# 智慧型演化計算 HW1-Optimal solution

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# 程式碼說明

將GA包成一個class,方便呼叫使用,在使用時即設定相關參數。

```
def __init__(self, pop_size, gene_size, cross_rate, mutation_rate, max_gen, func,
upper, lower, extremum, show_mode):
   self.pop_size = pop_size
                                    # 總染色體數
   self.gene_size = gene_size
                                    # 染色體
   self.cross_rate = cross_rate
                                    # 交配率
   self.mutation\_rate = mutation\_rate # 突變率
                                    # 最大迭代次數
   self.max_gen = max_gen
                                    # 染色體群體
   self.pop = []
                                    # 個體分數
   self.fitness_value = []
                                    # 交配池
   self.mating_pool = []
   self.func = func
                                    # 欲執行的函式名稱
                                    # 搜索範圍上限
   self.upper = upper
   self.lower = lower
                                    # 搜索範圍下限
   self.extremum = extremum
                                    # 找最大或最小值
                                    # 每一代的最佳fitness value
   self.best_result = []
                                    # 每一代最佳fitness_value的參數
   self.best_parameter = []
                                    # 執行時是否在終端顯示執行log
   self.show_mode = show_mode
```

因為是binary的GA·所以需要decode函式,會將只有1或0的list轉為一組在上下限範圍內的值(\$x\_1\$,\$y\_1\$)。

```
def decode(self, pop:list):
    """將染色體內的二進制資料轉為搜索範圍內的值

Args:
    pop (list): 一次一個pop進來‧格式為[1,0,0,1,1]

Returns:
    list: [x1,y1]
    """

decimal_1 = ''
    decimal_2 = ''
    # 因有兩個參數‧故將基因分成前後兩段
    for index in range(self.gene_size // 2): # 前半段
        decimal_1 += str(pop[index])
    for index in range(self.gene_size // 2): # 後半段
        decimal_2 += str(pop[index + self.gene_size // 2])

decimal_1 = int(str(decimal_1),2) # binary to
```

```
decimal decimal_2 = int(str(decimal_2),2)

decimal_1 = float(decimal_1) / (2 ** (self.gene_size//2)) # normalization to 0 ~ 1
decimal_2 = float(decimal_2) / (2 ** (self.gene_size//2))

result_1 = decimal_1 * (self.upper-self.lower) + self.lower # 線性轉換成上下限
範圍內的值
result_2 = decimal_2 * (self.upper-self.lower) + self.lower

return [result_1, result_2]
```

使用initialization()產生初始染色體群體。

```
def initialization(self):
    """產生初始population
    """
    for i in range(self.pop_size):
        temp_pop = []
    for j in range(self.gene_size):
        temp_pop.append(random.choice([0, 1]))
    self.pop.append(temp_pop)
```

使用evaluation()來評估個體的分數,首先先決定要計算哪個群體,接著將染色體內的基因解碼後代入指定的function,取得一數值就是該染色體之個體分數。

```
def evaluation(self, group:str):
    """計算每個pop帶入function內的值

Args:
    group (str): 輸入要計算哪個群體:'pop' or 'mating_pool'
"""

if group == 'pop':
    population = self.pop
elif group == 'mating_pool':
    population = self.mating_pool

self.fitness_value = []
for pop in population:
    result = self.decode(pop)
    value = self.func(result[0], result[1])
    self.fitness_value.append(value)
```

使用selection\_by\_RWS()來產生個別染色體的機率,並抽選至交配池內,此處採用softmax的方式來產生機率。

```
def selection by RWS(self):
    """利用softmax計算出個別的機率後,用輪盤法抽選至交配池內
    def softmax_max(x):
        x = [xi-max(x) \text{ for } xi \text{ in } x]
        e_x = [np.exp(-xi) \text{ for } xi \text{ in } x]
        return [x/sum(e_x) for x in e_x]
    def softmax_min(x):
        x = [xi-max(x) \text{ for } xi \text{ in } x]
        e_x = [np.exp(xi) \text{ for } xi \text{ in } x]
        return [x/sum(e_x) for x in e_x]
    if self.extremum == 'min' and sum(self.fitness_value) == 0:
        self.mating_pool = self.pop
    elif self.extremum == 'min':
        probability = softmax_min(self.fitness_value)
    elif self.extremum == 'max':
        probability = softmax max(self.fitness value)
    for _ in range(self.pop_size):
        random_pop = random.choices(self.pop, weights=probability)[0]
        random_pop = list(random_pop)
        self.mating_pool.append(random_pop)
```

使用crossover()來執行交配行為·先將交配池順序打亂·接著兩兩一組決定是否交配·接著再決定要交配的是x變數還是y變數(染色體內前半段為x·後半段為y)·決定變數後再決定交換的位置。

```
def crossover(self):
    """交配池內的染色體進行交配
   def swap_func(a,b):
       temp = a
       a = b
       b = temp
       return a,b
   shuffle mating pool = np.random.permutation(self.mating pool) # 打亂
mating pool順序
   shuffle_mating_pool = [list(x) for x in shuffle_mating_pool] # 轉為list
   for i in range(∅, len(shuffle mating pool), 2):
       cr = random.uniform(0,1)
       if cr < self.cross rate:</pre>
           x or y = random.choice([0,1]) # 決定要交換x或y 0:x, 1:y
           cross location = int(np.random.uniform(1, self.gene size//2 + 1)) # 決
定要從哪邊開始交換(uniform)
           if x or y == 0:
               shuffle_mating_pool[i][cross_location-1:self.gene_size//2],
shuffle_mating_pool[i+1][cross_location-1:self.gene_size//2] =
swap_func(shuffle_mating_pool[i][cross_location-1:self.gene_size//2],
shuffle_mating_pool[i+1][cross_location-1:self.gene_size//2])
```

使用mutation()來執行突變行為,遍歷交配池內的每個染色體,每條染色體中的基因都有機會發生突變。

```
def mutation(self):
    """交配池内的染色體進行突變
"""

    for p in self.mating_pool:
        for i in range(self.gene_size):
            mr = random.uniform(0,1)
        if mr < self.mutation_rate:
            if p[i] == 0:
                p[i] = 1
            else:
            p[i] = 0
```

使用execute()作為程式主要的執行流程,將上述函式整理成一個流程。

```
def execute(self):
    self.initialization()
    self.evaluation('pop')
    for gen in range(1, self.max_gen+1):
        self.selection by RWS()
        self.crossover()
        self.mutation()
        self.evaluation('mating pool')
       if self.extremum == 'max':
            best fitness = max(self.fitness_value)
        elif self.extremum == 'min':
            best fitness = min(self.fitness value)
        self.best_result.append(best_fitness)
        index = self.fitness_value.index(best_fitness) # 取得index
        parameter = self.decode(self.mating_pool[index]) # 轉為real value
        self.best parameter.append(parameter)
        if self.show mode:
            print(f'Generation {gen}:')
            print(f" best_value: {best_fitness:.4f} parameter:
{parameter[0]:.4f}, {parameter[1]:.4f}")
        self.pop = self.mating_pool # replace
        self.clean()
```

```
self.plot_iteration_result()
self.plot_best_result()
```

ga.py內須注意的地方為POP\_SIZE需為偶數·因為crossover那邊會用到·另一個是gene\_size = GENE\_SIZE\*2· 這邊\*2的原因是染色體內有兩個變數·所以我的GENE\_SIZE是表示一個變數。

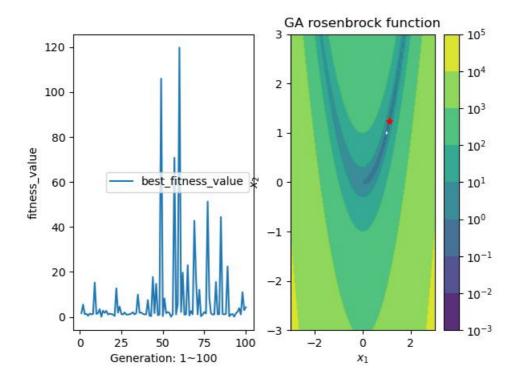
```
if run_select == 1:
   POP SIZE = 100 # even number for crossover
   GENE SIZE = 10
   CROSS_RATE = 0.8 # 0.8 to 0.6
   MUTATION_RATE = 0.2
   MAX_GEN = 100
   UPPER_BOUNDARY = 3
   LOWER_BOUNDARY = -3
   EXTREMUM = 'min'
    ga_rosenbrock = GeneticAlgorithm(pop_size = POP_SIZE,
                        gene_size = GENE_SIZE*2,
                        cross_rate = CROSS_RATE,
                        mutation_rate = MUTATION_RATE,
                        max gen = MAX GEN,
                        func = rosenbrock,
                        upper = UPPER_BOUNDARY,
                        lower = LOWER_BOUNDARY,
                        extremum = 'min',
                        show_mode = True)
    ga_rosenbrock.execute()
```

在執行ga.py時,只需修改run\_select變數以及相關參數,即可執行不同的function。

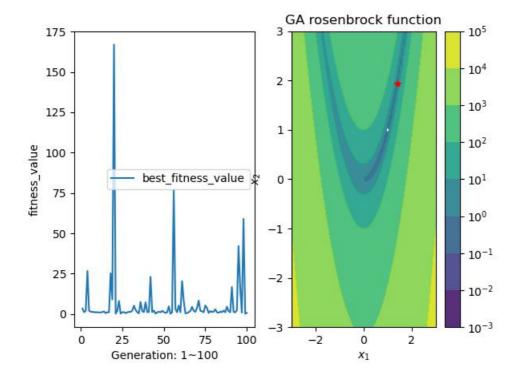
#### rosenbrock

GENE\_SIZE = 10固定不變

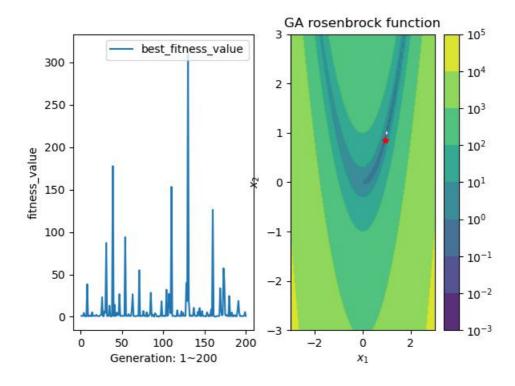
• POP\_SIZE = 100, CROSS\_RATE = 0.6, MUTATION\_RATE = 0.2, MAX\_GEN = 100



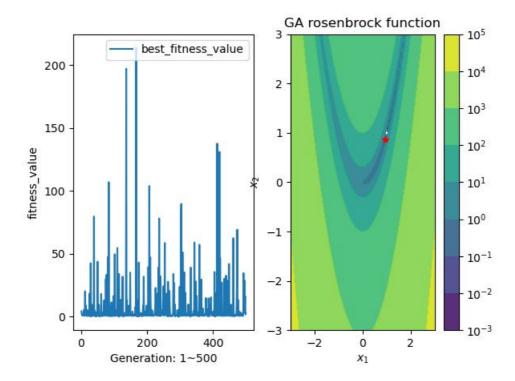
• POP\_SIZE = 100, CROSS\_RATE = 0.8, MUTATION\_RATE = 0.2, MAX\_GEN = 100



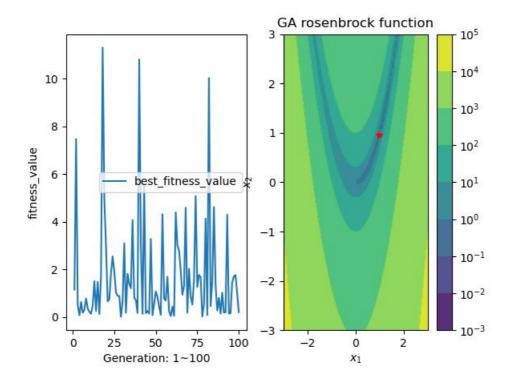
• POP\_SIZE = 100, CROSS\_RATE = 0.8, MUTATION\_RATE = 0.2, MAX\_GEN = 200



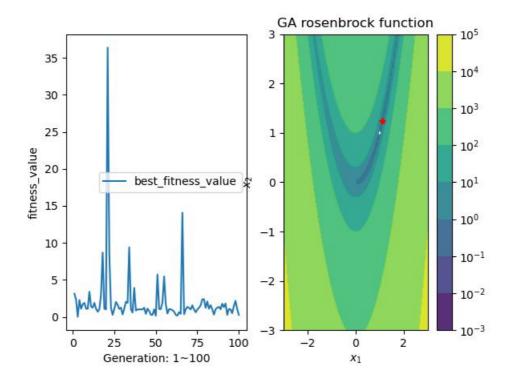
• POP\_SIZE = 100, CROSS\_RATE = 0.8, MUTATION\_RATE = 0.2, MAX\_GEN = 500



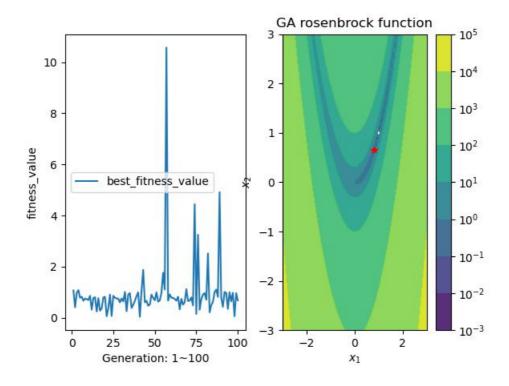
• POP\_SIZE = 100, CROSS\_RATE = 0.8, MUTATION\_RATE = 0.4, MAX\_GEN = 100



• POP\_SIZE = 200, CROSS\_RATE = 0.8, MUTATION\_RATE = 0.2, MAX\_GEN = 100



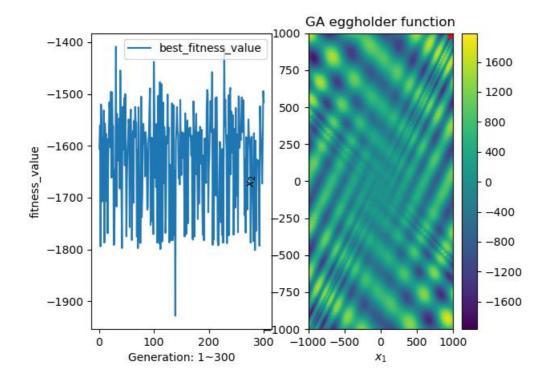
• POP\_SIZE = 300, CROSS\_RATE = 0.8, MUTATION\_RATE = 0.2, MAX\_GEN = 100



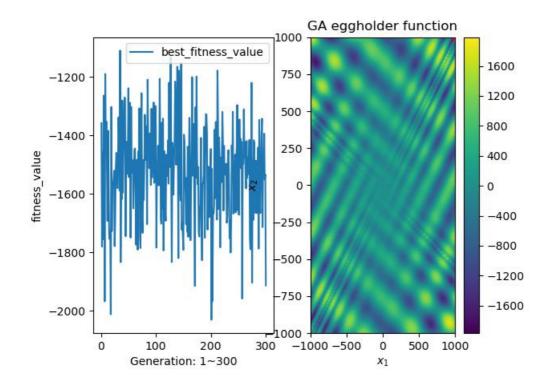
# eggholder

POP\_SIZE = 200, GENE\_SIZE = 16固定不變

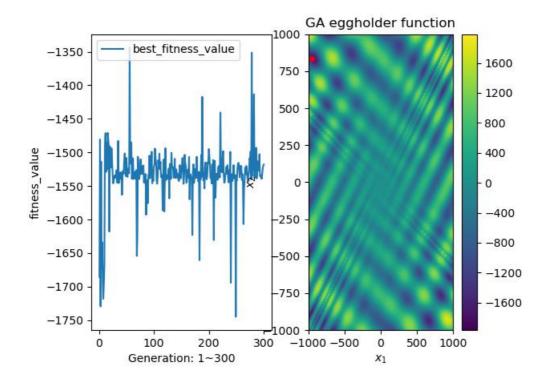
• CROSS\_RATE = 0.6, MUTATION\_RATE = 0.2, MAX\_GEN = 300



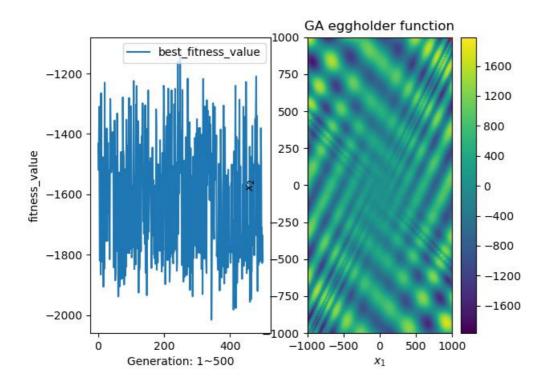
CROSS\_RATE = 0.6, MUTATION\_RATE = 0.4, MAX\_GEN = 300



• CROSS\_RATE = 0.8, MUTATION\_RATE = 0.2, MAX\_GEN = 300



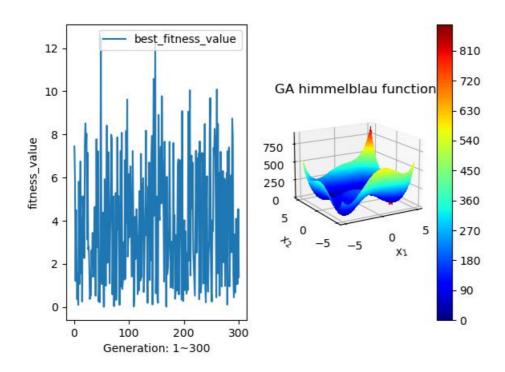
• CROSS\_RATE = 0.8, MUTATION\_RATE = 0.2, MAX\_GEN = 500



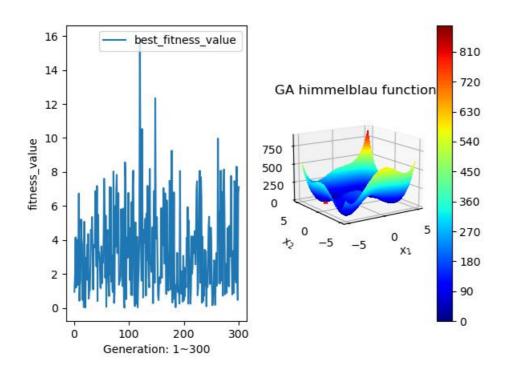
## himmelblau

POP\_SIZE = 200, GENE\_SIZE = 16固定不變

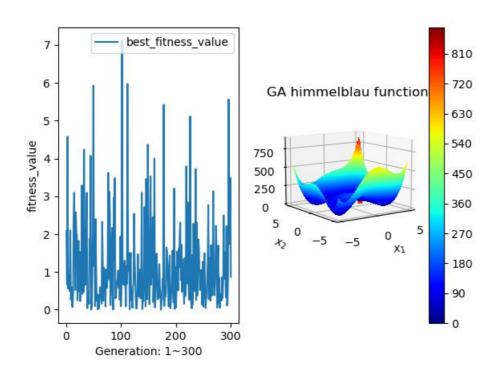
• CROSS\_RATE = 0.6, MUTATION\_RATE = 0.2, MAX\_GEN = 300



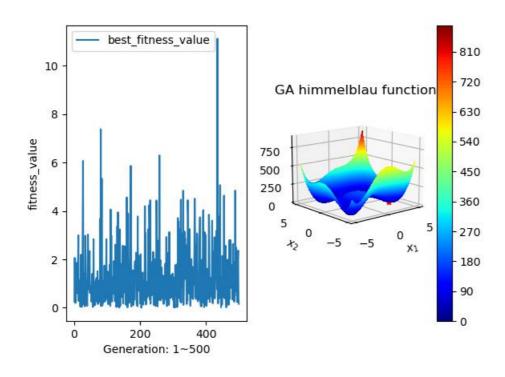
CROSS\_RATE = 0.8, MUTATION\_RATE = 0.2, MAX\_GEN = 300



• CROSS\_RATE = 0.8, MUTATION\_RATE = 0.4, MAX\_GEN = 300



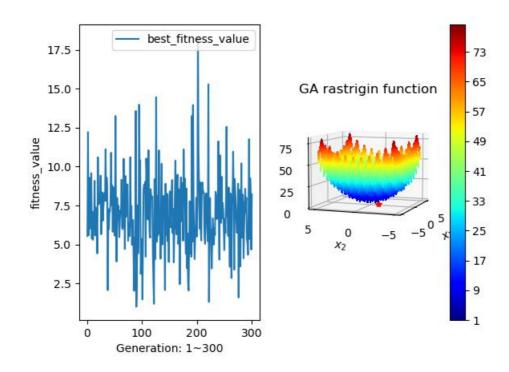
• CROSS\_RATE = 0.8, MUTATION\_RATE = 0.4, MAX\_GEN = 500



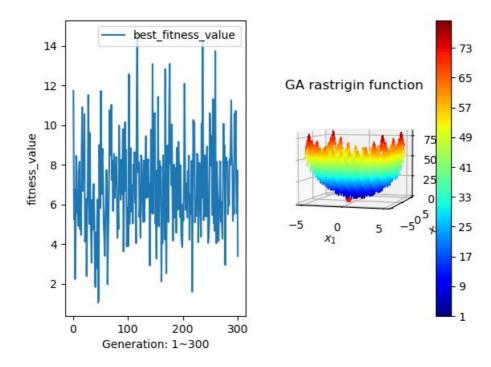
# rastrigin

POP\_SIZE = 200, GENE\_SIZE = 16, MAX\_GEN = 300固定不變

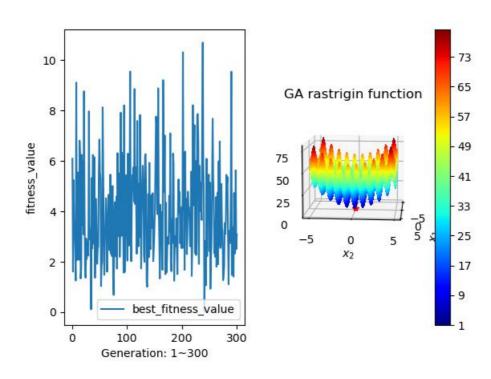
• CROSS\_RATE = 0.6, MUTATION\_RATE = 0.2



## • CROSS\_RATE = 0.8, MUTATION\_RATE = 0.2



## • CROSS\_RATE = 0.8, MUTATION\_RATE = 0.4



# 成果說明

#### rosenbrock:

提升POP\_SIZE為200或300 & 降低CROSS\_RATE至0.6 & 提升MAX\_GEN至200或500看起來效果都差不多,都很容易掉入local minimum裡面,將MUTATION\_RATE提升至0.4後更容易到達最低點。

#### • eggholder:

觀察執行結果發現常常最佳點都出現在右上或左上·此題感覺比較難找到最佳點·多次修改參數·結果都不相同。

#### • himmelblau:

此function的低點在四個象限,我實作出來的結果大多都在一、二和四象限,第三象限幾乎沒有出現。

### • rastrigin:

這題最低點應該會在[0,0]的地方,而我實作的結果大多都在[-1,1]之間,算接近了,但仍不是最佳。

# 心得

• 透過這次的作業,讓我了解到如何實作GA演算法,也對於GA演算法的流程更加的熟悉,未來若遇到可以轉為方程式的問題,就可以用這個方法來求解。這個方法參考生物的演化我覺得很有趣,交配與突變這個過程,就像現實中自己往自己所認為對的方向前進,殊不知因為自己的視野範圍小所以是往local的最佳值前進,此時就需要旁人的提醒或自身的醒悟來改變方向,往global最佳值前進。