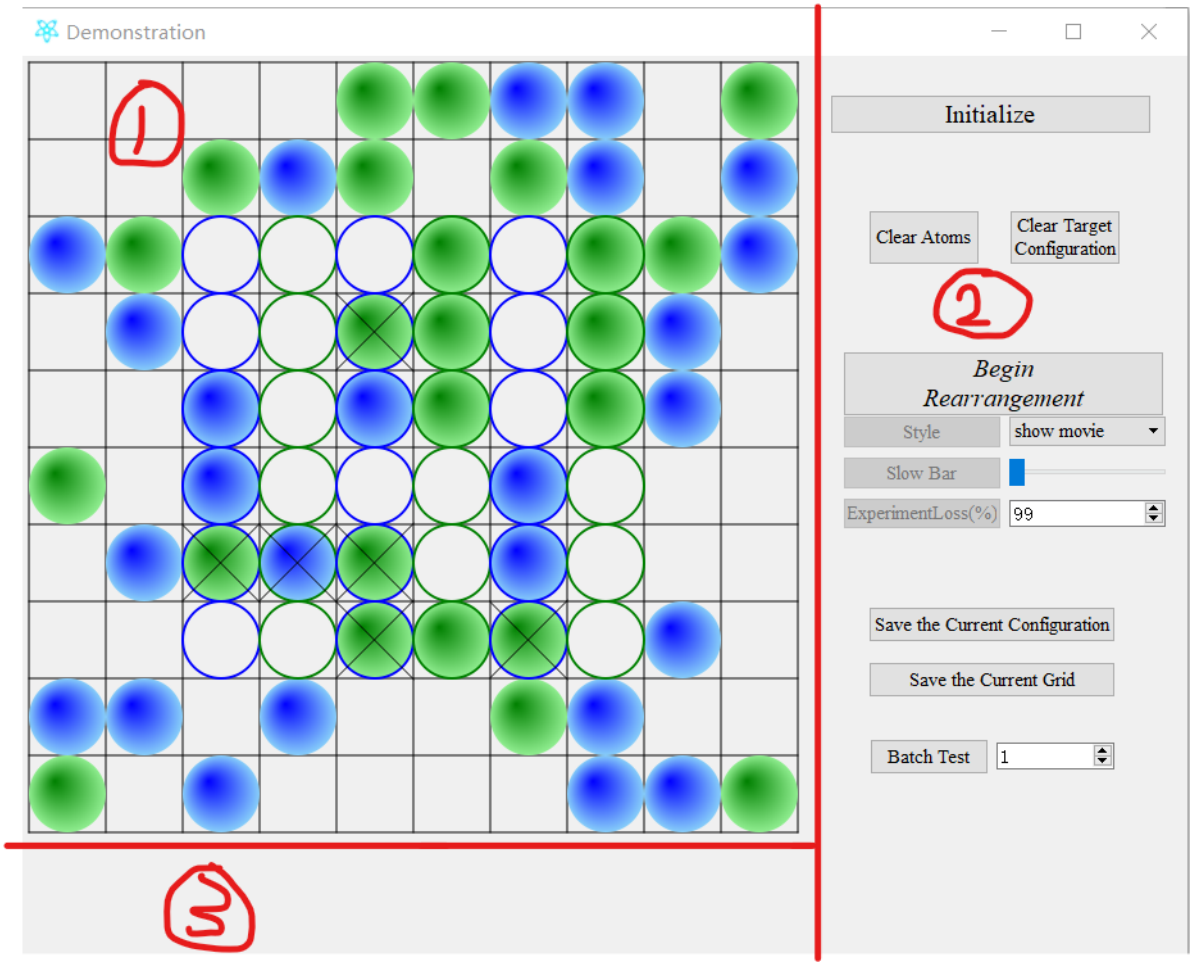
Help document for the HCOA demonstration app

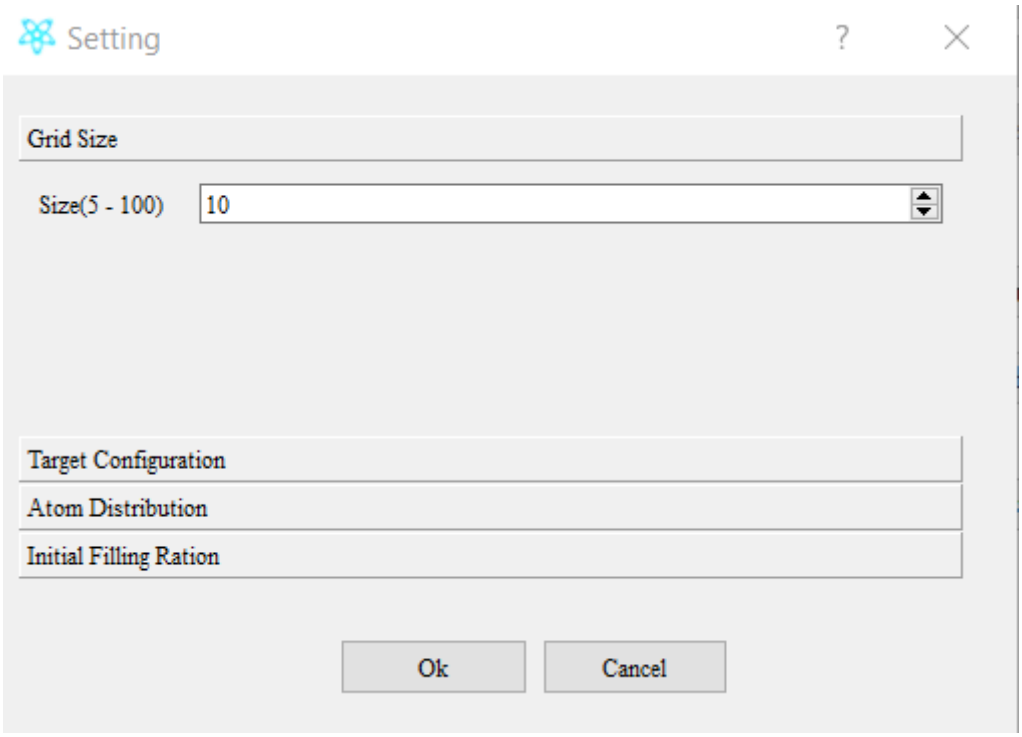
1.Overall configuration and functions



When you open this app, the user interface will appear like this picture. The graphical interface is divided into 3 regions. The first region is to show the initial atom distribution and user-defined target configuration. The blue balls and the green balls represent different kinds of atoms. The blue and the green circles represent the corresponding target configuration of atoms. Each square represents an optical trap and the cross will show on the atom which is misplaced in the target region. The second region is the button region, where you can click the corresponding button to set the grid size, generate the initial atom distribution, start playing the rearrangement movie and so on. The following will explain the buttons' functions in detail. The third region is to show the information of an rearrangement by the algorithm.

2. Set the initial state for rearrangement

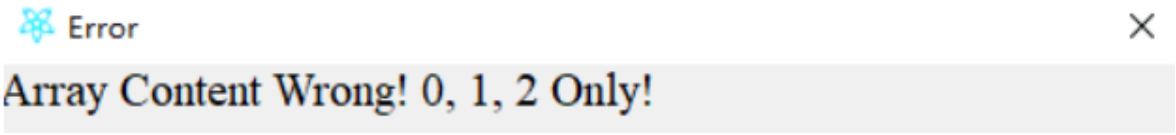
Obviously, you can click the "Initialize" button to set the initial state for rearrangement. When you click the button, a new interface appears like this:



1. The grid size can only be set in the range between 5-100, because the pixels are not enough to show a clear picture of the initial state when the grid size becomes too large.
2. In the target configuration setting, you can choose the three pre-defined target configurations, which are located in the center of the grid with the size of int(0.6*grid size). You can also choose the customized configuration in "csv" from your personal computer. The csv file must only store 0,1,2, where 0 represents no circle, 1 represents the blue circle and 2 represents the green circle.
3. In the atom distribution setting, you have two choices to generate the initial atom distribution. One is by inputting a rand seed, and then each square will generate a blue atom in the probability of 25%, a green atom in the probability of 25%, no atom in the probability of 50% stochastically by the input rand seed. The other choice is to read the csv file from your computer. The csv file must only store 0,1,2, where 0 represents no atom, 1 represents the blue atom and 2 represents the green atom.
4. Pay attention! One of the following error dialogs may appear, if your input csv file is not correct in the following ways.

(1) Your input csv file's size is not $L \times L$, where L is the grid size you have set in the grid size setting.

(2)Your input csv file's contains numbers different from 0,1,2.



5. Obviously, you can also adjust the initial filling fraction of each site.

Besides, you can also set the initial state by your mouse.

1. Press F3 to open the target configuration setting mode. In this mode, you can click the square to set the target configuration. Click your mouse's left button to set a blue circle and right button to set a green circle. If the square your mouse clicks has existed an circle, then the circle will be erased.
2. Press F2 to open the atom distribution setting mode. In this mode, you can set the atom distribution by mouse click. Click your mouse's left button to set a blue atom and right button to set a green atom. If the square your mouse clicks has existed an atom, then the atom will be erased.

3. Start rearrangement and play the rearrangement movie

When the initial state has been prepared, you can click the "Begin Rearrangement" button to rearrange. And then a new window will start to show the process of rearrangement. The information like the ideal number of atom moves, atom moves, cost time of the algorithm, total move distance will show in the third region in Fig1. You can set the play style to determine whether to show each step or just to show the rearrangement result. The slow bar slider is used to adjust the interval between the adjacent two steps in the movie. The minimum interval is 1ms when the slider lies in the most left while the maximum interval is 2000ms when the slider lies in the most right.

You can adjust the experiment loss ratio of each atom in the *experimentLoss* column to simulate the experimental loss.

4. Batch test to analyze the performance of the algorithm

Click the batch test button to test the performance of the algorithm with the initial target configuration shown in the first region in Fig1. The test time is set by users, and the computer will generate a file named "test.csv" in the current directory.