Spiking Neuron
IT3708

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March 4, 2013

1 Description

For this project I continued using the Evolutionary Algorithm(EA) that I developed for the previous project. Because of the modularity in the previous code not that much had to be changed apart from some minor changes to achieve better performance. As with the last project when needing to adapt the EA to a new problem one has to extend some core classes for which the default behaviour is not appropriate. For this project all the extended code can be found in the file *neuron.py* which contains all the code to simulate the task at hand.

For this project I decided that I wanted to change the crossover function in the genotype which meant that I had to extend the default genotype and create a new class. This is quite easy and only the code for the crossover needed to be changed. I will explain a bit more about why I wanted to change the default crossover below, but for now in *neuron.py* line 179 to 208 one can see the code for the neuron genotype.

1.1 Genotype

Since the phenotype of the spiking neuron relied on some values being in a certain range the code uses a variable amount of bits to represent these variables. The number of bits is user configurable to allow for testing of different sizes. The genotype then is just a bit array with 5xBITS where 5 represent the five variables. Since the genotype is just an array of bits I decided that for this project I would try out Gray Code to interpret those bits. This was done to ensure that mutation would not have the large impact it would have if regular conversion from a bit array to an integer was used. Gray code is another way of interpreting a bit array which tries to minimize the difference between two sequential numbers, e.g. 4 and 5 differ only by one bit. The genotype code does not need to do anything extra in order for this to apply and only in the conversion between genotype and phenotype is this extra bit of information used.

As mentioned above the crossover method was changed for this project. The change enables the crossover to take into consideration each of the five variables. This was done to make inheritance stronger. The change in code(listed in **??**) means that if we imagine the first variable representing a as the first 10 bits of the array, a child made from two such parents would inherit 50% of a from one parent and another 50% from the other. There is no crossover between different variables which should mean that the inheritance is stronger between parents and child and random bits from a variable will not be put into another variable. To illustrate a bit better I have tried to create an approximate figure in 1.

There is however a rather large problem with this. This way of doing crossover can lead to quite a bit of stagnation, which is clearly present as will be clear in the results. I decided that I wanted to do it this way however because it is quite easy coding wise and I wanted to see how the stagnation would affect the results and how the, stronger, inheritance would affect the results.

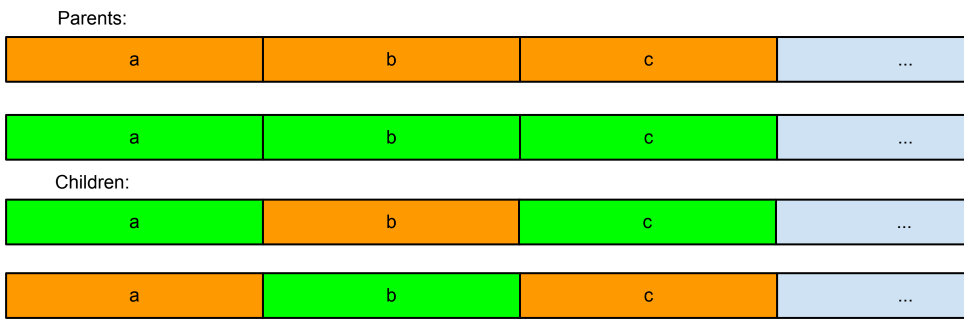


Figure 1: A representation of crossover in the neuron genotype

1.2 Fitness

To evaluate the fitness of each spike train I implemented the three different distance metrics suggested in the assignment. Since those metrics evaluated distance, meaning a smaller distance is better, and the EA code was set up for larger is better the natural choice was to just do 1.0/f(x), where f(x) is one of the three distance metrics. Since both *Spike Time Distance Metric(STDM)* and *Spike Interval Distance Metric(SIDM)* needed the peaks I created one more parent class which could calculate that. In listing 1 we can see the minimal code needed for SIDM[1].

Listing 1: The SIDM implementation

```python
class SIDM(NeuronFitness):
    '''Spike Interval Distance Metric fitness'''
    def sub_eval(self, pheno, population):
        spike_pheno = self.calc_spikes(pheno.get_spike_train())
        spike_data = self.spike_data
        s = 0
        n = min(len(spike_pheno), len(spike_data))
        for i in range(1, n):
            s += abs((spike_pheno[i][0]- spike_pheno[i - 1][0])
                 -
                   (spike_data[i][0] - spike_data[i - 1][0]))
                     **self.p
        s = s ** (1.0 / self.p)
        s += self.spike_penalty(len(spike_pheno), len(
            spike_data), len(self.data))
        n -= 1
        if n:
            s /= float(n)
        return 1.0 / s
```

[1]Note that this code does not include the code necessary for peak calculation

2 Results

Below are the results for the different test cases. The layout should be pretty similar so they should be quite easy to follow.

To get some good results I ran all of the test cases several times testing the different variables, these tests are not included here. One problem with this is that I can't know for certain that this is good, because it can easily end up in a local maximum regarding the different variables, e.g. I can test different mutation rates, but find the best one when considered with all of the others.

2.1 Test Case 1

In this test we are testing STDM with the test case *izzy-train1.dat*.

2.1.1 EA Parameters

Listing 2: Command-line to replicate the results

```
python src/main.py 350 5 50 --mutation=0.1 --cross_rate=0.8
    full_generational
tournament --k=5 --elite=3 stdm convert_neuron neuron_plot
    training\
data/izzy-train1.dat --bits_per_num=35 --e=0.02
```

Variable	Value
Generations	350
Population size	50
Mutation rate	0.1
Crossover rate	0.8
Protocol	Full generational replacement
Mechanism	Tournament selection, k=5 and e=0.02
Elitism	3
Bits per number	35

Table 1: EA parameters for test case 1

2.1.2 End Results

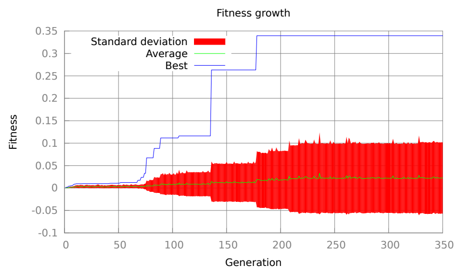
As we can see in figure 2b the end result is quite good for the STDM. Although for this test I had to up the bits per number to quite high and had to run with a higher population than I had initially wanted[2]. The end result is good and there is nothing really special about this. From the last project I found that *Tournament selection* was the better of the four mechanisms and that is reflected here, all the other did worse under the same conditions.

Looking at figure 2a we can see that the analysis about the new crossover was quite right. If we look at the standard deviation we can see that it is very low to begin with and then after some time, goes up. This is signs of stagnation, but because of the high mutation rate we get a good end result.

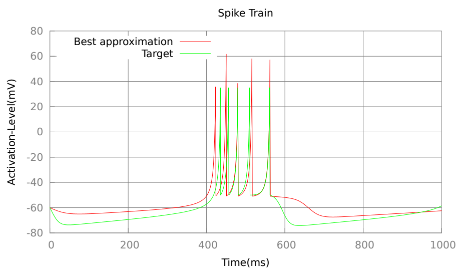
[2]Mostly do to performance concerns

a	b	c	d	k
0.0323	0.0441	-50.924	1.1294	0.0412

Table 2: The neuron variables which gave the best solution for test case 1



(a) Fitness progression for test case 1



(b) Spike train comparison for test case 1

Figure 2: Test case 1 result

2.2 Test Case 2

In this test we are testing SIDM with the test case *izzy-train1.dat*.

2.2.1 EA Parameters

Listing 3: Command-line to replicate the results

```
python src/main.py 350 5 50 --mutation=0.05 --cross_rate=0.8
    full_generational
tournament --k=5 --elite=3 sidm convert_neuron neuron_plot
    training\
data/izzy-train1.dat --bits_per_num=30 --e=0.02
```

2.2.2 End Results

In figure 3b we can see the spike train for this test case, and the story is quite different from the last case, but it is quite expected considering what SIDM

Variable	Value
Generations	350
Population size	50
Mutation rate	0.05
Crossover rate	0.8
Protocol	Full generational replacement
Mechanism	Tournament selection, k=5, e=0.02
Elitism	3
Bits per number	30

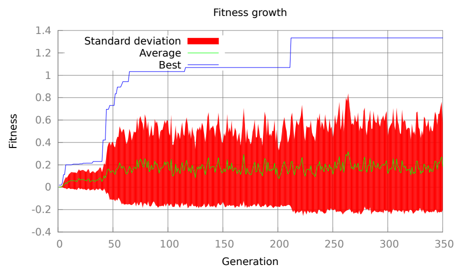
Table 3: EA parameters for test case 2

a	b	c	d	k
0.0010	0.0207	-55.985	5.2820	0.0497

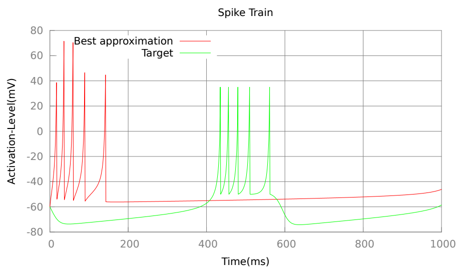
Table 4: The neuron variables which gave the best solution for test case 2

actually does. Since it is mostly conserned with the distance between spikes this technique is very good at getting the distance right, but the placement in the spike train is often wrong.

The fitness(see figure 3a) for this case is much closer to the previous case than the spike train. We can see that in the start the standard deviation is low, but then after some, lucky, mutations it grows and we get a more diverse population.



(a) Fitness progression for test case 2



(b) Spike train comparison for test case 2

Figure 3: Test case 2 result

2.3 Test Case 3

In this test we are testing WDM with the test case *izzy-train1.dat*.

2.3.1 EA Parameters

Listing 4: Command-line to replicate the results

```
python src/main.py 500 5 50 --mutation=0.05 --cross_rate=0.7
    full_generational
sigma --elite=3 wdm convert_neuron neuron_plot training\ data/
    izzy-train1.dat
--bits_per_num=20
```

2.3.2 End Results

The result for this one is very good, actually a lot better than I had initially though, but the result is very much a result of tweaking to get every thing to work at optimum. The strange thing this time was that Sigma scaling was better than Tournament selection. The number of generations also went up in this test, but that can be lowered or increased depending on what sort of result one wants. I tried increasing and got a slightly better result, which indicates

Variable	Value
Generations	500
Population size	50
Mutation rate	0.05
Crossover rate	0.7
Protocol	Full generational replacement
Mechanism	Sigma
Elitism	3
Bits per number	20

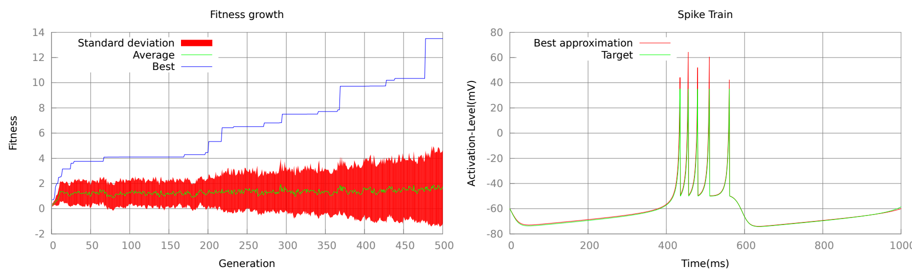
Table 5: EA parameters for test case 3

a	b	c	d	k
0.0246	0.1645	-49.704	1.9947	0.0401

Table 6: The neuron variables which gave the best solution for test case 3

that this probably could become perfect eventually, but I had to draw the line somewhere. If we look at figure 4b we can see that this is almost perfect.

The fitness plot this time around is quite familiar and nothing that special. Since this was run for a longer time than the two previous tests the standard deviation is a bit ”flatter”, but we can still see traces of early stagnation before some mutations kick in.



(a) Fitness progression for test case 3 (b) Spike train comparison for test case 3

Figure 4: Test case 3 result

2.4 Test Case 4

In this test we are testing STDM with the test case *izzy-train2.dat*.

2.4.1 EA Parameters

Listing 5: Command-line to replicate the results

```
python src/main.py 500 5 50 --mutation=0.1 --cross_rate=0.9
    full_generational
sigma --elite=3 stdm convert_neuron neuron_plot training\
```

Variable	Value
Generations	500
Population size	50
Mutation rate	0.1
Crossover rate	0.9
Protocol	Full generational replacement
Mechanism	Sigma scaling
Elitism	3
Bits per number	3

Table 7: EA parameters for test case 4

a	b	c	d	k
0.0229	0.2902	-47.672	5.7082	0.0470

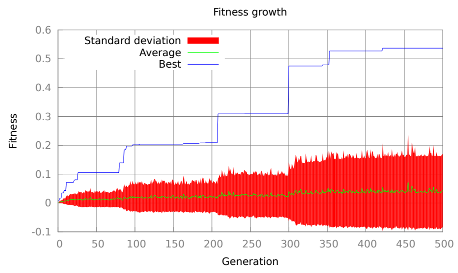
Table 8: The neuron variables which gave the best solution for test case 4

```
data/izzy-train2.dat --bits_per_num=40
```

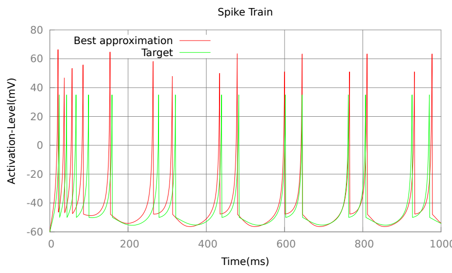
2.4.2 End Results

In this we can again see that STDM is quite good a placing the spike about where they should be, but it can't seem to place them perfect nor get the spacing completely correct.

The fitness is again quite representative for my earlier concerns, but high mutation combined with some elitism and crossover actually produce decent results. We can see that the standard deviation increases along with the best becoming better. This is again one which could probably run forever, but the later increases was not large enough for me to warrant the longer run times.



(a) Fitness progression for test case 4



(b) Spike train comparison for test case 4

Figure 5: Test case 4 result

2.5 Test Case 5

In this test we are testing SIDM with the test case *izzy-train2.dat*.

Variable	Value
Generations	250
Population size	20
Mutation rate	0.1
Crossover rate	0.8
Protocol	Full generational replacement
Mechanism	Tournament, k=5, e=0.02
Elitism	3
Bits per number	40

Table 9: EA parameters for test case 5

a	b	c	d	k
0.0313	0.1220	-43.496	7.9364	0.0502

Table 10: The neuron variables which gave the best solution for test case 5

2.5.1 EA Parameters

Listing 6: Command-line to replicate the results

```
python src/main.py 250 5 20 --mutation=0.1 --cross_rate=0.8
    full_generational
tournament --k=5 --e=0.02 --elite=3 sidm convert_neuron
    neuron_plot training\
data/izzy-train2.dat --bits_per_num=40
```

2.5.2 End Results

This was one of those cases which probably ended up in a local maximum, since changing any variable slightly would plummet the fitness far down. I chose to include it because it was so good and in many cases no other case, so far, have done as good with SIDM.

This case was again quite similar to the others in regard to fitness, it starts out low and then increases. Again this is a test case which could have ran longer, but trying to double the number of generations only gave an increase of about 0.02 which I felt was not good enough.

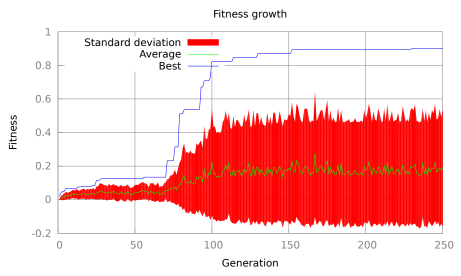
2.6 Test Case 6

In this test we are testing WDM with the test case *izzy-train2.dat*.

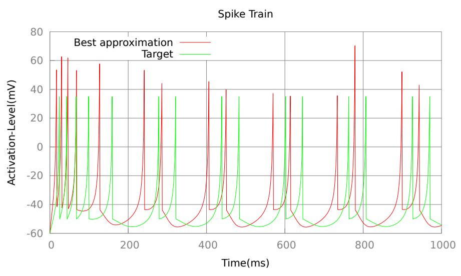
2.6.1 EA Parameters

Listing 7: Command-line to replicate the results

```
python src/main.py 400 5 50 --mutation=0.05 --cross_rate=0.9
    full_generational
sigma --elite=3 wdm convert_neuron neuron_plot training\
```



(a) Fitness progression for test case 5



(b) Spike train comparison for test case 5

Figure 6: Test case 5 result

Variable	Value
Generations	400
Population size	50
Mutation rate	0.05
Crossover rate	0.9
Protocol	Full generational replacement
Mechanism	Sigma
Elitism	3
Bits per number	40

Table 11: EA parameters for test case 6

```
data/izzy-train2.dat --bits_per_num=40
```

2.6.2 End Results

This test case seemed quite hard for WDM. No good results no matter the settings tried which is very strange. The choice of going with Sigma scaling for this was quite random as I tried several times with both this and Tournament selection which came very close to each other and in the end I went with Sigma.

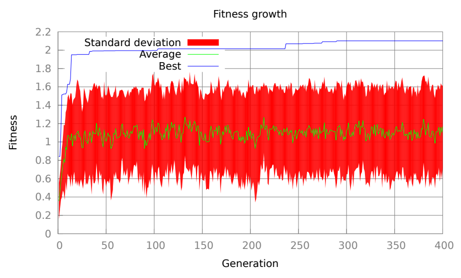
The fitness plot for this is also very strange, which again does not help explain the results.

2.7 Test Case 7

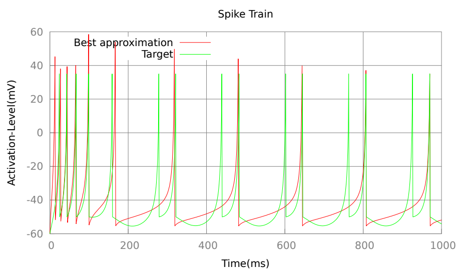
In this test we are testing STDM with the test case *izzy-train3.dat*.

a	b	c	d	k
0.0118	0.0538	-55.717	8.2982	0.0569

Table 12: The neuron variables which gave the best solution for test case 6



(a) Fitness progression for test case 6



(b) Spike train comparison for test case 6

Figure 7: Test case 6 result

Variable	Value
Generations	X
Population size	X
Mutation rate	X
Crossover rate	X
Protocol	X
Mechanism	X
Elitism	X
Bits per number	

Table 13: EA parameters for test case 7

2.7.1 EA Parameters

2.7.2 End Results

2.8 Test Case 8

In this test we are testing SIDM with the test case *izzy-train3.dat*.

2.8.1 EA Parameters

2.8.2 End Results

2.9 Test Case 9

In this test we are testing WDM with the test case *izzy-train3.dat*.

2.9.1 EA Parameters

2.9.2 End Results

2.10 Test Case 10

In this test we are testing STDM with the test case *izzy-train4.dat*.

a	b	c	d	k

Variable	Value
Generations	X
Population size	X
Mutation rate	X
Crossover rate	X
Protocol	X
Mechanism	X
Elitism	X
Bits per number	

Table 14: EA parameters for test case 8

a	b	c	d	k

Variable	Value
Generations	X
Population size	X
Mutation rate	X
Crossover rate	X
Protocol	X
Mechanism	X
Elitism	X
Bits per number	

Table 15: EA parameters for test case 9

a	b	c	d	k

Variable	Value
Generations	X
Population size	X
Mutation rate	X
Crossover rate	X
Protocol	X
Mechanism	X
Elitism	X
Bits per number	

Table 16: EA parameters for test case 10

a	b	c	d	k

2.10.1 EA Parameters

2.10.2 End Results

2.11 Test Case 11

In this test we are testing SIDM with the test case *izzy-train4.dat*.

2.11.1 EA Parameters

2.11.2 End Results

2.12 Test Case 12

In this test we are testing WDM with the test case *izzy-train4.dat*.

2.12.1 EA Parameters

2.12.2 End Results

Variable	Value
Generations	X
Population size	X
Mutation rate	X
Crossover rate	X
Protocol	X
Mechanism	X
Elitism	X
Bits per number	

Table 17: EA parameters for test case 11

a	b	c	d	k

Variable	Value
Generations	X
Population size	X
Mutation rate	X
Crossover rate	X
Protocol	X
Mechanism	X
Elitism	X
Bits per number	

Table 18: EA parameters for test case 12

a	b	c	d	k