

The minimum dissipative passband insertion loss $10 \log((1 - |S_{11}|^2)/|S_{21}|^2)$ including connectors was measured to be 0.1 dB. Assuming a dissipative loss contribution between 0 and 0.05 dB from the connectors, bond wires and contacts, an unloaded quality factor between $Q_0 = 6000$ and $Q_0 = 12000$ can be evaluated. Although even the latter value does not reach state-of-the-art quality factor values of planar HTS resonators [3, 7], one has to consider that very narrow strip conductors (40 μm) have been used to obtain a high degree of miniaturisation. Furthermore, an identical filter realised in copper would display a quality factor $Q_0 < 40$ and an insertion loss of ~ 16 dB.

A comparison between simulation and measurement shows good agreement although a frequency shift of ~ 27.5 MHz exists. This shift can be explained by taking into account that the material parameters of the substrate (thickness and permittivity) may differ from the assumed ideal values. To meet the correct centre frequency, several experimental iteration steps must be performed.

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M. Reppel, H. Chaloupka and S. Kolesov (University of Wuppertal, Fuhlrottstrasse 10, PO Box 100 127, D-42097 Wuppertal, Germany)

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Multi-objective genetic programming for nonlinear system identification

K. Rodríguez-Vázquez and P.J. Fleming

Genetic programming is applied to the identification of non-linear polynomial models. This approach optimises multiple objectives simultaneously, and the solution set provides a trade-off between the complexity and the performance of the models. This is achieved using the concept of the non-dominated or Pareto-optimal solutions. The approach is tested on the simple Wiener model.

Introduction: System identification, the problem of building a model from input–output observations of a given system, can be posed as a multi-objective optimisation problem where several aspects of the modelling process can be involved. Using the NARMAX model representation [1], this work introduces a non-linear system identification approach based on the concepts of multi-objective optimisation and genetic programming. The aim of this work is to exploit the dynamic representation scheme offered by the genetic programming paradigm to identify a set of valid and parsimonious models that satisfy the performance criteria.

NARMAX/genetic programming approach: Focused on non-linear systems, the NARMAX (non-linear autoregressive moving average with exogenous input) model [1] represents a means of describing the input–output relationship of a non-linear system. This model is an unknown non-linear function of degree l defined as

$$y(k) = F(y(k-1), \dots, y(k-n_y), u(k-1), \dots, u(k-n_u), \dots, e(k-1), \dots, e(k-n_e)) + e(k) \quad (1)$$

where $y(k)$, $u(k)$ and $e(k)$ represent the output, input and noise signals, respectively, and n_y , n_u and n_e are their associated maximum lags. Since $e(k)$ is unknown, this equation can be expressed in a simplified polynomial form as

$$y(k) = \theta_0 + \sum_{i_1=1}^n \theta_{i_1} x_{i_1}(k) + \sum_{i_1=1}^n \sum_{i_2=i_1}^n \theta_{i_1 i_2} x_{i_1}(k) x_{i_2}(k) + \dots + \sum_{i_1=1}^n \dots \sum_{i_l=i_{l-1}}^n \theta_{i_1 \dots i_l} x_{i_1}(k) \dots x_{i_l}(k) \quad (2)$$

where $n = n_y + n_u$ (the sum of the corresponding output and input maximum lags), θ_i are scalar coefficients and $x_i(k)$ represents lagged terms in y and u .

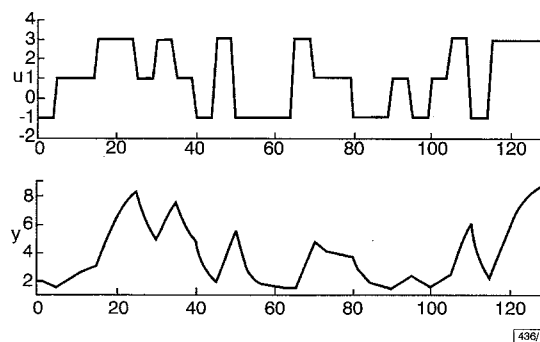


Fig. 1 Simple Wiener model input–output data

In this sort of model representation, the complexity of the identification process increases with the degree of nonlinearity and lag of the input, output and cross-coupled terms. Genetic programming (GP) is proposed here as an alternative means of determining the non-linear model structure for a given system. GP [2] is a branch of evolutionary computing (EC) methods that applies the theory of natural selection or survival of the fittest of a population of structures in a selection process. In the NARMAX-GP case, the population consists of tree-structured individuals that readily represent alternative structures for the application of the NARMAX approach. Potential models are encoded as hierarchical tree structures, thus providing a dynamic and variable representation, which are members of a population of different model structures. These structures consist of functions (internal nodes) and terminals (leaf nodes) appropriate to the problem domain. Hence, the function set is defined here as $F = \{\text{ADD}, \text{MULT}\} = \{+, *\}$, and the terminal set as $T = \{X_0, \dots, X_{n_y}, X_{n_y+1}, \dots, X_{n_y+n_u}\} = \{c, y(k-1), \dots, y(k-n_y), u(k-1), \dots, u(k-n_u)\}$.

An example of this hierarchical tree representation of the polynomial NARMAX model is expressed in Polish notation as (ADD (ADD X1 X4) (MULT (ADD X2 X3) (ADD X1 X2))). This is equivalent to the polynomial non-linear model defined as

$$y(k) = \theta_0 + \theta_1 y(k-1) + \theta_2 y(k-2) + \theta_3 u(k-1) + \theta_4 y(k-1)^2 + \theta_5 y(k-1)y(k-2) \quad (3)$$

where $\{X_0, X_1, X_2, X_3\} = \{1.0 \text{ (the constant term)}, y(k-1), y(k-2), u(k-1)\}$. A least squares algorithm is applied to compute the parameter vector θ to minimise the residual of errors between the model and measured data. Then, the population of the non-linear model is evolved by means of selection, crossover and mutation operators. In GP, crossing over two tree individuals produces a pair of offsprings by selecting a random node in each parent tree and exchanging the associated subexpressions. The mutation operation is performed by randomly selecting a node, which can be internal or terminal, and replacing the associated subexpression with a randomly generated subtree.

Multi-objective fitness function: To perform selection, all model measures considered in the identification are evaluated for each member of the population. The fitness value of each population member is assigned by means of a rank-based fitness method [3]. This fitness evaluation is based on the definition of Pareto-optimality or nondominance [3]. If we consider a minimisation problem, given two n component objective function vectors, f_u and f_v , we can say that f_u dominates f_v (is Pareto-optimal) if

$$\forall i \in \{1, \dots, n\}, f_{ui} \leq f_{vi} \wedge \exists i \in \{1, \dots, n\}, f_{ui} < f_{vi} \quad (4)$$

producing a set of possible and valid solutions known as the Pareto-optimal or nondominated set. Selection in the evolutionary process is made using a method of ranking which favours non-dominant members of the population [3].

Simulation results: The method described above is demonstrated on the simple Wiener model and compared with conventional identification techniques such as stepwise regression and orthogonal regression [4]. The differential equation of the linear dynamic part of the simple Wiener model is

$$10\dot{v}(t) + v(t) = u(t) \quad (5)$$

and the static non-linear part is expressed by

$$y(k) = 2 + v(k) + v^2(k) \quad (6)$$

The input-output data used here are defined in [4] (Fig. 1).

The multi-objective genetic programming (MOGP) approach was run considering five objectives representing the structure and the performance of the models. These were the number of terms, p , degree of non-linearity, DEG , maximum lag, LAG , residual variance, VAR , and long-term prediction error, $LTPE$. Crossover and mutation probabilities were 0.9 and 0.1, respectively, and the population consisted of 200 tree expressions. The MOGP method was run several times and gave similar families of solutions each time. Table 1 contains the results of one such run (MOGP₁₋₄ are representative solutions of this run).

Table 1: Comparative performance of the identification methods

Model	p	DEG	LAG	$VAR \times 10^{-3}$	$LTPE \times 10^{-3}$
MOGP ₁	6	2	1	2.3839	6.0221
MOGP ₂	6	2	2	2.1978	6.7967
MOGP ₃	7	2	2	1.6484	6.4279
MOGP ₄	7	2	2	1.6474	7.8151
Stepw. [4]	7	2	2	1.6808	7.8526
Orth. [4]	7	2	2	5.2243	26.8080

Polynomial NARMAX models obtained by the MOGP approach have similar model structures (Table 2) with some terms in common with the models obtained by conventional methods. All of the MOGP₁₋₄ results dominate stepwise regression and

orthogonal regression solutions when we consider both objectives. In the case of MOGP₃ and MOGP₄, improved variance results are achieved and the LTPE results are also better than the stepwise regression case (see Table 1).

Table 2: Simple Wiener model structures

Term	MOGP ₁	MOGP ₂	MOGP ₃	MOGP ₄	Stepw. [5]	Orth. [5]
c	x	x	x	x	x	x
$y(t-1)$	x	x	x	x	x	x
$y(t-2)$				x	x	x
$u(t-1)$	x		x			x
$u(t-2)$		x				x
$y(t-1)^2$	x	x	x	x	x	
$y(t-1)y(t-2)$				x		
$y(t-2)^2$					x	
$y(t-1)u(t-1)$	x	x		x	x	x
$u(t-1)^2$	x	x	x	x	x	x
$y(t-2)u(t-1)$			x			
$u(t-1)u(t-2)$			x			

Concluding remarks: A multi-objective evolutionary identification method, using a tree-based coding structure, has been shown to produce a similar and even better performance in some respects, in non-linear system identification, than conventional techniques. Although MOGP is demonstrated here using a simple model, at the present time it is being tested on more complex identification problems such as chaotic systems and data from gas turbine engine tests. For these applications, different statistical objectives for validating the models (e.g. autocorrelation of residuals and crosscorrelation tests) and different performance measures are being considered.

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K. Rodríguez-Vázquez and P.J. Fleming (*Automatic Control and Systems Engineering, University of Sheffield, Mappin Street, Sheffield S1 3JD, United Kingdom*)

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