

How to run NATALIE:

Here's where to find the binary file and codes for NATALIE. Everything is already compiled and you only need to run it.

All the files	/extra/wayne0/preserve/pashak/natalie
Binary	/extra/wayne0/preserve/pashak/natalie/build

The following line runs **NATALIE** on human and yeast networks. Replace 'human' or 'yeast' with the name of other wanted networks. Also replace 'output' with the wanted file name for the output file.

```
./natalie -if1 5 -if2 5 -r 1 -o output -g1 human.gw -g2 yeast.gw
```

Here are some of the most useful arguments for us:

```
-h    Help
-n    number of iterations to compute (default: -1 : no limit)
-t    time limit (wall) in seconds (default -1: no limit)

-if1  input file type for input 1 (5 is LEDA)
-if2  input file type for input 2
-o    output file name
-g1   first input name
-g2   second input name
-r    what relaxation to use
      0    $O(n^4)$  will not be practical for our networks
      1    $O(n^3)$ 
-sf   Specifies what score function to use (use -h for more details)
```

For more help on the arguments visit the following website. Note that the binary on the website is not update, so use the help in the binary file provided for the latest list of arguments.

<http://www.mi.fu-berlin.de/w/LiSA/Natalie>

And this is the link to the source code on GitHub <https://github.com/ls-cwi/natalie>. There was some problems with the LEDA parser so I have edited the code to fix the problem.