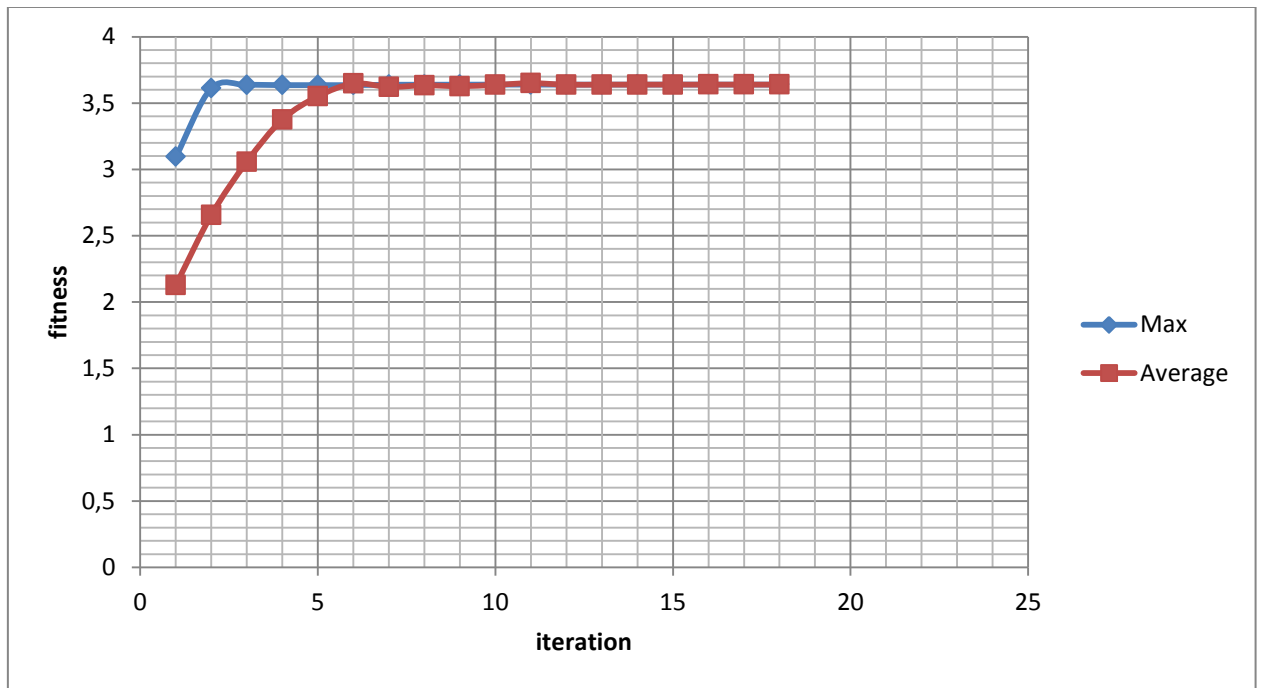
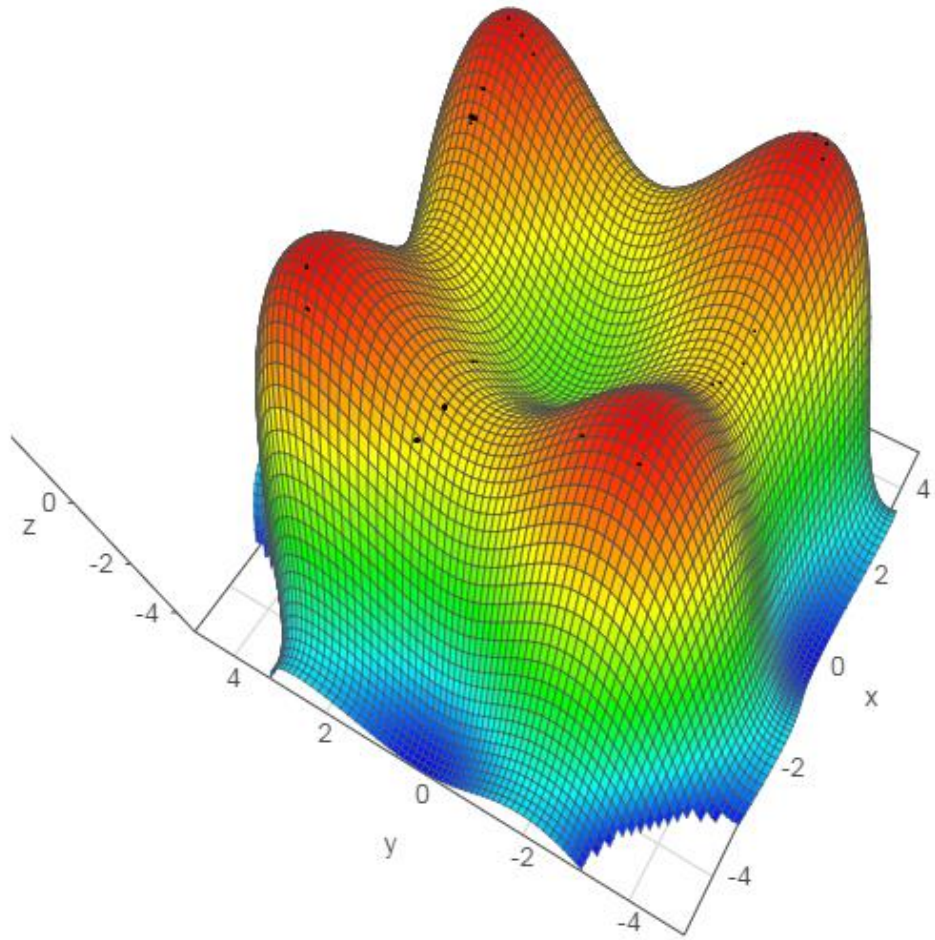
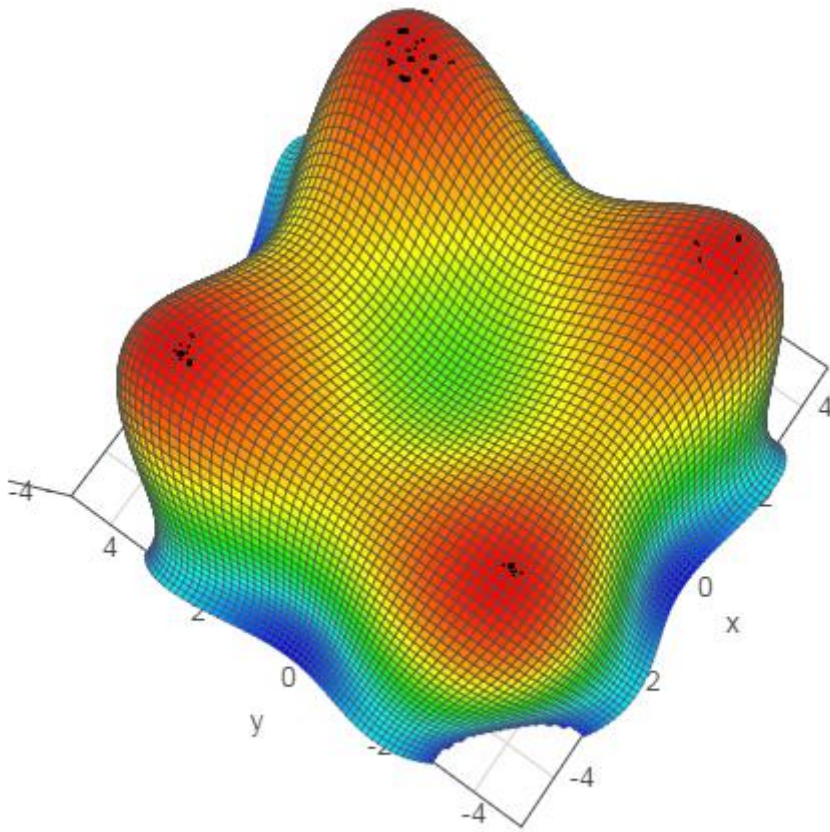




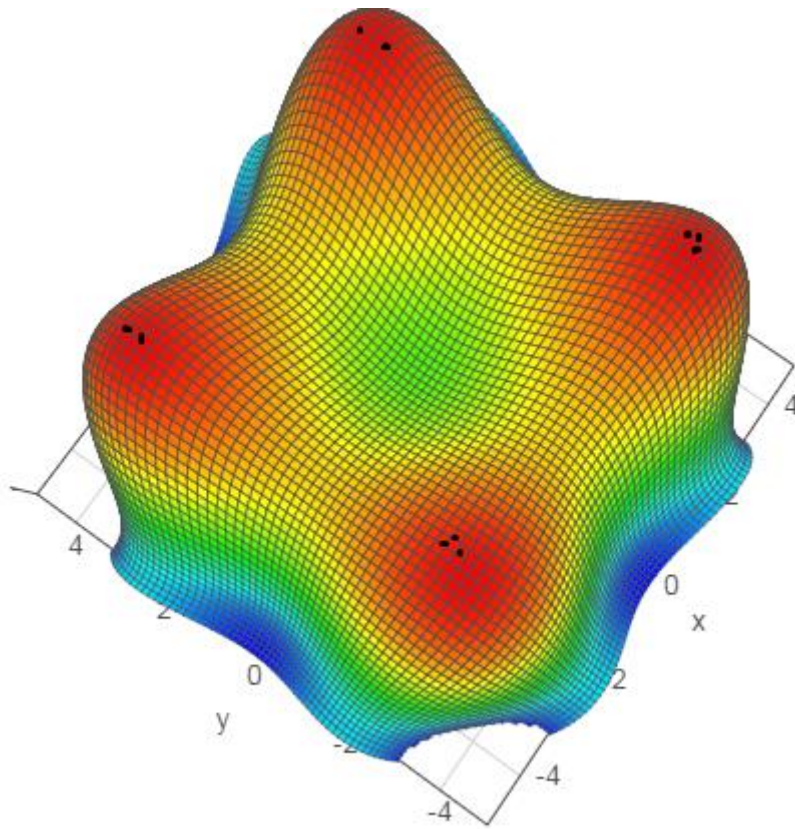
0:



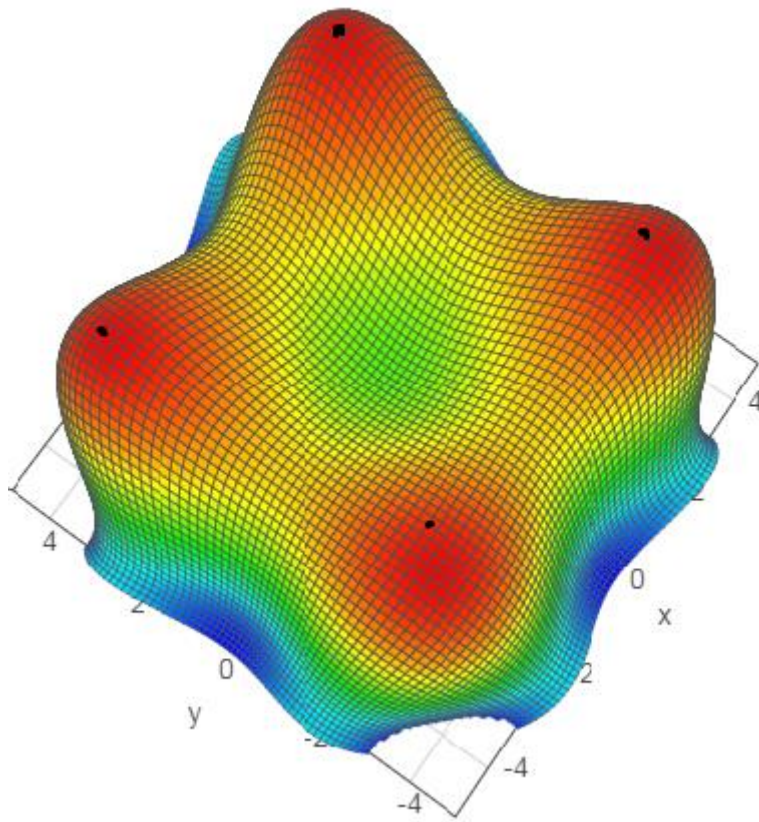
4:



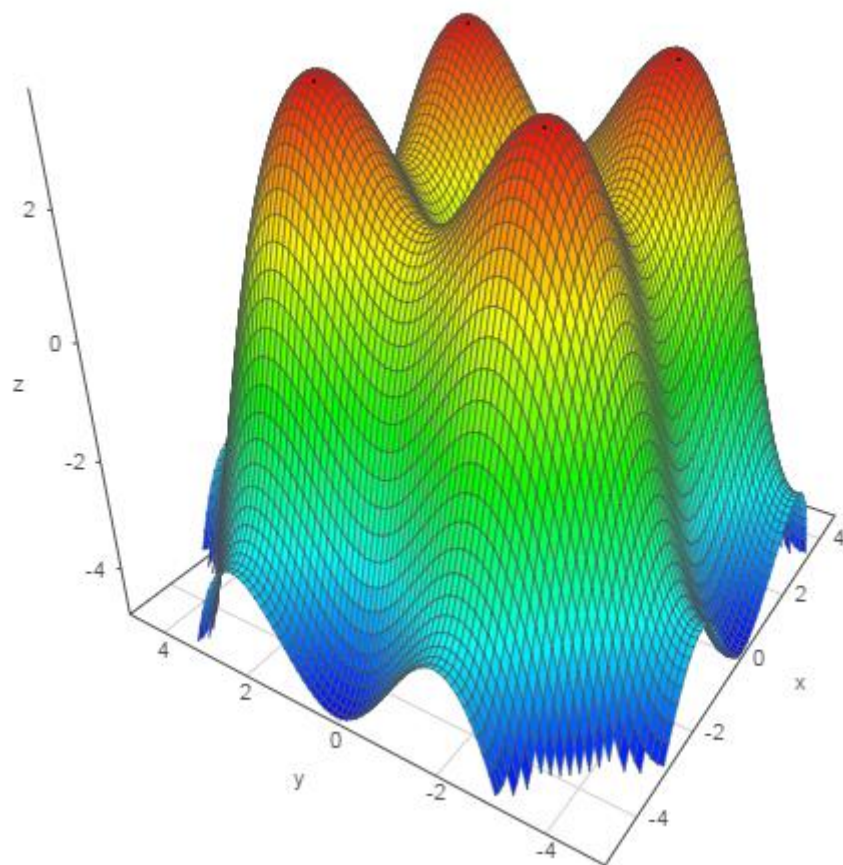
8:



12:



16:



0

x	y	z
2,158	-2,625	3,09386
-1,311	2,563	2,667856
-1,121	-2,375	2,655958
1,387	2,646	2,620707
1,46	2,705	2,594665
-0,969	-2,375	2,446098
-1,292	2,7	2,394991
1,985	0,747	2,324755
-1,97	0,742	2,31678
-1,89	0,635	2,170811
2,249	-0,5	1,991753
2,273	-0,5	1,975452
2,078	-0,315	1,913998
2,151	0,122	1,813897
1,414	3,154	1,684596
-2,3	-3,152	1,682929
-0,508	2,598	1,591241
0,867	-2,82	1,55235
-0,891	-2,834	1,549986
-2,117	-3,235	1,507775

4

x	y	z
1,985	1,997	3,635485
-2,053	1,934	3,626624
-1,975	1,938	3,624776
2,063	1,919	3,62193
1,99	1,919	3,621486
-1,907	1,953	3,612258
-1,907	1,953	3,612258
-1,907	2,109	3,610921
1,821	2,114	3,574091
-2,224	-1,899	3,563877
-2,263	-1,958	3,555075
-2,253	-1,895	3,544593
-2,327	-1,938	3,501978
2,253	-1,797	3,499625
-2,327	-1,895	3,48918
-2,371	2,061	3,470271
-2,38	2,041	3,461497
-2,38	2,061	3,460325
-2,38	2,061	3,460325
2,38	-2,09	3,45659

8

x	y	z
-2,024	2,017	3,639181
2,004	2,017	3,638414
2,004	-2,017	3,638414
-2,004	-1,997	3,637266
2,004	-1,997	3,637266
2,004	-1,997	3,637266
1,99	-2,017	3,637173
1,99	-2,017	3,637173
-1,985	-2,026	3,636825
1,985	2,017	3,636633
1,985	2,017	3,636633
1,985	2,017	3,636633
1,985	2,017	3,636633
1,985	2,017	3,636633
1,985	2,017	3,636633
1,985	2,017	3,636633
-1,985	2,017	3,636633
1,985	2,017	3,636633
-1,985	2,017	3,636633

12

x	y	z
2,029	2,017	3,639212
-2,024	2,017	3,639181
-2,024	2,017	3,639181
-2,024	2,017	3,639181
2,024	-2,017	3,639181
2,024	-2,017	3,639181
-2,024	-2,017	3,639181
2,024	-2,017	3,639181
-2,024	-2,017	3,639181
2,024	-2,017	3,639181
-2,024	-2,017	3,639181
2,024	-2,017	3,639181
-2,024	-2,017	3,639181
2,024	-2,017	3,639181
-2,024	-2,017	3,639181
2,024	-2,017	3,639181
-2,024	-2,017	3,639181
2,024	-2,017	3,639181
-2,024	-2,017	3,639181
2,024	-2,017	3,639181

16

x	y	z
-2,024	2,026	3,639372
2,024	2,026	3,639372
2,024	2,026	3,639372
2,029	-2,019	3,639284
2,029	-2,019	3,639284
2,029	2,019	3,639284
2,029	2,019	3,639284
-2,024	2,019	3,639253
-2,024	2,019	3,639253
-2,024	-2,019	3,639253
-2,024	-2,019	3,639253
-2,024	-2,019	3,639253
2,024	-2,019	3,639253
2,024	-2,019	3,639253
2,024	-2,019	3,639253
-2,024	-2,019	3,639253
2,024	-2,019	3,639253
-2,024	-2,019	3,639253
2,024	-2,019	3,639253
-2,024	-2,019	3,639253
2,024	-2,019	3,639253
-2,024	-2,019	3,639253
2,029	2,017	3,639212

CODE:

```
#include <iostream>
```

```
#include <vector>
```

```
#include <time.h>
```

```
#include <math.h>
```

```
#include <algorithm>
```

```
using namespace std;
```

```
typedef vector<int> Chromosome;
```

```
typedef vector<Chromosome> Population;
```

```
Population population;
```

```
Population population2;
```

```
Population makePopulation();
```

```
double fitness(Chromosome chromosome);
```

```
double s_function(Chromosome chromosome);
```

```
bool sortPopulation(const Chromosome &chromosome1, const Chromosome &chromosome2);
```

```
Population newPopulation();
```

```
double distance(const Chromosome &chromosome1, int k);
```

```
double sharing_fitness(Chromosome chromosome);
```

```
int main()
```

```
{
```

```
    srand(time(NULL));
```

```
    ofstream file("OutData.txt", ios::out);
```

```
    population = makePopulation();
```

```
    population2 = population;
```

```
    sort(population.begin(), population.end(), sortPopulation);
```

```

        population2 = population;

        double aver = 0.0;

for (int noChanged = 0, k = 0; noChanged < 30 && k < 500; k++)
{
    population = newPopulation();

    population2 = population;

    sort(population.begin(), population.end(), sortPopulation);

    population2 = population;

    double max = sharing_fitness(population[0]);

    double average = 0.0;

for (int i = 0; i < 20; i++)
{
    average += sharing_fitness(population[i]);
}

    average = average / 20;

if (average == aver)
{
    noChanged++;
}
else
{
    noChanged = 0;
}

    aver = average;

    file << max << "\t" << average << endl;
}

file.close();

system("pause");

return 0;

```



```

}

Population makePopulation()

{
Population result;
for (int i = 0; i < 20; i++)
{
    Chromosome chromosome;
        for (int j = 0; j < 22; j++)
        {
            chromosome.push_back(rand() % 2);
        }
        result.push_back(chromosome);
    }
    return result;
}

double fitness(Chromosome chromosome)
{
    int sum = 0;
    for (int i = 1; i < 11; i++)
    {
        sum += chromosome[i] * pow(2, (i - 1));
    }
    double x = sum / 1023.0 * 5.0;
    if (chromosome[0] == 0)
    {
        x = x * (-1.0);
    }
    sum = 0;
    for (int i = 12; i < 22; i++)

```

```

        {
            sum += chromosome[i] * pow(2, (i - 12));
        }

double y = sum / 1023.0 * 5.0;

    if (chromosome[11] == 0)

    {
        y = y * (-1.0);
    }

double z = x * sin(abs(x)) + y * sin(abs(y));

return z;

}

double distance(const Chromosome &chromosome1, int k)

{

int sum = 0;

for (int i = 1; i < 11; i++)

    {

        sum += chromosome1[i] * pow(2, (i - 1));

    }

double x1 = sum / 1023.0 * 5.0;

if (chromosome1[0] == 0)

    {

        x1 = x1 * (-1.0);

    }

sum = 0;

for (int i = 12; i < 22; i++)

    {

        sum += chromosome1[i] * pow(2, (i - 12));

    }

double y1 = sum / 1023.0 * 5.0;

```

```

if (chromosome1[11] == 0)
{
    y1 = y1 * (-1.0);
}

sum = 0;

for (int i = 1; i < 11; i++)
{
    sum += population2[k][i] * pow(2, (i - 1));
}

double x2 = sum / 1023.0 * 5.0;

if (population2[k][0] == 0)
{
    x2 = x2 * (-1.0);
}

sum = 0;

for (int i = 12; i < 22; i++)
{
    sum += population2[k][i] * pow(2, (i - 12));
}

double y2 = sum / 1023.0 * 5.0;

if (population2[k][11] == 0)
{
    y2 = y2 * (-1.0);
}

double dist = sqrt((x1 - x2)*(x1 - x2) + (y1 - y2)*(y1 - y2));

return dist;
}

double s_function(Chromosome chromosome)
{

```

```

double sigma = 0.6;

double s = 0.0;

for (int i = 0; i < population.size(); i++)
{
    double d = distance(chromosome, i);

    if (d < sigma)
    {
        s += (1 - (d / sigma));
    }
}

return s;
}

double sharing_fitness(Chromosome chromosome)
{
    double f = fitness(chromosome) / s_function(chromosome);

    return f;
}

bool sortPopulation(const Chromosome &chromosome1, const Chromosome &chromosome2)
{
    return sharing_fitness(chromosome1) > sharing_fitness(chromosome2);
}

Population newPopulation()
{
    int firstParent, secondParent;

    Population result;

    for (int i = 0; i < 10; i++)
    {
        firstParent = rand() % 10;

        secondParent = rand() % 10;
    }
}

```

```

        while (firstParent != secondParent)
        {
            secondParent = rand() % 10;
        }

        Chromosome child1, child2;
    for (int j = 0; j < 22; j++)
    {
        int mask = rand() % 2;

        if (mask == 0)
        {
            child1.push_back(population[firstParent][j]);
            child2.push_back(population[secondParent][j]);
        }
        else
        {
            child1.push_back(population[secondParent][j]);
            child2.push_back(population[firstParent][j]);
        }
    }

    result.push_back(child1);
    result.push_back(child2);
}

return result;
}

```