Efficient GA-inspired Macro-Modeling of General LTI Multi-Port Systems*

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Abstract

A numerically robust sampling and rational fitting method is introduced, that models the entire state-space matrix of Multiple-Input-Multiple-Output (MIMO) Linear Time-Invariant (LTI) systems. The algorithm adaptively builds an accurate rational pole-residue model, based on a minimal set of support samples. During the modeling process, no prior knowledge of the system's dynamics is required. The "survival-of-the-fittest" principle of a Genetic Algorithm (GA) provides a reliable way to detect convergence of the modeling process.

1. Introduction

Accurate simulation of complex multi-port LTI systems can be computationally very expensive and resource-demanding. One often wants to minimize the number of expensive data samples, in order to find an accurate broadband model in an acceptable amount of time. An earlier developed Adaptive Frequency Sampling technique [1] provides a reliable way to minimize the simulation cost by reducing the number of required support samples [2]. The selection of new samples, as well as the detection of convergence, was based on a set of heuristic rules, called Reflective functions [3]. Unfortunately, it's hard to define a reliable set of reflective functions, since it requires a lot of experience and know-how.

Recently, an alternative sampling strategy was introduced, based on the "survival-of-the-fittest" principle of genetic algorithms [4]. The major disadvantage of the technique is that it suffers poor numerical stability if the rational models require a large number of poles. If the behaviour of the system is highly dynamic, the convergence function becomes unreliable, and the algorithm converges prematurely. Rational spline interpolation with adaptive knot placement can provide an acceptable solution, although usually one global broadband macro-model is desired. In this paper the technology is refined, extended to MIMO systems, and the numerical issues are resolved by applying more robust fitting techniques.

2. Model representation

Most least-squares methods that are available to interpolate complex data by a rational function are numerically unstable, especially when the frequency range is rather broad or the model complexity is high. Orthogonalizing the basis of the numerator and denominator polynomials can improve the numerical stability [5][6][7], however it does not fully resolve all problems. In [8], a new robust iterative fitting technique, called Vector Fitting (VF), is introduced that builds accurate pole-residue models, based on frequency domain data samples. The technique is stable and resolves some of the numerical issues, that were encountered in [4].

*This work was supported by the Fund of Scientific Research Flanders

All elements of the state-space matrix are modeled by a rational pole-residue model, based upon a common set of support samples.

$$H(s_i) = \sum_{j=1}^{N} \frac{c_j}{s_i - a_j} + d + s_i h \qquad (1)$$

$H(s_i)$ represents the data samples simulated at the discrete complex frequencies s_i, $\forall i = 0, ..., m-1$. a_j and c_j are the poles and residues respectively, $\forall j = 1, ..., N$. d is a constant and h is a linear factor.

The Vector Fitting technique linearizes the non-linear identification problem. It starts with an initial set of N poles, and converges towards a global broadband solution in an iterative way by relocating the poles. The unknown system variables are estimated by solving 2 linear least-squares fits, and it is imposed that the poles and residues are real or occur in complex conjugate pairs. To enforce Bounded-Input-Bounded-Output (BIBO) system stability, unstable poles are flipped into the left half of the complex plane.

3. Sampling and modeling algorithm

The goal is to build an accurate global broadband system model, while minimizing the required number of data samples over the frequency range of interest [f_{min},f_{max}]. During the model building phase, all elements of the state-space matrix can be modeled separately. To avoid notational overhead, the modeling process of only one element will be described. However, during the sample selection phase, the complete matrix needs to be considered at once, as all elements share a single set of support samples.

The method used in this paper is based on the "survival-of-the-fittest" principle of the GA, but it is not a GA in the strict sense. Genetic concepts such as random populations, probability of selection, crossover and mutations aren't used. In fact, the algorithm is entirely deterministic.

3.1 Generation of chromosomes Let σ represent the set of selected data samples, used to solve the system identification problem. Initially (at evolution step 0), it consists of 3 or 4 samples equidistantly spaced over the frequency range of interest (Figure 1).

Several rational interpolants are built, each with a different order of numerator and denominator (Figure 2). The rational interpolants are also called the chromosomes of the modeling algorithm. The order of numerator and denominator is constrained by the number of available data samples, so the linear least squares system should always contain at least as many equations as there are unknowns, or degrees of freedom. In [4], only those rational models are considered, that exploit all degrees of freedom. It will be shown in the following sections that an overdetermined system can also provide useful information

during the modeling process. On the other hand, if the system is underdetermined, spurious poles can arise, and this can cause a highly inaccurate behaviour in between the samples. So this is not desired.

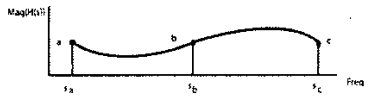

Figure 1 : Spectral response of $H(s)$ over frequency range $[s_a, s_c]$.

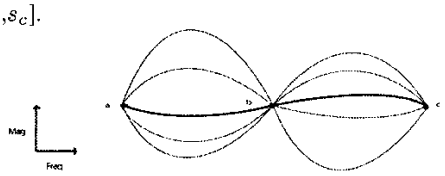

Figure 2 : Multiple rational interpolants, or chromosomes, built with a different order of numerator and denominator.

At evolution step t, the set of new interpolants is combined with the best, or most converged chromosomes of the previous evolution step (P_{t-1}), and this joint set of chromosomes will compete to join the new population at step t, represented by P_t.

Initially, at evolution step 0, the population of the previous evolution step (P_{-1}) is empty. Each time an additional sample is selected, the evolution step increases by 1. Note that a population of a previous evolution step consists of rational models, based upon a subset of the samples in σ. Some models can be overdetermined, such that they minimize the Euclidean norm of the residual vector instead of interpolating the samples.

Sufficient models should be built at each evolution step, such that the number of new interpolants exceeds, or at least equals the number of chromosomes of the previous evolution step. This constraint avoids that the population gets stuck in a suboptimal solution.

3.2 Assignment of fitness values The joint set of models consists of 'old' chromosomes, that were the fittest in previous evolution steps and 'new' chromosomes that are based on all the samples in σ. Each chromosome is compared to all other models, and an inverse fitness value (IFV) is assigned to it. Models that deviate a lot from the 'average' behaviour are assumed to be less fit, as compared to all models that are relatively close to each other over the frequency range of interest. To formalize this, some new definitions are introduced.

The difference between 2 chromosomes H^k and H^l at complex frequency s_i is defined as the Euclidean distance in the complex plane :

$$d^{(H^k,H^l)}(s_i) = |H^k(s_i) - H^l(s_i)| \tag{2}$$

For each chromosome H^k at complex frequency s_i, the distance to all the other models is summed and represented by :

$$\Psi_k(s_i) = \sum_{\forall l, k \neq l} d^{(H^k,H^l)}(s_i) \tag{3}$$

This concept is visualised in Figure 3, where the phase variation of the data is assumed to be zero, for ease of representation.

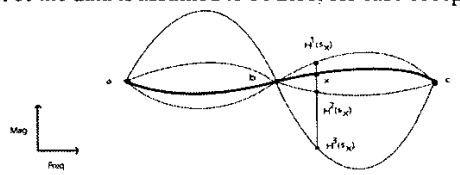

Figure 3 : Illustration of the distance at frequency s_x, for a theoretical example with zero-phase variation.

In Figure 3, the chromosome H^3 is the rational model that deviates the most from the group behaviour of the 2 other chromosomes at frequency s_x. In this case, calculating Ψ for all 3 interpolants gives following results :

$$\begin{aligned} \Psi_1(s_x) &= |H^1(s_x) - H^2(s_x)| + |H^1(s_x) - H^3(s_x)| \\ \Psi_2(s_x) &= |H^2(s_x) - H^1(s_x)| + |H^2(s_x) - H^3(s_x)| \\ \Psi_3(s_x) &= |H^3(s_x) - H^1(s_x)| + |H^3(s_x) - H^2(s_x)| \end{aligned} \tag{4}$$

At frequency s_x, it shows that $\Psi_2(s_x) < \Psi_1(s_x) < \Psi_3(s_x)$

The Inverse Fitness Value (IFV) is a measure for the deviation of a chromosome, say H^k, compared to the 'average' group behaviour. It is defined as follows :

$$IFV_k = \frac{\max(\Psi_k)}{N_c} \tag{5}$$

IFV_k is obtained by dividing the maximum of Ψ_k by the number of interpolants under consideration (N_c). This value represents the maximum average distance between chromosome k and the others. A low (high) IFV implies a high (low) fitness value of the chromosome or interpolant. So the goal is to minimize this value over all models.

Furthermore, this value provides a reliable estimate to detect convergence of the algorithm.

3.3 Selection - Population Only the fittest chromosomes (with the lowest IFV) are selected to fill population P_t at evolution step t, since they are likely to form the best approximation of the original data. The other models are dismissed, and the fitness value of all chromosomes in the population is recalculated, according to (3) and (5).

3.4 Convergence Convergence of the GA-based modeling algorithm is detected if the IFV value of all chromosomes H^k in population P_t is below a certain threshold ε.

$$IFV_k < \varepsilon \tag{6}$$

The population P_t consists of 3 types of chromosomes. Each of them is important for guaranteeing overall convergence :

- Chromosomes built on all samples in σ, and obtained from a system of equations that satisfies all interpolation conditions

- Chromosomes built on all samples in σ, and obtained from an overdetermined system of equations
- The fittest chromosomes of a previous generation, built on a subset of the samples in σ

If the criterium (6) is satisfied, the maximum average distance between the chromosomes is below the desired threshold, so it is assumed that all chromosomes lie within a so-called "ε-environment" of the unknown spectral reponse. In this case, the algorithm terminates and returns the best model. Otherwise, an additional sample is selected, and the algorithm goes on.

The second and third type of chromosomes in the population are particularly useful to detect oversampling. If the system is overdetermined, and the algorithm selects too many samples, all interpolation conditions are likely to be satisfied since the additional samples are already approximated quite well by the interpolant. Similarly, models based on a subset of those samples will also give a good approximation. An illustrative example is shown in Figure 4.

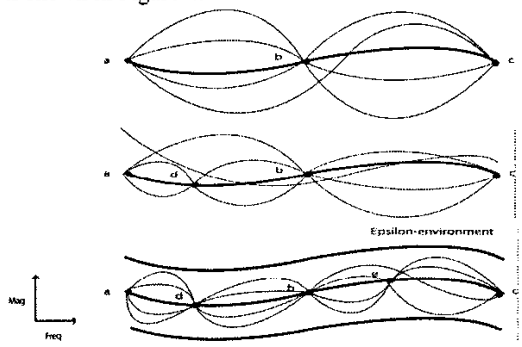

Figure 4 : The populations of three successive evolution steps converge after selecting 5 samples. The size of the populations is set to 4. (Zero-phase variation is assumed).

3.5 Sample selection For MIMO systems, all models share a common set of support samples. The rational models of the matrix element that exceed threshold ε (6) the most, will be used to select a new data sample.

In [4], new samples are selected at the frequency s_i where the models in the population P_t, differ the most :

$$\max\left(\sum_{\forall k,l,k<l} d^{(H^k,H^l)}(s_i)\right) \qquad (7)$$

If the population size is small, the new sample is selected at a good frequency location where the chromosomes differ the most. However, for highly dynamic systems, a small population doesn't provide sufficient information to detect convergence in a reliable way. On the other hand, increasing the size of the population compromises the optimality of the data samples. Moreover, with the adjustments made in this paper, the models in the population are no longer suited for sample selection since some of them are based on an overdetermined set of equations.

A more efficient solution, by combining the strengths of the sample selection techniques introduced in [1] and [4], is to consider two different sets of interpolants. The first set is the population P_t, which is used to detect convergence. The second set $\tilde{P}_t$ has a fixed size, and consists of the 3 most accurate models, based on all support samples in σ, as generated in section (3.1). This set will be used to select a new sample based upon formula (7). It is shown in [1], that the difference between the most accurate models forms a good alternative to select quasi-optimal samples, and the advantage will be illustrated with an example later on. This way, the convergence detection mechanism (based on the population P_t) is entirely independent of the sample selection (based on the set $\tilde{P}_t$).

Figure 5 demonstrates the selection of samples, for 3 successive evolution steps. The flow of the algorithm is illustrated in Figure 6.

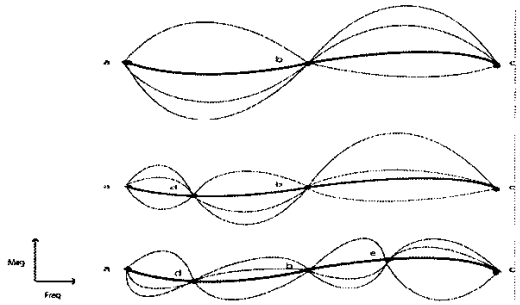

Figure 5 : Samples are selected where the most accurate models, based on all support samples in σ, differ the most.

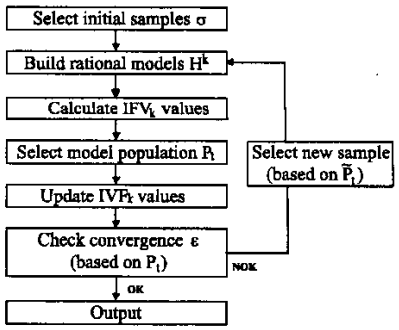

Figure 6 : Flowchart of the sampling and modeling algorithm

4. Example : Mismatched Transmission Line

The full scattering matrix of a 2-port mismatched transmission line is modeled over the frequency range [1 GHz - 51 GHz]. All data samples are simulated with the planar full-wave electro-magnetic simulator Agilent EEsof Momentum. The microwave structure is symmetric, so only S_{11} and S_{12} of the MIMO system need to be modeled.

The desired model accuracy of the S-parameters is -60dB or better, which corresponds to a maximal error on the magnitude of 0.001. The parameters of the GA-based modeling algorithm are chosen to be ε=0.0005 and population size 5. Note that ε is of the same order, but somewhat lower than the desired accuracy.

Decreasing ε improves the model accuracy (as all interpolants are required to lie within a smaller ε-environment),

while increasing the population size improves the model reliability (as more interpolants are required to lie with the ε-environment).

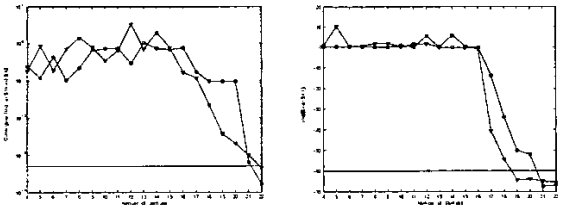

Figure 7 : Convergence function of the S_{11} ($\circ$) and S_{12} (∇) at left, and magnitude of the maximal absolute error between the best interpolants, and the response of S_{11} ($\circ$) and S_{12} (∇) respectively at right.

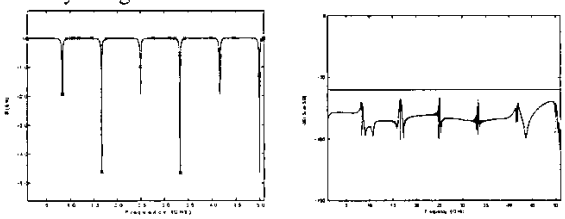

Figure 8 : Magnitude of S_{11} : selected samples ($\times$) and interpolated data (line) at left. Magnitude of abs. error between S_{11} and best interpolant at right.

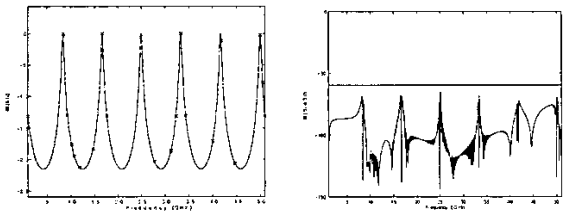

Figure 9 : Magnitude of S_{12} : selected samples ($\times$) and interpolated data (line) at left. Magnitude of abs. error between S_{12} and best interpolant at right.

Figure 7a shows that the modeling algorithm is converged after selecting 22 computational expensive data samples. Figure 7b shows that at least 21 samples are required to get the absolute error of both elements below the desired threshold of -60dB. Figure 8a and Figure 9a show the magnitude of S_{11} and S_{12} respectively, while Figure 8b and Figure 9b confirm that the desired accuracy is reached, since the difference between the rational model data and very densely sampled verification data (1000 samples) is below -60 dB.

5. Example : Influence of the population size

The influence of the population size on the reliability of the convergence function is demonstrated on a different (29-pole) example in Figure 10a. If the population size is set too small (3 or 4), the algorithm converges prematurely with 18 samples, since the accuracy of the final model is -37.2467dB. If the population size is increased to 5 or 6, the method becomes more reliable, and terminates with 31 samples. Note that if a higher population size is chosen, the algorithm does not necessarily require more samples. A clear resemblance can be seen between the 'real' error, shown in Figure 10b and the convergence function, shown in Figure 10a.

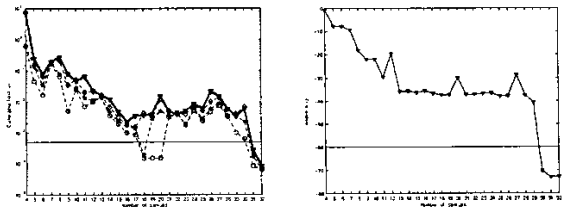

Figure 10 : Convergence function of a 29-pole example at left. Population size equals 3 ($\circ$), 4($*$), 5($\diamond$) and 6(∇). Magnitude of the maximum abs. error between the best interpolant and the spectral response at right.

6. Conclusions

A robust adaptive modeling technique, based on the "survival-of-the-fittest" principle of a genetic algorithm, is described that generates accurate and stable broadband pole-residue models for the entire system matrix. The algorithm adaptively selects a minimal set of support samples and converges without any prior knowledge of the system's dynamics. Some refinements of the algorithm make the convergence function more reliable, especially if the system is highly dynamic. The algorithm avoids oversampling and undersampling, as well as overmodeling and undermodeling, and guarantees numerical stable results.

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