Instructions

Overview

This C++ program simulates gene evolution that analyzed in the paper with or without spatial constraint.

The simulation procedure is divided into four stages: (i) initiation, (ii) mate selection, (iii) gamete generation and (iv) birth of the next generation.

An $n \times n$ matrix is used to simulate the mating procedure. Each element of the matrix that presented an individual is initialized by a pair of genes (*AA*, *Aa*, or *aa*), which randomly generated from *A* or *a* according to a given probability in stage (i). In stage (ii), (iii) and (iv), each element is randomly mated by one of its 4 neighbors (G_4), 6 neighbors (G_6) or 8 neighbors (G_8) in one loop. The loop stops till all elements constitute the same genes (either *AA* or *aa*). For the simulation without spatial constraint (Gnf), an element is randomly mated by any other element. When encounter boundary, a periodic boundary is applied to ensure that the neighboring condition of each element is the same. In each loop, number of gene *A*, gene *a*, and the distribution are recorded.

Simulation parameters are input manually and results are recorded in local text files.

progmain.cpp:
main function and program entry. Neighbor type and spatial condition are defined in _tmain() function. Initialized parameters are also input in *_tmain()*.

flower.h:
Defines *flower* class, which implements mating progress, and *files* class, which deals with iostream.

function.h:
Defines global functions that shared by all files.

Procedure

Input:

1. neighbor type should be predefined in **progrmain.cpp**.
2. after neighbor type is defined, run **progmain.cpp**.
3. In the end, the number of columns and rows, simulation times and random seed are requested to input in terminal.
4. When simulation finishes, the terminal will close automatically.

Output:

The number of generations for each simulation procedure and total time cost are recorded in *generation.txt* file. It will also generate a folder for each simulation named *00x, x* for indexing.

In each simulation folder, there are two text files named *distribution* and *scores* respectively. *distribution* records the constitution of genes for each element in all loop. *scores* records the number of different genes for each loop.

Code Access

All codes are available on github.
https://github.com/SJinping/hardy-weinberg-simulation

Environment Settings

This program has been successfully executed in the following environment.

Compiler: Microsoft Visual Studio 2013

OS: Windows 8 Enterprise, 64-bit