Graphical user interface for vonBertalanaffy User Manual.

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Tutorial

This is a GUI (Graphical user interface) for the vonBertalanffy toolbox.

Open the vonBertalanaffy interface by typing

```
> > vonBertalanffy
```

in the Command Window.

On the initial screen, as shown in figure **??**, are 4 buttons grouped together on the left. You start interacting with the button in the upper-left corner, then progress to the other three buttons below it.

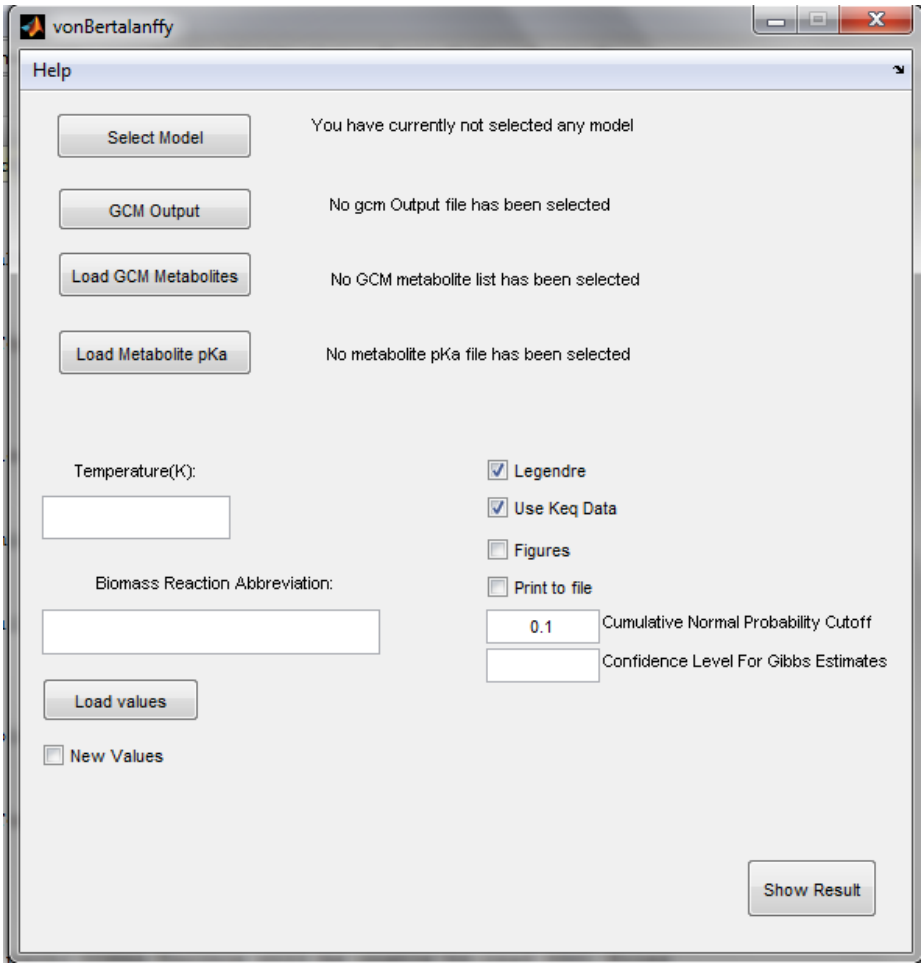

Figure 1: This is how the inital interface should be.

The first step is to select the model that we will be using. The model is a MATLAB structure array, created through the rBioNet package.

In this tutorial we will use an already existing model, available with the original console program.

By pressing the buttons a selection menu opens as shown in figure ?? where model and text files can be browsed and selected. Each button loads in one file. In this example we will use the Recon1 human network.

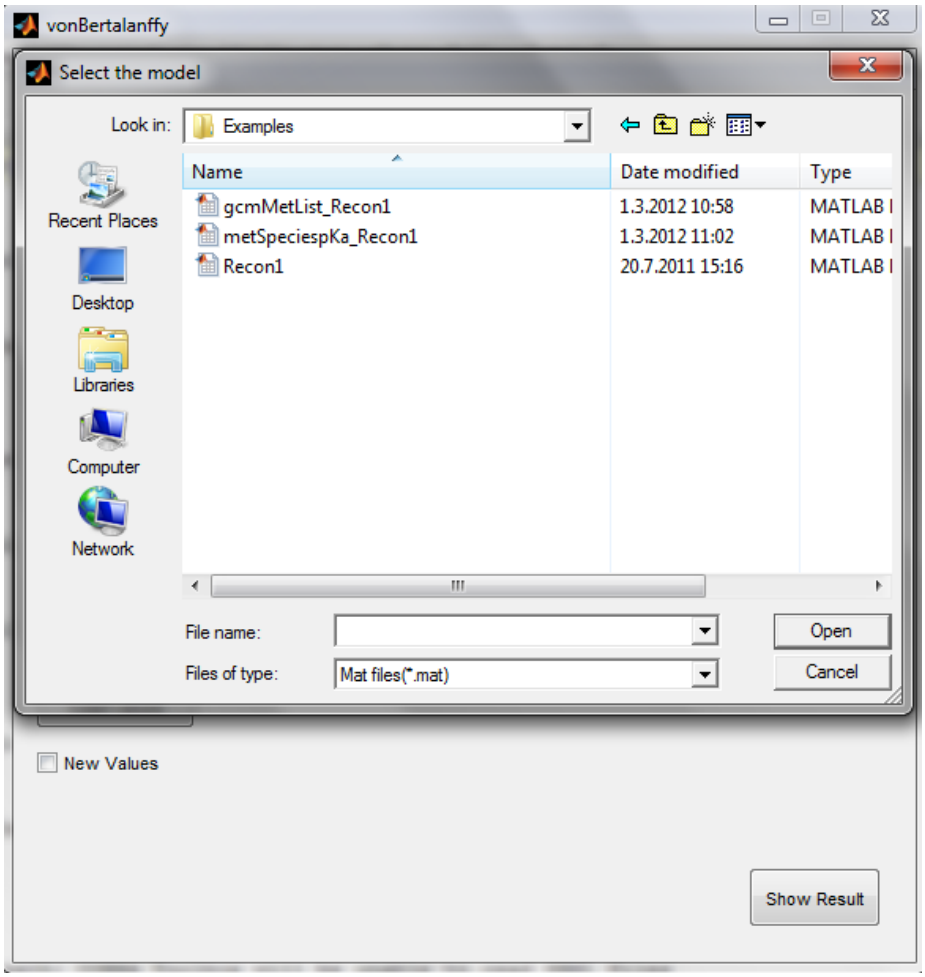

Figure 2: When the buttons in the right-left corner are pressed a selection menu opens where models and text files can be selected.

Every time a file is loaded, the text on the right changes to indicate that, and to remind you of which file you selected. The same is done for all 3 buttons. In total we find and load each of the following files:

Recon1.mat

gcmMetListRecon1.mat

metSpeciespKa-Recon1.mat

gcmOutputFile-Recon1.txt

Now a constant temperature is chosen. It is also necessary to know the abbreviation used for the biomass reaction. Lets choose the temperature 310.15 K. The biomass reaction abbreviation in this example is *biomass reaction*. The next step is to add in values for the ionic strength, pha and electronegativity of different chemicals.

There are two ways how to add these values in. One is to save the lines into a plain text file and load them with the "Load Values" button. The other is to check the checkbox "New Values" and then type in the abbreviation and value for each line and press *Add*. After typing in all the values that will be used the *Save values* button is pressed and a text file is created. The text file is then loaded in as the first method indicates.

In figure **??** is shown the second method in action. We are adding the pha value for c, which is suppose to be 7.2:

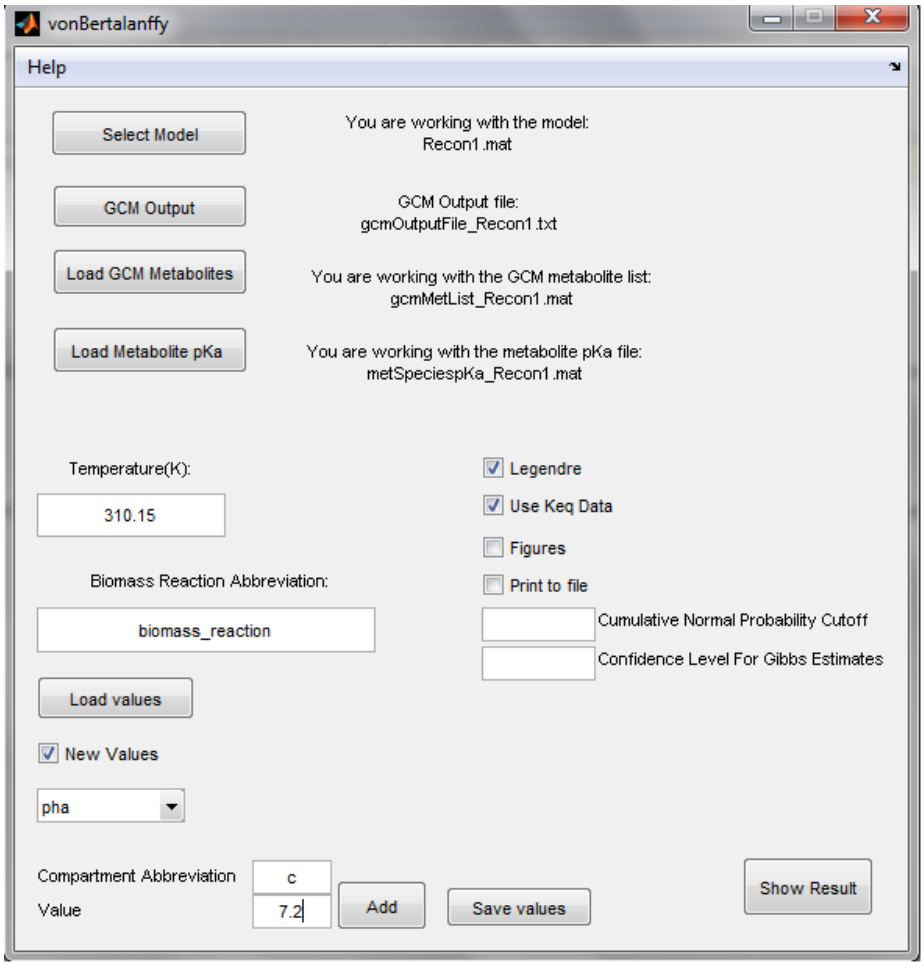

Figure 3: Temperature chosen, Biomass Reaction Abbrevation written and a value added for pha.c

In this tutorial we will check all the 4 checkboxes on the right and we will use the value 2 for the Cumulative normal probability cutoff and the value 0.2 for the Standard Deviation Group Contribution value. Now the screen should look like figure **??**

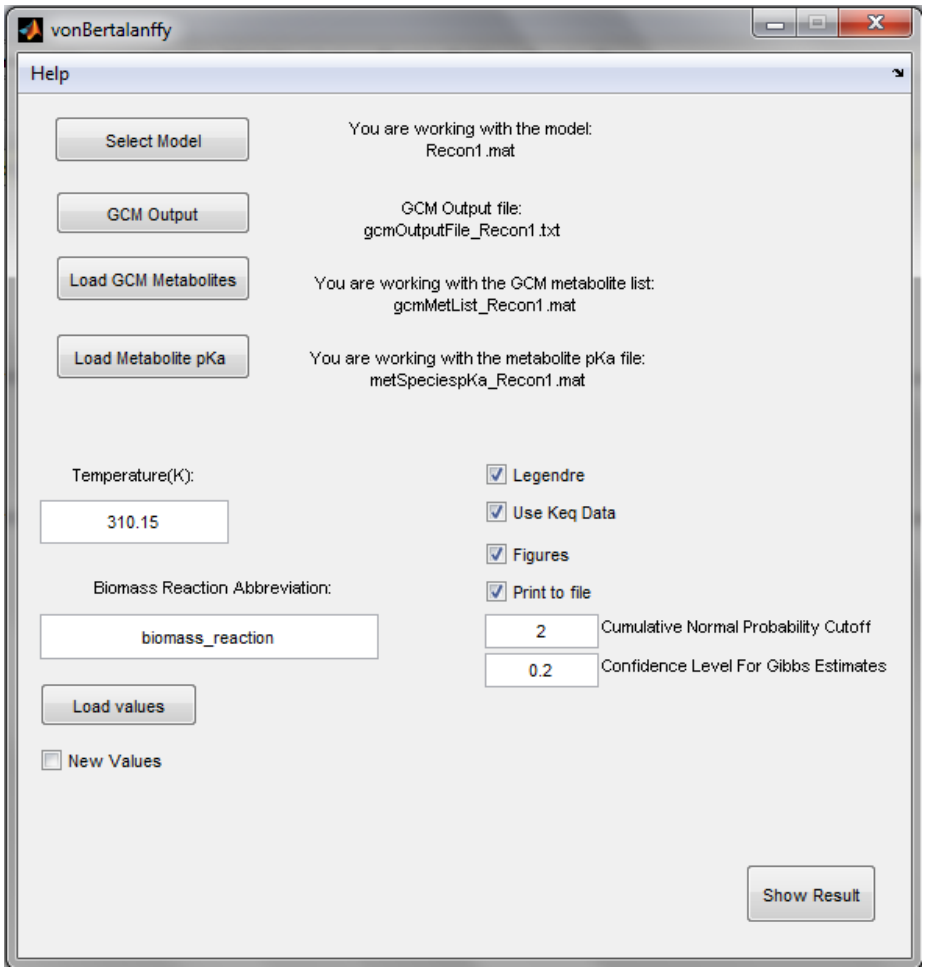

Figure 4: All the data has been registered and next the *Show Result* button is pressed

After this is done, we press the Show Result button. Now the console program will execute. You can keep track of the progressing of the program by watching output data in the matlab console. The console program will produce 24 graphs after the analysis is done.