

MetNetVR (simplified version for the paper submitted to bioinformatics)

The included MetNetVR and all support libraries are for linux. We already test them in RedHat Fedora Core 1 and Suse. The application runs in simulation mode, instead of in Virtual Reality platforms.

1 Prerequisite

1.1 OpenSG

Decompress the OpenSG library OpenSG.tar.gz using 'gunzip' and 'tar'. It contains a directory called 'opt'. Copy the whole directory into some place, e.g. '/usr/local/lib', and set the environment variable LD_LIBRARY_PATH. Below are the commands in C shell

```
setenv LD_LIBRARY_PATH ${LD_LIBRARY_PATH}:/usr/local/lib/opt
```

You can also download the OpenSG library from <http://www.opensg.org/>

1.2 VRJuggler

Download VRJuggler library from http://www.vrjuggler.org/vrjuggler/download-2_0.php#linux

You can decide the platforms (RedHat 8.0 plus GCC3.2, Fedora Core 1 plus GCC 3.3, Fedora Core 3, GCC 3.4, or SuSE 9.1)

Put the downloaded two files somewhere, e.g. '/home/vr/Juggler/2.0', and decompress using 'bunzip2' and 'tar'. If your platform is Fedora Core 1 plus GCC 3.3, these two files will be vrjuggler-2.0-beta2.linux-fc1.tar.bz2, and vrjuggler-2.0-beta2.linux-fc1-deps.tar.bz2

Set the environment variable VJ_BASE_DIR, VJ_DEPS_DIR, and LD_LIBRARY_PATH. Below is the commands in C shell

```
setenv VJ_BASE_DIR /home/vr/Juggler/2.0/vrjuggler-2.0-beta2.linux-fc1
setenv VJ_DEPS_DIR /home/vr/Juggler/2.0/vrjuggler-2.0-beta2.linux-fc1-deps
setenv LD_LIBRARY_PATH ${LD_LIBRARY_PATH}:${VJ_BASE_DIR}/lib/i686/opt
setenv LD_LIBRARY_PATH ${LD_LIBRARY_PATH}:${VJ_DEPS_DIR}/lib
```

1.3 R

Decompress the R library R.tar.gz using 'gunzip' and 'tar'. It contains a directory called 'R'. Copy the whole directory into some place, e.g. '/usr/local/lib', and set the environment variable LD_LIBRARY_PATH, R_HOME, and R_LIBS. Below are the commands in C shell

```
setenv R_HOME /usr/local/lib/R
setenv LD_LIBRARY_PATH ${LD_LIBRARY_PATH}:${R_HOME}/bin
setenv R_LIBS ${R_HOME}/library
```

You can also download R from <http://www.r-project.org/>

2 Run MetNetVR

2.1 Decompress MetNetVR.tar.gz using 'gunzip' and 'tar'. It contains a directory called MetNetVR

2.2 Go to the directory MetNetVR, use the command './runMetNetVR.sim' to run the system. Initially you will see for 4 windows

'SimWindow1': The main window for the application in simulation mode

'Wand Event Window': The Window to control the simulated wand device. In the real VR mode (opposite to the simulation mode), the wand device has 6 buttons and contains position and orientation information. All the buttons, position and orientation are simulated and controlled by Wand Event Window. The 6 buttons are labeled as 0, 1, 2, 3, 4, and 5. They are simulated by left, middle, and right buttons of the mouse and number key 3, 4, and 5 of the keyboard. Here we will use button0, button1, ..., button5 to call them.

'Head Event Window': The window to control the simulated head position and orientation of user

'Sim View Cameras Control': The window to control the Camera(viewpoint) position and orientation for rendering

You can omit 'Head Event Window' and 'Sim View Cameras Control' for the following reasons

- 1) In the real VR mode, these are controlled by the sensors attached to the user. In the simulation mode, their default values are already set for them.
- 2) All the users interaction are done by the wand device

2.3 Navigation and interactions

In the middle of SimWindow1, there is a ball (light blue) to simulate the user's head. There is a green gadget to simulate the wand; the red line casting from the wand is to indicate the orientation of the wand and do intersection with virtual objects.

In the SimWindow1, there are 3 virtual scenes; bottom left is the profiles for gene clusters; button right is the profiles for the genes for the currently selected cluster; and top is the metabolic network.

We use level-of-detail based on the distance between virtual objects and the user's viewpoint to accelerate rendering. The labels for nodes in the scene of the metabolic network will not appear until they are close to the user.

2.3.1 Navigation through the virtual scenes

Step 1) Put the mouse in 'Wand Event Window', press Ctrl and move mouse to control the orientation of wand.

Step 2) Press button0 (left button of mouse) to move forward along the wand orientation.

Step 3) Put the mouse in 'Wand Event Window' and press button3 (number 3 in keyboard) to turn left

Step 4) Put the mouse in 'Wand Event Window' and press button5 (number 5 in keyboard) to turn right

2.3.2 Switch layout between Gem3D and weighted Gem3D

Put the mouse in 'Wand Event Window'. Press button1, keep it pressed and then press button2. The buttons' status is

button1: On

button2: Toggle_on

All other buttons are Off

(There are 4 status for a button, On, Off, Toggle_on and Toggle_off)

2.3.3 Select a metabolite and display the reactions this metabolite takes part in

Step 1) Move to one of metabolites (yellow spheres in the top scenes).

Step 2) change the orientation of the wand according to the method in Step 1) of section 2.3.4 so that the red line casting from the wand intersects with the yellow sphere representing the metabolite of interest.

Step 3) Press button1 to do the selection. The buttons' status is

button1: Toggle_on
All other buttons are Off

Step 4) Press button1, keep it pressed and then press button5 to invoke the drawing of reactions the selected metabolite takes part in. The buttons' status is

button1: On
Button5: Toggle_on
all other buttons are Off

If you feel uncomfortable to do the intersection in simulation mode in Step 2 and 3 (It is much better in stereoscopic mode), we already chose a metabolite (also a gene, see section 2.3.4). You can use this one by press button4. The buttons' status is

button4: Toggle_on
All other buttons are Off

Then go to Step 4) do invoke the drawing

2.3.4 Select a gene from the gene profiles and display the reactions this gene takes part in

Step 1) Move to one of the connected lines representing the profiles of a gene (in the bottom right scene). In each gene's label, under the gene name, there is a word 'available' or 'unavailable'. This word indicates whether this gene is present in the currently loaded metabolic network. You need to choose a gene which is present.

Step 2) change the orientation of the wand according to the method in Step 1) of section 2.3.4 so that the red line casting from the wand intersects with any part of the connected line representing the gene profile.

Step 3) Press button1 to do the selection. The buttons' status is

button1: Toggle_on
All other buttons are Off

Step 4) Press button0, keep it pressed and then press button4 to invoke the drawing of reactions the selected gene takes part in. The buttons' status are

button0: On
Button4: Toggle_on
All other buttons are Off

If you feel uncomfortable to do the intersection in simulation mode in Step 2 and 3 (It is much better in stereoscopic mode), we already chose a gene (also a metabolite, see section 2.3.3). You can use this one by pressing button4. The buttons' status is

Button5: Toggle_on
all other buttons are Off

Then go to Step 4) do invoke the drawing

2.3.5 Select a gene from the gene profiles and pull out reactions this gene takes part in by animation

If you we already selected a current gene as describe in section 2.3.8, press button2 to invoke the animation. The buttons status is

button2: Toggle_on
All other buttons are Off

2.3.6 Select the current gene cluster to display

Step 1) Move to one of the connected lines representing the profiles of gene clusters (in the bottom left scene). You need to choose a cluster to be the current cluster to display (Initially it is the first cluster).

Step 2) change the orientation of the wand according to the method in Step 1) of section 2.3.4 so that the red line casting from the wand intersects with any part of the connected line representing the cluster profile.

Step 3) Press button1 to do the selection. The buttons' status are

button1: Toggle_on
all other buttons are Off

The bottom right scene will automatically change to the profiles for the genes of the select cluster.

Thank you!