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Toolbox for Discovering Dynamic System Relations via TAG Guided Genetic Programming

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Abstract: Data-driven modeling of nonlinear dynamical systems often requires an expert user to take critical decisions a priori to the identification procedure. Recently, an automated strategy for data-driven modeling of single-input single-output (SISO) nonlinear dynamical systems based on genetic programming (GP) and tree adjoining grammars (TAG) was introduced. The current paper extends these latest findings by proposing a multi-input multi-output (MIMO) TAG modeling framework for polynomial NARMAX models. Moreover, we introduce a TAG identification toolbox in Matlab that provides implementation of the proposed methodology to solve multi-input multi-output identification problems under NARMAX noise assumption. The capabilities of the toolbox and the modeling methodology are demonstrated in the identification of two SISO and one MIMO nonlinear dynamical benchmark models.

Keywords: Nonlinear system identification, Equation discovery, Tree Adjoining Grammar, Genetic Programming, Data-driven system modeling

1. INTRODUCTION

Control design for complex dynamic systems relies heavily on accurate system models. A way to obtain such models is through first principle modeling. While this method provides generic models with clear physical interpretation, it requires a considerable amount of time and user expertise. Another way to model the dynamical behaviour of a system is through data-driven system identification. Within this field there are numerous methods that require the user to take critical decisions (e.g. precisely selecting the model structure within prediction error methods (PEM)). In contrast, the machine learning strategies can automatically select or define model structures and features. Non-parametric machine learning methods for data-driven modeling such as Gaussian Process based Bayesian Estimators (Pillonetto et al., 2014), support vector machines (SVM) (Ming-guang Zhang et al., 2004) and artificial neuron networks (ANN), (Goodfellow et al., 2016), (Billings, 2013) describe large model spaces that can represent complex MIMO dynamics. However, the obtained models via these methods often lack interpretability and fail to provide generalization to unseen data or unseen operating regions of the system. On the other hand, the parametric machine learning methods, also known as symbolic regression, such as tree adjoining grammar guided genetic programming (TAG3P) (Khandelwal, 2020), and equation discovery (EQ) (Patelli and Ferariu, 2009) perform automated structure selection and yield time-domain solutions that directly represent the temporal modes of the system. In his doctoral thesis (Khandelwal, 2020), the author proposes a convenient way of defining the model set searching space through a novel TAG modeling framework and conveys the critical decision of selecting the right model structure into an automated evolutive procedure based on Genetic Programming. Moreover, this work shows how the proposed method can discover physical relation directly from data (Duffing oscillator). This latest development with respect to the modeling framework focused on the single-input single-output (SISO) polynomial NARMAX model set, but also included a considerable amount of variation (e.g. ability to embed sin(·), cos(·) or abs(·) nonlinear operators and TAG representation of Box-Jenkins models).

The current paper focuses on a novel grammar that extends the TAG modeling framework to multi-input multi-output (MIMO) polynomial NARMAX models. It is common for dynamic systems to have output channels with coupled dynamics. Our main contribution is to extending the framework such as multi-output candidate models are represented by only one compact syntactic tree. By this, the dynamic modes are created, evolved and parametrized with respect to all output signals at once, thus considering output couplings. Moreover, as our second contribution, a Matlab toolbox for identification with the TAG framework is provided. Using the toolbox, the user can easily select the structure searching space in terms of NARMAX (sub) model set(s). We have validated the modeling framework and Matlab implementation on two SISO and one MIMO
nonlinear benchmark models.

The paper is structured as follows: Section 2 details the novel TAG modeling framework. Section 3 describes the optimisation approach that drives the automated GP structure search procedure that is introduced in Section 4. Section 6 shows the identification results of several benchmark models. Section 5 describes the developed Matlab toolbox. In Section 7 we draw conclusions on our results and present several future research directions.

2. MODEL STRUCTURE VIA TAG

The symbolic regression identification problem consists of determining an appropriate dynamic structure and corresponding parameters of a data generating system. The solution space is described as \( S = W \times P \), where \( W \) is the a priori defined space of dynamic structures and \( P \in \mathbb{R}^n \) is its assigned parameter space, with \( n \) arbitrary large, but finite. Hence, naturally, a dual-optimization problem arises in the sense that finding the dynamic structure withing space \( W \) that minimizes the output error implies solving the parameters estimation problem within space \( P \).

For the proposed identification approach, TAG is used to describe the structure space \( W \). This chapter presents briefly the TAG modeling framework followed by a novel grammar proposal for MIMO polynomial NARMAX models. For a complete definition see (Kallmeyer, 2009) and (Khandelwal, 2020).

### Table 1. Sub model sets included in \( G_{\text{NARMAX}} \).

| Sub model       | Grammar       | Elementary trees |
|-----------------|---------------|-----------------|
| Input Poly.     | \( G_{\text{IP}} \) | \( \beta_1, \beta_4, \alpha_1 \) |
| LTI             | \( G_{\text{LTI}} \) | \( \beta_1, \beta_2, \alpha_1 \) |
| poly-NARX       | \( G_{\text{NARX}} \) | \( \beta_1, \beta_2, \beta_3, \alpha_1 \) |
| ext-NARX        | \( G_{\text{extNARX}} \) | \( \beta_1, \beta_2, \beta_4, \beta_5, \beta_6, \alpha_1, 2, 3, 4 \) |
| exp-NARX        | \( G_{\text{expNARX}} \) | \( \beta_1, \beta_2, \beta_4, \beta_5, \beta_6, \alpha_1, 5, 6 \) |

The structure of the elementary trees, imposed by the choice and position of the intermediate nodes \( v_{\text{int}} \) (e.g. \( \text{expr}_{0}, \ldots, \text{expr}_{6} \)), defines the rules that a certain grammar imposes over the shape of the derived trees \( \gamma \) (i.e. it defines what a model set is that can be generated from the recursive application of elementary operations by connecting trees via TAG adjunction and substitution operators). Each such derived tree \( \gamma \) represents a function \( F_{\gamma} \) via an interpreter function \( \mathcal{E}(\gamma) \) that transposes the tree structure into the mathematical function \( F \). In our context, the design of the elementary trees defines the TAG language \( \mathcal{E}(G) \) (all the trees \( \gamma \) that can be generated) thus, it directly defines the model set where \( F_{\gamma} = \mathcal{E}(\gamma) \) represents a model structure. Therefore, elementary trees can be designed such that a TAG can represent, via its language, an entire model set. TAGs are highly valuable as they allow to encode valid model representations and can seriously increase efficiency of GP based system identification as detailed in (Khandelwal, 2020).

### 2.1 TAG p-NARMAX modeling framework

Within this paper we focus on discrete-time MIMO polynomial NARMAX model set. Such a noise structure often provides enough flexibility to represent many dynamic systems in practice. Further, we consider systems of the form:

\[
Y(k) = \mathcal{F}(\{u_{i}(k-j)\}_{j=1}^{n_{u}}, \{y_{i}(k-m)\}_{m=1}^{n_{y}}, \{\xi_{i}(k-l)\}_{l=1}^{n_{\xi}}, i \in \{u,y,\xi\})
\]

\[
\begin{align*}
\beta_1 : & \quad C \times \text{expr}_3 \\
\beta_2 : & \quad L_U \times \text{op} \times U \\
\beta_3 : & \quad C \times \text{expr}_2 \\
\beta_4 : & \quad q^{-1} \times \text{expr}_2 \\
\beta_5 : & \quad L_U \times \text{op} \times Y \\
\beta_6 : & \quad q^{-1} \times \text{op} \times \text{expr}_2 \\
\alpha_1 : & \quad \Xi \times \sin \\
\alpha_2 : & \quad \text{preop} \\
\alpha_3 : & \quad \cos \times \text{abs} \\
\alpha_4 : & \quad \text{preop} \\
\alpha_5 : & \quad \text{inv} \times \text{exp} \\
\beta_7 : & \quad q^{-1} \times \text{op} \times \text{expr}_2 \\
\beta_8 : & \quad \text{preop} \times \text{op} \times \text{expr}_3
\end{align*}
\]
where \( U(k), Y(k) \) and \( \Xi(k) \) are multi-channel input, output and process noise signals respectively with dimensions \( r_{i(u,y,\xi)} \times k, r_{i(y,\xi)} \in \mathbb{N} \) and \( n_u, n_y \) and \( n_\xi \) are finite discrete time-delays with \( n_u, n_\xi \in \mathbb{N} \cup \{0\}, n_y \in \mathbb{N} \) and \( k \in \{1 \ldots N\} \) finite number of time samples. If the case (1) is restricted to polynomial relations, a suitable way to represent (1) for TAG modeling framework, is as follows:

\[
Y(k) = \sum_{i=1}^{p} C_i \prod_{j=0}^{q_i} L_{U,i,j} Y(k-j) \times \prod_{m=1}^{N_u} L_{Y,i,m} Y(k-m) \prod_{l=1}^{N_\xi} L_{\Xi,i,l} \Xi(k-l) + \Xi(k)
\]

where \( L_{(U,Y,\Xi)} \) is a so called linking array defined as:

\[
L_X \in \mathbb{R}^{1 \times r}, r = \text{dim}(X), L = [l_i]_{i=1}^r, l_i \in \{0,1\} \quad L_X \neq 0_{1 \times r}
\]

and \( p \in \mathbb{N} \). The operation: \( \prod_{s=1}^{0} L_{X,s} X(k-i) \) is defined as a right hand side matrix multiplication with \( X \) at time moment \( k-i \), \( s \) is a selector operator counter, \( L_{X,s} \) is a random linking array generated by (3) and \( g_i \) is the amount of right hand side multiplication of \( X(k-i) \) with itself (e.g. \( X(k-i)^2 \)). The form (2) can represent polynomial terms of all elements of the involved signals and their time-shifted representatives \( u_i(k-j), y_i(k-m) \) and \( \xi_i(k-l) \). A given function \( F(\cdot) \) within the model set (2) can be represented by a derived tree \( \gamma \). 

**Proposition 1.** TAG for MIMO p-NARMAX models

Let \( G_{NARMAX} = \langle \mathcal{N}, T, S, I, A \rangle \) be a TAG with:

- \( \mathcal{N} = \{expr_0, expr_1, expr_2, op, par\} \),
- \( T = \{U, Y, \Xi, +, C, \times, q^{-1}, L_Y, L_U, L_{\Xi}\} \), where \( L_Y, L_U \) and \( L_{\Xi} \) are "linking arrays", \( U, Y, \Xi \) are the input, output and process noise signals and \( C \) is the parameters vector.
- \( S = \{expr_0\} \),
- \( I = \{a_1\} \),
- \( A = \{\beta_1, \beta_2, \beta_3, \beta_4, \beta_5, \beta_6, \beta_7\} \), where the elementary trees \( \beta_i \) and \( a_1 \) are depicted in Figure 1.

The model set \( M(G_{NARMAX}) \) represents the set of all polynomial models defined by Equation (2) with \( p, n_y, n_\xi \in \mathbb{N} \) and \( n_u \in \mathbb{N} \cup \{0\} \).

Proposition 1 represents our main contribution over the TAG based modeling framework. As described in (Khandelwal, 2020), the TAG that represents the polynomial NARMAX model set can be enhanced or extended by considering \( \sin(\cdot), \cos(\cdot), \text{abs}(\cdot), \text{inv}(\cdot), \text{exp}(\cdot) \) functions over the polynomial variables enlisted above. This modeling extension is enabled in the TAG modeling framework by considering the \( \beta \) auxiliary tree and \( a_{2..6} \) initial trees depicted in the lower part of Figure 1. Similarly other functions can be added. Moreover, sub model sets included in \( G_{NARMAX} \) can be considered by selecting specific constituent elementary trees. Further extensions to the existed noise structure can be directly achieved as discussed in (Khandelwal, 2020) by extending the elementary trees with further elements over the noise structure. A list of useful model sets is shown in Table 1. An example of model set with TAG specification is given in: TAG3P_Call_Example.m.

### 3. IDENTIFICATION PROBLEM

Given a flexible model structure we would like to obtain an estimate of the underlying data generating system by finding a structure form with adequate complexity to achieve a desired level of approximation. This minimization can be formally defined as a dual optimization problem. Consider a TAG \( G_{Model} \) and its equivalent model set \( W_{Model} \) and a data generating system \( F_{\gamma_0}(\theta_0) \) described by a tree \( \gamma_0 \in \Sigma(G_{Model}) \), its tree-based equivalent model structure \( w_{\gamma_0} \) with the real parameters \( \theta_0 \) that yield the real output sequence \( y_0(w_{\gamma_0} | \theta_0, D_N) = Y_0(k) \), where \( D_N = \{U(k), Y_0(k)\}_{k=1}^{N} \) is a data set of length \( N \) with \( U(k) \) input sequence and \( Y_0(k) \) stochastic response. Let \( F_{\gamma}(\theta) = \mathcal{E}(\gamma) \) be a candidate model represented by tree \( \gamma \), its equivalent model structure \( w_\gamma \) and its assigned set of parameters \( \theta \). For the data set \( D_N \), the model \( F_{\gamma}(\theta) \) yields the one step ahead prediction response \( \hat{Y}_0(w_\gamma | \theta, D_N) = \hat{Y}_0(k) \) and simulation response \( \hat{Y}_0(w_\gamma | \theta, D_{S_N}) = \hat{Y}_0(k) \), where \( D_{S_N} = \{U(k), \hat{Y}_0(k)\}_{k=1}^{N} \). The two responses generate an error score \( E = (E_s, E_p) \in \mathbb{R}^2 \) where \( E_s \) is the root mean square simulation error (RMSs) produced by \( \hat{Y}_0(k) \) and \( E_p \) is the root mean square prediction error (RMSp) produced by \( \hat{Y}_0(k) \). The main aim of the identification strategy is to minimize the error score \( E \). Minimizing both errors is requested for reliable generalization property of the obtained models. (Khandelwal et al., 2019) Therefore the identification procedure searches for the solution of the following dual optimization problem:

\[
\min_{w_\gamma} J(w_\gamma, \theta) = \min \left( E \left(w_\gamma, \theta\right) \right) \quad \text{s.t.} \quad \theta = \min_{\theta} J_{\text{sub}}(\theta) = \omega_s E_s(\theta) + \omega_p E_p(\theta) \\
E_s(\theta) = \frac{1}{r_s} \sum_{i=1}^{r_s} \sqrt{\sum_{i=1}^{r_s} \frac{1}{N}s_i e_i s_i}, \quad E_p(\theta) = \frac{1}{r_p} \sum_{i=1}^{r_p} \sqrt{\sum_{i=1}^{r_p} \frac{1}{N}s_i e_i p_i} \quad \text{where} \quad e_{i,s,p} = [y_0(i,k) - \hat{y}_0(i,k)](w_\gamma, k | \theta, D_{S_N})_{k=1}^{N} \quad \text{is the simulation error weight and } \omega_p \text{ is the prediction error weight. The weight values play a role in determining what parameter estimation procedure can be deployed to solve the sub-optimization problem. They will be further detailed later.}
\]

4. ESTIMATION VIA GENETIC PROGRAMMING

To solve the multi-objective dual optimization problem described above, we designed and implemented a genetic programming (GP) algorithm that evolves a population of tree structures through TAG designed crossover and mutation genetic operators, perform parameter estimation for each structure and sorts each generation based on two fitness criterion RMSs and RMSp using the multi-objective non-dominating sorting algorithm.

4.1 Main Algorithm

The main steps of the GP algorithm are presented in Algorithm 1. The GP is initialized by defining the genetic parameters: population size \( \text{(Pop)} \), number of generations \( \text{(Gen)} \), number of maximum auxiliary trees that can be used in each derivation tree \( \text{(Complexity)} \) and crossover parameter \( \mu \in [0, 100\%] \). The genetic evolution starts from an initial population of randomly generated trees \( G(1) \). Inside the iterative loop, the crossover, mutation,
interpolator function, parameter estimation, evaluation and non-dominating sorting procedures are executed sequentially in order to propose, construct, evaluate and sort new dynamical structures. At the end, the solution is considered to be the first Pareto front of the last generation. Since within the Pareto solution the models do not dominate each other, in terms of the two considered fitness criterion, any of them can be selected as a final candidate model that minimizes problem (4). Next we will explain the main procedures in detail.

4.2 Crossover and Mutation genetic operators

In Crossover, two parents (individuals of population) have their genotype combined in order to form new individuals called offspring. Through crossover, no new information is added to the population. By switching strings of genotype between individuals, over generations, the genes that yield smaller fitness values tend to become more frequent in the population. In this way, a local exploration of the search space is performed. Consequently, via crossover, a population is exploring a local minimum of the cost score surface. The crossover operator is defined within the description of TAG3P+ in (Hoai et al., 2003). In Mutation, an offspring is proposed by eliminating or adjoining elementary trees starting from a derivation tree \( \Gamma \in G(i) \). In our implementation, for each structure of \( G(i) \) an offspring is created by mutation. By random addition or deletion of elementary trees to or from the parent derivation tree, the mutation operator is the procedure through which the evolution process performs global exploration of the searching space. Both crossover and mutation functions are called within \textbf{TAG\_GP\_Step1.m}.

4.3 Parameter estimation procedures

Every model constructed through crossover, mutation and random generation requires optimization of its parameters to assess its accuracy in terms of (4). The parameter estimation can be performed with respect to both simulation and prediction error (non zero \( \omega_s \) and \( \omega_p \) weights) or only prediction error (\( \omega_s = 0 \) and \( \omega_p = 1 \)). Considering both RMSs, in parameter estimation transforms the sub optimization problem into a non-convex optimization problem, making it considerable difficult and time-consuming to solve. If only the prediction error is considered, any model defined by a function \( F_\gamma \) with \( \gamma \in L(G\text{NARMAX}) \) can be rewritten as (7)

\[
\Psi = \Phi \Theta + E_\Theta
\]

where, for \( p \) polynomial terms as described in (2), \( \hat{\Psi} \in R^{N \times N_v} \) is the model output data set, \( \Phi \in R^{N \times p} \) is the evolution of each polynomial term over \( D_N \) and \( \Theta \in R^{p \times N_v} \) is the matrix corresponding to the parameter vector \( \Theta \). The set of parameters that minimize the sub optimization problem (4) is computed as

\[
\hat{\Theta} = (\Phi^T \Phi)^{-1} \Phi^T \Psi. \quad (8)
\]

The evolution of dynamical structure as presented above can be guided by a multi-objective criterion. In the presented algorithm, we have considered only simulation and prediction error (\( E_s, E_p \)), but other criterion like derivation tree complexity (see (Khandelwal, 2020)) can also be included. In the multi-objective genetic programming literature, most of the evolutionary strageties bases their findings on Pareto optimality criterion. Further, We introduce the Pareto dominance definition (Emmerich and Deutz, 2018).

Definition 2. Pareto dominance

Given two vectors in the objective space, \( O^{(1)}, O^{(2)} \in R^m \), then the point \( O^{(1)} \) said to Pareto dominate the point \( O^{(2)} \) \( \approx_{\text{Pareto}} O^{(2)} \), if and only if \( \forall i \in \{1, \ldots, m\} : O_i^{(1)} \leq O_i^{(2)} \) and \( \exists j \in \{1, \ldots, m\} : O_j^{(1)} < O_j^{(2)} \). In case that \( O^{(1)} \approx_{\text{Pareto}} O^{(2)} \) the first vector is not worse in each of the objectives and better in at least one objective than the second vector.

Based on the Pareto dominance \( \approx_{\text{Pareto}} \), one can group a set of candidates into fronts. Each candidate has a dominance level and it is based on the number of how many other candidates are Pareto dominated by it. A Pareto front, \( F_i \), can be seen as a contour on which all the candidates have the same dominance level. The order of dominance sorts the Pareto fronts. The Pareto optimal solution is the front that has the highest dominance level, as known as the set of non-dominated solution. A way to construct the Pareto fronts for a given set of dynamical structures is the NSGA-II algorithm detailed in (Deb et al., 2002) (see \textbf{NSGAI\_II.m}). The NSGA-II algorithm is called in \textbf{TAG\_GP\_Step4.m}. For the structure sorting procedure, the new models constructed through crossover and mutation in every generation are benchmarked against a test data set \( D_{N_{\text{test}}} \).

5. TOOLBOX MATLAB IMPLEMENTATION

The toolbox is publicly available at: gitlab.com/tu-e1/tag3p-matlab-toolbox. The repository contains an explanatory demo video that shows how to setup and run the algorithm by following the script \textbf{TAG3P\_Call\_Example.m}. After setting up the structures \textbf{Data, Parameters} and \textbf{ModelSpace}, the identification algorithm can be called by function \textbf{TAG3P.m}. The \textbf{Data} structure contains all the input output data sets arranged by role (\( D_{N_{\text{test}}}, D_{N_{\text{test}}}, D_{\text{val}} \)). Each input or output data set is defined as a matrix

\[
\begin{align*}
\text{Algorithm 1 TAG GP main} \\
\text{Define Pop} & \quad \triangleright \text{Define Population Size} \\
\text{Define Complexity} & \quad \triangleright \text{Define maximum complexity} \\
\text{Define Gen} & \quad \triangleleft \text{Define the maximum number of generations} \\
G(1) & \leftarrow \text{RandomPopulation} \quad \triangleright \text{Generate a random population of trees} \\
G(1) & \leftarrow \text{Interpreter(G(1))} \quad \triangleright \text{Construct the candidate model} \\
G(1) & \leftarrow \text{ParameterEstimation(G(1))} \\
G(1) & \leftarrow \text{Evaluate(G(1))} \quad \triangleright \text{Compute } E_s \text{ and } E_p \text{ for } G(1) \\
\text{while } i \leq \text{Gen} \text{ do} \\
\quad Q_1 & \leftarrow \text{CrossoverOffsprings(G(i))} \quad \triangleright \text{Card(Q}_1\text{) = Pop} \\
\quad Q_2 & \leftarrow \text{MutationOffsprings(G(i))} \quad \triangleright \text{Card(Q}_2\text{) = Pop} \\
\quad Q_1,2 & \leftarrow \text{ParameterEstimation(Q}_1,2\text{)} \quad \triangleright \text{see CreateTreeFunction.m} \\
\quad Q_1,2 & \leftarrow \text{Evaluator(Q}_1,2\text{)} \quad \triangleright \text{Compute } E_s \text{ and } E_p \text{ for } Q_1,2 \\
\quad R & \leftarrow G(i) \cup Q_1 \cup Q_2 \\
\quad R & \leftarrow \text{NSGA-II(R)} \quad \triangleright \text{Sorting R into Pareto fronts} \\
\quad G(i+1) & \leftarrow R(1 : \text{Pop}) \quad \triangleright \text{Select the first Pop candidates from the first Pareto fronts of R} \\
\text{end while} \\
\text{Save G(Gen)} & \quad \triangleright \text{collect the Pareto solution}
\end{align*}
\]
Table 2. RMS\textsubscript{s} and RMS\textsubscript{p} results of TAG3P Matlab Toolbox over the benchmark models in comparison with other system identification strategies from the literature.

| Benchmark model            | TAG          | RMS\textsubscript{s} | RMS\textsubscript{p} |
|----------------------------|--------------|----------------------|----------------------|
| Bouc-Wen hysteresis model  | G\textsubscript{NARX} | 6.52e−5              | 7.37e−6              |
| Full PLNSS (Esfahani et al., 2017) | 1.20e−5  | -                    |
| Decoupled PLNSS (Esfahani et al., 2017) | 1.40e−5  | -                    |
| LMN - NARX (Belz et al., 2017) | -          | 9.86e−6              |
| LMN - NFIR (Belz et al., 2017) | 1.63e−4     | -                    |
| Coupled electric drive     | RMS\textsubscript{s} | -                    | RMS\textsubscript{p} |
| Tag3P - G\textsubscript{estNARX} | 1.28e−1  | 3.27e−3               |
| Tag3P (Khandelwal, 2020) | 1.2e−1     | 3.73e−3               |
| GA + DE (Ayala et al., 2014) | 1.8e−1     | 4.0e−2               |
| Continuous Stirring Tank Reactor | RMS\textsubscript{s} | BFR                   |
| Tag3P - G\textsubscript{expNARX} | 1.6749     | 92.80%                |
| LPV-OBF (Tóth et al., 2010) | -          | 97.54%                |

\(x_\in\mathbb{R}^{n_x}\times N\). For this implementation all the data sets should contain the same amount of time-samples N. The function returns LastGeneration and Data structures. The former contains the Pareto solution alongside the last generation of models and the latter contains the input-output data structure with additional information. The function .\texttildelow/\texttildelow TAG\_main\_files\texttildelow/\texttildelow TAG3P\_ResultsPrint.m can be used to compute various error metrics and create simulation and prediction profiles for a chosen model over a validation data set.

### 6. RESULTS

We tested the TAG3P identification algorithm against two SISO and one MIMO benchmark models. For each model we considered three distinct data sets: \(D_N^{est}\) for parameter estimation, \(D_N^{est}\) for multi-objective sorting and \(D_N^{val}\) for computing validation RMS\textsubscript{s} and RMS\textsubscript{p} metrics described in Equations (5). These metrics are used to compare the results obtained through the proposed method with the ones presented in literature. For all benchmark systems, the comparison is shown in Table 2. For each benchmark model, out of the Pareto solution, we have selected the candidate model that yields the lowest average simulation error over the \(D_N^{val}\) data sets. For the MIMO benchmark model described in (Tóth et al., 2010), the authors measured their identification method performance in Best Fit Rate (BFR). Thus, for the MIMO case, alongside the RMS\textsubscript{s} value we have also computed a BFR metric.

Table 3. TAG and genetic parameters used for the benchmark problem.

| Benchmark model           | TAG          | Pop | Gen | Complexity |
|---------------------------|--------------|-----|-----|------------|
| BoucWen oscillator       | G\textsubscript{NARX} | 36  | 350 | 150        |
| Coupled electric drive    | G\textsubscript{estNARX} | 50  | 400 | 150        |
| Stirred tank model        | G\textsubscript{expNARX} | 60  | 350 | 120        |

#### 6.1 SISO benchmark models

**Bouc-Wen model** The Bouc-Wen model represents hysteretic effects and it is widely used in mechanical engineering. This benchmark is based on synthetic data and represents a challenging system to identify. The system has a dynamic nonlinearity that is governed by a non measurable internal variable. To identify this model we used the TAG with parameters Table 3.

For the parameter estimation and testing data sets (\(D_N^{est}\), \(D_N^{val}\)) we have generated 5 data sets of N = 4096 samples each using the algorithm indicated in (Noël and Schoukens, 2020). The validation data set \(D_N^{val}\) was considered the same sweep data set provided by the authors. For this data set, the identification results are reported in Table 2.

**Coupled electric drive model** The coupled electric drives consists of two electric motors that drive a pulley using a flexible belt. The pulley is held by a spring, resulting in a lightly damped dynamic mode. The drive control for the pulley is designed only for tracking the speed reference signal. A pulse counter is used to measure the angular speed of the pulley. Thus, the sign of the velocity is unknown. The available data sets are short (\(N = 500\)), and together with the absolute value component of the velocity profile make this system interesting from an identification point of view. For this system we used the extended TAG and genetic programming parameters in Table 3.

As described in (Wigren and Schoukens, 2017), the estimation data set \(D_N^{est}\) was constructed with u11 as input and z11 as output, while \(D_N^{est}\) and \(D_N^{val}\) data sets contained u12 as input and z12 as output.

The identification results, for the same validation data set, are fairly similar to the TAG3P implementation (in Mathematica) described in (Khandelwal, 2020). The result portrayed in Figure 2 and Table 2 shows that the new Matlab toolbox can match in error score the former Mathematica implementation.

#### 6.2 MIMO benchmark model

**Continuous Stirring Tank Reactor (CSTR) model** The main contribution of this paper is the extension of the TAG modeling framework to MIMO complex models. For this we tested the TAG3P MIMO identification procedure on an ideal, simulated, CSTR that is fully described in (Tóth et al., 2010). In short, the CSTR resembles a chemical conversion of an inflow substance into a product. The chemical conversion is described by a highly nonlinear dynamic relation between input signals \(U = [q, T_r, c_1]^T\) (input flow, coolant temperature and concentration of the inflow) and output signals \(Y = [T_2, c_2]^T\) (temperature in the reactor and concentration in the reactor). Since the benchmark model is fully known, ten \(D_N^{est}\), \(D_N^{est}\) and one \(D_N^{val}\) data sets were generated as described in (Tóth et al., 2010). Because of the known inverse and exponential terms within the model equations, to identify this model we used the extended TAG with parameters in Table

![Fig. 2. Validation results on the coupled electric drive system terms of simulation and prediction responses of the estimated model on \(D_N^{val}\).](image-url)
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