A LabVIEW-Based Target Optimization Genetic Algorithm for Biological Predators

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Abstract—Initial projection of a continuously repositioning target is a setback in genetic algorithm; a GA program needs constant input sampling to predict and declare a targets status. Another difficulty is the incorporation of GA to hardware and software which considered as the most important tool in sensor integration. Familiarity in programming is essential in utilizing the NI LabVIEW and NI myDAO environment. The aim of this research paper is to provide a solution for determining the locus (gene position) of a target through distinctly employed multiple sensors which employs low-frequency (LF) ground-wave oscillations as its signal sources. The targets' position as well as the speed is continuously monitored through virtual instrument (VI) software; the user will be able to visually analyze the constant system mutation plots and the number of completed generations. Upon completion on the number of generations, the plot points can be imported to a spreadsheet for further analysis. The multiplatform software will be able to plot the response under real-time circumstances.

Keywords: LabVIEW, locus, mutation, low-frequency, multiplatform

I. INTRODUCTION

Today, multiple programming methods are applied to perform different tasks; one of them is the genetic algorithm (GA). GA in artificial intelligence is a type of evolutionary computer algorithm in which symbols (often called "genes" or "chromosomes") representing diverse solutions undergo a process called crossover or sometimes addressed as breeding. This process involves recombination of possible genes and multiple mutations at a specific rate. GA mimics the way evolution acts and allows us to improve the performance of controllers or adapt them to different systems [1]. GA is a probabilistic behavior, global searching, and optimization algorithm which is primarily intended to solve complex problems [2].

In comparison with common classical algorithms, GA has loads of advantages, such as a widely viable solution, searching in small and large groups, assistance without further information on the target, internal heuristic random search, parallel computing, etc. [3]. GA is a process for solving both forced and unrestrained optimization problems that is based on natural selection; the mutation process drives biological evolution [4]. It is mainly an overall arbitrary search and optimization method which aims to emulate the natural biological evolution [5].

In the livestock industry, one of the major causes of destructive loss is reptilian predators; these are hunters that feed on fowls and their by-product. This research aims to employ this method under a different target such as predators and take consideration of some parameters such as speed of movement and location status. Through LabVIEW, a programming platform which is widely utilized due to its simple graphical environment yet able to adopt to diverse interface on various hardware and software [6], the user is enabled to analyze the result through point-plotting approach. Unlike other object-oriented programming, LabVIEW allows wiring graphical objects in block diagrams which function as various utilities and modules [7]. The NI DAQ (Data Acquisition) hardware is an external module interface of LabVIEW which consists of several modules that can imitate analog-to-digital converters (ADC), signal conditioners, isolators, filters, and interfacing circuits [8].

II. PRIOR RELATED WORK

LabVIEW GA is a virtual instrument that integrates fitness evaluation, mutations, crossovers and selection [9] through prediction modelling, determination of different signals coming from multiple sources where attenuation and interferences can occur can be used [10].

Animal behavioral studies have been recently being studied especially on the use of sound pressure [11], [12] especially on common reptiles such as snakes through

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vibration stimulation [13]. At 150–450 Hz in the range of 65–75 dBre at 20 mPa, Young and Aguiar observed a substantial decrease in the rattlesnake's *C. atrox* bodily movement and tongue flicking whilst showing a significant rise in numbers of head twitches and tail rattles [11]. Young and Morain added that olfactory-denervated and temporarily blinded Saharan sand vipers' (*Cerastes cerastes*) striking distance, angle, and accuracy were significantly reduced in capturing a free-running prey while employing only target vibrations [13]. Using GA, animal modeling rationalizes non-random mating and complex data organizations which utilizes parental phenotypes and offspring [14].

III. COMPONENTS AND SYSTEM ARCHITECTURE REQUIREMENTS

The system composition is a LabVIEW Virtual Instrument (VI) that employs a block diagram, front panel, and a DAQmx assistant which serves as a medium for acquiring data. The intent of the experiment is to record and plot multiple generations of data coming from the motion sensors. The sets of data that are sent to the computer are the position as well as the speed of the target. The program will be able to predict the succeeding point location where the target would move through a series of consecutive mutations and generations.

- A. The following are the hardware components of the GA system:
 - 1. Motion sensors/transducers
 - 2. Signal transceivers/tranducers
 - 3. NI myDAQ
 - 4. Personal computer/laptop
 - 5. NI LabVIEW
 - 6. Dual polarity power supply
- B. The following are the computer hardware specifications necessary to operate the GA structure:
 - 1. Pentium 4M processor or higher
 - 2. 1 GB of RAM or higher
 - 3. 32- or 64-bit Windows 7/8/8.1/10
 - 4. Free 20-GB hard drive storage for system software requirements
 - 5. Screen resolution of at least 1024×768 pixels



Fig. 1. System block diagram.

The system as shown in Figure 1 consists of two prepositioned transducers, a motion sensor for detecting the rate of the specimen movement, and an RF signal transducer comprised of a ground-wave oscillator for quantifying the position of the target.

The transducers continuously monitor the movement of the target such as change in speed and position and send it to the data acquisition hardware. The GA virtual instrument takes the samples (parents) and generates consecutive mutations within the user assigned number of iterations. The VI will display the optimum value of mutation and plots the activity. The accumulated results can be analyzed through an integrated spreadsheet.

The LabVIEW VI is composed of the following:

- 1. Waveform chart for signal analysis
- 2. Generation progress monitor
- 3. Value indicator
- 4. Generation control
- 5. Mutation probability control
- 6. Interrupter button
- 7. Time estimator
- 8. Time generation monitor
- 9. "Save on spreadsheet" button

The hardware and software system requirements stated are based upon the minimum requirements needed to run LabVIEW 2012 to 2015 and NI myDAQ. Higher specification computers can increase the boot speed of the program as well as the necessary modules; this will also affect the effectiveness of system simulation.

IV. HARDWARE AND SOFTWARE INTEGRATION

The hardware and software integration is implemented through the following procedures:

- A motion sensor is installed in a defined location with minimal irregular geographic terrain.
- An RF signal transducer is utilized to monitor the location of the specimen.
- The transducers are connected to an NI MyDAQ signal acquisition hardware to integrate LabVIEW.
- The LabVIEW program acquires the samples and applies genetic algorithm to perform mutations.
- The user defines the number of generations that will be iterated by the program.
- LabVIEW GA plots each performed mutation and restarts after completing the defined generations.

The circuit in Figure 2 is the RF oscillator that serves as an input to the signal transmitter. It is comprised of multiple square wave generators and sinusoid converters. The waveforms produced are generally combined by a masking stage and are used to generate ground wave oscillations.

Using roulette selection [15], let the population size be p, the population members be c_i for $\leq i \leq p$, and the fitness of chromosome be written f(c) and the wheel size W by

$$W = \sum_{i}^{p} f(c_i)$$

Selecting a chromosome,

$$j < \sum_{i}^{k} f(c_i)$$

where each f(c) slots corresponds to each chromosome. Assigning slot counts according to

$$f'(c) = F - f(c) + s$$

where

$$F = max f(c_i)$$

The fitness function is given by with if and only if x is a solution.

The loose fitness function satisfies with if x is a solution where the sum of any member of fitness functions with non-negative weights is also a fitness function.



Fig. 2. RF oscillator schematic diagram.

V. SYSTEM FUNCTIONALITY DEMONSTRATION

The block diagram, as shown in Figure 3, illustrates the main VI program of the GA system. It is also composed of multiple sub-VIs which perform the mutation of each input sample. The DAQ Assistant serves as the interface between the external experiment proper and the software. The speed of iterations varies depending upon the capacity of the simulating CPU.



Fig. 3. GA system block diagram.

The virtual instrument is simulated and displays the plot on the number of mutations and completed generations. The optimum mutation probability is 0.006. The most effective number of generations should be at least 100 before it reaches the best fitness.





Fig. 5. First-generation plot.

Figure 5 shows the plot of the first generation. First mutations are low, yet the best fit value generated by the VI reaches an almost constant score.



Fig. 6. Second-generation plot.

Figure 6 shows the plot of the second generation. First mutations are relatively lower than the first, yet the optimally fit value generated still reaches an almost constant score.

Fig. 4. Specimen and target setup.



Fig. 7. Third-generation plot.

In Figure 7, the first mutations are low, but while finding the best fitness, the program still arrived at the optimum score which is nearly constant.



Fig. 8. Fourth-generation plot.

In the fourth generation as shown in Figure 8, the first samples started extremely low but still managed to recover and attained a maximum score throughout the generation.

Figure 9 illustrates the four generations of mutations done by the system. As shown, multiple iterations are repeated for mutation of the acquired samples. At the start of the experiment, mutations are low; however, the system continuous to attempt a prediction on how the specimen would succeed in reaching its target. The VI requires at least 11 ms before it settles for the best fitness outcome.



Fig. 9. Mutation results.

VI. CONCLUSIONS AND RECOMMENDATIONS

The point plotting GA system was able to execute locus plots through the reception of sensor data. Mutations of several samples on the target specimen's velocity and position were obtained and monitored through NI LabVIEW as well as the importation on a spreadsheet summary for further analysis and assessment. The VI software can be modified to perform other tasks which allows gathering of other parameters of moving samples.

The system structure can be enhanced through several software and hardware modifications. These enhancements will improve genetic mutations on movement predictions, namely,

- Increase in CPU processing speed by utilizing greater hardware specifications,
- · Replacement of a higher sensitivity reception transducers,
- Modifications on the LabVIEW program for generation mutations, and
- Placement of transmitter and receiver transducers on terrains with less inclinations as well as geographical obstructions.

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