Homework 8 Advanced Analytics and Metaheuristics

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1. Genetic Algorithm

- (a) Finalize Code
 - i. To create the initial chromosomes, we kept it simple, generating a random number between -500 and 500. We used the global variable n as the number of dimensions.

```
def createChromosome(n):
    x = []
    for i in range(n):
        x.append(myPRNG.uniform(-500,500))
    return x
```

ii. For mutation, we played with this quite a bit. Originally we randomly selected an index and the just reseeded it with a random. This seemed to work but we wanted more control over it so we introduced a new parameter that we could tweak, mutationFactor. We used this to change one of the indicies by a random, $r \in [-1,1]$, with x[i] = x[i] + r * mutationFactor. We could then tweak this factor to get more or less mutation. We did check that it was inside the interval and if not, randomly reseed.

```
def mutate(x):
```

```
if mutationRate > myPRNG.random():
    i = myPRNG.randint(0,n-1)
    x[i] += mutationFactor*myPRNG.uniform(-1,1)
    if (x[i] > 500) or (x[i] <-500):
        x[i] = myPRNG.uniform(-500,500)</pre>
```

return x

iii. For cross over, we picked on index to swap start the swap. Everything after that index would be traded between the parents. This happened with a *crossOverRate*. Some times just the parents would be returned.

```
def crossover(x1,x2):
    p = myPRNG.random()
    if crossOverRate>p:
        z = myPRNG.randint(1,n-1)
        offspring1 = x1[:z] + x2[z:]
        offspring2 = x2[:z] + x1[z:]

else:
        offspring1 = x1[:]
        offspring2 = x2[:]
```

return offspring1, offspring2 #two offspring are returned

iv. Elitism was achieved by keeping the best numbering to *eliteSolutions* from the parent generation. It was important to resort these as the children were often better. We also made sure to change it so the minimum was first as desired here.

```
def insert(pop,kids):
```

```
newlist = []
for i in range(eliteSolutions):
    newlist.append(pop[i])
for kid in kids:
    newlist.append(kid)
popVals = sorted(newlist, key=lambda newlist: newlist[1], reverse = 1
return popVals
```

v. I want to share the code for computing the function. With *evaluate* we made sure to utilize the numpy speed in dealing with large dimensional data.

```
def evaluate(x):
    x = np.array(x)
    return 418.982887272443*n -sum(x*np.sin(np.sqrt(np.abs(x))))
```

(b) For parameters, I played around with the code a lot. I noticed for the small dimensional and chromosome, it was important to

have higher mutation rate. I found very good results with the following parameters

#number of dimensions in a solution n = 2

Generations = 300 #number of GA generations

crossOverRate = 0.8 #whether the couple breeds or just continues into next
mutationRate = 0.25 #rate at which mutation can occur
eliteSolutions = 10 #number of elite solutions form previous generation tha
mutationFactor = 50 # the largest number by which the mutation can change a
populationSize = 80 #size of GA population

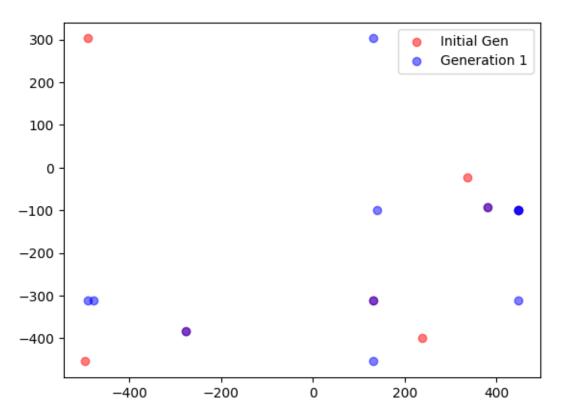
For the higher dimensions, we used

#number of dimensions in a solution n = 200

Generations = 1000 #number of GA generations

crossOverRate = 0.8 #whether the couple breeds or just continues into next mutationRate = 0.25 #rate at which mutation can occur eliteSolutions = 100 #number of elite solutions form previous generation th mutationFactor = 100 # the largest number by which the mutation can change a populationSize = 1000 #size of GA population

i. Here is my visualization of 8 chromosomes. We see some genes splicing and we see some repeats. It is also possible we see some mutations.



- ii. This had Best solution: [420.9337473832483, 421.0086992961223] as the best solution, accurate to three decimal places, 0.0003559856297670194
- (c) This was quite challenging. At 1000 generations, we were still seeing slight improvements. This is with an initial population of 1000 and keeping 100 elite solutions. We saw the value go as low as 18666. While this is nowhere as good as the 2D solution, we do see many entries with a value near the 420 optimal. The execution of this code was slow and with the generations not showing much improvement, do not think expanding beyond 1000 generations will improve the result by much. This problem is hard!

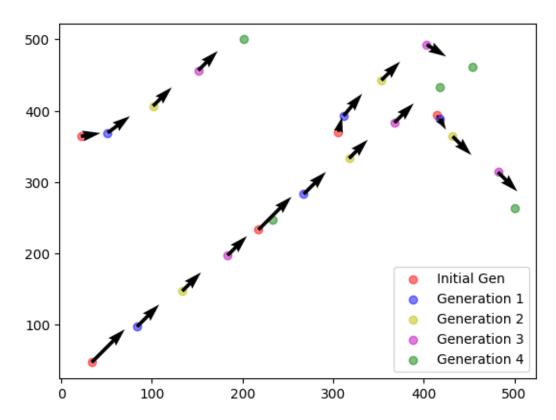
2. Particle Swarm Optimization

- (a) Code Basics
 - i. Particle Tracking:

```
def pbestUpdate(): #update the best lists
  particleUpdate = 0 #how many particles have been updated?
  globalUpdate = 0 #did the global best update
```

```
global phestestVal, phestest #get these variables from global environment
     for i in range(swarmSize): #iterate through swarm
       if curValue[i] < pbestVal[i]: #is the current better than current bes
         pbest[i] = pos[i][:] #since yes, change it up
         pbestVal[i] = curValue[i]
         particleUpdate +=1 #increment the counter
         if curValue[i] <pbestestVal: #since this is better than before, che
           pbestestVal = curValue[i] #since it is, update
           pbestest = pos[i][:]
           globalUpdate +=1
     return particleUpdate, globalUpdate #return counts for stopping criter:
ii. Velocity and Position updates
   def velocityUpdate(): #update velocities
     for i in range(swarmSize): #iterate through swarm
       for j in range(dimensions): #iterate through dimensions
         vel[i][j] = w*vel[i][j]+phi1*myPRNG.random()*(pbest[i][j]-pos[i][j]
         if vel[i][j] >maxVelocity: #check if outside of allowed values
           vel[i][j] = maxVelocity #just return max/min allowed
         if vel[i][j] <-1*maxVelocity:</pre>
           vel[i][j] = -1*maxVelocity
   def positionUpdate():#must be called after velocity update
     for i in range(swarmSize): #iterate through swarm
       for j in range(dimensions): #update all dimensions
         pos[i][j] = pos[i][j] + vel[i][j] #follow basic PSO
         if pos[i][j] > upperBound: #check if outside of feasible
           pos[i][j] = upperBound #if so, put on edge
         if pos[i][j] < lowerBound: #outside feasible?</pre>
           pos[i][j] = lowerBound
       curValue[i] = evaluate(pos[i]) #update currentvalue too
iii. Limits on particle positions are included in the position up-
   date. I only allow getting on the boundary
iv. Limits on velocity are included in velocity Update. Max ve-
   locity is a parameter that can be tweaked later.
```

- (b) 2D Schwefel
 - i. Here is a plot with just positions and velocities



ii. Here is a plot that includes the global best on each iteration

