

//แก้ไขจากตัวอย่างใน GAlib โดยใช้ binary to decimal genome และ สร้าง fitness function ใหม่

```
#include <ga/GASimpleGA.h>
#include <ga/ga.h>
#include <ga/std_stream.h>
#include <cmath>

#define cout      STD_COUT
#define NBITS    (3)
#define MIN_VALUE ((int)0)
#define MAX_VALUE ((int)7)
```

```
float Objective(GAGenome &);
bool isMet(int i1, int j1, int i2, int j2);
```

```
int main(int argc, char **argv)
{
    cout << "8-Queen\n\n";
    cout.flush();

    for(int ii=1; ii<argc; ii++) {
        if(strcmp(argv[ii+1],"seed") == 0) {
            GARandomSeed((unsigned int)atoi(argv[ii]));
        }
    }
}
```

```
GABin2DecPhenotype map;
for(int i = 0; i <= MAX_VALUE; i++)
{
    map.add(NBITS, MIN_VALUE, MAX_VALUE);
}
```

```
GABin2DecGenome genome(map, Objective);
```

```
int popsize = 100;
int ngen   = 10000;
float pmut  = 0.001;
float pcross = 0.9;
```

```
GASimpleGA ga(genome);
ga.populationSize(popsize);
ga.nGenerations(ngen);
ga.pMutation(pmut);
ga.pCrossover(pcross);
ga.evolve();
```

```

cout << ga.statistics().bestIndividual() << "\n\n";

system("PAUSE");
return 0;
}

float Objective(GAGenome& g) {
    GABin2DecGenome & genome = (GABin2DecGenome &)g;
    double score = 0;
    int met = 0;
    for(int i = 0; i < genome.nPhenotypes()-1; i++)
    {
        for(int j = i+1; j < genome.nPhenotypes(); j++)
        {
            if(isMet(i, (int)genome.phenotype(i), j, (int)genome.phenotype(j)))
            {
                met++;
            }
        }
    }
    score = 28-met;
    return score;
}

bool isMet(int i1, int j1, int i2, int j2)
{
    if(j1 == j2)
        return true;
    else if(abs(i1-i2) == abs(j1-j2))
        return true;
    else return false;
}

```

Output