

## Operator DEFI\_MODELE\_GENE

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### 1 Goal

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To create the total structure starting from the substructures in dynamic under-structuring (cf [R4.06.02]).

Within the framework of a calculation using the methods of dynamic under-structuring (analyzes modal or harmonic), the operator `DEFI_MODELE_GENE` allows to describe the total structure starting from the macronutrients resulting from `MACR_ELEM_DYNA` [U4.65.01] and of various connections which bind the substructures the ones to the others. A macronutrient can be used for the definition of several under - structures, whatever their orientation in the physical reference mark if the coupling is carried out by static modes (option `'CLASSICAL'`). This possibility makes it possible to take account of the repetition of a component in the total structure.

Product a structure of data of the type `modele_gene`.

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## 2 Syntax

```
mo_gene [modele_gene] = DEFI_MODELE_GENE (  
  
  ♦ SOUS_STRUC = _F (♦ NAME = nom_sstruc, [KN]  
                    ♦ MACR_ELEM_DYNA = macro_dy, [macr_elem_dyna]  
                    ♦ ANGL_NAUT = angl_naut, [l_R]  
                    ♦ TRANS = trans, [l_R]  
                    ),  
  ♦ CONNECTION = _F (♦ SOUS_STRUC_1 = 'nom_sstruc1', [KN]  
                    ♦ INTERFACE_1 = 'nom_int1', [KN]  
                    ♦ SOUS_STRUC_2 = 'nom_sstruc2', [KN]  
                    ♦ INTERFACE_2 = 'nom_int2', [KN]  
                    ♦ GROUP_MA_MAIT_1 = lgma1, [l_gr_maille]  
                    ♦ MAILLE_MAIT_1 = lma1, [l_maille]  
                    ♦ GROUP_MA_MAIT_2 = lgma2, [l_gr_maille]  
                    ♦ MAILLE_MAIT_2 = lma2, [l_maille]  
                    ♦ OPTION =/'CLASSICAL', [DEFECT]  
                    /'REDUCED',  
                    ),  
  
  ♦ VERIF = _F ( ♦ STOP_ERREUR =/'YES', [DEFECT]  
                /'NOT',  
                ♦ PRECISION =/prec, [R]  
                / 1.E-3, [DEFECT]  
                ♦ CRITERION =/'RELATIVE', [DEFECT]  
                / 'ABSOLUTE',  
                ),  
  ♦ INFORMATION=/1, [DEFECT]  
    / 2,  
  )
```

## 3 Operands

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### 3.1 Keyword SOUS\_STRUC

◆ SOUS\_STRUC

Keyword factor allowing to define all the substructures which compose the total structure. The definition of a substructure is done by the data of its name, the macronutrient which is associated to him and its orientation in the physical reference mark.

#### 3.1.1 Operand NAME

◆ NAME = 'nom\_sstruc'

Name of 8 characters maximum which will make it possible thereafter to indicate the substructure in:

- operator: DEFI\_MODELE\_GENE [U4.65.02], operands: CONNECTION and SOUS\_STRUC\_1,
- operator: DEFI\_SQUELETTE [U4.24.01], operand: SOUS\_STRUC,
- operator: ASSE\_VECT\_GENE [U4.65.05], operand: SOUS\_STRUC,
- operator: REST\_SOUS\_STRUC [U4.63.32], operand: SOUS\_STRUC.

#### 3.1.2 Operand MACR\_ELEM\_DYNA

◆ MACR\_ELEM\_DYNA = macro\_dyna

Name of the concept `macr_elem_dyna` resulting from the operator `MACR_ELEM_DYNA` [U4.65.01] which indicates the condensed model of the substructure. It is pointed out that a macronutrient can be used for the definition of several substructures.

#### 3.1.3 Operand ANGL\_NAUT

◇ ANGL\_NAUT = angl\_naut

List of the 3 nautical angles, in degrees, which make it possible to pass from the orientation of the model which has given rise to the macronutrient that of the substructure.

One will refer to the operator `AFFE_CARA_ELEM` [U4.42.01]: Operand `ORIENTATION` for the definition and the use of the nautical angles.

#### 3.1.4 Operand TRANS

◇ TRANS = trans

List of 3 components of translation which make it possible to build a news under - structure starting from the model which has given rise to the macronutrient, by applying an overall translation.

### 3.2 Keyword CONNECTION

◆ CONNECTION

Keyword factor allowing to define all the interfaces of connection between under - structures. A connection is defined by the names of the two substructures in opposite, and for each one of them, the name of the corresponding interface.

In the case of an incompatibility of grid between the two substructures in opposite, it is necessary to indicate that of both whose interface will be considered as Master (keywords

GROUP\_MA\_MAIT\* and/or MAILLE\_MAIT\*). The nodes slaves which are projected on the interface Master are definite first by DEFI\_INTERF\_DYNA [U4.64.01]. The “sticking together” of the 2 interfaces will be done by writing of linear relations between the degrees of freedom of the 2 faces.

**Note:**

*It is recommended that, in the case of incompatible interfaces, the main interface is the interface whose discretization is coarsest. In the case of the use of classical static modes (as much as degrees of freedom), it is thus advisable to use the interface with more the small number of degrees of freedom like main interface. In the case of the use of modes of couplings, this choice can be more delicate. The choice of the main interface can impact the quality of the result clearly if the two models present very different discretizations. See the discussion on this subject in the section 5.2.*

Displacements of the nodes of the face slave will be connected to displacements of their projections on the face Master. For each node of the face slave, one will write 2 (in 2D) or 3 (in 3D) linear relations.

An application of this functionality is for example the sticking together of a grid formed by linear elements (P1) on another quadratic grid (P2). In this case it is rather advised to choose like face “slave” the quadratic face.

It is possible to define a connection by reduced modes (or modes of interface) by the keyword OPTION.

### 3.2.1 Operand SOUS\_STRUC\_1

- ◆ SOUS\_STRUC\_1 = 'nom\_sstruc1'

Name of the first of the substructures put concerned on both sides of the connection. It must have been as a preliminary defined by the keyword: SOUS\_STRUC.

### 3.2.2 Operand INTERFACE\_1

- ◆ INTERFACE\_1 = 'nom\_int1'

Name of the interface of the first substructure intervening in the connection. It must have been as a preliminary defined by the operator DEFI\_INTERF\_DYNA [U4.64.01] for the macronutrient support of the substructure.

**Note:**

*In the case of the use of modes of couplings (operator MODE\_STATIQUE) with keyword MODE\_INTERF, it is essential that the dynamic interface is of type CRAIGB.*

### 3.2.3 Operand GROUP\_MA\_MAIT\_1, MAILLE\_MAIT\_1

- ◇ GROUP\_MA\_MAIT\_1 = lgma1
- ◇ MAILLE\_MAIT\_1 = lma1

This keyword makes it possible to indicate under structure Master, independently of the mesh or the group of mesh specified as starter. Operator DEFI\_MODELE\_GENE deals with the research of the meshes in opposite in all the cases, while being based on the definition of the interfaces in glance (operator DEFI\_INTERF\_DYNA – U4.64.01). If the interface is incompatible, and that the keyword is not indicated, it is under structure 1 which is defined like mistress.

### 3.2.4 Operand SOUS\_STRUC\_2

- ◆ SOUS\_STRUC\_2 = 'nom\_sstruc2'

Name of the second of the substructures put concerned on both sides of the connection. It must have been as a preliminary defined by the keyword SOUS\_STRUC.

### 3.2.5 Operand INTERFACE\_2

*Warning : The translation process used on this website is a “Machine Translation”. It may be imprecise and inaccurate in whole or in part and is provided as a convenience.*

◆ INTERFACE\_2 = 'nom\_int2'

Name of the interface of the second substructure intervening in the connection. It must have been as a preliminary defined by the operator DEFI\_INTERF\_DYNA [U4.64.01] for the macro - element support of the substructure.

**Note:**

*In the case of the use of modes of couplings (operator MODE\_STATIQUE) with keyword MODE\_INTERF, it is essential that the dynamic interface is of type CRAIGB.*

## 3.2.6 Operand GROUP\_MA\_MAIT\_2, MAILLE\_MAIT\_2

◇ GROUP\_MA\_MAIT\_2 = lgma2  
◇ MAILLE\_MAIT\_2 = lma2

This keyword makes it possible to indicate under structure Master, independently of the mesh or the group of mesh specified as starter. Operator DEFI\_MODELE\_GENE deals with the research of the meshes in opposite in all the cases, while being based on the definition of the interfaces in glance (operator DEFI\_INTERF\_DYNA – U4.64.01). If the interface is incompatible, and that the keyword is not indicated, it is under structure 1 which is defined like mistress.

## 3.2.7 Operand OPTION

◇ OPTION = / 'CLASSICAL',  
/ 'REDUCED',

Allows to choose between a classical under-structuring by static modes (method Mac - Neal, harmonic Craig-Bampton or not) or by modes of interface.

## 3.3 Keyword VERIF

◇ VERIF

Keyword factor allowing to check the coherence of the generalized model: it is checked that the connection is compatible with the orientations and the translations affected to under - structures. The nodes of the two interfaces do not have *a priori* not with being ordered so that they are two to two confused. If the nodes of the interfaces are not in opposite two to two, the code detects this state and reorders the nodes in order to give them in opposite.

### 3.3.1 Operand STOP\_ERREUR

Allows to carry out or not the checking of coherence of the generalized model.

### 3.3.2 Operands PRECISION/CRITERION

Indicate the threshold of precision to beyond which the connections are incompatible. It is the distance (relative or absolute following CRITERION) beyond which the nodes of connection are regarded as too distant being actually connected.

## 3.4 Keyword INFORMATION

Keyword allowing to specify level of impression.

## 4 Production run

The operator carries out a certain number of checks on the coherence of the connections if the connection does not present an incompatibility of grid:

- identical number of nodes on both sides of the connection,

- coherence, in each node, after orientation of the active degrees of freedom on both sides of the connection.

## 5 Matrices and conditions of connections calculated by DEFI\_MODELE\_GENE

### 5.1 In the case of the option 'CLASSICAL'

The operator calculates the matrices of directed connection intervening in the generalized model:

$$L_{j \text{ orientee}}^k = B_j^k R^k \Phi^k$$

where: the exhibitor  $k$  characterize the substructure,

the index  $j$  characterize the interface of connection,

$B_j^k$  is the matrix of extraction of the degrees of freedom of the connection  $j$ ,

$R^k$  is the matrix of rotation which makes it possible to pass from the orientation of the model which has given rise to the macronutrient that of the substructure,

$\Phi^k$  is the matrix column of the clean vectors of the substructure  $k$ .

Conditions of connection between substructures 1 and 2 being written:

$$q_{j \text{ orientee}}^1 = q_{j \text{ orientee}}^2, \text{ with } q_{j \text{ orientee}}^k = L_{j \text{ orientee}}^k \eta^k$$

where:  $q_j^k$  is the vector column of the physical coordinates of the connection  $j$  under - structure  $k$ ,

$\eta^k$  is the vector column of the generalized coordinates of the substructure  $k$ .

### 5.2 In the case of the option 'REDUCED'

The operator calculates the matrices of directed connection intervening in the generalized model:

$$L_{j \text{ orientee}}^k = B_j^k R^k \Phi^k$$

where: the exhibitor  $k$  characterize the substructure,

the index  $j$  characterize the interface of connection,

$B_j^k$  is the matrix of extraction of the degrees of freedom of the connection  $j$ ,

$R^k$  is the matrix of rotation which makes it possible to pass from the orientation of the model which has given rise to the macronutrient that of the substructure,

$\Phi^k$  is the matrix column of the clean vectors of the substructure  $k$ .

In the case of the option 'REDUCED', one restricts the generalized movements of the two interfaces. One ensures:

$$[\Phi_{\text{esclave}}]^T q_{j \text{ orientee}}^1 = [\Phi_{\text{esclave}}]^T q_{j \text{ orientee}}^2, \text{ with } q_{j \text{ orientee}}^k = L_{j \text{ orientee}}^k \eta^k$$

Indeed, in the case of the "CLASSICAL" option, the choice of the degrees of freedom Master and slave amount writing the equation of connection in the form

$$y_{\text{esclave}} - C y_{\text{maître}} = 0,$$



where  $y$  corresponds to the degrees of freedom. However, the use of a space of size reduced for the writing of the relation amounts imposing the following constraints:

$$\Phi_{\text{esclave}} q_{\text{esclave}} - C \Phi_{\text{maître}} q_{\text{maître}} = 0 .$$

One has, so more equations than unknown factors, the number of degrees of generalized freedom  $q_{\text{esclave}}$  being definitely lower than the number of physical degrees of freedom of the interface  $y_{\text{esclave}}$ . To ensure the good conditioning of the conditions of connection, one thus projects this relation on the restriction on the interface of the modes of under structure slaves, and the relation to be checked becomes then:

$$\Phi_{\text{esclave}}^T \Phi_{\text{esclave}} q_{\text{esclave}} - \Phi_{\text{esclave}}^T C \Phi_{\text{maître}} q_{\text{maître}} = 0$$

The choice of under structure Master thus conditions the quality of the sticking together in the case of strongly incompatible interfaces.

**Note:**

*It is appropriate, in the case of the use of the option particularly to pay attention to the choices of the main interfaces and slave, insofar as the kinematic relation between the interfaces is written on the degrees of physical freedom, but that the relation is then projected on the modes of the interface slave. If two modelings are identical (3D – 3D, or 2D-2D), and the discretization equivalent, then the main interface will be the interface presenting more a large number of modes. In the case of different modelings, it will have to be made sure that one has an equivalent number of modes of interface for each one of under structures, ideally a little less for under structure slave, and to choose like interface Master that presenting the coarsest discretization. In all the cases, while waiting for the development of tools making it possible to evaluate the quality of the sticking together, it will be necessary to carry out a visual checking of the results.*