A Genetic Algorithm for the Characterization of Biological Samples through Smart Microgrippers

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***Abstract*—In this paper, a novel technique for the viscoelastic characterization of biosamples is presented. The measuring tool consists of MEMS-technology based tweezers. A mechanical model is developed for the nonlinear dynamics of the microsystem, composed of the tweezers and of the sample to be analyzed. The identification of the viscoelastic parameters is performed by implementing a genetic algorithm.**

***Index Terms*—MEMS Microgripper, Micromanipulation, Viscoelastic Characterization, Genetic Algorithms**

I. INTRODUCTION

The identification of the mechanical characteristics of biomaterials is necessary for understanding the role of material mechanics in disease diagnosis, for replacing tissues and for validating the constitutive models [1], [2]. The mechanical characterization of the biosample can be formulated as a parameter estimation problem, where the unknowns are the stiffness and damping coefficients of the determined model. Hence, the estimation problem can be solved by using Kalman filtering methods or genetic algorithms [3].

In this investigation, a novel identification strategy is presented, based on the simultaneous actuation of both the arms of a microgripper. The Maxwell liquid drop model is considered for the sample, and the estimation problem is solved by implementing a genetic algorithm.

II. EXPERIMENTAL TECHNIQUE

The experimental technique adopted for the viscoelastic characterization of the biosamples resorts to the use of the MEMS-based microgripper shown in Figure 1. Each arm is actuated by a rotary comb drive that exerts the necessary torque to perform the gripping task, that are are applied in two phases: torques application ($1.6 \times 10^{-3}\,\mu$Nm for 200 s) and relaxation ($0.32 \times 10^{-3}\,\mu$Nm for 200 s, to maintain the grip with the sample). The rotation of one arm is recorded throughout the gripping time, and it is assumed that a 10% random noise is present on the measured rotation response.

III. MECHANICAL MODEL

The compliant structure of the microgripper can be modeled considering the rigid-body replacement method [4], as reported in Figure 2. The system configuration can be described by means of reference, target and incremental variables. The

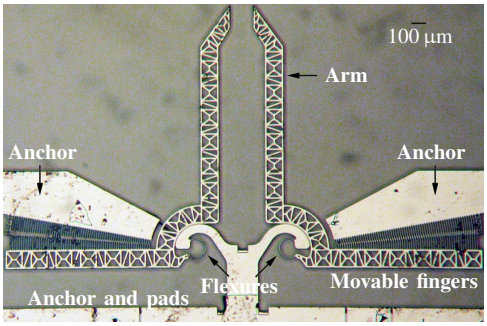

Fig. 1. Optical microscope image of the silicon microgripper.

reference variables ($\hat{v}$) define the system in the symmetrical configuration, where the gripper arms are in contact to the sample but no deformations occur. The target variables ($\tilde{v}$) define the system in the deformed configuration. Therefore, the incremental variables are defined as $v = \tilde{v} - \hat{v}$. The model parameters are listed and defined in Table I.

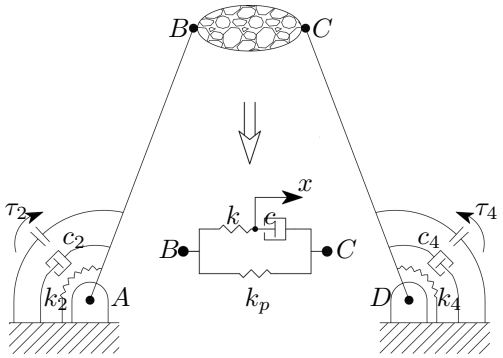

Fig. 2. Gripper-cell model.

Assuming the inertia of the sample to be negligible, the dynamical model of the system can be described by means of the following approximate linear equations,

$$\begin{aligned} &I_2\ddot{\theta}_2 + c_2\dot{\theta}_2 + c_p l^2\left(\dot{\theta}_2\sin\hat{\theta}_2 - \dot{\theta}_4\sin\hat{\theta}_4\right)\sin\hat{\theta}_2 \\ &+k_2\theta_2 + kl\left(l\theta_2\sin\hat{\theta}_2 - x\right)\sin\hat{\theta}_2 \\ &+k_p l^2\left(\theta_2\sin\hat{\theta}_2 - \theta_4\sin\hat{\theta}_4\right)\sin\hat{\theta}_2 = \tau_2, \end{aligned} \tag{1}$$

TABLE I
NOMENCLATURE AND PARAMETERS VALUES

Par.	Unit	Value	Definition
d	[m]	5.47e−4	length of AD
l	[m]	1.50e−3	length of AB and DC
$\hat{u}$,	[m]	150e−6	reference length of BC
$\hat{\theta}_2$	[rad]	1.44	reference orientation of AB
$\hat{\theta}_4$	[rad]	1.70	reference orientation of DC
k_2, k_4	[Nm]	0.30e−6	arm torsional stiffness
c_2, c_4	[Nsm]	1.24e−12	gripper damping coefficients
I_2, I_4	[kgm^2]	1.25e−14	arm moment of inertia
$\tilde{u}$, u	[m]		BC length (target/incremental)
$\tilde{\theta}_2$, θ_2	[rad]		AB orientation (target/incremental)
$\tilde{\theta}_4$, θ_4	[rad]		DC orientation (target/incremental)
τ_2, τ_4	[Nm]		comb drive input torques
k, k_p	[Nm^{-1}]		sample stiffness coefficients
c	[Nsm^{-1}]		sample damping coefficient

$$
\begin{aligned}
&I_4\ddot{\theta}_4 + c_4\dot{\theta}_4 + cl^2\left[\dot{\theta}_4\sin\hat{\theta}_4 - \dot{x}\right]\sin\hat{\theta}_4 + k_4\theta_4 \\
&-c_p l^2\left[\dot{\theta}_2\sin\hat{\theta}_2 - \dot{\theta}_4\sin\hat{\theta}_4\right]\sin\hat{\theta}_4 \qquad (2)\\
&+k_p l^2\left(\theta_2 - \sin\hat{\theta}_2 + \theta_4 + \sin\hat{\theta}_4\right)\sin\hat{\theta}_4 = \tau_4,
\end{aligned}
$$

$$
k\left(l\theta_2\sin\hat{\theta}_2 - x\right) + c\left(\dot{x} - l\dot{\theta}_4\sin\hat{\theta}_4\right) = 0. \qquad (3)
$$

The system (1)-(3) is a system of second order linear differential equations with three state variables: θ_2, θ_4, and x. The linear coefficients depend nonlinearly on the system configuration that can be measured (i.e. $\hat{\theta}_2$ and $\hat{\theta}_4$).

IV. GENETIC ALGORITHM IMPLEMENTATION

Genetic algorithms procedure generally consists of four steps, that are initialization, crossover, selection and mutation. Genetic coding of parameters and formulation of fitness function have also to be considered in the algorithm implementation. In this study, it is required to encode three independent parameters: the stiffness coefficients k and k_p, and the damping coefficients c. Each one of these values is encoded into the chromosome using three independent genes, one defining the order of magnitude, and the other two genes defining the first two significant digits of the parameter, as:

$$
\begin{aligned}
k &= 10^{g_{k_1}}\left(0.1g_{k_2} + 0.01g_{k_3}\right),\\
k_p &= 10^{g_{k_{p1}}}\left(0.1g_{k_{p2}} + 0.01g_{k_{p3}}\right),\\
c &= 10^{g_{c_1}}\left(0.1g_{c_2} + 0.01g_{c_3}\right).
\end{aligned} \qquad (4)
$$

The proposed algorithm does not assume the order of magnitude of each parameter value known *a priori*, that is indeed provided by the identification procedure. The initial population of models is set to 500 individuals and evolves into the next generation by three genetic operators: crossover, mutation, and selection.

V. SIMULATIONS AND RESULTS

The cell model is generated for each individual transcoding the parameter values, according to eqn. 4. A dynamic simulation of the system is performed to acquire the time history of the left arm rotation (θ_2), and to compare it to the target one. For each individual, the fitness function is the root mean square of the difference between the simulated dynamic response of the system and the reference one.

A numerical simulation is performed by considering an endothelial cell (T^c) [5] model characterized by the linear viscoelastic behavior defined in Table II. A comparison between the target response of the system and the best fit solution, obtained at the 70$^{\text{th}}$ generation, is reported in Figure 3. The comparison between identified and reference values in Table II shows that k_p and c have a negligible error, whereas the error on k is lower than the noise level added to the reference signal.

TABLE II
COMPARISON OF TARGET AND IDENTIFIED MODEL VALUES

Parameter	Unit	Target	Identified	Error [%]
k	[Nm^{-1}]	35.0	32.8	6.1
k_p	[Nm^{-1}]	12.3	12.3	0
c	[Nsm^{-1}]	299.9	302.5	−0.8

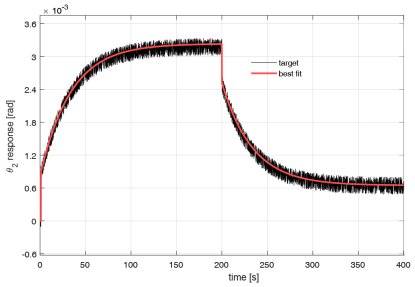

Fig. 3. Comparisons between system response and best fit solution of GA.

VI. CONCLUSIONS

In this paper, a novel experimental technique, based on the use of a MEMS microgripper with a symmetric actuation scheme, has been introduced to evaluate the mechanical characteristics of biomaterials. A genetic algorithm has been implemented to solve the estimation problem. The simulations results confirm the feasibility of the approach that appears to be robust with respect to measurement noise and does not require to assume a priori the parameters order of magnitude.

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