Poor Man's TBR: A Simple Model Reduction Scheme

Joel Phillips Cadence Berkeley Laboratories Cadence Design Systems San Jose, CA 95134, U.S.A. jrp@cadence.com

L. Miguel Silveira INESC ID/IST, Cadence Laboratories Technical University of Lisbon Lisbon, Portugal

ABSTRACT

This paper presents a model reduction algorithm motivated by a connection between frequency domain projection methods and approximation of truncated balanced realizations. The method produces guaranteed passive models, has near-optimal error properties, is computationally simple to implement, contains error estimators, and can incorporate frequency weighting information in a straightforward manner. Examples are shown to prove that the method can outperform the standard order reduction techniques by providing similar accuracy with lower models or superior accuracy for the same size model.

1. INTRODUCTION

Model reduction algorithms are now standard techniques in the integrated circuits community for analysis, approximation, and simulation of models arising from interconnect and electromagnetic structure analysis. Krylov subspace projection methods such as PVL [1] and PRIMA [2] have been the most widely studied over the past decade. They are very appealing due mostly to their simplicity and their overall strong performance in terms of efficiency and accuracy.

However, Krylov projection methods are known to have two drawbacks in practical application. First, there is no general agreement on how to control error in these methods. Error estimators do exist for some methods [3] but they are seldom used in practice. The drawbacks of these estimators are that they require additional computation, which can be expensive and awkward to implement, and produce error estimates only at single frequency points, which leaves open the problem of error estimation over a range of frequencies. Second, moment based methods such as PRIMA are known in some cases to produce models that are "too high" in order with the obvious consequences in terms of analysis or simulation cost [4, 5, 6]. Multipoint rational approximations produce more compact models than moment matching, but error theory is even less well developed [7].

An alternate class of model reduction schemes are the truncated balanced realization (TBR) family [8]. These are purported to produce "nearly optimal" models and have easy to compute a-posteriori error bounds. As the TBR methods are too expensive to directly apply to integrated circuit problems, various two-stage and iterative Krylov methods have been proposed [5, 9, 10, 11, 12, 17] that combine Krylov subspace projection and TBR. While these hybrid techniques do a fairly good job of addressing the excessive order issue, the error bound properties are weakened. Sec-

ond, they are awkward in treating non-symmetric, particularly very unbalanced systems, when two separate projection subspaces must be combined. Third, the methods are perceived as being complicated to implement, and so have not been widely used in practice. Implementation of the TBR techniques requires considerable machinery from control theory and multiple numerical procedures that are tricky to implement in a stable way: solution of Lyapunov equations, balancing transformations and/or eigendecompositions of matrix products.

The main contribution of this paper is to illustrate a direct connection between two existing algorithms: multipoint rational approximation techniques and TBR. As a side benefit, this connection motivates a new algorithm, PMTBR, whose major attraction is its simplicity. It possesses some of the advantages of both techniques: the straightforward implementation of the projection methods and the excellent compaction properties of TBR. In fact, the techniques presented here turn out to perform better than TBR in many cases, as it turns out that the "near-optimal" approximation properties of TBR are only "near-optimal" for classes of problems never encountered in practical circuit analysis. A side benefit is to provide further theoretical basis for the empirically observed excellent performance of multipoint projection. PMTBR also appears to have promising properties with respect to order control and error estimation, which, while not as powerful as TBR's error control, appears to be an advance over multipoint projection.

2. MODEL REDUCTION BACKGROUND

2.1 **Projection Framework**

Many modern interconnect modeling technologies rely heavily on projection-based model reduction algorithms. For simplicity of exposition, consider for the moment the restricted case linear system models

$$\frac{dx}{dt} = Ax + Bu, \quad y = Cx \tag{1}$$

with input *u* and output *y*, that are described by the matrices $A \in \mathbb{R}^{n \times n}$, $B \in \mathbb{R}^{n \times p}$, $C \in \mathbb{R}^{p \times n}$. These algorithms take as input a linear system of the form (1) and produce a reduced model

$$\frac{dz}{dt} = \hat{A}z + \hat{B}u, \quad y = \hat{C}z \tag{2}$$

where $\hat{A} \in \mathbb{R}^{q \times q}, B \in \mathbb{R}^{q \times p}, C \in \mathbb{R}^{p \times q}$. This is achieved by constructing matrices *W* and *V* whose columns span a "useful" subspace, and projecting the original equations in the column spaces of *W* and *V* as

$$\hat{A} \equiv W^T A V \quad \hat{B} \equiv W^T B \quad \hat{C} \equiv C V.$$
(3)

Most common choices are based on picking the columns of W, V to span a Krylov subspace [1, 2]. Different choices will lead to

different algorithms with slightly different properties but an overall similar "flavour".

2.2 Truncated Balanced Realizations (TBR)

Model reduction via balanced truncation is based on analysis of the controllability and observability Gramians X, Y respectively. The Gramians are usually computed from the Lyapunov equations

$$AX + XA^T = -BB^T, (4)$$

$$A^T Y + Y A = -C^T C. ag{5}$$

Reduction is performed by projection onto the invariant subspaces associated with the dominant eigenvalues of the product of Gramians *XY* [8, 13]. For example, the approach of [13] corresponds to the projection procedure above with *W*,*V* the orthonormal bases arising from the Schur decomposition. One of the important features of TBR is an absolute bound on the error of approximation. If we let σ_k denote the square root of the *k*th largest eigenvalue of *XY* (*XY* always has real eigenvalues) then the error in the transfer function of the order *k* TBR approximation is bounded by $2\sum_{i=k+1}^{N} \sigma_k$ [14].

2.3 Multipoint rational approximation

A more sophisticated approach is to construct the projection matrix V from a rational, or multipoint, Krylov subspace [7, 15, 9]. For a given model order the multipoint approximants tend to be more accurate, but are usually more expensive to construct. Given M complex frequency points s_k , a projection matrix may be constructed whose kth column is

$$z_k = (s_k I - A)^{-1} B. (6)$$

This leads to multipoint rational approximation. Multipoint projection is known to be an efficient reduction algorithm in that the number of columns, which determines the final model size, is usually small for a given allowable approximation error, at least compared to pure moment matching approaches. Of course there are many practical questions to ponder in an actual implementation: how many points s_k should be used, and how should the s_k be chosen? How is error determined? How is linear independence of the columns of V enforced?

Consider enforcing linear independence. An obvious strategy is to perform an SVD on the vectors z_k computed as above. The main point of this paper is that constructing projection matrices by multipoint frequency sampling, as in (6), followed by an SVD, in fact converges to the TBR algorithm. The singular values obtained from such a procedure approximate the Hankel singular values, and can thus be used for order and error control.

3. APPROXIMATION IN FREQUENCY DO-MAIN

3.1 Controllability Analysis

For simplicity consider the case $A = A^T$, $C = B^T$ and further assume that A is stable. This case is of more than theoretical interest as it occurs in RC circuit analysis, and the standard TBR algorithm is known to produce passive approximants [12]. It it is easy to see that in this symmetrized case, both Gramians are equal and in the standard TBR procedure are obtained by solving the Lyapunov equation

$$AX + XA^T = BB^T. (7)$$

The more fundamental definition of the Gramian X is obtained from the state evolution operator, also called the fundamental solution, of

the differential equation dx/dt = Ax + Bu. The Gramian can also be computed in the time domain as

$$X = \int_0^\infty e^{At} B B^T e^{A^T t} dt.$$
(8)

However, noting that the Laplace transform of e^{At} is $(sI - A)^{-1}$, it follows immediately from Parseval's theorem that the Gramian *X* can also be computed from the expression

$$X = \int_{-\infty}^{\infty} (j\omega I - A)^{-1} B B^{T} (j\omega I - A)^{-H} d\omega.$$
(9)

where superscript *H* denotes Hermitian transpose. Consider evaluating *X* via applying numerical quadrature to (9). Given a quadrature scheme with notes ω_k and weights w_k , and defining

$$z_k = (j\omega_k I - A)^{-1} B, \qquad (10)$$

an approximation \hat{X} to X can be computed as

$$\hat{X} = \sum_{k} w_k z_k z_k^H.$$
(11)

Let *Z* be a matrix whose columns are z_k , and *W* a diagonal matrix with diagonal entries $W_{kk} = \sqrt{w_k}$. Eqn (11) can be written more compactly as

$$\hat{X} = ZW^2 Z^H. \tag{12}$$

3.2 Model Reduction

To derive a model reduction procedure consider the eigendecomposition

$$X = V_L \Sigma V_L^T. \tag{13}$$

Note that $V_L^T V_L = I$ since X is real symmetric in this special case. An obvious candidate for reduction would be to pick a projection matrix formed from the columns of V corresponding to the dominant eigenvalues of X. If the quadrature rule is accurate, \hat{X} will converge to X, which by perturbation analysis of invariant subspaces [16] implies the dominant eigenspace of \hat{X} converges to the dominant eigenspace of X. Now consider the singular value decomposition of ZW.

$$ZW = V_Z S_Z U_Z \tag{14}$$

with S_Z real diagonal, V_Z and U_Z unitary matrices. Clearly

$$\hat{X} = V_Z S_Z^2 V_Z^T \tag{15}$$

so in fact the dominant singular vectors in V_Z , as can be identified from the singular values in S_Z , give the eigenvectors of \hat{X} . Therefore V_Z converges to the eigenspaces of X, and the Hankel singular values are obtained directly from the entries of S_Z . V_Z can then be used as the projection matriz in a model order reduction scheme.

It seems likely that the singular values of the matrix Z would have something to do with approximation error. The above illustrates that the correspondence is in fact precise – the SVD of Z reveals the same information revealed by TBR (modulo the weights W).

An obvious question is: how fast does the proposed scheme converge, in particular, how fast do the dominant singular vectors of ZW approach the dominant eigenvectors of X? As we will demonstrate, it turns out that very good models can be obtained with a fairly small number of sample points, in agreement with previous experience with multipoint approximation. For this reason, we denote our method "Poor Man's" TBR (PMTBR), since the quantities computed are cheap approximations to full TBR.

Surprisingly, as we shall shortly demonstrate, in many *practical* applications, PMTBR performs *better* than TBR in the sense of

giving more accurate models for a given model size or amount of effort. This unexpected bonus demonstrates the virtues and rewards of frugality.

4. PRACTICAL IMPLEMENTATION

4.1 Descriptor Systems

Usually in circuit analysis is it inconvenient, and possibly prohibitively expensive, to translate to the form in Eq. (1). In the more general case, with the state-evolution equation given by Edx/dt = Ax + Bu, the controllability Grammian can be obtained from

$$AXE^T + EXA^T + BB^T = 0. (16)$$

Not surprisingly, the frequency domain equation is

$$X = \int (j\omega E - A)^{-1} B B^{T} (j\omega E - A)^{-H} d\omega$$
 (17)

and the above procedure follows exactly with the change that the columns of Z are given by

$$z_k = (s_k E - A)^{-1} B. (18)$$

Formally, to removing the system symmetry restrictions on *A* and *C* we would need to compute vectors $y_k = (s_k E^T - A^T)^{-1}C^T$, but in most IC problems using an orthogonal projector computed from the z_k and congruence transforms for reduction is an effective scheme. Such an approach has the additional advantage of guaranteeing the passivity of the reduced order model.

4.2 Finite Bandwidths and Frequency Weighting

Consider evaluating Eqn. (17) by breaking the integral into partial sums I_k each of which is an integral over a section S_k of the imaginary axis:

$$X = \sum_{k=1}^{\infty} I_k \tag{19}$$

$$I_k = \int_{S_k} (j\omega E - A)^{-1} B B^T (j\omega E - A)^{-H} w(\omega) d\omega \quad (20)$$

where $\bigcup_{i=1}^{\infty} S_i$ amounts to the whole imaginary axis.

Each I_k gives the contribution to X from the system's behavior over the interval S_k . X is the Gramian of the operator that maps input to state; its singular values give the norm of that operator. This suggests interpreting I_k as the contribution from the input u over the frequency interval S_k . The standard TBR procedure, having no a-priori knowledge of the frequency content of the input, weights each frequency equally. However, in almost all practical problems we have some knowledge of the actual frequency distribution of the inputs. Often, the inputs are bandlimited, or nearly so, or we might be interested only in the behavior of the system around some finite frequency interval. We propose truncating the sum in Eqn. (19) to finite intervals, and using the resulting "finite-bandwidth" Gramian for model reduction. Since the resulting Gramian places more emphasis on frequencies of relevance, we expect to achieve better performance, for a given model order, on problems with finite bandwidth inputs. More generally, we may define a "frequency-weighted" Gramian as

$$X_{FW} = \int_{-\infty}^{\infty} (j\omega E - A)^{-1} B B^T (j\omega E - A)^{-H} w(\omega) d\omega.$$
(21)

where $w(\omega)$ is the "weighting" function (the notational similarity with quadrature weights is deliberate). The more appropriate the weighting function to our problem at hand, the better we expect the

performance of the reduction algorithm to be. Seen from this viewpoint, TBR is a generic, somewhat naive, algorithm as it presumes complete ignorance of frequency content. The weighting function in "standard" TBR is most appropriate for white noise inputs where nothing is really known about frequency content.

In a practical implementation, with a finite number of frequency samples, weighting can be accomplished by adjusting the weights w_k and/or location of samples ω_k . In fact, every ZW-matrix implicitly defines a frequency weighting scheme. For this reason, it is better to choose points/weights in PMTBR (perhaps adaptively) according to the expected frequency profile of the system and the inputs, than to try to achieve convergence to the TBR Gramians themselves.

While it seems to be widely believed that the TBR methods are more mathematically sound than projection methods, in fact it now appears that the opposite is true: TBR is a naive implementation of more powerful, problem-specific multipoint projection schemes.

This argument also explains the empirically observed fact that multipoint projection can exhibit better relative error performance than generic TBR. Multipoint projection more highly weights points in (21) than the standard TBR weighting, resulting in better relative performance in those areas.

4.3 Error Estimation

The above arguments can be extended to a generalized process of error estimation. The singular values obtained from the weighted Gramians can be intepreted as gains between "filtered" inputs and "weighted" outputs. Singular values from truncated modes can be interpreted as errors on the "filtered" system, i.e. finite-bandwidth or weighted errors. The singular value information can be used in three ways to guide model order control.

First, if enough samples are taken that good estimates of the true Gramians are obtained, then the singular values obviously provide error bounds, through the connection to TBR.

Second, the singular values can guide an adaptive point selection scheme. With reasonable spaced sampling of points, as projection vectors are added to the *ZW*-matrix, convergence of the singular values indicates convergence of the error, which guides when to stop adding vectors to *ZW*.

Third, we have found that, again assuming "reasonable" sampling density, the singular values usually give a fairly good guide to model order well before convergence is achieved. Our experiments indicate that when, for a number of samples in excess (e.g. twice) of the model order, the singular value distribution exhibits a small "tail" (that is, for a "small" ε , $\exists k : \varepsilon > \sum_{i=k+1}^{\infty} \sigma_i$), then sufficient order and point placement has been achieved. Again this is, as one would expect, strikingly similar to the usual TBR concepts.

5. COMPUTATIONAL EXPERIMENTS

5.1 Convergence to TBR

In our first example we consider an RC circuit model of a clock distribution network. This circuit, to a good approximation, is finite bandwidth. We use this example to illustrate the asymptotic equivalence of the TBR and PMTBR methods. Figure 1 illustrates the singular values of the ZW matrix resulting from a moderate number (50) of sample points w_k . It can be seen that the estimated singular values, while not exact, are good approximations, and follow the general trend of the exact solution. It is interesting that the approximate singular values continue to rapidly decrease over nearly fifteen orders of magnitude, even with a relatively low accuracy approximation of the Grammians. PMTBR appears to capture the fact that this RC model is intrinsically low-order. Of course,

adding sample points would increase the accuracy of the singular value approximations, as we will show later.



Figure 1: Hankel singular values as computed from exact Gramians (solid line) and estimated from PMTBR (dashed line).

More critical for model reduction is the estimation of the projection subspaces. Figure 2 shows convergence of one *angle* between projection subspaces. In this case we chose the second principal vector to estimate within the first four leading subspaces of PMTBR. Even for small numbers of sample points, the subspaces are fairly closely aligned, and alignment increases with increasing number of samples. This indicated convergence of PMTBR to TBR for this example. The leveling out of the curve is due to the fact that the model under study has non-zero response outside the finite bandwidth used to compute the PMTBR results. By increasing the bandwidth over which we perform PMTBR we could continue to decrease the subspace angles, but at some point the accuracy obtained thereby ceases to be of interest, because in a real problem negligible signal strength exists outside finite bandwidths.



Figure 2: Angle between second principle vector and PMTBR singular subspaces.

5.2 Comparison to PRIMA



Figure 3: Error of approximations of resistance obtained with PRIMA and PMTBR for increasing order models on the spiral inductor example.



Figure 4: Spiral inductor example, convergence of singular values of *ZW*.

In our next example we use a model for an on-chip spiral inductor to demonstrate how PMTBR can outperform the standard model order reduction method PRIMA. Particularly for the real part of the inductor's impedance (i.e. the resistance), PRIMA converges slowly on this example. Figure 3 shows a comparison of the error in the inductor's resistance for approximations obtained with PRIMA and PMTBR of increasing sizes. From the plot one can see that the PMTBR approximation produces a more accurate approximation at any given order, and converges more quickly. As thirty frequency samples were used to compute the PMTBR model, at each order, more work was also required to compute the approximations for a given order. However, as about sixty PRIMA vectors are required to obtain 1% accuracy in the resistance, the overall work is still less.

Next we demonstrate the order control and error estimation capabilities of PMTBR. Figure 4 shows the convergence of the five largest singular values of \hat{X} as the number of frequency domain sample points (aka quadrature nodes w_k) is increased. In this example we used a very crude uniform sampling/weighting that would correspond to the "rectangle rule"in quadrature. We see that the



Figure 5: Admittance transfer function error and error estimates for the spiral inductor example.

largest five singular values have mostly converged by the time we reach 100 sample points. Figure 5 shows the error vs. order for PMTBR models using 100 sample basis points, as well as the error estimates computed using the singular values. First, we can see that increasing the order of the approximation beyond ten or twelve benefits very little, as the corresponding singular values are certainly below the relevant error and quickly approaching machine precision. Second, we see that, for the orders corresponding to the well-estimated singular values, the error estimates are very good. Estimates for higher orders are not as good, but do indicate correctly that the actual error is small and rapidly approaching zero.

Note that as indicated above for this example a much smaller number of samples was required to achieve excellent error performance on this model. Singular value plots with this sample size (not shown) show that a model of size 5-7 is indeed enough to achieve acceptable accuracy with this number of sample points.

5.3 Comparison to multipoint projection

Of course, an obvious question is, since the PMTBR technique uses the same information as multipoint projection, whether there is any advantage in using PMTBR over multipoint projection. To answer this, we show results from an example introduced in [1], a lumped-element equivalent circuit for a three-dimensional problem modeled via PEEC.

Figure 6 shows a comparison of the errors incurred with approximations of increasing order obtained using a multipoint projection method and PMTBR for this PEEC example. The plots clearly show the superior accuracy of PMTBR for similar size models (equivalently, PMTBR is able to generate more compact size models for the same accuracy). Furthermore it is interesting to note that for high accuracy this difference actually increases, as the error of the projection method goes down very slowly with order increase. This is clearly due to the ability of PMTBR to prune out "redundant" information from the model. Note that in [1] an order 60^{th} approximation computed with PVL was needed to obtain good approximation of the transfer function of the equivalent circuit.

It is interesting to observe that, just as the multipoint projection method did, the PMTBR technique is able to circumvent any difficulties involved with having singular A or G matrices. This is a matter of practical relevance as many systems obtained applying the modified nodal formulation to some discretized model often have singular A and/or E matrices (typically in those cases A would



Figure 6: Comparison of error in multipoint projection method (MPPROJ) and PMTBR for the PEEC example.

be related to the conductance matrix and E to the capacitance matrix). Applying "standard" TBR to such systems involves some complicated preprocessing, see [12] for a discussion. Note also that PMTBR was quite accurate on this example, despite the fact that it contains sharp resonances that cause difficulty for quadrature (compare Figure 1 where the singular value estimates are not exact). PMTBR does not produce the exact same singular value estimates as TBR, as it weights the contributions to the projection subspaces differently, the subspaces produced contain the system information relevant to the point selection chosen.

5.4 Finite Bandwidth

A final question to resolve is whether there is any advantage to PMTBR compared to a standard projection technique followed by standard TBR. We show results from an 18 pin shielded connector structure that was previously used to illustrate a PEEC formulation based on PRIMA that generates passive reduced-order models [6]. While the resulting model was indeed provably passive, disappointing reductions were reported, which were attributed to limitation in the PRIMA algorithm in dealing with the "relevant modes of the system". In order to address this issue, in [17] the same example was used to illustrate a two-step algorithm for RLC order reductions were reported after the 2^{nd} step of reduction as TBR is able to determine that those modes are not observable nor controllable. Therefore it is a good model system on which to compare PMTBR and TBR.

Figure 7 shows a plot of the exact transfer function of the connector, as well as approximations obtained with TBR and PMTBR. For this particular example we were interested in testing the ability of the PMTBR algorithm to produce approximations on a finite bandwidth. We decided to illustrate approximation over a finite range of zero to 8 GHz. Samples were generated to cover the frequency range from DC to 8*GHZ* and these samples were used to generate an order 18 PMTBR approximation. At the same time, a TBR approximation of order 30 was also generated (we found that 30 was the minimum order required for TBR to provide reasonable representation of *any* features in the 0-8GHz range). From the figure we can see that the PMTBR approximation does indeed show very good accuracy in the frequency range of interest. The figure also shows, rather dramatically, the inability of the TBR approximation to produce an accurate model at the frequency of interest, even with the higher order approximation. Furthermore, the TBR approximation seems to be accurately picking some features of the system but these happen to fall out of the bandwidth of interest. We believe TBR concentrates effort around 15GHz because of the relative amplitude of the transfer function. PMTBR is easily focused on the 8GHz and below range merely by selection of sampling points, and does not waste effort with approximation at higher frequencies.



Figure 7: Transfer function approximations for the connector example. Note PMTBR has better finite-bandwidth performance than TBR.

6. CONCLUSIONS

In this work we discussed a connection between truncated balanced realization (TBR) model reduction methods and multipoint rational approximation/projection techniques. While primarily of theoretical interest, this connection leads to a potentially useful new algorithm, PMTBR. PMTBR was shown to have some advantages over existing algorithms, particularly in generating smaller reduced models, and possibly in order control and error estimation. In retrospect, the connection of TBR and PMTBR is not surprising: both the TBR procedure and the SVD used in PMTBR are principal components analyses. TBR is a principal components analysis of the functionals defined by the state-space model, and naturally arises from time-domain theory of state-space systems. PMTBR arises naturally from a numerical approximation viewpoint of frequency domain data.

Possible extensions of this work include integration of adaptive point selection estimation with error control, and extension of the PMTBR approach to the positive-real TBR [12] algorithms.

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