Setting Up FracMap and Mishchenko's T-matrix Code

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1 I. Installing FracMap

First, go to `http://lasso.dri.edu/fracmap/` and download the source code for Microsoft Visaul Studio 2010 package. After downloading, you will get .zip file. Within this file, there is a file called unix-fractal, this is the file you are going to use. Navigate to through the unix-fractal file until you find a file called main.cpp. Replace this main.cpp with the modified version, you can get the modified version by email me *aldahlaw@seattleu.edu* or email your advisor Dr. Boness. Next, open up a terminal window. This could be done by using the search bar in unix machines and search for an application called terminal. After doing so, you will get a window which is similar to $figure1$ below.

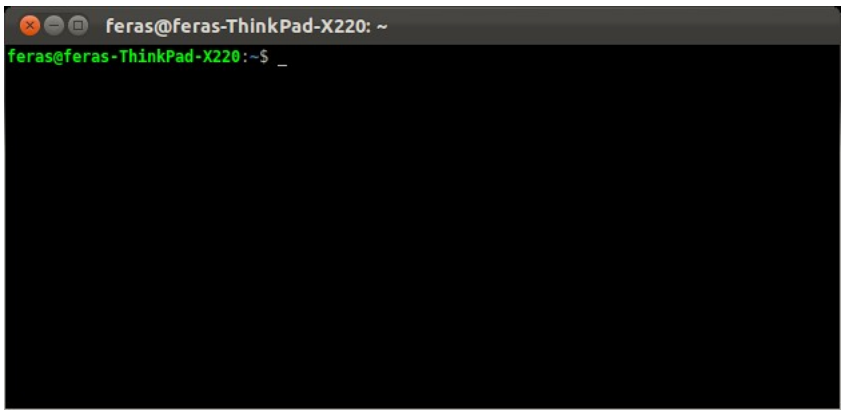

Figure 1: Linux/Ubuntu terminal window

Notice that you will have a different name than mine. Currently, I am in my home directroy. Type **cd** and hit **enter** to go to the home directory. Once you are in your home directroy, navigate to your unix-fractal folder using the change directory command **cd**. Just type **cd #next-dirctory**. If you do not know which files/directories are in the current directory type **ls** to show you a

list of possible directories to move to from your current directory. e.g. If you want to go to your desktop,desktop is where I save my FracMap folder, type **cd Desktop**. Note that the commands are case sensetive.

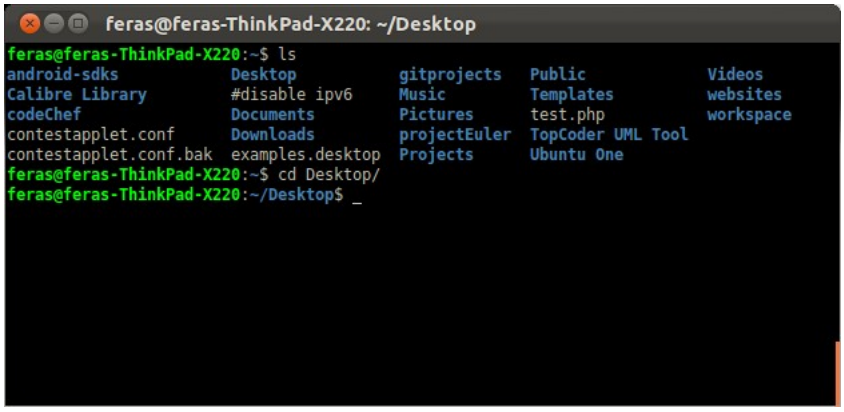

Figure 2: navigating to Desktop

Now you are in your desktop, or whatever you choose to navigate to. From Deskto, type ls again to see files/folders available in the Desktop. Type **cd wxFracMap** to navigate to the wxFracMap folder. Then type **cd unix_ fractal**

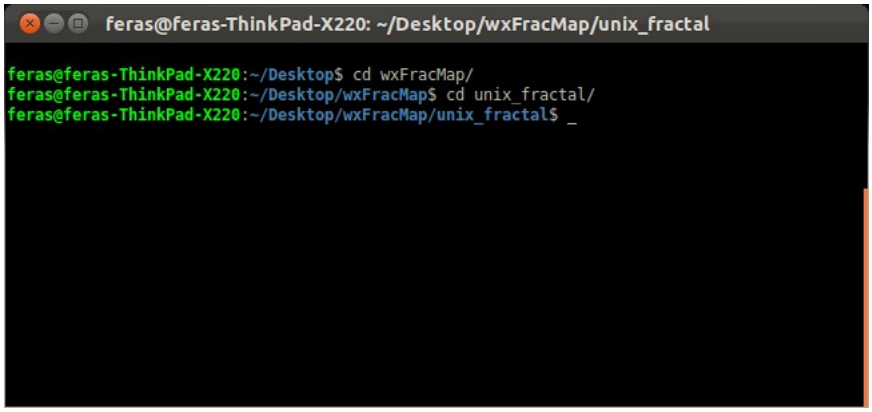

Figure 3: navigating to unix_ fractal

Once you are in unix_ fractal, build the source code by type **make**. Wait a few seconds until the project has been built. You will notice a new executable file called **fractal** is been created. To run this executable file, type **./fractal #fractal-dimension #prefactor #number-of-monomers** Where fractal-dimension is a number between 1.0 and 2.0. prefactor is any floating point number greater than 0, and number of monomers is an integer greater than 0. e.g. **./fractal 1.83 2.0 8**. the output shown in the figure below.

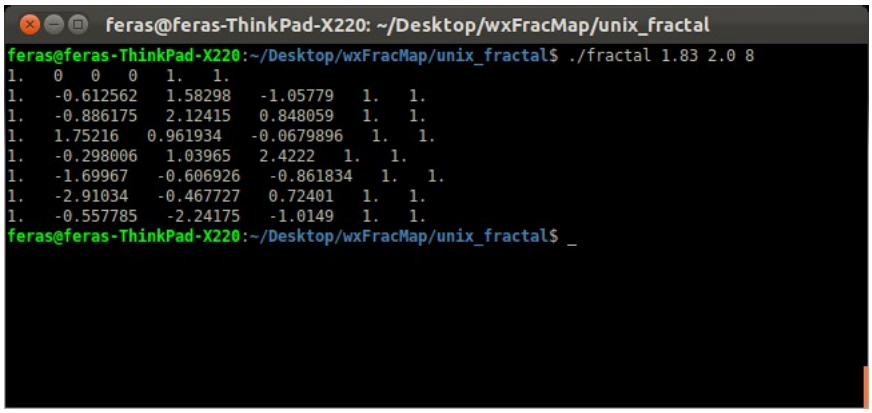

Figure 4: trial run of FracMap

Congratulations! you have FracMap set up on you Unix machine.

2 II. Installing and setting up Mishcheko's T-matrix code

go to `http://eng.auburn.edu/users/dmckwski/scatcodes/` and downloads the files. Copy all the files and place it in the unix_ fractal folder. This is important to avoid complication in automating the process of generating and analyzing fractals using two different programs. After doing so, open the terminal window and navigate to the unix_ fractal directory. (see section I for more information on how to do this). Run the command to build the mstm source code. After running the command, you will notice a new file called mstm.out. This is the executable file for the mstm code. Go ahead and try out the mstm program. Note that you have to give it an input file as an argument otherwise it will provide default value. Type the command **./mstm.out mstm.inp**. Read the MSTM manual to understand the arguments in the input file.

Congratulations! you have MSTM code set up and running on your machine.

3 III. Automation

Since we will look at a huge amount of data, it is good to have an automation mechanism to avoid the tedious and error prone human interaction. Remember when you replace main.cpp file with the revised main.cpp? The only modification done is that the program will output the position of the monomers instead of unrelated data. Inorder to redirect the output to a file, run the command **./fractal #fractal-dimension #prefactor #number-of-monomers ¿¿ #output-filename.txt**. e.g. **./fractal 1.50 7.0 100 ¿ positions.pos** (Note the .pos extension). In *positions.pos* you will find the position of the

monomers created by FracMap. Now ,in msmt.inp file, make sure that you have the sphere_ position_ file is equal to you .pos file name. Changing eaither you output file name of the entry under sphere_ position_ file will do the trick. After that, create a scripot file with extension .sh. You can name it anything you want, I named it script.sh. In this script file, add the following lines of code:

```
#!bin/bash
./fractal 1.0 3.0 70 > positions.pos
./mstm.out mstm.inp
```

Note that this script has to be in the same folder as FracMap and MSTM. In order to make this shell script executable, run the command **chmod +x script.sh**. This will allow you to run the script from the terminal window. Go ahead and try it out by typing **bash script.sh** in you terminal window. This script will run fractal program and then pass the output to mstm.out to be analyzed. Read more about bash scripting to caputer the power of automating the analysis of the data.

if you have any further question, just email me at *aldahlaw@seattleu.edu*.