

Addendum 1 of Appendix D, Economics – Attachment 3: Lock Capacity: Optimized Tows and Genetic Algorithm

Inner Harbor Navigation Canal (IHNC) Lock – Lock Replacement, Orleans Parish, Louisiana General Reevaluation Report

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Attachment 3 - Optimized Tows and Genetic Algorithm: IHNC Lock

1. Summary

The 110 feet by 900 feet lock project will allow users of the waterway to transit in fewer cuts, as the expanded chamber dimensions will accommodate more barges per cycle. This reduction in cuts will have a non-linear impact on average transit times through the project. During high traffic periods, delays during additional cuts will simultaneously impact all waiting users.

This improvement in efficiency is a function of the character of expected traffic, namely the lengths, widths, and barge counts of flotillas, as only flotillas that are either wider or longer than the chamber will experience a decrease in necessary cuts to transit. Additional efficiency gains however can be achieved if traffic through the project is able to reconfigure to better make use of the additional chamber size.

For IHNC, existing traffic is largely one or two barge tows. This composition is due to a number of reasons, but among them are the existing chamber dimensions and the increased delay costs incurred by larger tows. Over 67% of IHNC traffic transits only this project (five-year average, 2019-2024), so the majority of tow configurations would not be influenced by the dimensions of up or downstream project chambers.



Figure 1 - Historic Tow Size Distribution

To evaluate the potential efficiencies from re-configuration of IHNC traffic, alternative characterizations of traffic were created, based on the existing traffic documented in the historic LPMS data. These alternative characterizations are essentially the existing historical traffic, reconfigured to most optimally transit the new project dimensions, while maintaining the same equipment, tonnage, and commodities as in the LPMS data.

To achieve this optimization, and to develop the baseline estimate of FWP traffic, historic traffic was disaggregated into individual barges, and then a genetic algorithm was used to optimize reaggregation into a new set of flotillas.

A genetic algorithm is an optimization algorithm that uses the basic principles of evolution to arrive at an optimized solution without needing to evaluate the entirety of the solution space. To do this, the algorithm first creates a 'population' of solutions to the optimization problem. Each is a purely randomly determined 'answer' to the problem, encoded in a chromosome. This initial population is evaluated using a fitness test, which represents the strength of each possible solution, and those members of this population that have the highest assigned fitness score reproduce to create the next generation. This reproduction involves a combining of the chromosomes from a pair of population members, with possible mutation. The process is then continued for a set number of iterations, or generations, and the chromosome associated with highest fitness score from the final generation decoded to produce the optimized solution.

2. Flotilla Groupings

To optimize IHNC project traffic, the existing traffic was first separated into bins with like characteristics, and the barges/flotillas within these individual bins optimized. Flotillas were categorized by arrival month, predominant barge class, and hazardous cargo flag. This was done to preserve traffic seasonality, to ensure that barges of significantly different size or type were not paired with each other in a flotilla, and that barges with hazardous cargo were not paired with those without.

For each bin, the solutions were encoded as a chromosome with three gene sequences, as shown in the figure below. The first gene sequence contains in each allele a random sequential integer (with possible repeated values) that represents the index of the newly created Flotilla. Repeated indices will indicate multiple barges added to the same newly created flotilla. The second gene sequence contains a series of random, non-repeating integers that represent the barge index within the bin to be added to the new flotilla. This value is also used to indicate the position in the newly created flotilla's tow packet of that barge. Finally, the third gene sequence contains a random integer representing the index of the flotilla archetype within the bin from which to draw the powered vessel to associate with the newly created optimized flotilla.

Figure 2 - Chromosome Example

| 0 | 3 | 3 | 4 | 2 | 1 |
|---|---|---|---|---|---|
| 1 | 5 | 4 | 2 | 0 | 3 |
| 0 | 0 | 3 | 2 | 2 | 1 |

Newly created Flotilla index Barge index (and tow packet position) Previous Flotilla index (Powered Vessel)

3. Fitness Testing

Once a population is generated as described above, the fitness test is the total number of cuts necessary for the entire subset of created optimized flotillas to transit the project. This is estimated by decoding each chromosome into a shipment list and estimating the required cuts for each created tow. The lowest total number of required cuts are assigned the highest fitness scores, and vice versa.

To decode the chromosome Flotillas are created from the first gene sequence, and barges added to them from the second. The second chromosome however encodes a one-dimensional sequence of indices. To convert from this to a two-dimensional arrangement of barges, a target dimension is required, in this case the new FWP chamber dimensions. This target dimension is used to bound the addition of each barge, by index in the chromosome, sequentially. Just as with the chamber packing algorithm used in ARNOLT simulations, barges are added by column, then by row. If a barge cannot be added to the tow packet in the current column without exceeding the target dimensions, it is instead added to the start of the next row. This is illustrated in Figure 3 below.

Figure 3 - Tow Packet Decoding



4. Reproduction

Reproduction after fitness scores are computed for each generation is done by vertical crossover, whereby a random point along the gene sequence is selected and the sequence split at that point. The 'child' chromosome is the created by combining the left and right ends of the split chromosomes and applying random mutation (where alleles are randomly swapped).

One hundred generations were evaluated as described above before selecting the optimized traffic configuration. Figure 4 below shows a comparison in tow-sizes between the previous, historical traffic reflected in LPMS, and the results of the genetic algorithm optimization.



Figure 4 - Tow Size Distribution Comparison

5. Summary

The benefits of the optimization on transit times and overall project throughput and efficiency can be better intuited when these tow-sizes are broken out by barge class or barge size. IHNC traffic predominantly consists of barges of three sizes, representing between them nearly 70% of all barge traffic. These are, in descending order of overall size, barges that are 290-300' long x 50-54' wide, barges 200-259' x 28-36', and 195-200' x 28-36'.

The following figures present the expected number of barges of these various sizes that could viably transit the FWP chamber in a single cut, alongside increase in average tow-sizes by each barge type, showing the increases in efficient utilization of the project.





50-54 x 290-300

Figure 6 - Single Cut Tow Sizes - 28-36' x 200-259'



28-36 x 200-259



Figure 7 - Single Cut Tow Sizes - 28-36' x 195-199'

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