

MULTIOBJECTIVE GENETIC PROGRAMMING FOR GAS TURBINE ENGINE MODEL IDENTIFICATION

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Abstract. A Genetic Programming-NARMAX approach has been successful applied to the identification of non-linear systems. This evolutionary identification method has been extended to a multiobjective form with the aim of simultaneously optimising different measures of the system model under investigation. So far, this novel approach has only been tested on simulated data. Here, we demonstrate a practical application of this technique to obtain a model of the relationship between the fuel feed and the shaft speed dynamics of a gas turbine engine.

Keywords: System Identification, Gas Turbine Engine, Genetic Programming, Multiobjective Optimisation.

INTRODUCTION

In the field of system identification, the problem of building a model from input-output observations of a system, non-linear system identification remains a difficult task. In many cases, no initial information is generally available about the system structure. For non-linear system identification problems, Leontaritis and Billings (6) introduced a means of describing the input-output relationship of a non-linear system, known as the NARMAX (Non-linear AutoRegressive Moving Average with extra inputs) model. This model is an unknown non-linear function of degree l defined as,

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

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 form as

$$y(k) = F(y(k-1), \dots, y(k-n_y), u(k-1), \dots, u(k-n_u)) \quad (2)$$

Leontaritis and Billings have also demonstrated that the polynomial representation is one of the most common formulations and has been shown to work well

in practical applications. Thus, a polynomial NARX model of degree l is expressed as,

$$y(k) = \theta_0 + \sum_{i_1=1}^n \theta_{i_1} x_{i_1}(k) + \sum_{i_1=1}^n \sum_{i_2=1}^n \theta_{i_1 i_2} x_{i_1}(k) x_{i_2}(k) + \dots + \sum_{i_1=1}^n \dots \sum_{i_l=1}^n \theta_{i_1 \dots i_l} x_{i_1}(k) \dots x_{i_l}(k) \quad (3)$$

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 . This non-linear difference equation model can represent a wide class of non-linear systems and it is the basis for this work. As the complexity of the identification process increases with the degree of non-linearity and lag of the input, output and cross-coupled terms, Evolutionary Computing (EC) methods have proved useful for structure and term selection.

GENETIC PROGRAMMING

EC methods apply the Neo-Darwinian theory of Natural Selection or *survival of the fittest* of a population of structures and terms in a selection process. In an attempt to alleviate the increasing complexity in NARMAX model identification problems with increased degrees of non-linearity and numbers of possible terms, previous work by (Rodríguez-Vázquez et al. (8) has investigated an identification approach based on genetic programming, Koza (4) and (5). Genetic programming (GP) is a branch of evolutionary algorithms in which the population consists of tree-structured individuals which 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 here defined as $F = \{\text{ADD, MULT}\} = \{+, *\}$, and the terminal set as $T = \{X_0, \dots, X_{n_y}, X_{n_y+1}, \dots, X_{n_y+n_u}\} = \{c, y(k-1), \dots, y(k-n_y), u(k-1), \dots, u(k-n_u)\}$. The population evolves by means of crossing over and mutating these structures. In GP, crossing over two tree individuals produces a pair of offspring by selecting a random node in each parent

tree and exchanging the associated subexpressions. The mutation operation is performed by randomly selecting a node, that can be internal or terminal, and replacing the associated subexpression with a randomly generated subtree.

An example of this hierarchical tree representation of the polynomial NARMAX model is shown in Fig.1. This model is written 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

$$y(k) = \theta_0 + \theta_1 y(k-1) + \theta_2 y(k-2) + \theta_3 u(k-1) + \theta_4 y(k-1)^2 + \theta_5 y(k-1)y(k-2) \quad (4)$$

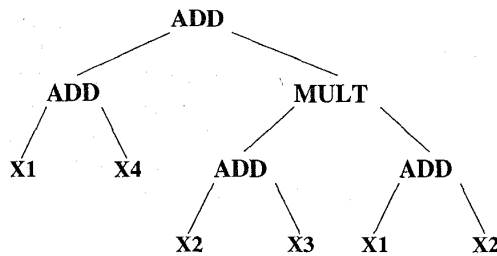


Figure 1: Polynomial NARMAX model represented as a hierarchical tree.

where X1, X2, X3 and X4 are 1.0 (the constant term), $y(k-1)$, $y(k-2)$ and $u(k-1)$, respectively. Then, a least squares algorithm is applied to compute the parameter vector θ .

Multiobjective Genetic Programming

In a further study, Rodríguez-Vázquez et al. (9), this method was transformed into a multiobjective genetic programming approach that is based on the combination of the notion of preferability, Fonseca and Fleming (3), with the concept of Pareto-Optimality or non-dominance, Ben-Tal (1). The Pareto-optimal concept means that when considering a minimisation problem and given two n components objective function vectors, \bar{f}_u and \bar{f}_v , one can say that \bar{f}_u dominates \bar{f}_v (is Pareto-optimal) if

$$\forall i \in \{1, \dots, n\}, f_{u_i} \leq f_{v_i} \wedge \exists i \in \{1, \dots, n\}, f_{u_i} < f_{v_i} \quad (5)$$

producing a set of possible and valid solutions known as the pareto-optimal or nondominated set. Fig. 2

illustrates graphically the nondominated solution set for a bi-objective problem.

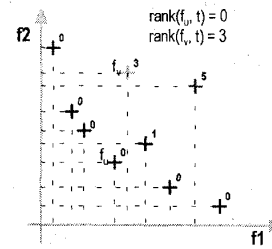


Figure 2: Pareto-ranking without preference information.

Additionally, preference information can be introduced in the form of a goal vector which provides a means of evolving only a specific region of the search space. From Fig. 2 it is seen that the individuals which satisfy their goals (g_1 and g_2) are preferable to, and therefore have a lower rank than, all of the remaining ones.

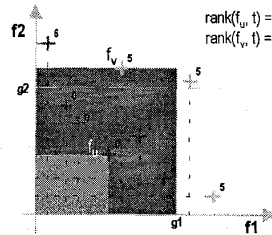


Figure 3: Pareto-ranking with preference information.

Fitness Assignment (Cost Function)

Fonseca and Fleming (2) introduced a multiobjective genetic algorithm that uses a rank-based fitness assignment where the rank of a certain individual x_i at generation t is related to the number of individuals $p_i(t)$ in the current population by which it is dominated. This is expressed as

$$\text{rank}(x_i, t) = p_i(t). \quad (6)$$

All non-dominated individuals are assigned rank 0 and the remaining ones are penalised according to the above equation.

The fitness (cost function) is assigned by interpolating from the model that shows the best performance and has the simplest structure (rank=0) to the worst. Then, the fitness assigned to models with the same rank is averaged where the global population fitness is kept constant.

Thus, in the context of system identification based upon the NARMAX model, the multiobjective approach has the aim of optimising different measure requirements within the identification process such as residual errors, long-term prediction error, the validation of identified models by means of the evaluation of statistical tools and model parsimony. Results of these studies proved encouraging although the GP-NARMAX identification approach was applied to simulated data only, Rodríguez-Vázquez et al. (9).

GAS TURBINE ENGINE DATA: A PRACTICAL APPLICATION

This section reports the application of the multiobjective genetic programming-NARMAX approach to model the relationship between the fuel feed and the shaft speed dynamics of a gas turbine engine. The input-output data measured on a Spey engine at DERA Pyestock is used for the identification purpose.

In addition to the use of a variety of performance measures, the multiobjective framework is demonstrated to be a useful tool for simultaneously identifying and validating models using different test signals at the same operating points; or, alternatively, the same test signal at different operating points. Thus, in a first experiment, the identification is based upon a multisine input signal considering different operating conditions. Besides the objectives related to the model structure such as the number of terms (NT), degree (DG) and lag (LG) of the model, the residual variance (VAR) and the k-step ahead prediction error (K-PE) at each of the operating points (53.8%, 75.45, 75.3% and 88.7% mean NH) are also optimised. A population of 100 individuals (potential models) and crossover and mutation probabilities of 0.9 and 0.1, respectively, are used.

Table 1 summarises the results obtained in this run and Fig. 4 shows the multiobjective trade-off graph. The eleven objectives are ranged along the x-axis and the performance achieved for each objective is indicated in the y-direction. For presentational purposes, these objectives are normalised with respect to each other; "X" denotes the target posed for each objective. A number of solutions (indicated by individual lines) satisfy all the objectives and are also non-dominated, i.e. no solution is deemed better than any other (refer to Eqn (5)). Interestingly, although non-linear terms were available for creation within the tree structure, a linear representation was the most satisfactory solution. This will be discussed further in a subsequent section.

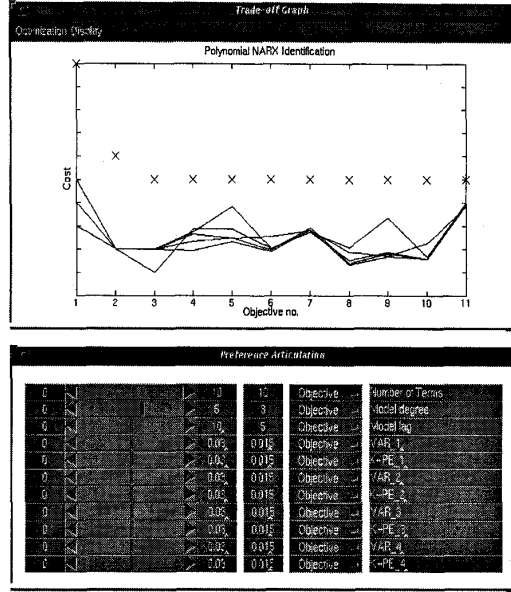


Figure 4: Multiobjective Genetic Programming Framework. Run 1.

In a second experiment, five test signals at the same 75% NH operating point are used for the identification process which are (i) no-imposed input, (ii) a multisine input, (iii) Inverse-Repeat Maximum Length Binary Signal (IRMLBS), (iv) a multisine at an input amplitude of $\pm 10\%$ of the steady state fuel flow, (v) a IRMLBS at $\pm 25\%$ of the input amplitude fuel flow. The family of models identified in this experiment are the same linear models as obtained in the previous run. Table 2 shows the terms involved in each linear model and Figure 5 represents the results of this second experiment. Although the engine shows to be non-linear (next section), these linear models are shown to predict well but they are not statistically valid models.

MODEL VALIDATION BY MEANS OF STATISTICAL TOOLS

The autocorrelation function ACF of the residuals and the crosscorrelation function CCF between the residuals and input are measures for statistically validating models. These correlation tests are respectively defined as

$$ACF = \min \Phi_{\xi\xi}(\tau) \quad \tau \neq 0 \quad (7)$$

$$CCF = \min \Phi_{u\xi}(\tau) \quad \forall \tau \quad (8)$$

and

$$\Phi_{\xi\xi}(\tau) = E[\xi(t-\tau)\xi(t)] \quad (9)$$

$$\Phi_{u\xi}(\tau) = E[u(t-\tau)\xi(t)] \quad (10)$$

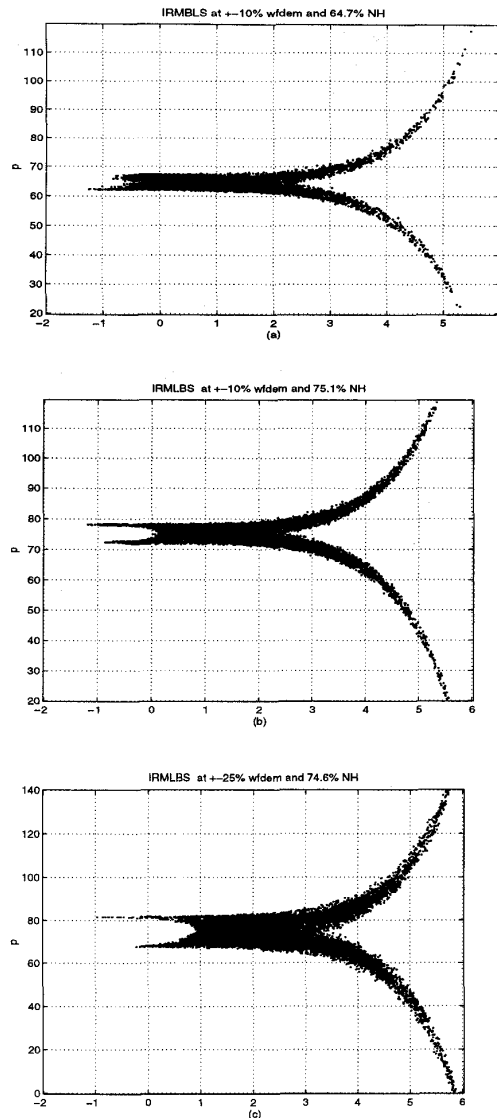


Figure 7: HP tendency. Fixed points location.

CONCLUSIONS AND FUTURE WORK

Since this is a multiobjective identification approach, there is no single solution but a family of models and the modeller is left to select the most suitable model depending on the purpose of the modelling.

It has been shown that a set of simple linear models predict well at different operating conditions although they are not statistically valid models. Introducing the correlation tests - autocorrelation and crosscorrelation, the search process has centred on a region of non-linear models. It has also been pointed out that the non-linearity of the engine is affected by the amplitude of the fuel flow.

This work has basically focused on the analysis of the HP shaft speed dynamics, but, the relation between the fuel flow and the LP shaft speed can be examined in a similar way.

In terms of the validation of the non-linear system description, the two correlation functions evaluated in this work are necessary conditions but not sufficient. Therefore, higher order correlation tests have to be considered.

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TABLE 1 - Multiobjective genetic programming identification of a multisine input signal at different operating conditions. The identified models are all linear models.

Model	NT	LAG	VAR ₁	K-PE ₁	VAR ₂	K-PE ₂	VAR ₃	K-PE ₃	VAR ₄	K-PE ₄
1	3	1	8.6190	8.6035	6.1151	8.2585	6.1856	10.093	5.0191	12.013
2	4	2	7.0341	7.4798	7.6930	8.4910	5.6612	5.1242	6.8299	11.581
3	4	2	7.9635	7.4308	5.9626	8.8259	4.1407	5.4512	4.7378	12.095
4	4	2	8.2633	11.566	6.1481	8.2645	4.5760	5.6710	4.7652	11.770
5	5	2	5.8557	7.0325	5.6946	8.5667	3.9777	5.0554	4.7346	11.910

* The residual variance and the k-step prediction error have the exponent 10^{-3} .

TABLE 2 - Identified linear models.

Model\Term	c	y(t-1)	y(t-2)	u(t-1)	u(t-2)
1	x	x		x	
2	x	x		x	x
3	x		x	x	x
4	x	x		x	x
5	x	x	x	x	x