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Sampled-Data Vectors: A New Means for Biological System Identification

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Abstract

The concept of the sampled-data vector is defined. It is shown that, single-valued as well as double-valued nonlinear biological models, however complicated, may be expressed by means of the sampled-data nonlinearity vector. By using this vector-valued model, a direct correlation may be established between the nonlinearity and its equivalent gain. This is obtained by means of linear transformations using numerically known (invariant) matrices, i.e. matrices which are independent of the nonlinear model. Likewise, for linear frequency-dependent biological models, the step-response sampled-data vector as well as the real frequency sampled-data vector are defined. By means of these vectors, a direct correlation may be established between the time and frequency domains. This is a linear transformation too, using invariant matrices. The matrices permitting the inverse transformation (i.e. the identification) are given and, it is shown that, these transformations may be associated with a linear (or quadratic) programming procedure in order to get linear as well as nonlinear biological models, subject to some constraints. This leads to the conditional identification concept, which allows the use of our prior knowledge about the biological system in the identification procedure. Two examples concerning the identification procedure (a linear and a nonlinear model) are given and, it is shown that since invariant matrix operators in connection with customary optimization algorithms are used, the identification procedure is a computer-oriented one. Thus, by starting directly from the test-data and by observing some accuracy or stability constraints, various biological models may be obtained in a simple and general manner.

Zusammenfassung

Der Begriff des Abtastvektors wird definiert und gezeigt, daß sowohl ein- als auch mehrdeutige, beliebig komplizierte nichtlineare biologische Modelle mit Hilfe des Abtastvektors der Nichtlinearität ausgedrückt werden können. Zur Anwendung dieses vektoriellen Modelles wird eine direkte Beziehung zwischen der Nichtlinearität und ihrer äquivalenten Verstärkung aufgestellt. Dies geschieht mittels einer linearen Transformation, unter Anwendung zahlenmäßig bekannter, folglich vom nichtlinearen Modell unabhängiger Matrizen. Ebenso werden für lineare, frequenzabhängige biologische Modelle der Übergangs- und Realteilvektor definiert. Mit Hilfe der letzteren kann man – durch eine lineare Transformation – eine direkte Beziehung zwischen dem Zeit- und Frequenzgebiet herstellen, indem man ebenfalls invariante Matrizen anwendet. Es werden die umgekehrte Transformation ermöglichende Matrizen gegeben und man sieht, daß diese Transformationen mit einem linearen (oder quadratischen) Programmierungsverfahren verknüpft werden können, um sowohl lineare als auch nichtlineare, verschiedenen Einschränkungen unterworfene biologische Modelle zu erhalten. Dies führt zu dem Konzept der bedingten Identifikation, welche die Anwendung vorheriger Kenntnisse über das biologische System im Identifikationsverfahren ermöglicht. Zwei dieses Verfahren betreffende Beispiele (ein lineares und ein nichtlineares Modell) werden gegeben und es wird gezeigt, daß die Anwendung invarianter Matrixoperatoren zu einem für Computer geeigneten Identifikationsverfahren führt. Wenn man also direkt von den Testdaten ausgeht und bestimmte, die Genauigkeit oder die Stabilität des Modelles betreffende Einschränkungen berücksichtigt, kann man verschiedenartige nichtlineare und lineare biologische Modelle auf einfache und allgemeingültige Art erzielen.

Introduction

There are a lot of physiological as well as biological areas in which nonlinear model identification occurs such as dynamic control in a circulatory system (Kenner, 1971; Baertschi *et al.*, 1971; Kenner *et al.*, 1970; Levison *et al.*, 1966; Stegemann and Geisen, 1966), dynamics of pupillary reflex (Milsum, 1966; Swan, 1969), etc. Moreover, linear (or approximate-linear) model identification occurs in many biological problems (Allison and Sagawa, 1970; Wetterer and Kenner, 1968; etc.). According to this increasing interest in the biological model identification, various methods derived from the conventional or modern control theory had been designed, but not all of them may be used in all identification problems. Thus, many identification procedures are in use at present, such as numerical deconvolution, autocorrelation, and cross-correlation, spectral density, sinusoidal response as well as learning model procedures (Cuenod and Sage, 1967; Bellman *et al.*, 1964; Eyckhoff and Smith, 1962). As a general purpose, in all these procedures, the task is to determine the mathematical model, starting from deterministic and/or stochastic responses. It is to notice, however, that, unlike the case of linear models, there are only a few methods for nonlinear model identification. Furthermore, these methods lead, in general, to poor accurate models. For example, in the case of the circulatory system, it has been found (Baertschi *et al.*, 1971; Kenner *et al.*, 1970) that the

magnitude of the open loop carotid sinus gain is amplitude-dependent and decreases with increasing input pressure amplitude. As a consequence, the nonlinear model (Kenner, 1971)

$$G(dp)=G_0\left(\frac{\alpha}{dp_0}\right)^n \tag{1}$$

had been suggested, where $G(dp)$ is the amplitude dependent gain, G_0 is the constant gain, α is a dimensional constant, dp_0 the carotid sinus input pressure amplitude and $n\in(0.5, 0.75)$ is the subject dependent parameter. Obviously, such a memory-less model may not express the input-output phase dependence, which, however, would lead to a better understanding of the nonlinear phenomenon under consideration. On the other hand, almost all methods for nonlinear identification are of a very particular kind. Thus, if one wishes to determine the model of a given nonlinear phenomenon, there is a possible way to solve the Volterra equation (Teodorescu, 1972a)

$$n(A)=\frac{k}{A^2}\int_0^A\frac{xN_1(x)}{(A^2-x^2)^{1/2}}dx \tag{2}$$

that is

$$N_1(x)=\frac{1}{x}\frac{d}{dx}\int_0^x\frac{\eta^2 n(\eta)}{(x^2-\eta^2)^{1/2}}d\eta \tag{2a}$$

in which $n(A)$ is the real describing function and $N_1(x)$ is the nonlinear function to be identified. However, this method may be applied only to particular cases, namely when the describing function $n(A)$ is known in analytic form. It is to notice that, for complicated nonlinearities, the procedures to obtain solution (2a) are quite cumbersome. Furthermore, the way to solve Eq. (2a) is related to the nonlinearity type and, consequently, it depends on the researchers ability.

An alternative identification procedure, of special interest for nonlinear models, had been derived starting from Wiener's theory of nonlinear systems (Wiener, 1958; Lee and Schetzen, 1961; Lee and Schetzen, 1965). Following this method, the unknown system parameters are determined as coefficients of an operator in the Hilbert space. To achieve this, the input $u(t)$ of the system is expanded in a Laguerre function series. Thus, the n-th Laguerre function is

$$g_n(t)=\begin{cases}e^{-\frac{t}{2}}L_n(t) & t\geqq 0\\ 0 & t<0,\end{cases} \tag{3}$$

where $L_n(t)$ is the Laguerre polynomial, i.e.

$$L_n(t)=\frac{1}{(n-1)!}e^t\frac{d^{n-1}}{dt^{n-1}}[t^{n-1}e^{-t}],\qquad n=1,2\ldots. \tag{3a}$$

Note that functions $g_n(t)$ are orthonormal for all $t\in(0,\infty)$. Now, with the assumption that the input used to excite the system response is a Gaussian white noise, it can be shown (Wiener, 1958) that Laguerre functions are uncorrelated Gaussian random processes with equal variances. On the other hand, since Hermite polynomials are also orthonormal ($\forall\, t\in-\infty,\infty$), it is reasonable to expand the system operator in Hermite functions

$$H_n(u)=e^{-\frac{u^2}{2}}\eta_n(u), \tag{3b}$$

where $\eta_n(u)$ is the n-th Hermite polynomial. Thus, the transformation from the Laguerre coefficient input space to the output can be written in terms of Hermite functions as

$$x(t)=\lim_{p\to\infty}\sum_{i=1}^{\infty}\sum_{j=1}^{\infty}\cdots\sum_{k=1}^{\infty}a_{ij\ldots k}\cdot H_i(u_1)H_j(u_2)\ldots H_k(u_p) \tag{4}$$

in which the coefficients $a_{ij\ldots k}$ may be obtained by crosscorrelating the system input with the Hermite polynomials, i.e.

$$a_{ij\ldots k}=(2\pi)^{p/2}\lim_{T\to\infty}\frac{1}{2T}\cdot\int_{-T}^{T}u(t)\eta_1(u_1)\eta_j(u_2)\ldots\eta_k(u_p)dt. \tag{4a}$$

In connection with Wiener's method, it is to observe that, there are an infinite number of operations involved in the expression (4a). Thus, it is necessary to truncate all limiting operations both with regard to measurement time and also to the number of terms taken in series for the input $u(t)$. On the other hand, an error analysis of the effect of this truncation seems to be exceptionally difficult (Cuenod and Sage, 1967). Further difficulties are generated by the fact that special test signals must be applied over a long interval of time. Finally, the requirement to convert Wiener coefficients in model parameters is often not a simple task.

Despite the aforementioned fact that for linear biological model identification there are many procedures in use, only a few ones may be applied for large model classes. Moreover, the accuracy of these procedures may be also poor, leading in some practical identification problems to inadequate results. Thus, one may conclude that, more general and accurate methods than the conventional ones are needed for nonlinear as well as linear biological model identification. According to this fact, the present paper has the following aims:

a) to use some general relationships between a certain vector expressing the nonlinear model and the vector which express the equivalent gain, in order to

obtain an identification procedure valid for large classes of nonlinear biological models;

b) to apply some general correlations between the vector which express the step response and a certain vector expressing the real-part frequency function of the linear model, in order to derive an identification procedure valid for large classes of linear biological models;

c) to suggest new identification procedures permitting to obtain nonlinear as well as linear models, subject to some restrictions. The latest ones are imposed by the prior knowledge of the actual process features. Thus, with respect to the conventional methods, such a procedure may be regarded as a "conditional or constrained identification".

The above mentioned correlations as well as the identification procedures, are based on the sampled-data concept. Let us first define this particular identification mean.

2. The Sampled-Data Vector Concept

Consider the function

$$y=f(x) \qquad x\in(x_0, x_m) \tag{5a}$$

or, equivalently, the mapping

$$\left|\begin{matrix} y_0 y_1 y_2 \dots y_m \\ x_0 x_1 x_2 \dots x_m \end{matrix}\right| \tag{5b}$$

and note

$$x_p - x_{p-1} = \Delta x \qquad \forall\, p\in(1, m)\,.$$

Then

$$\boldsymbol{y} = [y_0 y_1 y_2 \dots y_m]^T \tag{5c}$$

is the *sampled-data (or specific) vector of the function (mapping) y, with the sampling period Δx, over the interval* (x_0, x_m). There are many kind of sampled-data vectors. The following ones are of special interest to our problem:

a) Nonlinearity sampled-data vector (n.s.v.)

b) Equivalent-gain sampled-data vector (e.g.v.)

c) Step-response vector (s.r.v.), and

d) Real (imaginar) part frequency sampled-data vector (r.f.v.) (i.f.v.).

These vectors will be considered in the following development.

3. Nonlinearity Sampled-Data Vector and Nonlinear Model Identification

The nonlinearity sampled-data vector was defined firstly in (Teodorescu, 1971) in order to express, in a more general manner, the single-valued nonlinearities which occur in control systems. According to this definition, the n.s.v. is a column vector $\boldsymbol{z}$ the elements of which are equal to the values of the nonlinear function $N(x)$ at positive, equal and consecutive sampling periods Δx (see Fig. 1). In a similar manner may be defined the equivalent gain vector, which express the equivalent gain of the nonlinearity in the sense of describing-series (Teodorescu, 1970). This is a vector $\boldsymbol{n}$ the elements of which are equal to the values of the equivalent gain function $n(A)$ at equal and consecutive sampling intervals ΔA (A is the input amplitude). The definition is illustrated in Fig. 1. By using these definitions, it is shown (Teodorescu, 1971) that, for the whole class of symmetric single-valued nonlinearities, the sampled-data vectors $\boldsymbol{z}$ and $\boldsymbol{n}$ are related by the linear transformations

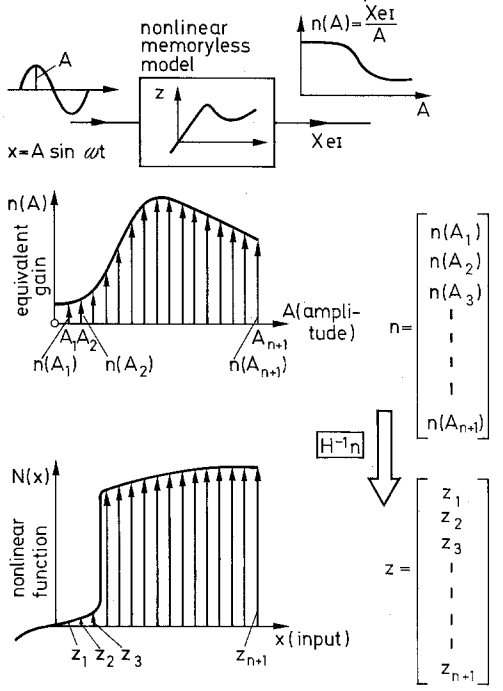

Fig. 1. Identification of nonlinear memory-less models by means of the matrix $\boldsymbol{H}^{-1}$ and definition of the sampled-data vectors $\boldsymbol{z}$ and $\boldsymbol{n}$

$$\boldsymbol{H}\boldsymbol{z} = \boldsymbol{n}\,, \tag{6}$$

$$\boldsymbol{H}^{-1}\boldsymbol{n} = \boldsymbol{z}\,, \tag{7}$$

where matrices $\boldsymbol{H}$, $\boldsymbol{H}^{-1}$ are independent of the nonlinearity shape. Equations (6) and (7) are also valid for nonlinear functions with a bounded number of finite discontinuities. The invariant matrices $\boldsymbol{H}$, $\boldsymbol{H}^{-1}$ are given in the monograph (Teodorescu, 1973), in which various synthesis procedures based on transformations (6), (7) are presented. They permit to determine the

correction nonlinearity $N_c(x)$ (i.e. the sampled-data vector z_c) which, introduced in the control system, allow one to obtain a desired steady-state and/or transient behaviour. By using the same relationships, in the present paper we shall consider the converse problem, i.e.

Given a nonlinear biological system with unknown model, tested by means of a sinwave with constant frequency and controlled amplitude, find the sampled-data vector z which express the model subject to some accuracy constraints. Such a problem may arise, for example, in pupillary light reflex model identifications (Schwan, 1969; Blesser, 1969) as well as in eyeball dynamics (oculomotor subsystem) investigations (Milsum, 1966). Of course, once the sampled-data vector z is found, the mathematical model of the nonlinear function under consideration may be easily determined by applying the methods used in the conventional approximation theory (Talbot, 1970; Rice, 1969) such as Tchebysheff approximation, L_2 norm approximation, etc.

In this context of a special interest is the restrictions problem and, it is to observe that, there are many characteristic features of the model which are desirable and may be obtained by using appropriate restrictions. More precisely, the identified nonlinear function must fulfil some restrictive conditions, in order to be easy to handle and sufficiently accurate, such that:

a_1) *Smoothing Restrictions.* A smooth nonlinear function is, of course, desirable, since it allows to get the mathematical model in a more straightforward manner. Unfortunately, measurement noise perturbations exist in all concret cases. Thus, in order to be realistic and to obtain smooth nonlinear models also, smoothing restrictions must be observed. This may be obtained by performing transformation (7) subject to a "minimum length" restriction for the nonlinear function $N(x)$ expressed by the vector z. As will be shown later, this leads to a quadratic programming problem.

b_1) *Sign Restrictions.* In certain cases, there is some prior information about the model, concerning the sign of the nonlinear function $N(x)$ for given domains of the variable x. For example, in deriving the threshold phenomena model as a basic property of the nerve membrane (Schwan, 1969; Noble and Stern, 1966) we know that, regardless the state of the membrane (narcosis, relatively refractory state, etc.) the response must be positive for any positive stimulus. To use such a positivity restriction in the identification procedure is, obviously, favourable since wrong interpretations of the results (as a consequence of some identification errors) are thus avoided.

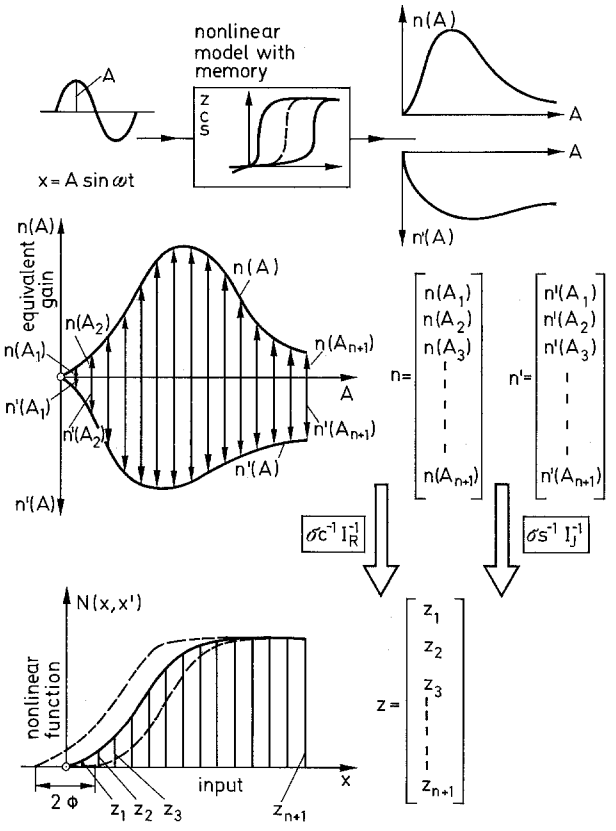

Fig. 2. Identification of nonlinear models with memory by means of matrices I_R^{-1}, I_J^{-1}, σ, and definition of the sampled-data vectors $\boldsymbol{n}$, $\boldsymbol{n}'$, and z (the hysteresis loop width 2Φ is expressed by the matrices c^{-1}, s^{-1})

c_1) *Slope-Sign Restrictions.* As shown in (Teodorescu, 1971), in the case of double-valued nonlinearities having a loop width of 2Φ, the definition of the sampled-data nonlinearity vector z is valid for the resulting nonlinearity, when $\Phi=0$, that is $|N(x,\dot{x})|_{\Phi=0}$. The definition is illustrated in Fig. 2, where $\boldsymbol{n}$ and $\boldsymbol{n}'$ are the real-respectively imaginar sampled-data vectors expressing the equivalent gain of the nonlinearity. According to (Teodorescu, 1971) the hysteresis loop width is expressed in terms of the sampled-data vectors method by means of the diagonal matrices

$$\begin{matrix} c^{-1} \\ s^{-1} \end{matrix} = \begin{bmatrix} \cos^{-1}\frac{\pi}{\Theta}\Phi & \cdot & \cdots & 0 \\ \sin^{-1}\frac{\pi}{\Theta}\Phi & & & \\ \cdot & \cos^{-1} 3\frac{\pi}{\Theta}\Phi & & \cdot \\ & \sin^{-1} 3\frac{\pi}{\Theta}\Phi & & \\ \cdot & & \cdot & \cdot \\ \cdot & & \cdot & \cdot \\ 0 & \cdot & \cdot & \cos^{-1}(2n+1)\frac{\pi}{\Theta}\Phi \\ & & & \sin^{-1}(2n+1)\frac{\pi}{\Theta}\Phi \end{bmatrix} \tag{8}$$

under the assumption that

$$\cos(2n+1)\frac{\pi}{\Theta}\Phi \neq 0 \qquad \sin(2n+1)\frac{\pi}{\Theta}\Phi \neq 0\,, \tag{9}$$

where Θ is the nonlinearity period. Thus, the n.s.v. of the nonlinearity under consideration (whose equivalent gain is expressed by the vectors $\boldsymbol{n}$, $\boldsymbol{n}'$) is given by

$$\boldsymbol{z} = \boldsymbol{E}\boldsymbol{n} \tag{10}$$

or alternatively by

$$\boldsymbol{z} = \boldsymbol{F}\boldsymbol{n}' \tag{10a}$$

in which the real-part transformation matrix is

$$\boldsymbol{E} = \boldsymbol{\sigma}\boldsymbol{c}^{-1}\boldsymbol{I}_R \tag{11}$$

while the imaginary-part one is

$$\boldsymbol{F} = \boldsymbol{\sigma}\boldsymbol{s}^{-1}\boldsymbol{I}_J\,. \tag{11a}$$

Note that matrices $\boldsymbol{I}_R$, $\boldsymbol{I}_J$, $\boldsymbol{\sigma}$ [given in the monograph (Teodorescu, 1973)] like matrices $\boldsymbol{H}$, $\boldsymbol{H}^{-1}$, are invariant with respect to the nonlinearity shape. Moreover, it is to observe that, in order to use matrices $\boldsymbol{\sigma}$, $\boldsymbol{I}_R$, $\boldsymbol{I}_j$, $\boldsymbol{H}$, $\boldsymbol{H}^{-1}$, for nonlinearities with an arbitrary period (width) Θ, a scale transformation must be performed as shown in (Teodorescu, 1973).

From the definition in Fig. 2 (the double-valued nonlinearity is obtained by a $\pm\Phi$ parallel shifting of the symmetrical single-valued nonlinearity $N(x,\dot{x})|_{\Phi=0}$), it follows that a positive (or zero) slope of the single-valued nonlinearity $N(x,\dot{x})|_{\Phi=0}$, expressed by the vector $\boldsymbol{z}$, is a desirable condition. It may be obtained if in the identification problem some slope sign restrictions are observed. Of course, such restrictions may be observed by the single-valued nonlinearities also, if there is some prior information about the slope sign of the nonlinear model under consideration. As will be shown in the example that follows, in many cases, by observing sign restrictions as well as slope-sign ones, smooth nonlinear models are obtained, without considering in the identification problem any smoothing condition.

3.1. Conditional Identification of Nonlinear Biological Models

To outline the identification procedure consider again Eq. (7) in connection with Fig. 3, in which the definition of the error-vector $|\varepsilon|$ is illustrated. By using them the loss-function

$$w = \boldsymbol{\alpha}^T|\boldsymbol{\varepsilon}| \tag{12}$$

(expressing the inaccuracy of the identified model) may be defined. Observe that components of the vector $|\varepsilon|$

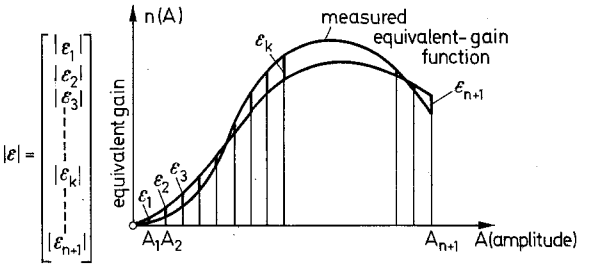

Fig. 3. Definition of the error-vector $|\varepsilon|$ which expresses the inaccuracy of the models equivalent-gain vector with respect to the measured equivalent-gain vector $\boldsymbol{n}$

are absolute values of the components of the vector

$$\boldsymbol{\varepsilon} = [\varepsilon_1\varepsilon_2\varepsilon_3 \ldots \varepsilon_{n+1}]^T \tag{13}$$

while $\boldsymbol{\alpha}$ is the weighting vector.

Thus, Eq. (7) may be rewritten as

$$\boldsymbol{\lambda}_{(H-1)q}(\boldsymbol{n} \pm \boldsymbol{\varepsilon}) = z_q \qquad q \in (1, n+1) \tag{14}$$

in which $\boldsymbol{\lambda}_{(H-1)q}$ are line-vectors of the matrix $\boldsymbol{H}^{-1}$, z_q are components of the nonlinearity sampled-data vector, while $\boldsymbol{n}$ is the vector expressing the measured equivalent-gain of the nonlinearity.

Now, if we consider

$$\boldsymbol{\varepsilon} = \boldsymbol{\varepsilon}^+ - \boldsymbol{\varepsilon}^- \qquad \boldsymbol{\varepsilon}^+ \geqq 0 \qquad \boldsymbol{\varepsilon}^- \geqq 0 \tag{15}$$

which is a customary notation in control optimization problems with loss functions like Eq. (12) (Boudarel *et al.*, 1967, Tome 2, p. 231), Eq. (15) leads to

$$|\boldsymbol{\varepsilon}| = \boldsymbol{\varepsilon}^+ + \boldsymbol{\varepsilon}^- \tag{15a}$$

and, consequently, Eqs. (12) and (14) may be rewritten as a linear programming problem, i.e.

$$\boldsymbol{\lambda}_{(H-1)r}(\boldsymbol{n} + \boldsymbol{\varepsilon}^+ - \boldsymbol{\varepsilon}^-)\{\geqq, \leqq\}0\,, \qquad r+p \in (1, n)\,, \tag{16a}$$

$$\boldsymbol{\lambda}_{(H-1)(p+1)}(\boldsymbol{n} + \boldsymbol{\varepsilon}^+ - \boldsymbol{\varepsilon}^-) - \boldsymbol{\lambda}_{(H-1)p}(\boldsymbol{n} + \boldsymbol{\varepsilon}^+ - \boldsymbol{\varepsilon}^-)\{\geqq, \leqq\}0\,, \tag{16b}$$

$$\min \boldsymbol{\alpha}^T(\boldsymbol{\varepsilon}^+ + \boldsymbol{\varepsilon}^-)\,. \tag{17}$$

Observe that (16a) are sign restrictions (i.e. $z_r\{\geqq, \leqq\}0$) while (16b) are slope-sign ones (i.e. $z_{(p+1)}\{\geqq, \leqq\}z_p$). Problems (16) and (17) may be solved by using a customary simplex algorithm. The following example is given to illustrate the procedure.

Example. Consider the measured equivalent-gain function shown in Fig. 4a, which (because of the measurement noise perturbations) is expressed by the equivalent-gain sampled-data vector

$$\boldsymbol{n} = [0.02 \quad -0.15 \quad 0 \quad -0.15 \quad 0.6 \quad 0.86 \quad 0.81 \quad 0.81 \quad 0.74 \quad 0.72 \quad 0.70 \quad 0.645 \quad 0.64]^T$$

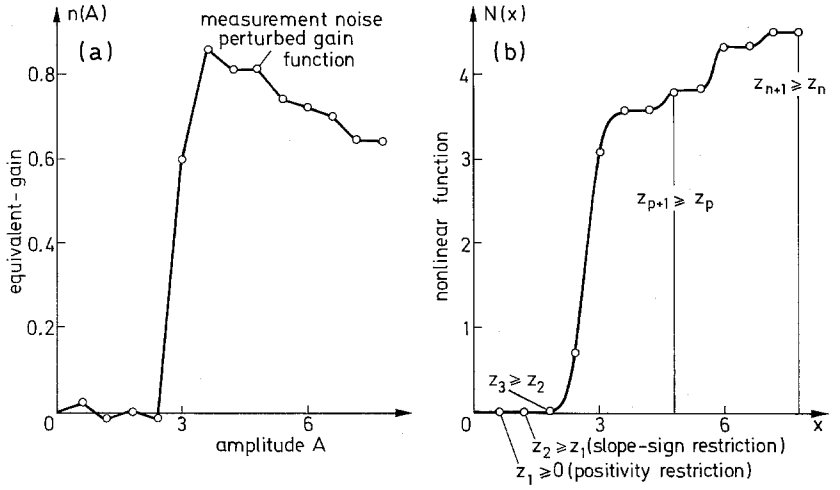

Fig. 4a and b. Measured equivalent-gain function (a) and the corresponding nonlinear model (b)

rather than by the function $n(A)$ itself. By solving problems (16) and (17) and by observing sign restrictions ($z_1 \geqq 0$) as well as slope sign ones ($z_{p+1} \geqq z_p$, $p \in (2, n)$) the nonlinear model (n.s.v.)

$$z = [0 \quad 0 \quad 0 \quad 0.698 \quad 3.073 \quad 3.582 \quad 3.582 \quad 3.779 \quad 3.779 \quad 4.317 \quad 4.317 \quad 4.510 \quad 4.510]^T$$

is obtained. The corresponding nonlinear function is illustrated in Fig. 4b, in which the restrictions of the linear programming problem are also shown. The minimum value of the loss function is $w = 0.245$.

As mentioned before (a_1) another way to derive smooth nonlinear biological models is to observe smoothing restrictions in the identification procedure. This becomes possible if one considers with the notations in Fig. 1 the loss function

$$g = z_1^2 + (z_1 - z_2)^2 + (z_2 - z_3)^2 + \ldots (z_n - z_{n+1})^2 + (n+1)\Delta x^2 \tag{18}$$

expressing the nonlinearity "length". Observe that, for a given matrix $\boldsymbol{H}$, the term $(n+1)\Delta^2 x$ is a positive constant and, as a consequence, if one notes by $f = g - (n+1)\Delta^2 x$, the identification problem may be stated as follows:

Find the nonlinearity sampled-data vector z corresponding to the minimum of the strict convex loss function

$$f = \tfrac{1}{2} z^T \boldsymbol{C} z \tag{18a}$$

with matrix $\boldsymbol{C}$ positive-definite, on the restriction set

$$\boldsymbol{r}_i^T z \leqq \boldsymbol{b}_i \qquad i \in (1, 2, \ldots m). \tag{19}$$

This is, obviously, a quadratic programming problem in which matrix $\boldsymbol{C}$ is

$$\boldsymbol{C} = \begin{bmatrix} 2 & -1 & 0 & \cdots & \cdots & 0 \\ -1 & 2 & -1 & & & \vdots \\ 0 & -1 & 2 & -1 & & \vdots \\ \vdots & & & \ddots & & \vdots \\ \vdots & & & & \ddots & \vdots \\ \vdots & & & & -1 \quad 2 & -1 \\ 0 & \cdots & \cdots & \cdots & 0 \quad -1 & 2 \end{bmatrix} \tag{20}$$

while the restrictions matrix in Eq. (19) is

$$\boldsymbol{R} = \begin{bmatrix} \boldsymbol{I} \\ \hline \boldsymbol{H} \end{bmatrix}. \tag{21}$$

Clearly, $\boldsymbol{R}$ is an $m \times (n+1)$ matrix in which the unity matrix $\boldsymbol{I}$ is introduced in order to observe positivity conditions for the components of the n.s.v. z. Note that, as a consequence of Eqs. (19) and (21), restrictions may be considered directly for the components of the e.g.v. $\boldsymbol{n}$ [see Eq. (6)]. Problems (18a) and (19) may be solved by using the Theil-Van de Panne algorithm. A similar problem is discussed in (Teodorescu, 1974) in connection with a new control system synthesis procedure and some examples are given.

It is to observe that, identification of nonlinear models with memory may be performed in a similar way, by using transformations (10) in connection with a linear (or quadratic) programming procedure. Note also that, in this case, the problem is a parametric one, having the hysteresis loop width Φ as parameter. Moreover, the identification of asymmetric nonlinear models, may be performed by using the same pro-

cedures as above. In addition, transformations given in (Teodorescu, 1973) for asymmetric nonlinearities must be observed.

3.2. *The Analytical Nonlinear Model*

Once the vector-valued nonlinear model z (i.e. the n.s.v.) is obtained, in order to get the corresponding polynomial model the problem may be stated as follows:

Given the sampled-data vector z, find the polynomial $P(x)$ which enables the best approximation in R_{n+1} of the vector z to be obtained.

Note that, the best approximation is considered here in terms of the minimum square error, although other criteria (Tchebyshew, etc.) may be used. Thus, if the approximation polynomial is

$$P(x)=A_0x^{p-1}+\ldots A_{p-1}x+A_p \qquad p<n \tag{22}$$

the coefficients A_p may be obtained by solving the system (Angot, 1961)

$$\begin{aligned} &A_0\textstyle\sum_{i=1}^{n+1}x_i^{2p}+A_1\sum_{i=1}^{n+1}x_i^{2p-1}+\ldots+A_p\sum_{i=1}^{n+1}x_i^{p}=\sum_{i=1}^{n+1}z_ix_i^{p}\\ &\qquad\vdots\qquad\qquad\vdots\qquad\qquad\qquad\vdots\qquad\qquad\vdots\\ &A_0\textstyle\sum_{i=1}^{n+1}x_i^{p}+A_1\sum_{i=1}^{n+1}x_i^{p-1}+\ldots+A_p\sum_{i=1}^{n+1}1=\sum_{i=1}^{n+1}z_i, \end{aligned} \tag{23}$$

where z_i are the components of the n.s.v. corresponding to the input values $x=x_i$.

It is to observe that, as compared with the Wiener method, the sampled-data vector procedure allows:

– to obtain conditional models, i.e. models subject to given constraints;

– to get biological models with controlled accuracy;

– to perform the identification by using invariant operators, in connection with computer-oriented techniques.

4. Step-Response Vector and linear Model Identification

As already shown, correlations (6), (7), (10), and (11), based on the sampled-data vector concept, are valid for very large classes of nonlinear models. This generality (somewhat unusual for the nonlinear domain) leads to the following, naturally, question: which are the corresponding transformations in the linear domain? However, such a transformation, relating the time domain with the frequency one, may be easily obtained, by using the step-response vector (s.r.v.) concept (Teodorescu, 1972b). This is a vector $\boldsymbol{a}$, the components of which are equal to the values of the step-response function $a(t)$ at positive, equal and consecutive sampling intervals Δt. The definition is illustrated in Fig. 5. Likewise, *a real-part frequency sampled-data vector* (r.f.v.) may be defined as a vector $\boldsymbol{u}$ the components of which are equal to the values of the real-part frequency function $u(\omega)=\mathrm{Re}\,L(j\omega)$ at positive, equal and consecutive sampling intervals $\Delta\omega$. By using these concepts, it is shown that, under certain conditions (Teodorescu, 1974), the sampled-data vectors $\boldsymbol{a}$ and $\boldsymbol{u}$ are related by the linear transformation

$$\boldsymbol{A}\boldsymbol{u}=\boldsymbol{a}, \tag{24}$$

$$\boldsymbol{A}^{-1}\boldsymbol{a}=\boldsymbol{u}, \tag{25}$$

in which matrices $\boldsymbol{A}$, $\boldsymbol{A}^{-1}$ are invariant with respect to the time and frequency scales. Matrix $\boldsymbol{A}^{-1}$ of the order $q=16$ with $\Delta t=0.45$ ($\Delta\omega=0.45$) is given in Table 1. However, in order to use this matrix in identification procedures, starting from a s.r.v. $\boldsymbol{a}$ with an arbitrary final time (t_{n+1}), a scale transformation with the *scale coefficient*

$$k_T^{-1}=\frac{t_{n+1}}{q\Delta t} \tag{26}$$

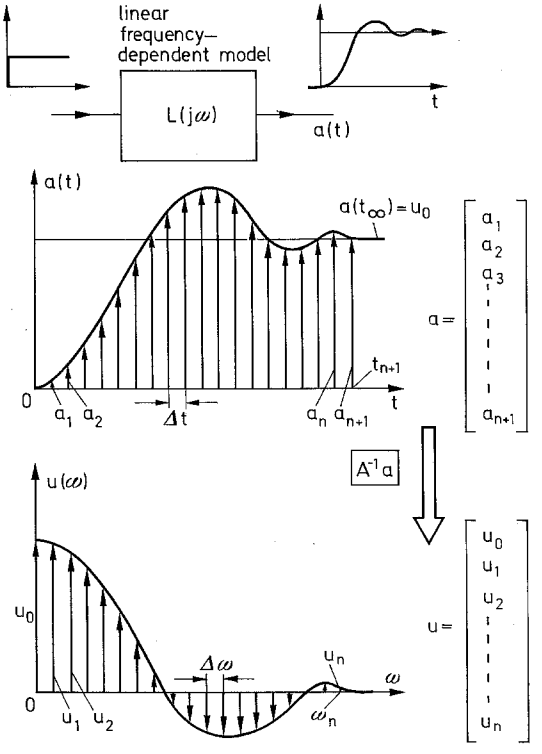

Fig. 5. Identification of linear frequency-dependent models by means of the matrix $\boldsymbol{A}^{-1}$ and definitions of the sampled-data vectors $\boldsymbol{a}$ and $\boldsymbol{u}$

Table 1. Matrices A^{-1} and B of 16-th order $\Delta t=0.45$ ($\Delta\omega=0.45$)

A^{-1}	0,00001	-0,00002	0,00004	-0,00006	0,00010	-0,00014	0,00018	-0,00025	0,00035	-0,00048	0,00072	-0,00120	0,00237	-0,00695	0,49549	0,50984
	0,04072	0,07981	0,11557	0,14672	0,17165	0,18996	0,19994	0,20251	0,19577	0,18246	0,15965	0,13345	0,09629	0,06813	-0,47541	-0,51064
	0,15962	0,29331	0,37966	0,40442	0,36407	0,26432	0,12243	-0,04005	-0,19500	-0,31988	-0,39087	-0,40189	-0,34222	-0,24029	0,41565	0,51303
	0,34676	0,56948	0,58836	0,39675	0,06301	-0,29291	-0,54459	-0,60064	-0,44272	-0,12502	0,23535	0,51477	0,60428	0,49074	-0,31750	-0,51708
	0,58669	0,80900	0,52900	-0,07964	-0,63859	-0,80140	-0,46584	0,15804	0,68500	0,78503	0,39963	-0,23710	-0,72095	-0,77039	0,18341	0,52283
	0,85865	0,90995	0,10513	-0,79829	-0,95118	-0,20917	0,72919	0,98228	0,31068	-0,65184	-1,00325	-0,40797	0,56546	1,02029	-0,01661	-0,53028
	1,13895	0,79336	-0,58601	-1,20197	-0,25092	1,02655	0,96688	-0,35398	-1,21217	-0,49222	0,87160	1,09594	-0,10207	-1,18086	-0,17884	0,53959
	1,40085	0,42781	-1,27021	-0,81571	1,02095	1,12786	-0,67711	-1,33383	0,26876	1,41724	0,16214	-1,36464	-0,58461	1,19994	0,39810	-0,55092
	1,61807	-0,15924	-1,60227	0,31660	1,57156	-0,47179	-1,52443	0,62079	1,46460	-0,76649	-1,38682	0,89927	1,30461	-1,04203	-0,63561	0,56428
	1,76499	-0,87905	-1,32733	1,54054	0,55956	-1,81869	0,34554	1,64744	-1,16734	-1,06445	1,69538	0,22341	-1,81278	0,69420	0,88495	-0,57985
	1,81967	-1,59690	-0,41813	1,96356	-1,30443	-0,81946	2,02413	-0,95755	-1,18279	1,99386	-0,56443	-1,50220	1,88893	-0,17045	-1,13931	0,59790
	1,76424	-2,15400	0,86573	1,09716	-2,20571	1,59664	0,25555	-1,90776	2,07261	-0,62134	-1,31642	2,23240	-1,41607	-0,48771	1,39084	-0,61836
	1,58706	-2,40391	2,05412	-0,70763	-0,98194	2,19445	-2,34117	1,35073	0,29634	-1,80143	2,43466	-1,88994	0,43479	1,21527	-1,63151	0,64162
	1,28279	-2,24013	2,62918	-2,35116	1,47653	-0,22692	-1,08110	2,11585	-2,61505	2,45276	-1,67081	0,46919	0,84428	-1,92702	1,85130	-0,66724
	0,85640	-1,63283	2,25737	-2,67155	2,83692	-2,73818	2,38492	-1,81029	1,06797	-0,22784	-0,63073	1,42636	-2,08159	2,52533	-2,03690	0,69402
	0,62529	-1,24480	1,85020	-2,43501	2,99259	-3,51622	4,00047	-4,43951	4,82760	-5,16002	5,43114	-5,63411	5,76135	-5,79038	4,31933	-1,43142
B	0,	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	0,27699	0,13940	0,19939	0,11379	0,12866	0,05194	0,04767	-0,02547	-0,03545	-0,10386	-0,10779	-0,17166	-0,15191	-0,24135	-0,17747	0,00661
	0,53003	0,18593	0,20648	-0,07004	-0,13714	-0,34071	-0,35705	-0,42805	-0,33330	-0,26686	-0,08994	0,05362	0,20359	0,38850	0,37619	-0,02180
	0,73862	0,06828	-0,04941	-0,53953	-0,53826	-0,58947	-0,21805	0,04143	0,46243	0,54820	0,60851	0,26844	0,05002	-0,51518	-0,50137	0,01606
	0,88200	-0,23285	-0,47759	-0,91036	-0,41365	0,04831	0,72291	0,74225	0,47766	-0,23431	-0,67756	-0,78755	-0,38173	0,38965	0,69292	-0,03686
	0,94989	-0,69445	-0,82830	-0,76270	0,46369	0,88950	0,79339	-0,33134	-0,88200	-0,85585	0,22953	0,82647	0,97198	-0,29240	-0,73264	0,01382
	0,93027	-1,22761	-0,84637	0,01068	1,32507	0,53533	-0,63872	-1,24656	-0,00148	1,05157	0,89195	-0,54106	-1,23878	-0,14290	0,89279	-0,03767
	0,82773	-1,72902	-0,35676	0,94473	1,16225	-1,01484	-1,10504	0,34767	1,51783	-0,18002	-1,27427	-0,53039	1,49909	0,39096	-0,81062	-0,01004
	0,64244	-2,06148	0,56059	1,33869	-0,19095	-1,72081	0,69313	1,37008	-0,58656	-1,51649	0,89998	1,31627	-1,00899	-0,99594	0,92069	-0,01438
	0,39739	-2,14032	1,64822	0,65684	-1,46797	-0,34322	2,00023	-0,97823	-1,20967	1,28685	0,86712	-2,04277	0,54633	1,14183	-0,67116	-0,07034
	0,10440	-1,88928	2,45284	-0,86314	-1,24551	1,59698	0,14158	-1,97219	1,80193	0,21344	-1,85035	1,32358	0,68202	-1,66070	0,71987	0,04786
	-0,19181	-1,35458	2,64751	-2,42108	0,72541	1,19134	-1,88124	0,83535	1,11543	-2,44627	2,12784	-0,43634	-1,23594	1,34573	-0,22701	-0,19512
	-0,47236	-0,59050	2,01919	-2,90194	2,70061	-1,44601	-0,29930	1,72328	-2,16464	1,43840	0,06939	-1,57867	2,26754	-1,54740	0,21267	0,17777
	-0,65527	0,16583	0,86086	-2,00577	2,90205	-3,27894	3,01466	-2,16102	0,92765	0,37129	-1,39422	1,85075	-1,54963	0,32748	0,73002	-0,46113
	-0,72357	0,77676	-0,45844	-0,09957	0,79293	-1,52417	2,20169	-2,74267	3,07823	-3,15713	2,94564	-2,42180	1,55162	-0,16972	-0,79737	0,45520
	-0,38872	0,56250	-0,62163	0,59708	-0,50337	0,34819	-0,13550	-0,13352	0,46102	-0,85298	1,32265	-1,89856	2,64891	-3,79516	3,61675	-1,36157

is to be performed. Note that transformations (24) and (25) are valid only for stable linear models. Moreover, in order to obtain a good accuracy $\Delta\omega$ must be sufficiently small, which, in fact, means that ω_n must be correctly chosen. This fact is important especially if matrices $\boldsymbol{A}$, $\boldsymbol{A}^{-1}$ with small order are used. However, computer facilities allows to apply transformations (24) and (25) with satisfactory results in any identification problem, by using matrices with high order.

The inverse transformation (25) enables to obtain in a simple way the r.f.v. $\boldsymbol{u}$ of the model starting from the measured s.r.v. $\boldsymbol{a}$. Of course, to obtain the mathematical model, the *imaginary part frequency sampled-data vector* (i.f.v.) is necessary too. By using a similar definition as for the vector $\boldsymbol{u}$ (Fig. 5) we may define the i.f.v. as a vector $\boldsymbol{v}$, the components of which are equal to the values of the imaginary-part function $v(\omega)=\mathrm{Im}L(j\omega)$ at positive, equal and consecutive sampling intervals $\Delta\omega$. It follows that

$$\boldsymbol{\lambda}=\boldsymbol{u}+j\boldsymbol{v} \tag{27}$$

may be regarded as the *polar vector* of the model, corresponding to the polar locus $L(j\omega)$. Thus, according to the proof in (Teodorescu, 1974) the sampled-data vector $\boldsymbol{v}$ is related to the s.r.v. $\boldsymbol{a}$ by the linear transformation

$$\boldsymbol{v}=\boldsymbol{B}\boldsymbol{a} \tag{28}$$

in which, under similar conditions as with matrices $\boldsymbol{A}$, $\boldsymbol{A}^{-1}$, matrix $\boldsymbol{B}$ is invariant with respect to the time and frequency scales. Matrix $\boldsymbol{B}$ of the 16-th order with $\Delta t=0.45$ ($\Delta\omega=0.45$) is given in Table 1. Observe that, Eqs. (24), (27), and (28) lead to equation

$$\boldsymbol{\lambda}=(\boldsymbol{A}^{-1}+j\boldsymbol{B})\boldsymbol{a} \tag{29}$$

which is a complex linear transformation, allowing to transform the s.r.v. $\boldsymbol{a}$ in the polar vector $\boldsymbol{\lambda}$ and thus to get, in a simple and general manner, the vector-valued model of the biological system under consideration.

However, in applying transformation (29) in the identification procedure there are some particular restrictions which must be observed i.e.

a_2) *Stability Restrictions.* Suppose that, starting from the measured s.r.v. $\boldsymbol{a}$ of the biological system under investigation, the sampled-data vectors $\boldsymbol{u}=\boldsymbol{A}^{-1}\boldsymbol{a}$ and $\boldsymbol{v}=\boldsymbol{B}\boldsymbol{a}$ are obtained. Now, the following step is to determine the mathematical model of the system. Obviously, since the investigated system is a stable one, in order to be realistic in deriving the mathematical model, some stability constraints must be observed.

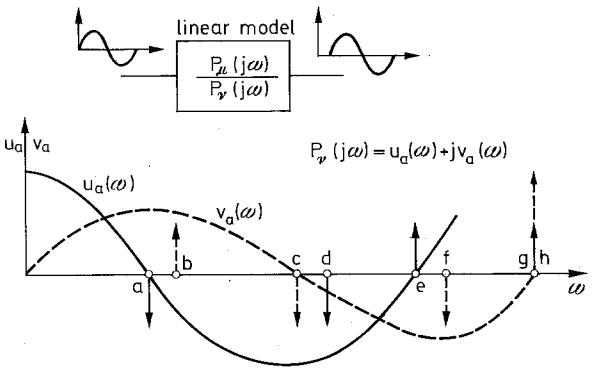

Fig. 6. Stability restrictions ($a, b, c \ldots h$) according to the Michailov criterion

To achieve this, consider the set of biological systems with the general transfer function (model)

$$\frac{P_\mu(s)}{P_\nu(s)}=\frac{a_0+a_1s+a_2s^2+\ldots a_\mu s^\mu}{b_0+b_1s+b_2s^2+\ldots b_\nu s^\nu} \qquad \mu \leqq \nu . \tag{30}$$

According to the Michailov stability criterion (Oppelt, 1966; Teodorescu, 1974) the conditions which must be fullfilled by the real part $u_a(\omega)=\mathrm{Re}\,P_\nu(j\omega)$ of the characteristic equation may be expressed by restrictions a, d, e, etc., in Fig. 6, while the imaginary-part $v_a(\omega)=\mathrm{Im}\,P_\nu(j\omega)$ must fullfill restrictions b, c, f, etc. It follows that, in order to obtain a stable biological model, restrictions like

$$b_0-\omega_s^2b_2+\omega_s^4b_4+\ldots\{\geqq,\leqq\}0, \tag{31}$$

$$\omega_tb_1-\omega_t^3b_3+\omega_t^5b_5+\ldots\{\geqq,\leqq\}0, \tag{32}$$

must be observed in the identification procedure. Observe that, in Eqs. (31) and (32), the frequencies which are associated to the stability restrictions are noted by ω_s, ω_t, to avoid confusions.

On the other hand, the sampled-data vectors $\boldsymbol{u}$ and $\boldsymbol{v}$ determined previously, which contain the information about the biological system structure, may be approximated by using the error-vectors $\boldsymbol{\delta}^u$, $\boldsymbol{\delta}^v$. Thus, in order to approximate the first i components of the vectors $\boldsymbol{u}$ and $\boldsymbol{v}$ (corresponding to the frequencies $\omega_1, \omega_2 \ldots \omega_i$) by a linear programming procedure, we suppose that the components of the error vectors

$$\boldsymbol{\delta}^u=[\delta_1^u\delta_2^u\ldots\delta_i^u]^T, \qquad \boldsymbol{\delta}^v=[\delta_1^v\delta_2^v\ldots\delta_i^v]^T$$

are sufficiently small, so that

$$\lim\frac{P_\mu(j\omega)}{P_\nu(j\omega)(u_i+jv_i)+\delta_i^u+j\delta_i^v}=1 \tag{33}$$

$$\delta_i^{u,v}\to 0 .$$

It follows that the restrictions of the identification problem may be written as

$$(a_0-\omega_i^2a_2+\omega_i^4a_4+\ldots)-u_i(b_0-\omega_i^2b_2+\omega_i^4b_4+\ldots)$$
$$+v_i(\omega_ib_1-\omega_i^3b_3+\omega_i^5b_5+\ldots)+\delta_i^u=0 \qquad i\in(1,i) \tag{34}$$

for the real part, and

$$(\omega_ia_1-\omega_i^3a_3+\omega_i^3a_5+\ldots)-u_i(\omega_ib_1-\omega_i^3b_3+\omega_i^5b_5+\ldots)$$
$$-v_i(b_0-\omega_i^2b_2+\omega_i^4b_4+\ldots)+\delta_i^v=0 \qquad i\in(1,i) \tag{35}$$

for the imaginary one.

By observing restrictions (31), (32), (34), and (35), the identification problem may be stated as follows:

Given the sampled-data vectors $\boldsymbol{u}=\boldsymbol{A}^{-1}\boldsymbol{a}$ and $\boldsymbol{v}=\boldsymbol{B}\boldsymbol{a}$ which express the biological model, find the coefficient vectors

$$\boldsymbol{\alpha}_0=[a_1a_3a_5\ldots]^T \qquad \boldsymbol{\alpha}_e=[1\ a_2a_4\ldots]^T$$
$$\boldsymbol{\beta}_0=[b_1b_3b_5\ldots]^T \qquad \boldsymbol{\beta}_e=[b_0b_2b_4\ldots]^T$$

[i.e. the model $P_\mu(s)/P_\nu(s)$] which minimize the loss function

$$p=\boldsymbol{c}^T|\boldsymbol{\delta}^u|+\boldsymbol{d}^T|\boldsymbol{\delta}^v|, \tag{36}$$

where

$$|\boldsymbol{\delta}^u|=\boldsymbol{\delta}^{u+}+\boldsymbol{\delta}^{u-} \qquad |\boldsymbol{\delta}^v|=\boldsymbol{\delta}^{v+}+\boldsymbol{\delta}^{v-} \tag{37}$$

subject to restrictions (31), (32), (34), and (35). Observe that in Eq. (36) $\boldsymbol{c}$ and $\boldsymbol{d}$ are weighting vectors.

It follows that the identification problem may be rewritten as

$$\boldsymbol{Q}_e\boldsymbol{\beta}_e\{\geqq,\leqq\}0, \tag{38}$$
$$\boldsymbol{Q}_0\boldsymbol{\beta}_0\{\geqq,\leqq\}0, \tag{39}$$
$$\boldsymbol{P}_e\boldsymbol{\alpha}_e-\boldsymbol{U}_i\boldsymbol{P}_e\boldsymbol{\beta}_e+\boldsymbol{V}_i\boldsymbol{P}_0\boldsymbol{\beta}_0+\boldsymbol{I}\boldsymbol{\delta}^u=0, \tag{40}$$
$$\boldsymbol{P}_e\boldsymbol{\alpha}_0-\boldsymbol{U}_i\boldsymbol{P}_0\boldsymbol{\beta}_0-\boldsymbol{V}_i\boldsymbol{P}_e\boldsymbol{\beta}_e+\boldsymbol{I}\boldsymbol{\delta}^v=0, \tag{41}$$
$$\min[\boldsymbol{c}^T(\boldsymbol{\delta}^{u+}+\boldsymbol{\delta}^{u-})+\boldsymbol{d}^T(\boldsymbol{\delta}^{v+}+\boldsymbol{\delta}^{v-})], \tag{42}$$

in which $\boldsymbol{Q}_e(\boldsymbol{Q}_0)$ are even (odd) matrices having as components the frequencies $\omega_s^k(\omega_t^k)$, which are associated to the stability restrictions (Fig. 6); $\boldsymbol{P}_e(\boldsymbol{P}_0)$ are even (odd) matrices having as components frequencies ω_i^k, $i\in(1,i)$; $\boldsymbol{U}_i(\boldsymbol{V}_i)$ are diagonal matrices formed by means of the first components of the vectors $\boldsymbol{u}(\boldsymbol{v})$, while $\boldsymbol{I}$ is the unity matrix. Clearly, (38)–(42) is a customary linear programming problem, which may be solved by using the simplex algorithm. The following example is given to illustrate the procedure.

Example. Let us consider a biological system having the step-response vector (Fig. 7, full line)

$$\boldsymbol{a}=[0.6277\ \ 1.4193\ \ 1.7898\ \ 1.7518\ \ 1.4896\ \ 1.1869$$
$$0.9600\ \ 0.8486\ \ 0.8368\ \ 0.8835\ \ 0.9471\ \ 0.9993$$
$$1.0277\ \ 1.0348\ \ 1.0271\ \ 1.0141]^T .$$

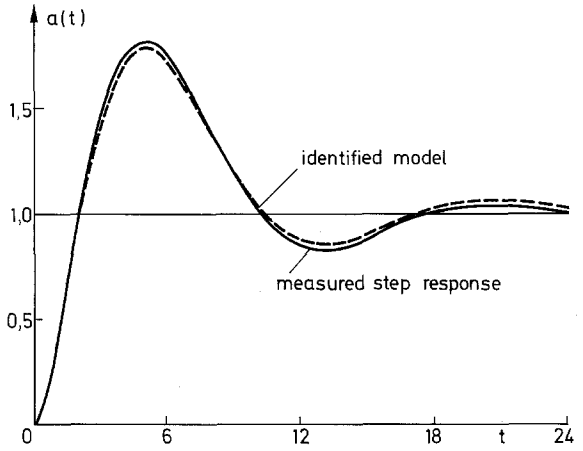

Fig. 7. Comparison between the measured (full line) step response and the response of the identified model (dashed line)

By applying transformations with matrices $\boldsymbol{A}^{-1}$, $\boldsymbol{B}$ (Table 1), then by solving problem (38)–(42) with $(\omega_i = \omega_1 \ldots \omega_6)\ \omega_1 = 0; \omega_2 = 0.135; \omega_3 = 0.27; \omega_4 = 0.405; \omega_5 = 0.54; \omega_6 = 0.675$ and $\omega_s = 0.5; \omega_t = 2$ the coefficient vectors

$$\boldsymbol{\alpha}_e = [1]$$
$$\boldsymbol{\alpha}_0 = [4.486]$$
$$\boldsymbol{\beta}_e = [0.980 \quad 6.520]^T$$
$$\boldsymbol{\beta}_0 = [2.775 \quad 4.338]^T$$

are obtained. Consequently the mathematical model of the system under investigation is

$$\frac{P_u(s)}{P_y(s)} = \frac{4.486s + 1}{4.338s^3 + 6.520s^2 + 2.775s + 0.980}.$$

The (unweighted) loss function, expressing the inaccuracy of the identification is 0.449636. Furthermore, the accuracy of the identified model may be easily checked, if the step response of the model is computed by applying the well-known Laplace transform procedure. This leads to the step response shown in Fig. 7 (dashed line). Now, if the responses in Fig. 7 are compared, the accuracy of the identified model becomes obvious.

5. Discussion

Thus, it is shown that, by using the sampled-data vector concept, some new identification procedures are derived which enables to obtain, in a simple way, the mathematical models of biological systems. The identification methods are based on linear transformations, using invariant matrices, associated with linear (or quadratic) programming procedures. As a consequence, the methods under consideration are computer-oriented ones, since there are obvious reasons to include such general operators in subrutines. Moreover, the identification is made with controlled accuracy, the error being expressed by the loss function of the programming problem itself. Thus, various identification problems, concerning linear as well as nonlinear biological systems may be solved in a general manner, by using computer facilities. This fact is, perhaps, significant since there are clear reasons to use, in concrete cases, more general biological models than the analytical ones. Indeed, the conventional biological models [say the open loop carotid sinus gain model in Eq. (1)] are expressed by analytic forms with one or more subject-dependent parameters. Consequently, the model may be used in a given concrete case once these parameters are estimated. This fact leads, however, to undesirable constraints (for the concrete model under investigation) determined by the analytical model itself. Obviously, the analytical model having one or two adjustable parameters, like a Procust-bed, may not be in accordance with the characteristic features of any concrete model. Thus, an alternative way is considered here, i.e.

a) to use a vector-valued model (like the sampled-data vectors $\boldsymbol{z}$, $\boldsymbol{u}$, $\boldsymbol{v}$) instead of the analytical one; clearly, the vector-valued model being related to the actual process by some invariant matrix operators, which are valid for very large model classes, undesired constraints are avoided;

b) to use an optimization procedure, in which actual constraints (determined by the prior knowledge of the model) are observed, instead of approximating the subject-dependent parameters of the analytical model;

c) to express the accuracy of the model by using a loss function.

Thus, following this way, the sampled-data vectors become useful tools, leading to identification methods of wide applicability and controlled accuracy.

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