select node: The user can select a node in order to get more information about it; 6. Select item in menu: It allows the user interact with the menu, for instance to filter the nodes by enabling or disabling the checkboxes from the filtering menu; 7. Oculus menu: It opens the menu from oculus and pauses GeneNet VR; 8. Teleport: It teleports the user to another position on the floor of the VR scene.

As for the use of the Oculus Quest HMD (Head Mounted Display), this is placed in the head and it has a belt that is used to adjust the headset to the head. This will help the user feel more comfortable while wearing the HMD. Another important aspect that we have taken into account in GeneNet VR is that the user can use the application and explore the network by sitting on a chair. This is possible thanks to the locomotion techniques implemented that allows the user to move around with the controllers. We will go into more detail later in this chapter about this.

We will explain now in the following subsections the different interaction techniques that we have used and also what benefits they bring for the visualization and interaction of the network.

2.1.1 Locomotion

Locomotion is one of the most important ways of interaction in virtual reality experiences. It can be defined as a self-proppelled movement in the virtual world. Even though moving around is not the main goal in most of VR applications, it is an important aspect for the user's perspective in order to move the user's viewpoint in the virtual world and navigate around it.

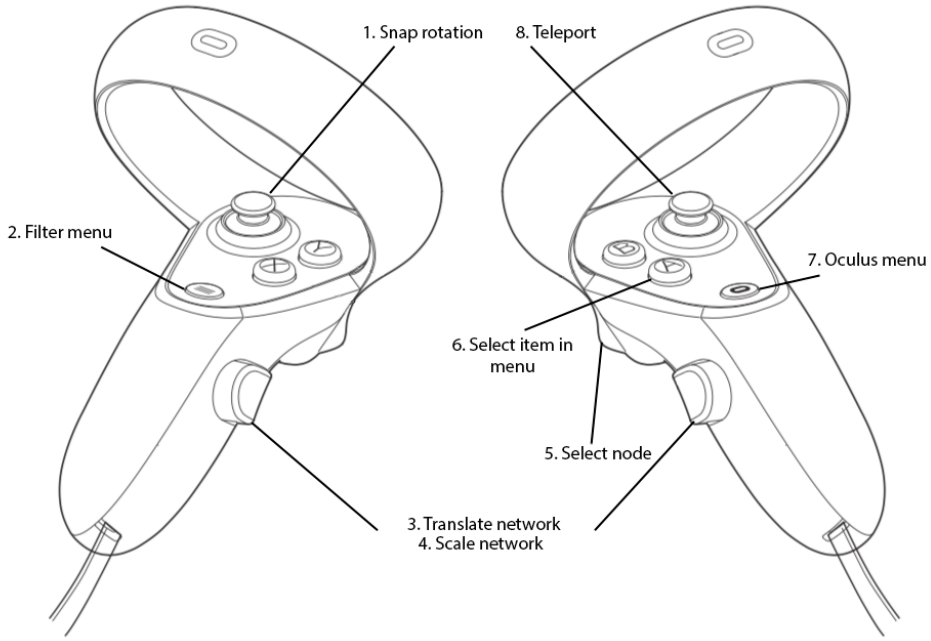


Figure 2.2: Mapping of the Oculus Quest controllers for the different actions implemented in GeneNet VR: 1. Snap rotation. 2. Filter menu. 3. Scale environment. 4. Translate environment. 5. Pointer. 6. Select item in menu. 7. Oculus menu. 8. Teleport. Adapted figure from Oculus developer's page [15].

Locomotion can have an strong influence in the user's experience. A poorly designed locomotion technique can reduce the user's immersion and even introduce motion sickness, which is related to the movement that the technique produces. HMDs like Oculus Quest allow the users to control the position and the orientation of the viewpoint by moving their heads and walking; however, large virtual environments such as GeneNet VR need a big physical tracked area, which cannot be covered by just walking around. It is for this reason that we need to use a locomotion technique that makes it possible to move around without having to walk around in the physical world [2]. In addition, as research has shown, when the user is stationary both in the virtual and real world, the motion sickness produced by VR is less likely [18].

The locomotion technique that we use in GeneNet VR is called teleportation. It consists in choosing a spot on the floor were we want to teleport to. To do this the user has to move forward the thumbstick from the right controller (see "8. Teleport" from Figure 2.2). Furthermore, it is possible to choose which direction the user will face once the teleportation is completed. To do this we just need to rotate the same thumbstick to the desired direction. Once the

user releases the thumbstick, a black flash will be followed by the new position in the space. This black flash is very important when implementing some of the locomotion techniques because it prevents from producing motion sickness and disorientation. Without the black flash, the transition to the new position would be too abrupt and it may disorient the user.

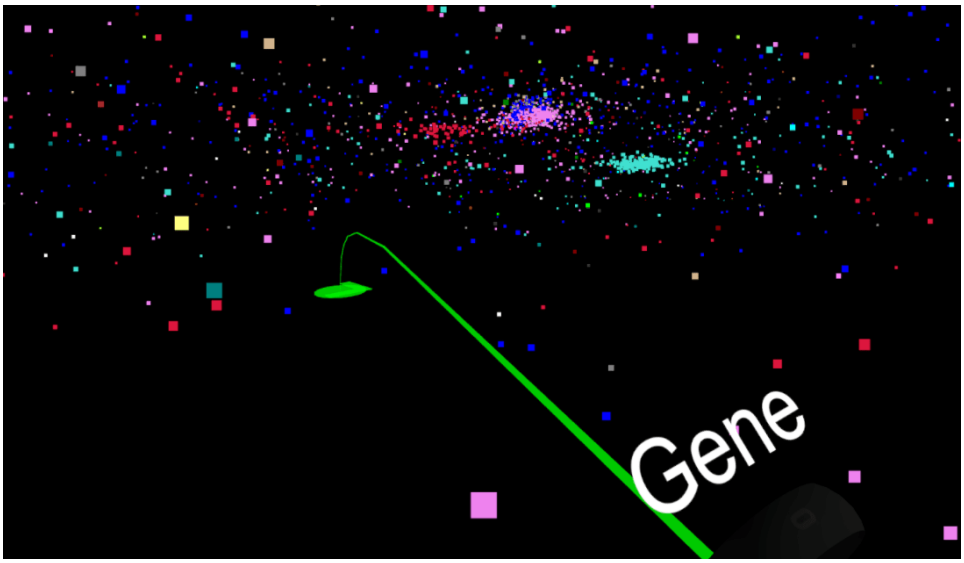


Figure 2.3: Teleportation technique. The user can use the jystick from the right controller to teleport to a different spot. To choose the spot a parabolic arc will appear.

In Figure 2.3 we can see an example of how the teleportation technique is used in GeneNet VR. A parabolic arc is created in the 3D space with a circle representing the spot where we are goint to teleport to. It can be seen as if we are throwing an object to the spot where we want to teleport to. The green circle includes also an arrow, indicating the direction that we will face once we are teleported.

In addition to the teleportation, it is also possible to rotate to the left or to the right with the Oculus controllers so that the user doesn't have to rotate the head to look around in the scene. This action is triggered using the thumbstick on the left hand (See 1. Snap rotation in Figure 2.2). By moving the thumbstick to the left side, the camera will rotate 45° to the left side, and 45° to the right side if the user moves it to the right side. A black transition is also used in this case before the rotation happens to avoid motion sickness, for the same reason as in the teleportation technique.

2.1.2 Translation of the network

By teleporting to different places in the environment, we allow the user visualize the network from different perspectives; however, it is also interesting to be able to move the network and specially move it in a precise way, so that the user has more control over what it is being visualized. The user might for instance be able to see the network or a specific node or cluster from above or also from below. To do this we have implemented a functionality to translate the network in the 3D space.

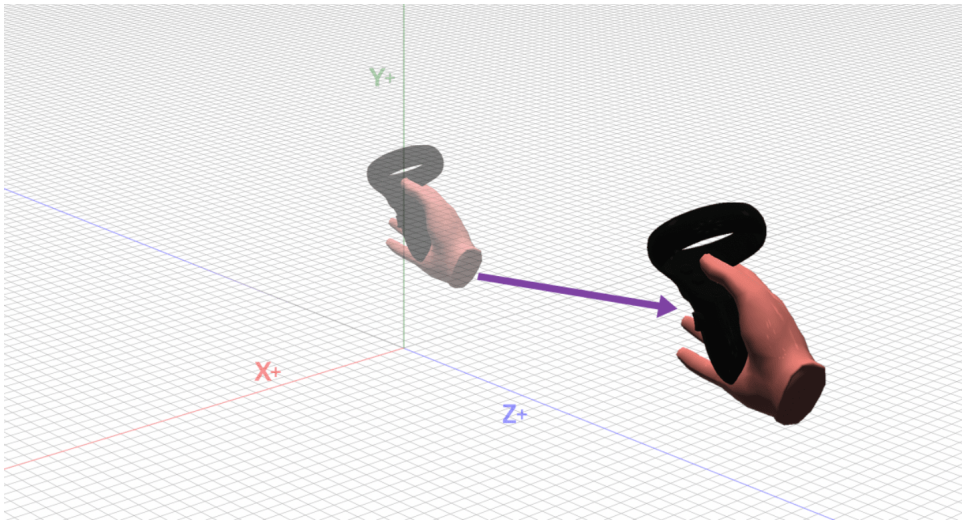


Figure 2.4: Translation of the network functionality. The user holds the translation button on the Oculus controller and moves the hand to the direction where he or she wants the network to translate.

To translate the network in GeneNet VR, the user needs to press on the hand trigger from the right controller (see "3. Translate network" in Figure 2.2). Then the user needs to keep holding this trigger down and move the hand to the direction to which we want the network to move to (see Figure 2.4). This intuitive approach feels like we are just pulling from a rope tied to the network and we just move it to the direction we want.

2.1.3 Zooming in the network

When exploring a big network with hundreds of nodes and several clusters, sometimes the information can be too crowded. In our example dataset that we use in GeneNet VR, there are some clusters of nodes that have too many nodes close to each other and it gets very hard to visualize them properly. A way to cope with this problem is for instance by "zooming" in the part of the network

that we want to explore better. We implement then a scaling functionality that makes the network bigger or smaller.

The way we implemented the zooming functionality in GeneNet VR is by using the hand triggers with the name "4. Scale network" (see the reference in Figure 2.2). In the first place the user needs to press and hold these triggers from both controllers, and then we need to expand or contract the arms, as if we were stretching out or contracting the network itself. This is also an intuitive action to do since the user might think that we are actually stretching the network with the hands.

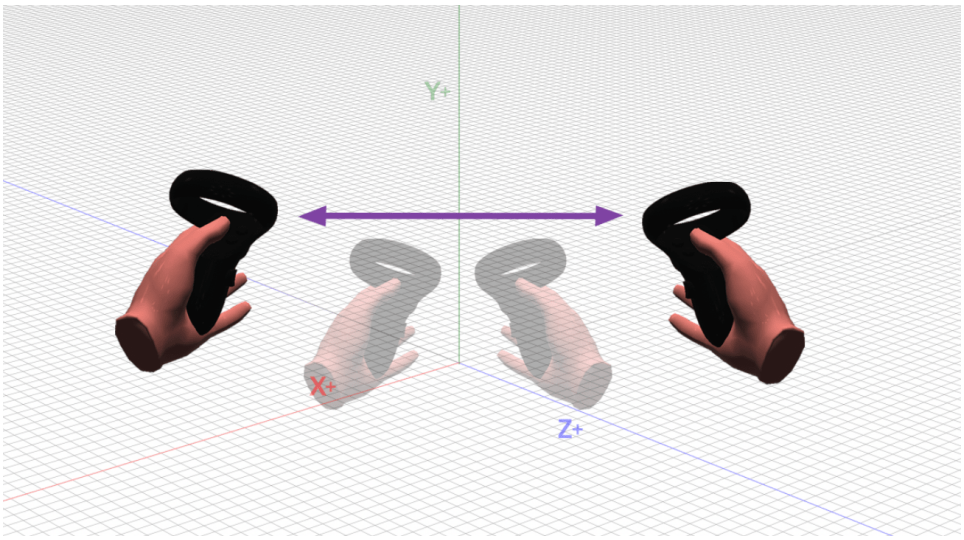


Figure 2.5: Zooming in the network functionality. The user can hold the scaling buttons on the Oculus controller to make the network bigger or smaller. In this example if we strech our hands outside, the network will expand.

In Figure 2.5 there is a visual example of how the zooming works using the Oculus controllers. In this example the user is stretching the hands out in order to make the network bigger. The user starts in an initial position, then holds the zooming triggers from both controllers and then moves the hands out. If we wanted to make the network smaller we would do the opposite action, by contracting the hands to the inside.

2.1.4 Interaction with the nodes

GeneNet VR provides also information about the data that is being displayed. The user can interact with the nodes of the network to obtain information about each of them. In our example, the nodes represent genes and the user might be interested in knowing which gene name corresponds to a specific node.

The action that we need to do to obtain the name of the gene is to get close with the right controller to the node that we are interested in and press the "5. Select node" index trigger on the right controller (see Figure 2.2). When we press this trigger, we can select a node from the network. By selecting a node, we will get the name of that gene node that will be displayed in a rendered text, and we will also visualize the edges from this node to other nodes. The node is selected with an algorithm that searches for the node closest to our right controller.

2.1.5 Node relationships

Finally, our dataset has information about the relationships between the nodes. GeneNet VR is implemented to show also this information. Because there can be too many relationships in the dataset, we don't show them all at the same time. Therefore, we can only see those of the node that the user has selected. The way that these relationships are represented is with lines between the nodes.

2.2 Scalable network in Unity and data structures

GeneNet VR uses files from an external source with data that will be used to be the network. The first file contains the information about the nodes and what category the node belongs to; The second one has information about the relationships between each of the nodes. As for the content of the files look like, in Table 2.1 and Table 2.2 we show an extract from them. Originally the files are in CSV format. CSV [4] stands for Comma-Separated Values where each record is located on a separate line within the file, delimited by a line break. In addition, each record can contain one or more fields, separated by commas.

For our example we represent the extract from the CSV files using tables, which are more illustrative. Table 2.1 contains an extract from the file with information about the genes and the categories to which each gene belongs to. Here each row is a category and as we can see, the second cell contains all the gene names for that specific category. These categories are named by colors and these color names will be used by GeneNet VR to color each node from the network. As for the second table, Table 2.2, this one shows an extract with the information about the relationships between the genes. This file can be very large since each row in the CSV file corresponds to a relationship between two

genes and one gene can be related with multiple genes. For instance one of the CSV files that GeneNet VR uses to build the relationships contains almost 90k lines.

category	genes
brown	ARHGAP30 FERMT3 ARHGAP25 CD53 PLEK IRF8 DOCK2
cyan	SAFB MOB3A RAB35 ABR ASCC2 CDC37 ANKFY1 GLTSCR1
darkgrey	RAB40C ZNF213 ZNF263 PIGQ RHBDF1 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.

The following diagram shown in Figure 2.6 schematizes the steps that we follow to build the network in Unity. We start with the 2 CSV files described before, containing the data about the nodes and the relationships. We process these CSV files in order to store the data in data structures in GeneNet VR. During the process of storing this data we also apply a clustering algorithm that will set the correct position for each node in the network. After doing this we can easily access the information about the nodes, their position, color and to which nodes they are related to in order to draw the edges. Finally, the network is created using a particle system as we will explain later.

Now that we know how sources of information to build the network in GeneNet VR, let's take a look at how the network itself is represented in Unity and what algorithms and data structures we use for that. These will have an impact in the scalability of the network, and therefore it's important to choose a good solution. We have three elements from the network that have more weight in its scalability: the nodes, the edges and the cluster algorithm used. We are going to explain each of them in more detail now.

The nodes in GeneNet VR are represented using a particle system. In Unity a particle system [20] is defined an array of particle objects. Each particle is a defined structure in Unity that contains properties like the life duration of the particle, start color, start size or position in the 3D space. Particle systems in Unity are very useful to render some special effects like fire, steam, fireworks

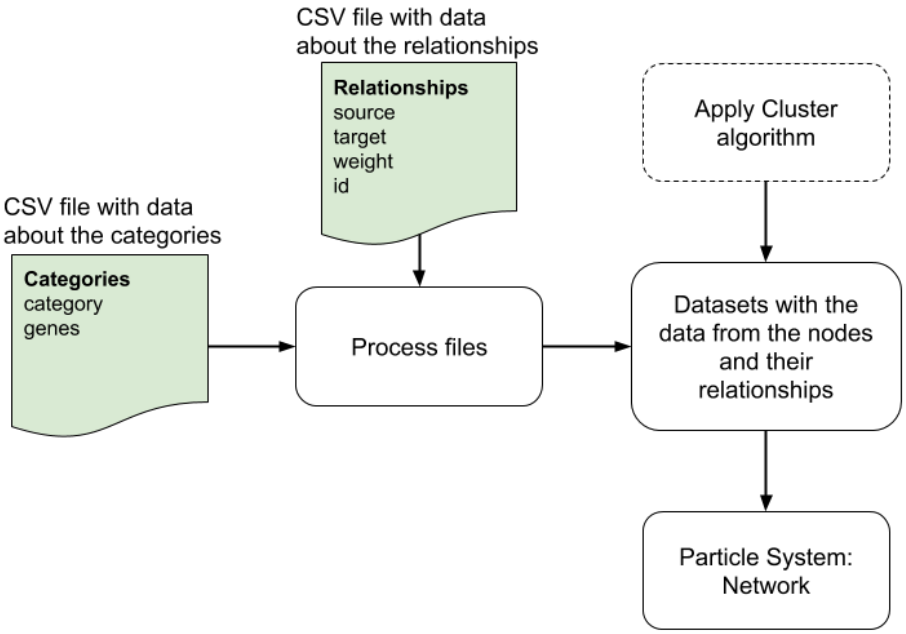


Figure 2.6: Diagram: steps for the creation of the network from the 2 CSV files.

or projectiles. They are also very powerful because they give plenty of control to the developer over the particles. In GeneNet VR we take advantage of this, allowing us to structure the network in the way we want. Usually particles have a lifetime, which means that for instance they can start in a position with a particular colour and finish or disappear after a few seconds in a different position and colour. In GeneNet VR, the particles are static and have a very long lifetime, giving the perception that the network is a rigid structure. As for the way the particles are rendered, a 2-dimensional square is shown in the scene for each particle or node. Finally, in order to store the information of each node or particle we have a dictionary object in GeneNet VR that looks like this:

```
private Dictionary<string, ParticleSystem.Particle> particles;
```

A dictionary in C# is a data structure that contains a set of keys and each key has a single associated value. In our case the key corresponds to the name of the node, the name of the genes in this case, and the value is a particle object.

The edges between the nodes are represented with 2-dimensional lines in GeneNet VR. A line in Unity is created with a Line Render component [19]. These lines are very flexible and can be used to draw anything from a straight

line to a spiral. They also have properties like color, texture mode, possibility to have different widths along the line, etc. In our case we want to render straight lines, so we need to know the start and the end points where the line will be rendered. This information is taken from the CSV file with the edges information. To store this information, we also use a Dictionary, where the key is the name of a node and the value is a list with all the nodes to which this node is connected to. This looks like this in C#:

```
private Dictionary<string, List<string>> edges;
```

Showing all the edges at the same time in GeneNet VR would make it very hard to visualize the network. For this reason we show only the edges of the node that the user has selected. Also, in GeneNet VR the edges are shown dynamically, meaning that they are created every time the user selects a node. When the user selects a different node, the current edges are removed and a new set of edges are rendered for the new node. This process can be a bit CPU-consuming in Unity. Every time an edge has to be rendered an edge object is instantiated with the CreateInstance method from Unity. The edge object in the scene from what is called a prefab in Unity. A prefab [21] is basically a reusable asset, which in our cause is the line with some defines properties like the width and the colour.

The algorithm used to cluster the nodes in the network is another important aspect that can influence in the scalability. In GeneNet VR we use a linear algorithm that clusters the nodes in the 3d space depending on the module where they belong too. In this way the user can visualize each module as single clusters with a distinct colour per cluster.

2.3 Other features of GeneNet VR

GeneNet VR provides some features that help in the process of visualization and interaction with the network. They have a complementary purpose, and they don't influence much in the scalability of the system.

2.3.1 Filtering information in the network

Another feature that GeneNet VR uses to improve the visualization of networks is a filtering menu. When we have huge amounts of data in large networks, it is sometimes necessary to show less or more data. By filtering the nodes we can visualize only the part that we are interested in.

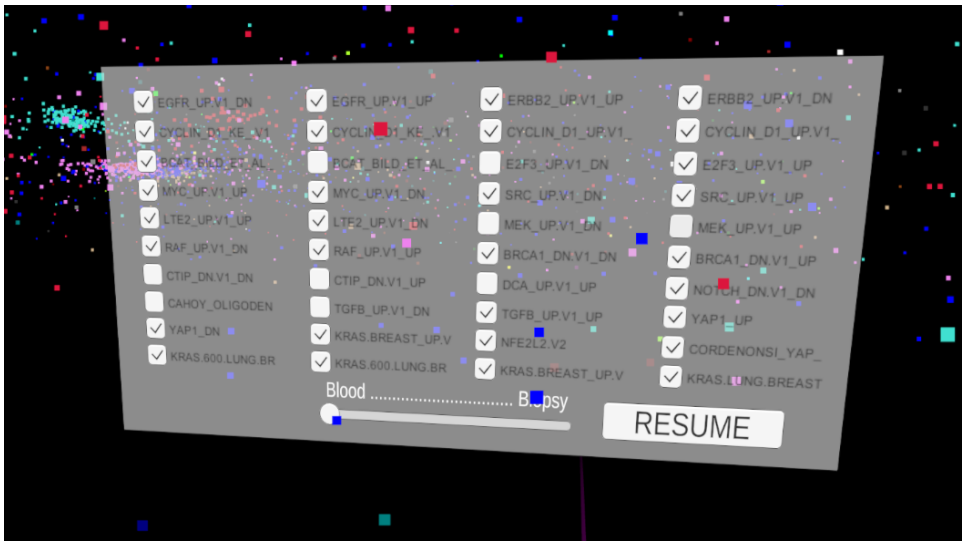


Figure 2.7: Filtering menu in GeneNet VR.

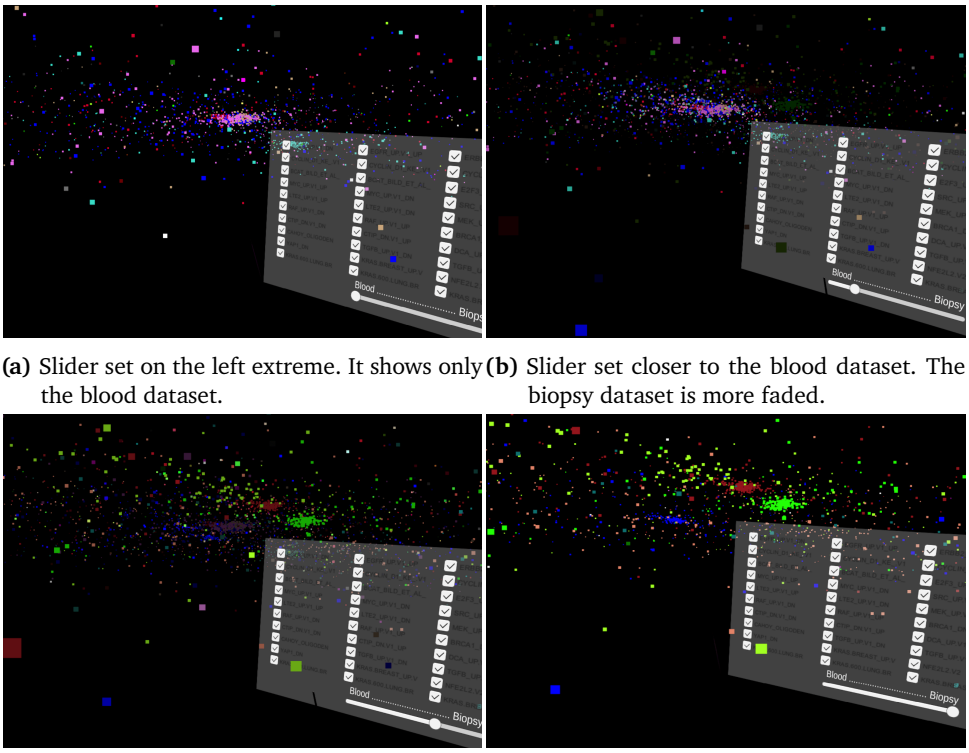
We have built a 2 dimensional menu in Unity, see Figure 2.7, to filter the data in our example network. We use checkboxes for the filtering. From a starting point, all the boxes are checked, and if the user wants to hide a part from the visualization it is done by unchecking the box. To show the filtering menu we need to press on the menu button from the left controller, see the "2. Filter menu" in Figure 2.2. The to check or uncheck the boxes we need to use the A button from the right controller, named "6. Select item", see Figure 2.2.

2.3.2 Network morphing

GeneNet VR has also the possibility to morph from one network to another. This can be done in the filtering menu by pressing the menu button from the left controller and there we can see a slider as in Figure 2.7 which we can move to the right or to the left in order to morph the network. In Figure 2.8 we can see an example of how the network morphs, showing 4 states of the morphing process. In a) the network is showing the blood network state and on d) the biopsy state. In b), the slider is moved slightly to the right, but closer to the blood state. We can see that in this state, the biopsy network is starting to show. Also, some nodes from the blood network are starting to move to relocate to their position in the biopsy network. In c) the slider is set closer to the biopsy state (to the right extreme) and we can appreciate more clearly the biopsy dataset, but the blood one is less visible.

This morphing tool help us visualize two datasets at the same time and compare them. The slider has values from 0 to 10. When the value is set to 0 we visualize

the blood dataset, and when it is set to 10, we visualize the biopsy dataset. For the values that are neither 0 nor 10, we can see both datasets at the same time. Depending on if the value is closer to 0 or 10, the nodes from one dataset or the other will be more visible. In addition, the position of the nodes that are found in both datasets, is interpolated and there for we can see how this nodes move from one dataset to the other one by using the slider. Something that this tool doesn't allow us to do, is the selection of nodes and edges to render. We can only select the nodes if we are in either the blood or the biopsy state.



(a) Slider set on the left extreme. It shows only the blood dataset.

(b) Slider set closer to the blood dataset. The biopsy dataset is more faded.

(c) Slider set closer to the biopsy dataset. The blood dataset is more faded.

(d) Slider set on the right extreme. It shows only the biopsy dataset.

Figure 2.8: Network morphing from the blood dataset to the biopsy dataset.

2.4 Implementation details

Unity (version 2018.4.10f1 [24]) is the software that was used to build the system. It is a multi-platform game engine. It is known to be easy to use and for having a big community of creators and asset designers [9]. Even though it is intuitive to use, it also has low-level access for developers. As for Virtual Reality, Unity has been up-to-date with the new VR technologies thanks to professionals and amateurs in this area who have built an integration for Unity.

In our case, our device is an Oculus Quest, and for this reason we use the Oculus integration for Unity [25]. In addition, we have used VRTK, a collection of scripts and assets that help build VR solutions [26]. Finally, the programming language used in Unity to implement the system is C#.

2.5 Architecture and design

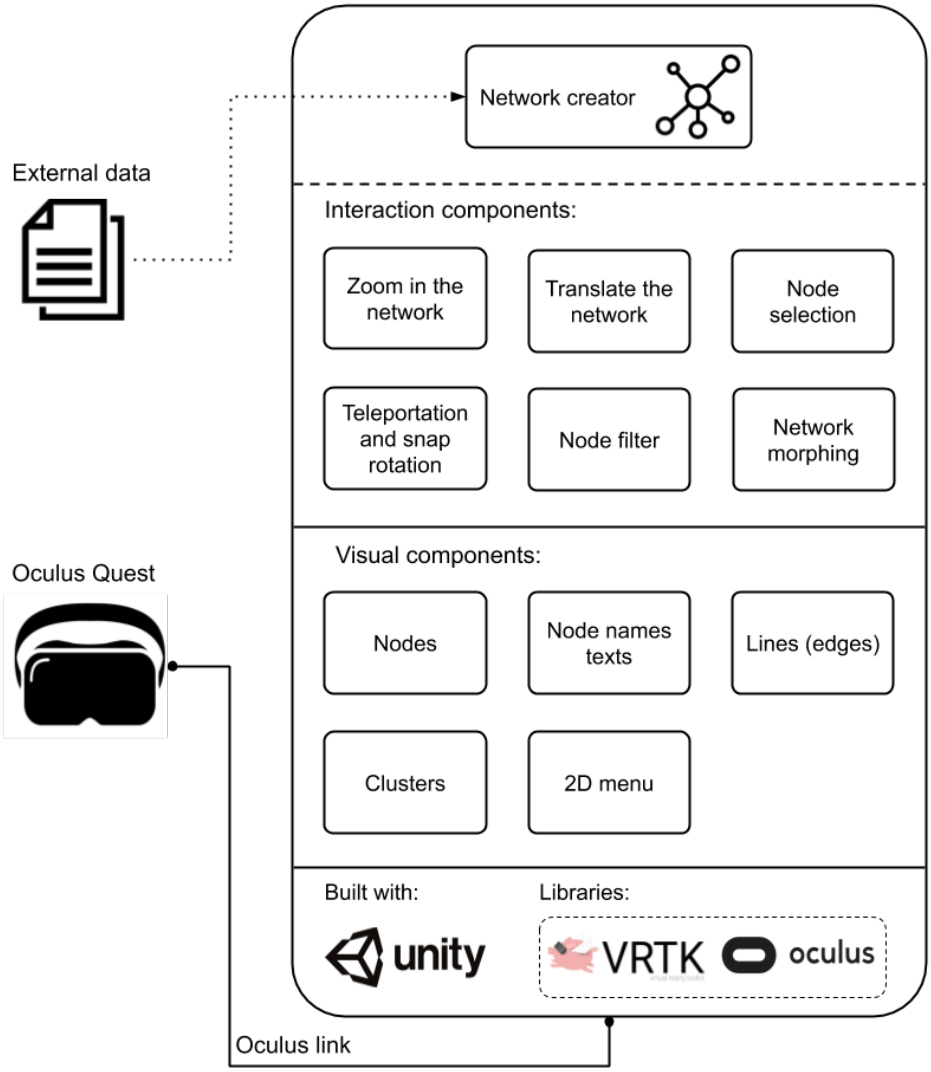


Figure 2.9: Architecture and design of GeneNet VR.

GeneNet VR is a VR application built in Unity. For the implementation of the different visualization and interaction components I programmed some C#

scripts, used also solutions that are native in Unity like the particle systems and made use of the VRTK library and the Oculus library for Unity.

In Figure 2.9 we have an overview of the architecture of GeneNet VR. The big box represents the Unity application and it contains all the components and functionalities that I have developed for the project. We can see that the big box is divided in 4 regions. The first one, starting from the top, is the network creator component that uses external data in order to build the network. In the second region we have the different interaction components that are available for the user to interact with the network and the environment. The third region contains the visual components that help the user visualize the data. Finally, the last region contains the technologies and libraries that I have used to build the application. We can also see the Oculus Quest headset represented down on the left. Here the user can visualize the network and use the controllers to interact. As we can see in the figure, the Oculus Quest can be connected to the PC using an Oculus Link, which is basically a high-quality USB 3 C to C or USB A to C cable with proven performance [14]. This allows the user run GeneNet VR on the PC. Another possibility is also load GeneNet VR in the Oculus Quest and run it in the hardware of the headset without any cable or PC. We are going to explain now in more detail how each of the interaction components of GeneNet VR were implemented. I will use some flowcharts to explain some algorithms. In this section we will also mention some actions that are triggered using the Oculus controllers. These are specified in Figure 2.2.

The network creator (see Figure 2.10) initializes and builds the networks using the data files that were previously stored in the application's directory. It processes the data from the CSV files and stores the information in hash maps that can be later be used by the interaction components to transform or read the data of the networks like the node positions or colors. During this process of building the network, we apply a cluster algorithm as well. This algorithm consists of a loop of 10 iterations where for each iteration we go through each of the relationships from the relationship file. For each relationship we update the position of the nodes so that the ones that are connected are closer to each other in the space, resulting into clusters of nodes depending on how related they are.

For the *zoom in the network* component I wrote a C# script where I use the Oculus integration to communicate with the Oculus Quest controllers. The algorithm is run every time the user enables the action for zooming (see Figure 2.11 for the algorithm). What the script does is to find out if the user is stretching or contracting the arms. For this, when the user triggers the action, the system stores the current position of the left and right controllers in the 3D space and calculates the distance between these 2 points. This position is called initial position. Until the user releases the triggers, the system calculates for every

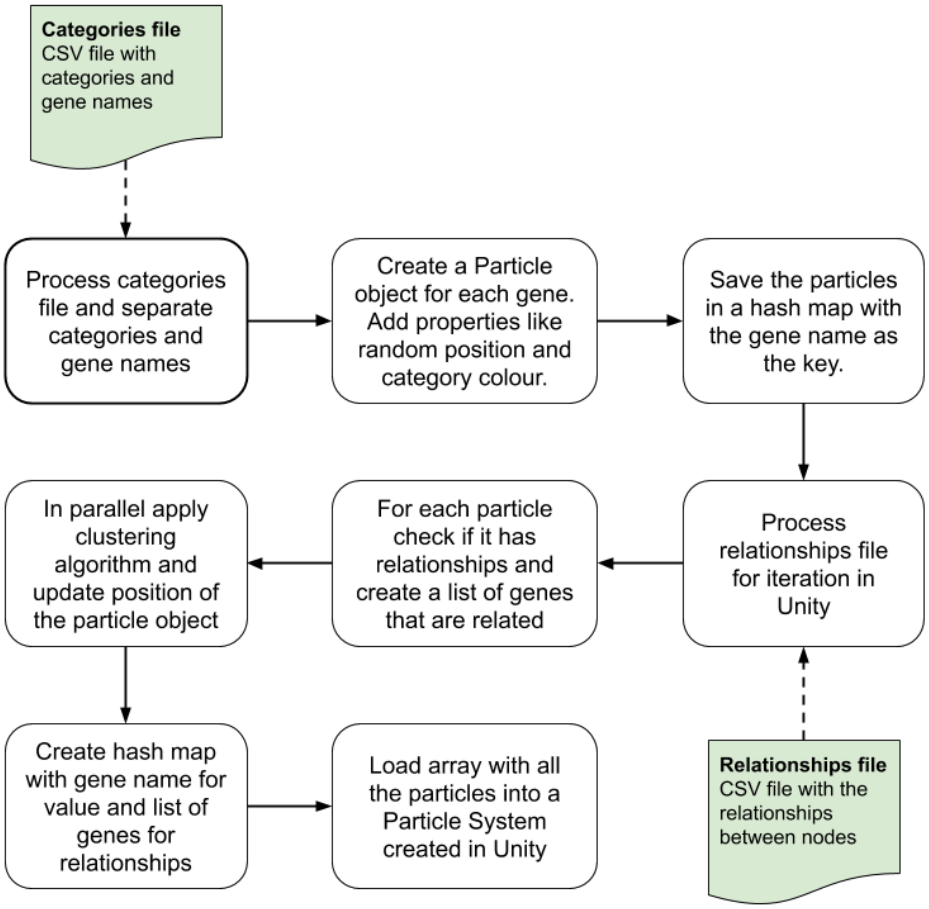


Figure 2.10: Network creator algorithm.

frame the current distance between the two controllers and compares it with the initial distance that was stored right before the user triggered the action. If the new distance is smaller than the initial one, the network will shrink; if it is bigger, the network will grow up.

The *translate the network* component consists is implemented in C# as well (see Figure 2.12). Here we do something similar to the *zoom in the network* component. When the action for the translation of the network is triggered, the position of the right controller is stored as the initial position. Then, while the user is holding the trigger of the right controller, the current position for the controller is calculated for every frame. A vector is calculated like (current_position - initial_position) and normalized. With this we obtained the direction of the vector where the user is trying to move the network to. We add up that vector with a constant to update the position of the network in the 3D space.

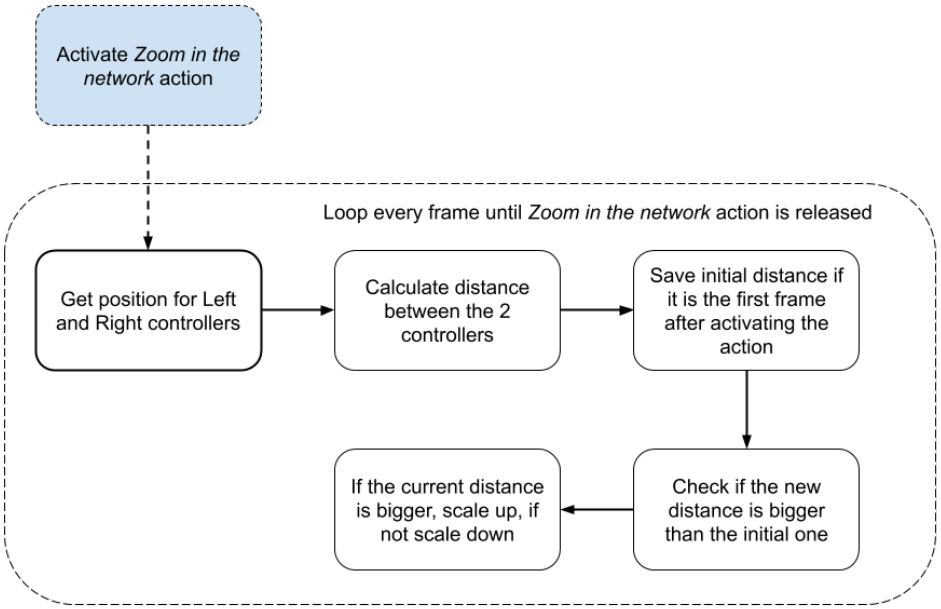


Figure 2.11: Algorithm for zooming in the network.

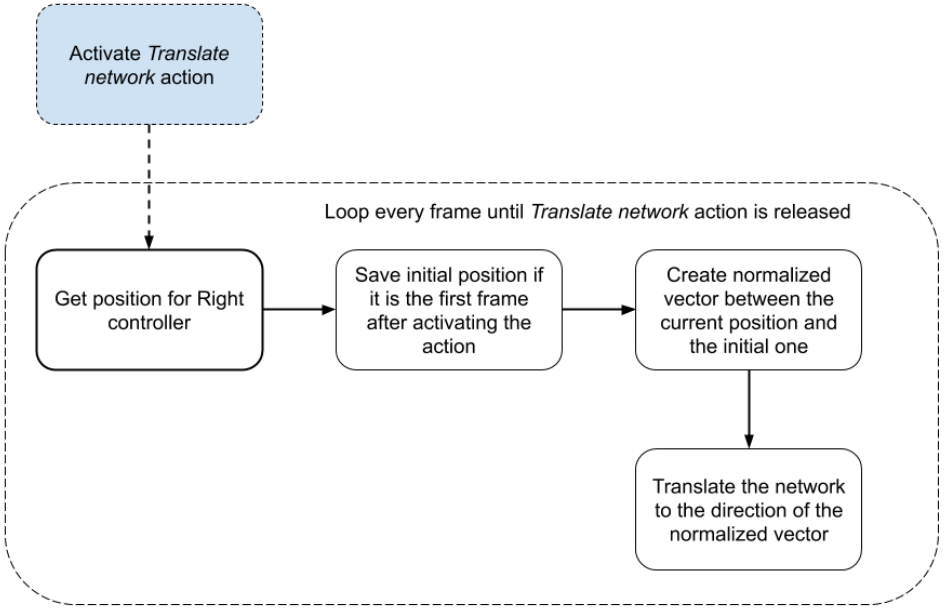


Figure 2.12: Algorithm for translating the network.

For the *select node* component, when the user triggers the *select node* action, an algorithm is used to calculate which node is the one that the user is trying to point at. In Figure 2.13, we can see a flowchart of the algorithm that we

implemented. I used C# to code a script for this functionality. A laser pointer comes out from the right controller when the user triggers the action. In the algorithm we make use of this laser information which consists of a vector. In order to select the node that we are pointing at, we calculate for each node in the network a vector product composed by the laser vector and a vector that goes from the right controller position to each node position. The result is another vector where we extract its magnitude. The magnitude that is smaller will correspond with the node that is closer to the laser pointer. We will select this node with the smaller magnitude value. When a node is selected, the algorithm also draws the lines corresponding to the relationships of this node in the scene. If there were any lines before the new node is chosen, these are removed.

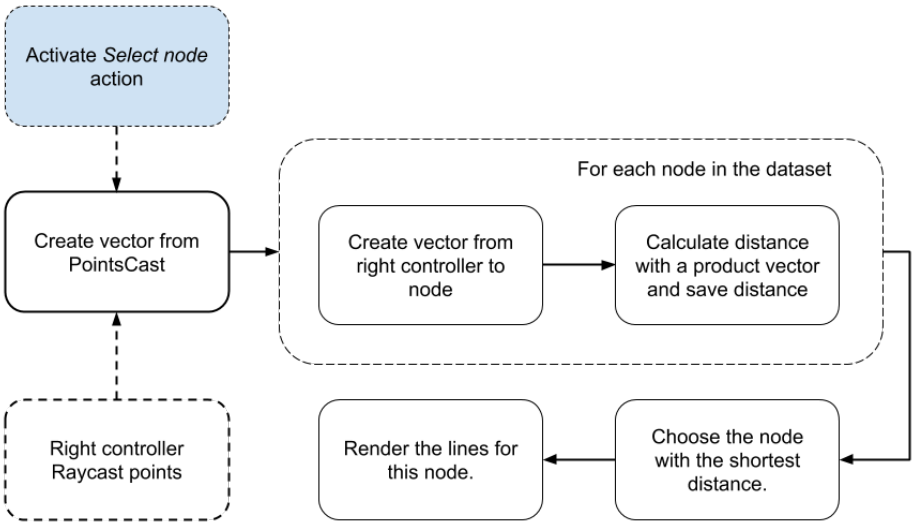


Figure 2.13: Algorithm for the selecton of the nodes in the scene.

The *network morph component* (see Figure 2.14) consists of a UI slider element that is in the menu and a method where we pass the value of the slider as a parameter. The values from the slider range from 0 to 10 and as the algorithm shows, value 0 will show the blood network in the scene and value 10 will show the biopsy one. When the value is greater than 0 or lower than 10, we interpolate the color and the position of the nodes. For the colour interpolation, we use a linear interpolation function from Unity called Color.Lerp. The position interpolation is only applied to the nodes that are in both the blood and the biopsy dataset. For this interpolation, we create a vector that goes from the node in the blood dataset to the node in the biopsy one. We divide this vector into 10 and multiply it for the slider value. This will be the new position for the node.

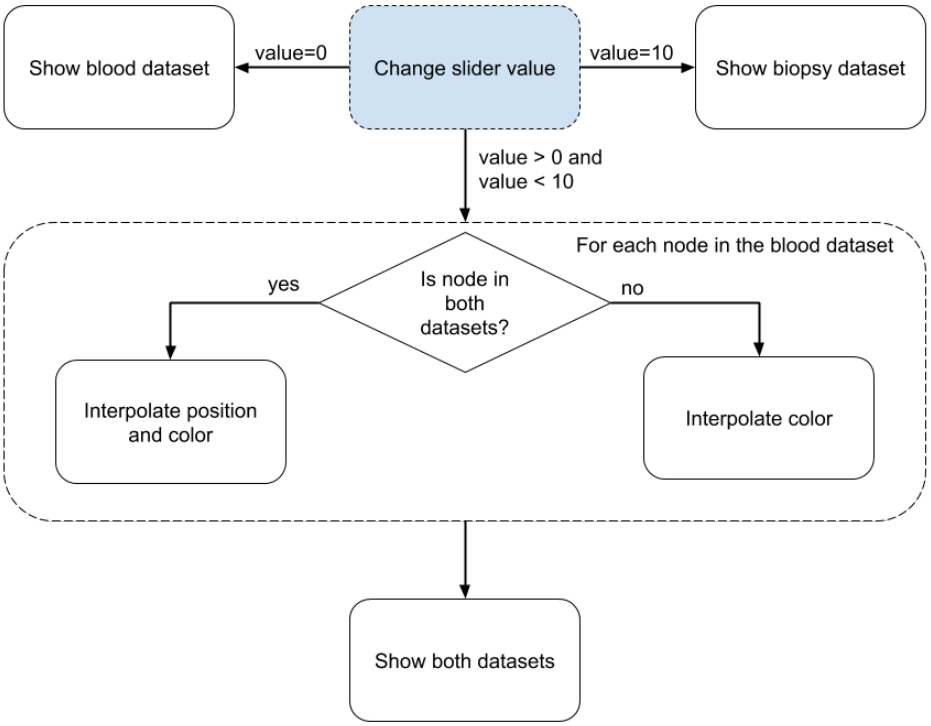


Figure 2.14: Algorithm for the network morph.

For the *node filter component*, a UI interface is used in Unity. This interface contains several checkboxes that are switched on by default. In addition, each checkbox has attached a function that is run every time the user switches it off or on. This function receives as a parameter a string value that is different from each checkbox. When the user switches the checkbox, the algorithm looks into a hash map that looks like this:

```
private Dictionary<string, string[]> oncoGroups;
```

We use the string variable that is passed to the function to look up the oncoGroups hash map, where each key corresponds to the name of each checkbox. We obtained a list of nodes that we need to turn on or off from the network.

Finally, for the *Teleportation and snap rotation component* we have used some scripts and prefabs that come with the VRTK library. I used as a reference some techniques to develop these locomotion solutions from a course on Unity[1].

1. https://learn.unity.com/course/oculus-vr

2.6 Discussion

2.6.1 Unity vs Unreal Engine

Unity3D[2] and Unreal Engine[3] are two popular software for the development of videogames as well as virtual reality games and other applications. They offer an integration for Oculus Quest and other VR devices in the market.

I chose Unity for the development mostly because I had some experience with it. In addition, when I researched about VR development, I found that Unity is good integrated with Oculus Quest and there is the VRTK library. I also found several tutorials about VR development in Unity as well as documentation for the Oculus integration and about VRTK. Unity is also known to be easier to learn. There is a study where they teach Unity and Unreal Engine to students, and they concluded that Unity is little less complicated to learn [6]. On the other hand, Unreal can create more professional looking results. For this project, we are not looking for realistic graphics, since we are dealing with abstract data.

2.6.2 VR toolkits and frameworks

Apart from the Oculus integration for Unity, there are some 3rd party toolkits and frameworks that we can use to accelerate the development process for VR. I used VRTK in my project, as I have mentioned before. This toolkit contains several scripts and prefabs that can be used to build several VR solutions. In my case I used this library to build the teleportation and snap rotation locomotion techniques. VR Interaction Framework[4] is another toolkit for VR development, but it is not open source. In addition, Unity comes with XR, a support for XR platform integration.

2.6.3 VR headsets

We can find numerous VR headsets nowadays in the market[5], from simple headset solutions like Google Cardboard to more advanced ones like HTC Vive Focus. In order to choose which headset we wanted to target our application to, we had into account the price, performance and the features that the headsets have. We chose Oculus Quest because the price was not very high (5799,- kr in

2. https://unity.com
3. https://www.unrealengine.com
4. http://beardedninjagames.com/vr-framework
5. https://versus.com/en/vr-headset

2019) and it was also a standalone device, which is not so common among the VR headsets. Oculus Quest also has an advantage as for the performance, it can be connected to a PC where we can run heavier applications. In this way, this headset is very versatile and the price is affordable for many people and especially for research entities. Other features that Oculus Quest has is that it comes with two controllers that have free movement and inputs as buttons, triggers and grips that can be used for the interactions in the VR application. Other headsets from a lower price range like the Oculus Go have fewer inputs in the controllers and are more stationary.

3

Visualizing MIxT in VR

What is MIxT used for? And how would users do it in VR? How the MIxT application is implemented in GeneNet VR and what it does. What are typical network characteristics for this (type of) application? Size, clusters, edges, connectivity, etc?

4

Related work

I will focuse in this chapter on similar works found in the literature for the visualization of bioinformatic data in VR.

4.1 Virtual Reality Chemical Space

Virtual Reality Chemical Space is a VR application for the interactive exploartion of chemical space populated by Drugbank compounds[17]. It is also developed in Unity using C# and the VRTK library. They use a particle system to render the particles of the chemical space. To render the particles, they use shaders instead of geometrical spheres as well, optimizing the number of vertices per datapoint in the scene. In order to reduce the motion sickness they have introduced a floor in the form of a grid acting as a static frame of reference. Also instead of letting the user move through the VR environment, they use a controller to move the point cloud. In Figure 4.1 we can see an screenshot from the VR application. As we can notice in the screenshot, there is a subtle rendering of an outer space scene as an independent visual background. This is another technique to reduce the motion sickness that helps the user keep the notion of space. This is an interesting technique that we could have tried in GeneNet VR.

They conclude in the article that the application that they have developed doesn't visualize an environment with an analogue in the real world, but instead

a mathematical construct. Also some of the drawbacks that VR has compared to traditional solutions is that the VR headsets are not so comfortable as well as often-occurring eye strain and virtual reality sickness. They also conlcude that the application of VR in chemistry has more potential in the fields of education and training as for the current state of technology. The tools for chemistry need to be further evaluated wether they should be extended to VR.

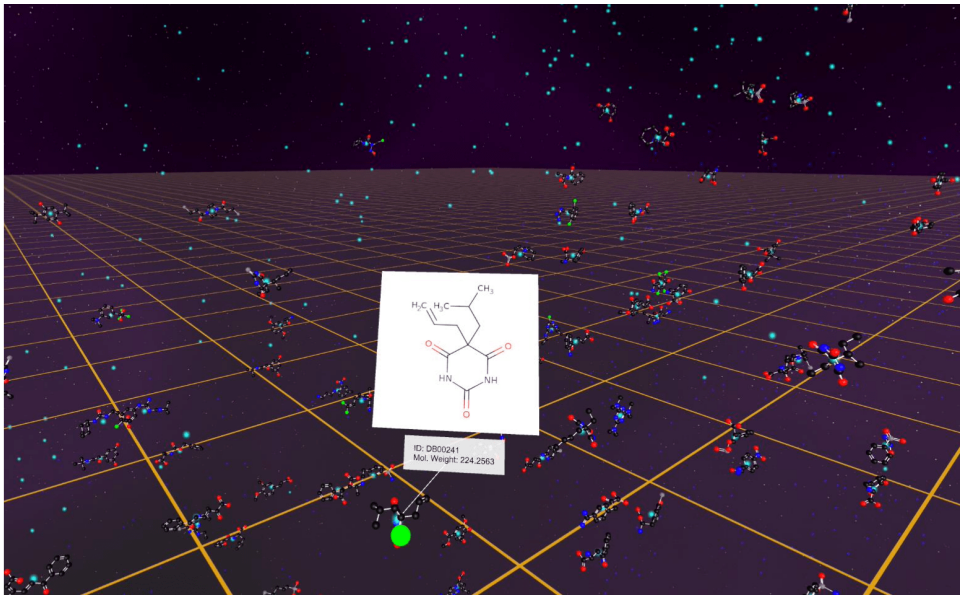


Figure 4.1: Optimized virtual reality chemical space. Figure taken from [17].

4.2 BioVR

BioVR is an interactive VR platform for integrated visual analysis of DNA/RNA protein structures[30]. It is built in Unity and using C#. The headset that they targeted the application to is Oculus Rift. One big difference between BioVR and our application is that in BioVR they use the hands for the interactions rather than the controllers. This can be very attractive and it could have worked very well for GeneNet VR, since most of the interactions can be done with hand gestures. Also since early 2020, hand tracking has been integrated in Oculus Quest, making it easier for dveleopment[1]. An screenshot of BioVR can be seen in Figure 4.2. The user in BioVR can visualize the virtual hands in the virtual world and they are used for the interaction with the nucleotide sequence and UI menus. In GeneNet VR instead of the hands we show the controllers, which help the user orientate in the space. The research concludes that using VR

1. https://developer.oculus.com/documentation/unity/unity-handtracking

helps in create new workflows for researchers to view DNA/RNA sequence and protein structures. They also of VR is that it is easy to integrate 2D user interfaces in the virtual world, as we can see in Figure 4.2 B.

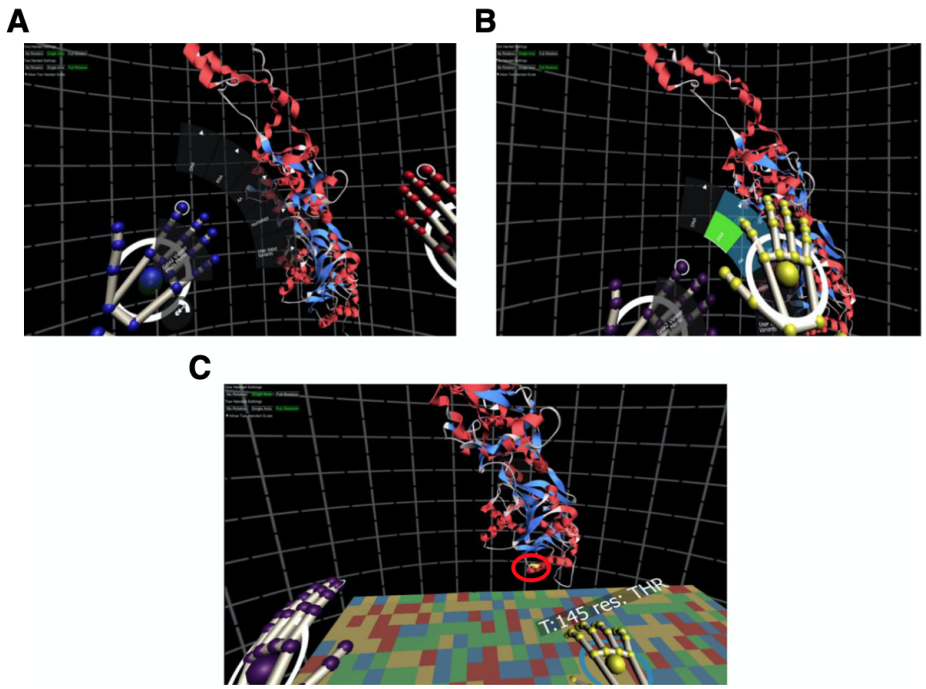


Figure 4.2: Screenshot from BioVR. Figure taken from [30].

4.3 CellexalVR

CellexalVR is a virtual reality envirnoment for the visualization and analysis of single-cell RNAseq experiments that help researchers undertand their data[11]. The system is divided in two parts: the first one consists on the VR interface and the second is an R package called cellexalvrR that does back-end calculations and also provides functions that allows the user export the scRNAseq data from an R session for CellexalVR to read. CellexalVR was developed in Unity for HTC Vive (Pro). They used Unity and C# and R for the implementation. They used libraries like VRTK, OpenVR and SteamVR as well in the implemenation.

Something that is interesting in CellexalVR is that it allows a multi-user mode via the Photon Unity Networking. This works sending information about the events to each user using Remote Procedure Calls. In Figure 4.3 we can see an screenshot from CellexalVR where two users participate in the same session. Other users can also be in the same session but just be watchers and be in like

a "ghost mode". This is something interesting that could be used in GeneNet VR as well. Espcially the "ghost mode" could be useful so that other people can visualize the network at the same time from other perspectives.

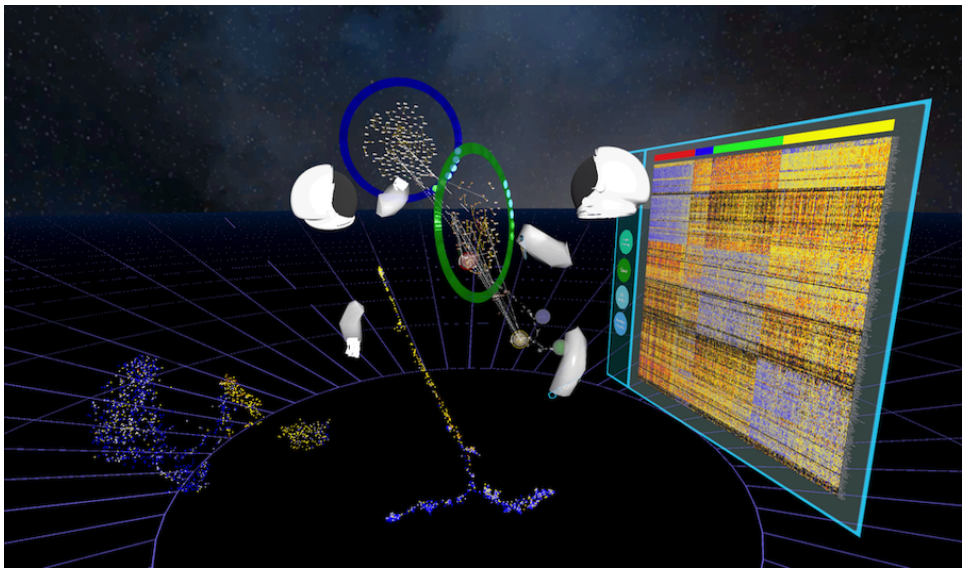


Figure 4.3: Screenshot from CellexalVR. Two users using CellexalVR at the same time. The head models were taken from NASA. Figure taken from [11].

4.4 BigTop

BigTop is a visualization framework in VR for the rendering of Manhattan plots in three dimensions[27]. Manhattan plots are usually 2-dimensionals, where genomic coordinates are displayed in the x-axis and the negative log-10 of the association P-value for each single nucleotide polymorphism (SNP) displayed on the Y-axis. Each dot on the Manhattan plot signifies a SNP then. In BigTop, the z-axis is used to display minor allele frequency of each SNP. This allows the identification of allelic variants of genes. As for the interaction, BigTop allows the user to select a node in order to obtain more information like the SNP name. BigTop is built in JavaScript with the React and A-Frame frameworks. It can also be rendered in any commercially available VR headsets and also in 2D web browsers.

To move around the scene in BigTop the user can take steps (in the VR version) or using the arrow keys from the keyboard. The user can select the nodes by pointing with a laser at the nodes in the scene in the VR version (See Figure 4.4 for a screenshot of BigTop showing the selection of a node). In the browser version it is possible to select them using the pointer from the mouse. Also in

order to look around, the user needs to move the head around using the VR headset, or by isong click and drag with the mouse (in the browser). In GeneNet VR we have focused only into building a visualization system for a VR headset. We have used better locomotion techniques that improves the comfortability. However the locomotion technique that they use to move around could be a good idea for GeneNet VR as well.

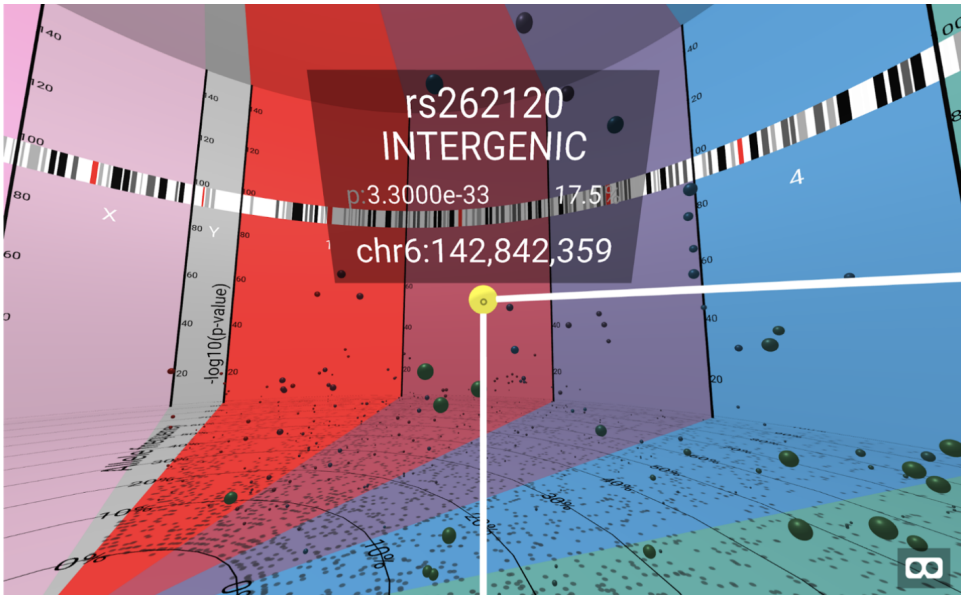


Figure 4.4: Screenshot from BigTop where a node is selected. Figure taken from [27].

5

Evaluation and discussion

GeneNet VR has been developed to explore biological networks that contain genetic information. For this project, we have used two datasets from MIxT [7], where we applied several VR techniques to build a visualization and interaction system. In this chapter we want to evaluate GeneNet VR, focusing on its scalability and performance. Since we are visualizing networks with genetic information, we want to know if the system that we built can be used for larger sizes of this type of datasets. As part of the evaluation process, we designed a list of questions that we will try to answer along this chapter. The questions are:

1. For which interactions do we achieve the recommended FPS (72) when scaling the network?

2. What characteristics of the network influence the scalability?

3. What is the performance by using a PC with Oculus Link and the performance using just the Quest hardware?

4. How do users perceive the interaction of the network?

Question one is based on the Oculus' performance guidelines[22], that say that an application should meet the following:

- 72 FPS for Oculus Quest (required by Oculus).

- 50-100 draw calls per frame.
- 50,000-100,000 triangles or vertices per frame.

We will evaluate the performance for the interactions we use most for the visualization of the networks. These are: translation of the network, scaling of the network and node selection (including the line rendering for the relationships).

As for the second question, we want to know what characteristics influence the scalability of the system. Some parts of the application will have more impact on the performance than others. To keep it simple, we will evaluate the impact in the performance done by the following elements, that are the most important for the visualization: number of nodes, number of lines and number of clusters. However, since the cluster algorithm is applied when initializing the network, we will just focus on the number of nodes and the number of lines.

We will also evaluate the performance of the application being run in the Oculus Quest hardware and compare it with the performance in the PC. The hardware of the Oculus Quest is not as powerful as the one of the machine that was used for the development. We would like to know if the performance in the Oculus Headset is good enough for the visualization of MIxT.

Finally, we want to know how the users perceive the interaction and visualization of the network. We will evaluate this with a qualitative method with a demo of the application using the MIxT datasets and also an interview.

5.1 Experimentation plan

An experimentation plan was designed to ensure that the experiments are consistent and that they can be reproduced several times in order to get realistic measurements. We take into consideration the following aspects for our experiments:

1. Scalability for different interactions.
2. Network characteristics.
3. Bottlenecks.
4. User study.

5. Hardware and software specification.

As we mentioned before, we will evaluate the performance of the system when we translate, scale and select nodes in the network. We will focus on the number of nodes and lines that the network has to have an idea of how the network scales. While studying the performance we will also see if there are bottlenecks and what is causing them. We will describe in Table 5.1 the elements of the system that can more impact in the scalability.

Element	**Description**
Clusters	The algorithm used to create the clusters is run in the initialization of the system, before everything renders. This can be time consuming because it involves many operations to process the text files (they have several thousands of lines). However this is only called at the beginning and not after the system is initialized.
Nodes	Represented as 2D squares in the space, they consist of 2 triangles. They are always showing in the scene and they position change while scaling and translating the network.
Lines	They represent relationships between the nodes. Everytime a node is selected, line objects are added to the scene. They are 2-dimensional and consist of 2 triangles. Depending on the node we might need to render several hundreds of these lines in the scene.

Table 5.1: Elements of the network that have influence in the scalability.

We have designed a series of experiments that can be reapeated several times. We ran each experiment 4 times and calculate the average in order to get realistic results. We also created a benchmark in Unity using C# where we reproduce the interactions that we want to evaluate. The experiments are coded in the benchmark using scripts so that we can always reproduce them. For the networks translation and network scale we use mathematical functions to translate the network around the scene and to scale the network up and down. For the node selection we have chosen a set of nodes.

As for the hardware specification, we ran the experiments in a machine with Windows 10. In Table 5.2 we can see the hardware specification for the machine. The GPU is also specified in Table 5.3. The hardware specification of the Oculus Quest is shown in Table 5.4.

The experiments were run in Unity, the same software that we used for the development. We used the version 2018.4.10f1 of Unity for the whole project

Machine specification	
Processor	Intel(R) Xeon(R) CPU E3-1275 v6 @ 2.80GHz 3.79 GHz
RAM memory	64.0 GB
System type	64-bit Operating System

Table 5.2: Machine specification.

GPU specification	
Adapter type	NVIDIA GeForce GTX 1080 Ti
Chip Type	GeForce GTX 1080 Ti
DAC Type	Integrated RAMDAC
Available memory	45025 MB

Table 5.3: GPU specification.

Oculus Quest specifications	
Panel Type	Dual OLED 1600x1440
Supported Refresh Rate	72Hz
Tracking	Inside out, 6DOF
CPU	Qualcomm® Snapdragon 835
GPU	Qualcomm® Adreno™ 540 GPU
Memory	4GB total

Table 5.4: Oculus Quest specifications.

and experimentation. In Unity we used the OpenGL graphic API.

In order to find bottlenecks, we used a profiling tool in Unity. A profiler is used to get an overview of the performance of the application. We used the built-in profiler in Unity. This gave us information about per-fram CPU performance metrics. In addition, Unity also provides some metric information that we can be displayed in the Unity editor. We got information about the number of vertices in the scene, triangles, frames per second, etc.

5.2 Performance evaluation

We will explain in this section the experiments to evaluate the performance. We will also show the results that we obtained and discuss them. As we mentioned before, we will focus on the performance for several actions that the user usually does when exploring the networks. These are translation of the network, scale up or down the network and select nodes in the network as well as render the lines for the relationships. All the experimens are run 4 times and we show the

averages.

We ran all the experiments on the PC and we used the blood dataset from MIxT. We chose this dataset because it is bigger than the biopsy one. We also ran each experiment for different sizes of the blood dataset: the whole dataset (2693 nodes), half size of the dataset (1346 nodes) and a third part (897 nodes). In order to analyse the performance, we obtained the deltaTime for each frame. In Unity, this variable privides the time between the current and the previous frame. Once we obtain all the times for all the frames that the experiments last, we extract make the following calculations: the average of all the times of the frames, the 0.25% worst of all the frames and the 0.1% worst of all the frames.

5.2.1 Performance when translating the network

In this experiment, we evaluate the performance when translating the network. To translate the network around in the scene, we have used a sine function in the y axis and a constant function in the z axis. For every frame we update the y and z position of the network object, creating a wave motion. We obtain the delta time for every frame during a total of 700 frames (starting from frame number 501 until frame 1200). In Table 5.5 we can see the results obtained in the experiment for all the network sizes and with the averages.

Dataset size	1% average low	0.25% average low	Average
size	12.174	20.111	6.553
size/2	12.791	21.996	6.498
size/3	13.516	23.28	6.495

Table 5.5: Performance results when translating the network.

The average for all the sizes is quite similar. We can also see that the average time is slightly lower when the network is smaller. For the 1% column, we calculate the average for the 7 frames with highest times. For the 0.25% column, we do something similar; we show the time of the frame with the worst time. As we can see, the times for these percentages are actually higher when the network is smaller, something that we didn't expect. We would have expected that the time was lower when the number of nodes was lower as well. However, for the total averages, this tendency meets our expectations.

5.2.2 Performance when scaling the network

In this experiment, we evaluate the performance when scaling up and down the network. We use a sine function as well. we update the size of the network object for every frame and since we use a sinus function, the network scales up an down several times. We obtain the delta time for every frame during a total of 700 frames, as well as in the translation performance experiment. See Table 5.6 for the results obtained.

Dataset size	1% average low	0.25% average low	Average
size	13.418	22.816	6.505
size/2	12.685	22.607	6.485
size/3	13.631	23.015	6.494

Table 5.6: Performance of scale the network.

The results from this experiment are similar to the ones obtained in the previous one about the translation of the network, but we find some differences. The average time for all the nodes (3rd column) is slightly different, the time for size/3 is higher than size/2, somthing that we would have expected the opposite. All the results for the size/2 are lower than for size/3.

5.2.3 Performance when selecting nodes

In this experiment we want to evaluate the performance when selecting nodes. When a node is selected in GeneNet VR, several things are done during this process. First, an algorithm finds the node that the user is trying to select. Second, two text objects are updated with the new names of the gene node. Thrid, the relationships from that node are rendered in the scene. There are many things going on during this process and we evaluate the performance for the entire pipeline.

As for the experiment design, we took into consideration the number of the relationships (lines) that had to be drawn in the scene. In the blood dataset, a node can have between 1 and 1607 edges. We wanted to have a balanced number of this for our experiment, so we decided to select several nodes that cover this range.

In Figure 5.1 we show a scatter plot where the X axis represents the the number of edges in ascendent order and the Y axis represents the number of nodes that have that number of edges. As we can see, most of the nodes have less than 100 edges. For instance, there are 117 nodes that have 2 edges, and 231 nodes that have just 1 edge. This suppose already the 12,92% of all the nodes

in the dataset. However there also a few nodes that have several hundred of lines. Because it was a bit hard to make a balanced selection, we just selected several nodes from the range 1 to 1607. The nodes that we select during the experiment are the following (in parenthesis the number of edges that they have): TGFBR3 (1), EPSTI1(11), SMNDC1(90), HNRNPH3(290), ANGEL2(586), ACTR6(756), ARGLU1(1607).

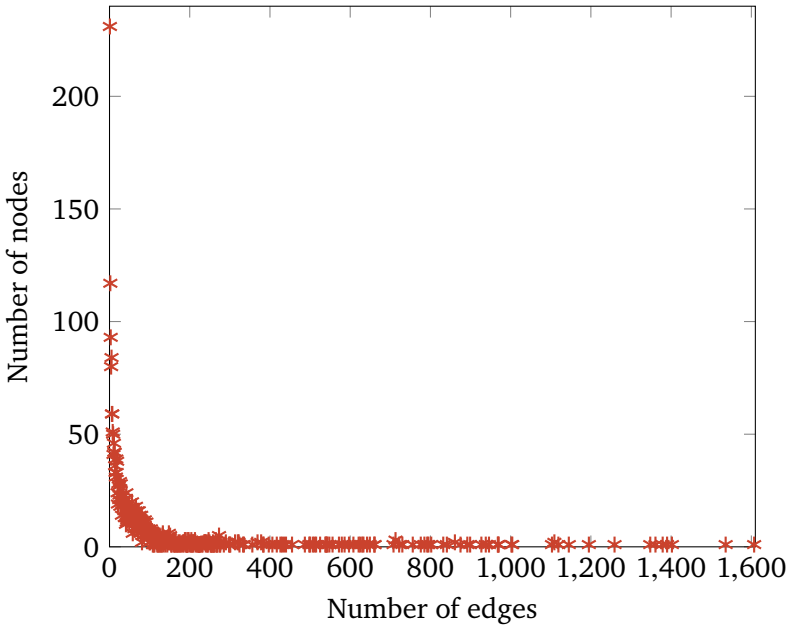


Figure 5.1: Scatter plot showing a distribution of the number of edges in the blood dataset. The X axis shows the number of edges and the Y axes shows the number of nodes that have that number of edges in the blood dataset.

In the experiment, we select the nodes that we mentioned before. We select one node every 100 frames, starting from the TGFBR3 node and following the order from the list. We calculate the averages after all the nodes have been selected. We also have a total of 700 frames, like in the previous experiments. In Figure 5.7 we can see the results.

Dataset size	1% average low	0.25% average low	Average
size	65.569	100	8.711
size/2	56.389	100	8.638
size/3	56.385	100	8.583

Table 5.7: Performance of select node.

The average delta time is a bit higher than the ones in the translation and scaling experiments (around 2 milliseconds more). In the low percentages we can see a big difference though. For the 0.25%, it's always 100ms. And for the

1% everage low, it's 65ms for the whole size and 56ms for size/2 and size/3. We can see that the node selection can have much more impact in the performance than the translation and scale of the network.

5.2.4 Performance discussion

We can see from the results, that the number of nodes in the dataset doesn't have that much impact in the performance. It would be interesting to analyse the performance wiht datasets that have more than 2693 nodes. For instance with 5000 and 10000 nodes, but for our project, we have just focused on the datasets MIxT, and the blood dataset is the biggest one. For a future work, it would be interesting to analyse larger datasets to see if the number of nodes could influence more in the performance.

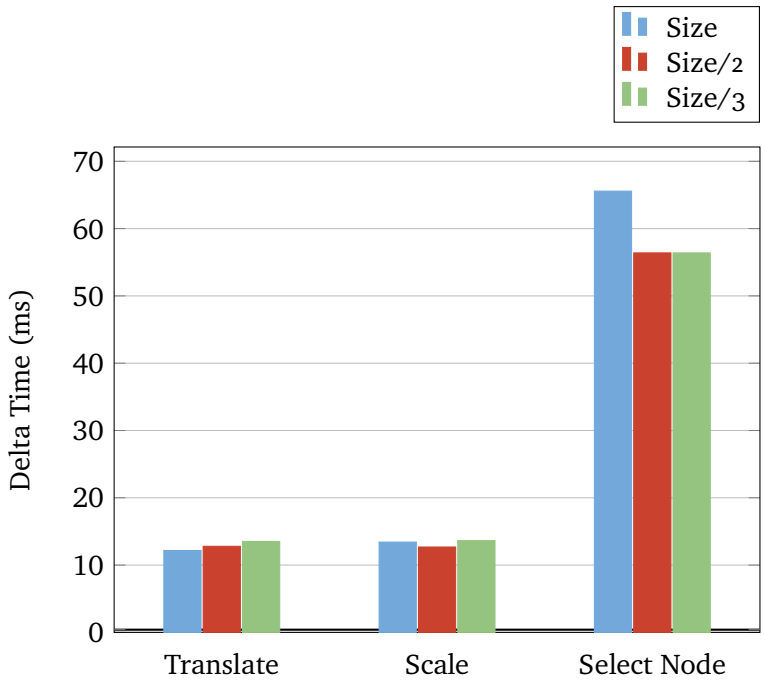


Figure 5.2: Bar graph showing a summary of the performance results for the 1% lowest average (7 frames with worst performance or higher times).

In general, the performance is good for the experiments that we ran. Having an average of 7-8 milliseconds for all the frames means that we meet the 72 FPS that the Oculus' performance guidelines suggest. However, for the node selection, we have seen that the performance can be a lot worse than for the other interactions, see Figure 5.2 for a summary of the results. In this bar graph we can see a summary of the 1% worst time for the different interactions. We can see that the time for the node selection interaction is much higher.

One important observation is that in the experiment we just select 7 nodes, one every 100 frame. However, when we use GeneNete VR, it's easy to select many nodes in just a few frames. This is because the select node function is run for every frame when we trigger the action for it, and if we point at a region where there are many nodes together, it will be easy to select several of them in a short period of time. Another point to take into account is that not all the nodes have the same number of edges to render. It would be interesting to know if the number of edges could decrease the performance as well. We will analyse in the following section if the selection of nodes and the number of edges could have more impact in the performance and scalability of the network.

5.3 Scalability evaluation

As we saw in the performance experiment for selecting the nodes, the time to render the frames can be very high. This could have influence in the quality of the application and generate some unconformity in the user's experience. It could happen that the application freezes for some milliseconds and that the application doesn't run smoothly when selecting the nodes. In this section we evaluate the performance when selecting the nodes and rendering the edges for the nodes. This will also help us study the scalability of the application so that it can be used for larger datasets.

We would like to know if the number of edges that we need to render in the scene can decrease the performance. We designed an experiment where we test the delta time (the time that a frame takes to render) for different amount of edges to render. In Figure 5.1 we showed the distribution between the number of edges and the number of nodes that have that amount of edges. We used this data and created a new dataset where we have a node from every "edge category" and then we selected each of the nodes and calculated the delta time. To put it simple we try to render the edges for each of the possible number of edges that we can find in the blood dataset and calculate the time for each of them.

In Figure 5.3 we can see the results for this experiment. In our benchmark we run the select node action for each of the nodes from the dataset that we created for this. We select a new node in each frame. We show the results using an scatter plot. The X axis represents the number of edges to render. The Y axis represents the total time that it took to render that amount of edges.

We would have expected that when there are more edges to render, more time it would be needed for that. However, that is not as clear in the experiments results. We can see that when there are less than 200 edges, many of the times

are less than 20ms. Nevertheless, some nodes that have less than 200 edges take more than 40 or even 50 ms to render. On the right side of the plot we can see that some nodes with several hundreds of edges take more than 60 ms to render, but in some cases they take less than 20 ms. This is not very consisten and we conclude here that the number of edges might influnce in the performance, but we can see that there are many other things that influence the performance as well. Unity is a complex game engine, and there are many things going on when we run the experiments.

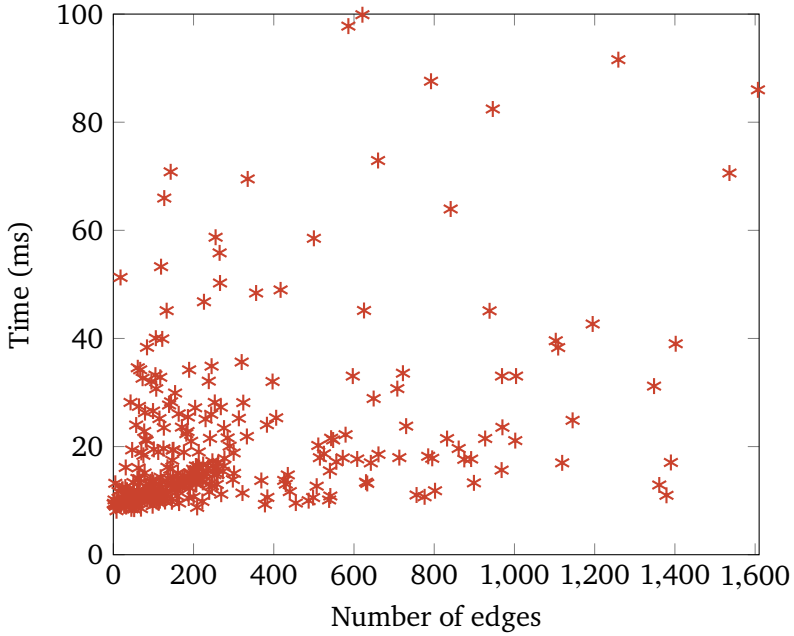


Figure 5.3: Scatter plot showing the relation between the number of edges to render and the time that it takes to render for the blood dataset.

After running this experiment we ran the profiler from Unity to see what could be the cause for taking so much time when selecting some nodes. We profiled the selection of the node ARGLU1(1607), which has the maximum number of edges. In Figure 5.4, we can see an screenshot of the profiler in Unity. In the profiler window we can see a graph where the Y axis shows the amount of time that each frame took to render. we are selecting a frame in the middle, where we can see a spike (althugh it's a bit hard to see because of the selection bar). This frame corresponds with the selection of the node. It took 121.23ms to render. In the Overview window we can see a list of functions that are called during this frame. Also there are several columns and the the total column indicates the percentage of the time that a particular function took. As can see in the screenshot, we don't get much information about where the proble could be. But we can see that 65.4% of the total time comes from the BehaviourUpdate function.

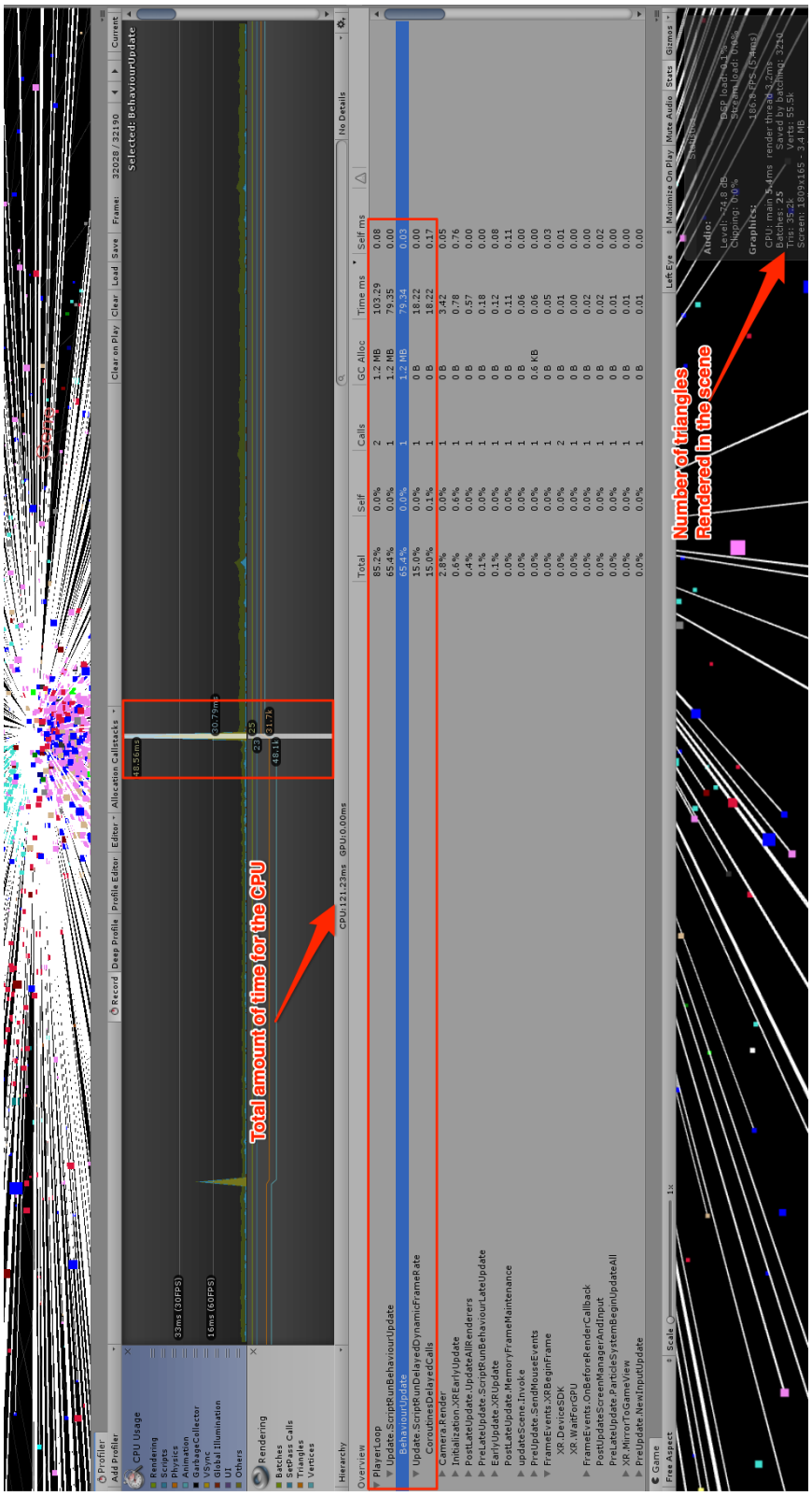


Figure 5.4: Profiling the selection of the node ARGLU1(1607), which has the highest number of edges. We study what is the cause for the high amount of time that this takes to render.

We get also some other metric information from this screenshot (see the region far below and the small black grey square with the Statistics title), like the number of triangles that the scene is rendering. This is the selection of the node with the highest number of edges and there are a total of 35.2k verteces, which is inside of the Oculus' performance guidelines.

5.4 Oculus Quest vs Computer

We developed the application in a PC and tested it in Oculus Quest, an standalone headset. We did the testing using a USB C cable that connects the headset to the PC. However when we run the application in this way, we use the PC's hardware. The previous experiments were also run in the PC. We want to evaluate in this section, if the performance in the Oculus Quest is good enough when running GeneNet VR. The hardware for the Oculus Quest is not as good as for the machine, so we expect that the performance in the Oculus Quest is goin to be worse.

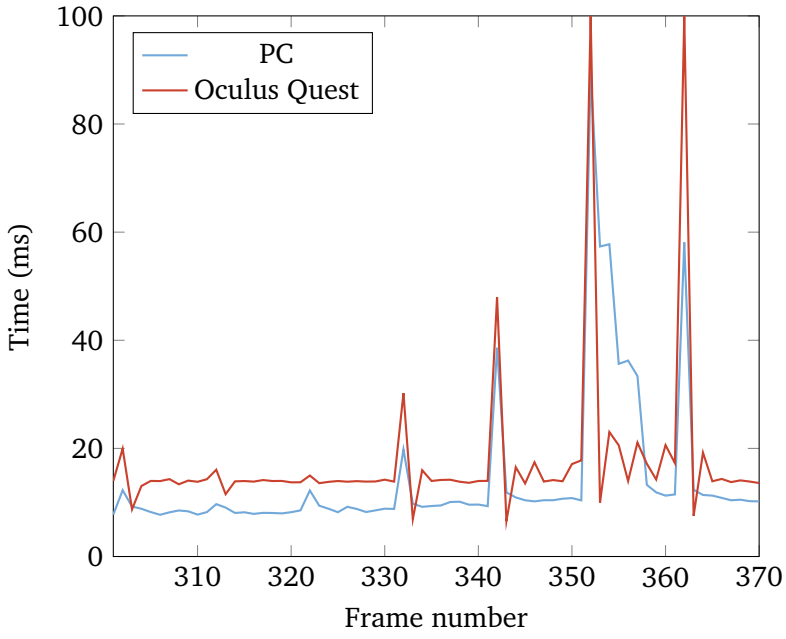


Figure 5.5: Performance running the application in a machine vs on Oculus Quest.

We designed an experiment that we could run in the PC and in the Oculus Quest to measure the performance for each of the machines. In the experiment we run several things at the same time. We used a combination of the three performance experiments that we explained before and use them together for this experiment. For a short period of time we translate the network, scale it

and select several nodes, everything at the same time. The experiment lasts for 70 frames; it starts in frame 300 and ends in frame 370.

In Figure 5.5, we can see the results from the experiment, represented with a graph. The X axis represents the frame number (like a timeline). The Y axis represents the amount of time that a particular frame took to render in milliseconds. We can see that the performance for the Oculus Quest is a bit worse than for the PC; however, the difference is not very big. We can also see some peaks in the graph. This is due to the select node action. We select 7 nodes during the experiment. A new node is selected every 10 frames. The node selection starts in frame 300 with a node that doesn't have many edges and the last node of the experimen (in frame 360 has many nodes). Each new node selected has more edges that the previous one. We can see this refleted in the graph; every 10 frames there is a new picks, starting from frame 330, and this pick is higher. We can say that the number of edges has an impact with the performance.

5.5 Demo and interview

One of the questions that we asked ourselves during the evaluation process was about the comfortability of using BigNext VR to explore a biological network. This is an important aspect when building VR applications. Some of the aspects to take into account are for instance the motion sickness or the intuitiveness. In order to evaluate this we made a questionnaire for bioinformaticians that would test the application. Unfortunately, due to the Covid-19 situtation[5], we were not able to carry out the questionnaire with people. The reason is because it wasn't possible to test GeneNet VR with people on a single Oculus Quest device without avoiding the social distancing rules. We estimated to have around 10 participants with knowdledge in bioinformatics to test the application. With this number of participants we could have made some statistics and obtained feedback for future improvement.

The following questionnaire is divided in four sections; a general section about VR headsets, a section about comfortability exploring the network using GeneNet VR, a section about the different actions in GeneNet VR and finally a section about feedback.

To complete the questionnaire, the teste has to indicate the level of agreement or disagreement with each of the statements, mark yes or no when it is asked and in the feedback section reply the questions with constructive feedback if possible.

6

Conclusion and future work

In this section we will conclude the thesis and describe what we can do to improve the project and the future work.

6.1 Future work

Bibliography

[1] Corey J. Bohil, Bradly Alicea, and Frank A. Biocca. "Virtual reality in neuroscience research and therapy." In: *Nature Reviews Neuroscience* 12.12 (2011), 752–762. DOI: 10.1038/nrn3122.

[2] Evren Bozgeyikli et al. "Point & Teleport Locomotion Technique for Virtual Reality." In: *Proceedings of the 2016 Annual Symposium on Computer-Human Interaction in Play - CHI PLAY 16* (2016). DOI: 10.1145/2967934.2968105.

[3] "Commentary on Rose, F.D., Brooks, B.M., & Rizzo, A.A., Virtual Reality in Brain Damage Rehabilitation: Review." In: *CyberPsychology & Behavior* 8.3 (2005), 263–271. DOI: 10.1089/cpb.2005.8.263.

[4] *Common Format and MIME Type for Comma-Separated Values (CSV) Files*. URL: https://tools.ietf.org/html/rfc4180.

[5] *Coronavirus*. URL: https://www.who.int/emergencies/diseases/novel-coronavirus-2019.

[6] Paul E. Dickson et al. "An Experience-based Comparison of Unity and Unreal for a Stand-alone 3D Game Development Course." In: *Proceedings of the 2017 ACM Conference on Innovation and Technology in Computer Science Education* (2017). DOI: 10.1145/3059009.3059013.

[7] Vanessa Dumeaux et al. "Interactions between the tumor and the blood systemic response of breast cancer patients." In: *PLOS Computational Biology* 13.9 (2017). DOI: 10.1371/journal.pcbi.1005680.

[8] Bjørn Fjukstad et al. "Building Applications for Interactive Data Exploration in Systems Biology." In: *Proceedings of the 8th ACM International Conference on Bioinformatics, Computational Biology,and Health Informatics - ACM-BCB 17* (2017). DOI: 10.1145/3107411.3107481.

[9] Jason Jerald et al. "Developing virtual reality applications with Unity." In: *2014 IEEE Virtual Reality (VR)* (2014). DOI: 10.1109/vr.2014.6802117.

[10] KE. Laver et al. "Virtual reality for stroke rehabilitation." In: *Cochrane Database of Systematic Reviews* 11 (2017). ISSN: 1465-1858. DOI: 10.1002/14651858.CD008349.pub4. URL: https://doi.org//10.1002/14651858.CD008349.pub4.

[11] Oscar Legetth et al. "CellexalVR: A virtual reality platform for the visualisation and analysis of single-cell gene expression data." In: *bioRxiv* (2019). DOI: 10.1101/329102. eprint: https://www.biorxiv.org/

content/early/2019/07/16/329102.full.pdf. URL: https://www.biorxiv.org/content/early/2019/07/16/329102.

[12] Mike May. "LIFE SCIENCE TECHNOLOGIES: Big biological impacts from big data." In: *Science* 344.6189 (2014), pp. 1298–1300. ISSN: 0036-8075. DOI: 10.1126/science.344.6189.1298. eprint: https://science.sciencemag.org/content. URL: https://science.sciencemag.org/content/344/6189/1298.

[13] Matthias Minderer et al. "Virtual reality explored." In: *Nature* 533.7603 (2016), 324–325. DOI: 10.1038/nature17899.

[14] *Oculus Link Compatibility*. URL: https://support.oculus.com/444256562873335/.

[15] *OVRInput*. URL: https://developer.oculus.com/documentation/unity/unity-ovrinput/.

[16] Georgios A. Pavlopoulos et al. "Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future." In: *GigaScience* 4.1 (2015). DOI: 10.1186/s13742-015-0077-2.

[17] Daniel Probst and Jean-Louis Reymond. "Exploring Drugbank in Virtual Reality Chemical Space." In: (2018). DOI: 10.26434/chemrxiv.6629150.

[18] R.a. Ruddle. "The effect of environment characteristics and user interaction on levels of virtual environment sickness." In: *IEEE Virtual Reality 2004* (). DOI: 10.1109/vr.2004.1310067.

[19] Unity Technologies. *Line Renderer*. URL: https://docs.unity3d.com/Manual/class-LineRenderer.html.

[20] Unity Technologies. *ParticleSystem*. URL: https://docs.unity3d.com/ScriptReference/ParticleSystem.html.

[21] Unity Technologies. *Prefabs*. URL: https://docs.unity3d.com/Manual/Prefabs.html.

[22] *Testing and Performance Analysis*. URL: https://developer.oculus.com/documentation/unity/unity-perf/?device=QUEST.

[23] David A. Thorley-Lawson, Karen A. Duca, and Michael Shapiro. "Epstein-Barr virus: a paradigm for persistent infection – for real and in virtual reality." In: *Trends in Immunology* 29.4 (2008), 195–201. DOI: 10.1016/j.it.2008.01.006.

[24] *Unity 2018.4.10*. URL: https://unity3d.com/unity/whats-new/2018.4.10.

[25] *Unity Integration*. URL: https://developer.oculus.com/downloads/package/unity-integration/1.29.0/.

[26] *Welcome to VRTK · VRTK - Virtual Reality Toolkit*. URL: https://vrtoolkit.readme.io/docs/summary.

[27] Samuel T. Westreich, Maria Nattestad, and Christopher Meyer. "BigTop: A Three-Dimensional Virtual Reality tool for GWAS Visualization." In: (2019). DOI: 10.1101/650176.

[28] James Xia et al. "Three-dimensional virtual-reality surgical planning and soft-tissue prediction for orthognathic surgery." In: *IEEE Transactions*

on Information Technology in Biomedicine 5.2 (2001), 97–107. DOI: 10.1109/4233.924800.

[29] Yuting Yang et al. "Integration of metabolic networks and gene expression in virtual reality." In: *Bioinformatics* 21.18 (July 2005), pp. 3645–3650. ISSN: 1367-4803. DOI: 10.1093/bioinformatics/bti581. eprint: http://oup.prod.sis.lan/bioinformatics/article-pdf/21/18/3645/520673/bti581.pdf. URL: https://doi.org/10.1093/bioinformatics/bti581.

[30] Jimmy F Zhang et al. "BioVR: a platform for virtual reality assisted biological data integration and visualization." In: (2018). DOI: 10.1101/307769.

[31] Jimmy F. Zhang et al. "BioVR: a platform for virtual reality assisted biological data integration and visualization." In: *BMC Bioinformatics* 20.1 (2019). DOI: 10.1186/s12859-019-2666-z.