

Brain Explorer for Connectome Analysis (BECA) Software Manual (Genome Explorer)

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1. Launch the application

Double click on the BECA icon as shown in Figure 1.

If nothing shows up, you may need to launch it in compatible mode by following steps shown in Figure 2:

- a. Right click on the BECA icon and select 'Properties'
- b. Select 'Compatibility' tab
- c. Check 'Run this program in compatibility mode for' and then select 'Windows 7' in the combo box below.
- d. Click the 'OK' button and try to run it again.



Figure 1. BECA application icon

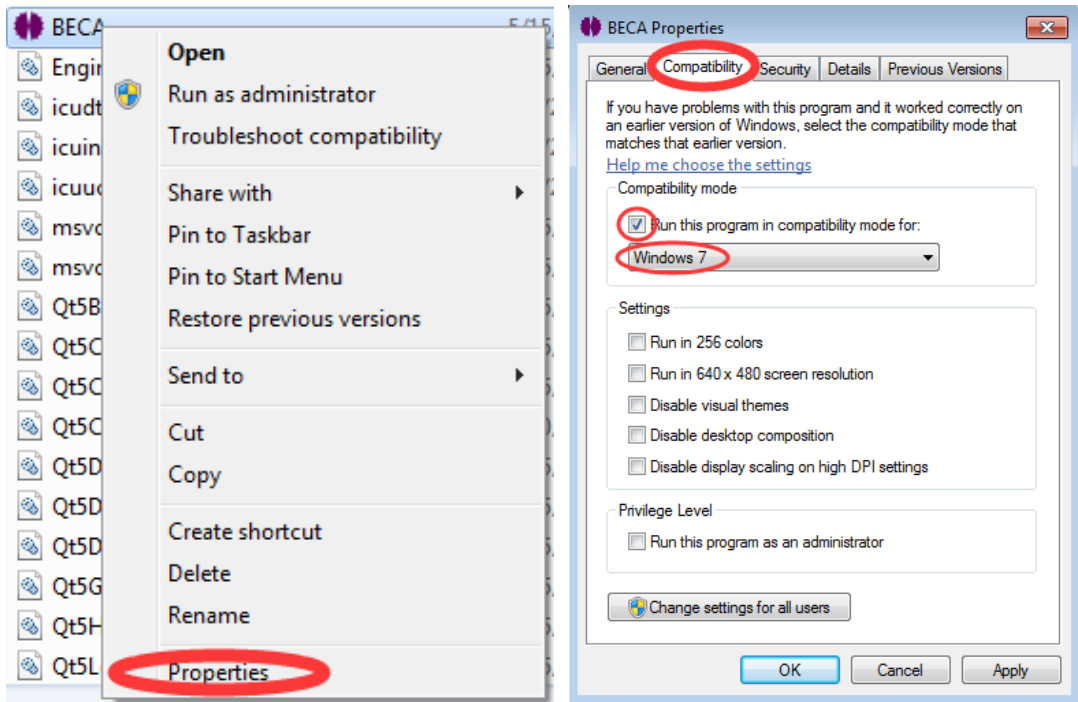


Figure 2. Run it in compatible mode

2. Launch the CUDA server

***A NVIDIA graphic card is required to run the CUDA server**

Launch the CUDA server by double clicking 'BECAServer.bat'. A window will show up with information about the NVIDIA graphics card that the server is currently using, as shown in Figure 3.

```
C:\WINDOWS\system32\cmd.exe

C:\Users\Huang\Desktop\BECA\Release>BServer.exe
Basic GPU Server is running ...

** GeForce GTX 1080 present.
    Major = 6, Minor = 1
```

Figure 3. CUDA GPU server is running

3. Load genotype, phenotype and MRI data

Follow the steps in Figure 4 to load the genotype (genotype.txt) and phenotype (phenotype.bin) data in 'example_data' folder.

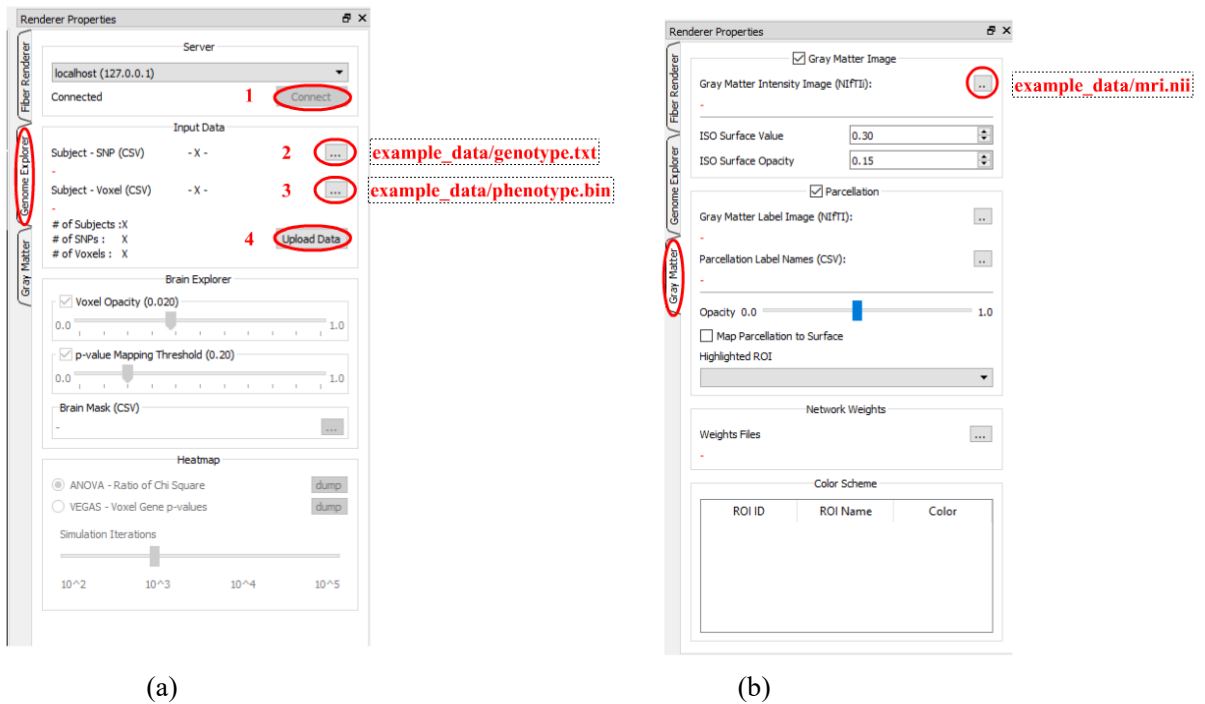


Figure 3. (a) Loading genotype and phenotype data. (b) Loading MRI data

4. Explorer data in genome explore

The user interface is shown in Figure 4. In the lower left-hand corner, a 3-dimensional model of a reference brain is displayed, color-mapped with the ANOVA of the association between each voxel and the current SNP or gene. At the top of the user interface is the SNP explorer. This region displays the $-\log_{10}(\text{p-value})$ of the association between each SNP or gene and the current voxel.

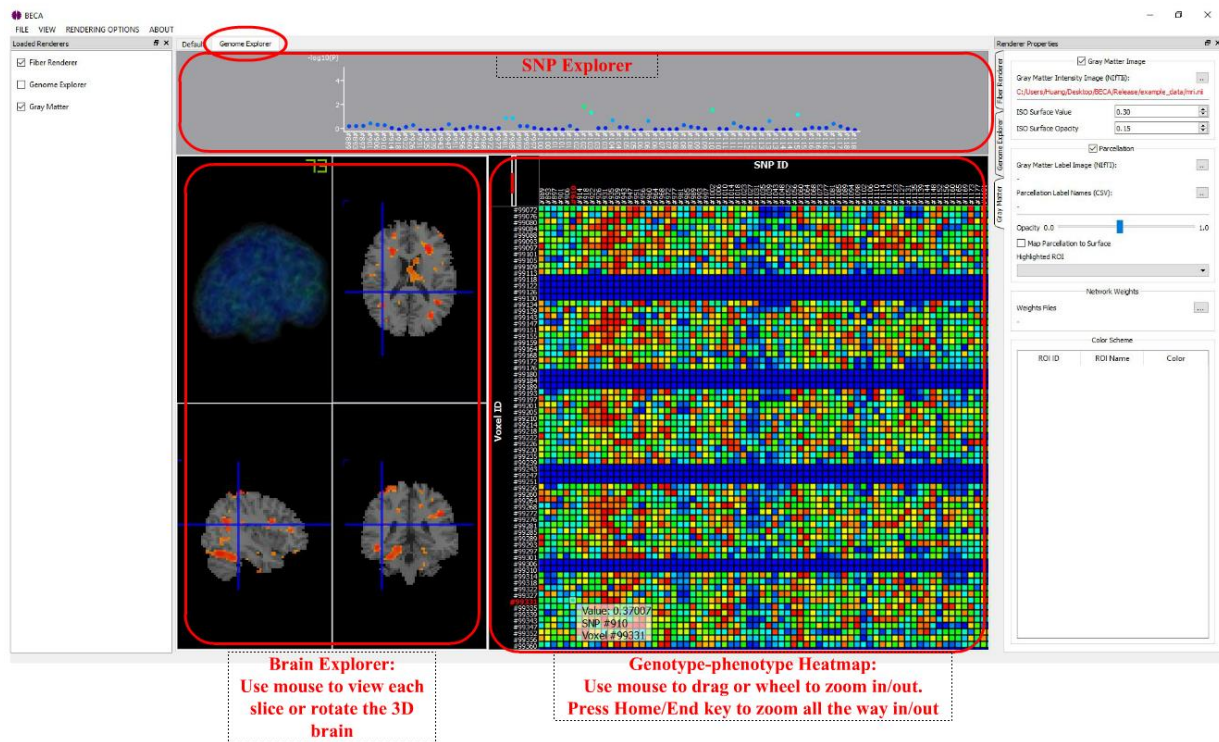


Figure 4. User interface for the neuroimaging genome browser, which consist of SNP explorer (top), brain explorer (bottom left), and heat map (bottom right).

Appendix

Input data format

If you want to use the genome explorer with custom data instead of the example data, you can prepare your data in the following format.

Genotype data: (example_data/genotype.txt)

You can load this file with Excel. Each row is a subject, and each column is a SNP

Phenotype data: (example_data/phenotype.bin)

This file is a N by M matrix in binary format. The first 8 bytes are two 32bit integers indicating the number of subjects (N) and the number of measurements (M) for each subject, which is followed by NxM 32bit float-point numbers. The matrix is written in row major format.