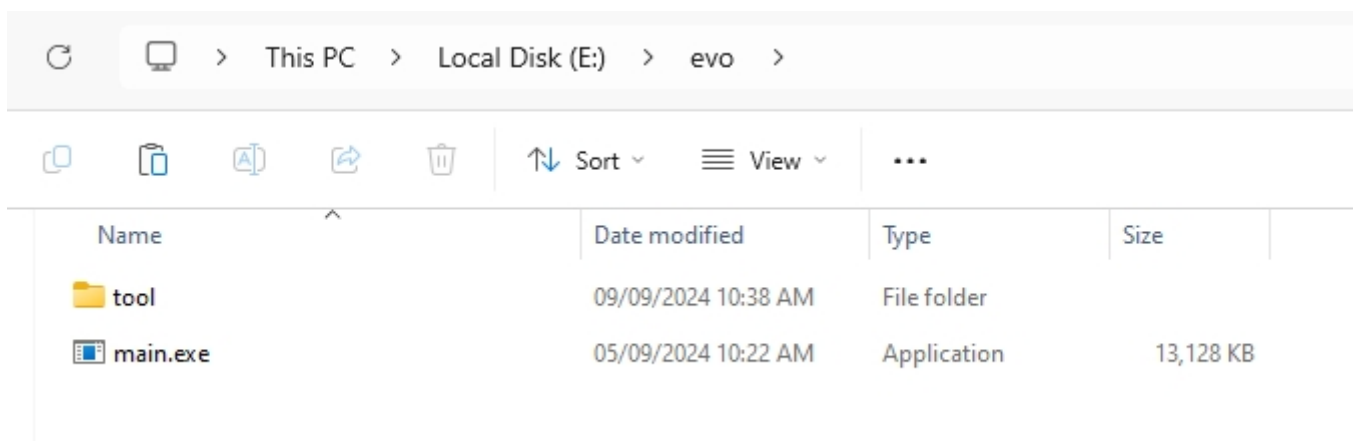


# 4x4 Gene-Type BitLife Hackathon Must Read Script

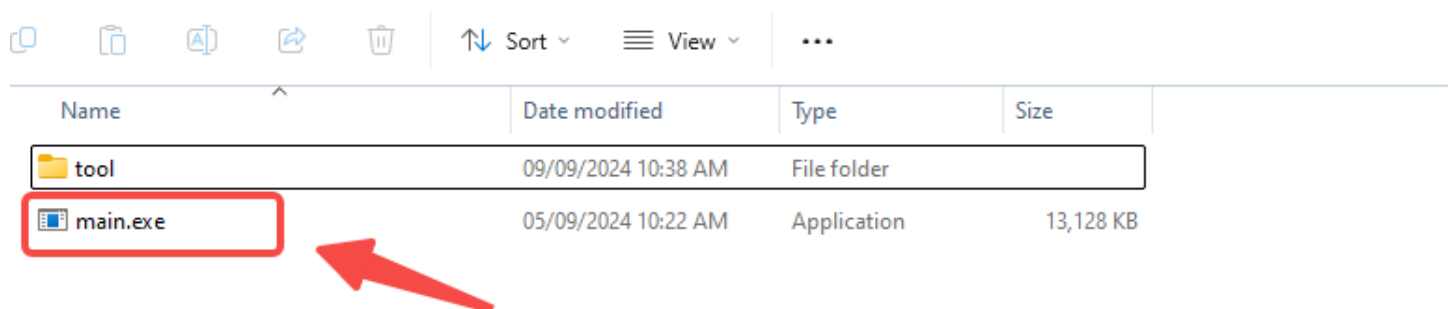
## Tutorial

**Note: Currently, the server-side evolution tool only supports Windows systems.**

Step 1: After you download the code, you can see the file directory as follows. In the example, I downloaded the script tool to E:\evo



Step 2: Double-click to open main.exe without additional operations. When you see the following screen, it means that the script tool is running normally.



```

evolution end :2024-09-05 10:28:59
Not meeting the conditions, abandon
evolution start:2024-09-05 10:28:59
evolution end :2024-09-05 10:28:59
Not meeting the conditions, abandon
evolution start:2024-09-05 10:28:59
evolution end :2024-09-05 10:28:59
Not meeting the conditions, abandon
evolution start:2024-09-05 10:28:59
evolution end :2024-09-05 10:28:59
Not meeting the conditions, abandon
evolution start:2024-09-05 10:28:59
evolution end :2024-09-05 10:29:00
Not meeting the conditions, abandon
evolution start:2024-09-05 10:29:00
evolution end :2024-09-05 10:29:00
Not meeting the conditions, abandon
evolution start:2024-09-05 10:29:00

```

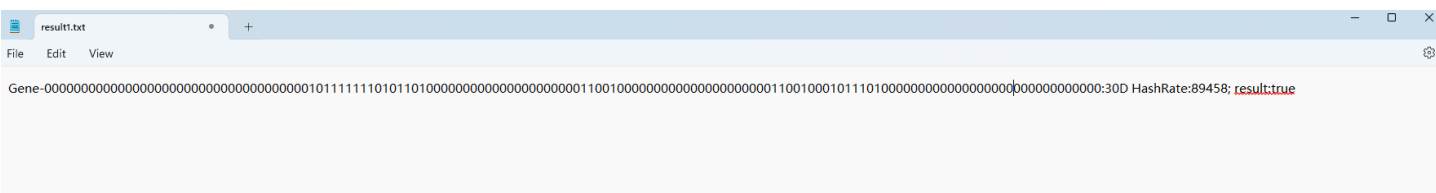
When you see his prompt as "**Not meeting the conditions,abandon**" means the current random genotype. **If the conditions are not met, it will be discarded and the next random combination evolution will be carried out.**

Step 3: If a genotype that meets the expectations is generated, a file named resultX.txt will be generated in the same directory of the script tool. After opening it, you can see that it contains the binary string that meets the conditional genotype and 30DAY. hashrate value

--Under the current file, as shown below:

Name	Date modified	Type	Size
tool	09/09/2024 10:38 AM	File folder	
main.exe	05/09/2024 10:22 AM	Application	13,128 KB
result1.txt	09/09/2024 10:52 AM	Text Document	0 KB

Open result1.txt to see the genotype information that meets the conditions. Each line represents a genotype that meets the conditions. **Whenever a new genotype that meets the conditions is calculated, it will be appended to the file.**



**\*\*Do not delete the generated resultX.txt. If you delete the file by mistake while the program continues to execute, it will not affect the process of the program. When a new genotype that meets the conditions is found, the file will still be generated and the output will satisfy the conditions. genotype information, but previously deleted genotype information may not be retrieved.**

## Other questions

**Question 1:** Then how do I know that I have found the genotype that meets the requirements?

**Answer:** If resultX.txt does not appear, it means that no genotype that meets the conditions appears (the condition is: 30Day Hashrate>18329471)

**Question 2:** If I obtain a genotype that meets the requirements, how do I submit the results?

**Answer:** If you get a genotype that meets the requirements

**\*\*Users with development capabilities can submit your results through the following methods**

After a genotype that meets the requirements appears, the submission method is the interface request method:

[illegible]

**\*\*Users without development capabilities can submit through the synthesis platform and intercept every 12 strings of "010..." in the text to obtain a genotype dot matrix diagram. An example is as follows:**

1. Wrap every 12 lines, and you can get something similar to the picture below.

```
00000000000000
00000000000000
```

```

00000000000000
0 11 001101000
00000000000000
00000000000000
00000000000000
00000000000000
00000000000000
00000000000000
0 0000011100 0
00000000000000

```

- In cellula, each bitlife is composed of 2 to 16 BitCells, and each cell is composed of different cell points. In the abstract, each BitCell is a 3\*3 square grid with blank areas. area with cells

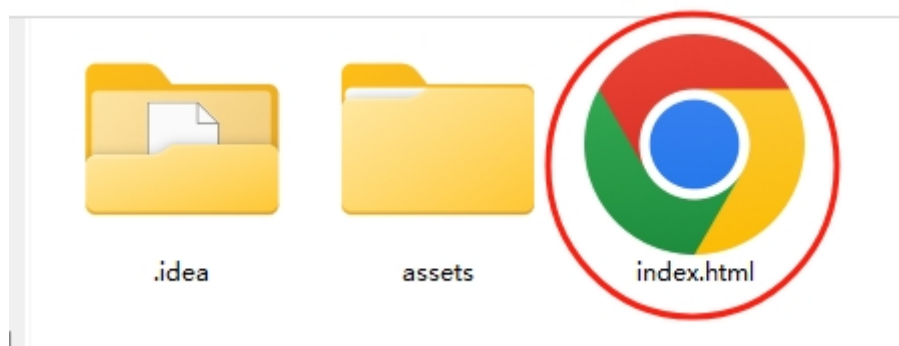


- We treat the area with cells in the code as 1, and the area without cells as 0. Write every 3 horizontally and 3 vertically into a grid, and you can parse the "0101..." string. The example is as follows



## Google plug-in tool example:

1. Download it, open the project folder and double-click index.html

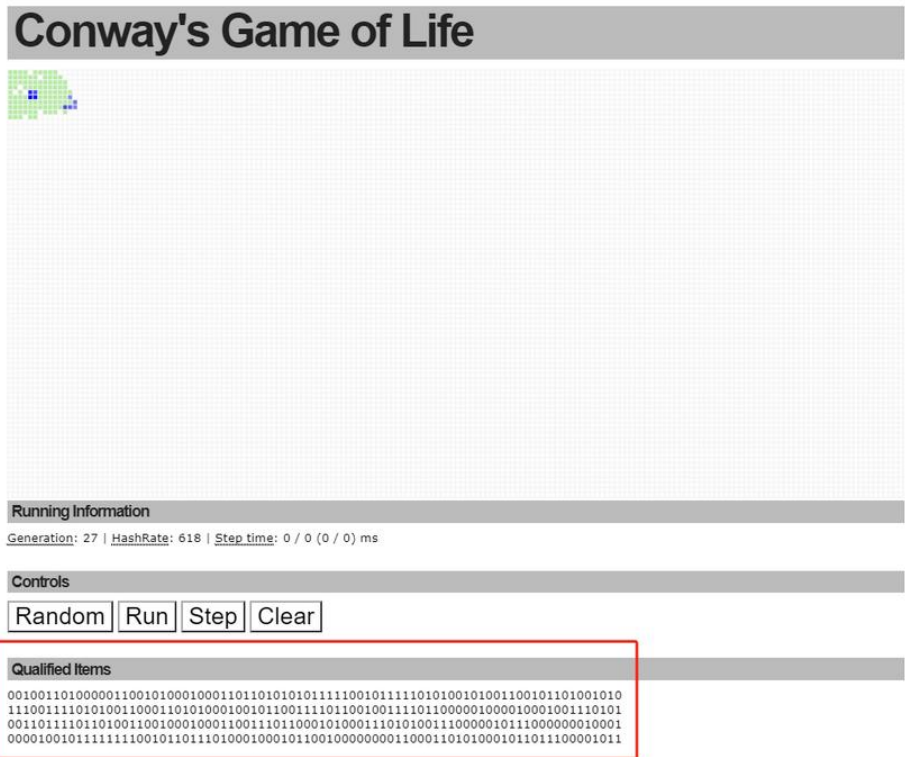


After opening the page, click Run to automatically start evolution.

## Conway's Game of Life

The screenshot shows the web application for Conway's Game of Life. It features a large grid for the game state. Below the grid is a 'Running Information' section with text: 'Generation: 0 | HashRate: 0 | Step time: 0 / 0 (0 / 0) ms'. To the right of this is a yellow hint box that says 'Hint: hit the Run button!'. Below the running information is a 'Controls' section with four buttons: 'Random', 'Run', 'Step', and 'Clear'. The 'Run' button is highlighted with a red border. At the bottom is a 'Qualified Items' section, which is currently empty.

Eligible genotypes will automatically be recorded in the list below



After a genotype that meets the requirements appears, the submission method is the interface request method:

- [illegible]