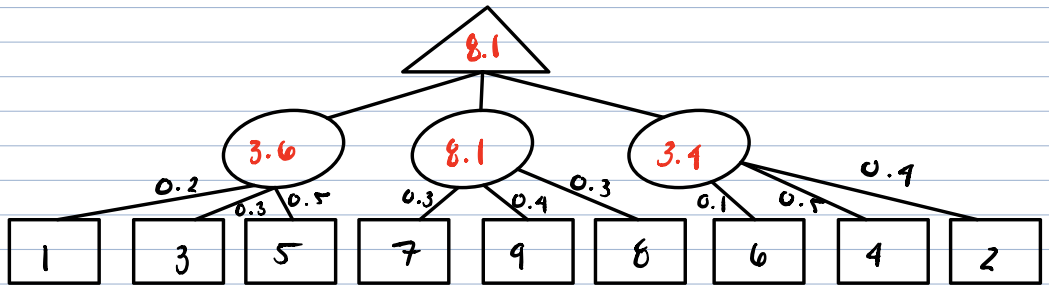
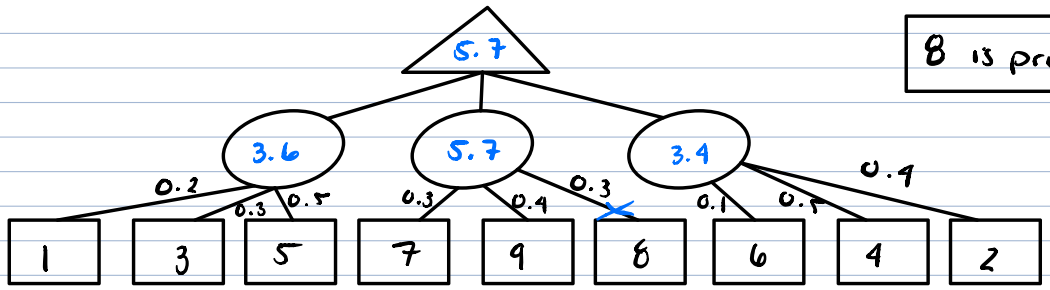
1)



$(1 \cdot 0.2) + (3 \cdot 0.3) + (5 \cdot 0.5)$ $(7 \cdot 0.3) + (9 \cdot 0.9) + (8 \cdot 0.3)$ $(6 \cdot 0.1) + (4 \cdot 0.5) + (2 \cdot 0.9)$

$0.2 + 0.9 + 2.5 = 3.6$ $2.1 + 3.6 + 2.4 = 8.1$ $0.6 + 2 + 0.8 = 3.4$

2)

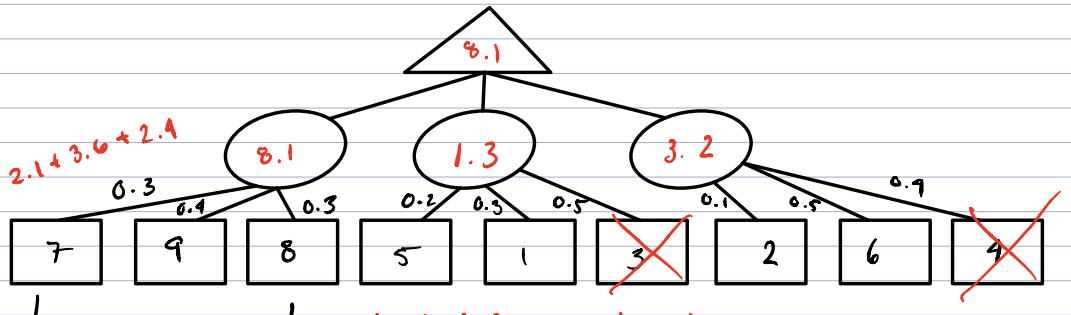


8 is pruned

$0.2 + 0.9 + 2.5 = 3.6$ $2.1 + 3.6 = 5.7$ $0.6 + 2 + 0.8 = 3.4$

→ We can see the probabilities, but not the values. We must visit the first 3 nodes due to lack of information, the center branch looks at the first node, calculates that probability which is 2.1, still less than the left-most branch, goes next, and even with a tested value of 9, the chance node has the opportunity to be higher than the left most node, we check it, get 3.6 to add up to 5.7, this is now the highest value so we don't care about the next value. We go to the rightmost node and see 0.1, we check it to get 0.6, we look next, see 0.5, if we test with 9, we get 4.5 which leaves a remainder of 0.4 to multiply to something and possibly give you a greater value, we check it and get 2, we are now at 2.6, we see 0.4, test it with 9 to get 3.6, which added to 2.6 will give you a greater value than 5.7, we check it, it's a 2 and we total 3.4.

3)



These 3 run always

$1 + 0.3 + \text{Max}(0.5 \cdot 8)$

$1.3 + 4 = 4.3$

$0.2 + 3 + \text{Max}(0.4 \cdot 9)$

$3.2 + 3.6 = 6.8$

Exercise 2

1. The simplest genotype would be binary composed digits that represent the angles of each bend. The values that the individual genes can have would be in the form of vectors that represent each dimension in which the bend lays. The binary would allow for easy crossover and the vector for easy pin-pointing of which dimension the bend is in.
2. Crossover can be performed by taking the two bends/angles with the best fitness function and splitting each of them into portions that can be shared. These combined attributes from each angle forms a new, fitter, generation.
3. The termination condition is when there is no result better than our greatest distance of at least 100 km.
   Ex/Clarification: if the best value is 150 and it can't get BETTER than 150, then thats when we stop.

* Note to Self *

* each gene should have a vector of 3 values that can represent 3D space (x, y, z)

< 5, 8, 1 > - maybe binary encode
- this should give us where each bend is and would allow 4 easy crossover.