

A Novel Non-Iterative Method for Real-Time Parameter Estimation of the Fricke-Morse Model

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Abstract—Parameter estimation of Fricke-Morse model of biological tissue is widely used in bioimpedance data processing and analysis. Complex nonlinear least squares (CNLS) data fitting is often used for parameter estimation of the model, but limitations such as high processing time, converging into local minimums, need for good initial guess of model parameters and non-convergence have been reported. Thus, there is strong motivation to develop methods which can solve these flaws. In this paper a novel real-time method for parameter estimation of Fricke-Morse model of biological cells is presented. The proposed method uses the value of characteristic frequency estimated from the measured imaginary part of bioimpedance, whereupon the Fricke-Morse model parameters are calculated using the provided analytical expressions. The proposed method is compared with CNLS in frequency ranges of 1 kHz to 10 MHz (beta-dispersion) and 10 kHz to 100 kHz, which is more suitable for low-cost microcontroller-based bioimpedance measurement systems. The obtained results are promising, and in both frequency ranges, CNLS and the proposed method have accuracies suitable for most electrical bioimpedance (EBI) applications. However, the proposed algorithm has significantly lower computation complexity, so it was 20-80 times faster than CNLS.

Index Terms—bioimpedance, biological system modeling, estimation, filters, signal processing.

I. INTRODUCTION

Development of non-invasive techniques for analysis of the properties of living tissues has been a subject of research for decades. One of the widely used techniques is electrical bioimpedance spectroscopy which offers rapid, straightforward and cost-effective approach for biological tissue monitoring. It is based on measurement of bioimpedance and fluctuations of bioimpedance due to tissue changes. More complex analysis can be conducted with introduction of models of biological tissues [1, 2], with parameters of the models related to the specific part of tissue (i.e. intracellular or extracellular) or process (changes in the size, shape, number or organization of cells, etc.) In general, if there is a change in tissue, the specific parameter will change and that can be used in analysis of organ state, cancer detection [3], *in vivo* human lung tissue analysis [4], *in vivo* real-time myocardium tissue characterization [5, 6], *ex vivo* electrical impedance measurements on excised

hepatic tissue from human patients with metastatic colorectal cancer [7], total body water estimation [8], etc.

Structure of the models of biological tissues depends on available measurement equipment as well as required accuracy and applications. Thus complexity varies from single cell models such as cellular Potts model, center-based single-cell model, models with lattice-free center-based cells, deformable ellipsoidal cell model [9], to more complex models such as model of complex tissues with individual viscoelastic cells, Fricke-Morse [1] and Cole models [2] which, compared to the single cell models, can be used for analysis of wider groups of tissues or parts of the body. Single cell models are most often used in analysis of biophysical and molecular interactions between cells [9].

However, model of complex tissues with individual viscoelastic cells and Cole model are mathematical models, thus these models cannot provide explanations related to the underlying structures and physical processes at the cellular level. Their electrical properties cannot be represented with equivalent electrical circuits. In contrast, Fricke-Morse model employs basic concepts of electrical circuit theory to represent similar properties in biological materials. Since the introduction of the Fricke-Morse model of biological cell in 1925 [1], the model has been widely used in bioelectrical impedance analysis due to its simplicity, direct physical interpretation and its ability to describe the main dispersion in the frequency range of 1 kHz to 10 MHz (β -dispersion) [1]. Main advantage of Fricke-Morse model over other models is direct physical interpretation (there are no semi-empirical elements such as constant phase element). With Fricke-Morse model (Fig. 1) cells are modeled with just three elements as 2R-1C circuit.

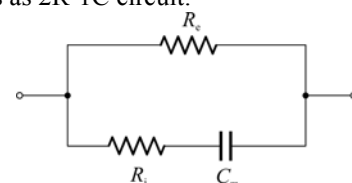


Figure 1. Fricke-Morse model of biological cell.

The impedance of a cell according to Fricke-Morse 2R-1C model, at some angular frequency, $\omega = 2\pi f$ [rad/s], is given with:

$$Z(\omega) = \frac{R_e(1 + j\omega R_i C_m)}{1 + j\omega(R_i + R_e)C_m} \quad (1)$$

where R_e presents the extracellular space, while the intracellular space and the membrane are presented as a

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series of resistor R_i and a capacitor C_m , respectively.

Non Linear Least Squares (NLLS) is the method widely used to obtain the values of parameters of the given model which best fit experimentally obtained bioimpedance data. Complex nonlinear least squares (CNLS) is a NLLS method which simultaneously fits the proposed model to the real and imaginary parts (or modulus and phase) of bioimpedance. Compared to the fitting done independently for the two parts of the bioimpedance, CNLS approach reduces statistical errors and generally yields very high resolution and accuracy [10, 11]. Despite the fact that CNLS fitting is widely used for parameter estimation of electrical bioimpedance models, it is important to emphasize some limitations and disadvantages of this approach: (a) CNLS is a time consuming process [4], (b) post-processing of the data is also a difficult task [4], (c) CNLS requires high quality initial guess for the model parameters [12], (d) there is always a possibility of converging into a local minimum [12], and (e) CNLS non-convergence is a common issue [12]. Based on the above-mentioned facts, new approaches for Fricke-Morse model parameter estimation are continuously developed, such as using differential impedance analysis [4], multisine electrical impedance spectroscopy [5], the vector impedance analysis [6], singular value decomposition [13], etc. However, the proposed methods are not optimized for low-cost systems with a low power processing unit because they require complex mathematical operations and are typically implemented on PC-based platforms.

In our research, a novel non-iterative approach for parameter estimation of Fricke-Morse model of biological tissue is developed. The proposed method uses the value of characteristic frequency estimated from the measured imaginary part of bioimpedance, whereupon the Fricke-Morse model parameters are calculated using the provided analytical expressions. The distinguished feature of the proposed method is low computation complexity, so it is suitable for use in on-line monitoring and characterization of biological tissues with low-cost microcontroller-based wearable devices such as [14-17]. The presented approach has been compared with CNLS data fitting regarding estimation accuracy and processing time in frequency ranges of 1 kHz to 10 MHz (β -dispersion) and 10 kHz to 100 kHz, which is more suitable for low-cost microcontroller-based bioimpedance measurement systems. Possible practical applications are related to the general-purpose bioimpedance analysis as well as in applications where use of methods proposed in literature is limited: parameter estimation in real-time of time-varying bioimpedance (lung composition, myocardium tissue characterization, breathing rate, etc.) with low-cost microcontroller-based measurement devices.

II. PARAMETER ESTIMATION OF FRICKE-MORSE MODEL

A. A Novel non-iterative method

Real part of the impedance of Fricke-Morse 2R-1C model (1) can be written as:

$$\text{Re}\{Z(\omega)\} = K \frac{\omega^2 + zp}{\omega^2 + p^2} \quad (2)$$

and imaginary part as:

$$\text{Im}\{Z(\omega)\} = K \frac{(p-z)\omega}{\omega^2 + p^2} \quad (3)$$

where K , z and ω_c are defined as

$$K = \frac{R_e R_i}{R_e + R_i} \quad (4)$$

$$z = \frac{1}{C_m R_i} \quad (5)$$

$$p = \frac{\omega_c}{2\pi} = \frac{1}{C_m (R_e + R_i)} \quad (6)$$

There are three unknowns (K , z and p) in the system (2)-(3), while only two values ($\text{Re}\{Z(\omega)\}$ and $\text{Im}\{Z(\omega)\}$) are known. Thus, to analytically solve this system one more equation is required.

As can be seen from (4), K can be estimated as impedance of the 2R-1C circuit at very high frequency (theoretically it should be infinite frequency) where influence of the C_m is negligible, while (6) implies that p can be estimated as characteristic frequency f_c of the 2R-1C impedance. With knowledge of one of these two parameters, system (2)-(3) can be solved analytically with a unique solution.

However, the estimation of K from measured impedance of the 2R-1C circuit at very high frequency is not reliable, especially with low-cost microcontroller-based systems with narrow frequency range.

As mentioned above, from experimentally obtained bioimpedance data, characteristic frequency can be estimated as frequency at which absolute value of the imaginary part has maximum value. Therefore, if \hat{p} is estimated from the set of measured data, from system of equations (2) and (3), parameters \hat{z}_i and \hat{K}_i can be calculated for each measurement angular frequency ω_i , $i=1, \dots, N$, where N is the number of data points included in the measurements, as:

$$\hat{z}_i = -\frac{\text{Im}\{Z(\omega_i)\}\omega_i^2 - \text{Re}\{Z(\omega_i)\}\hat{p}\omega_i}{\text{Im}\{Z(\omega_i)\}\hat{p} + \text{Re}\{Z(\omega_i)\}\omega_i} \quad (7)$$

and:

$$\hat{K}_i = \frac{(\hat{p}^2 + \omega_i^2)(\text{Im}\{Z(\omega_i)\}\hat{p} + \text{Re}\{Z(\omega_i)\}\omega_i)}{\omega_i^3 - \omega_i \hat{p}^2} \quad (8)$$

If K_i , p and z_i are known, from system of equations (4)-(6), parameters of 2R-1C Fricke-Morse model can be calculated as:

$$R_e(\omega_i) = \frac{\hat{z}_i \hat{K}_i}{\hat{p}} \quad (9)$$

$$R_i(\omega_i) = \frac{\hat{K}_i R_e(\omega_i)}{R_e(\omega_i) - \hat{K}_i} \quad (10)$$

$$C_m(\omega_i) = \frac{R_e(\omega_i) - \hat{K}_i}{\hat{z}_i \hat{K}_i R_e(\omega_i)} \quad (11)$$

for each measurement angular frequency ω_i . Finally, the estimated values \hat{R}_e , \hat{R}_i and \hat{C}_m can be obtained as means of calculated values $R_e(\omega_i)$, $R_i(\omega_i)$ and $C_m(\omega_i)$, $i=1, \dots, N$, respectively.

At this point, it must be emphasized that parameter estimation with the proposed method, largely depends on the quality of the characteristic frequency estimation from

bioimpedance data, which can be strongly affected with noise. Because of that, in this research appropriate filter design and implementation are discussed in Section II.B.

Compared to the CNLS data fitting approach, advantages of the proposed method are:

1. shorter processing time because there is no need to simultaneously solve a set of equations,
2. there is no possibility of converging into a local minimum or non-convergence because the proposed method is not iterative,
3. the estimated solution (set of \hat{R}_e , \hat{R}_i and \hat{C}_m) is unique which usually is not the case with CNLS data fitting [4], and
4. the presented algorithm has low computation complexity so it is expected that it can be used in portable and autonomous low-cost microcontroller-based systems for bioimpedance measurement in real-time.

B. White Gaussian noise reduction

For implementation of systems for real-time bioimpedance measurement, it is required to have appropriate filter because noise presence is a common issue. In such applications, general requirements for filter design can be summarized as: simple structure with low level computation complexity and high reduction of white Gaussian noise. For such applications, moving average filter is widely used [18]. It averages M measurements to produce filtered signal. This can be written as:

$$y[i] = \frac{1}{M} \sum_{j=0}^{M-1} x[i+j] \quad (12)$$

where x is the measurement, y is the filtered signal and M is the number of points in the average.

As an alternative, the group of points from the input signal can be chosen symmetrically around the output point, which can be written as:

$$y[i] = \frac{1}{M} \sum_{j=-\frac{M-1}{2}}^{\frac{M-1}{2}} x[i+j] \quad (13)$$

where M must be an odd number.

The moving average filter can be implemented also in multiple-pass moving average form, in which the input signal is passed through a moving average filter two or more times. In this research, data was filtered with symmetrical two-pass moving average filter with the number of points in the average set to 13.

III. EXPERIMENTAL RESULTS

We analyzed parameter estimation of the Fricke-Morse model with the proposed method and CNLS data fitting for six common EBIs: Total Body Composition (TBC), Respiration Rate (RR), Trunk-Trunk (TT), Leg-Leg (LL), Lung Composition (LC) and Arm-Arm (AA). Reference values for the model parameters (R_e , R_i and C_m) have been used as obtained in [19].

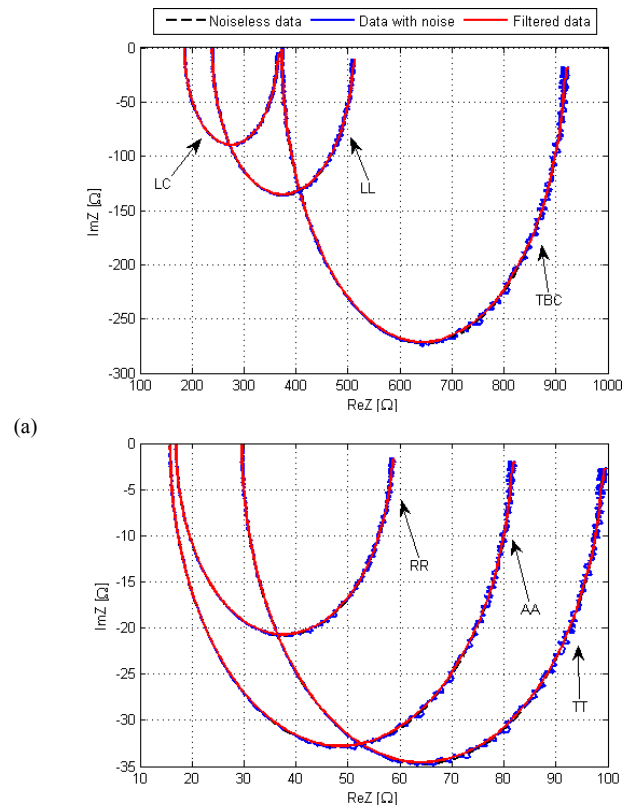
In [19], experimental bioimpedance measurements (TBC, AA, LL, RR, LC and TT) were performed with commercial ImpediMedSFB7 device in the frequency range of 4 kHz to 1 MHz, while values of the parameters of the 2R-1C model have been extracted with associated BioImp software. Test subject was 24 years old male, height: 173

cm and weight: 79 kg.

Our proposed method has been compared with CNLS fitting regarding accuracy and processing time in frequency range of 1 kHz to 10 MHz and frequency range of 10 kHz to 100 kHz. CNLS data-fitting was performed in MATLAB® with *Levenberg-Marquardt* algorithm [20]. Maximum number of function evaluations and maximum number of iterations were set to 10^3 , while termination tolerance on the function value and termination tolerance on estimated vector were set to 10^{-9} . To increase the speed of estimation, a user-calculated Jacobian was supplied to the solver.

A. Estimations in frequency range of 1 kHz - 10 MHz

Using reference values for the model parameters, EBIs of TBC, AA, LL, RR, LC and TT have been calculated in frequency range of 1 kHz to 10 MHz in 512 points with logarithmic frequency distribution, as used by many commercial bioimpedance measurement devices (Xitron Hydra 4200, ImpediMedSFB7, Bodystat1500MDD, etc.). To create more realistic test bioimpedance, Gaussian white noise with SNR of 40 dB has been added to these reference bioimpedances. Nyquist plots of noiseless EBIs, EBIs with added white noise and EBIs filtered as explained in Section III. B. in frequency range of 1 kHz to 10 MHz are presented in Fig. 2.



(b) Figure 2. Nyquist plots in frequency range of 1 kHz to 10 MHz of (a) TBC, LL and LC (b) RR, AA and TT bioimpedance.

From EBIs data, characteristic frequency, \hat{f}_c , was estimated using procedure described in [14]. The estimated values of characteristic frequency of analyzed EBIs were compared with the characteristic frequencies calculated with reference values of the model parameters, given in Table I as f_c in [Hz]. The relative errors of the characteristic frequencies estimations were calculated and the obtained results are presented in Table I. As can be seen, the

characteristic frequencies were estimated with the maximum relative error of 0.881% (for AA) for the noiseless data, while for the data with added white Gaussian noise the maximum relative error was 6.947% (for LC). In the case of filtered data, the maximum relative error was 1.320% (for LL), while for all other EBI-s it was lower than 1%, which is very close to the values obtained for the noiseless data.

TABLE I. COMPARISON OF RELATIVE ERRORS IN CHARACTERISTIC FREQUENCY ESTIMATION

EBI	f_c [Hz]	Noiseless data [%]	Filtered data [%]	Data with noise [%]
TBC	30091.52	0.232	0.232	2.055
RR	25515.09	0.509	0.509	4.198
TT	25599.14	0.179	0.179	3.856
LL	25310.90	0.490	1.320	4.013
LC	33002.79	0.009	0.009	6.947
AA	34521.45	0.881	0.922	2.757

With known \hat{p} , parameters \hat{K}_i and \hat{z}_i , and after that, $R_e(\omega_i)$, $R_i(\omega_i)$ and $C_m(\omega_i)$ can be calculated. For obtained values, mean values (\hat{R}_e , \hat{R}_i and \hat{C}_m) and standard deviations ($\delta\hat{R}_e$, $\delta\hat{R}_i$ and $\delta\hat{C}_m$) are calculated as shown in Table II. In this table, the reference values for R_e , R_i and C_m [19] are given as well. As can be seen, parameters of 2R-1C circuit have been estimated with maximum standard deviation of 0.93% in the case of the noiseless data (\hat{R}_i estimation for AA), while for the data with added white Gaussian noise maximum standard deviation was 14.93% (\hat{R}_i estimation for LC). For the filtered data, maximum standard deviation was 1.66% (\hat{R}_i estimation for LL).

TABLE II. MEAN VALUES \pm STANDARD DEVIATION OF ESTIMATED VALUES OF MODEL PARAMETERS WITH PROPOSED METHOD

	EBI	R_e [Ω]	R_i [Ω]	C_m [nF]
Ref. values	TBC	917.5	629.0	3.42
	RR	58.5	23.9	75.7
	TT	99.0	42.3	44.0
	LL	510.0	450	6.55
	LC	81.46	19.64	47.7
	AA	364.6	379.0	6.2
	EBI	$\hat{R}_e \pm \delta\hat{R}_e$ [Ω]	$\hat{R}_i \pm \delta\hat{R}_i$ [Ω]	$\hat{C}_m \pm \delta\hat{C}_m$ [nF]
Noiseless data	TBC	916.70 \pm 0.53	628.05 \pm 1.77	3.42 \pm 0.003
	RR	58.36 \pm 0.09	23.78 \pm 0.19	75.6 \pm 0.093
	TT	98.92 \pm 0.05	42.23 \pm 0.11	44.0 \pm 0.020
	LL	510.87 \pm 0.56	450.99 \pm 2.40	6.57 \pm 0.013
	LC	81.50 \pm 0.00	19.60 \pm 0.00	47.7 \pm 0.001
	AA	365.58 \pm 0.68	380.49 \pm 3.55	6.23 \pm 0.024
Data with noise	TBC	910.51 \pm 6.95	620.67 \pm 15.78	3.38 \pm 0.030
	RR	57.41 \pm 0.77	22.91 \pm 1.52	74.5 \pm 0.862
	TT	97.32 \pm 1.21	40.75 \pm 2.41	43.4 \pm 0.481
	LL	517.30 \pm 5.51	458.37 \pm 20.42	6.72 \pm 0.113
	LC	84.53 \pm 2.14	22.26 \pm 3.32	48.5 \pm 0.621
	AA	361.62 \pm 2.90	374.50 \pm 11.01	6.10 \pm 0.080
Filtered data	TBC	917.64 \pm 1.53	626.54 \pm 4.33	3.42 \pm 0.011
	RR	58.44 \pm 0.00	23.71 \pm 0.32	75.5 \pm 0.285
	TT	99.05 \pm 0.19	42.12 \pm 0.36	44.0 \pm 0.133
	LL	508.19 \pm 1.21	446.43 \pm 7.43	6.50 \pm 0.045
	LC	81.61 \pm 0.20	19.52 \pm 0.21	47.7 \pm 0.150
	AA	363.88 \pm 0.62	376.58 \pm 4.60	6.17 \pm 0.036

A common way for parameter estimation of the 2R-1C model is data fitting with CNLS approach. In Table III, relative errors ($\Delta\hat{R}_e$, $\Delta\hat{R}_i$ and $\Delta\hat{C}_m$) in parameter estimation of 2R-1C model with the proposed method and CNLS are compared. Both approaches were tested with the same noiseless data, data with added noise and filtered data.

TABLE III. COMPARISON OF RELATIVE ERRORS FOR ESTIMATED VALUES OF MODEL PARAMETERS WITH PROPOSED METHOD AND CNLS

	EBI	$\Delta\hat{R}_e$ [%]	$\Delta\hat{R}_i$ [%]	$\Delta\hat{C}_m$ [%]
Proposed Method - Noiseless data	TBC	0.087	0.151	0.119
	RR	0.233	0.520	0.191
	TT	0.081	0.176	0.069
	LL	0.170	0.219	0.299
	LC	0.005	0.002	0.002
	AA	0.268	0.393	0.557
Proposed Method - Data with noise	TBC	0.762	1.325	1.025
	RR	1.862	4.162	1.526
	TT	1.693	3.676	1.448
	LL	1.432	1.861	2.536
	LC	3.722	13.57	1.753
	AA	0.818	1.188	1.677
Proposed Method - Filtered data	TBC	0.016	0.391	0.081
	RR	0.104	0.776	0.207
	TT	0.047	0.429	0.819
	LL	0.355	0.794	0.741
	LC	0.133	0.416	0.035
	AA	0.196	0.638	0.491
CNLS - Noiseless data	TBC	0.000	0.000	0.000
	RR	0.000	0.000	0.000
	TT	0.000	0.000	0.000
	LL	0.000	0.000	0.000
	LC	0.000	0.000	0.000
	AA	0.000	0.000	0.000
CNLS - Data with noise	TBC	0.010	0.004	0.117
	RR	0.014	0.006	0.101
	TT	0.014	0.005	0.103
	LL	0.015	0.012	0.165
	LC	0.006	0.014	0.063
	AA	0.007	0.011	0.136
CNLS - Filtered data	TBC	0.028	0.114	0.066
	RR	0.035	0.149	0.061
	TT	0.034	0.145	0.062
	LL	0.020	0.097	0.103
	LC	0.045	0.221	0.039
	AA	0.022	0.097	0.077

From the obtained results, it can be seen that the proposed method extracted mean values for \hat{R}_e , \hat{R}_i and \hat{C}_m with relative errors lower than 0.557% for analyzed EBIs in the case of noiseless data. CNLS data fitting estimated values with relative errors lower than 0.0005%. As it was expected, accuracy of both algorithms is affected when white noise is presented: maximum relative error for the proposed approach was 4.162 %, while for CNLS it was 0.165 %. This difference can be easily explained if Table I is analyzed. A disadvantage of the proposed method is that it cannot recover from the big error in parameter \hat{p} estimation, while CNLS with its iterative algorithm can. Thus, filtering of the bioimpedance measurement data is required. For the filtered data, maximum relative error was

0.819%, which is acceptable for most EBI applications and very similar to the results obtained in [4], where relative error was in range $\pm 1\%$ in the case of the noiseless data.

Presented approach is compared with CNLS regarding processing time as well. In Table IV, execution time of both algorithms in milliseconds is given. Time required for filtering was not included because filtering was treated as the part of measurement and data acquisition process.

TABLE IV. PROCESSING TIMES FOR PROPOSED METHOD AND CNLS IN MILLISECONDS

	TBC	RR	TT	LL	LC	AA
Proposed method	0.198	0.190	0.191	0.497	0.183	0.191
CNLS	9.419	8.081	8.728	11.39	7.687	7.945

As can be seen from Table IV, presented method is from 20 to 50 times faster than CNLS in estimating model parameters since it is a non-iterative method and uses analytical expressions for calculation of Fricke-Morse model parameters. Thus, it can be expected that the proposed method can be implemented in systems for real-time parameter estimation of Fricke-Morse model.

B. Estimations in frequency range of 5 kHz - 100 kHz

Because the proposed method has low computation complexity and short processing time, its main purpose is to be used in portable and autonomous low-cost microcontroller-based systems for bioimpedance measurement in real-time. Such devices, usually have limited frequency range from few kHz to 100 kHz [14-17]. Thus, in our study an analysis of parameter estimation in the frequency range of 5 kHz - 100 kHz is conducted as well. Bioimpedance has been calculated in 128 points with logarithmic frequency distribution.

Following the same procedure as in the frequency range of 1 kHz to 10 MHz, the first step was estimation of the characteristic frequency, \hat{f}_c , for each EBI in case of noiseless data, data with white noise and filtered data. Estimated values are compared with calculated characteristic frequencies, given in Table V as f_c in [Hz], and relative errors of estimations are calculated. The obtained results are presented in Table V.

TABLE V. COMPARISON OF RELATIVE ERRORS IN CHARACTERISTIC FREQUENCY ESTIMATION

EBI	f_c [Hz]	Noiseless data [%]	Filtered data [%]	Data with noise [%]
TBC	30091.52	0.208	0.208	4.807
RR	25515.09	0.223	0.223	2.159
TT	25599.14	0.550	0.550	1.823
LL	25310.90	0.582	0.582	2.983
LC	33002.79	0.008	0.008	2.379
AA	34521.45	0.211	0.211	5.052

As can be seen from Table V, with the proposed method characteristic frequencies were estimated with the maximum relative error of 0.582% (for LL) for the noiseless data, while for the data with added white Gaussian noise maximum relative error was 5.052% (for AA). Maximum relative error for filtered data was 0.582% (for LL), while for all other EBIs it was very close to the values obtained from the noiseless data.

Calculated mean values (\hat{R}_e , \hat{R}_i and \hat{C}_m) and standard

deviations ($\delta\hat{R}_e$, $\delta\hat{R}_i$ and $\delta\hat{C}_m$) for model parameters in frequency range of 5 kHz to 100 kHz are shown in Table VI. Reference values for R_e , R_i and C_m [19] are given as well. As can be seen, the parameters of a 2R-1C circuit have been estimated with maximum standard deviation of 0.63% in the case of the noiseless data (\hat{R}_i estimation for TT), while for the data with added white Gaussian noise maximum standard deviation was 4.31% (\hat{R}_i estimation for TBC). For the filtered data, maximum standard deviation was 1.83% (\hat{R}_i estimation for LC).

TABLE VI. MEAN VALUES \pm STANDARD DEVIATION OF ESTIMATED VALUES OF MODEL PARAMETERS WITH PROPOSED METHOD

	EBI	R_e [Ω]	R_i [Ω]	C_m [nF]
Ref. values	TBC	917.5	629.0	3.42
	RR	58.5	23.9	75.7
	TT	99.0	42.3	44.0
	LL	510.0	450	6.55
	LC	81.46	19.64	47.7
	AA	364.6	379.0	6.2
	EBI	$\hat{R}_e \pm \delta\hat{R}_e$ [Ω]	$\hat{R}_i \pm \delta\hat{R}_i$ [Ω]	$\hat{C}_m \pm \delta\hat{C}_m$ [nF]
Noiseless data	TBC	917.97 \pm 0.35	630.68 \pm 1.16	3.42 \pm 0.002
	RR	58.54 \pm 0.03	23.99 \pm 0.06	75.7 \pm 0.031
	TT	99.18 \pm 0.12	42.69 \pm 0.27	44.1 \pm 0.046
	LL	509.27 \pm 0.50	447.57 \pm 2.14	6.53 \pm 0.011
	LC	81.50 \pm 0.00	19.60 \pm 0.00	47.7 \pm 0.001
	AA	364.46 \pm 0.11	378.16 \pm 0.59	6.20 \pm 0.004
Data with noise	TBC	929.15 \pm 9.58	669.07 \pm 28.86	3.48 \pm 0.050
	RR	58.12 \pm 0.47	23.03 \pm 0.59	75.2 \pm 0.509
	TT	98.47 \pm 0.75	41.04 \pm 0.87	43.8 \pm 0.029
	LL	506.56 \pm 4.16	437.87 \pm 10.74	6.47 \pm 0.065
	LC	80.94 \pm 0.71	18.18 \pm 0.73	47.5 \pm 0.300
	AA	361.55 \pm 3.55	359.67 \pm 13.34	6.09 \pm 0.094
Filtered data	TBC	917.52 \pm 1.76	631.69 \pm 4.30	3.42 \pm 0.010
	RR	58.52 \pm 0.13	24.07 \pm 0.21	75.7 \pm 0.020
	TT	99.13 \pm 0.26	42.82 \pm 0.31	44.0 \pm 0.097
	LL	509.16 \pm 1.04	448.69 \pm 4.34	6.53 \pm 0.026
	LC	81.43 \pm 0.18	19.62 \pm 0.36	47.7 \pm 0.162
	AA	364.31 \pm 0.68	375.54 \pm 3.06	6.19 \pm 0.023

In Table VII, relative errors in parameter estimation of a 2R-1C model with the proposed method and CNLS are presented. Both approaches were tested on the same noiseless data, data with added noise and filtered data.

From the obtained results, it can be seen that the proposed method extracted mean values for \hat{R}_e , \hat{R}_i and \hat{C}_m with relative errors lower than 0.921% for analyzed EBIs in the case of noiseless data. CNLS data fitting approach estimated values with relative errors lower than 0.0005%. As it was expected, the accuracy of both algorithms is again affected when white noise is presented: maximum relative error for the proposed approach was 7.230%, while for CNLS it was 0.391%. For the filtered data, maximum relative error for proposed method was 1.22%.

The proposed method is compared with CNLS regarding processing time as well. In Table VIII, execution of time of both algorithms in milliseconds is given. As can be seen, proposed method was from 30 to 80 times faster than CNLS.

TABLE VII. COMPARISON OF RELATIVE ERRORS FOR ESTIMATED VALUES OF MODEL PARAMETERS WITH PROPOSED METHOD AND CNLS

	EBI	$\Delta\hat{R}_e$ [%]	$\Delta\hat{R}_i$ [%]	$\Delta\hat{C}_m$ [%]
Proposed Method - Noiseless data	TBC	0.051	0.267	0.070
	RR	0.073	0.385	0.060
	TT	0.178	0.921	0.152
	LL	0.142	0.539	0.251
	LC	0.002	0.024	0.001
	AA	0.038	0.220	0.080
Proposed Method - Data with noise	TBC	1.270	6.370	1.671
	RR	0.652	3.647	0.596
	TT	0.538	2.975	0.526
	LL	0.674	2.696	1.286
	LC	0.681	7.230	0.376
	AA	0.837	5.100	1.832
Proposed Method - Filtered data	TBC	0.002	0.428	0.034
	RR	0.027	0.694	0.003
	TT	0.133	1.220	0.095
	LL	0.164	0.291	0.354
	LC	0.090	0.079	0.067
	AA	0.081	0.123	0.107
CNLS - Noiseless data	TBC	0.000	0.000	0.000
	RR	0.000	0.000	0.000
	TT	0.000	0.000	0.000
	LL	0.000	0.000	0.000
	LC	0.000	0.000	0.000
	AA	0.000	0.000	0.000
CNLS - Data with noise	TBC	0.117	0.136	0.150
	RR	0.126	0.179	0.081
	TT	0.125	0.172	0.085
	LL	0.123	0.057	0.183
	LC	0.115	0.391	0.055
	AA	0.111	0.117	0.236
CNLS - Filtered data	TBC	0.031	0.428	0.034
	RR	0.000	1.151	0.002
	TT	0.002	1.119	0.000
	LL	0.032	0.704	0.039
	LC	0.006	2.150	0.072
	AA	0.052	0.867	0.193

TABLE VIII. PROCESSING TIMES FOR PROPOSED METHOD AND CNLS IN MILLISECONDS

	TBC	RR	TT	LL	LC	AA
Proposed method	0.145	0.146	0.163	0.168	0.340	0.087
CNLS	4.438	5.890	6.651	13.14	9.724	6.588

IV. CONCLUSION

A novel non-iterative approach for real-time parameters estimation of Fricke-Morse model of biological tissue has been presented. Compared to the CNLS data fitting method, proposed method showed shorter processing time with accuracy suitable for the most EBI applications. Proposed method has low computation complexity so it suitable for use in on-line monitoring and characterization of biological tissues with low-cost wearable devices.

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