

EMG-Torque correction on Human Upper extremity using Evolutionary Computation

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Abstract. There have been many studies indicating that control system of rehabilitative robot plays an important role in determining the outcome of the therapy process. Existing works have done the prediction of feedback signal in the controller based on the kinematics parameters and EMG readings of upper limb's skeletal system. Kinematics and kinetics based control signal system is developed by reading the output of the sensors such as position sensor, orientation sensor and F/T (Force/Torque) sensor and there readings are to be compared with the preceding measurement to decide on the amount of assistive force. There are also other works that incorporated the kinematics parameters to calculate the kinetics parameters via formulation and pre-defined assumptions. Nevertheless, these types of control signals analyze the movement of the upper limb only based on the movement of the upper joints. They do not anticipate the possibility of muscle plasticity. The focus of the paper is to make use of the kinematics parameters and EMG readings of skeletal system to predict the individual torque of upper extremity's joints. The surface EMG signals are fed into different mathematical models so that these data can be trained through Genetic Algorithm (GA) to find the best correlation between EMG signals and torques acting on the upper limb's joints. The estimated torque attained from the mathematical models is called simulated output. The simulated output will then be compared with the actual individual joint which is calculated based on the real time kinematics parameters of the upper movement of the skeleton when the muscle cells are activated. The findings from this contribution are extended into the development of the active control signal based controller for rehabilitation robot.

1. Introduction

This research utilizes both EMG readings and kinematics parameters to best predict the correlation between EMG signals and the individual torque of the upper limb's joints. Each individual torque acts as a feedback signal of the sub-component in the control system to control the actuators driving the exoskeleton's joints. Electromyography (EMG) is clinically used to identify the abnormality of muscle cells. It is then incorporated into the control system of rehabilitative robot to read the action potential of muscle cells and translate them into kinetics parameters of joints (force and torque). Rigorous researches have been done in utilizing EMG signals as the foundation to establish the control system [1, 2, 3, 4, 5] Some of the challenges that are encountered by many researchers are the methodologies to convert



the EMG signals of multiple muscles into the generated torque of the upper extremity's joints [6, 7] This is because the action potentials of muscle cells are dependent not only on the skeletal movement [8] but also on the proportion of slow and fast fibers [9], thickness of fat under the skin [5], placement of electrodes, age [6] and muscle temperature [8]. Due to these independent variables which vary between individuals, there is still a debate on the relationship between EMG signals and force/torque of upper extremity. Some has proven that they are exponentially related [9, 10] while another has integrated both curve fit polynomials and exponential to describe their relationship [11]. There are also many other works that have investigated EMG-force/torque relationship of single joint at upper extremity. However, it has been proven that improvement of torque estimation of single joint led to the unpredictable errors to the multi joints prediction [12]. The clinical results of the implementation of predicting control signal of single joint only showed good results in the restoration of the transmission path at the early stage of rehabilitation process. Nevertheless, full restoration requires the coordination of several joints to perform the functional task in daily activities. Therefore, it highlights the importance of this research in which it aims at predicting the multi torques of upper extremity based on EMG readings of different muscle cells.

Genetic Algorithms have been widely used in the field of engineering as an alternative method in problem solving especially in the search and optimization problems. It is said to be better than other traditional methods [13] and conventional AI [13] due to its robustness. GAs are also proven to be able to offer substantial benefits over many other typical heuristic search algorithm such as linear programming, depth-first, breath-first, etc. [14]. According to David [15], they are good at having a huge search spaces and also directing the direction of search to look for optimal combinations of the array of parameters producing solutions that might not be found in a lifetime. Hence, GAs are chosen to be the training/search algorithm to search for the optimized/best possible relationship between EMG signals and the exerted torques of the upper limb's joints

2. Methods

2.1. Design of Algorithm

The fitness function is the evaluation criteria for the candidate solutions to determine if they are good or bad solutions by assigning values to the individual chromosome. Given the current problem, the fitness function is represented by the mathematical models as mentioned in Eqns 1-10. Each of the mathematical models consists of the inputs which are the EMGs signals of different muscles, outputs (simulated torque of shoulder, elbow and wrist joint) and the trained coefficients. These coefficients are denoted as a_i , b_i , c_i , and d_i in the equation. Since the EMGs signal has already been acquired and known, the value of the simulated torque can only be tweaked by changing the value of the coefficient parameters so that the difference between actual and simulated torque is very small. The coefficient parameters are trained under the supervision of GA.

$$\tau_{simulated} = \sum_{i=1}^N a_i x_i \quad (1)$$

$$\tau_{simulated} = \sum_{i=1}^N a_i x_i^2 + b_i x_i + c_i \quad (2)$$

$$\tau_{simulated} = \sum_{i=1}^N a_i x_i^3 + b_i x_i^2 + c_i x_i + d_i \quad (3)$$

$$\tau_{simulated} = \sum_{i=1}^N a_i (e^{x_i})^2 + b_i e^{x_i} \quad (4)$$

$$\tau_{simulated} = \sum_{i=1}^N a_i \log(x_i)^2 + b_i \log(x_i) \quad (5)$$

$$\tau_{simulated} = \sum_{i=1}^N a_i \log(x_i) + b_i(e^{x_i}) \tag{6}$$

$$\tau_{simulated} = \sum_{i=1}^N a_i \cos(x_i) + b_i \sin(x_i) \tag{7}$$

$$\tau_{simulated} = 1 / (\sum_{i=1}^N a_i \cos(x_i) + b_i \sin(x_i) + c_i \log(x_i)) \tag{8}$$

$$\tau_{simulated} = \sum_{i=1}^N a_i \cos(x_i) + b_i \sin(x_i) + c_i(e^{x_i}) \tag{9}$$

$$\tau_{simulated} = \sum_{i=1}^N a_i \cos(x_i) + b_i \sin(x_i) + c_i \log(x_i) + d_i(e^{x_i}) \tag{10}$$

where, $\tau_{simulated}$: the simulated torque of the upper joints
 N : number of muscles
 x_i : EMG measurement of muscle i
 a_i, b_i, c_i, d_i : the coefficients of muscle i (the trained parameters)

Encoding the fitness value of a chromosome based on the fitness function is one of the problems encountered in GAs. There are two alternative methods to determine the fitness value of the chromosomes. The first method is averaging all the error percentages of a chromosome from all data points as illustrated in Equation 11.

$$fitness_value = \frac{\sum_{i=1}^{data_points} \left(\frac{simulated_{(i)} - actual_{(i)}}{actual_{(i)}} \right) \times 100\%}{data_points} \tag{11}$$

All participants are required to perform a simple shoulder abduction adduction movement for 20 seconds with a sampling rate of 247 Hz. The same movement is repeated for 1- cycles with a 5 minutes resting time in between the execution of each cycle. Resting time is introduced to allow muscle cells to rest so that the effect of muscle fatigue can be minimized. Muscle fatigue reduces the overall energy stimulated by muscle cells affecting the prediction of the control signal. Hence, the inconsistent error in the control signal can be minimized by reducing the possibility of having muscle fatigue. The procedure and the criteria of all participants of these experimental studies have been approved by MUHREC .

Table 1. The physical properties of the participants.

Subjects #	Age	Weight (kg)	Height (cm)
Subject #1	(Female) 25	43	150
Subject #2	(Female) 27	48	154
Subject #3	(Male) 27	63	178
Subject #4	(Male) 28	67	175

2.2. Kinematics data acquisition and processing

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The acquisition system consists of Motion Tracking System [16, 17] and EMG system. The tracking system tracks and records the tracking markers and converts them into path trajectory to generate the

kinematics parameters of the movement. Each of the tracking markers is placed onto the upper limb based on the arm anatomy and together, they form the anatomy landmarks of the upper limb. These parameters are then exported to Visual3D to calculate the kinetics data of the individual joint of the upper limb. Using the static marker as the reference and the exported data, the proximal and distal forces and torques of the upper limb joints can be calculated. The skeletal model of Visual3D is illustrated in Figure 1.

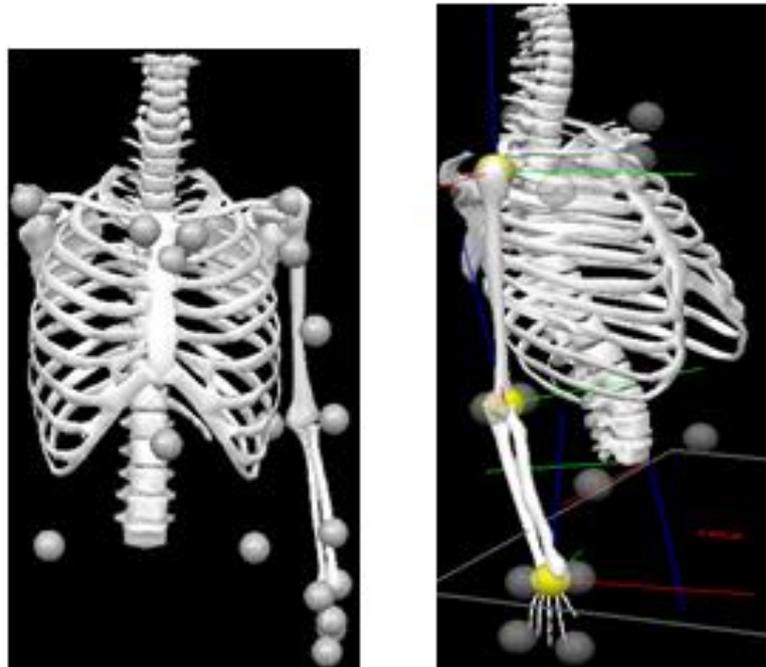


Figure 1. The skeleton modeled by Visual3D based on the tracking markers. The red, blue and green represent the xyz reference. Each joint (point of rotation) has its respective reference frame.

2.3. EMG signal acquisition and processing

EMG system is equipped with a built in amplifier with a gain of 100 to amplify the miniscule magnitude of the muscle's electrical activity. The system uses electrodes to detect the electrical activity generated by the muscle cells by attaching the electrodes onto the skin where the muscles of interest lie beneath it. Numerous investigations have been done to study the implication of different attachment of electrodes in relation to the measured readings and their characteristics [18,19, 20]. This then raises doubts in the reliability of EMG signals prior to data acquisition which then questions the integrity of the collected data. SENIAM (Surface EMG for Non-Invasive Assessment of Muscles) has documented the general assessment of electrode placement which is widely implemented and recognized [21, 22, 23, 24, 25]. This research follows SENIAM's assessment strictly to generalize the assessment of signal and maintain the integrity of the findings. Also, the signal's assessment has complied with the theory presented by [26, 27] and been verified by signal analysis done by [28].

All electrical activities recorded by bio-electrodes without built in filter are called raw EMG signals and they are all consisted of interferences and positive and negative characteristic of stimulated energy. The interference may be originated from the neighboring electrical hardware, electrical noise within the hardware, cross talk, etc. This interference causes the existence of baseline and artifact noise in the signal and thus, raw EMG signals have to be processed to minimize all unforeseen variables that can affect the performance of control signal and controller. Rectification of signal is encouraged because the total energy from the raw signal cannot be measured due to positive and negative characteristics of EMG signal. Hence, raw signal is fully rectified to calculate the total energy of the muscle but still, preserving the information stored in the signal.

3. Results and Discussions

The coefficients a_i , b_i , c_i and d_i of the mathematical models play an important role in determining the simulated torque based on the EMG signals. These coefficients are represented as genes in the training algorithm known as Genetic Algorithm. In GA, there are many techniques of training the parameters by using different selection methods, crossover operators and mutation operators. For comparison study, all the simulated results addressed in this work are trained with linear ranking selection, BLX- α crossover operator and random mutation operator. This research addressed the performance of the simulated results that are generated from training the different non-linear mathematical models. The non-linear mathematical models are illustrated in Equation 1-Equation 4.

The simulation results have shown that quadratic polynomial has better performance than cubic polynomial. Cubic polynomial has steeper slope which can be seen from the narrow graph of the simulated torque. Figure 2 illustrates the simulated results from training the EMG signals based on the quadratic polynomial and cubic polynomial function. It is evident that the simulated graph of quadratic polynomial is able to cover more area under the actual torque in comparison to the cubic polynomial. Hence, its error percentage is lower. Quadratic polynomial has an average error of 49.368% while cubic polynomial has an average error of 58.48%. The average error is calculated by averaging the total average errors from 100 generations.

On the other hand, both exponential and trigonometry function have the worst performance against the other non-linear mathematical models. It was found that the average error percentage generated by these functions exceeded 500% which is not tolerable. The problems encountered in training EMG signals based on these functions are the behavior of the baseline and height of the slope of the simulated graph when the training parameters are altered. Figure 3a and Figure 3b illustrates the behavior of the simulated torque when the range of value of the coefficients are set within (0.5, 1) and (1, 2) respectively. By increasing the range of value of the coefficients, the baseline is also increased significantly. This can be proven by the increment of the baseline by $\pm 2\text{N.m}$ in the graph below. Nevertheless, the height of the slope is not affected significantly. Hence, by altering the value of the genes and exploring new candidate solutions are not improving the performance of the simulated output. In comparison with the exponential function, polynomial functions do not have issue with the baseline and the height of the slope. For polynomial functions, increasing the range of value of the coefficients, the baseline is not affected significantly but the height of the slope is affected significantly. The behavior of the simulated graph is more favorable in mimicking the actual torque.

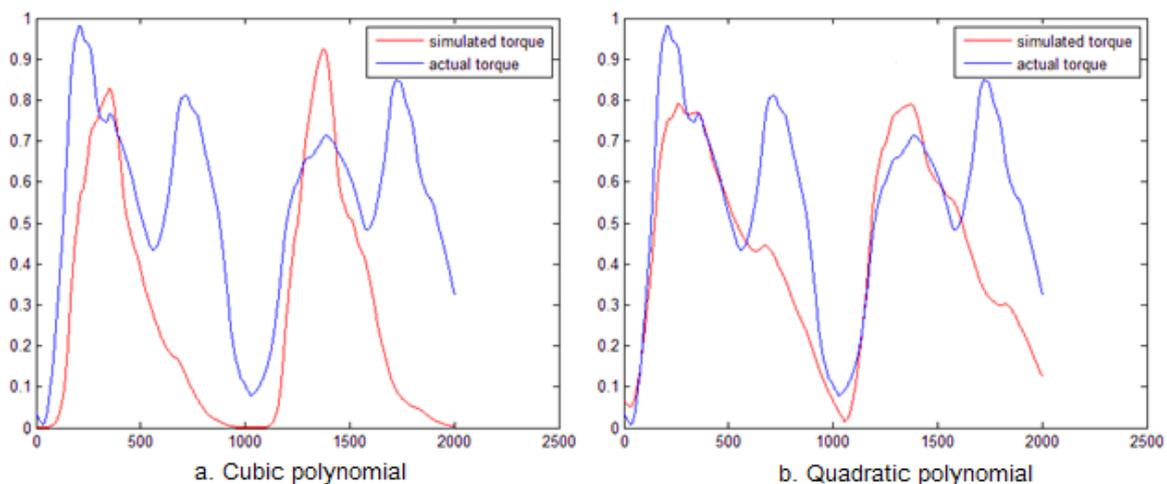


Figure 2. The actual and simulated torque generated from the EMG signals training based on (a) cubic polynomial function and (b) quadratic polynomial function.

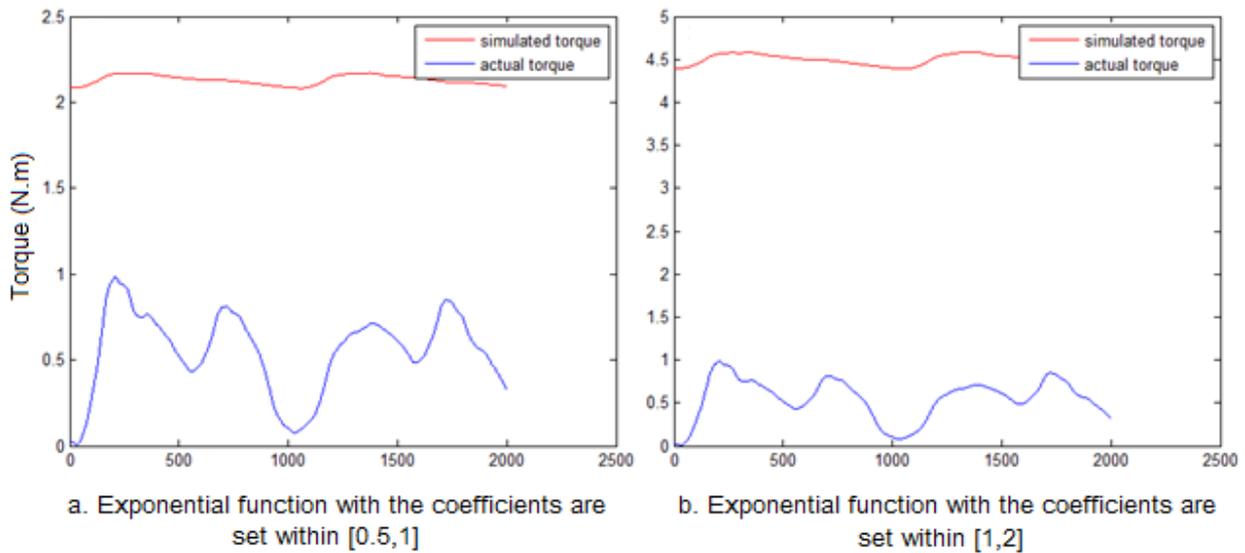


Figure 3. The actual and simulated torque of exponential function with different coefficients

Table 2. The results comparison between cubic and quadratic polynomial

	Cubic polynomial	Quadratic polynomial
Equation	$\sum_{i=1}^N a_i x_i^3 + b_i x_i^2 + c_i x_i + d_i$	$\sum_{i=1}^N a_i x_i^2 + b_i x_i + c_i$
Elapsed time	4336 seconds	3779 seconds
Number of coefficients (genes)	30 genes	20 genes
Average error (%)	58.48%	49.368%

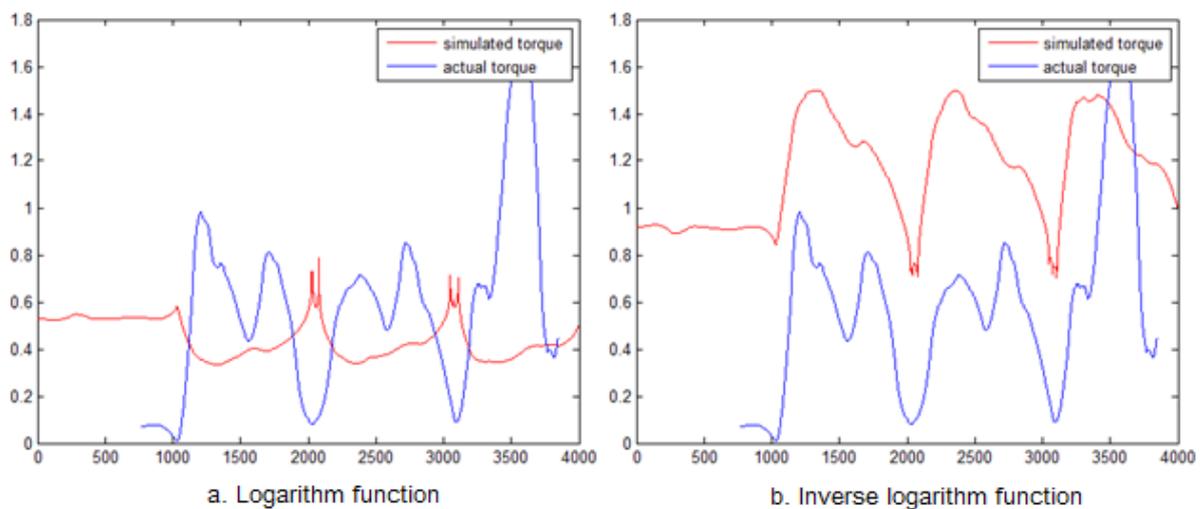


Figure 4. The actual and simulated torque of a) logarithm function and b) inverse logarithm function

Table -2 summarizes the performance of both quadratic polynomial and cubic polynomial. Based on the summary, it is evident that quadratic polynomial is a better mathematical representation than cubic polynomial. Quadratic polynomial achieved smaller average error with lesser computational time than cubic polynomial.

Another mathematical model to be investigated is logarithm function. An inverse relationship is discovered while investigating the behavior of the simulated graph when the logarithm function is trained which can be seen in Figure 4(a) The actual torque decreases when the simulated torque increases and vice versa. Hence, *Equation 1* is introduced and its coefficients are trained to analyze the simulated torque generated by inverse log which results in Figure 4(b). Further investigation has then revealed that the increased value of the coefficients increases both the baseline value and the rise of the slope.

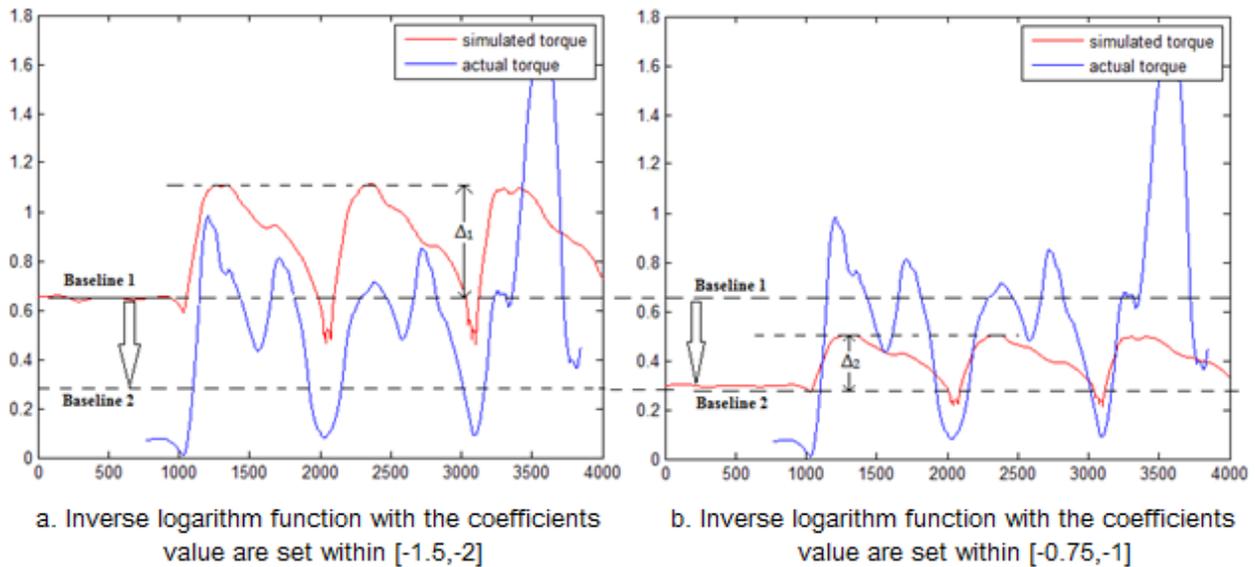


Figure 5. The graph comparison of inverse logarithm functions when the value range of the chromosomes is changed. Left – The simulated graph is generated when the initial chromosomes are set to [-0.05,-0.075] whereas right – the initial chromosomes are within [-0.15,-0.2].

The value range of the chromosomes is increased significantly to minimize the baseline offset between the graphs. *Figure 5* illustrates how the simulated graph is affected when the values of the coefficients (chromosomes) are changed. Should the value increases, the baseline offset is reduced as shown with the error in the graph. However, Δ_1 is also reduced resulting in Δ_2 . Thus, to preserve the value of Δ but still minimizing the error of the baseline; *Equation 2* is introduced. While the logarithm function sets the value of Δ , the constant b maintains the position of the graph to be near the baseline. Comparing the simulated torque of the quadratic polynomial (and the inverse logarithm (*Equation 2*)), the average error of the inverse logarithm is calculated to be $\pm 32\%$ which is smaller than quadratic polynomial. It also has lesser computational time than quadratic polynomial. Hence, the EMG-torque relationship is best described as the inverse logarithm with a variable b . With inverse logarithm used as the fitness function to evaluate the quality of the solutions generated by the training algorithm, the torque acting on the shoulder, elbow and wrist joint is estimated based on the EMG signals.

Equation 1. Inverse logarithm

$$\tau_{simulated} = \sum_{i=1}^N 1/a_i \log(x_i)$$

Equation 2. Inverse logarithm with constant b

$$\tau_{simulated} = \left(\sum_{i=1}^N 1/a_i \log(x_i) \right) - b$$

4. Conclusion

It can be concluded that exponential offers the worst prediction in estimating the actual torque of upper limb's joints during shoulder abduction adduction. It is then followed by both quadratic and cubic polynomials which present an average error of $\pm 49\%$ and $\pm 58\%$ respectively. The source of the error mainly originated from the narrow gap of the slope; made it difficult to cover certain areas under the actual graph. Since cubic polynomial has steeper slope, it does make sense that the average error is higher than quadratic polynomial. On the other hand, the inverse log function (Equation 2) produces a much better prediction in comparison to the other non-linear mathematical models with an average error of 32% throughout 100 generations. Hence, it is the best mathematical model estimating the simulated torque at the multi joints during shoulder abduction adduction.

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