

מעבדה 2 חלק א

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implemented in fitness selector

```
class fitness_selector:
    def __init__(self):...

    def distance_fitness(self, object, target, target_size):...

    def bul_pqia(self, object, target, target_size):...

    # fitness for NQueens:
    def n_queens_conflict(self, object, target, target_size):...

    def n_queens_conf_based_on_place(self, object, row, col):...

    def bins_fitness(self, object, target, target_size):...

    def levinshstine_distance(self, a, b, target_size=0):...

    def kendallTauDistance(self, values1, values2):...
```

## Implementation

```
def levinshstine_distance(self, a, b, target_size=0):
    """ if one of them is of length 0 return the length of the other """
    if len(a) == 0:
        return len(b)
    elif len(b) == 0:
        return len(a)
    # if the first character matches then go farther in the strings
    elif a[0] == b[0]:
        return self.levinshstine_distance(a[1:], b[1:])
    # x calculate distance between the first string without the first character with the second string
    # y same as x but cuts down b by one( takes the tail of b with full a
    # z compares both tales of a and b
    else:
        x, y, z = self.levinshstine_distance(a[1:], b), self.levinshstine_distance(a,
                                                                                       b[1:]), self.levinshstine_distance(
            a[1:], b[1:])
        return 1 + min(x, y, z)

def kendallTauDistance(self, values1, values2):
    """Compute the Kendall tau distance."""
    n = len(values1)
    assert len(values2) == n, "Both lists have to be of equal length"
    i, j = numpy.meshgrid(numpy.arange(n), numpy.arange(n))
    a = numpy.argsort(values1)
    b = numpy.argsort(values2)

    ndisordered = numpy.logical_or(numpy.logical_and(a[i] < a[j], b[i] > b[j]),
                                   numpy.logical_and(a[i] > a[j], b[i] < b[j])).sum()
    return ndisordered / (n * (n - 1))
```

self.gene\_dist is the distance function that we get from fitness type class , so that we can use it in the algorithm as we please

```
class genetic_algorithm(algorithm):
    def __init__(self, target, tar_size, pop_size, problem_spec, crosstype, fitness_type, selection,
                  surviving_mechanism, mutation, gene_dist):
        algorithm.__init__(self, target, tar_size, pop_size, problem_spec, fitness_type, selection)
        self.cross_func = cross_types().select[crosstype]
        self.surviving = surviving_mechanism
        self.mutation_type = mutation
        self.gene_dist = self.problem_spec().fitness_type[gene_dist]
```

## סעיף 2:

previously the ranking system was done in each selection function , now we changed it to be done on the population and just send a probabilities array to the selection function

selection pressure:

- in case of RWS and SUS and Tournament: we use the probability of selection that exists in fitness array (it's a probability array of each individual) to find the probability of selecting best individual and the average individual

```
def probabilities_rank_based(self):
    # depending on the selection scheme get probabilities from ranking system !
    multiplier = 1 if self.selection == SUS or RWS else 0.5 # for now keep it like this
    # scale fitness values with linear ranking for sus and RWS
    if self.selection == SUS:
        mio = self.pop_size
        self.fitness_array = numpy.array([p_linear_rank(mio, int(i)) for i in range(self.pop_size - 1, -1, -1)])
    # get accumulative sum of above values
    elif self.selection == RWS:
        mean = numpy.mean(self.fitness_array)
        std = numpy.std(self.fitness_array)
        # linear scale
        self.fitness_array = numpy.array([i for i in range((self.pop_size + 1) * 10, 10, -10)])
        # sigma scale
        self.fitness_array = numpy.array(
            [max((f - mean) / (2 * std), 1) if std > 0 else 1 for f in self.fitness_array])
        sum = self.fitness_array.sum()
        self.fitness_array = numpy.array([i / sum for i in self.fitness_array])
    else:
        # fps for tournament selection
        self.fitness_array = numpy.array([pop.fitness for pop in self.population])
        sumof_fit = self.fitness_array.sum()
        sumof_fit = sumof_fit if sumof_fit else 1
        self.fitness_array = numpy.array([(pop.fitness + 1) / sumof_fit for pop in self.population])

    # selection pressure :
    self.selection_pressure = self.fitness_array[0] / numpy.mean(
        self.fitness_array) if self.fitness_array.any() else 0
    if self.selection_pressure and (self.selection != SUS and self.selection != RWS):
        self.selection_pressure = 1 / self.selection_pressure
```

## Diversity :

- to calculate diversity we calculate the distance of each individual with the full population , then average it out and store it
- then add all individual diversities and average them out to indicate the diversity of the whole population

```
def calc_diversity(self):
    # if the distance is levishtine distance we can aproximate it by calculating the difference
    # between 2 strings on all the population
    # by that we mean the distance between all the population and one string
    # and then using a+b<c to approximate it !
    # Distance_hash = {}
    mean = 0
    self.pop_diversity = 0
    counter = 0
    counter2 = 0
    # print(len(self.population),"pop size")
    for i in range(self.pop_size):
        self.population[i].diversity = 0
        mean += self.population[i].fitness
        # for j in sample:
        for j in range(self.pop_size):
            # calculate diversity for each individual with a hash table so that we don't
            # calculate the same string twice
            strings = self.population[i].hash(self.population[j])
            strings2 = self.population[j].hash(self.population[i])
            if strings in self.Distance_hash.keys():
                self.population[i].diversity += self.Distance_hash[strings]
                counter += 1
            elif strings2 in self.Distance_hash.keys():
                counter += 1
                self.population[i].diversity += self.Distance_hash[strings2]
            else:
                counter2 += 1
                self.Distance_hash[strings] = self.gene_dist(self.population[i].object, self.population[j].object)
                self.population[i].diversity += self.Distance_hash[strings]
        self.population[i].diversity = self.population[i].diversity / self.pop_size
        self.pop_diversity += self.population[i].diversity
    self.pop_mean = mean / self.pop_size

    # divide by all population to get population diversity
    # print("hashed",counter,"first time hash ",counter2)
    old_pop_diversity = self.pop_diversity
    self.pop_diversity /= self.pop_size

    self.trigger_mutation = True if old_pop_diversity < self.pop_diversity else False
```

## סעיף 3:

### תוצאות :

population size	exploration to exploitaion	Hyper triggered	mutation parameter=0.25
100	generation:33 ,runtime: 31	generations:28 ,runtime:32	generation:35 ,runtime: 35.7
300	generation:21 ,runtime: 209	generations:19 ,runtime:182	generation:20 ,runtime: 195

As we have seen in previous lab ,our perfect mutation rate was 0.25 so we used it , as we have tried lower or higher , and it wasn't optimal

#### Results :

- when the population is small both Hyper triggered and linear exploration to exploitation both work better than a fixed mutation rate.
- When the population is bigger:
  - we can see that the linear exploration to exploitation is worst than both , but this result does not reflect the full truth , as in bigger populations our linear function should be adjusted to the appropriate ratio between population size and the linear value that we add to the original mating probability
  - Hyper triggered is faster than a fixed mutation rate. And gets out of local optima much faster

## מעבר הדרגתי מ exploration ל exploitation :

Population size=100

```
selection pressure: 1.9527472527472527 Diversity: 3.5922
Best:h,e,l,d,o,l,w,o,r,l,d,r, ,fitness: 90 Mean: 176.7 ,Variance: 86.69999999999999 Time : 24.2154452 ticks: 24.21562361717224
0.23000000000000012

selection pressure: 2.844262295081968 Diversity: 3.5838000000000001
Best:h,e,l,d,o,l,w,o,r,l,d,l, ,fitness: 60 Mean: 172.5 ,Variance: 112.5 Time : 25.117565799999998 ticks: 25.118208646774292
0.23500000000000013

selection pressure: 2.770491803278689 Diversity: 3.6748000000000003
Best:h,e,l,d,o,l,w,o,r,l,d,l, ,fitness: 60 Mean: 168.0 ,Variance: 108.0 Time : 26.0116635 ticks: 26.011826515197754
0.24000000000000013

selection pressure: 2.6032786885245898 Diversity: 3.4731999999999994
Best:h,e,l,d,o,l,w,o,r,l,d,l, ,fitness: 60 Mean: 157.8 ,Variance: 97.80000000000001 Time : 26.922158200000002 ticks: 26.922679662704468
0.24500000000000013

selection pressure: 2.411475409836066 Diversity: 3.1922000000000001
Best:h,e,l,d,o,l,w,o,r,l,d,l, ,fitness: 60 Mean: 146.1 ,Variance: 86.1 Time : 27.755675999999998 ticks: 27.75644826889038
0.25000000000000001

selection pressure: 2.249180327868852 Diversity: 2.9308000000000014
Best:h,e,l,d,o,l,w,o,r,l,d,l, ,fitness: 60 Mean: 136.2 ,Variance: 76.19999999999999 Time : 28.646290899999998 ticks: 28.64706540107727
0.25500000000000001

selection pressure: 2.254098360655738 Diversity: 2.8630000000000001
Best:h,e,l,d,o,l,w,o,r,l,d,l, ,fitness: 60 Mean: 136.5 ,Variance: 76.5 Time : 29.4281168 ticks: 29.428019523620605
0.26000000000000001

selection pressure: 4.145161290322582 Diversity: 2.5974
Best:h,e,l,d,o,l,w,o,r,l,d,l, ,fitness: 30 Mean: 127.5 ,Variance: 97.5 Time : 30.200909900000003 ticks: 30.200867176055908
0.26500000000000001

selection pressure: 4.048387096774194 Diversity: 2.7429999999999994
Best:h,e,l,d,o,l,w,o,r,l,d,l, ,fitness: 30 Mean: 124.5 ,Variance: 94.5 Time : 30.990103800000004 ticks: 30.990882873535156
0.27000000000000001

selection pressure: 122.49999999999999 Diversity: 2.6938
Best:h,e,l,d,o,l,w,o,r,l,d,l, ,fitness: 0 Mean: 121.5 ,Variance: 121.5 Time : 31.6987353 ticks: 31.698997974395752
number of generations : 33
Overall runtime : 31.6987812
```

## Population size=300

```
selection pressure: 2.2296703296703293 Diversity: 5.196088888888889
Best:d,e,l!,o ,w,o,r,h,d!, ,fitness: 90 Mean: 201.9 ,Variance: 111.9 Time : 127.85266419999999 ticks: 127.85233640670776
0.17000000000000007

selection pressure: 2.1252747252747253 Diversity: 5.002133333333335
Best:d,e,l!,o ,w,o,r,h,d!, ,fitness: 90 Mean: 192.4 ,Variance: 102.4 Time : 137.4043643 ticks: 137.40465712547302
0.17500000000000007

selection pressure: 5.754838709677419 Diversity: 4.627888888888888
Best:h,e,l,h,o ,w,o,r,l,d!, ,fitness: 30 Mean: 177.4 ,Variance: 147.4 Time : 146.480774 ticks: 146.48031497001648
0.18000000000000008

selection pressure: 5.345161290322581 Diversity: 4.245888888888891
Best:h,e,l,h,o ,w,o,r,l,d!, ,fitness: 30 Mean: 164.7 ,Variance: 134.7 Time : 155.5897098 ticks: 155.5895025730133
0.18500000000000008

selection pressure: 4.938709677419356 Diversity: 4.003488888888887
Best:h,e,l,h,o ,w,o,r,l,d!, ,fitness: 30 Mean: 152.1 ,Variance: 122.1 Time : 164.61762050000002 ticks: 164.6176633834839
0.19000000000000009

selection pressure: 4.632258064516129 Diversity: 3.941155555555557
Best:h,e,l,h,o ,w,o,r,l,d!, ,fitness: 30 Mean: 142.6 ,Variance: 112.6 Time : 173.6350033 ticks: 173.63465404510498
0.19500000000000001

selection pressure: 4.4161290322580635 Diversity: 3.628888888888893
Best:h,e,l,h,o ,w,o,r,l,d!, ,fitness: 30 Mean: 135.9 ,Variance: 105.9 Time : 182.7402023 ticks: 182.73967719078064
0.20000000000000001

selection pressure: 4.103225806451613 Diversity: 3.512444444444444
Best:h,e,l,h,o ,w,o,r,l,d!, ,fitness: 30 Mean: 126.2 ,Variance: 96.2 Time : 191.5082353 ticks: 191.50839710235596
0.20500000000000001

selection pressure: 3.8161290322580634 Diversity: 3.254755555555557
Best:h,e,l,h,o ,w,o,r,l,d!, ,fitness: 30 Mean: 117.3 ,Variance: 87.3 Time : 200.3478611 ticks: 200.3475923538208
0.21000000000000001

selection pressure: 116.3 Diversity: 3.048222222222221
Best:h,e,l,l,o ,w,o,r,l,d!, ,fitness: 0 Mean: 115.3 ,Variance: 115.3 Time : 209.0021326 ticks: 209.00203108787537
number of generations : 21
Overall runtime : 209.0022042
```

## Hyper triggered:

### Population size=100:

```
selection pressure: 3.9709677419354845 Diversity: 2.673399999999999
Best:h,e,l,l,o ,w,o,r,e,d!, ,fitness: 30 Mean: 122.1 ,Variance: 92.1 Time : 25.496625899999998 ticks: 25.49640727043152

selection pressure: 4.087096774193549 Diversity: 2.7175999999999998
Best:h,e,l,l,o ,w,o,r,e,d!, ,fitness: 30 Mean: 125.7 ,Variance: 95.7 Time : 26.666620199999997 ticks: 26.666279315948486

selection pressure: 3.816129032258064 Diversity: 2.6528000000000005
Best:h,e,l,l,o ,w,o,r,e,d!, ,fitness: 30 Mean: 117.3 ,Variance: 87.3 Time : 27.830959299999996 ticks: 27.83047080039978

selection pressure: 3.8935483870967738 Diversity: 2.4547999999999996
Best:h,e,l,l,o ,w,o,r,e,d!, ,fitness: 30 Mean: 119.7 ,Variance: 89.7 Time : 28.7527641 ticks: 28.75200653076172

selection pressure: 3.7677419354838695 Diversity: 2.4080000000000004
Best:h,e,l,l,o ,w,o,r,e,d!, ,fitness: 30 Mean: 115.8 ,Variance: 85.8 Time : 29.8185669 ticks: 29.81815528869629

selection pressure: 3.709677419354838 Diversity: 2.5027999999999992
Best:h,e,l,l,o ,w,o,r,e,d!, ,fitness: 30 Mean: 114.0 ,Variance: 84.0 Time : 30.8594808 ticks: 30.85938024520874

selection pressure: 3.8838709677419345 Diversity: 2.5512
Best:h,e,l,l,o ,w,o,r,e,d!, ,fitness: 30 Mean: 119.4 ,Variance: 89.4 Time : 31.923028099999996 ticks: 31.922614812850952

selection pressure: 114.40000000000002 Diversity: 2.3918
Best:h,e,l,l,o ,w,o,r,l,d!, ,fitness: 0 Mean: 113.4 ,Variance: 113.4 Time : 32.8786104 ticks: 32.87814378738403
number of generations : 28
Overall runtime : 32.8786612
```

## Population size=300

```
selection pressure: 2.5142857142857147   Diversity: 5.792177777777773
Best:e,e,l,h,o, ,w,r,r,l,d,!, ,fitness: 90   Mean: 227.8 ,Variance: 137.8   Time : 102.6090923   ticks: 102.6088194847107

selection pressure: 2.261538461538461   Diversity: 5.470266666666667
Best:e,e,l,h,o, ,w,r,r,l,d,!, ,fitness: 90   Mean: 204.8 ,Variance: 114.80000000000001   Time : 112.1589257   ticks: 112.15904355049133

selection pressure: 3.1049180327868857   Diversity: 4.941111111111112
Best:h,e,l,h,o, ,w,r,r,l,d,!, ,fitness: 60   Mean: 188.4 ,Variance: 128.4   Time : 121.142664   ticks: 121.1427993774414

selection pressure: 2.8950819672131143   Diversity: 4.537777777777775
Best:h,e,l,h,o, ,w,r,r,l,d,!, ,fitness: 60   Mean: 175.6 ,Variance: 115.6   Time : 130.1224863   ticks: 130.12253212928772

selection pressure: 5.31290322580645   Diversity: 4.071911111111111
Best:h,e,l,h,o, ,w,o,r,l,d,!, ,fitness: 30   Mean: 163.7 ,Variance: 133.7   Time : 138.9716439   ticks: 138.97207188606262

selection pressure: 4.874193548387097   Diversity: 3.6676222222222234
Best:h,e,l,h,o, ,w,o,r,l,d,!, ,fitness: 30   Mean: 150.1 ,Variance: 120.1   Time : 147.8177689   ticks: 147.81776213645935

selection pressure: 4.470967741935484   Diversity: 3.5062888888888946
Best:h,e,l,h,o, ,w,o,r,l,d,!, ,fitness: 30   Mean: 137.6 ,Variance: 107.6   Time : 156.64445039999998   ticks: 156.64502954483032

selection pressure: 4.3193548387096765   Diversity: 3.453555555555559
Best:h,e,l,h,o, ,w,o,r,l,d,!, ,fitness: 30   Mean: 132.9 ,Variance: 102.9   Time : 165.3450614   ticks: 165.3455469608307

selection pressure: 4.2548387096774185   Diversity: 3.4222222222222203
Best:h,e,l,h,o, ,w,o,r,l,d,!, ,fitness: 30   Mean: 130.9 ,Variance: 100.9   Time : 173.7330652   ticks: 173.73295617103577

selection pressure: 122.49999999999999   Diversity: 3.096844444444443
Best:h,e,l,l,o, ,w,o,r,l,d,!, ,fitness: 0   Mean: 121.5 ,Variance: 121.5   Time : 182.0372577   ticks: 182.0370054244995
number of generations : 19
Overall runtime : 182.03730560000002
```

## Fixed mutation parameter:

Mutation rate=0.25:

Population size=100:

```
selection pressure: 4.667741935483871   Diversity: 3.1178
Best:h,e,l,r,o, ,w,o,r,l,d,!, ,fitness: 30   Mean: 143.7 ,Variance: 113.69999999999999   Time : 30.776093300000014   ticks: 30.775875329971313

selection pressure: 4.570967741935484   Diversity: 3.2325999999999993
Best:h,e,l,r,o, ,w,o,r,l,d,!, ,fitness: 30   Mean: 140.7 ,Variance: 110.69999999999999   Time : 31.782166100000004   ticks: 31.782013177871704

selection pressure: 4.3   Diversity: 3.1522000000000001
Best:h,e,l,r,o, ,w,o,r,l,d,!, ,fitness: 30   Mean: 132.3 ,Variance: 102.30000000000001   Time : 32.818920900000002   ticks: 32.81911778450012

selection pressure: 4.203225806451615   Diversity: 3.0341999999999999
Best:h,e,l,r,o, ,w,o,r,l,d,!, ,fitness: 30   Mean: 129.3 ,Variance: 99.30000000000001   Time : 33.777676400000002   ticks: 33.777637243270874

selection pressure: 3.9225806451612897   Diversity: 2.9193999999999996
Best:h,e,l,r,o, ,w,o,r,l,d,!, ,fitness: 30   Mean: 120.6 ,Variance: 90.6   Time : 34.776272000000006   ticks: 34.7761652469635

selection pressure: 123.39999999999998   Diversity: 2.7810000000000014
Best:h,e,l,l,o, ,w,o,r,l,d,!, ,fitness: 0   Mean: 122.4 ,Variance: 122.4   Time : 35.725356700000002   ticks: 35.72544026374817
number of generations : 35
Overall runtime : 35.725403299999998
```

## Population size=300:



```

selection pressure: 2.32967032967033   Diversity:  6.0029111111111107
Best:h,e,!,l,o, ,e,o,r,!,d,!, ,fitness: 90   Mean: 211.0 ,Variance: 121.0 Time :  123.51850289999999   ticks: 123.51901435852051

selection pressure: 2.1736263736263743   Diversity:  5.6620000000000001
Best:h,e,!,l,o, ,e,o,r,!,d,!, ,fitness: 90   Mean: 196.8 ,Variance: 106.80000000000001 Time :  132.83431650000006   ticks: 132.83461451530457

selection pressure: 3.055737704918032   Diversity:  5.3229111111111114
Best:h,e,l,l,o,o,w,o,r,l,d,w, ,fitness: 60   Mean: 185.4 ,Variance: 125.4 Time :  142.10310280000004   ticks: 142.10357117652893

selection pressure: 5.425806451612904   Diversity:  5.0580444444444447
Best:h,e,l,l,o,!,w,o,r,l,d,!, ,fitness: 30   Mean: 167.2 ,Variance: 137.2 Time :  151.4614337   ticks: 151.46148252487183

selection pressure: 4.8096774193548395   Diversity:  4.3552444444444448
Best:h,e,l,l,o,!,w,o,r,l,d,!, ,fitness: 30   Mean: 148.1 ,Variance: 118.1 Time :  160.70845049999997   ticks: 160.70830154418945

selection pressure: 4.4161290322580635   Diversity:  3.9321333333333293
Best:h,e,l,l,o,!,w,o,r,l,d,!, ,fitness: 30   Mean: 135.9 ,Variance: 105.9 Time :  169.5769366   ticks: 169.57731676101685

selection pressure: 4.106451612903224   Diversity:  3.5228222222222225
Best:h,e,l,l,o,!,w,o,r,l,d,!, ,fitness: 30   Mean: 126.3 ,Variance: 96.3 Time :  178.40248300000002   ticks: 178.40223503112793

selection pressure: 4.019354838709678   Diversity:  3.3190666666666667
Best:h,e,l,l,o,!,w,o,r,l,d,!, ,fitness: 30   Mean: 123.6 ,Variance: 93.6 Time :  187.12032330000005   ticks: 187.12085580825806

selection pressure: 122.59999999999998   Diversity:  3.0111555555555553
Best:h,e,l,l,o, ,w,o,r,l,d,!, ,fitness: 0   Mean: 121.6 ,Variance: 121.6 Time :  195.63413510000004   ticks: 195.6339144706726
number of generations :  20
Overall runtime : 195.63420279999997

```

## סעיף 4:

## Implementation of GA with speciation:

```

class Genetic_speciation(genetic_algorithm):

    def __init__(self, target, tar_size, pop_size, problem_spec, crosstype, fitness_type, selection,
                  surviving_mechanism, mutation, gene_dist, speciation, mutation_probability=0):
        genetic_algorithm.__init__(self, target, tar_size, pop_size, problem_spec, crosstype, fitness_type, selection,
                                    surviving_mechanism, mutation, gene_dist, mutation_probability)
        self.mate_for_species = mate_for_species(target, tar_size, pop_size, problem_spec, crosstype, fitness_type,
                                                  selection,
                                                  surviving_mechanism, mutation, gene_dist, mutation_probability)

        self.groups = []
        self.speciation=SpeciationType().type[speciation]
        self.speciationType=speciation
        # threshold speciation factor to control threshold
        self.distance_factor=0
        self.threshold=0
        self.species_count=0.05*pop_size

    # this function returns an array for each species , how many are elite
    # so that we can choose the appropriate amount of genes from species and so that the population size stays the same
    def how_many_of_each_species(self, size):...

    # uses a function to divide population into species
    # def threshold_speciation(self, threshold):
    #     return threshold_speciation(self.Distance_hash, threshold, self.population)

    def mate(self, gen):...
    def init_population(self):...

    def algo(self, i):...

```

## Explanation of each parameter :



1. Groups is an array that has k clusters where k is defined from either threshold speciation or k-means clustering .
2. distance\_factor : is a minimal distance metric between two identical genes that one of them was mutated.
3. Speciation : a function that returns clusters in an array .
4. SpeciationType : dictates which algorithm to use for speciation ,i.e. threshold speciation or k-means clustering
5. Self.threshold: is used either as k or as the current threshold based on the speciationType

## Explanation of each function :

### 1. how\_many\_of\_each\_speciey(self,size)

- specifies the number and positions of the elite member in each cluster/specie

### 2. def mate(self, gen):

- treats each specie as a single population and mates only the ones that are in the cluster/specie
- after going over all cluster , this function puts all genes of all kind of species in the buffer as separate genes.(not as clusters)

```
def mate(self, gen):
    |  esize = self.serving_genes()
    |  # cross function for initial GA algo
    |  elite_individuals = self.how_many_of_each_speciey(esize)
    |  for index, group in enumerate(self.groups):
    |      temp_buffer = self.mate_for_species.mate_pop(group, gen, elite_individuals[index])
    |      self.buffer[esize:esize + len(group) - elite_individuals[index]] = temp_buffer[:]
    |      esize += len(group) - elite_individuals[index]
```

### 3. def init\_population(self)

- this function initiates the population as it was done in previous implementations and calculates the distance\_factor or k so that we can use those parameters in the speciation itself

### 4. def algo(self, i):

- This is the algorithm itself:
  - o First calculate diversity for all population
  - o Sort them by fitness
  - o Change current threshold based on previous iteration
  - o Rank population for selection methods
  - o Use the new mate function to mate the population

- o Then new hash is created for distance measurements

## Implementation of speciation types:

```
def spicieation_threshold(most_recent_thresh, minimal_distance, numOfspieces, spieces_count):...

def Minimal_distance(gene, distance_function, prob_spec):...

class SpeciationType:
    def __init__(self):
        self.type = {1: self.threshold_speciation, 2: self.optimal_k_clustering}

    # threshold functions:

    def threshold_speciation(self, hash, thresh, pop):...

    # k means functions
    # given centroids and population, hash of distances create the clusters
    def k_means_clustering(self, hash, k, pop):...

    def optimal_k_clustering(self, hash, k, pop):...

    def sub_k_means(self, hash, pop, centroids, clusters, clusters_means, distances):...

    # finds the closest distance from the centroid
    def find_closest_val(self, array, value):...

    def silhouette_score(self, clusters, hash):...
```

1. `def spicieation_threshold`
  - returns the new threshold
2. `def Minimal_distance(gene, distance_function, prob_spec)`
  - returns the minimal distance to reduce or add to threshold
3. `def threshold_speciation(self, hash, thresh, pop):`
  - returns the new clusters
  - basically starts with the first gene checks if the threshold condition applies then adds member to a cluster
  - after insertion of first 2 genes in a specific cluster, the distance check is used on all members of the specific cluster
  - continues to add clusters and members until it finishes going over the full population
4. `def optimal_k_clustering(self, hash, k, pop):`
  - starts with k=3 up to maximum k
  - uses k-means clustering until silhouette\_score returns True , i.e. until k is optimal
5. `def k_means_clustering(self, hash, k, pop):`
  - Creates iterations of sub\_k\_means until population converges ,i.e. until centroids do not change from previous iteration
6. `def sub_k_means(self, hash, pop, centroids, clusters, clusters_means, distances):`
  - Appoints genes to centroids based on minimal distance from centroid
  - Returns new clusters with mean of distances in each cluster

Comparison between Threshold Speciation and k-means Clustering Speciation :

Runs on strings matching (bul pgiaa):

	Threshold			K-means clustering
population size	5 % of poulation size	15% of population	30	
100	generation:30 runtime: 34.5	generations:34 runtime:30	generation:90 runtime: 90	generation:28 runtime: 25
200	generation:30 runtime: 118	generations:29 runtime:129	generation:33 runtime: 143.5	generation:27 runtime: 111
512	generation:17 runtime: 502	generations:23 runtime:637	generation:17 runtime: 492	generation:11 runtime: 340

There are 2 main metrics to consider when comparing the two algorithms

1. Time to get to the solution
2. The quality of the solution

The results above are quite clear:

1. The time to get to the solution in k means is a lot faster than threshold speciation ,although in small populations it doesn't amount to much difference but in larger populations we can see a significant time reduction /
2. The quality of the solution on both algorithms is outstanding ,as we see in the mock trials below of the code running :
  - On both we can see that the initial mating of the species produces better solutions, we can see that in the fitness value and mean of the fitness value in both algorithms
  - But we can see that k means clustering handles local minima much better than threshold speciation as it takes 3 to 4 iterations on average for threshold speciation to get out of local minima, yet K-means hardly stumbles on local minima







## Threshold=30 , population size=100

```
selection pressure: 12.400000000000002   Diversity:  6.940600000000002
Best:h,e,l,l,o, ,w,w,r,l,d,!, ,fitness: 30   Mean: 383.4 ,Variance: 353.4 Time :  89.4666832   ticks: 89.46652626991272
5.7374000000000045

number of groups
30

selection pressure: 12.40967741935484   Diversity:  6.945000000000001
Best:h,e,l,l,o, ,w,w,r,l,d,!, ,fitness: 30   Mean: 383.7 ,Variance: 353.7 Time :  90.39105699999999   ticks: 90.39104533195496
5.7374000000000045

number of groups
30

selection pressure: 12.467741935483867   Diversity:  6.909399999999998
Best:h,e,l,l,o, ,w,w,r,l,d,!, ,fitness: 30   Mean: 385.5 ,Variance: 355.5 Time :  91.30266990000001   ticks: 91.30260944366455
5.7374000000000045

number of groups
30

selection pressure: 385.9   Diversity:  6.947199999999997
Best:h,e,l,l,o, ,w,o,r,l,d,!, ,fitness: 0   Mean: 384.9 ,Variance: 384.9 Time :  92.206042   ticks: 92.20600366592407
number of generations :  90
Overall runtime : 92.206091
```

## Threshold=30 , population size=200

```
selection pressure: 9.075806451612902   Diversity:  7.1239500000000024
Best:h,e,w,l,o, ,w,o,r,l,d,!, ,fitness: 30   Mean: 280.35 ,Variance: 250.35000000000002 Time :  128.4891239   ticks: 128.48921370506287
.7986500000000002

number of groups
32

selection pressure: 9.066129032258065   Diversity:  6.950299999999995
Best:h,e,w,l,o, ,w,o,r,l,d,!, ,fitness: 30   Mean: 280.05 ,Variance: 250.05 Time :  132.2722001   ticks: 132.2726731300354
.7986500000000002

number of groups
31

selection pressure: 9.15322580645161   Diversity:  6.970400000000001
Best:h,e,w,l,o, ,w,o,r,l,d,!, ,fitness: 30   Mean: 282.75 ,Variance: 252.75 Time :  136.21359909999998   ticks: 136.2136423587799
.7986500000000002

number of groups
21

selection pressure: 8.645161290322582   Diversity:  6.314250000000003
Best:h,e,w,l,o, ,w,o,r,l,d,!, ,fitness: 30   Mean: 267.0 ,Variance: 237.0 Time :  139.9451324   ticks: 139.9453318119049
.7986500000000002

number of groups
18

selection pressure: 218.79999999999998   Diversity:  4.809250000000002
Best:h,e,l,l,o, ,w,o,r,l,d,!, ,fitness: 0   Mean: 217.8 ,Variance: 217.8 Time :  143.5349767   ticks: 143.5352373123169
number of generations :  33
Overall runtime : 143.53502840000002
```



## Threshold=32 , population size=200

```
selection pressure: 3.8426229508196723   Diversity:  5.2272
Best:h,e,l,l,o,d, ,o,r,l,d, ,fitness: 60   Mean: 233.4 ,Variance: 173.4 Time :   27.319917599999997   ticks: 27.320194005966187
4.7639999999999994

number of groups
20

selection pressure: 3.631147540983607   Diversity:  4.8538
Best:h,e,l,l,o,d, ,o,r,l,d, ,fitness: 60   Mean: 220.5 ,Variance: 160.5 Time :   28.1871485   ticks: 28.186877250671387
4.7639999999999994

number of groups
15

selection pressure: 7.638709677419354   Diversity:  5.153999999999998
Best:h,e,l,l,o,w,o,r,l,d, ,fitness: 30   Mean: 235.8 ,Variance: 205.8 Time :   29.024954   ticks: 29.02518343925476
6.7639999999999994

number of groups
17

selection pressure: 223.9   Diversity:  4.760600000000001
Best:h,e,l,l,o, ,w,o,r,l,d, ,fitness: 0   Mean: 222.9 ,Variance: 222.9 Time :   29.913575899999998   ticks: 29.913987398147583
number of generations :   34
Overall runtime : 29.913627499999997

run again ? press y for yes n for no
```

## Threshold=76 , population size=512

```
selection pressure: 9.239037298387098   Diversity:  7.964141845703125
Best:h,e,r,l,o, ,w,o,r,l,d,!, ,fitness: 30   Mean: 285.41015625 ,Variance: 255.41015625 Time :   560.9696586   ticks: 560.9696047306061
i.831573486328125

number of groups
47

selection pressure: 8.01990927419355   Diversity:  6.886566162109375
Best:h,e,r,l,o, ,w,o,r,l,d,!, ,fitness: 30   Mean: 247.6171875 ,Variance: 217.6171875 Time :   586.5479199   ticks: 586.548680305481
..831573486328125

number of groups
71

selection pressure: 7.622983870967739   Diversity:  6.554359436035156
Best:h,e,r,l,o, ,w,o,r,l,d,!, ,fitness: 30   Mean: 235.3125 ,Variance: 205.3125 Time :   611.9149315   ticks: 611.9154055118561
i.831573486328125

number of groups
253

selection pressure: 236.25390625000003   Diversity:  6.442481994628906
Best:h,e,l,l,o, ,w,o,r,l,d,!, ,fitness: 0   Mean: 235.25390625 ,Variance: 235.25390625 Time :   637.0892768   ticks: 637.0895440578461
number of generations :   23
Overall runtime : 637.0893292000001
```

# K-means clustering with optimal k each iteration:

Population size =200

```
number of groups
5

selection pressure: 4.696774193548387   Diversity: 3.5159
Best:h,e,l,l,o,d,w,o,r,l,d!, ,fitness: 30   Mean: 144.6 ,Variance: 114.6 Time : 96.05234590000009   ticks: 96.05201053619385

number of groups
5

selection pressure: 4.551612903225807   Diversity: 3.4112000000000005
Best:h,e,l,l,o,d,w,o,r,l,d!, ,fitness: 30   Mean: 140.1 ,Variance: 110.1 Time : 99.80817610000008   ticks: 99.80760431289673

number of groups
3

selection pressure: 4.449999999999999   Diversity: 3.410799999999999
Best:h,e,l,l,o,d,w,o,r,l,d!, ,fitness: 30   Mean: 136.95 ,Variance: 106.94999999999999 Time : 103.60291129999996   ticks: 103.60225081443787

number of groups
5

selection pressure: 4.358064516129033   Diversity: 3.2804999999999995
Best:h,e,l,l,o,d,w,o,r,l,d!, ,fitness: 30   Mean: 134.1 ,Variance: 104.1 Time : 107.4616039   ticks: 107.46128559112549

number of groups
3

selection pressure: 133.14999999999998   Diversity: 3.1217499999999996
Best:h,e,l,l,o, ,w,o,r,l,d!, ,fitness: 0   Mean: 132.15 ,Variance: 132.15 Time : 111.20828830000005   ticks: 111.2076563835144
number of generations : 27
Overall runtime : 111.20833739999989
```

# Population size=512

```
set population size: 512
choose algorithm : 1:GA 2:P50 3:Minimal conflicts 4:first fit
choose problem to solve : 1:8ul Pgia 2:N Queens 3:Bin Packing Prob
choose surviving strategy : Elite: 1 ,Age: 2
if you want to use cx make sure that the string doesn't have 2 matching letters !
type string: h,i,l,d,r,h
choose cross function : One Cross: 1 Two Cross: 2 Uniform: 3 PMX: 4 CX: 5
choose selection function : RAND: 0 SUS: 1 RWS: 2 tournament:3
choose fitness function : 0:Distance 1:8ul Pgia
choose mutation scheme: random mutation: 1 ,swap_mutate: 2 ,insertion_mutate: 3
for hyper press 1 for normal press 0
choose speciation type : 1: threshold speciation 2:k-means clustering 3: none

number of groups
3

selection pressure: 1.4729770740843509 Diversity: 11.835258483886719
Best:9,! ,d,r,h , ,w,o,n,s,0,h,! , ,fitness: 900 Mean: 1326.15234375 ,Variance: 426.15234375 Time : 28.557068399999935 ticks: 28.55730485916137

number of groups
3

selection pressure: 1.4897169729542303 Diversity: 11.574974060058594
Best:9,! ,d,r,h , ,w,o,n,s,0,h,! , ,fitness: 720 Mean: 1073.0859375 ,Variance: 353.0859375 Time : 57.09125599999993 ticks: 57.09132647514343

number of groups
3

selection pressure: 1.6652855919765168 Diversity: 10.83721923828125
Best:o,! ,d,r,z , ,w,o,n,s,0,h,! , ,fitness: 510 Mean: 849.9609375 ,Variance: 339.9609375 Time : 85.1940356 ticks: 85.19385488880737

number of groups
3

selection pressure: 1.9167886140483381 Diversity: 9.697769165039662
Best:e,e,h,h,h , , ,o,s,! ,l,! , ,fitness: 330 Mean: 633.45703125 ,Variance: 303.45703125 Time : 113.31910069999981 ticks: 113.31883430488995

number of groups
3

selection pressure: 3.1252845612582787 Diversity: 8.783477783203125
Best:e,e,l,d,h , ,w,o,r,! ,l,! , ,fitness: 150 Mean: 470.91796875 ,Variance: 320.91796875 Time : 144.98684149999985 ticks: 144.98631465830381

number of groups
3

selection pressure: 2.3127328228476824 Diversity: 8.170608520507812
Best:e,e,l,d,h , ,w,o,r,! ,l,! , ,fitness: 150 Mean: 388.22265625 ,Variance: 198.22265625 Time : 172.24802980000012 ticks: 172.24894516983031

number of groups
5

selection pressure: 3.0494934752747254 Diversity: 7.1603240966796875
Best:h,! ,l,d,o , ,w,o,r,l,d,! , ,fitness: 90 Mean: 276.50390625 ,Variance: 186.50390625 Time : 199.83003739999998 ticks: 199.82998156547546

number of groups
10

selection pressure: 2.600703983516483 Diversity: 6.701873779296875
Best:h,! ,r,d,o , ,w,o,r,l,d,! , ,fitness: 90 Mean: 235.6640625 ,Variance: 145.6640625 Time : 227.72627820000002 ticks: 227.72590327262878

number of groups
15

selection pressure: 3.5243340163934436 Diversity: 6.404731750488281
Best:h,e,o,l,o , ,w,o,r,h,d,! , ,fitness: 60 Mean: 213.984375 ,Variance: 153.984375 Time : 258.16022379999998 ticks: 258.15962386131287

number of groups
5

selection pressure: 3.338947233606557 Diversity: 6.051788330078125
Best:h,e,o,l,o , ,w,o,r,h,d,! , ,fitness: 60 Mean: 202.67578125 ,Variance: 142.67578125 Time : 287.36067989999997 ticks: 287.36041498184204

number of groups
17

selection pressure: 2.960489241803279 Diversity: 5.463844299316406
Best:h,e,o,l,o , ,w,o,r,h,d,! , ,fitness: 60 Mean: 179.58984375 ,Variance: 119.58984375 Time : 316.48416650000013 ticks: 316.4840660095215

number of groups
11

selection pressure: 167.9921875 Diversity: 5.096824645996094
Best:h,e,l,l,o , ,w,o,r,l,d,! , ,fitness: 0 Mean: 166.9921875 ,Variance: 166.9921875 Time : 343.71980729999973 ticks: 343.71956157684326
number of generations : 11
Overall runtime : 343.71986799999999

run again ? press y for yes n for no
```

## תוצאות כלליות בשביל ניתוח סופי :

population size	exploration to exploitaion	Hyper triggered	mutation parameter=0.25
100	generation:33 ,runtime: 31	generations:28 ,runtime:32	generation:35 ,runtime: 35.7
300	generation:21 ,runtime: 209	generations:19 ,runtime:182	generation:20 ,runtime: 195
	Threshold		K-means clustering
population size	5 % of poulation size	15% of population	30
100	generation:30 runtime: 34.5	generations:34 runtime:30	generation:90 runtime: 90
200	generation:30 runtime: 118	generations:29 runtime:129	generation:33 runtime: 143.5
300			Generations:16 runtime=163
512	generation:17 runtime: 502	generations:23 runtime:637	generation:17 runtime: 492
			generation:11 runtime: 340

## k-means-clustering + population 300:

```

selection pressure: 2.5252747252747247 Diversity: 5.396488888888884
Best:w,e,l,l,o ,d,o,r,l,l,! ,fitness: 90 Mean: 228.8 ,Variance: 138.8 Time : 106.2283879 ticks: 106.22867345809937

number of groups
3

selection pressure: 2.3373626373626375 Diversity: 5.142777777777778
Best:w,e,l,l,o ,d,o,r,l,l,! ,fitness: 90 Mean: 211.7 ,Variance: 121.69999999999999 Time : 115.6401703 ticks: 115.64037680625916

number of groups
5

selection pressure: 2.1934065934065936 Diversity: 5.029466666666668
Best:w,e,l,l,o ,d,o,r,l,l,! ,fitness: 90 Mean: 198.6 ,Variance: 108.6 Time : 124.75799219999999 ticks: 124.7581045627594

number of groups
13

selection pressure: 3.0918032786885243 Diversity: 4.786711111111111
Best:h,e,l,l,o ,w,o ,l,h,! ,fitness: 60 Mean: 187.6 ,Variance: 127.6 Time : 134.5002608 ticks: 134.49991154670715

number of groups
4

selection pressure: 2.973770491803279 Diversity: 4.736422222222222
Best:h,e,l,l,o ,w,o ,l,h,! ,fitness: 60 Mean: 180.4 ,Variance: 120.4 Time : 143.8581286 ticks: 143.8582375049591

number of groups
4

selection pressure: 5.296774193548387 Diversity: 4.290199999999999
Best:h,e,l,l,o ,w,o,r,l,l,! ,fitness: 30 Mean: 163.2 ,Variance: 133.2 Time : 153.763551 ticks: 153.76414942741394

number of groups
6

selection pressure: 150.6 Diversity: 3.923133333333333
Best:h,e,l,l,o ,w,o,r,l,d,! ,fitness: 0 Mean: 149.6 ,Variance: 149.6 Time : 163.5336277 ticks: 163.5342104434967
number of generations : 16
Overall runtime : 163.53367830000002

run again ? press v for yes n for no

```

## סעיף 6+7:

מכיוון שלא הצלחנו לשחזר את random immigrants שאיבדנו עם רוב חלק ב אזי נשווה את הפתרון האופטימלי שקיבלנו מ k-means clustering :

א. שלימות : האלגוריתם עם k means תמיד מביא לפתרון סופי , כיוון שהוא תמיד יוצא מ local optima ובכל האיטרציות שהרצנו , למראת שגם כן האלגוריתם הקודם תמיד היה מוציא פתרון , אך לא היה מוגבל מבחינת ריצות ואז היה רץ עד max iterations אך בסופו של דבר שניהן מגיעות לפתרון גם אם לא היה האופטימלי.

ב. מכיוון ש k-means יוצא מ local optima מצאנו שבכל המקרים שעברנו עליהן מול האלגוריתם הישן היה תמיד מוצא את הפתרון האופטימלי אך בפחות צעדים , ספציפית עם אוכלוסייה קטנה כמו 100 האלגוריתם הישן לא היה תמיד מגיע לפתרון למראת ה k-means.

ג. כמו שאמרנו בסעיפים קודמים , הפתרונות הן איכותיות יותר למשל ב k-means עם אוכלוסייה קטנה size=100, הגענו לפתרון תוך 28 generations למראת האלגוריתם הישן שהגיע תוך 35 generations שהיה עם mutation rate=0.25 . (כל התוצאות הללו נמצאות בטבלות בסעיפים הקודמים ) , גם כן נראה שבאוכלוסיות יותר גדולות לאלגוריתם החדש לוקח 16 generations למראת הישן שלוקח 20 generation .

ד. מבחינת זמן אין הרבה מה להשוות כיוון שכל אטירציה שיש בה חישוב של diversity של כל האוכלוסייה לוקחת יותר זמן מהאלגוריתם הישן כדי למצוא תשובה .  
הכוונה שהאלגוריתם של המעבדה קודמת היה מסיים בפחות משניה לפעמים למרות האלגוריתם החדש שלוקח לא פחות מ 5 שניות במקרה הטוב ביותר .

## שיפורים אפשריים בעתיד:

1. Distance function ליניארי , או לפחות יותר טוב ממה שיש לנו עכשיו , אולי שימוש ב hamming distance או Euclidian distance היו אופציות יותר הגיוניות .
2. אלגוריתם random immigrants והאלגוריתם הממטי היה מדהים ומעניין , אך לא הצלחנו לשחזר אותו, לכך עלינו להיות יותר זהירים בעתיד.
- 3.
4. למראת שכל הפונקציות כלליות עלינו לעשות אותם מודולריות בעתיד.

## חלק ב :

כמו ששלחנו קודם בבקשה לאיחור, לא הספקנו לשחזר אותו .