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DEVELOPMENT AND COMPARATIVE ANALYSIS OF NOVEL COMPONENT MODE SYNTHESIS METHODS FOR STRUCTURAL AND ACOUSTIC APPLICATIONS

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ABSTRACT

This paper introduces two novel Component Mode Synthesis (CMS) techniques. It begins with an overview of existing CMS approaches. A dual assembly method using fixed-interface modes is formulated based on the Craig-Bampton approach and a further condensation of the interface degrees-of-freedom (DOF) as in MacNeal's Method is carried out. Then, a dual assembly method employing free-interface modes is derived by integrating the principles of the Dual Craig-Bampton Method with simplifications from MacNeal's Method. Finally, the proposed methods are evaluated against established techniques through two examples spanning structural and acoustic models. This comparison is conducted in both the modal and frequency domains, providing a detailed analysis of their performance and computational efficiency.

Keywords: *simulation, CMS, FEM, substructuring, acoustics*

1. INTRODUCTION

Advances in computing power now allow for solving very large linear systems with millions of degrees of freedom. However, dynamic analysis often requires solving multiple linear systems, which makes CMS a key method for efficient analysis. CMS divides models into subcomponents, represented by reduced bases, while ensuring compatibility of DOF and equilibrium of interface forces.

Dividing models into components has several benefits. It improves the sharing of models among design teams, reduces the computational cost by lowering the DOF of substructures, and enables contribution analysis in dynamic studies. This last benefit supports the efficient application of Numerical Transfer Path Analysis.

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2. COMPONENT MODE SYNTHESIS

The concepts presented in this section are a summary of the most studied methods in CMS, and its review is based on the work of Gruber and Rixen [1], De Klerk [2] and Allen, Rixen et al [3]. The last subsections are dedicated to two new novel CMS methods.

2.1 Primal and dual assemblies

This subsection is a summary of the work presented by Gruber and Rixen [1]. Let us consider a finite element model of a global domain that is partitioned into N non-overlapping substructures. In this division, each node belongs to exactly one substructure, except for the nodes located on the interface boundaries. The linear or linearized equation of motion for an individual substructure that contains no damping can be expressed as:

$$M^{(s)}\ddot{u}^{(s)} + K^{(s)}u^{(s)} = f^{(s)} + g^{(s)} \tag{1}$$

Where the superscript (s) refers to a particular substructure. $M^{(s)}$, $K^{(s)}$, and $u^{(s)}$ are the mass matrix, stiffness matrix, and the displacement vector of the substructure,

respectively. The external force vector $f^{(s)}$ and the interface force vector $g^{(s)}$, resulting from the interaction between adjacent substructures, are the excitation loads of the equation of motion. By assembling the model, the equations of motion of the N substructures can be rewritten in a block-diagonal format as:

$$M\ddot{u} + Ku = f + g \tag{2}$$

The assembly of all the N subdomains can be performed establishing two conditions: compatibility of DOF and equilibrium of interface forces. The compatibility condition can be expressed using the constraint matrix B that enforces equal DOF at adjacent interfaces. For that, it selects the interface DOF corresponding to each subdomain.

$$Bu = 0 \tag{3}$$

The equilibrium condition is expressed using the localization matrix L. This localization matrix separates the internal terms of each of the subdomains from the interface DOF.

$$L^T g = 0 \tag{4}$$

The localization matrix L can be built using a matrix that selects only the internal nodes of each substructure and the interface constraint matrix using the following relation:

$$L = \begin{bmatrix} B_{ii}^T & B_{bb}^T A_{bb}^T \end{bmatrix} = \begin{bmatrix} B_{ii}^T & B_{eq}^T \end{bmatrix} \tag{5}$$

With B_{ii} and B_{bb} matrices that select internal and interface nodes of every substructure, A_{bb} a matrix that imposes the compatibility condition from the interface set, and B_{eq} the matrix that establishes the compatibility condition from the global set.

2.1.1 *Primal Assembly*

The displacements of N substructures can be divided in internal DOF u_i and interface DOF u_b using the previously defined localization matrix (5).

$$u = L \begin{bmatrix} u_i \\ u_b \end{bmatrix} \tag{6}$$

With u_b a unique set of interface DOF. Equation (6) implicitly establishes the compatibility condition, since it enforces a unique set of interface DOF from the entire assembly. Thus, the compatibility condition (3) results:

$$Bu = BL \begin{bmatrix} u_i \\ u_b \end{bmatrix} = 0 \quad \forall \begin{bmatrix} u_i \\ u_b \end{bmatrix} \neq 0 \tag{7}$$

Resulting in L as the nullspace of B. Substitution of equation (6) into equation (2), and by multiplying L^T on the left in equation (2), the system of equations is transformed into primal assembly, for which the equilibrium condition is inherently satisfied:

$$M_a \begin{bmatrix} \ddot{u}_i \\ \ddot{u}_b \end{bmatrix} + K_a \begin{bmatrix} u_i \\ u_b \end{bmatrix} = f_a \tag{8}$$

with the subindex a indicating that it is projected onto the primal subspace.

2.1.2 *Dual Assembly*

Interface compatibility can be enforced using interface forces as unknowns. In this case, the interface forces are represented by their force intensities, also known as Lagrange multipliers λ:

$$g = -B^T \lambda \tag{9}$$

And this condition automatically satisfies the equilibrium condition, since L is the nullspace of B (7). The equation of motion (2) and the compatibility condition (3) can be rewritten in the following assembled system of equations, integrating the definition of the interface forces by Lagrange Multipliers, the dual assembly equation of motion is established:

$$\begin{bmatrix} M & 0 \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \ddot{u} \\ \ddot{\lambda} \end{bmatrix} + \begin{bmatrix} K & B^T \\ B & 0 \end{bmatrix} \begin{bmatrix} u \\ \lambda \end{bmatrix} = \begin{bmatrix} f \\ 0 \end{bmatrix} \tag{10}$$

This system of equations, once solved, allows us to obtain the interface forces between subcomponents, together with the displacement DOF of the system. No division of internal and interface DOF is required.

2.2 Fixed-Interface methods

Fixed-interface methods refer to CMS procedures that use modes of the internal degrees of freedom and constraint modes at the interfaces. These attempt to reduce the description of the internal domain, while keeping a non-reduced description of the interface behavior.

2.2.1 *Craig-Bampton Method (CBM)*

The CBM [4] is the most popular CMS procedure. It is a fixed-interface method in a primally assembled fashion. The primal assembled system of equations (8) can be expressed in terms of internal and interface components of the assembly matrices:

$$\begin{bmatrix} M_{ii} & M_{ib} \\ M_{bi} & M_{bb} \end{bmatrix} \begin{bmatrix} \ddot{u}_i \\ \ddot{u}_b \end{bmatrix} + \begin{bmatrix} K_{ii} & K_{ib} \\ K_{bi} & K_{bb} \end{bmatrix} \begin{bmatrix} u_i \\ u_b \end{bmatrix} = \begin{bmatrix} f_i \\ f_b \end{bmatrix} \tag{11}$$

with the subindices *i, b* corresponding to internal and interface terms of the matrices and vectors. Considering only the first equation line, the internal DOF can be seen excited by the interface DOF:

$$M_{ii}\ddot{u}_i + K_{ii}u_i = f_i - M_{ib}\ddot{u}_b - K_{ib}u_b \tag{12}$$

An approximation of u_i can be achieved using the internal modes of each substructure and a static correction.

$$u_i \simeq \Phi_i u_{m,i} + u_{i,\text{stat}} \tag{13}$$

With Φ_i a diagonal block matrix containing a truncated set of internal modes of each substructure and $u_{m,i}$ the corresponding modal participation factors. The static correction can be obtained from (12), when only u_b excites the system in a static condition:

$$u_{i,\text{stat}} = -K_{ii}^{-1}K_{ib}u_b = \Psi_{ib}u_b \tag{14}$$

With the term Ψ_{ib} referring to the interface constraint modes. Since K_{ii} corresponds to the stiffness matrix of the internal DOF, meaning that the interface DOF have been fixed, the resulting matrix is invertible. The CBM transformation is thus performed using internal and interface constraint modes:

$$\begin{bmatrix} u_i \\ u_b \end{bmatrix} \simeq \begin{bmatrix} \Phi_i & \Psi_{ib} \\ 0 & I \end{bmatrix} \begin{bmatrix} u_{m,i} \\ u_b \end{bmatrix} = T_{CB} \begin{bmatrix} u_{m,i} \\ u_b \end{bmatrix} \tag{15}$$

Inserting transformation (15) into the equation of motion in primal assembly representation (8), and multiplying the system by T_{CB}^T on the left, we obtain the CBM reduced equation of motion:

$$M_{CB} \begin{bmatrix} \ddot{u}_{m,i} \\ \ddot{u}_b \end{bmatrix} + K_{CB} \begin{bmatrix} u_{m,i} \\ u_b \end{bmatrix} = f_{CB} \tag{16}$$

The reduced CBM matrices condense the information of the primal assembly mass and stiffness matrices, while keeping the interface DOF in physical domain, thus, preserving an accurate description of the interaction between subcomponents.

2.3 Free-Interface methods

Free-interface CMS methods refer to procedures that assemble subdomains using free-interface modes. Since the reduced matrices generally have a lack of information at the adjacent interfaces because of dropping high-order modes, flexibility attachment modes are used to improve the coupling.

Recall the equation of motion of the entire assembly (2) . If now, the degrees of freedom are approximated by a truncated set of eigenmodes Φ of each component, leveraged by the modal participation factors u_m and the superposition of local static solutions u_{stat}, the DOF of the entire domain can be expressed as:

$$u \simeq \Phi u_m + u_{\text{stat}} \tag{17}$$

And the static solution can be obtained by solving the system in static conditions, only using the interface forces as loads:

$$u_{\text{stat}} = K^{-1}g = K^{-1}B_{bb}^T g_b \tag{18}$$

with g_b the interface components of the interface force vector g. The matrix K^{-1} is a block matrix containing the inverses of the components' stiffness matrices. If K is singular, because there are not enough boundary conditions to prevent its rigid body motion, then K^{-1} is obtained by a procedure that constrains K to be invertible and suppresses the rigid body modes [5]. Since a portion of the subspace defined by Φ is already incorporated in K^{-1}, the residual flexibility matrix G_r can be used instead:

$$G_r = K^{-1} - \Phi\Omega^{-2}\Phi^T \tag{19}$$

With Ω^{-2} being the block diagonal matrix containing the reciprocal first eigenvalues of K. The approximation of the N substructures results:

$$u \simeq \begin{bmatrix} \Phi & G_r B_{bb}^T \end{bmatrix} \begin{bmatrix} u_m \\ g_b \end{bmatrix} = T_1 \begin{bmatrix} u_m \\ g_b \end{bmatrix} \tag{20}$$

Inserting the transformation into the equation of motion (2), and multiplying by T_1^T on the left, we obtain the free-interface system:

$$M_{\text{free}} \begin{bmatrix} \ddot{u}_m \\ \ddot{g}_b \end{bmatrix} + K_{\text{free}} \begin{bmatrix} u_m \\ g_b \end{bmatrix} = f_{\text{free}} + g_{\text{free}} \tag{21}$$

This equation is not fully assembled, since neither the compatibility nor the equilibrium conditions are yet established. The free interface matrices are built by the following terms:

$$M_{\text{free}} = \begin{bmatrix} I & 0 \\ 0 & M_{r,bb} \end{bmatrix}, \quad K_{\text{free}} = \begin{bmatrix} \Omega^2 & 0 \\ 0 & G_{r,bb} \end{bmatrix} \tag{22}$$

with I the identity matrix and the rest terms as:

$$M_{r,bb} = B_{bb}G_r M G_r B_{bb}^T, \quad G_{r,bb} = B_{bb}G_r B_{bb}^T \tag{23}$$

2.3.1 Rubin's Method (RM)

The RM [6] assembles the free-interface reduced equation of motion (21) in a primal approach, enforcing a strong compatibility condition. For that, the force DOF g_b are transformed back to the interface displacements u_b. Take equation (20) and multiply it by B_{bb} on the left:

$$u_{b,0} = B_{bb}u \simeq \Phi_b u_m + G_{r,bb}g_b \tag{24}$$

The sub-index 0 in $u_{b,0}$ denotes that the interface DOF are not assembled. The force g_b and the modal DOF u_m can then be expressed in terms of u_m and $u_{b,0}$:

$$\begin{bmatrix} u_m \\ g_b \end{bmatrix} \simeq \begin{bmatrix} I & 0 \\ -K_{r,bb}\Phi_b & K_{r,bb} \end{bmatrix} \begin{bmatrix} u_m \\ u_{b,0} \end{bmatrix} = T_2 \begin{bmatrix} u_m \\ u_{b,0} \end{bmatrix} \tag{25}$$

With $K_{r,bb}$ the inverse of $G_{r,bb}$. To impose compatibility of displacements, $u_{b,0}$ can be expressed by the common interface DOF u_b. This expression imposes the compatibility condition:

$$\begin{bmatrix} u_m \\ u_{b,0} \end{bmatrix} \simeq \begin{bmatrix} I & 0 \\ 0 & A_{bb}^T \end{bmatrix} \begin{bmatrix} u_m \\ u_b \end{bmatrix} = T_3 \begin{bmatrix} u_m \\ u_b \end{bmatrix} \tag{26}$$

with A_{bb} a matrix that enforces compatibility, as defined in equation (5). Finally, the DOF of the free-interface equation of motion (21) can be assembled using the previous transformations:

$$u \simeq T_1 \begin{bmatrix} u_m \\ g_b \end{bmatrix} = T_1T_2T_3 \begin{bmatrix} u_m \\ u_b \end{bmatrix} = T_{RM} \begin{bmatrix} u_m \\ u_b \end{bmatrix} \tag{27}$$

The equation of motion (2) can be thus transformed using T_{RM} that performs the Rubin reduction with primally assembled interface DOF:

$$M_{RM} \begin{bmatrix} \ddot{u}_m \\ \ddot{u}_b \end{bmatrix} + K_{RM} \begin{bmatrix} u_m \\ u_b \end{bmatrix} = f_{RM} \tag{28}$$

2.3.2 MacNeal's Method (MNM)

The MNM [7] is identically derived as the RM, using the exact same ingredients: free-interface modes assembled using primal assembly. The only difference is that the residual mass term $M_{r,bb}$ is neglected in (20), resulting in a simplified mass matrix. This assumes that the interface DOF u_b have no associated inertia in the equation of motion. The modified Rubin mass and stiffness matrices are:

$$M_{RM}^* = \begin{bmatrix} M_{RM,mm} & 0 \\ 0 & 0 \end{bmatrix}, \quad K_{RM}^* = K_{RM} \tag{29}$$

The second line of the equation of motion (28) can be rearranged, so the interface DOF u_b can be expressed in terms of u_m. The resultant transformation is:

$$u \simeq T_{RM} \begin{bmatrix} I \\ -K_{RM,bb}^{-1}K_{RM,bm} \end{bmatrix} u_m = T_{MNM}u_m \tag{30}$$

With sub-indices *m* and *b* corresponding to the modal and interface terms of the Rubin reduced matrices. The equation of motion (2) can thus be transformed using T_{MNM} that performs the MacNeal's reduction:

$$M_{MN}\ddot{u}_m + K_{MN}u_m = f_{MN} \tag{31}$$

2.3.3 Dual Craig-Bampton Method (DCBM)

The Dual Craig Bampton method [8] is a dual assembly method that uses free-interface modes and attachment modes. Recall the approximation of the displacement DOF by using free-interface component modes (21) and the definition of the interface forces by using Lagrange Multipliers (9). The DOF of the dual assembly can be approximated as:

$$\begin{bmatrix} u \\ \lambda \end{bmatrix} \simeq \begin{bmatrix} \Phi & -G_rB^T \\ 0 & I \end{bmatrix} \begin{bmatrix} u_m \\ \lambda \end{bmatrix} = T_{DCB} \begin{bmatrix} u_m \\ \lambda \end{bmatrix} \tag{32}$$

Inserting this transformation into the equation of motion of the dual assembly in the physical domain (10), and multiplying it on the left by T_{DCB}^T, we obtain the DCBM matrices:

$$M_{DCB} \begin{bmatrix} \ddot{u}_m \\ \ddot{\lambda} \end{bmatrix} + K_{DCB} \begin{bmatrix} u_m \\ \lambda \end{bmatrix} = f_{DCB} \tag{33}$$

This method relaxes the compatibility condition, setting a strong equilibrium condition. This is exactly the opposite as in the Rubin Method.

3. NOVEL METHODS

3.1 Condensed Craig-Bampton Method

The Condensed Craig-Bampton Method (CCBM) is a simplified version of the CBM that condenses the interface DOF u_b in the equation of motion. The derivation of this method is achieved through an additional transformation of the CBM transformation matrix that neglects the inertial contributions in the transformation, similarly as in MNM (31).

Recall the second line of the equation of motion where internal and interface components are separated in the primal assembly (8):

$$M_{bi}\ddot{u}_i + M_{bb}\ddot{u}_b + K_{bi}u_i + K_{bb}u_b = f_b \tag{34}$$

Substitution of u_i by the approximation of internal modes and constraint modes of equation (13), the previous equation can be rearranged to the following expression:

$$\begin{aligned}(K_{bi}\Psi_{ib} + K_{bb})u_b \simeq f_b - \big(M_{bi}\Phi_{ii}\ddot{u}_{m,i} \\ +M_{bi}\Psi_{ib}\ddot{u}_b + M_{bb}\ddot{u}_b + K_{bi}\Phi_{ii}u_{m,i}\big)\end{aligned} \tag{35}$$

By assuming that f_b, $M_{bi}\Phi_{ii}\ddot{u}_{m,i}$, $M_{bi}\Psi_{ib}\ddot{u}_b$ and $M_{bb}\ddot{u}_b$ are negligible, u_b can be expressed as a function of $u_{m,i}$. The transformation from CBM to CCBM is thus:

$$\begin{bmatrix} u_{m,i} \\ u_b \end{bmatrix} \simeq \begin{bmatrix} I \\ -(K_{bi}\Psi_{ib} + K_{bb})^{-1}K_{bi}\Phi_{ii} \end{bmatrix} u_{m,i} \tag{36}$$

Combining the previous relation with the Craig-Bampton transformation (15) gives the CCBM transformation:

$$\begin{aligned}\begin{bmatrix} u_i \\ u_b \end{bmatrix} \simeq T_{CCB}u_{m,i} = \\ \begin{bmatrix} \Phi_{ii} - \Psi_{ib}(K_{bi}\Psi_{ib} + K_{bb})^{-1}K_{bi}\Phi_{ii} \\ -(K_{bi}\Psi_{ib} + K_{bb})^{-1}K_{bi}\Phi_{ii} \end{bmatrix} u_{m,i}\end{aligned} \tag{37}$$

Inserting this relation into the primal assembly equation of motion (8), the condensed equation is obtained:

$$M_{CCB}\ddot{u}_{m,i} + K_{CCB}u_{m,i} = f_{CCB} \tag{38}$$

This equation contains less DOF as the CBM. It might be beneficial for systems with a high number of interface DOF.

3.2 Condensed Dual Craig-Bampton Method (CDCBM)

In Gruber [1] and Allen, Rixen [3], it is stated that if the residual mass component M_r is equal to 0 in the DCBM, then the compatibility condition is strongly enforced and the reduced system is equivalent to the MNM. This citation is referred to Rixen [8]. The equivalence between the two methods was newly introduced in the last paragraph of Gruber [1] p.457, but a derivation with equations was not provided, neither in [8] nor in [1]. In this section, we clarify this procedure.

Consider the DCBM matrices. As done in the MNM, Section 2.3.2, the inertial interface terms are neglected. The modified DCBM matrices are thus:

$$M^*_{DCB} = \begin{bmatrix} M_{DCB,mm} & 0 \\ 0 & 0 \end{bmatrix}, \quad K^*_{DCB} = K_{DCB} \tag{39}$$

With this simplification in the equation of motion of the DCBM (33), λ can be expressed as a function of u_m. The transformation from DCBM to CDCBM results:

$$\begin{aligned}\begin{bmatrix} u \\ \lambda \end{bmatrix} \simeq T_{DCB}\begin{bmatrix} I \\ -K^{-1}_{DCB,\lambda\lambda}K_{DCB,\lambda m} \end{bmatrix} u_m \\ = T_{CDCB}u_m\end{aligned} \tag{40}$$

with the subindex λ corresponding to the interface terms. Inserting this transformation on the dual assembly equation of motion (10), the CDCBM system of equations is obtained:

$$M_{CDCB}\ddot{u}_m + K_{CDCB}u_m = f_{CDCB} \tag{41}$$

This system of equations condenses the interface force intensities λ into the equation of motion, resulting in a reduced system of equations respect to the DCBM.

The resulting mass and stiffness matrices differ in the MNM in how the compatibility and equilibrium conditions are set. In the case of MNM, derived from the RM, the compatibility condition is *a priori* satisfied, when in CDCBM, derived from DCBM, the equilibrium condition is intrinsically satisfied.

4. EXAMPLES AND DISCUSSION

4.1 Acoustic example - 1 DOF

The CMS methods presented in the paper are compatible to structural and confined acoustic domains. The equation of motion of N enclosed acoustic interconnected subdomains is equivalent to the one used for structural domains (2), since the fundamental equation of motion is equivalent [5]. In this case, the DOF is the pressure p.

The acoustic example (see Figure 1) is composed by four acoustic subdomains, connected at the red-colored interfaces. The material and model properties are summarized under the *Acoustic* column in Table 1.

The Natural Frequency Relative Error (NFRE), computed as $(\omega - \omega_{ref})/\omega_{ref}$, with ω_{ref} the natural frequencies of the primal assembly model, is shown in Figure 2. All methods have a good performance. As explained in previous sections, the CDCBM method is equivalent to the MNM and this is shown in how the results align. The coupled modal shapes are also compared using the Modal Assurance Criterion (MAC) [9] in Figure 3, using the primal assembly modes as reference, and the same trend can be observed.

A random excitation in the domain f_1 is applied to study the response of the system using the different CMS

Table 1. Acoustic and structural model properties

	Acoustic	Structure
Domains	4	7
Type	3D solid	3D shell
Nodes	6646	4256
DOF	6646	32322
ρ [kg/m^3]	1.225	7850
c [m/s]	346.25	
E [GPa]; ν		200; 0.3

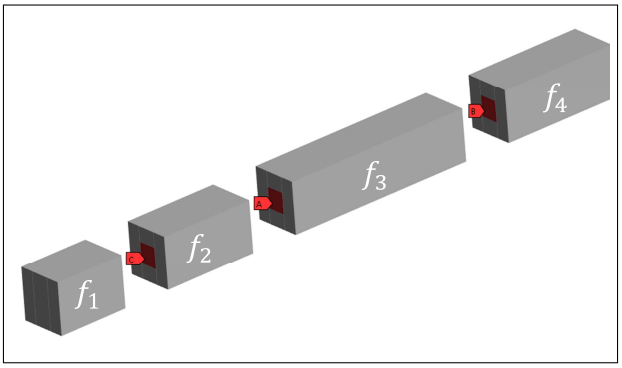

Figure 1. Example of connected acoustic domains.

approaches. In Figure 4 the Acoustic Potential Energy [5] is studied as a global indicator to compare the different methods. All of them have a good performance respect to the primal assembly.

In terms of computational demands, Table 2 contains a summary of the CPU time and the maximum RAM required in each CMS method, for the computation of the modes, and for the harmonic response. As one can observe, there is no gain in applying CMS instead of solving the modes directly from the primal assembly, since the CPU and RAM requirements are low. CMS is quite expensive in RAM due to the computation and use of the flexibility component's matrices.

For the harmonic response analysis, the CPU time is much longer when no reductions are applied than using CMS. Even though, this gain could also be achieved using a simple modal reduction.

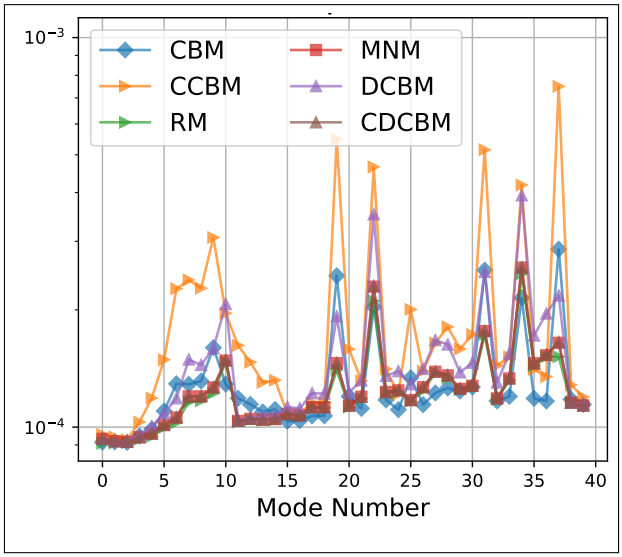

Figure 2. NFRE [-] of different CMS models in the acoustic example.

Table 2. Summary of CPU time [s] and maximum used RAM [GB] for different CMS methods in the acoustic example. Calculation of coupled modes and harmonic response.

	Modes		Response	
	CPU	RAM	CPU	RAM
A_{sparse}	3,16	0,08	1882,34	0,16
CB	32,94	2,26	1,77	0,12
CCB	33,99	2,27	1,31	0,12
RM	44,28	1,85	1,77	0,12
MNM	43,51	1,83	1,37	0,12
DCBM	43,4	1,83	1,32	0,12
CDCBM	43,46	1,83	1,28	0,11

4.2 Structural domain - 6 DOF

The structural example of Figure 5 (see properties in Table 1) consists of seven shell subdomains. Each node of the FE mesh contains six DOF, in comparison to the acoustic example, where there was only a single DOF per node.

In this case, we can see many differences in the CMS methods. None of the free-interface methods can correctly predict any natural frequency, as it is observed in Figure 6.

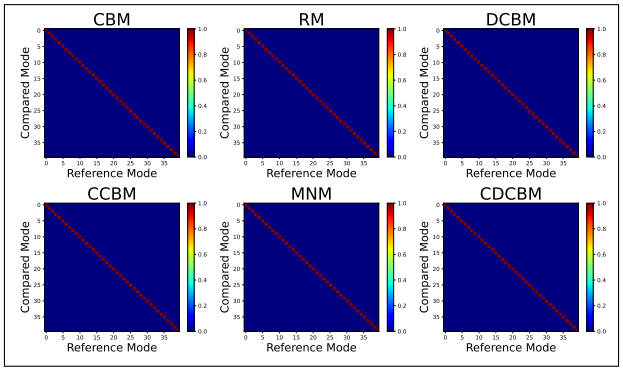

Figure 3. MAC values of different CMS models in the acoustic example.

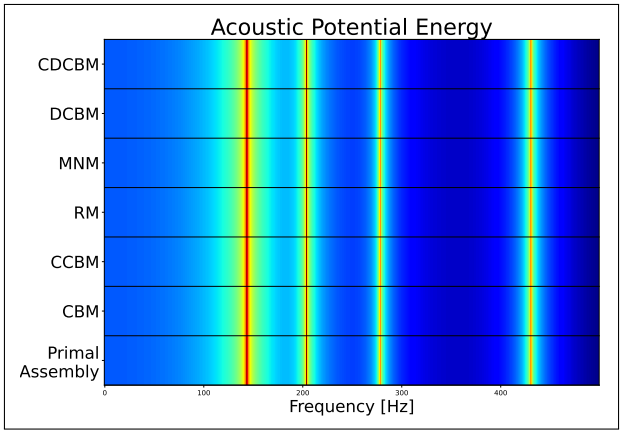

Figure 4. Harmonic response of acoustic domain using different CMS method.

Only the CBM and the novel CCBM can achieve a good accuracy. Here, we can observe the slight deviation between CBM and CCBM, exhibiting the second a greater error. This is due to the simplifications of the method.

In terms of harmonic response, a randomly distributed force is introduced in subdomain s_1. Figure 7 shows the Structural Kinetic Energy [5] of the different CMS models. The CBM and the CCBM are the only methods that can produce accurate results respect to the primal assembly response. In this case, the computation time of the CCBM is better than the CBM (see Table 3), since the number of DOF to solve contains only the number of modes of each subdomain.

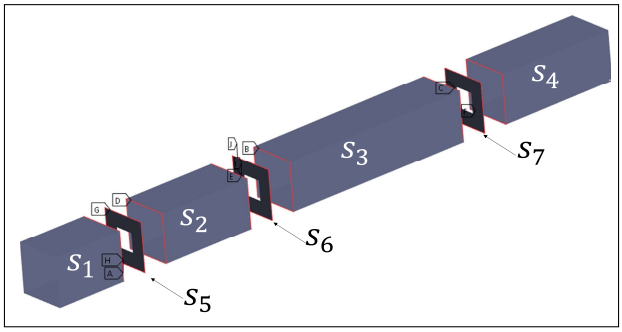

Figure 5. Example of connected structural domains.

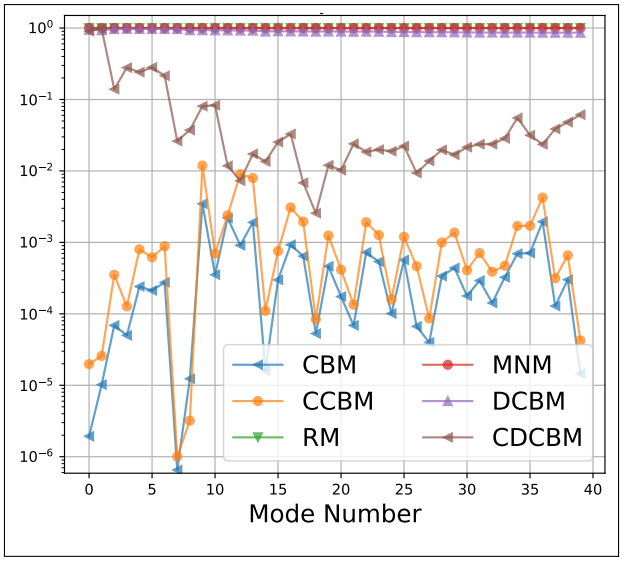

Figure 6. NFRE [-] of different CMS models in the structural example.

5. CONCLUSIONS

This paper introduced interesting novel CMS methods: Condensed Craig-Bampton Method and Condensed Dual Craig-Bampton Method. The first method is derived from the Craig-Bampton method after transforming it in dual assembly and further simplification of inertias. The second method is derived from the Dual Craig-Bampton Method with the simplifications of the MacNeal's method.

The different methods have been compared and benchmarked in terms of accuracy and computational efficiency through two examples: one acoustic and one structural. Free-interface methods (RM, MNM, DCBM and CDCBM) failed in predicting the coupled behavior of

Table 3. Summary of CPU time [s] and maximum used RAM [GB] for different CMS methods in the structural example. Calculation of coupled modes and harmonic response.

	Modes		Response	
	CPU	RAM	CPU	RAM
A_{sparse}	22,91	0,3	24011,40	0,36
CBM	209,66	11,3	33,27	0,67
CCBM	199,77	9,2	7,89	0,31
RM	1044,74	16,1	105,45	1,05
MNM	402,26	17,2	7,27	0,31
DCBM	460,35	12,3	54,68	0,66
CDCBM	291,44	10,1	6,46	0,31

the structural assembly, whereas fixed-interface methods maintain this accuracy. The CMS methods are in general more demanding than sparse eigenvalue solvers of the assembly model. However, they remain useful for models that demand substructuring for other purposes.

The CCBM exhibited a good performance, comparable to CBM, and it is slightly less demanding since it reduces the number of DOF of the reduced CMS system. In the case of the CDCBM, it is less demanding than the DCBM and it is slightly more accurate. Nevertheless, as the rest of free-interface methods, it is not reliable for complex structural assemblies.

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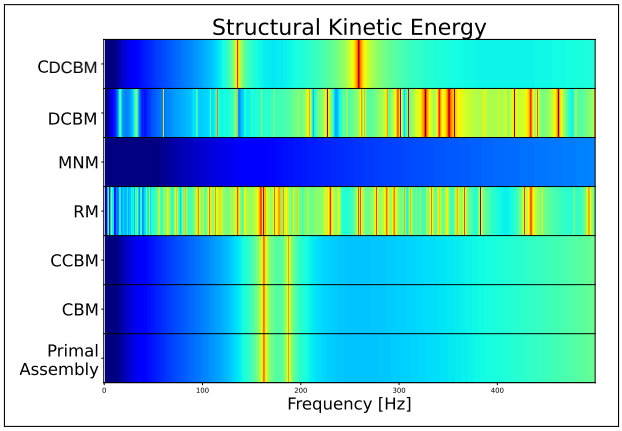

Figure 7. Harmonic response of structure using different CMS method.