NARMAX Model Identification Using a Set-Theoretic Evolutionary Approach

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Abstract

A method is presented for identification of system models that are linear in parametric structure, but arbitrarily nonlinear in signal operations. The fundamental parameter estimation task uses a set-theoretic analysis of the data to deduce feasible sets of solutions in light of certain model assumptions. In turn, measurable set solution properties are used to assess the viability of nonlinear regressor functions that “compete for survival” as components of the model best fit to represent the system. The strategy blends traditional system identification methods with three modeling strategies that are not commonly employed in signal processing: linear-time-invariant-in-parameters models, set-based parameter identification, and evolutionary selection of the model structure. The algorithm can identify nonlinear model structure and estimate parameters in the presence of different unknown noise scenarios, especially correlated noise. This paper reports the theoretical foundation of the methods and the simulation studies to illustrate the performance benefits.

Keywords:

Set-membership estimation, model structure selection, nonlinear system identification, evolutionary algorithm

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1. Introduction

At its core, signal processing (SP) is not a new discipline. Most of the roughly half-century-long profession is built on a solid foundation of linear mathematics and models that were researched, tested, and refined for several centuries before anyone conceived of an “FFT,” or a “digital model” expressed as a “computer program.” Yet, SP en-

gineers have been brilliantly insightful in shaping, out of this bedrock of mathematics, theories, products, and services that have exploited and synergistically advanced the state of modern networks and digital devices. A rich set of theories and methods based on linear, time-invariant (LTI) models is now familiar to the SP practitioner and it is these LTI models that have largely supported the spectacular technological change we have witnessed over a few short decades. The 21st century SP engineer, however, is increasingly likely to encounter system analysis and design problems in which LTI models are just not sufficient [1]. Biologically-motivated solutions are but one extremely compelling current example of this trend.

Nonlinear and / or time-varying models are difficult around which to design, analyze, and compute solutions. Arduous research over decades

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(again based in classical mathematics) has led to a sufficient body of theoretical and applied knowledge in nonlinear systems to support graduate course offerings at many universities (e.g., [2]). *Ad hoc* applications of nonlinear systems occupy a small but increasing number of pages in the scholarly literature, an SP-based example being the re-emergence of neural network of massive scale in “deep learning” of the structure of speech (e.g., [3]). This progress notwithstanding, the general class of nonlinear models is relatively poorly understood in contrast to the treasury of theoretical and practical LTI knowledge available to the SP practitioner. One approach to accounting for non-LTI system properties, without abandoning the rich SP toolkit for LTI systems is to employ models that are ***LTI in parameters*** (LTiP). For some SP endeavors, nonlinear models that LTiP are useful and only marginally more difficult to work with than systems with purely LTI properties [4]. It is upon this “bridge” class of nonlinear systems that we shall focus in this paper.

Contemporary linear system theory represents a blend of seminal efforts arising in mathematics and statistics, systems and control engineering, and SP. The model structures employed are often known as “time series models,” a name used by early developers of the methods prior to the era of modern SP. The models were initially viewed as structures to explain the spectra of random process realizations (e.g., [5, 6]). With the advent of laboratory-scale computing machines in the 1970s, time series models began to receive significant attention following the publication of the widely-read text by Box and Jenkins [6]. Economists were among the first academicians to have employed these models extensively in their research (e.g., [7]), while the nascent field of SP found applications of the methods in speech processing and spectrum estimation [8, 9, 10, 11]. Even though the early SP work was principally concerned with linear prediction – hence with a “blind input” type of model equivalent to the time-series AR model (see below) – the SP applications represent a subtle shift in the view of the model to one of a *system*, rather than strictly as a model of process (signal) generation. The name “AR

model” was not initially employed by the SP community, but, over the decades, time-series models names have been adopted by many signal and systems engineering researchers to refer to variations of canonical linear constant-coefficient difference equations models with, and sometimes without, stochastic signal components.³ Currently, the autoregressive moving average with exogenous input (ARMAX) model, including the special cases of autoregressive (AR), autoregressive moving average (ARMA), and autoregressive with exogenous input (ARX) models, are the most commonly used for linear system identification, which remains a very active research field [12, 13, 14].

A much wider variety of system nonlinearities leads to a much broader class of potential nonlinear model forms. Different insights, approximations, and application requirements have led to many model structures. Historically, nonlinear system identification has focused on a few specific models that can be tightly defined, albeit limited. Early work, based on the Volterra series, generalizes the linear convolution concept to accommodate nonlinear systems. While different identification methods are still actively studied [4, 15, 16], system identification based on the Volterra (and related Wiener) series remains a challenging problem in general. The identification of Volterra series often requires restrictive inputs like Gaussian white noise [17] that are not always consistent with applications. Moreover, the Volterra series can require a very large number of parameters to appropriately represent an output process in terms of inputs, even when the physical model is of relatively low order [18]. More recently, research into nonlinear identification has turned to more constrained models including block-structured models, such as the Hammerstein and Wiener models [19, 20, 21]. Due to the simple structure of such models, their identification can be very efficient, but the model forms are limited, and accurate *a priori* system information is required for satisfactory performance.

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³The cross-disciplinary use of the models has not always sustained a purity of terminology, but we take care in this paper to use the model names in accordance with generally accepted definitions.

The nonlinear-ARMAX (NARMAX) model was introduced by Leontaritis and Billings [22] as a new representation for a wide class of nonlinear systems. As the extension of the linear system ARMAX system, the NARMAX model, of which the nonlinear AR (NAR) and ARX (NARX) models are special cases,⁴ is the most concise and comprehensive representation for nonlinear dynamic system identification [23]. The essence of the NARMAX model is that past outputs are included in the expansions. This makes the model more concise since fewer terms are required to represent systems, but it also means that noise in the output must be taken into account when estimating the model coefficients [18]. The Volterra series, block-structured models, and many network (e.g., radial basis network, neural network) architectures can be considered special cases of the NARMAX model as well. Identification of NARMAX models, which are applicable to a wide class of nonlinear systems, is of great importance in system modeling.

The NARMAX model can be represented as the LTIIP system form. The most challenging problem in any LTIIP model identification is the determination of the model structure. The procedure must be designed to select the correct model terms (regressor signals) and estimate the model parameters from measurements of system inputs and outputs in the presence of correlated or nonlinearly dependent noise. A simple approach is to estimate a model which includes all of the nonlinear terms and then to prune (backward elimination) the insignificant components [24]. This approach is known to cause numerical and computational problems [18]. Another approach is residual-based selection, in which one term is selected at each time according to some measure of goodness of fit (forward selection) [24]. An example of this approach is the FROLS algorithm proposed by Billings *et al.* [23] which is based on the orthogonal least squares (OLS) estimator. However, in order for FROLS to achieve unbiased parameter estimation in the presence of colored or more complex noise, the algorithm must repeat-

edly refit the noise model. Moreover, the forward selection is greedy in only adding one term at a time [25].

In the approach to be presented, the fundamental parameter estimation task uses set-theoretic analysis of the data to deduce feasible sets of solutions in light of certain model assumptions. Several well-known batch and recursive methods can be used to identify *point* estimates of LTIIP systems, but ***set-membership*** algorithms provide *sets* of feasible parameter vectors rather than a single point estimate [26, 27, 28]. This is achieved through successive refinements of an initial solution set, consistent with *a priori* constraints on the signal or system model. In the present work, measurable set solution properties are used to assess the viability of nonlinear regressor functions that compete for “survival” as components of the model best suited to represent the system. Specifically, we describe an evolutionary approach to the selection of regressors. The framework presented simultaneously addresses both selection of the model and the parameter estimation. A very significant advantage of the algorithm is the lack of need for assumptions about stationarity or distributional characteristics of the noise. This feature makes the algorithm especially beneficial for NARMAX model identification.

2. Identification Framework

Consider a single-input–single-output discrete-time system with input x and output ζ , each typically assumed to belong to some well-behaved space, $\mathfrak{X} \subset \mathbb{R}^{\mathbb{Z}}$ (e.g., ℓ_2). Let $\mathbb{F}_{\theta} : \mathfrak{X} \rightarrow \mathfrak{X}$ denote the system operator mapping x to ζ , which is parametrized by a real vector $\theta \in \mathfrak{p} \subset \mathbb{R}^Q$,

$$\zeta = \mathbb{F}_{\theta}(x) \quad (1)$$

The system is said to be ***linear-in-parameters*** if, for any $x \in \mathfrak{X}$, for all $\theta, \theta' \in \mathfrak{p}$, and for all $\alpha, \alpha' \in \mathbb{R}$,

$$\mathbb{F}_{\alpha\theta + \alpha'\theta'}(x) = \alpha\mathbb{F}_{\theta}(x) + \alpha'\mathbb{F}_{\theta'}(x). \quad (2)$$

We assume that $\mathbb{F}_{\theta}$ is a continuous operator so that eq. (2) extends to countable additivity (e.g., [29]).

⁴As are, of course, AR, ARX, and ARMAX.

The internal processing of the system is based on a subset of a *candidate set* of nonlinear regressor functions, $\Xi_\varphi = \{\varphi_q\}$, of size $|\Xi_\varphi|$. Each regressor is a mapping $\varphi_q : \mathbb{R}^{r_q+s_q} \rightarrow \mathbb{R}$, operating on a set of r_q past and present system inputs, and s_q past outputs. The LTLiP *observation model*, $\mathbb{O}_{\theta_*, \varphi_*}$, for $t \in \mathbb{Z}$, is given by

$$\begin{aligned} \mathbb{O}_{\theta_*, \varphi_*} : \quad \zeta[t] &= \sum_{q=1}^Q \theta_{q*} \varphi_{q*} (x_{-\infty}^t, \zeta_{-\infty}^{t-1}) + e_*[t] \\ &\stackrel{\text{def}}{=} \theta_*^T \varphi_* (x_{-\infty}^t, \zeta_{-\infty}^{t-1}) + e_*[t], \end{aligned} \quad (3)$$

with $\theta_* \in \mathbf{p}$, and $e_* \in \mathbb{R}^{\mathbb{Z}}$ an error sequence (properties described below) representing uncertainties in the model. The “*” subscript indicates a “true,” but unknown, quantity associated with the observation model.⁵ The arguments, $x_{-\infty}^t$ and $\zeta_{-\infty}^{t-1}$, of the regressor signals φ_q (or vector φ) indicate that a finite number of elements are selected from the subsequences $\{\dots, x[t-1], x[t]\}$ and $\{\dots, \zeta[t-2], \zeta[t-1]\}$ by each φ_q for processing at time t . For conservation of space, we define the vectors of signal samples,

$$\mathbf{u}_{q*}[t] \stackrel{\text{def}}{=} \begin{bmatrix} \text{column vector of } r_q \text{ inputs from} \\ x_{-\infty}^t, \\ \text{and } s_q \text{ outputs from } \zeta_{-\infty}^{t-1}, \text{ used} \\ \text{by } \varphi_{q*} \text{ at } t \end{bmatrix}, \quad (4)$$

and the matrix $\mathbf{U}_*[t] = [\mathbf{u}_{1*}[t] \ \dots \ \mathbf{u}_{Q*}[t]]$. Given observations of x and ζ sufficient to compute outputs on time interval $t = 1, 2, \dots, \mathfrak{T}$, we pose an *estimation model*, formulated as a function of the parameters and regressor signals,

$$\begin{aligned} \mathbb{M}_{\theta, \varphi} : \quad \zeta^p(t, \theta, \varphi) &= \sum_{q=1}^Q \theta_q \varphi_q (\mathbf{u}_q[t]) \\ &\stackrel{\text{def}}{=} \theta^T \varphi (\mathbf{U}[t]) \end{aligned} \quad (5)$$

⁵Because the index q in φ_q has been defined as an enumeration of the elements of the candidate set Ξ_φ , the functions in (3) should be indexed as φ_{q_i*} , $i = 1, \dots, Q$, but we use the slightly abusive notation φ_{q*} for simplicity. It is to be understood that φ_{q*} is the q^{th} element *selected from* Ξ_φ , rather than the q^{th} element of Ξ_φ .

in which each φ_q is drawn from the set Ξ_φ (see Footnote 5), $\theta \in \mathbf{p}$, and the $\mathbf{u}_q[t]$ and $\mathbf{U}[t]$ are defined similarly to (4). The superscript on ζ^p connotes “prediction,” as this estimation model corresponds to the classical prediction-error method of Ljung [30] and others. If the observation equation is modeled stochastically, and $\mathcal{E}\{e_*[t]\} = 0$ for each $t \in \mathbb{Z}$. The expectation then

$$\mathcal{E}\{\zeta[t] \mid \theta_*, \varphi_*\} = \theta_*^T \varphi_* (\mathbf{u}_*[t]) = \zeta^p(t \mid \theta_*, \varphi_*), \quad (6)$$

where the “conditioning” notation $(\dots \mid \theta_*, \varphi_*)$ is used in a deterministic function merely to emphasize that the conditioning quantities are to be treated as fixed values. Thus, if the “true” parameters and regressors can be found using the estimation model, the prediction sequence will represent the minimum-mean-square-error (MMSE) estimate of the observed sequence. That is, $\zeta^p(t, \theta, \varphi)$ is the MMSE predictor of the sequence produced by $\mathbb{O}_{\theta_*, \varphi_*}$. The prediction residual sequence associated with the general estimation model $\mathbb{M}_{\theta, \varphi}$ is

$$\begin{aligned} \varepsilon(t, \theta, \varphi) &= \zeta[t] - \zeta^p(t, \theta, \varphi) \\ &= (\theta_* - \theta)^T \varphi_* (\mathbf{U}_*[t]) + e_*[t] \\ &\quad + \theta^T [\varphi_* (\mathbf{U}_*[t]) - \varphi (\mathbf{U}[t])] \end{aligned} \quad (7)$$

indicating error components due to the possible misadjustment in the parameter estimates as well as the possible improper selection of regressor functions. Assuming that the “true” parameters and regressor signals can be found for use in the estimation model, then, eq. (7) reduces to

$$\varepsilon(t \mid \theta = \theta_*, \varphi = \varphi_*) = e_*[t], \quad (8)$$

the asymptotic best-case residual.

The estimation algorithm to be developed has the objective of determining the appropriate regressor signal forms concomitantly with the estimation of parameters in a modeling application. The regressor set is chosen by a genetic algorithm based on an evolutionary view of the selection process. The parameters are identified using a set-theoretic approach which supports the evolution by contributing model fitness measures.

3. Set-Theoretic Parameter Estimation

3.1. Overview of Conventional Methods

Set-membership (SM) estimation and filtering have been widely researched and broadly applied, but have received significantly more interest and attention among the systems and control research communities.⁶ Recent interest in signal processing is evidenced by publications in this journal [35, 36]. In this paper we feature the **optimal bounding ellipsoid** (OBE) algorithms, an important subclass of recursive SM algorithms which have significant application potential in engineering – especially in their extended forms in this work which accommodates wide classes of nonlinear systems. The classic (linear-systems) methods developed here provide enhancements to approaches that are traditionally applied to tasks involving system identification, detection, tracking, and adaptive filtering, and data compression and security. Moreover, the enhanced procedures have the potential to make advances in methods that identify and process nonlinear dynamics. The estimation methods are particularly attractive to SP researchers due to their familiar and readily interpretable structures (e.g., [33]). In this section, we sketch the basic principles of the OBE class of algorithms.

We begin by positing the existence of a “true” observation model of form (3), $\mathbb{O}_{\theta_*, \varphi_*}$, in which, *for the purposes of introducing the OBE algorithm*, we assume the “true” regressor signals $\varphi_{q*}(\mathbf{u}_{q*}[t])$ are known. The “true” parameters, of course, are unknown and to be estimated based on observed values of the sequences ζ and x . Hence, for development purposes only, we use the conditioned estimation model, $\mathbb{M}_{\theta|\varphi_*}$,

$$\zeta^p(t, \theta | \varphi_*) = \theta^T \varphi_*(\mathbf{U}_*[t]) \quad (9)$$

OBE algorithms are based on the assumption of unknown but bounded disturbances in the observation model. We assume the existence of a sequence of error bounds,

$$|e_*[t]| < \gamma_t, \quad t \in \mathbb{Z}. \quad (10)$$

At each t , the observation model of eq. (3) in conjunction with the bound γ_t implies the existence of two hyperplanes in the parameter space $\mathbf{p} \subset \mathbb{R}^Q$,

$$\begin{aligned} \mathcal{H}_t^+ &= \{\theta \in \mathbf{p} : \zeta[t] = \theta^T \varphi_*(\mathbf{U}_*[t]) + \gamma_t\}, \quad \text{and} \\ \mathcal{H}_t^- &= \{\theta \in \mathbf{p} : \zeta[t] = \theta^T \varphi_*(\mathbf{U}_*[t]) - \gamma_t\} \end{aligned} \quad (11)$$

between which θ_* must lie. The intersection of these pairs of hyperplanes over time forms a convex polytope, say $\bar{\mathbb{P}}_t \subset \mathbf{p}$. The set of points interior to $\bar{\mathbb{P}}_t$, say $\mathbb{P}_t$, is called the **feasibility set**, at time t . $\mathbb{P}_t$ is the exact set of all parameters in $\mathbb{R}^Q$ that could have possibly produced the observed signal using the selected $\mathbb{O}_{\theta_*, \varphi_*}$ model, while adhering to the assumed constraint on the error bounds, γ_t . The convex polytopes are difficult to track without adding significant complexity to the recursion. However, the existing structure of any OBE-updating procedure readily admits a reasonable set approximation to $\bar{\mathbb{P}}_t$ in the form of an hyperellipsoid, say $\bar{\mathbb{E}}_t$, which overbounds the polytope $\bar{\mathbb{P}}_t$. The set of interior points of $\bar{\mathbb{E}}_t$, say $\mathbb{E}_t$, called the **membership set**, is therefore guaranteed to contain the feasibility set $\mathbb{E}_t \supseteq \mathbb{P}_t$. OBE optimization strategies involve minimization of some measure of the “size” of $\mathbb{E}_t$, thus seeking a tight approximation to the feasibility set. Moreover, the updating is very sparse (typically $\ll 10\%$ of the observations are innovative) leading to a very efficient estimation procedure.

In general, a hyperellipsoidal set in $\mathbb{R}^Q$ is a collection of points

$$\mathbb{E} \stackrel{\text{def}}{=} \{\theta \in \mathbb{R}^Q : (\theta - \theta_c)^T \mathbf{K}(\theta - \theta_c) < 1\} \quad (12)$$

in which θ_c is the centroid of the set, and $\mathbf{K} \in \mathbb{R}^Q$ is a nonnegative-definitive matrix. In an OBE algorithm, the hyperellipsoidal membership set at time $t \geq Q$ is given by

$$\begin{aligned} \mathbb{E}_t &\stackrel{\text{def}}{=} \{\theta \in \mathbb{R}^Q : (\theta - \theta_t)^T \kappa_t^{-1} \mathbf{C}_t(\theta - \theta_t) < 1\} \\ &= \{\theta \in \mathbb{R}^Q : (\theta - \theta_t)^T \mathbf{C}_t(\theta - \theta_t) < \kappa_t\} \end{aligned} \quad (13)$$

in which $\mathbf{C}_t$ is the sample covariance matrix of

⁶Historical accounts of the field with extensive reference lists are found, for example, in [28, 31, 32, 33, 34].

the observed regressor signals

$$\mathbf{C}_t \stackrel{\text{def}}{=} \sum_{n=1}^t \boldsymbol{\varphi}(\mathbf{U}[n]) \boldsymbol{\varphi}^T(\mathbf{U}[n]) \quad (14)$$

κ_t is a positive scalar, and $\boldsymbol{\theta}_t$ is the ellipsoid center which can be used as a point estimator of $\boldsymbol{\theta}_*$ if desired. Because hyperellipsoidal membership set is structured using second-order statistics, the updating recursions for the OBE-class algorithms are closely related to the weighted recursive least squares (WRLS) algorithm [31]. The recursive updating equations for a generic OBE algorithm [31] are as follows. With $\mathbf{P}_t \stackrel{\text{def}}{=} \mathbf{C}_t^{-1}$ (functional dependencies other than that on t are suppressed), for $t=1,2,\dots$,

$$\begin{aligned} G_t &= \boldsymbol{\varphi}_*^T[t] \mathbf{P}_{t-1} \boldsymbol{\varphi}_*[t] \\ \varepsilon[t] &= \zeta[t] - \boldsymbol{\theta}_{t-1}^T \boldsymbol{\varphi}_*[t] \\ \mathbf{P}_t &= \frac{1}{\alpha_t} \left[\mathbf{P}_{t-1} - \frac{\lambda_t \mathbf{P}_{t-1} \boldsymbol{\varphi}_*[t] \boldsymbol{\varphi}_*^T[t] \mathbf{P}_{t-1}}{\alpha_t + \lambda_t G_t} \right] \\ \boldsymbol{\theta}_t &= \boldsymbol{\theta}_{t-1} + \lambda_t \mathbf{P}_t \boldsymbol{\varphi}_*[t] \varepsilon[t], \\ \kappa_t &= \alpha_t \kappa_t + \lambda_t \gamma_t^2 - \frac{\alpha_t \lambda_t \varepsilon^2[t]}{\alpha_t + \lambda_t G_t}, \end{aligned} \quad (15)$$

$\{\alpha_t\}$ and $\{\lambda_t\}$ are nonnegative weighting sequences. The process is typically initialized with $\boldsymbol{\theta}_0 = 0$, $\kappa_0 = 1$ and $\mathbf{P}_0 = \frac{1}{\mu} \mathbf{I}$ (μ is a small number).

Different members of the OBE family are distinguished by the forms of the weighting sequences $\{\alpha_t\}$ and $\{\lambda_t\}$, and the criteria by which optimal values of these weights are determined. Two of the three optimization criteria used in the development of OBE algorithms are directly related to the “size” of $\mathbb{E}_t$ at each t . These are: ① to minimize the determinant of the inverse ellipsoid matrix, $\mu_t^{\text{vol}} \stackrel{\text{def}}{=} \det\{\kappa_t \mathbf{P}_t\}$, which is proportional to the square of the volume of the ellipsoid; ② to minimize the trace of the inverse ellipsoid matrix, $\mu_t^{\text{tr}} \stackrel{\text{def}}{=} \text{tr}\{\kappa_t \mathbf{P}_t\}$ which is proportional to the sum of squares of the ellipsoid’s semi-axes; and, ③ to minimize the parameter κ_t which is guaranteed to reduce ellipsoid volume though not to the minimum possible, and which has complex interpretations described in, for example, [35, 36, 37].

Optimization in each iteration generally consists of solving a quadratic function to determine

the existence of optimal weights λ_t in the sense of shrinking the ellipsoid size. If such weights do not exist, the observation can be discarded and the effort of updating avoided. Efficient checks for innovation in the data can be used to circumvent the computation involved in direct solution for weights (e.g., [28, 33, 31]). The process is mildly dependent on the particular OBE strategy used, and the details are carefully documented in the cited references.

In addition to the very sparse and efficient updating procedure used by OBE methods, a significant advantage for application is the lack of need for assumptions about stationarity or distributional characteristics of the error sequence e_* . Further, OBE algorithms yield a feasible set of solutions that can be exploited (see below), whereas the centroid of the set provides a conventional estimate which is interpretable as a weighted least square error estimate.

Obtaining the advantages of the OBE algorithm requires knowledge of noise bounds which are unavailable in many applications. This issue is particularly poignant in the present deployment of the method because shifting sets of regressor signals in $\mathbb{O}_{\boldsymbol{\theta}_*, \boldsymbol{\varphi}_*}$ can have significant effects on the error bounds in the model. In the analysis above, we have assumed known regressor signals. We next introduce innovations into the OBE structure to account for the potential for erroneous error bounds as the model undergoes “evolution.”

3.2. Technical Adjustments for Evolving Regressor Signals

To mitigate the problem of unknown error bounds, we incorporate the **automatic bound estimation** (ABE) procedure [38]. ABE has been studied in a probabilistic setting in which conditions have been proven for stochastic convergence of OBE methods that use the method. The basis for ABE is that, starting with overestimated error bounds, there exists, with nonzero probability, an interval $\mathbb{I}$ of any length $\mathcal{N}$ over which no update takes place. Empirically, the need to adjust the bound is indicated by a sufficiently long period

without updates⁷. When such an interval occurs, ABE invokes a bound re-estimation recursion,

$$\gamma_t = \begin{cases} \gamma_{t-1} - d_J, & \text{if } d_J > 0 \\ \gamma_{t-1}, & \text{otherwise} \end{cases} \quad (16)$$

where, $d_J = (\kappa_{J-1})G_J/Q - \epsilon(2\sqrt{\gamma_{t-1}} - \epsilon)$
and $J = \arg \max_{t \in \mathbb{I}} \varepsilon^2[t]$

in which ϵ is a small number, and γ_t denotes the sequence of estimated bounds with $\gamma_0 > \gamma_*$ (true bound).

Furthermore, an immediate and simple check for the ellipsoid regularity is incorporated into the algorithm. For meaningful parameter estimation, the ellipsoid $\mathbb{E}$ must have non-negative volume. In turn, this condition requires that $\kappa_t > 0$. The generalized method, **OBE with evolved regressor signals** (OBE-ERS), is given in Algorithm 1. While the enhancements can be incorporated into any OBE algorithm, here we employ the OBE algorithm version known as *set-membership-stochastic approximation (SM-SA)*. In the SM-SA algorithm, the volume of the ellipsoid (proportional to $\det\{\kappa_t P_t\}$) is minimized at each iteration by letting $\lambda_t = \beta_t$ and $\alpha_t = 1 - \beta_t$ in eq. (15), and seeking the optimal β_t in light of the current measurements [31].

Several evolutionary fitness measures can be derived from the final membership set. For instance, the conventional prediction error energy associated with the centroid of the set (point estimator) can be calculated as a quality measure. Additionally, the estimated bounds and the set-related-properties, such as the volume of the ellipsoid, and the shape of the ellipsoid, can be used as measures of viability. Naturally, the best fitting model should have the minimum estimation error, the smallest ellipsoid volume, and the smallest estimated error bound. A good model will also arise from an ellipsoidal set of “balanced dimensions,” so that no redundant regressors are included in

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Algorithm 1: OBE-ERS

Data: Observation subsequences x, ζ

Result: Parameter membership set

Initialization

1. $\theta_0 = \mathbf{0}, \kappa_0 = 1$ and $\mathbf{P}_0 = \frac{1}{\mu} \mathbf{I}$;
2. γ_0 a overestimated bound;
3. window length $\mathcal{N}$ and $\epsilon = 0.02$.

/* Parameter estimation starts */

for each data pair (x, ζ) do

    if $\kappa_t > 0$ then

        if data is innovate then

            execute eq. (15);   /* OBE

            updates */

        else if $\mathbb{I} > \mathcal{N}$ then

            execute eq. (16);   /* ABE */

$\mathbb{I} = 0$;

        else

$\mathbb{I} = \mathbb{I} + 1$;

        end

    end

end

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the model. In the next section, these properties characterize the performance of models in the estimation model set, and are exploited by an evolutionary algorithm to guide the exploration of better models.

4. EVOLUTIONARY MODEL SELECTION

4.1. “Cell Biology” of the LTIIP Model

An evolutionary algorithm is a generic population-based meta-heuristic optimization algorithm. Falling under the category of evolutionary algorithms, the genetic algorithm solves optimization and search problems using processes inspired by natural evolution [39, 40, 41]. Genetic algorithms often exhibit excellent performance in nonlinear and discrete optimization problems. Here, we use a genetic algorithm to aid in system modeling. The model structure detection problem, which is a NP-hard problem, can be mapped coherently into the standard genetic algorithm framework.

In the present formulation, a LTIIP model is an “*organism*” with a single “*chromosome*.”

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⁷The OBE-ABE has been proven for stochastic convergence [38]. In application, large data samples M and $\mathcal{N}$ ($=\sqrt{M}$, for example) are chosen to achieve high probability convergence.

In contrast to the complex chemical structure of chromosomes in living cells, the LTtiP chromosome is a simple, finite, binary sequence in which each bit indicates the presence or absence of a particular “*gene*.” To stretch the analogy, a binary “1” represents a region of “*coding DNA*” along the model chromosome, while a “0” represents “*non-coding DNA*.” Whereas the information in a biological gene is encoded in its sequence of nucleotides, the information in a model gene is merely in its position along the chromosome. In particular, each gene “codes for” a particular regressor function in the model. By analogy, a regressor function, as a “building block” of the model which is indicated by a particular gene, plays the role of a “*protein*” in the model organism.

Let $\Xi_\varphi = \{\varphi_q\}$, of set size $|\Xi_\varphi|$ elements, contain the regressor functions available with which to create models. A chromosome is a string of $|\Xi_\varphi|$ bits which is in one-to-one correspondence with a model. A unity bit in the ℓ^{th} binary position of the chromosome is a “gene” that codes for regressor φ_q^ℓ in its model. In principle, then, there are $(2^{|\Xi_\varphi|} - 1)$ different chromosomes, corresponding to an equal number of distinct models. A viable model is one with an effective set of regressor functions and parameter values that allow it to accurately produce the observed ζ from the observed x . Although they appear in the “*phenotype*,” the parameters in some sense represent “*regulators of expression*” of the genes, the desired expression being the linear mix of proteins that give the model the highest “*survival potential*.” As in biology, survival depends on the inherent suitability of an individual’s genetic makeup for meet the challenges of the environment (reflected in x and ζ), and also in the realization of that genetic potential resulting from an effective parameter set.

4.2. Survival Fitness Measures

The set-theoretic aspects of the identification constrain the sets of parameters to those that are feasible in light of the observations and the error constraints. In turn, they determine the range and statistical viability of phenotypes, and ulti-

Table 1: Adaptation of system modeling to a genetic algorithm

Cell Biology	System Model
Chromosome	LTtiP model
Gene	Regressor function
Regulator of gene	Parameter

mately the plight of the chromosomes. The algorithm starts with a population $\mathbb{P}$, a set of candidate models,

$$\mathbb{P}[\tau] = \{\zeta_j^p[\tau] \mid \zeta_j^p \in \mathbb{M}_{\theta, \varphi}\} \quad (17)$$

where $j = 1, 2, \dots, |\mathbb{P}|$ indexes individuals in the population, and $\tau = 1, 2, \dots$ is the generation index. The parameters of each model is determined by the OBE-ERS algorithm, and the performance of each model (corresponding to a chromosome) is evaluated via a fitness function derived from the set properties of the resulting ellipsoid.

Different fitness functions can be used for model selection [42, 43]. One option is to use the Akaike Final Prediction Error (FPE) [44] as fitness function to evaluate different models. The FPE, which is broadly used for measuring model quality and determining model orders in linear models, is given by

$$FPE = \frac{N + \sigma Q}{N - \sigma Q} V \quad (18)$$

where N is the data length, Q is the number of model terms, σ is an adjustable parameter, and $V = \frac{1}{N} \sum_1^N (\zeta - \zeta_j^p)^2$, which is the sum of squared one-step prediction errors. FPE represents bias and variance trade-offs in model fitting. A useful interpretation of FPE is that the criterion provides a measure by simulating the situation in which the model is tested on a different data set. The goal is to minimize the fitness function defined by FPE criterion.

An alternative quality measure based on the properties of the ellipsoid set is designed empirically:

$$f = Q \times b^2 \times R \quad (19)$$

where Q is the number of regressor signals, b is the estimated bound of the error sequence, and

R is the ratio of the maximum and the minimum axes of the ellipsoid. The OBE-ERS algorithm starts with an over-estimated error bound, and estimates the error bound recursively. A good model will explain more variations in the data, and approach the ‘true’ error bound asymptotically as in eq. (8). Conversely, a bad model as in eq. (7) (irrelevant regressors or wrong parameters) will have a larger estimated error bound. In this sense, b serves as a measure of how well a model fits the data. In addition, the parameter hyperellipsoid will approximate a hypersphere if all the chosen regressors contribute equally to the model fitting. Thus, a good model has a smaller b and R . Q is added to avoid model overfitting. Notice that both R and Q contribute to the pruning of model parameters. Other fitness functions can also be designed based on the properties of the membership set (e.g., the volume of the ellipsoid).

Each individual is assigned a fitness value derived from the fitness function, which is then used in the selection to bias the new population toward the inclusion of better individuals. Highly-fit individuals (in our case, smaller fitness values) have a high probability of being selected for reproduction. The process continues through subsequent generations. The average fitness of the population improves as more fit individuals appear and interbreed, and the unfit individuals are selected out. The evolutionary algorithm is terminated when a predefined number of generations is reached or the fitness values in the population reaches a prescribed minimum.

4.3. Evolutionary Operations

The genetic algorithm begins by creating a random initial population. At each step, the algorithm uses the current population to create the offspring that comprise the next generation. The algorithm selects a group of individuals in the current population, called parents, which contribute their genes to their children. The algorithm usually selects parents that have better fitness values. The operations of selection, crossover, and mutation affect the evolutionary process. Algorithm 2, evolutionary model selection, outlines this pro-

cess, and the details regarding these operators are described as follows. Further details are found in [45, 46].

Selection directs the algorithm towards fitter solutions. Selection must favor fitter candidates over weaker ones. Among different schemes, **tournament selection** is widely used [40]. The method randomly partitions the populations into “tournaments” and select winners. The winners are the parents which are then used by the crossover and mutation operators to produce children.

Crossover is used to vary the chromosomes from one generation to the next. After selection, parent solutions are chosen to reproduce potentially fitter child solutions with probability p_c . A unity probability indicates that all the selected chromosomes are used in reproduction. In the **uniform crossover** [40] scheme, a random binary vector is created by selecting the genes where the vector is a 1 from the first parent, and the genes where the vector is a 0 from the second parent, and combines the genes to form the child.

Mutation is used to introduce random alteration of the genes. It is analogous to biological mutation and typically occurs infrequently. Mutation inverts each bit in a single parent with a low probability p_m .

Replacement determines which children survive in the next generation. We employ the elite scheme. Elite children are the individuals in the current generation with the best fitness values. These individuals automatically survive to the next generation. The elite children, together with crossover and mutation children, form the next generation.

5. Experiments and Discussion

The evolutionary model selection algorithm can be applied to a broad class of identification problems spanning many disciplines. In this section, we report on the use of the method in identifying NARMAX systems. Several factors are common to the experiments. In the initialization of the algorithm, the population size is 50 per generation, the maximum number of iterations $N_{max} = 100$. The crossover rate is $p_c = 1$ and the mutation rate is $p_m = 0.1$. For each generation, other than

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Algorithm 2: Evolutionary Model Selection

Data: Observation subsequences x, ζ

Result: Best fitting model

Initialization

1. population $\mathbb{P}$ of size $|\mathbb{P}|$
2. maximum generation $N_{\max}$
3. crossover and mutation rate
4. OBE-ERS algorithm initialization

```

/* Regressor selection starts      */
for  $\tau \leftarrow 1$  to  $N_{\max}$  do
  for  $j \leftarrow 1$  to  $|\mathbb{P}|$  do
    OBE-ERS ;
    calculate fitness values  $f^j$  of each
    individual;
  end
  selection;
  crossover and mutation;
  replacement;
end

```

---

two elite children, 80% of the children come from crossover, and 20% from mutation. By design, the candidate set of regressors, Ξ_{φ} , contains various linear and nonlinear functions. In practice, knowledge of the system can be used to guide the creation of this set, which might include, for example, polynomials and the hyperbolic tangent. For the simulation study in this section, the candidate set contains linear and polynomial nonlinear functions (up to order three, including cross-terms) of delayed inputs and outputs with maximum delay of three (i.e. $\zeta[t-1], \zeta[t-2], \zeta[t-3], x[t-1], x[t-2], x[t-3]$), totally 55, for instance, $x[t-1]\zeta^2[t-2]$. Thus, the length of the chromosome is 55 genes, with each bit coding for a regressor, yielding $(2^{55} - 1)$ possible estimation models.

5.1. System 1

For simplicity, we begin with a two parameter NARX system

$$\zeta[t] = x[t-1] + 0.25x[t-2]\zeta[t-3] + e_*[t] \quad (20)$$

Figure 1: System 1: Residual and linear correlation Test: the horizontal line on the second figure is the 95% confidence interval. Using the proposed OBE-ERS identification algorithm, the residual appears to be white in accordance with the true system as in eq. (20)

in which the input sequence x is an uncorrelated Gaussian process, $x \sim \mathcal{G}(0, 2)$, and $e_*[t]$ is uniformly-distributed i.i.d white noise, $e_* \sim U(-0.1, 0.1)$. The noise is assumed unknown *a priori* and the noise bound is to be estimated. 1024-point signal observations (input-output pairs) are generated. The observation dataset is divided into a 512-point training set and a 512-point test set. The training set is used to identify the model, while the test set is used to assess the performance of the identified model.

Using the FPE criterion of eq. (18) as the fitness function with $\sigma = 1$, the estimated model is

$$\begin{aligned} \zeta^p[t] = & 1.0001x[t-1] + 0.2494x[t-2]\zeta[t-3] \\ & - 0.0009\zeta[t-1]\zeta[t-2] \end{aligned} \quad (21)$$

From the result, we can see that the key structure (the first and second regressor terms) has been detected and the estimated parameters are accurately estimated using the algorithm. The parameter associated with the extra term $\zeta[t-1]\zeta[t-2]$ is so small as to make the term negligible. The residual and the autocorrelation of the residual are shown in Fig. 1, where the residual appears to be white in accordance with the true system as in eq. (20).

The Model Predicted Output (MPO) [18] is

Figure 2: System 1: Identification results: True data (continuous curve) and estimated data (dash-dot curve). For visualization purpose, only 100 samples are shown. The identified model exhibits excellent tracking ability.

calculated using the test set. The system output is initialized by a few measured output values and then MPO is calculated from the identified model driven by only the given input. The result is shown in Fig. 2. For clear visualization, only 100 samples are shown. The selected model exhibits excellent tracking ability. The Pearson correlation coefficient of the true and estimated output is 0.9996. To further verify that the extra term $-0.0009\zeta[t-1]\zeta[t-2]$ is negligible, the MPO is calculated with the small term excluded. The correlation coefficient remains 0.9996, which means that the term is insignificant at least to $O(10^{-4})$ in this measure.

Using the same setup with only the fitness function changed, another experiment was implemented using the set measure related fitness function of eq. (19). The estimated model is

$$\begin{aligned} \zeta^p[t] = & 1.0001x[t-1] + 0.2494x[t-2]\zeta[t-3] \\ & - 0.0028\zeta[t-1]\zeta[t-3] \end{aligned} \quad (22)$$

The set property related measure is also successful in identifying the nonlinear system. The correlation coefficient of the original and estimated output is 0.9996. The result indicates that other than using only the prediction error as conventional point estimate method, the OBE-ERS algorithm provides more useful options as model quality measures and model selection criteria.

5.2. System 2

A significant advantage of the OBE estimation is the lack of need for assumptions about stationarity or distributional characteristics of the error sequence. The model selection algorithm can identify the system under different noise conditions, a useful ability for NARMAX model identification with exotic noise conditions.

5.2.1. Additive Colored Noise

In this case the system output is contaminated by colored noise, and there are no cross products between the noise and the system input and output measurements. A three parameter system with colored noise is simulated (NARMAX)

$$\zeta[t] = 0.5\zeta[t-1] + x[t-2] + 0.1x^2[t-1] + e_*[t] \quad (23)$$

where colored noise $e_*[t]$ is uniformly-distributed i.i.d. white noise sequence $v[t] \sim U(-0.1, 0.1)$ by lowpass filtering,

$$e_*[t] = -0.9e_*[t-1] + v[t]. \quad (24)$$

A 1024-point signal observation (input-output pairs) is generated with 512 points for training and 512 points for testing.

Using the FPE criterion ($\sigma = 1$) as the fitness function, the estimated model is

$$\begin{aligned} \zeta^p[t] = & 0.5078\zeta[t-1] + 0.9983x[t-2] \\ & + 0.0999x^2[t-1] \\ & + 0.0009\zeta[t-1]\zeta[t-2]x[t-1] \end{aligned} \quad (25)$$

The key structure is detected, and very importantly, the estimated parameters are unbiased in the colored noise environment. The residual, as shown in Fig. 3, is colored noise, which corresponds to the true situation. The autocorrelation of the residual measures the linear dependence between the lagged estimated error sequence. The MPO on the 512-point testing dataset is shown in Fig. 4. The correlation coefficient is 0.9938.

5.2.2. General Noise

In the NARMAX model, the noise can be nonlinearly dependent and have some cross terms involving the input and output [18]. A simulated

Figure 3: System 2 with colored noise: Residual and linear correlation test: the horizontal line on the second figure is the 95% confidence interval. The residual appears to be correlated, which is in accordance with the true system as in eq.(24). The algorithm can identify correct models in colored noise scenario.

system to include nonlinear noise terms is as follows:

$$\begin{aligned} \zeta[t] = & 0.5\zeta[t-1] + x[t-2] + 0.1x^2[t-1] \\ & + 0.5e_*[t-1] + e_*[t] + 0.1x[t-1]e_*[t-2] \end{aligned} \quad (26)$$

Using the FPE criterion ($\sigma = 1$) as the fitness function, the algorithm accurately estimated the model

$$\zeta^p[t] = 0.4970\zeta[t-1] + 0.9980x[t-2] + 0.1007x^2[t-1] \quad (27)$$

The residual and autocorrelation are shown in the Fig. 5. The correlation coefficient on the test set is 0.9992.

The ability to identify the correct model with unbiased parameters without explicit noise modeling makes the algorithm appealing for real system identification, since, in practice, complex noise properties may be unknown.

5.3. System 3

A more complex system is simulated to test the algorithm

$$\begin{aligned} \zeta[t] = & 0.8\zeta[t-1] - 0.6\zeta[t-2] \\ & + x[t-1] - 0.2x^2[t-1] \\ & + 0.01\zeta[t-1]\zeta[t-2]x[t-2] + e_*[t]. \end{aligned} \quad (28)$$

As before, 512 points are used for estimation and 512 points for testing. Using the FPE criterion

Figure 4: System 2 with colored noise: Identification results: True data (continuous curve) and estimated data (dash-dot curve). The identified model exhibits excellent tracking ability.

($\sigma = 1$) as the fitness function, the estimated model is

$$\begin{aligned} \zeta^p[t] = & 0.8020\zeta[t-1] - 0.6005\zeta[t-2] \\ & + 0.9973x[t-1] - 0.1984x^2[t-1] \\ & + 0.0100\zeta[t-1]\zeta[t-2]x[t-2] \end{aligned} \quad (29)$$

Again, the algorithm has correctly identifies the system model. The correlation coefficient on the test set is 0.9997.

5.4. System 4

Finally, to compare the performance of the evolutionary method with some of the most current research, we turn to recent work on Hammerstein systems by Yu, Zhang, and Xie [20]. The improvements in our study as compared to Yu *et al* are as follows:

- The disturbance in the Hammerstein model used by Yu *et al*. is restricted to a stationary white output error, whereas the method of this paper can identify models with much broader classes of noise with no specific distributional or dependence requirements.
- The Hammerstein model is of fixed parametric form with the objective of the Yu research being the identification of parameter values within this form. The present paper seeks to co-identify the model structure and the parameters within the optimal structure.

Figure 5: System 2 with general noise: Residual and linear correlation test: the horizontal line on the second figure is the 95% confidence interval. The residual has the same autocorrelation characteristics as in the true system eq. (26). This example demonstrates the algorithm can identify the correct model even in complex noise conditions.

- In the present work, there is no need for parameter convergence analysis like that appearing in [20, Figs. 4-6] since the parameter convergence is implicit in the set-bounding algorithm. This convergence has been extensively researched in previous papers [31, 38].

Each of these factors represent benefits of the present method over the previous work, if the new method can be shown to perform at parity or better on the Hammerstein model relative to the Yu method. This experiment is designed to test that question.

The model studied by Yu *et al.* is a Hammerstein system with a static nonlinearity at the input followed by a linear dynamical system,

$$\begin{aligned} z[t] &= 1 - 0.5x[t] + 0.7x^2[t] \\ \zeta[t] &= 0.3\zeta[t-1] + 0.4\zeta[t-2] \\ &\quad + z[t] - 2.5z[t-1] + z[t-2] + e_*[t] \end{aligned} \quad (30)$$

where the system input $x[t]$ and output $\zeta[t]$ are measurable but the intermediate signal $z[t]$ is unmeasurable. The $x[t]$ is an uncorrelated Gaussian process, $x \sim \mathcal{G}(0, 2)$, and $e_*[t]$ is uniformly-distributed i.i.d white noise. 512-point signal observation is generated for estimation and 512-points for testing. Whereas Yu begins with the known

model form, a significant difference in the current work is starting point in which both the model structure and parameters are unknown, both to be determined from the input, output dataset. With some manipulation, eq. (30) can be expressed as the NARX model,

$$\begin{aligned} \zeta[t] &= 0.3\zeta[t-1] + 0.4\zeta[t-2] - 0.5x[t] \\ &\quad + 0.7x^2[t] + 1.25x[t-1] - 1.75x^2[t-1] \\ &\quad - 0.5x[t-2] + 0.7x^2[t-2] - 0.5 + e_*[t] \end{aligned} \quad (31)$$

With eq. (31) as the surrogate for Yu’s model of eq. (30), the evolutionary model selection algorithm is applied to the dataset. The candidate set is modified to contain linear and polynomial nonlinear functions (up to order three, including cross-terms) of present and delayed inputs, and delayed outputs with maximum delay of two (i.e. $\zeta[t-1], \zeta[t-2], x[t], x[t-1], x[t-2]$). A constant regressor is also included for total of 56 possible terms. Using the FPE criterion ($\sigma = 1$) as the fitness function, the estimated model is

$$\begin{aligned} \zeta[t] &= 0.2977\zeta[t-1] + 0.3987\zeta[t-2] - 0.5013x[t] \\ &\quad + 0.6999x^2[t] + 1.2490x[t-1] - 1.7492x^2[t-1] \\ &\quad - 0.4997x[t-2] + 0.6964x^2[t-2] - 0.5056 \end{aligned} \quad (32)$$

The algorithm has not only correctly estimated the parameter values, but, critically, has properly identified the system model form. The correlation coefficient on the test set is 0.9969.

Beyond demonstrating the critical advantage of automatic determination of the model form with comparable test set correlation, it should also be noted that the algorithm can be applied when the system is corrupted by correlated or even more complex noise. Asymptotic convergence of the parameter estimation is guaranteed by the OBE algorithm [38] as part of the evolutionary process.

6. Conclusions

This paper has suggested a step toward the development of “non-LTI” methods in one important area of SP – parametric model identification.

A framework has been presented in which nonlinear models can be identified without completely abandoning well-understood and tested methods developed for LTI models.

We first introduced the LTiiP modeling concept in which the signal observations can be (in principle) arbitrarily nonlinear, while the LTiiP property preserves the ability to exploit LTI identification. An LTiiP model can be viewed as a “LTI” model in a world in which the original signals have become morphed into nonlinear combinations that are, nevertheless, if observable, a transformed set of signals. Thus LTI methods can theoretically be used to identify the model parameters in conventional ways. The LTiiP framework, however, has spawned new thinking about model identification, one of the most intensely-researched areas being that of set-membership based system identification. These methods produce sets of solutions that are consistent with *a priori* model assumptions, rather than conventional point solutions that result from conventional statistical optimization.

While previous research in conventional and set-theoretic identification has focused on the estimation of parameters, the work presented here simultaneously addresses the selection of the model and the parameter estimation. Measures of quality of set solutions over different configurations of models can be used to assess viability of the underlying models. Models with high “fitness” measures in the set solution space are placed in evolutionary competition with one another in genetic algorithms adapted for the problem setup. The underlying hypothesis of the work is that nonlinear models that are highly tuned to observed signal data will emerge with sufficient opportunity for the models to selectively reproduce and mutate within this competition.

The algorithm has been tested on four varied systems and exhibits excellent performance. As shown in the experiments, the proposed algorithm can identify system models in different noise scenarios. Unlike conventional algorithms, the algorithm can identify NARMAX model without an explicit noise model which is always unknown in the real system. The algorithm has significant

potential for further theoretical and applied development.

7. Reference

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