

Genetic Vehicle Routing Problem

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Part 1 - Problem Description



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- Trucks have a set capacity



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- 2D problem with Euclidean coordinates and Euclidean distance



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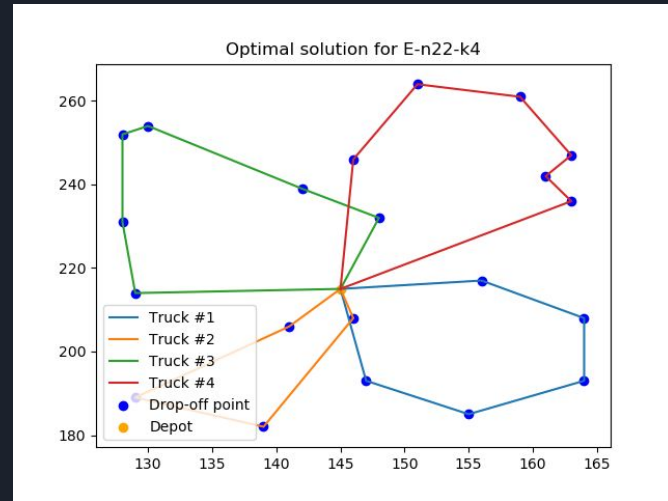


Problem description

- Trucks have a set capacity
- 2D problem with Euclidean coordinates and Euclidean distance
- All trucks start at the depot and must return to the depot at the end
- Drop-off points require a set quantity to be satisfied
- We want to minimize the total distance traveled by the trucks

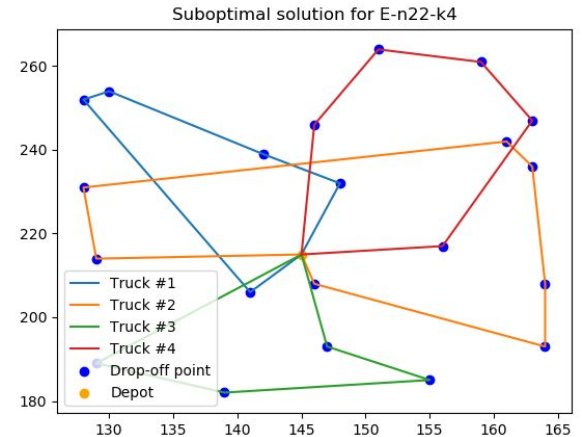
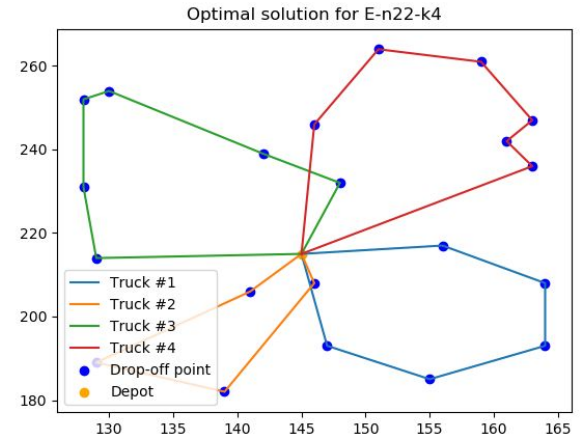
A visual example

- Optimal length is 375



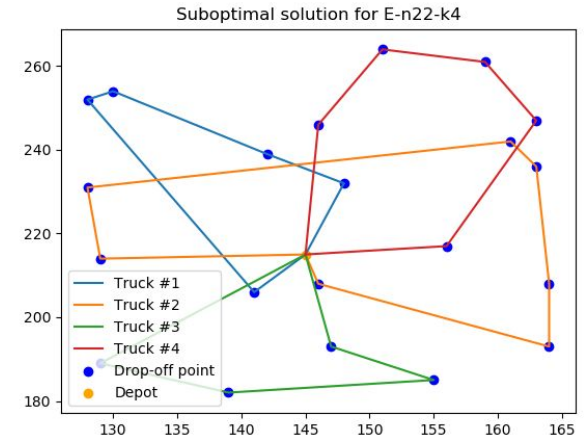
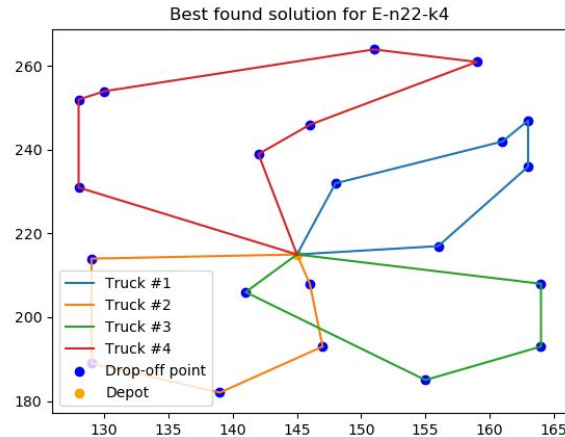
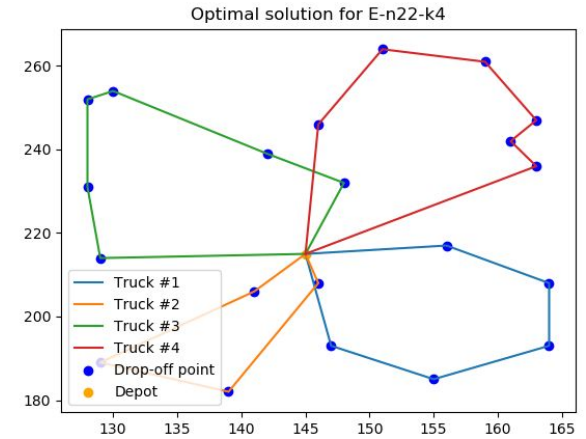
A visual example

- Optimal length is 375
- Suboptimal solution has length 461.06



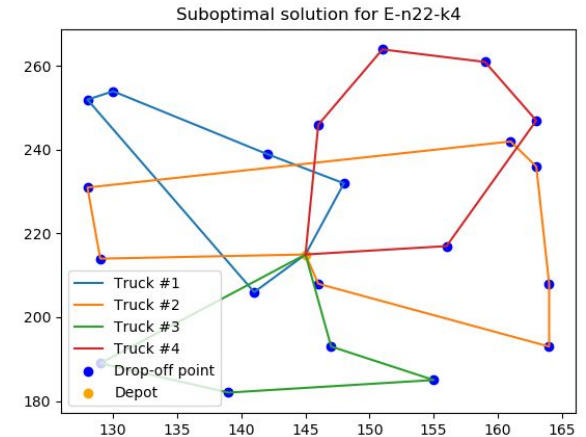
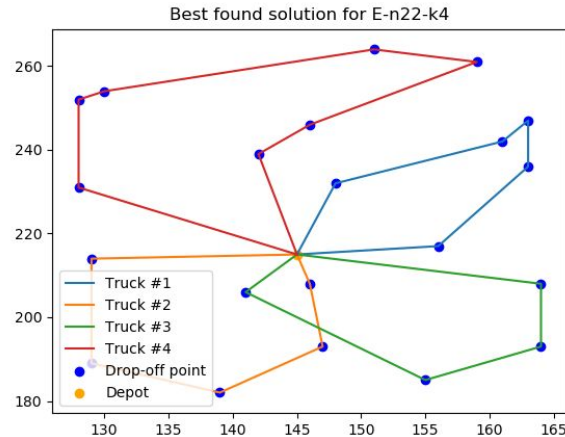
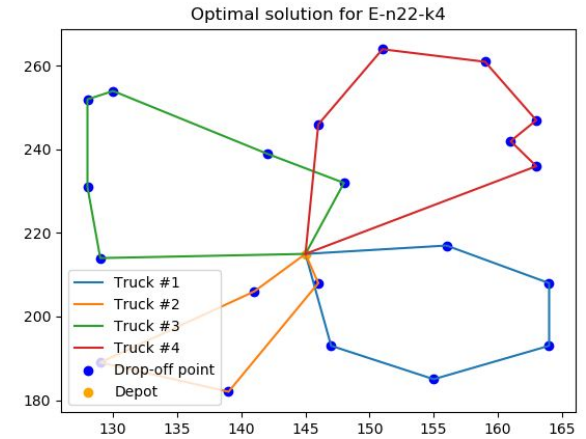
A visual example

- Optimal length is 375
- Suboptimal solution has length 461.06
- Best found solution has length 383.87

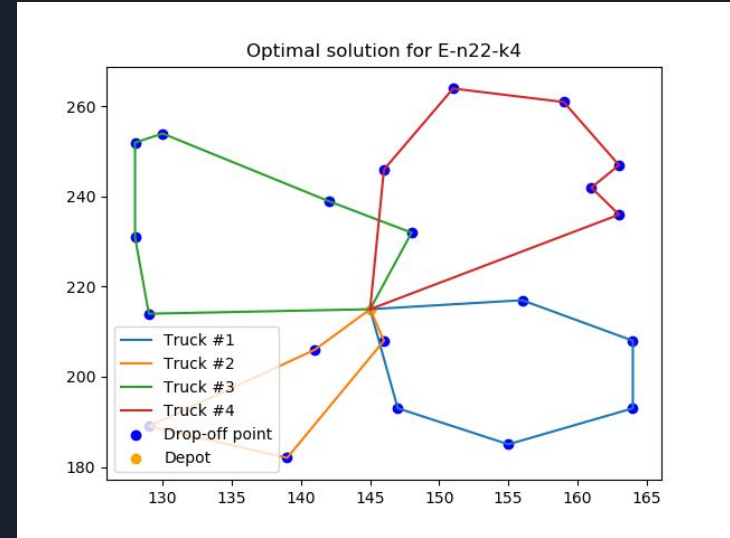
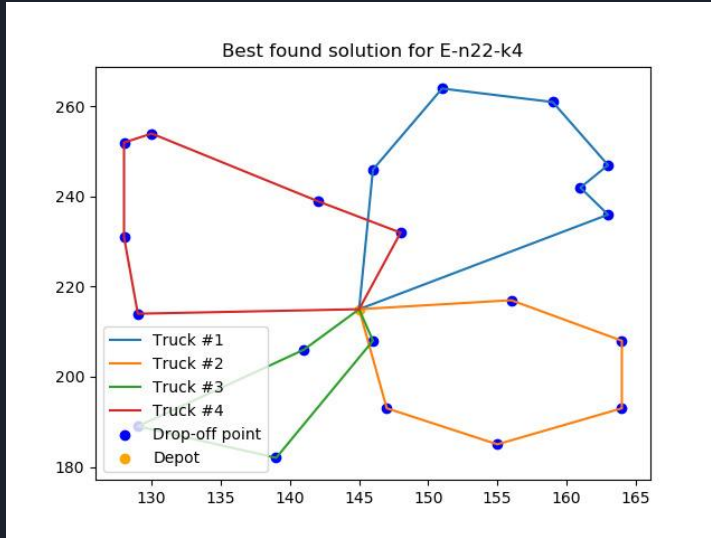


A visual example

- Optimal length is 375
- Suboptimal solution has length 461.06
- Best found solution has length 383.87
- Even near-optimal solutions are very different



Best solution after enough generations





Part 2 - Genetic Algorithm



Genetic algorithm

- Individuals represented by genomes, similar to DNA.



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- Initially, individuals start with random genes, and evolve in time to find better solutions
- Population is represented by multiple individuals in a generation.
- Evolution takes place over multiple generations.
- Survival of the fittest: better performing individuals have a greater chance to reproduce and keep their genes in the gene pool.



Representing VRP Solution as a Genome

- Genome format

3.353225, 3.374998, 1.496267, 1.425025, 3.482352, 1.611691, 3.629004, 1.875911,
3.834087, 3.005951, 2.134070, 2.846377, 2.427292, 2.993102, 2.495519



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- Each chromosome has the following format: {truck_number . order}
- A point is visited by a truck only after all points with smaller order are visited
- Size of the genome is as big as the number of Drop-off points



Genetic parts - Fitness Calculator

- Fitness calculator
- Computes the total cost of all vehicle routes using a fitness function



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 - Computes the total cost of all vehicle routes using a fitness function
 - Fitness function greatly punishes trucks that are overloaded



Genetic parts - Fitness Calculator

- Fitness calculator
 - Computes the total cost of all vehicle routes using a fitness function
 - Fitness function greatly punishes trucks that are overloaded
 - While encouraging trucks with shorter routes



Genetic parts - Selector

- Fitness calculator
- Selector
- Selects the pairs of individuals that will reproduce



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- Selects the pairs of individuals that will reproduce
- Sorts individuals and creates pairs of parents that create offspring



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Genetic parts - Selector

- Fitness calculator
- Selector
- Selects the pairs of individuals that will reproduce
- Sorts individuals and creates pairs of parents that create offspring
- Elitism: A small fraction of the best performers also survive
- Introduce new individuals with completely random genomes



Genetic parts - Crossover Calculator

- Fitness calculator
- Selector
- Crossover calculator
- Creates new individuals from the computed pair of parents



Genetic parts - Crossover Calculator

- Fitness calculator
- Selector
- Crossover calculator
- Creates new individuals from the computed pair of parents
- Uniform crossover: Each gene is selected randomly from one of the parent chromosomes.



Genetic parts - Mutator

- Fitness calculator
 - Selector
 - Crossover calculator
 - Mutator
- Randomly mutates the genome with a small chance



Genetic parts - Mutator

- Fitness calculator
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 - Crossover calculator
 - Mutator
- Randomly mutates the genome with a small chance
 - Trigger global mutations after a set number of generations, representing major environment changes



Part 3 - Locating the bottleneck



Bottleneck - Empirical Approach

- Manually analyzing the algorithm points out to the Fitness Calculator as being the bottleneck
- It has the biggest asymptotic complexity of $O(\text{num_cars} * \text{num_dropoff})$
- Best candidate for parallelization
- This is the only part that is worth parallelizing

```
void VRP::LinearFitnessCalculator::calculateInterval(double *genome, int len, int genomeSize, vector<double> &fitness) {  
    for (int i = 0; i < len; i++) {  
        fitness[i] = calculate(genome + i * genomeSize, genomeSize);  
    }  
}
```

Bottleneck - Confirmation via Profiling

- Running Intel VTune Profiler for linear implementation confirms the previous claim
- Out of all the functions we've implemented it's the most time consuming by a huge margin
- It is trivial to parallelize
- Next function in the profiling is the Crossover which takes only 3.7% of total CPU time

| Hotspots ? | | | | |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------|------------------|-----------|---------------|
| Analysis Configuration Collection Log Summary Bottom-up Caller/Callee Top-down Tree Flame Graph Platform | | | | |
| Function | CPU Time: Total | CPU Time: Self | | |
| | | Effective Time ▼ | Spin Time | Overhead Time |
| std::vector<std::pair<double, int>, std::allocator<std::pair<double, int>>>::push_back | 40.3% | 35.002s | 0s | 0s |
| std::sort<__gnu_cxx::__normal_iterator<std::pair<double, int>*, __gnu_cxx::__normal_iterator<std::pair<double, int>*, int>>, std::less<std::pair<double, int>>>::__stl_sort | 17.2% | 8.214s | 0s | 0s |
| VRP::LinearFitnessCalculator::calculate | 86.4% | 8.016s | 0s | 0s |
| __gnu_cxx::__normal_iterator<std::pair<double, int>*, __gnu_cxx::__normal_iterator<std::pair<double, int>*, int>>::operator++ | 4.5% | 5.528s | 0s | 0s |
| std::sqrt<int> | 3.7% | 4.610s | 0s | 0s |
| std::make_pair<double, int> | 3.4% | 4.176s | 0s | 0s |



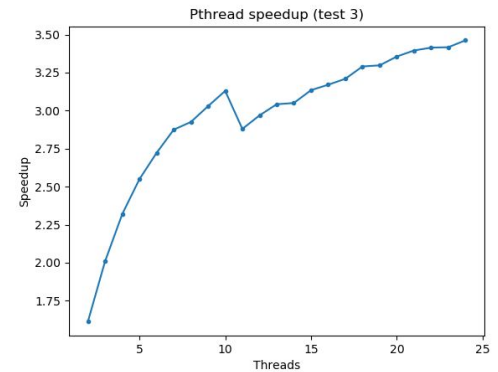
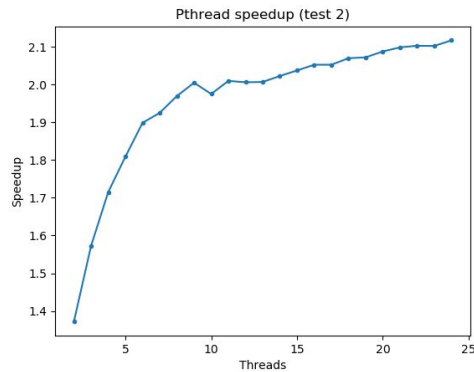
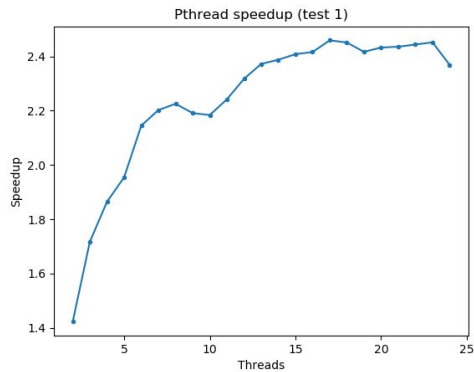
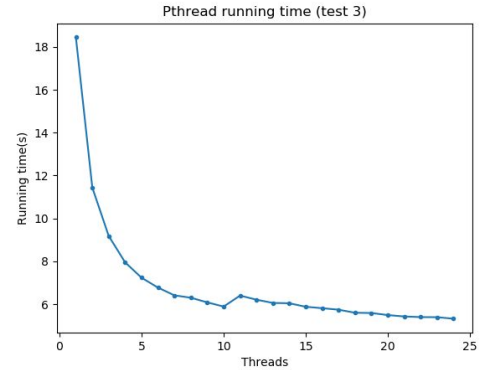
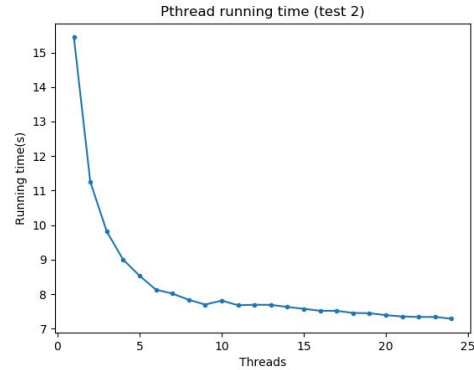
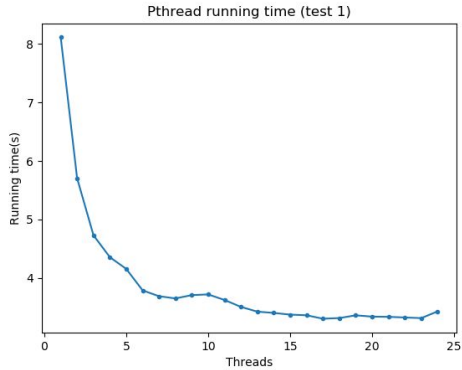
Part 4 - Implementation comparison



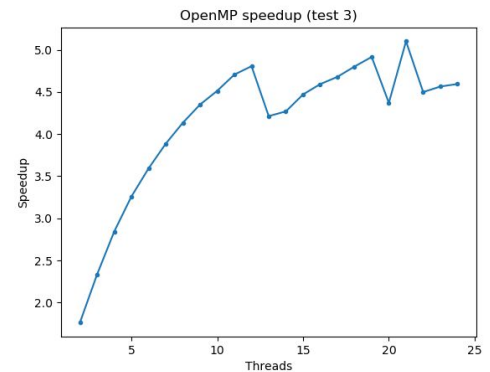
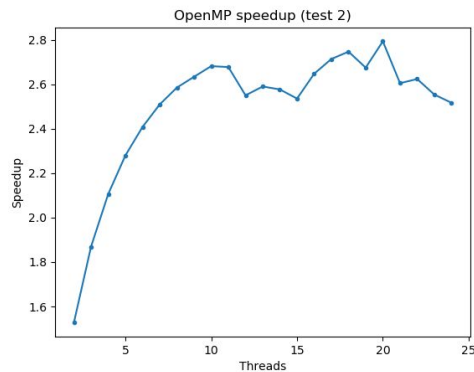
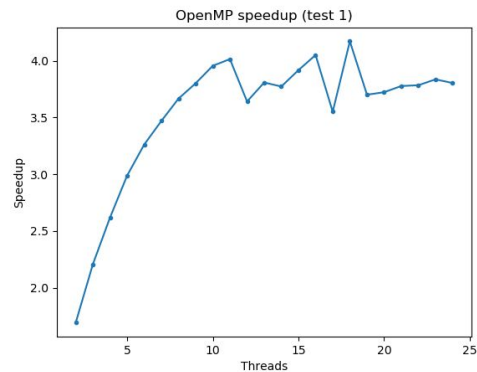
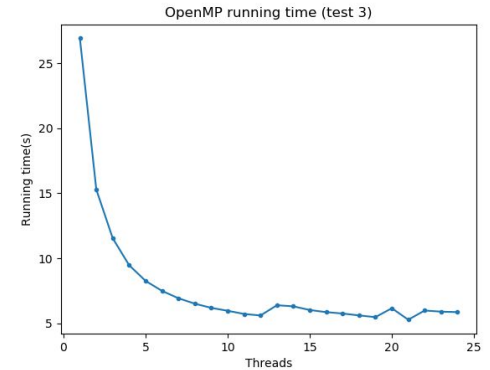
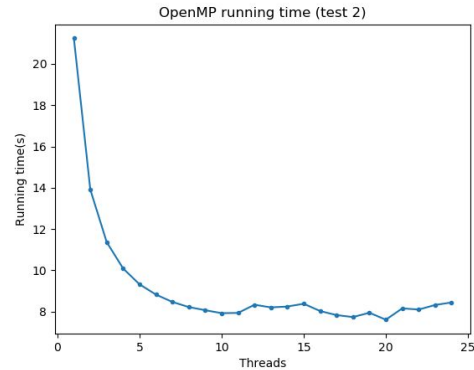
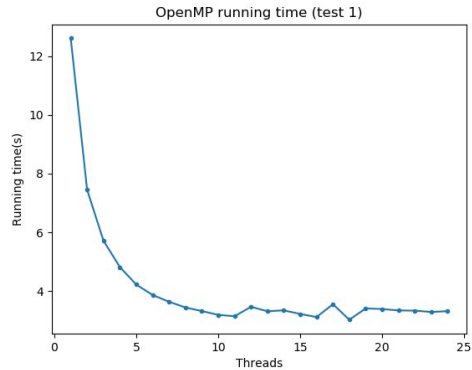
A starting point - Linear implementation

- For all the tests we chose the following parameters
 - Genome size - 400
 - Number of generations - 3000
- We ran our implementations on 3 different tests
- The times for the linear implementation are:
 - Test #1 - 12.705s
 - Test #2 - 21.237s
 - Test #3 - 26.891s

Pthread implementation results



OpenMP implementation results



MPI implementation results

