

Implementation of calculation by dynamic under-structuring

Summary:

The purpose of this document is to help and give advices to the users for the realization of a study utilizing the dynamic technique of under-structuring.

One presents initially the general approach for the implementation of the technique.

One describes thereafter the sequences of the operations necessary in order to get exploitable results. The presentation is illustrated for three examples treating a modal calculation, a transitory calculation of answer and a harmonic calculation of answer.

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1 Of what does consist the dynamic under-structuring?

The dynamic under-structuring consists with partitionner the structure of several substructures in order to reduce the size of the digital model and to be able to study each substructure independently. The overall model is obtained thereafter by assembling the models of the various substructures. Each substructure is projected on a judiciously selected basis of vectors. This projection makes it possible to reduce the size of the model of each substructure and consequently the size of the model of the assembled structure.

2 Why use the dynamic under-structuring?

The increasing complexity of the mechanical structures makes difficult the estimate of its behavior dynamic under imposed request. The digital modeling of the complete structure would require an important investment as well on the level memory capacity as cost calculation. Besides the reduction of the size of the model, the dynamic technique of under-structuring makes much more modular the modeling of the structure total.

3 A small reminder of methodology

Here only the principles fundamental of the technique are pointed out. For more detail, the reader is invited to consult the reference document [R4.06.02].

The fact of projecting the substructure on a reduced basis, involves necessarily an approximation on the got results. The role of the modelisator is to choose a rather rich base in order to be able to seize the dynamic behavior of the substructure. The quality of the results depends on the choice of this base of projection. The techniques most used for the choice of this base are the technique of Craig Bampton and the technique of Mac Neal. To these two techniques the use of modes of interface is added who is an alternative of these two techniques where one carries out a condensation of the degrees of freedom of connection.

- The technique of Craig-Bampton consists in choosing as bases projection, modes normal and constrained modes. The normal modes are clean modes of the substructure where one blocks all the nodes of the interfaces with the adjacent substructures. A constrained mode is defined by the static deformation obtained by imposing a displacement unit on a degree of freedom of connection, the other degrees of freedom of connection being blocked. The base of projection contains normal modes and all the all constrained modes associated with all the degrees of freedom of connection.
- The technique of Mac Neal consists in choosing as bases projection, modes normal and modes of fastener. In this case, the normal modes are clean modes of the substructure with free interface. A mode of fastener is defined by the static deformation obtained by imposing a unit force on a degree of freedom of connection, the other degrees of freedom of connection being free. The base of projection contains normal modes and all the modes of fastener associated with all the degrees of freedom with connection.
- Use of modes of interface: One can note that the dimension of the base of projection can become very large if the number of degree of freedom of connection is important. One then defines the concept of mode of interface which consists to carry out a condensation of the behavior of the structure on the degrees of freedom of interface and to solve the problem with the eigenvalues associated. That makes it possible to express the behavior of the reduced structure to the interface. One limits oneself to preserve like basic vectors the first modes calculated in complement of the normal modes. Indeed, SI one remains within the framework of the dynamic low frequency, the whole of the constrained modes (or fastener) is not necessary to represent the dynamics of the problem. Nevertheless, it is recommended to control a posteriori the relevance of the base chosen by checking for example the continuity of displacements to the interfaces.

One can list hereafter the various stages of the approach:

- For each substructure:

- Calculation of the base of projection: normal modes and modes of connection or modes of interface
- Calculation of the generalized matrices of the substructure: projection of the matrices of mass and rigidity of the substructure on the reduced basis
- Assembly of the substructures by the formulation of the continuity of displacement to the interfaces and the nullity of the work of the bonding strengths. One thus obtains a generalized model of the assembled structure
- Calculation of the answer in generalized coordinates
- Restitution of the results on physical basis
- control of the got results
- postprocessing (calculation of constraint, calculation of energy,...)

4 Implementation in Code_Aster

4.1 Concept of macronutrient dynamic

A dynamic macronutrient is a scale model (generalized) of a substructure. It understands:

- the projection of the model (matrices of mass and rigidity) of the substructure on the reduced basis,
- information on the interfaces where will be connected the adjacent substructures and the matrices of connection associated with these interfaces.

Normally, one builds as much dynamic macronutrient than of substructure. If one is in the presence of substructures which differ only by their position in space, only one macronutrient is sufficient. One applies thereafter, a rotation and/or translation of the macronutrient during the assembly.

4.2 Course of a study

- For each substructure: creation of the dynamic macronutrient
 - Calculation and assembly of the matrices of mass, rigidity and the loading of the substructure: (CALC_MATR_ELEM, ASSE_MATRICE, CALC_VECT_ELEM, ASSE_VECTEUR)
 - Calculation of the basic vectors of projection: normal modes, static modes, modes of interface (CALC_MODES, MODE_STATIQUE, DEFI_BASE_MODAL)
 - Definition of the interfaces (DEFI_INTERF_DYNA)
 - Projection of the matrices of the substructure on the basic vectors (MACR_ELEM_DYNA)

The sequence of these operations can be carried out with only one call to the operator CREA_ELEM_SSD. Cand operator allows to create a dynamic macronutrient by informing only information about the model and the interfaces. He calculates the basic vectors of projection (normal modes and modes of connection), defines the interfaces and projects the matrices of rigidity and mass on the calculated basis. He connects the following operators: CALC_MATR_ELEM, ASSE_MATRICE, CALC_MODES, MODE_STATIQUE, DEFI_INTERF_DYNA, DEFI_BASE_MODAL, MACR_ELEM_DYNA.

- Assembly of the various substructures
 - Definition of the generalized model of the assembled structure: connection between substructures and classification of the degrees of freedom of the system (DEFI_MODELE_GENE, NUME_DDL_GENE)
 - Assembly of the generalized matrices of the substructures (ASSE_MATR_GENE, ASSE_VECT_GENE)

These operations of assembly of dynamic macronutrients can be realized by using the operator ASSE_ELEM_SSD. It defines the generalized model and assembles the generalized matrices of the various substructures. It connects the following operators: DEFI_MODELE_GENE, NUME_DDL_GENE, ASSE_MATR_GENE.

- Calculation of answer on the generalized model (CALC_MODES, DYNA_VIBRA)

- Restitution of the results in physical coordinates of the substructure or on a grid skeleton (`REST_SOUS_STRUCT`)
- Back testing of the results by checking the continuity of the field of displacement to the interfaces (`POST_RELEVE_T`, `TEST_TWHITEBAIT`) and the nullity of the work of the bonding strengths (`CALC_CORR_SSD`)

4.3 Practical advices

- For the standard cases: to use the operator `CREA_ELEM_SSD` for the creation of the dynamic macronutrient and the operator `ASSE_ELEM_SSD` for the assembly of the macronutrients. That facilitates to a significant degree the writing of the command file.
- For the nonstandard cases (bases particular projection), it is times, necessary to be allocated to the elementary operators. Current limitations of `CREA_ELEM_SSD` and `ASSE_ELEM_SSD` are:
 - conservative structure (without damping)
 - base projection: normal modes + modes of connection (Craig-Bampton, Mac Neal, N first modes of interface)
 - All the components of the degrees of freedom of the nodes interfaces are considered for the calculation of the modes of connection (the keyword `MASK` who allows to select the active components of the nodes interfaces is not active for `CREA_ELEM_SSD`)
 - The normal modes are calculated by using the operator `CALC_MODES`, the options on the dimension of the subspace of search for modes are those taken by default by this operator.
- If one is in the presence of a specific interface or with low number of ddl, the use of the classical methods (Craig-Bampton or Mac Neal) is recommended.
- The modes of interface are adapted for the interfaces distributed (nonspecific). The quality of the results depends amongst modes on interface taken into account in the base on projection. A back testing of the results is always indicated. This control can be done by checking the continuity of the field of displacement to the interfaces and/or the nullity of the work of the bonding strengths. It is necessary to increase the number of modes of interface if one observes an separation on the level of the interfaces or if the work of the bonding strengths is not negligible.
- To choose well the normal modes which are used as basic vectors of projection. The subspace generated by these basic vectors must at least contain the deformation of the substructure after assembly. One cannot, for example, to observe the torsion of the substructure if one does not put a deformation of torsion among the basic vectors.
- For an interface of the type Mac Neal, it should be made sure that the substructure is maintained some share in order to avoid the rigid movement of body.

5 Some examples of calculation

One presents three cases to illustrate the implementation of the technique.

The first case corresponds to a standard modal calculation with use of the operators `CREA_ELEM_SSD` and `ASSE_ELEM_SSD`.

The second case corresponds to a calculation of transitory answer. A double projection is carried out. The first projection is carried out during the creation of the dynamic macronutrient and the second projection is carried out on the generalized model of the assembled structure for calculation of answer.

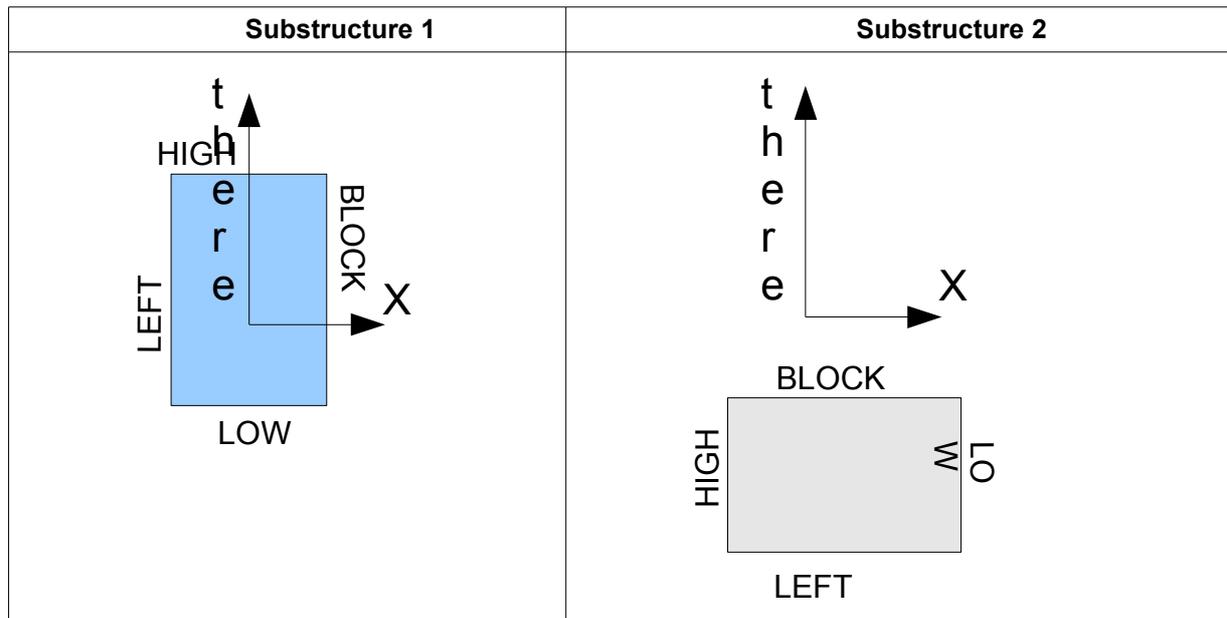
The third case corresponds to a calculation of harmonic answer on a dissipative structure. One describes the sequence of the elementary operators necessary for the creation of the dynamic macronutrients and the assembly of the generalized matrices of the substructures.

5.1 An example of modal calculation

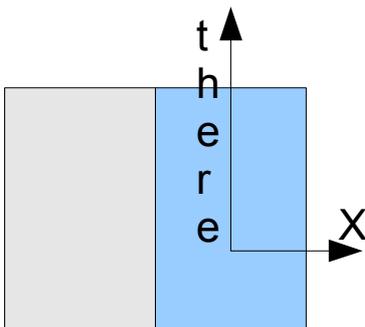
It is modeling E of the case test SDLS106 [V2.03.106].

In this case test, one wishes to calculate the clean modes of a structure made up of two substructures defined in two different reference marks. The association of these two substructures is judicious to obtain a plate in condition pressed on its edges.

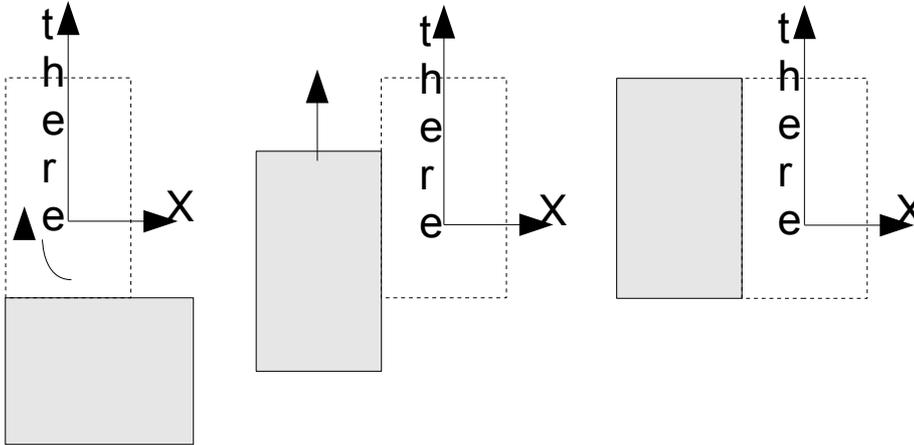
One can schematize it as follows:



The assembled structure is a rectangular plate resting against these edges.



To lead to this assembled structure, one carries out a rotation and a translation of substructure 2. Indeed, the two substructures must be expressed in the same reference mark.



Rotation -90 degrees around DZ + Translation according to DY

One will present the stages for the creation of the dynamic macronutrient of substructure 1, the dynamic macronutrient of substructure 2 east creates in a similar way.

Definition of the boundary conditions of substructure 1:

One wishes to use a base of the type Craig-Bampton, it is thus necessary to embed the degrees of freedom of the interface which are associated here with the group of nodes `LEFT`. The other conditions correspond to the boundary conditions of the substructure.

```
CHARGE_1=AFFE_CHAR_MECA ( MODELE=MODELE1, DDL_IMPO= (
  _F (GROUP_NO = 'BLOCKS', DX = 0.0, DY = 0.0, DZ = 0.0),
  _F (GROUP_NO = 'LEFT', DX = 0.0, DY = 0.0, DZ = 0.0,
      DRX = 0.0, DRY MARTINI = 0.0, DRZ =
0.0),
  _F (GROUP_NO = 'LOW', DX = 0.0, DY = 0.0, DZ = 0.0),
  _F (GROUP_NO = 'HIGH', DX = 0.0, DY = 0.0, DZ = 0.0)))
```

- Creation of the dynamic macronutrient :

The operator is used `CREA_ELEM_SSD` for the creation of the dynamic macronutrient,

There is an interface distributed here, one wishes to use **modes of interface** like modes of connection. Under the keyword factor `BASE_MODALE`, a base of the type is chosen `RITZ` and one seizes the number of modes of interface to be used.

The keyword factor `CALC_FREQ` inform about the numbers of normal modes to use.

```
MACEL1 = CREA_ELEM_SSD (
  MODEL = MODELE1,
  LOAD = CHARGE_1,
  CHAM_MATER = CHAMAT1,
  CARA_ELEM = PARAM1,
  INTERFACE = _F (NAME = 'LEFT',
                  TYPE = 'CRAIGB',
                  GROUP_NO = 'LEFT'),
  BASE_MODALE = _F ( TYPE = 'RITZ',
                    NMAX_MODE_INTF = 20, ),
  CALC_FREQ = _F (NMAX_FREQ = 6, ),
)
```

One creates same manner the dynamic macronutrient of substructure 2.

- Assembly of the various substructures:

One carries out the assembly of the substructures by using the operator `ASSE_ELEM_SSD`

The keyword factor `RESU_ASSE_SSD` allows to name the concepts results (model, classification of the generalized ddl, matrices generalized).

The keyword factor `SOUS-STRUCT` allows to name the various substructures. It is in this keyword factor that one affects the possible rotation and the translation of the macronutrient (one carries out initially rotation `ANGL_NAUT` and then translation `TRANS`).

The keyword `CONNECTION` allows to define the interfaces between substructures. If one uses modes of interfaces as modes of connection, it is necessary to specify `REDUCED` under the keyword `OPTION`.

The group of meshes `GROUP_MA_MAIT_*` pilot the field of displacement to the interface. If the interfaces are not compatible (the nodes are not in opposite), it is advised to choose like main mesh, the finest mesh. If not, by defaults, the meshes of substructure 1 are defined like mistresses.

The choice `ELIMINATE` under the keyword `METHOD` mean that one numbers the degrees of freedom generalized by taking of account the equations of connection by the method of elimination of the constraints.

```
ASSE_ELEM_SSD (
    RESU_ASSE_SSD = _F (
        MODEL = CO ('MODEGE'),
        NUME_DDL_GENE = CO ('NUMEGE'),
        RIGI_GENE = CO ('RIGGEN'),
        MASS_GENE = CO ('MASGEN'),
    ),
    SOUS_STRUC = (
        _F (NAME = 'CARRE1',
            MACR_ELEM_DYNA = MACEL1, ),
        _F (NAME = 'CARRE2',
            MACR_ELEM_DYNA = MACEL2,
            ANGL_NAUT = (- 90. , 0. , 0. ) , ),
        TRANS = (0. , 0.5, 0.) ,
    ),
    CONNECTION = (
        _F (SOUS_STRUC_1 = 'CARRE1',
            INTERFACE_1 = 'LEFT',
            GROUP_MA_MAIT_1 = 'CALCULATION',
            OPTION = 'REDUCED',
            SOUS_STRUC_2 = 'CARRE2',
            INTERFACE_2 = 'BLOCKS' , ),
    ),
    VERIF = _F (STOP_ERREUR = 'YES',
        PRECISION = 1.E-6,
        CRITERION = 'RELATIVE' ) ,
    METHOD = 'ELIMINATES',
),
```

- Calculation of the clean modes of the assembled structure:

One carries out modal calculation on the assembled generalized matrices. The modal deformations obtained are expressed in generalized coordinates.

```
RESGEN=CALC_MODES (MATR_RIGI=RIGGEN,
    MATR_MASS=MASGEN,
    OPTION = 'PLUS_PETITE',
    CALC_FREQ=_F (NMAX_FREQ=10, ),
    SOLVEUR_MODAL=_F (METHODE=' SORENSEN' , ),
    VERI_MODE=_F (PREC_SHIFT=5.0E-3,
        STOP_ERREUR=' NON' ,
```

```
                STURM=' NON',  
                SEUIL=9.9999999999999995E-01),  
        STOP_BANDE_VIDE=' NON',  
    )
```

- Restitution on physical basis:

For the analysis of the results, it necessary to restore them on the physical basis.

```
MODCOT1=REST_SOUS_STRUC (RESU_GENE=RESGEN,  
                        TOUT_ORDRE=' OUI',  
                        SOUS_STRUC=' CARRE1',);
```

```
MODCOT2=REST_SOUS_STRUC (RESU_GENE=RESGEN,  
                        TOUT_ORDRE=' OUI',  
                        SOUS_STRUC=' CARRE2',);
```

- Quality control of the results:

The quality of the got results can be controlled by checking the continuity of displacements to the interface. That makes it possible to validate the selected number of modes of interface.

In this case test, one compares the displacement of the node N9 substructure 1 with that of the node N70 substructure 2. These two nodes are in opposite.

```
T1_DZ=POST_RELEVE_T (ACTION=_F (INTITULE=' CARRE1',  
                                NOEUD= ('N9'),  
                                RESULTAT=MODCOT1,  
                                NOM_CHAM=' DEPL',  
                                TOUT_ORDRE=' OUI',  
                                NOM_CMP=' DZ',  
                                OPERATION=' EXTRACTION',  
                                ),);
```

```
T2_DZ=POST_RELEVE_T (ACTION=_F (INTITULE=' CARRE2',  
                                NOEUD= ('N70'),  
                                RESULTAT=MODCOT2,  
                                NOM_CHAM=' DEPL',  
                                TOUT_ORDRE=' OUI',  
                                NOM_CMP=' DZ',  
                                OPERATION=' EXTRACTION',  
                                ),);
```

```
F_DZ=FORMULE (NOM_PARA= ('DZ_C1', 'DZ_C2'),  
             VALE=' ABS (DZ_C1 - DZ_C2)')
```

```
TC_DZ=CALC_TABLE (TABLE=T1_DZ,  
                 ACTION= (_F (OPERATION=' RENOMME',  
                             NOM_PARA= ('DZ', 'DZ_C1')),  
                          _F (OPERATION=' COMB',  
                             TABLE=T2_DZ,  
                             NOM_PARA= ('NUMÉRIQUE_ORDRE',)),  
                          _F (OPERATION=' RENOMME',  
                             NOM_PARA= ('DZ', 'DZ_C2')),  
                          _F (OPERATION=' OPER',  
                             NOM_PARA=' ECART',  
                             FORMULE=F_DZ)),  
                 ),  
                 TITRE=' Comparison DZ ssd 1/ssd 2')
```

```
TEST_TABLE (  
    TABLE = TC_DZ,
```

```
NOM_PARA = 'VARIATION' ,  
TYPE_TEST = 'SOMM' ,  
VALE = 0. ,  
CRITERION = 'ABSOLUTE' ,  
PRECISION = 3.E-3 ,  
REFERENCE = 'ANALYTICAL' , )
```

One calculates here the sum of the absolute values of the variations. The keyword `PRECISION` allows to define the tolerated maximum variation.

One can also check the nullity of the work of the bonding strengths by using the operator `CALC_CORR_SSD`. This calculation is rather consuming time CPU.

```
CALC_ENR=CALC_CORR_SSD (MODELE_GENE=MODEGE,  
RESU_GENE=RESGEN,  
SHIFT=1. ,  
UNITE=6)
```

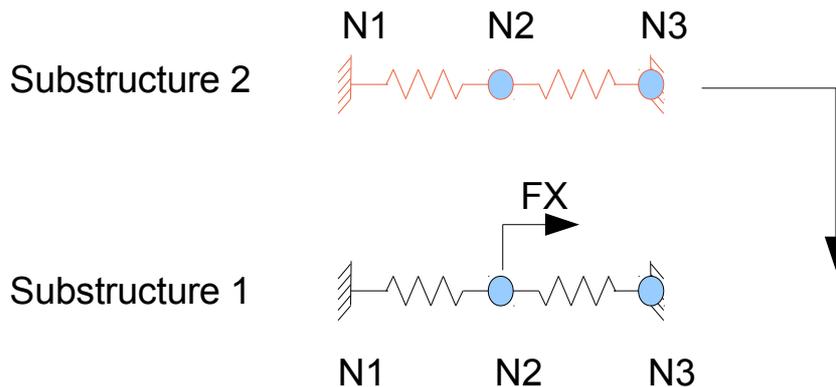
A summary of the got results is deposited, by default, in the file of the messages. One can enrich the base if it is noted that the work of the bonding strengths is not negligible. One can take as a starting point the modeling has case test `SDLS122 [V2.03.122]` for the implementation of this enrichment of the base of projection.

5.2 An example of transitory calculation of answer

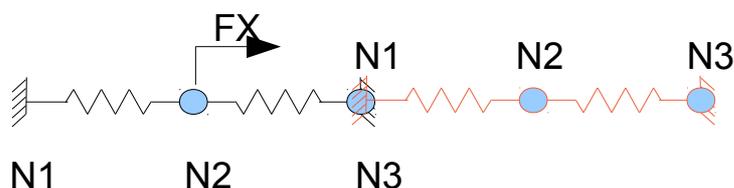
It is modeling E of the case test `SDLD102 [V2.01.102]`.

The substructures are made up of discrete elements. The first substructure is requested by a specific force.

One uses the same model and the same grid for the definition of the two substructures.



The complete structure is obtained by assembling the two substructures.



Definition of the boundary conditions of the substructure:

One wants to use a base of the type **Classical Craig-Bampton**, the node with the interface must be blocked (node *N3* for substructure 1 and node *N1* for under structure 2).

```
CHARGE_L=AFPE_CHAR_MECA (MODELE=MODELE,  
                          DDL_IMPO= (  
                              _F (NOEUD=' N2 ',  
                                  DY=0.,  
                                  DZ=0.,  
                                  DRX=0.,  
                                  DRY=0.,  
                                  DRZ=0.),,  
                              _F (NOEUD=' N1 ',  
                                  DX=0.),,  
                              _F (NOEUD=' N3 ',  
                                  DX=0.),),),);
```

- Creation of the dynamic macronutrients:

The loading is applied **FX** on this substructure 1, it is then necessary to seize a classification for the degrees of freedom of the substructure. This classification will be used later on at the time of the definition of the loading on the assembled model.

```
MACEL1 = CREA_ELEM_SSD (  
    MODELE=MODELE,  
    CARA_ELEM=PARAM,  
    CHARGE=CHARGE_L,  
    CHAM_MATER = CHAMAT,  
    NUME_DDL=CO ('NUMDDL_L'),  
    INTERFACE=_F (NOM=' DROITE',  
                 TYPE=' CRAIGB',  
                 NOEUD=' N3',),,  
    BASE_MODALE = _F ( TYPE = 'CLASSICAL',),,  
    CALC_FREQ = _F (NMAX_FREQ = 1),,  
)
```

Creation of the dynamic macronutrient of substructure 2:

```
MACEL2 = CREA_ELEM_SSD (  
    MODELE=MODELE,  
    CARA_ELEM=PARAM,  
    CHARGE=CHARGE_L,  
    CHAM_MATER = CHAMAT,  
    INTERFACE=_F (NOM=' GAUCHE',  
                 TYPE=' CRAIGB',  
                 NOEUD=' N1',),,  
    BASE_MODALE = _F ( TYPE = 'CLASSICAL',),,  
    CALC_FREQ = _F (NMAX_FREQ = 1),,  
)
```

- Assembly of the various substructures:

```
ASSE_ELEM_SSD (  
    RESU_ASSE_SSD = _F (  
        MODEL = CO ('MODEGE'),  
        NUME_DDL_GENE = CO ('NUMEGE'),  
        RIGI_GENE = CO ('RIGGEN'),  
        MASS_GENE = CO ('MASGEN'),  
    ),  
    SOUS_STRUC= (_F (NOM=' COTE1',
```

```
MACR_ELEM_DYNA=MACEL1, ),
_F (NOM=' COTE2',
MACR_ELEM_DYNA=MACEL2,
TRANS= (0.2, 0. , 0.), ), ),
LIAISON=_F (SOUS_STRUC_1=' COTE1',
INTERFACE_1=' DROITE',
SOUS_STRUC_2=' COTE2',
INTERFACE_2=' GAUCHE', ),
VERIF=_F (STOP_ERREUR=' OUI',
PRECISION=1.E-6,
CRITERE=' RELATIF', ),
);
```

- Calculation of the transitory answer of the assembled structure:
Definition and assembly of the vector loading:

```
CHARTRAN=AFFE_CHAR_MECA (MODELE=MODELE,
FORCE_NODALE=_F (NOEUD=' N2',
FX=1., ), );
V_ELEM=CALC_VECT_ELEM (OPTION=' CHAR_MECA',
CHARGE=CHARTRAN, );
```

The loading must be expressed in same classification as the vectors of projection (classification of the degrees of freedom of substructure 1).

```
V_ASSE=ASSE_VECTEUR (VECT_ELEM=V_ELEM,
NUME_DDL=NUMDDL_L, );
```

Assembly of the vector loading on the model generalized (loading applied to the substructure COTE1):

```
FGEN=ASSE_VECT_GENE (NUME_DDL_GENE=NUMEGE,
CHAR_SOUS_STRUC=_F (SOUS_STRUC=' COTE1',
VECT_ASSE=V_ASSE, ), );
```

Definition of the base of projection for the transitory calculation of answer (in the majority of the cases, the base is made up of clean modes of the system):

```
RESGEN=CALC_MODES (MATR_RIGI=RIGGEN,
MATR_MASS=MASGEN,
OPTION=' PLUS_PETITE',
CALC_FREQ=_F (NMAX_FREQ=3, ),
TITRE=' CALCULATION OF THE CLEAN MODES OF STRUCTURE
GLOBALE',
);
```

Classification of the degrees of freedom of the base of calculation:

```
NUMEMODE=NUMERIQUE_DDL_GENE (BASE=RESGEN,
STOCKAGE=' DIAG', );
```

Projection of the matrices assembled on the basis of calculation:

```
MASPRO=PROJ_MATR_BASE (BASE=RESGEN,
NUME_DDL_GENE=NUMEMODE,
MATR_ASSE_GENE=MASGEN, );
```

```
RIGPRO=PROJ_MATR_BASE (BASE=RESGEN,
NUME_DDL_GENE=NUMEMODE,
MATR_ASSE_GENE=RIGGEN, );
```

Projection of the loading on the basis of calculation:

```
VECPRO=PROJ_VECT_BASE (BASE=RESGEN,
NUME_DDL_GENE=NUMEMODE,
```

```
VECT_ASSE_GENE=FGEN,);
```

By defaults, displacement and speed are worthless at the initial moment. One shows hereafter how to seize the initial condition of the system.

One creates the field on the grid of the substructure with same classification as that of the macronutrient.

```
CHAMP_0 = CREA_CHAMP (OPERATION=' AFFE', TYPE_CHAM=' NOEU_DEPL_R',  
                      MAILLAGE=MAILLA,  
                      NUME_DDL=NUMDDL_L,  
                      AFFE=_F ( ALL = 'YES',  
                                NOM_CMP = ('DX', 'DY', 'DZ', 'DRX', 'DRY'  
MARTINI', 'DRZ',)),  
                      VALE = (0., 0., 0., 0., 0., 0.,))  
                      )
```

Projection of the field on the assembled generalized model:

```
VGEN_0=ASSE_VECT_GENE (NUME_DDL_GENE=NUMEGE,  
                      CHAR_SOUS_STRUC=_F (SOUS_STRUC=' COTE1',  
                                          VECT_ASSE=CHAMP_0,)),);
```

The second projection of the field on the basis of calculation of answer:

```
DEPINI=PROJ_VECT_BASE ( BASE=RESGEN, VECT_ASSE_GENE=VGEN_0,  
                       NUME_DDL_GENE=NUMEMODE,  
                       TYPE_VECT=' DEPL')
```

```
VITINI=PROJ_VECT_BASE ( BASE=RESGEN, VECT_ASSE_GENE=VGEN_0,  
                       NUME_DDL_GENE=NUMEMODE,  
                       TYPE_VECT=' VITE')
```

The transitory calculation of answer can be carried out by using the order `DYNA_VIBRA`. One uses the technique of resolution by projection on a basis of calculation.

Calculation of the transitory answer on the model assembled project:

```
TRANGEN1=DYNA_VIBRA (TYPE_CALCUL=' TRAN', BASE_CALCUL=' GENE',  
                    SCHEMA_TEMPS=_F (SCHEMA=' EULER',),  
                    MATR_MASS=MASPRO,  
                    MATR_RIGI=RIGPRO,  
                    INCREMENT=_F (INST_INIT=0.,  
                                   INST_FIN=82.,  
                                   PAS=0.01,),  
                    ETAT_INIT=_F (DEPL = DEPINI,  
                                   QUICKLY = VITINI,),  
                    ARCHIVAGE=_F (PAS_ARCH=10,),  
                    EXCIT=_F (VECT_ASSE=VECPRO,  
                              COEF_MULT=1.,),);
```

- Restitution on physical basis:

One can restore the results directly on the substructure or a grid of visualization called grid skeleton which should be defined as a preliminary.

Creation of the grid of visualization:

```
SQUEL=DEFI_SQUELETTE (MODELE_GENE=MODEGE,  
                     SOUS_STRUC= (_F (NOM=' COTE1',  
                                       GROUP_MA=' RESSORT'  
                                       ),  
                                   _F (NOM=' COTE2',  
                                       GROUP_MA=' RESSORT'  
                                       ),),);
```

Restitution of the base of calculation on the grid of visualization:

```
MODGLO=REST_SOUS_STRUC (RESU_GENE=RESGEN,  
                        TOUT_ORDRE=' OUI',  
                        SQUELETTE=SQUEL,);
```

Restitution of the answer on the grid of visualization (for a resolution with double projection, not to forget to specify the restitution of the base of calculation on the substructure or the skeleton):

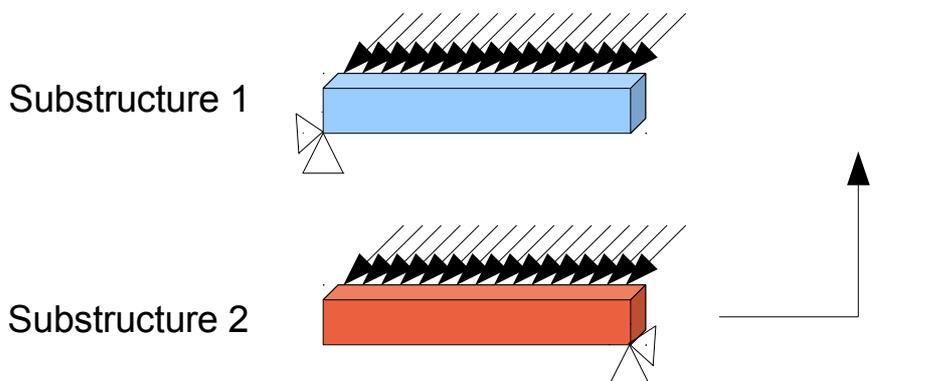
```
TRAN1=REST_GENE_PHYS (RESU_GENE=TRANGEN1,  
                      MODE_MECA=MODGLO,  
                      LIST_INST=LISTE_R,  
                      INTERPOL=' LIN',  
                      TOUT_CHAM=' OUI',  
                      NOEUD=' NO3',);
```

It is thus pointed out that for a calculation of temporal answer, one carries out a double projection. The first projection of the substructure on the basis made up of normal modes and modes of connection and the second projection of the model assembled small-scale on the basis of calculation of answer.

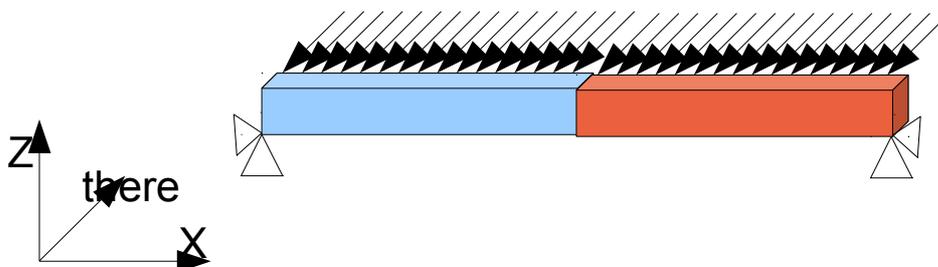
5.3 An example of harmonic calculation of answer

In the majority of the cases, a harmonic calculation of answer is carried out on a dissipative model. Operators `CREA_ELEM_SSD` and `ASSE_ELEM_SSD` treat only the conservative structures. One details in this example the elementary operations subjacent, necessary for the realization of a harmonic calculation of answer per dynamic under-structuring.

The case test SHLV301A is used to illustrate the presentation. It is about a bar with rectangular section modelled with quadratic voluminal elements. One applies a sinusoidal pressure to a side face of the bar.



The assembled structure:



Definition and assignment of material:

```
MAT=DEFI_MATERIAU ( ELAS=_F (RHO = 7.8E03, NAKED = 0.3, E = 2.1E11,  
                             AMOR_ALPHA = 1.6E-5, AMOR_BETA = 16.))
```

```
CHMAT=AFFE_MATERIAU (  MAILLAGE=MAYA,  
                        AFFE=_F (ALL = 'YES',  
                                MATER = CHECHMATE))
```

Description of the loading:

```
PRESSION=AFFE_CHAR_MECA (  MODELE=POVOL,  
                           PRES_REP=_F (  GROUP_MA = 'PRESSURE',  
                                         CLOSE = 50.E4))
```

Description of the boundary conditions (One wishes to use a base of projection of the type **Mac Neal** : the nodes of the interface is free):

```
FIXAT1=AFFE_CHAR_MECA (  MODELE=POVOL,  
                         DDL_IMPO= (  _F (  GROUP_NO = 'COND1',  DY = 0.),  
                                     _F (  GROUP_NO = 'CONDZG',  DZ = 0.),  
                                     _F (  NODE = 'N26',  DX = 0.),  
                                     _F (  GROUP_NO = 'RIGHT',  DX = 0.)))
```

- Creation of the dynamic macronutrients:

Creation of the elementary matrices of substructure 1:

```
K_ELEM1=CALC_MATR_ELEM (  MODELE=POVOL,  
                          CHAM_MATER=CHMAT,  
                          OPTION=' RIGI_MECA',  
                          CHARGE= (FIXAT1,)  
                          )
```

```
M_ELEM1=CALC_MATR_ELEM (  MODELE=POVOL,  
                          CHAM_MATER=CHMAT,  
                          OPTION=' MASS_MECA',  
                          CHARGE= (FIXAT1,)  
                          )
```

```
A_ELEM1=CALC_MATR_ELEM (  MODELE=POVOL,  
                          CHAM_MATER=CHMAT,  
                          OPTION=' AMOR_MECA',  
                          RIGI_MECA=K_ELEM1,  
                          MASS_MECA=M_ELEM1,  
                          CHARGE= (FIXAT1,)  
                          )
```

Creation of the elementary vector of the loading for substructure 1:

```
V_ELEM1=CALC_VECT_ELEM (  OPTION=' CHAR_MECA',  
                          CHARGE=PRESSION)
```

Assembly of the elementary matrices and vector:

```
NUM1=NUMÉRIQUE_DDL (  MATR_RIGI=K_ELEM1)
```

```
K_ASSE1=ASSE_MATRICE (  MATR_ELEM=K_ELEM1,  
                       NUME_DDL=NUM1)
```

```
M_ASSE1=ASSE_MATRICE (  MATR_ELEM=M_ELEM1,  
                       NUME_DDL=NUM1)
```

```
A_ASSE1=ASSE_MATRICE (  MATR_ELEM=A_ELEM1,  
                       NUME_DDL=NUM1)
```

```
V_ASSE1=ASSE_VECTEUR (  VECT_ELEM=V_ELEM1,
```

```
NUME_DDL=NUM1)
```

Calculation of the normal modes:

```
MODES1=CALC_MODES (MATR_RIGI=K_ASSE1,  
                   MATR_MASS=M_ASSE1,  
                   CALC_FREQ=_F (NMAX_FREQ = 20))
```

Definition of the interface for a base of the type Mac Neal:

```
INTERF1=DEFI_INTERF_DYNA ( NUME_DDL=NUM1,  
                           INTERFACE=_F (NAME = 'RIGHT',  
                                         TYPE = 'MNEAL',  
                                         GROUP_NO = 'RIGHT'),  
                           INFO=2)
```

Definition of the base of projection:

```
BAM01=DEFI_BASE_MODAL ( CLASSIQUE=_F (INTERF_DYNA = INTERF1,  
                                       MODE_MECA = MODES1,  
                                       NMAX_MODE = 20),  
                        INFO=2)
```

Creation of the dynamic macronutrient:

It is specified that one wishes to take into account damping by seizing the matrix of damping to be projected.

```
MACRO1=MACR_ELEM_DYNA ( BASE_MODAL=BAM01,  
                        MATR_AMOR=A_ASSE1 )
```

One builds same manner the dynamic macronutrient of substructure 2.

- Assembly of the various substructures:

Definition of the generalized model: one names each substructure and one specifies the interfaces between the various substructures

```
MODEGE=DEFI_MODELE_GENE (SOUS_STRUC= (_F (NAME = 'COTE1',  
                                           MACR_ELEM_DYNA = MACRO1,  
                                           TRANS = (0. , 0. , 0. ,),  
                                           ANGL_NAUT = (0. , 0. , 0. ,),),  
                              _F (NAME = 'COTE2',  
                                   TRANS = (1. , 0. , 0. ,),  
                                   ANGL_NAUT = (0. , 0. , 0. ,),  
                                   MACR_ELEM_DYNA = MACRO2)),  
                          LIAISON=_F (SOUS_STRUC_1 = 'COTE1',  
                                       SOUS_STRUC_2 = 'COTE2',  
                                       INTERFACE_1 = 'RIGHT',  
                                       INTERFACE_2 = 'LEFT'))
```

Definition of a classification of the degrees of freedom of the assembled generalized system:

```
NUMEGE=NUMERIQUE_DDL_GENE ( MODELE_GENE=MODEGE)
```

Assembly of the generalized matrices of the various substructures:

```
RIGGEN=ASSE_MATR_GENE ( NUME_DDL_GENE=NUMEGE,  
                        OPTION=' RIGI_GENE')
```

```
MASGEN=ASSE_MATR_GENE ( NUME_DDL_GENE=NUMEGE,  
                        OPTION=' MASS_GENE')
```

```
AMOGEN=ASSE_MATR_GENE ( NUME_DDL_GENE=NUMEGE,  
                        OPTION=' AMOR_GENE')
```

Assembly of the vector generalized loading:

```
VECTGEN=ASSE_VECT_GENE ( NUME_DDL_GENE=NUMEGE,  
                          CHAR SOUS_STRUC= (
```

```
_F ( SOUS_STRUC = 'COTE1',  
      VECT_ASSE = V_ASSE1),  
_F ( SOUS_STRUC = 'COTE2',  
      VECT_ASSE = V_ASSE2)))
```

- Calculation of the harmonic answer of the assembled structure:

```
DYNGEN=DYNA_VIBRA (TYPE_CALCUL=' HARM',BASE_CALCUL=' GENE',  
                  MATR_MASS=MASGEN,  
                  MATR_RIGI=RIGGEN,  
                  MATR_AMOR=AMOGEN,  
                  SOLVEUR=_F (METHODE=' LDLT',),  
                  FREQ=F,  
                  TOUT_CHAM=' OUI',  
                  EXCIT=_F (VECT_ASSE = VECTGEN,  
                             COEF_MULT = 1.))
```

- Restitution on physical basis:

One carries out here a restitution on substructure 1 (COTE1) :

```
DYNHAR1=REST_SOUS_STRUC ( RESU_GENE=DYNGEN,  
                          SOUS_STRUC=' COTE1')
```

It is thus pointed out that for a harmonic calculation of answer, as for modal calculation, one directly carries out calculation on the generalized model of the assembled structure without making the second projection on a basis of calculation.