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a direct collocation method for optimization of wrist joint EMG-driven musculoskeletal model

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***Abstract*— EMG-driven musculoskeletal model has been broadly used to detect human intention in rehabilitation robots. This approach computes muscle-tendon force and translates it into a joint kinematics model with muscle-tendon parameters. However, these parameters are difficult to measure in *vivo* and varied across subjects. In this study, a direct collocation method is proposed to optimize the subject-specific parameters in a wrist musculoskeletal model. The resultant optimized parameters are used to estimate the wrist flexion/extension motion. The estimation performance is compared with the parameters optimized by the genetic algorithm. Experiment results show that the direct collocation method requires less optimization time and achieved the same performance, compared with the genetic algorithm.**

I. Introduction

Decoding users' intention based on the electromyography (EMG) signals can provide an intuitive control scheme for rehabilitation robots. The interest in using EMG-driven musculoskeletal (EMG-MS) model to estimate the joint motion has risen recently [1]–[3]. This approach transfers the muscle activities to the muscle-tendon force, using the muscle activation dynamics and muscle contraction dynamics respectively [4]. Together with the explicit representation of the joint geometry, the joint kinematics can be computed regarding the given EMG signals [5]–[7]. However, the force output of the musculoskeletal model is influenced by the muscle-tendon parameters significantly, i.e., maximum isometric force, optimal muscle fibre length, tendon length and pennation angle [8], [9]. It is difficult to determine these parameters in *vivo* and they are closely related to the gender, age and activity level. Therefore, these parameters are required to be optimized across users in order to establish a subject-specific EMG-MS model.

To date, several methods have been used to determine the muscle-tendon parameters. A linear scaled method was proposed which optimized the parameters from the anatomical dimension based on the reference model in a biomechanical software, e.g., OpenSim [10], [11]. However, this method determines the subject-specific parameters from the user's anatomical data solely. Alternatively, the inverse (or forward) dynamics methods are widely used to optimize the subject-specific parameters, which minimizes the difference between the experimental joint moment/motion and the model estimated joint moment/motion [5]–[7]. The resultant parameter optimization problem composes a large number of the muscle-tendon parameters according to the related muscles. Thus, the heuristic algorithms, e.g., genetic algorithm, are commonly employed to find the best match of parameters. However, due to a large amount of muscle-tendon parameters and the corresponding large search space, the heuristic algorithms may require the long optimization time, which may lead to barriers for implementing the EMG-MS model in the clinical environment [12]. For instance, in [13], an average optimization time of 20 hours was reported in a lower limb EMG-MS model for estimating the multiple degrees-of-freedom joint moments. Pau *et al.,* has used the genetic algorithm to tune 24 muscle parameters in an EMG-MS model, which requires an average one hour for each trial [5]. Moreover, Crouch *et al.,* reported the execution time of optimization taking approximately 20 hours in a lumped-parameter EMG-MS model using the simulated annealing algorithm [6].

In contrast to the heuristic algorithms, this parameter optimization problem can be solved by formulating the EMG-MS model into an optimal control problem [15]. However, solving the optimal control problem straightforward is computationally expensive, i.e., indirect method [16]. Instead, the direct collocation (DC) method is a computationally efficient method in finding the solutions in the EMG-MS model related problems. The DC method becomes popular to determine the muscle activities [17], internal joint contact force [18] or the optimal trajectories [19]. Furthermore, with a given movement and EMG signals, DC method is able to determine the muscle-tendon parameters. Falisse *et al.* applied the DC method to estimate the value of tendon slack length and optimal muscle fibre length by minimizing the joint moment between model's estimation and measured joint moment in a lower-limb musculoskeletal model [14]. However, they have only optimized two kinds of muscle-tendon parameters and compared them with the linear scaled method.

This paper proposes a direct collocation method to optimize the muscle-tendon parameters in a wrist joint musculoskeletal model, which includes maximum isometric force, optimal muscle fibre length, tendon length and pennation angle. By formulating the wrist joint EMG-MS model into an optimal control problem, the direct collocation method converts it into a non-linear programming (NLP) problem. In order to determine the muscle-tendon parameters, a vector including the discretized state variables, control variables and muscle-tendon parameters is generated. Then the gradient matrix and the constraint Jacobian matrix are computed for the NLP solver. The optimized parameters are used to estimate the wrist flexion/extension motion. Based on the same objective function, maximum iteration number and stop

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criteria, the estimation performance using optimized parameters through the DC method is compared with the genetic algorithm. Results show that the optimized parameters by the DC method can estimate the wrist flexion/extension accurately. Under the same performance, the direct collocation method requires less optimization time.

In this paper, the remaining sections are organized as follows. In section II, the experiment protocol and the description of the direct collocation methods are presented. Section III gives the results regarding the optimized muscle-tendon parameters and the comparison with the genetic algorithm, followed by a conclusion in Section IV.

II. Methods

A. Experiment

Subjects are informed to seat on an armchair with the fully straight torso. The right shoulder is abducted at 90° and elbow is flexed at 90°. Continuous wrist motion ais recorded using the 8 motion capture cameras (Vicon Motion Systems Ltd. UK). The VICON upper limb model is used to compute the measured joint trajectory [20]. 16 reflective markers are placed over the subjects' right upper limb, which are allocated over the spinous process of the 7^{th} and the 10^{th} thoracic vertabra, right scapula, xiphoid, acromio-clavicular joint, clavicle, lateral/medial humerus medial epicondyle, right radial/ulnar styloid, middle forearm and the right third metacarpus. The motion data are sampled at 250 Hz.

Five EMG channels (Delsys Trigno^{TM} system) are placed over flexor carpi radialis, flexor carpi ulnaris, extensor carpi radialis longus, extensor carpi radialis brevis and extensor carpi ulnaris, according to the SENIAM recommendation [21]. The arm is shaved and skin is cleaned up using an alcohol wipe to minimize the impedance. EMG signals are recorded sampled at 2000 Hz. A trigger module is used to synchronize the EMG signals and motion data. To alleviate the effect of wrist muscles, the metacarpophalangeal joint is keeping fully relaxed during the experiment. The isometric maximum voluntary contraction is recorded before the experiment. The continuous wrist flexion/extension movement is recorded in the experiment. Each trial last about 15-20 seconds and Five repetitions are performed for each subject. A three-minute break is given between trials to prevent muscle fatigues. One cycle of wrist flexion/extension movement is extracted from the first trial in order to tune the parameters through the DC method and genetic algorithm respectively. The remaining motion trials are used to validate and compare the estimation performance between the DC method and genetic algorithm.

This experiment is approved by the MaPS and Engineering Joint Faculty Research Ethics Committee of the University of Leeds (MEEC 18-002). The consent forms are signed by five healthy subjects.

B. EMG-MS model

The EMG-MS model in this study is used to established to estimate the flexion/extension motion of the wrist joint, comprising the muscle activation dynamics, muscle-tendon dynamics and Joint kinematic estimation model.

1) Muscle activation dynamics: The muscle activation dynamics is derived by a first order differential equation and a non-linear equation. The raw EMG signals are first filtered using a 2^{nd} order butterworth band-pass filter at cut-off frequencies between 25 Hz and 450 Hz to remove baseline and artefact noise, and then fully rectified. The rectified signals are then low-pass filtered using 4^{th} order butterworth low-pass filter at a corner frequency of 4 Hz. Filtered signals are normalized by dividing the peak value of isometric maximum voluntary contraction, resulting the enveloped signal $e_i(t)$. Then a first order differential equation is used to compute the muscle excitation $s_i(t)$, which is written as [22]:

$$\frac{ds_i(t)}{dt} = (\frac{e_i(t)}{t_{act}} + \frac{1 - e_i(t)}{t_{deact}})(e_i(t) - s_i(t)) \tag{1}$$

where the t_{act} and t_{deact} are the activation time and deactivation time, are set to $15\,\mathrm{ms}$ and $50\,\mathrm{ms}$ respectively [23]. A non-linear function is used to transfer the $e_i(t)$ to muscle activation $a_i(t)$, which is represented as [4]:

$$a_i(t) = \frac{e^{As_i(t)} - 1}{e^A - 1} \tag{2}$$

where the non-linear shape factor A has the range of -3 to 0.01.

2) Muscle-tendon model: The muscle-tendon force F_i^{mt} is computed by the muscle-tendon model, comprising a tendon in series with a muscle fibre. The muscle fibre includes a contractile element (CE) in parallel with passive elastic element (PE). Thus the F_i^{mt} can be derived by the the summation of the active force $F_{CE,i}$ and the passive force $F_{PE,i}$, which can be written as,

$$F_i^{mt} = (F_{CE,i} + F_{PE,i})\cos\phi_i. \tag{3}$$

where the $F_{CE,i}$ and $F_{PE,i}$ are

$$F_{CE,i} = F_{o,i}^m f_a(\frac{l_i^m}{l_{o,i}^m(\lambda(1 - a_i(t)) + 1)}) f(\overline{v}_i) a_i(t) \tag{4}$$

$$F_{PE,i} = F_{o,i}^m f_p(\frac{l_i^m}{l_{o,i}}) \tag{5}$$

where $F_{o,i}^m$ is the maximum isometric force. l_i^m and $l_{o,i}^m$ represent the muscle fibre length and the optimal muscle fibre length respectively. λ is a constant, which is set to 0.15 [24]. Note that the muscle tendon force F_i^{mt} is fully derived by the variation of the l_i^m because the tendon length is assumed to be constant in this study. The muscle fibre length l_i^m is computed by

$$l_i^m = (l_i^{mt} - l_i^t)\cos^{-1}\phi_i \tag{6}$$

where l_i^{mt}, l_i^t and ϕ_i are the muscle-tendon length, tendon length and pennation angle respectively. The equations for the force/length relationship of the Hill's muscle model are provided in Appendix.

3) Joint kinematic estimation: In this study, the joint kinematics is computed by the coordinate relative to the wrist joint, where is located at the mid of the radial and ulnar styloid. It is assumed that the hand is a rigid segment and is rotated around the joint centre in the sagittal plane. Thus, the equation of motion is written as

$$I\ddot{\theta} + mgLsin(\theta) + C\dot{v} = \tau \tag{7}$$

where I is the moment of inertia of hand. $\ddot{\theta}$ is the angular acceleration. m and L represent the mass of subject's hand and the length of the hand. θ and $\dot{v}$ represent the wrist joint angle and angular velocity respectively. C is the damping coefficient representing the elastic and viscous effects from tendon, ligaments. τ is the joint torque, which is calculated by ($i = 1 \dots 5$):

$$\tau = \sum_{i=1}^{2} M_{flexor,i} - \sum_{i=3}^{5} M_{Extensor,i} \tag{8}$$

where $M_{flexor,i}$ and $M_{extensor,i}$ represent joint torque computed by the wrist flexor and extensor respectively.

$$M_i = F_i^{mt} r_i. \tag{9}$$

The l^{mt} and r_i are presented using the second-order Fourier equations according the estimation from OpenSim [25]

$$l_i^{mt} = b0 + \sum_{n=1}^{2} b_n cos(nw\theta) + c_n sin(nw\theta) \tag{10}$$

$$r_i = d0 + \sum_{n=1}^{2} d_n cos(nw\theta) + h_n sin(nw\theta) \tag{11}$$

where the coefficient b_i, c_i, d_i and h_i are the Fourier parameters. Therefore, the EMG-MS model can estimate the wrist joint motion according to the given EMG signals.

4) Parameter optimization: In order to provide accurate motion estimation for each subject, the muscle-tendon parameters containing optimal muscle fibre force, tendon slack length, maximum isometric force, and pennation angle are required to be optimized for each subject. Therefore, a parameter p including the non-shape factor A is generated for the optimization, which is represented as

$$p = [F_{o,i}^{m^T}, l_{o,i}^{m^T}, l_{o,i}^{t^T}, \phi_i^T, A] \tag{12}$$

In this study, genetic algorithm and DC method are used to optimize the parameter vector respectively. This parameter estimation problem is solved by an objective function, which is written as,

$$\Psi = \int_{t_1}^{t_f} (\theta_{measured} - \theta_{estimated})^2 dt \tag{13}$$

where $\theta_{measured}$ and $\theta_{estimated}$ represent the measured joint angle and estimated joint angle respectively. The t_1 and t_f represent the initial time and end time respectively. In addition, the boundary conditions of parameters for both optimization method are set as

$$\begin{aligned} 10 \le F_{o,i}^m(\mathrm{N}) &\le 1000 \\ 0.06 \le l_{o,i}^m(\mathrm{m}) &\le 0.1 \\ 0.2 \le l_i^t(\mathrm{m}) &\le 0.4 \\ 0 \le \phi_i(\mathrm{rad}) &\le \frac{\pi}{2} \\ -3 \le A &\le 0.01. \end{aligned} \tag{14}$$

C. Genetic algorithm

The genetic algorithm mimics the natural evolutionary process by representing the parameters as a 'chromosome'. The algorithm randomly generates a set of possible solutions for the parameter estimation problem. The best fitness at each generation to generate the "offspring" and finally the best set of parameters can be reached. Furthermore, the genetic algorithm is commonly used in the musculoskeletal model [5]. It can evaluate multiple solutions in the search space, and reduced the risk of falling into local minima. Thus, to determine the best match of the subject-specific parameters, the genetic algorithm is set to

$$\hat{p} = \arg\min_{p} \{\Psi(p)\} \tag{15}$$

where $\hat{p}$ is the optimized parameters. In this study, the MATLAB global optimization toolbox is used to solve this optimization problem. The tolerance is set to $1 \times e^{-4}$ and the maximum iteration number is set to 1000, other settings are set to the default value.

D. Direct Collocation Method

The DC method transcribes the EMG-MS model related optimal control problem into the finite-dimension NLP problem, which treats the states, control and muscle-tendon parameter vector p as an unknown vector [15]. Furthermore, the musculoskeletal model comprising the differential equations which allows computing the Jacobian matrix for the NLP solver.

In the wrist EMG-MS model, the state variables contain the joint angle θ, velocity v and muscle excitation $s_i(t)$, which can be represented by

$$x(t) = [\theta, v, s_i(t)]. \tag{16}$$

The enveloped EMG signals $e_i(t)$ are introduced as the control variables

$$u(t) = [e_i(t)]. \tag{17}$$

Thus, the estimated joint trajectory can be represented as the function of the state/control variable and the parameter vector p which is $\theta_{estimated}(x(t), u(t), p)$ in (13). Furthermore, the control variables and state variables are discretized simultaneously into number of grid points N with respect to the time history, which are collected into a vector Y,

$$\begin{aligned} Y = [x_1^T, u_1^T, x_2^T, u_2^T, x_1^T, u_1^T, \dots, x_N^T, u_N^T, p], \\ 0 = t_1 < t_2 < t_3 < \cdots < t_N = t_f \end{aligned} \tag{18}$$

The parameter vector p is added at the end of Y that it can be optimized by the NLP solver.

1) Constraint functions: The constraint functions are imposed by the muscle activation dynamics and muscle contraction dynamics are the implicit formulations are used [26]. The constraint functions at each grid can be presented by

$$f(x_k, \dot{x}_k, u_k, p) = \begin{cases} \dot{\theta}_k - v_k \\ I\dot{v}_k + mgl\cos(\theta_k) + Cv_k - \tau_k \\ \dot{s}_{i,k} - (e_{i,k} - s_{i,k})(\frac{e_{i,k}}{t_{act}} + \frac{1-e_{i,k}}{t_{deact}}) \end{cases} \tag{19}$$

where $k = 1, 2, 3 \ldots N-1$. $\dot{\theta}_k$, $\dot{v}_k$ and $\dot{s}_{i,k}$ represent the derivatives of the state variables. Furthermore, the constraint function are converted into the the algebraic constraints using the finite differential approximation, where the mid-point rule is used in this study,

$$c_k = f(\frac{x_{k+1} + x_k}{2}, \frac{x_{k+1} - x_k}{t_{k+1} - t_k}, \frac{u_{k+1} + u_k}{2}, p) = 0 \tag{20}$$

where c_k is the algebraic constraints at each grid. Furthermore, task constraints are also introduced to restrict the motion is consistent with measured data at the initial and end condition.

$$\begin{aligned} s_i(t_0) &= 0 \\ \theta(t_0) = \theta(t_f) &= 0 \\ v(t_0) = v(t_f) &= 0 \end{aligned} \tag{21}$$

In addition to (14), the boundary conditions of the control and state variables are restricted by

$$\begin{aligned} 0 < e_i, s_i &\leq 1 \\ -70^\circ \leq \theta &\leq 70^\circ \\ -\infty \leq v &\leq \infty. \end{aligned} \tag{22}$$

Therefore, the boundary conditions for the DC method can be reformulated as

$$\begin{aligned} UB &= \{x_U(t1), u_U(t1), x_U(t2), u_U(t2), \ldots, p_U\} \\ LB &= \{x_L(t1), u_L(t1), x_L(t2), u_L(t2), \ldots, p_L\} \end{aligned} \tag{23}$$

Where the UB and LB represent the upper bound and lower bound respectively. Note that the length of the bounds in DC method should have the same with the parameter vector Y.

2) Implementation: This optimal musculoskeletal model contains 7 states variable (2 joint kinematics and 5 muscle activations), 5 controls variables (5 enveloped EMG signals) and 21 parameters. The optimization trial is discretized into 101 equal interval ($N = 101$), the resulted NLP problem contains 1233 variables in vector Y and 710 equalities constraints. To solve this NLP problem, the gradient matrix $\frac{\partial \Psi}{\partial Y}$ and the Jacobian matrix $\frac{\partial c}{\partial x}$, $\frac{\partial c}{\partial \dot{x}}$ and $\frac{\partial c}{\partial u}$ are calculated according to [15]. Additionally, the partial derivates of the constraint functions with respect to the muscle-tendon parameter are calculated by:

$$[-\frac{\partial \tau}{\partial F^m_{o,i}}^T - \frac{\partial \tau}{\partial l^m_{o,i}}^T - \frac{\partial \tau}{\partial l^t_{o,i}}^T - \frac{\partial \tau}{\partial \phi_i}^T] \tag{24}$$

This NLP is solved used the IPOPT solver with Hessian matrix approximation. The tolerance is also set to $1 \times e^{-4}$ and the maximum iteration number is set 1000. Other settings are remaining default.

III. Results and Discussion

A. Constraint Jocabian matrix

The Jacobian matrix of the constraint functions with respect to the variables are illustrated in Fig 1, which results in a large sparse matrix. It is can be easily solved by the linear algebra operations of the NLP solver. Last 10 rows represent the task constraints at the beginning and end of the optimization trial respectively. Last 21 columns are also non-zero elements because the partial derivatives of the constraint functions with respect to the muscle-tendon parameters are always computed in the muscle-tendon dynamics, which are represented by the thick blue line. Besides, the constraint functions are computed by two adjoint grids, each row contains two non-zero blocks.

Fig. 2 presents a 7-by-12 matrix that describes the non-zero elements of the constraint Jacobian matrix at each grid. The first row indicates the partial derivatives of motion dynamics with respect to the kinematic state variable, θ and v. The second row contains the partial derivatives of the muscle-tendon model equations ((3) – (9)) with respect to all state variables. The last 5 rows are the piratical derivates of muscle activation equations ((1)) with respect to the muscle excitation $s_i(t)$ and enveloped EMG signals $e_i(t)$.

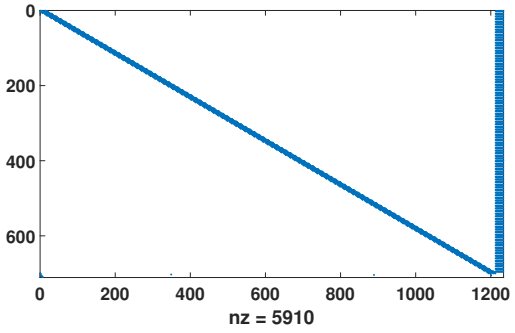


Fig. 1. The partial derivatives of constraint functions with respect to the parameter Y, contains 5190 non-zero elements ($N = 101$). Last 21 columns represent the partial derivatives of the constrains function to muscle-tendon parameters.

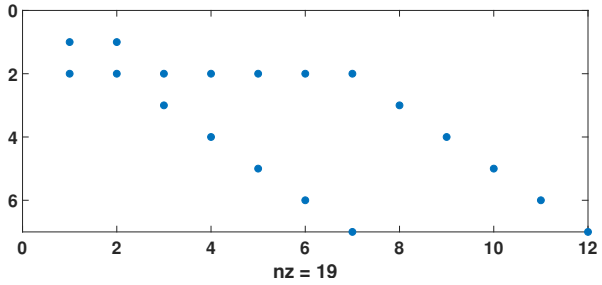
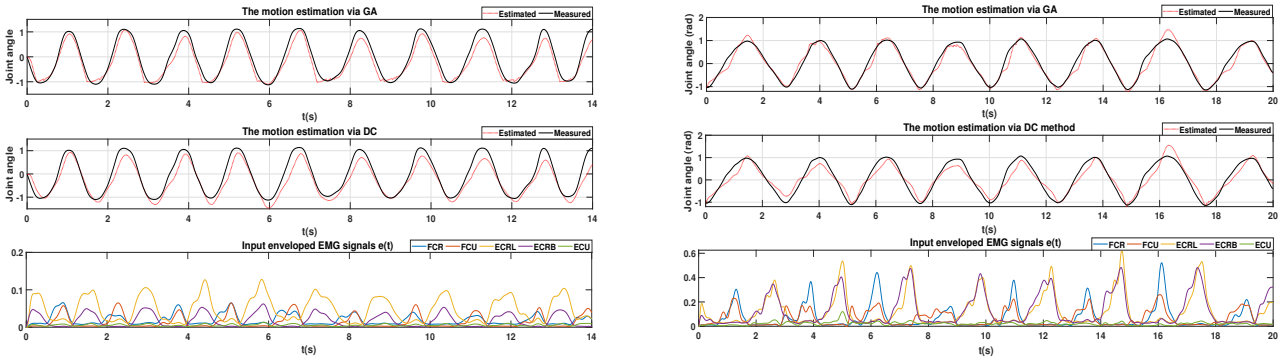


Fig. 2. The partial derivatives of the constrains function to the control and state variables at each grid. Rows corresponds to each constrain function and columns correspond to the control and state variables.



(a) (b)

Fig. 3. Comparison of estimation performance using two different optimization methods in subject 3 and 5, respectively. Each panel shows the estimation performance using the GA-based parameters and the estimation performance using the DC-based parameters respectively. The bottom figure corresponds to the enveloped EMG signals $e_i(t)$.

B. Verification of the optimized parameters

The parameters optimized by the DC method and genetic algorithm are verified by the continuous wrist motion trials. Root-mean-square-error (RMSE) and coefficient of determination R^2 are used to evaluate model's estimation performance compared with the measured joint trajectories. Hereinafter, the parameters optimized by genetic algorithm and direct collocation method are referred to GA-based parameters and DC-based parameters in the following sections.

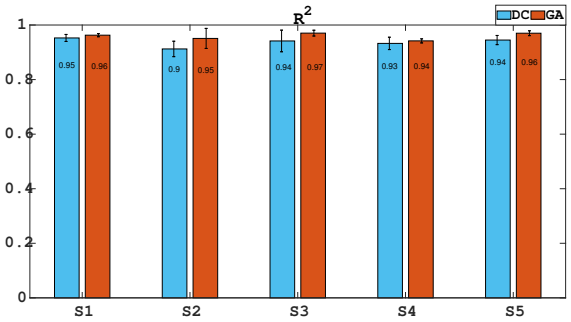


Fig. 4. The mean R^2 across all subjects are 0.93 and 0.96 for direct collocation method and genetic algorithm respectively.

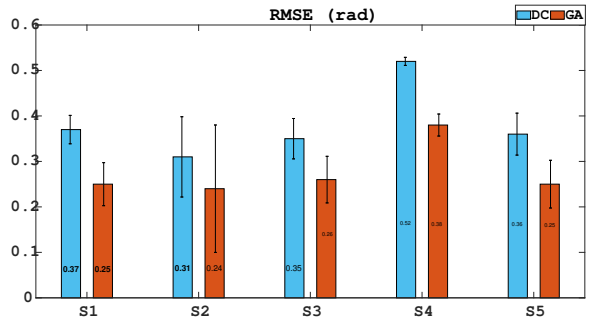


Fig. 5. The mean RMSE across all subjects are $0.38\,\mathrm{rad}$ and $0.27\,\mathrm{rad}$ for direct collocation method and genetic algorithm, respectively.

Fig 3(a) and Fig. 3(b) illustrate the estimation performance with the optimized parameters using two different methods in subject 3 and subject 5, respectively. The R^2 are similar in both subjects, but RMSE increase from $0.25\,\mathrm{rad}$ to $0.32\,\mathrm{rad}$ and from $0.17\,\mathrm{rad}$ to $0.23\,\mathrm{rad}$ when the DC-based parameters are used.

Fig 4 illustrates the mean R^2 across all subjects. The correlation of the DC method based are slightly less than the genetic algorithm based but overall R^2 are high ($R^2 > 0.9$). Both methods have shown the capabilities to estimate the continuous wrist flexion/extension motion with the optimized parameters. Fig 5 presents mean RMSE across subjects, which are $0.27\,\mathrm{rad}$ and $0.38\,\mathrm{rad}$ for the GA-based parameters and DC-based parameters respectively. The mean RMSE of the genetic algorithm is less than the DC method based parameters, which indicates using the genetic algorithm can provide the better motion estimation in terms of the amplitude of wrist flexion/extension motion. The differences in RMSE between the two methods are caused by the difference of two optimized parameters. Because both methods cannot determine the unique optimized parameters due to the large parameters search space. Thus, the variations of the parameters generate the different muscle-tendon force ((3)-(6)), which results in different joint kinematics accordingly. It is worthy to note that the high RMSE is commonly occurred in most of the EMG-MS models, even using the genetic algorithm. This is because the EMG-driven model is an 'open-loop' estimation model. For controlling the rehabilitation robots, the feedback signals are used to reduce the estimation errors. Moreover, the EMG signals are non-stationary signals and the subject cannot perform the same muscle activations in the same movement, as illustrated in Fig 5.

The variations of the optimized parameters of subject 5 with respect to the initial value are listed in the Table I. The variations of the non-linear shape factor A are 67.825% and 4.21% for GA and DC method respectively. The optimized optimal muscle length, tendon length and pennation angle

TABLE I

COMPARISON OF THE OPTIMIZED PARAMETERS IN SUBJECT 5 USING TWO DIFFERENT APPROACHES

	$F^m_{o,i}$ **(N)**		$l^m_{o,i}$ **(m)**		$l^t_{o,i}$ **(m)**		ϕ_i **(rad)**	
Muscles	Variation (GA)	Variation (DC)	Variation (GA)	Variation (DC)	Variation (GA)	Variation (DC)	Variation (GA)	Variation (DC)
FCR	135.72%	117.90%	149.75%	138.48%	104.20%	123.73%	60.51%	213.86%
FCU	59.28%	98.42%	100.06%	131.07%	132.41%	140.37%	166.97%	132.24%
ECRL	49.32%	111.44%	130.01%	153.34%	111.55%	113.95%	2051.60 %	1796.20%
ECRB	27.82 %	164.67 %	121.74%	150.53%	106.42%	126.64%	146.58%	10.14%
ECU	247.95%	261.04%	129.25%	135.87%	167.47%	133.10%	225.18%	243.52%

GA = Genetic algorithm. DC = Direct collocation method.

increase in both approaches, compared with the initial value. The most deviations occur at the pennation angle. However, according to the equation((3)), the variations of the pennation angle should have fewer effects on the muscle-tendon force output, which varied between 0 and 1. The muscle-tendon length and optimal muscle fibre length are increased after optimization for both approaches, which affect the muscle-tendon force output significantly [8], [9]. The most difference in two parameter sets is the optimized maximum isometric force of the FCR, FCU and ECRB. In GA, these parameters decreased significantly while they are increased in the DC method.

Table II presents the mean optimization time for the genetic algorithm and the DC method. Both optimization approaches are run several times within the limited maximum number (1000) of the iterations to calculate the mean optimization time and the best value of the objective function are selected with the same stop criteria (tolerance = $1\times e^{-4}$). Therefore, the most prominent differences between the genetic algorithm and the DC method are the optimization time, which are $1697\,\mathrm{s}$ and $75\,\mathrm{s}$ respectively. The optimization time using DC method is significantly reduced, which reaches our goal. The lager sparse constraint Jacobian matrix has been used in the DC method, which is more easily computed using the linear algebra operations [26]. Furthermore, the larger number of parameters with the wide boundaries, i.e., maximum isometric force, is also an important aspect to cause the more computational cost in the genetic algorithm. Although the GA-based parameters show the better performance as the GA can reduce the risk to be trapped in local minima, DC method has much less optimization time which has potential to be applied in the clinical environment.

TABLE II

THE OVERALL PERFORMANCE AND MEAN OPTIMIZATION TIME

	Optimization time (s)	R^2	RMSE (rad)
Genetic algorithm	1697	0.96	0.27
Direct collocation	75	0.93	0.38

IV. CONCLUSION

A direct collocation method is proposed to optimize the subject-specific parameters in the EMG-MS model. After formulating the EMG-MS related optimal control problem, this method transcribes to a non-linear programming problem by discretizing the control variables and state variables into a number of grid points. By adding the parameters into the unknown vectors, the subject-specific parameters are optimized through the NLP solver.

The optimized parameters through the DC method are verified and compared with the optimized parameters using the genetic algorithm. Experiment results indicate both methods can estimate the wrist flexion/extension motion accurately. There are no such significant differences in terms of the R^2 but the RMSE is higher in the DC-based parameters. Future studies will provide a detailed investigation of convergence and grid refinement of the DC-method.

APPENDIX

The active force-length relationship $f_a(\bar{l}^m_{a,i})$ addresses the muscle force at different fibre length,

$$f_a(\bar{l}^m_{a,i}) = e^{-(\bar{l}^m_{a,i}-1)^2 k^{-1}} \tag{A.1}$$

where $\bar{l}^m_{a,i}$ the muscle fibre length with respect to the muscle activations $a_i(t)$, as shown in equation ((4)). k is a constant to approximate the force-length relationship [27]. The function $f(\overline{v}_i)$ represents the force-velocity relationship between the l^m_i and the normalized contraction velocity $\overline{v}_i$ [23]. To simplify the partial derivatives in constant Jacobian matrix, the $f(\overline{v}_i)$ is set to 1 in this paper. The passive force F_{PE} is the forced produced by the PE which can be calculated according to

$$F_{PE,i} = f_p(\bar{l}_i) F^m_{o,i} \tag{A.2}$$

where

$$f_p(\bar{l}_i) = \frac{e^{10(\bar{l}^m_i - 1)}}{e^5}. \tag{A.3}$$

Note that the tendon length is assumed to be constant in order to alleviate the burden of numerical integration.

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