

The program is written in C and is provided as source files. The source files must be compiled to produce the simulation program. We mainly used Intel C compiler (icc, version 16.0.4), but the GNU C compiler (gcc) will also work (although the outcome of a simulation will change due to different optimization to numerical calculations).

Installation (Run the default mode)

By default, the program evolves TRNs under selection for filtering out a short spurious signal, and allows the signal to regulate the effector directly. The program runs on 10 CPU cores (Haswell V3 28 core processor), and usually takes 1-3 days.

We suggest using a Linux system to facilitate the installation. To run the program in the default mode, follow these steps:

1. Copy all source files (files with suffix .c and .h, and the *makefile*) to one directory.
2. Under the same directory, create a folder and name it **result**. The folder will be used to hold output files.
3. Change directory into the directory that contains the source file. Compile source files using the command

```
make simulator CC=icc
```

This command will create several files with suffix `.o` and an executable program named `simulator`. “`CC=icc`” compiles the source files with `icc`. The default compiling option is `-O3` for simulation speed, and `-fp-model precise` `-fp-model source` to ensure arithmetic operations are accurate and reproducible.

To compile with `gcc`, change “`CC=icc`” to “`CC=gcc`” and comment out `-fp-model precise` `-fp-model source` in *makefile*. We have noticed that when compiled with `gcc`, the simulation produces result different from when compiled with `icc`. Enabling safe arithmetic options in `gcc` may solve the problem, but we haven’t tested it.

4. Execute simulator to start. On Linux, this is done with the following command

```
./simulator
```

Output

The simulation will generate several files when it begins to run. The size of some files, e.g. `evolutionar_summary_5.txt`, will keep increasing. Samples of output files and a description to their content can be found in folder **output_sample**.

Run neutral evolution

Neutral evolution is simulated with one CPU and finishes in minutes. To enable this mode, modify line 33 of netsim.h to

```
#define NEUTRAL 1
```

Then compile the source file and run the simulator.

Make selection condition for signal recognition

The selection condition is specified in main.c. By default, the program selects for filtering out a short spurious signal. To create selection for signal recognition, modify line 118 - 127 of main.c to

```
selection.env1.signal_on_strength=1000.0;
selection.env1.signal_off_strength=0.0;
selection.env2.signal_on_strength=1000.0;
selection.env2.signal_off_strength=0.0;
selection.env1.signal_on_aft_burn_in=1;
selection.env2.signal_on_aft_burn_in=1;
selection.env1.t_signal_on=200.0;
selection.env1.t_signal_off=0.0;
selection.env2.t_signal_on=0.0;
selection.env2.t_signal_off=200.0;
```

If the signal is not allowed to directly regulate the effector (see Additional settings), a burn-in condition of evolution is required. To enable burn-in, set line 260 of main.c to

```
burn_in.MAX_STEPS=1000;
```

and line 171 to

```
selection.MAX_STEPS=51000;
```

Also set line 242 – 251 to

```
burn_in.env1.signal_on_strength=1000.0;  
burn_in.env1.signal_off_strength=0.0;  
burn_in.env2.signal_on_strength=1000.0;  
burn_in.env2.signal_off_strength=0.0;  
burn_in.env1.signal_on_aft_burn_in=1;  
burn_in.env2.signal_on_aft_burn_in=1;  
burn_in.env1.t_signal_on=200.0;  
burn_in.env1.t_signal_off=0.0;  
burn_in.env2.t_signal_on=0.0;  
burn_in.env2.t_signal_off=200.0;
```

Output expression levels of genes over time

This mode samples the concentration of proteins over time. It uses the `accepted_mutations_x.txt` file of a previous simulation to replay evolution, and reproduce the genotype at a given evolutionary step. To enable this mode, following these steps:

1. Modify line 34 of `netsim.h` to

```
#define PHENOTYPE 1
```

2. Copy `accepted_mutaton_5.txt` file (see folder **output_sample**) to `result`.

3. Modify line 171 of `main.c`

```
selection.MAX_STEPS=n;
```

The network that evolves at evolutionary step `n` will be reproduced.

4. Compile the source code and run the simulator

This mode can be run on one or multiple CPUs and finishes in minutes. The program runs replicate of developmental simulation under environment A and B, and samples instantaneous fitness and protein concentrations during simulation. The default sampling interval is 1 minute in developmental time. See **readme_output.pdf** in folder **output_sample** for the output files.

Run perturbation analysis

In this mode, the program replays mutation and attempt perturbation on TRNs at the given evolutionary steps. The program will exclude a TRN if it is not suitable for the perturbation. If a TRN can be perturbed, the program calculates the fitness before and after the perturbation. To enable the perturbation mode, following these steps:

1. Modify line 35 of netsim.h to

```
#define PERTURB 1
```

2. Specify the type of perturbation in line 63 – 68 of netsim.h.

Example 1: converting AND-gated isolated C1-FFLs to fast-TF-controlled isolated C1-FFLs by adding a strong binding site

```
#define WHICH_MOTIF 0
#define WHICH_CIS_TARGET 0
#define WHICH_TRANS_TARGET 1
#define ADD_TFBS 1
#define ADD_STRONG_TFBS 1
```

Example 2: convert AND-gated FFL-in-diamonds to AND-gated isolated diamonds

```
#define WHICH_MOTIF 1
```

```
#define WHICH_CIS_TARGET 2
#define WHICH_TRANS_TARGET 1
#define ADD_TFBS 0
#define ADD_STRONG_TFBS 1
```

3. Copy *accepted_mutation_x.txt* file and *evo_summary_x.txt* to result.
4. By default, the program tries to perturb TRNs at the last 10,000 evolutionary steps. Line 171 of `main.c` specifies the last evolutionary step to modify, and line 416 of `netsim.c` specifies the number of evolutionary steps to modify.
5. Compile the source files and run simulator.

Because the program needs to measure the fitness of many TRNs, it is recommended to run the program with multiple CPUs. See **readme_output.pdf** in folder **output_sample** for the output files.

Additional settings

1. Change random number seed

Random number seed is set at line 37 of `main.c`. It mainly controls the initial genotypes.

2. Change the number of parallel

threads

By default, the program runs on 10 threads. To change, modify line 41 of netsim.h. Note that N_REPLICATES (line 42 of netsim.h) must be divisible by N_THREADS!

3. Direct regulation of signal to effector

By default, the program allows the signal to evolve to directly regulate the effector. To disable this, change line 56 of netsim.h to 1. Burn-in is recommended if direct regulation is not allowed.

4. Penalty of undesirable effector

By default, the effector is harmful if expressed in a wrong environment. To remove the harm (the cost of expressing the effector still applies), set 162 of main.c to 1.

5. Count near-AND-gated motifs

By default, near-AND-gated motifs are not counted. Set line 74 of netsim.h to count them. Note that counting near-AND-gated motifs is available only when PHENOTYPE = 1.

6. Excluding weak TFBSs when

scoring motifs

By default, TFBSs with up to 2 mismatches are included when scoring motifs. Line 82 - 85 of `netsim.h` set the maximum number of mismatches in a TFBS.