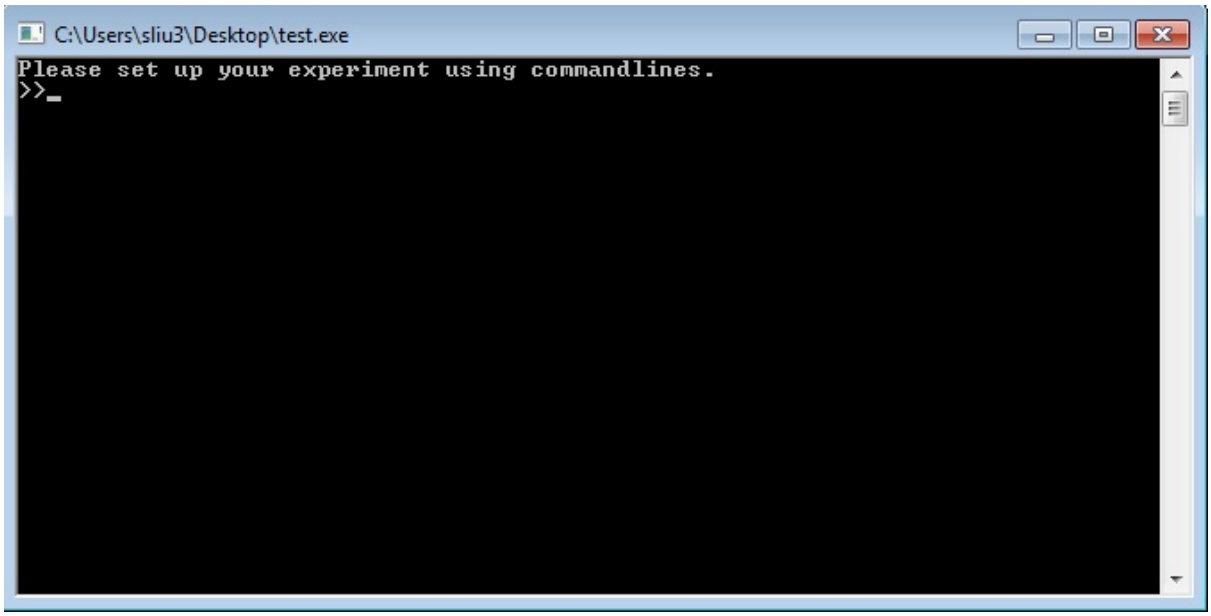
There are four steps for carrying out a simulation with PolyIsle:

1. Start the program;
2. Set parameters;
3. Run simulation;
4. Terminate the program, and collect outputs.

1. Start the program

Start the program “PolyIsle.exe”. A window as below pops up, and immediately three “txt” files will be generated in the same folder. The files are “profile.txt”, “burnin.txt”, and “simulation.txt”.



“profile.txt”: it records the parameter settings of the simulation, and the time taken for the simulation.

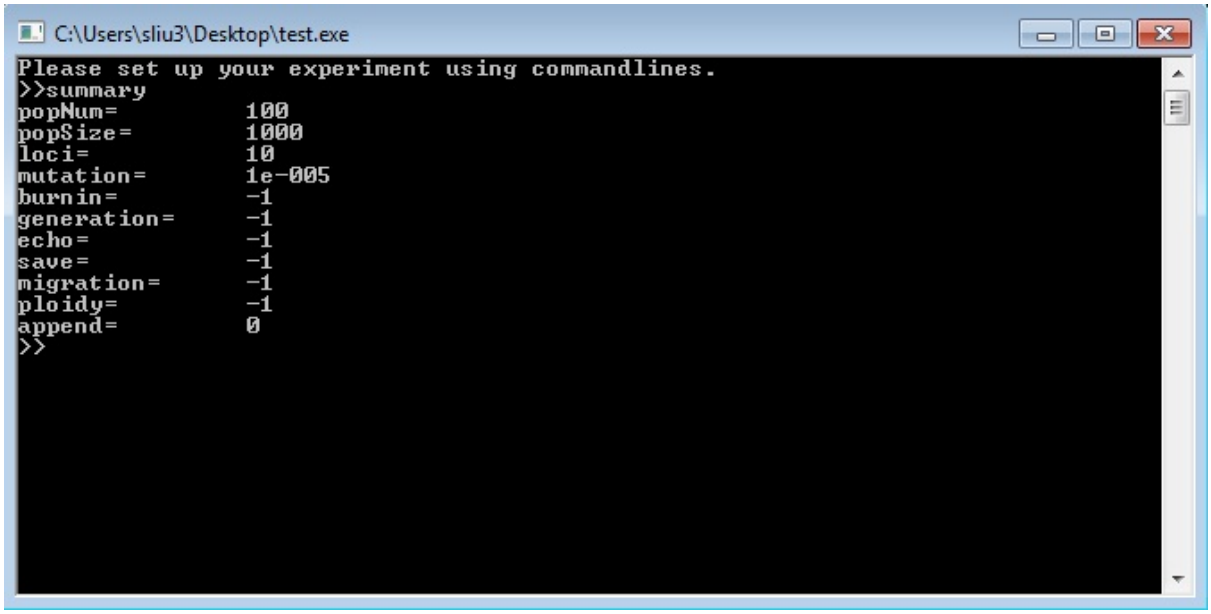
“burnin.txt”: it stores the output of heterozygosities (HO, HS, HT) during the burn-in period.

“simulation.txt”: it stores the output of heterozygosities during the simulation period.

2. Set parameters

Parameters are set through commandlines. There are three types of commandlines, summary commandline, parameter commandline, and start commandline. This section will introduce the first two types. Start commandline will be introduced in next section.

Summary commandline is implemented by simply typing in “summary” followed by an Enter key. It provides a summary over all parameters and their values, as is shown in the picture below.



The meanings of the parameters are:

“popNum”:	number of populations
“popSize”:	population size
“loci”:	number of loci
“mutation”:	mutation rate
“burnin”:	number of generations for burn-in period
“generation”:	number of generations for real simulation
“echo”:	how often to echo to the screen (unit: generation)
“save”:	how often to output heterozygosities (unit: generation)
“migration”:	migration rate
“ploidy”:	ploidy level
“append”:	continue from a previous simulation (“append=1”) or not (“append=0”)

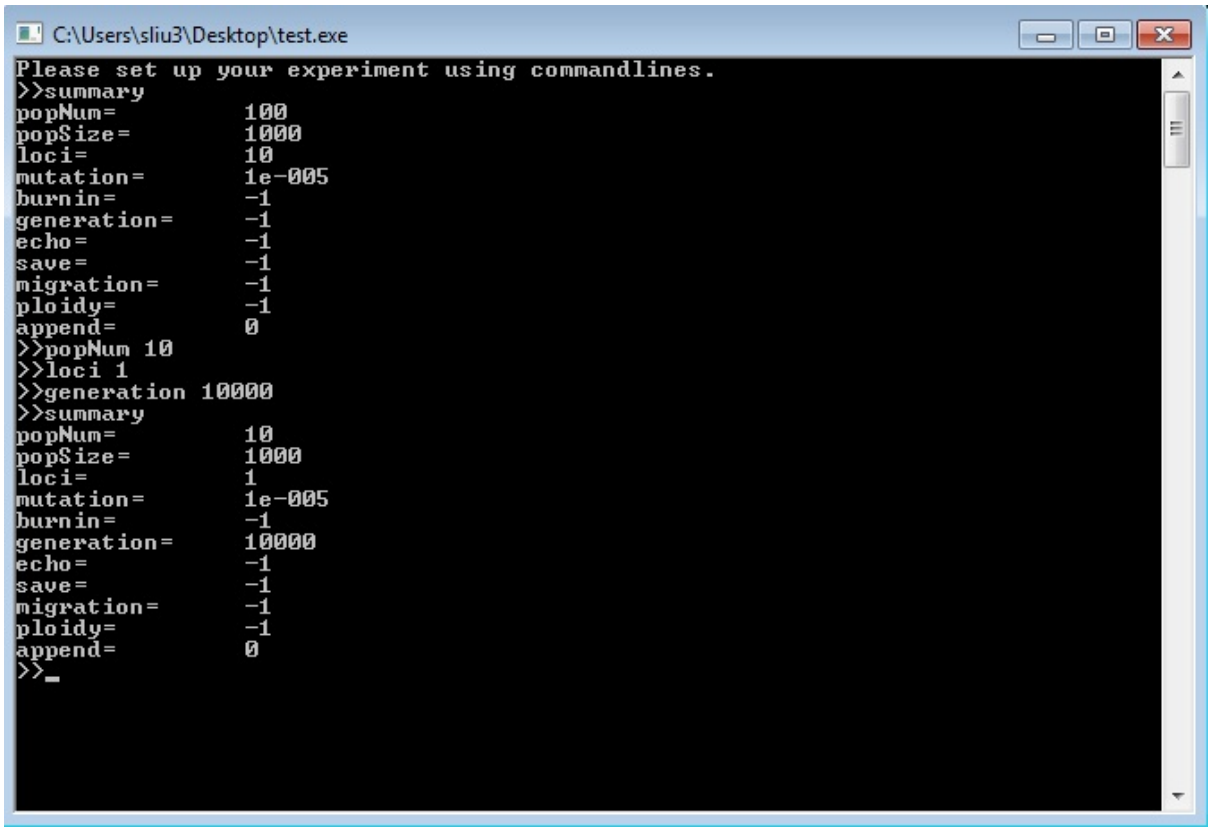
“popNum”, “popSize”, “loci”, “mutation”, and “append” have meaningful default values as shown in the picture above. But all the other parameters are set as “-1” in default, which means they need to be assigned with meaningful values so that the simulation can be initialized.

Parameter commandlines are used to set or change the values of the parameters. They have the same syntax as:

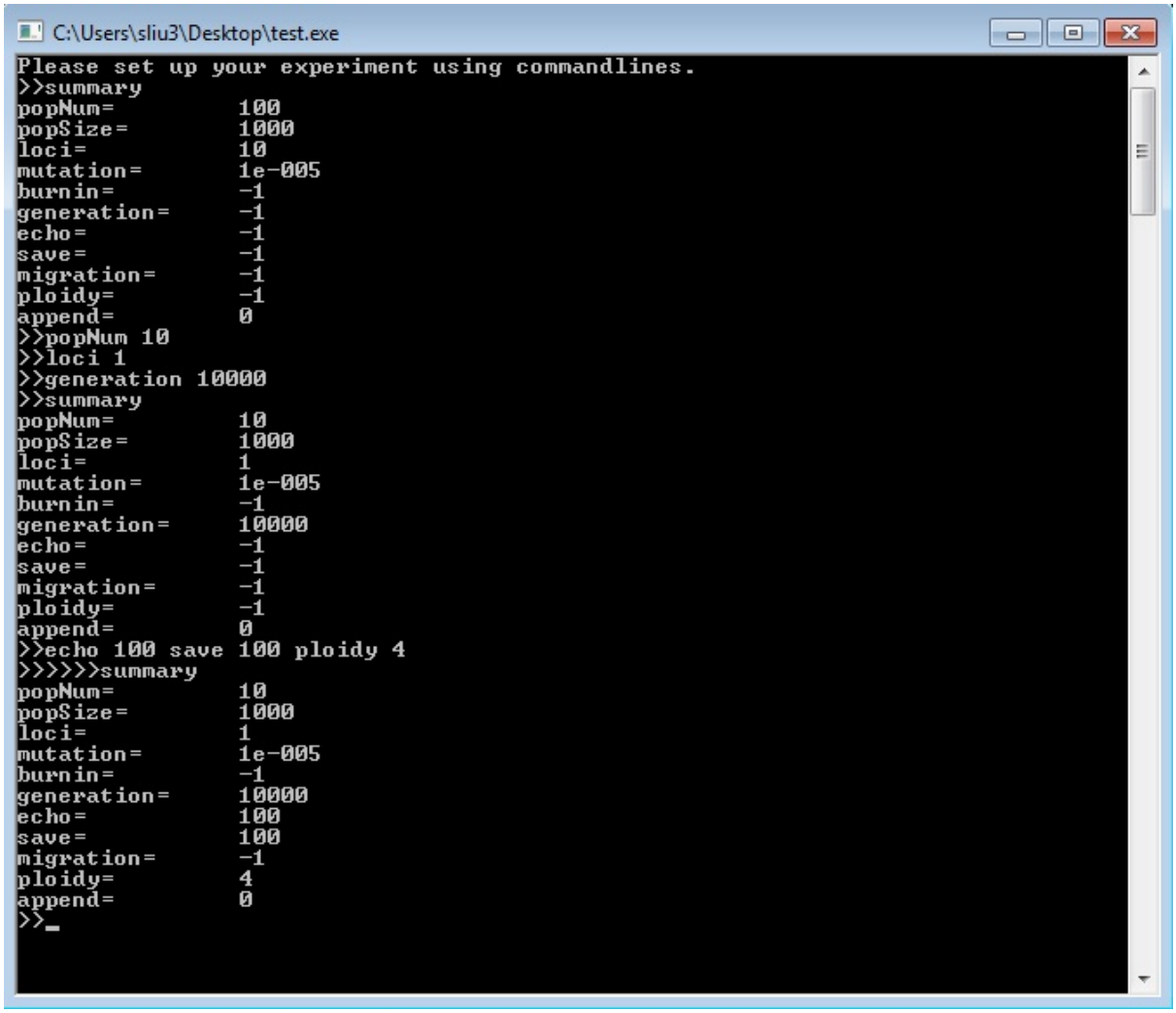
PARAMETER_NAME VALUE

For example, to change the number of populations from the default value of 100 to 10, we need to type in “popNum 10” followed by an Enter key. Other parameters follow the same manner. The

picture below shows that the values of “popNum”, “loci”, and “generation” were changed. Of course, the new status of the parameters can be reviewed with summary commandline as well.

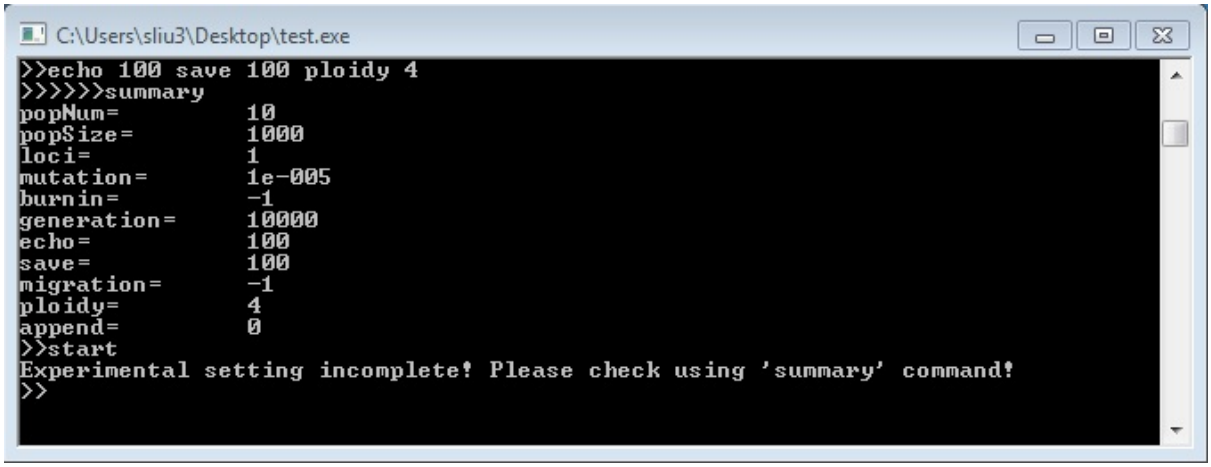


It should be noted that the commandlines can be concatenated. For example, in the picture below, I concatenated 3 commands together by typing in “echo 100 save 100 ploidy 4” followed by an Enter key. In this way, the values of “echo”, “save”, and “ploidy” were changed together. In fact, all commandlines can be concatenated, including summary commandline and start commandline.

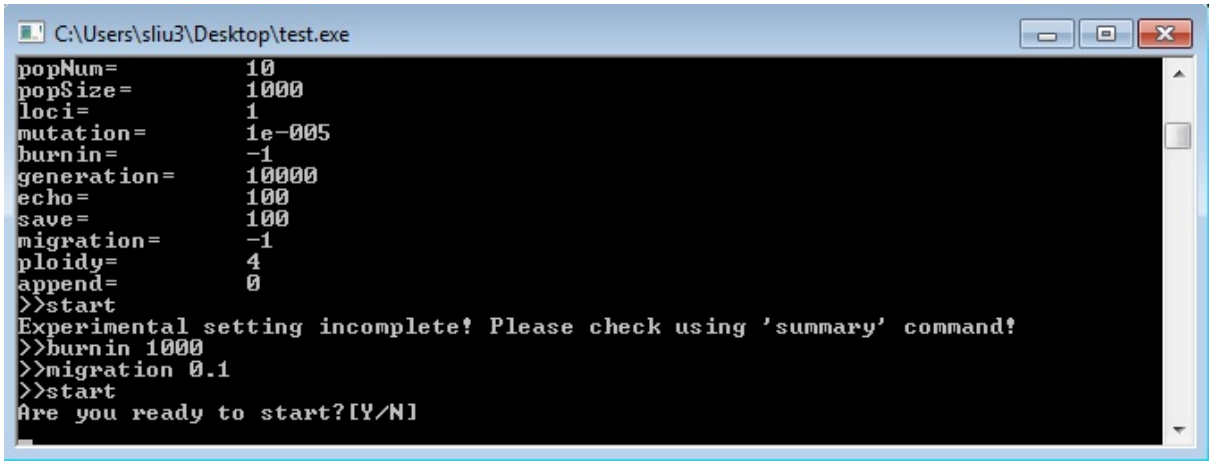


3. Run simulation

Start commandline is “start”. It tells the program to start the run. But you have to make sure every parameter has been assigned with a meaningful value. Otherwise, the program will refuse to run, as is shown in the picture below.

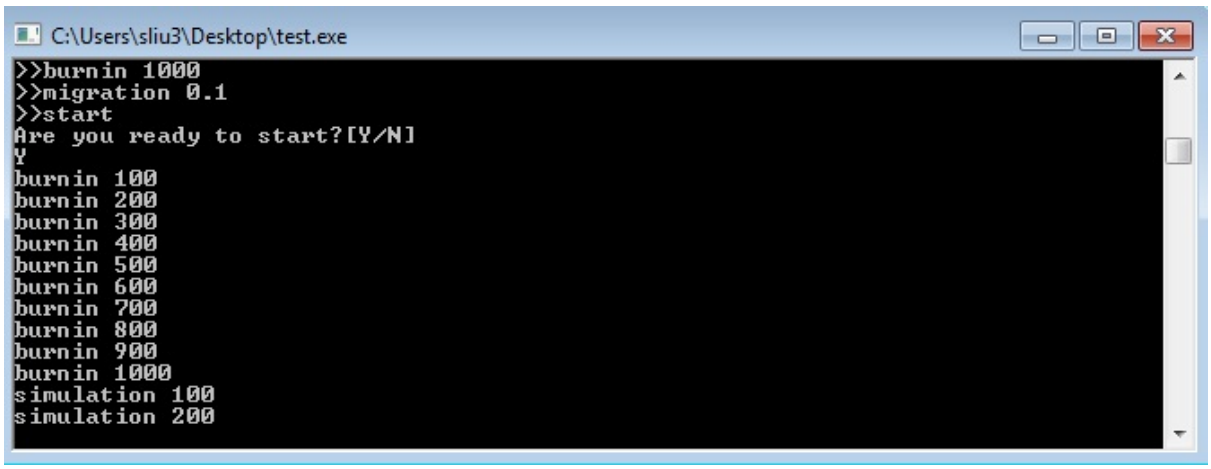


When all parameters are well set, the program will respond as:



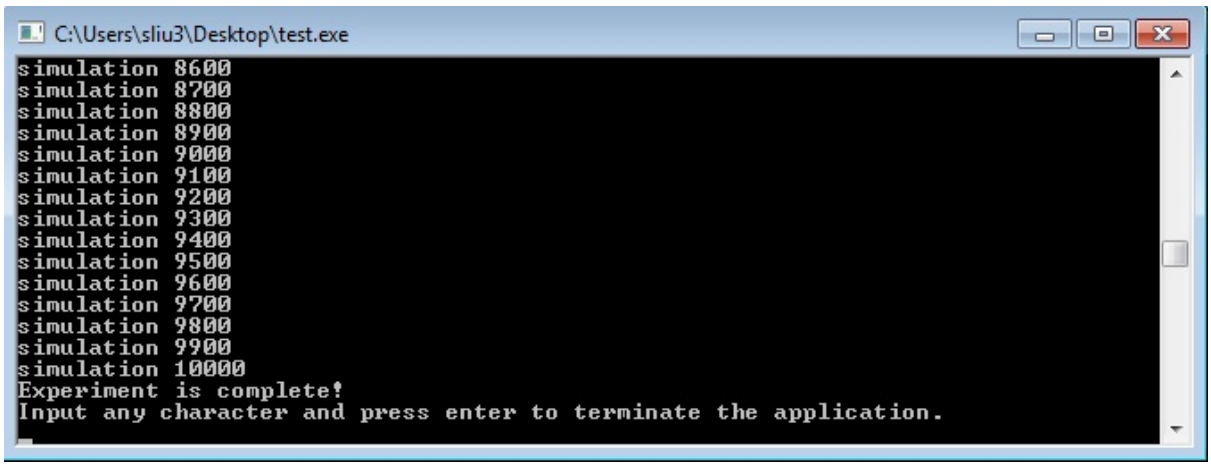
Input “Y” to start the run, or “N” to keep setting parameters.

When the simulation is under run, the screen looks like this:



4. Terminate the program, and collect outputs

When the simulation is complete, it shows:



At the end of the simulation, another “txt” file will be generated, called “state.txt”. It stores the final status (genotypes of all individuals) of the metapopulation.

When multiple simulations are to be run in the same folder in sequence, the four output files must be renamed or transferred to another folder at the end of each simulation. Otherwise, the files will be overwritten by next simulation. For the same reason, multiple simulations must not be run simultaneously under the same directory.