# CS572 Project 3 Report

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### Abstract

In this project, I have implemented an genetic programming algorithm for the Sante Fe trail problem. By including the prog2, prog3 and isFoodAhead non-terminals, and left, right, and forward terminals, with completely no control of the tree generation except initial depth, the implementation creates an static ant(where all the nodes/individuals share the same ant), and the ant is able to evolve and behave evolutionarily and becomes smarter to pick up more and more food. The algorithm works with potential that by modifying and enforcing isFoodAhead non-terminal's forward node, or even an isFood2StepsAhead non-terminal, the algorithm could even work better or perfectly. In one work, the algorithm works great. According to the results that I have some records, the ant could pick up at least 64 food from in total 90 food.

algorithms	Steady-state
Population Size	100
Selection Method	Tournament Selection of size 10 each generation
Elitism(if used)	Yes, one copy of parent though it's not necessary, included to speed up the process
Crossover Method	One-point Subtree crossover
Crossover rate	1, happened 90% on Non-terminal & 10% on Terminal
Mutation Method	Node mutation with probability of 0.05 at each node for the individual
Operator/non-terminal Set	pro2, pro3, isFoodAhead
Terminal Set	left, right, forward
Fitness function	The counts of food has been taken by the individual

Tournament selection selects the one with smaller size if both share same fitness.

### ${f 1}$ Algorithm Emphasize

Size control(if any)

#ifndef ANT\_H

### 1.1 Project Implementation Ideas

For this project, different upon the last project2 is that I used an static ant object in the node object so that I always have an ant for all the individual. Since the ant is static, for all the individuals, I initialize the ant once, and I will always reset my ant so that I can evaluate the fitness for all individuals without extra troubles. The "ant.h" interface is listed below as the reference.

```
void getAnt();
                      // write the trail my ant has moved when reach certain fitness
   void left();
                      // move left
   void right();
                      // move right
                      // move forward
   void forward();
   bool isFoodAhead(); // check if there is food ahead
#endif
```

### Non-terminal / Operator Set 1.2

};

The non-terminal in this project includes prog2, prog3 and isFoodAhead. And the terminals in this project include left, right, and forward. The prog2 and isFoodAhead has two terminal nodes, and the pro3 non-terminal has three terminal node. All the non-terminal nodes and terminal nodes are generated completely randomly. So I give up the control of looking ahead if there is food ahead.

To make an smarter ant, I suppose I should modify my tree generation method so that my isFoodAhead nonterminal will always has a node called "forward". That way the "isFoodAhead" function can take effect and make my ant smarter. But for the sake of trying to finish the project on time and focus on some other tasks, I didn't bother to take my effect to try that, but I understand that there are still plenty potentials to improve my results.

### 1.3Crossover of two subtrees

By using tournament selection, I can get two above average individuals. Though I have used Steady-state algorithm, to help make the population converges faster, I still keep one copy of the best two individuals untouched in my new generation. And for the same propose of facilitating the population to converge faster, I replaced the worst two individuals in the population by the best two parent. I copied the best two individuals to the memory position where the two worst population individuals originally at, I do crossover of the best two sample individuals on place. The crossover of two subtrees obey the 90-10 rule for selecting crossover points; in picking a crossover point

there is a 90% chance that it will be an internal node and only a 10% chance that it will be a leaf node. And for specific detail, it will include cases like one root node swap with another expression tree's internal node. But if it happens that require both parent tree swap from root node, then for that specific generation, I didn't do the crossover, but mutation only. From implementation point of view, the crossover is done by first decide if we do internal node swap of leaf

nodes swap, then by modifying Dr. Soule's calc size recursion function, we can count down the node number by passing the crossover point randomly generated non-terminal number by reference, we would be able to get the node pointer to the specific internal or terminal node, and also the pointer to its parent. We will get four pointers pointing to two pair of nodes for two individuals.

We can finishes the crossover of two subtrees by conduction the following steps:

### 1.3.1crossover key steps

- plcurr for pointer to pl node, plprt for pointer to pl's parent;
- p2curr for pointer to p2 node, p2prt for pointer to p2's parent;
- find p1prt's branches index i, set p1prt's branches[i] = p2curr;
- set p2curr's parent = p1prt;
- find p2prt's brandches index j, set p2prt's branches[j] = p1curr;
- set p1curr's parent = p2prt;

Special consideration needs to be given to conditions like, when one individual's parent node pointer is null, which means the whole expression tree will be considered as a subtree for swapping. Theory is the same, just the corner case need some attention.

```
void Population::swapSubtree(int winIdx1, int winIdx2, int cnt)
   int fst = winIdx1;
   int snd = winIdx2;
   int one;
   int two;
   bool oneFlag = true, twoFlag = true; // flag for non-terminal
   popu[fst].calc_size();
   popu[fst].evaluate();
   popu[snd].calc_size();
   popu[snd].evaluate();
   // generate node number for expression tree 1
   if (rand() % 100 / 100.0 < 0.90 && popu[fst].non_terms) { // non-terminal swap
        one = rand() % popu[fst].non_terms;
        oneFlag = true;
   } else {
        oneFlag = false;
        one = rand() % popu[fst].terms;
   }
   // generate node number for expression tree 2
   if (rand() % 100 / 100.0 < 0.90 && popu[snd].non_terms) { // non-terminal swap
        two = rand() % popu[snd].non_terms;
        twoFlag = true;
   } else {
        twoFlag = false;
        two = rand() % popu[snd].terms;
   }
   while ( (one == two && (one == 0 || two == 0))
            || (oneFlag != twoFlag) )
   {
        if (rand() % 100 / 100.0 < 0.90 && popu[fst].non_terms) { // non-terminal swap
            one = rand() % popu[fst].non_terms;
            oneFlag = true;
        } else {
            oneFlag = false;
            one = rand() % popu[fst].terms;
        }
        if (rand() % 100 / 100.0 < 0.90 && popu[snd].non_terms) { // non-terminal swap
            two = rand() % popu[snd].non_terms;
            twoFlag = true;
        } else {
            twoFlag = false;
            two = rand() % popu[snd].terms;
        }
   }
   twoPtr p, q;
   int onecnt = 0, twocnt = 0;
   // get node pointers for current node and current node's parent
   if (!oneFlag) {
        popu[fst].getTermNodePtr(popu[fst].the_indiv, one, onecnt);
        p = popu[fst].term[0];
        popu[fst].getNonTermNodePtr(popu[fst].the_indiv, one, onecnt);
        p = popu[fst].nonterm[0];
   }
```

```
onecur = p.cld;
    twoprv = q.prt;
    twocur = q.cld;
    // swap two parts of subtrees from two individuals
    // special conditions still needs to be worked on
    if (!oneprv && !twoprv){;} // do nothing here
    else if (!oneprv && onecur && twoprv) {
        for (int i = 0; i < MAX_ARITY; ++i) {</pre>
            if (twoprv->branches[i] == twocur) {
                 twoprv->branches[i] = onecur;
                 onecur->parent = twoprv;
            }
        }
        popu[fst].the_indiv = NULL;
        popu[fst].copy(twocur);
        (popu[fst].the_indiv)->parent = NULL;
    } else if (!twoprv && twocur && oneprv) {
        for (int i = 0; i < MAX_ARITY; ++i) {</pre>
            if (oneprv->branches[i] == onecur)
                 oneprv->branches[i] = twocur;
                 twocur->parent = oneprv;
            }
        popu[snd].the_indiv = NULL;
        popu[snd].copy(onecur);
        (popu[snd].the_indiv)->parent = NULL;
    } else {
        for (int i = 0; i < MAX_ARITY; ++i)</pre>
            if (oneprv && oneprv->branches[i] == onecur)
                 oneprv->branches[i] = twocur;
                 twocur->parent = oneprv;
            }
            if (twoprv && twoprv->branches[i] == twocur)
                 twoprv->branches[i] = onecur;
                 onecur->parent = twoprv;
            }
        }
    }
}
     Mutation
1.4
I have done node mutation for this project. There is floating point mutation rate to control the probability of
mutating each node for the expression tree. The floating mutation rate is a passed in argument and used recursion
```

// get node pointers for current node and current node's parent

popu[snd].getTermNodePtr(popu[snd].the\_indiv, two, twocnt);

popu[snd].getNonTermNodePtr(popu[snd].the\_indiv, two, twocnt);

if (!twoFlag) {

node\* oneprv; node\* onecur; node\* twoprv; node\* twocur;

oneprv = p.prt;

}

q = popu[snd].term[0];

q = popu[snd].nonterm[0];

```
while ( type == tmp->type)
                 type = NUM_NON_TERMS + rand() % NUM_TERMS;
            tmp->type = type;
    } else if (tmp) {
        switch(tmp->type) {
        case 0: //pro2:
        case 2: // ifFoodAhead:
             for (int i = 0; i < 2; ++i)
                 mutate(tmp->branches[i], mutRate);
            break;
        case 1: // pro3:
             for (int i = 0; i < MAX_ARITY; ++i)</pre>
                 mutate(tmp->branches[i], mutRate);
            break;
        }
    }
}
int cnt = step;
the_indiv->evaluate(cnt);
```

to recursively execute from root down to leaves.

void Individual::mutate(node\* tmp, float mutRate) {

if (tmp && rand()% 100/100.0 < mutRate)
 if (tmp->type < NUM\_NON\_TERMS ) {</pre>

type = rand() % NUM\_NON\_TERMS;
while (type == tmp->type)

Codes are included as reference;

int type;
if (!tmp) {

### 1.5 Selection

I have used the Tournament selection method. I used two members of the tournament-al selected individuals as the two parent. If the two parent's fitness equals, I keep the one as parent whose expression tree size is smaller, so that I have some selection pressure on minimizing tree size. And I will repeat this process with the tournament size of 5 to select another parent until I find a second parent whose fitness is not equal any more. By this repeating process,

actually I have increase the tournament selection pressure because potential I have selected two parent from 15 sample or 20 samples. But since my population could not converge fast any way, I did not care that much for this

# 2 Results

The simply project works pretty well with all the codes Dr. Soule has handed to us, especially those recursive ones. I have printed out the minimum fitness in the population and the average fitness as well.

# 2.1 Fitness vs Generation Count

Figure 1 indicates that the crossover and node mutation works pretty well in that aspect that the best individual fitness from the population reduced down smoothly.

From the above figure 1 we can also see that the average fitness has several peaks, that was due to the offspring outliers when two parent from previous generation crossover and node mutated. If I apply some tricks to filter out these outliers, and then calculate the population average, it should be able to get smoothly increasing average fitness as well.

### Fitness vs Generation

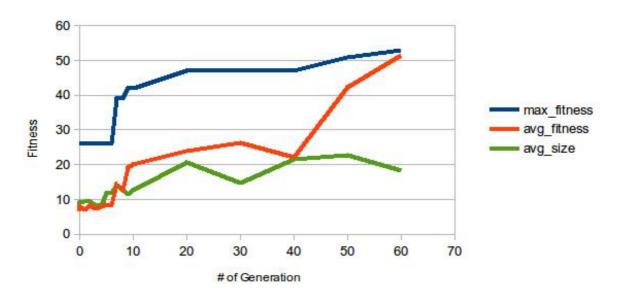
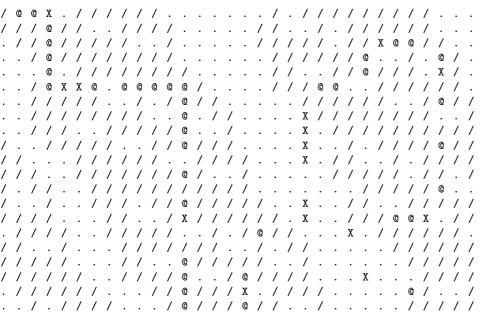


Figure 1: Average and best fitness for the Sante Fe Trail problem. Best fitness (max fitness) has the perfect trend, but average fitness has several peaks due to the offspring outliers resulted from parent crossover and node mutation.

Since I have used the Steady-state algorithm, for each generation, I keep the two parent selected using Tournament selection method in the new generation just to speed up the evolving process, which is not necessary for the Steady-state algorithm. And I crossover the parent, so there would be two parent individuals got one-point crossover, and followed by node mutation for the crossover individuals. Since the ant is behaving smart, I didn't try enough generations to track even further behaviours, and the figure above all showed only the first 60 generations. But later on for more scientific researches, I will need to remember to dig deep enough to draw sound conclusions.

# 2.2 Applying best function on test points

table 1: An ant that I have got with the fitness between 65 and 75, lost track of which one works corresponding to the fitness. The '@' represents that the food has been taken by the ant, the '/' means the ant has stepped there, and '.' means the ant has not been there yet. and the 'X' means it is food and the ant has not been able to take it yet.



/	/	/	/	/	/			/				Х	/		/	/	/	/	/	/	/	/				Х	/	/	/	
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restricted the crossover to be non-terminal to non-terminal swap, or terminal to terminal swap, but I should have allow non-terminal to terminal or terminal to non-terminal as well. And as mentioned earlier, I didn't bother to apply the isFoodAhead boolean function (which means if there is food ahead, my ant does not necessarily move forward and pick up the food. Instead my ant will behave according to the individual's tree instruction), which means if I have controlled the forward node of the isFoodAhead non-terminal, the ant should be able to behave smarter(move forward if there is food ahead), and potentially being able to pick up more food, getting better fitness.

solutions. With deeper consideration of good-bad codes side-effects, and individual expression tree size control, together with better understanding of the relationship between the non-terminal and terminals having been applied and the behaviour of the ant, by modifying and enforcing the isFoodAhead non-terminal's "forward" terminal node,

`

# 3 Conclusions

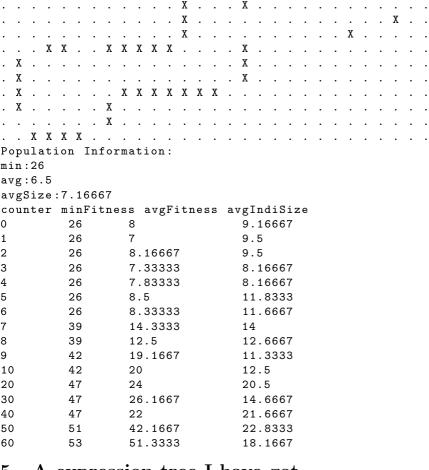
In order be able to do genetic programming, we need certain data structures that would allow us be able to swap the evolutionary algorithms data in the middle functionally as if we have swapped programs. Like this project, we

used the tree structure. As far as we understand the Genetic Programming theory and C++ pointer, the project turned out to be not that hard. And so far, it works pretty well. And compared with project 2, I included an static ant in the node object so that the static ant is shared among all the node sub-sequentially individuals and

static ant in the node object so that the static ant is shared among all the node, sub-sequentially individuals and population. But in order to separate among individuals, the ant gets reset to evaluate for each new individual. But still, as can be easily seen from table 1, it works well, but there are quite some distance from the expert

and potentially including an isFood2StepsAhead, which looks ahead 2 steps away, potentially my static ant will still behaviors smarter and smarter. But it is good to see that the ant is smarter enough to evolve evolutionary genetic programming like, which means the algorithms in this project works.

# 4 example results I got before bad<sub>alloc</sub>



### $\mathbf{5}$ A expression tree I have got

This fitness function is used for the test points plot, because this is the best tree that I have been able to save the expression tree results. Previous ones, like some function fitness can reach up to 64, but I lost tract of the individuals when I got  $bad_{alloc}$  from running the programs. popu[1]:

Size: 31 Fitness: 64

R->4

L->3

P3->1

P2->0

P3->1

P3->1

P2->0

P3->1

P2->0

P2 - > 0

R->4L->3 P2->0

R->4L->3

P2->0

iFA->2

R->4L->3

> L->3 F->5

R->4

F->5

R->4F->5

P2->0

R->4 L->3 iFA->2 L->3 F->5