

## Structure of data sd\_nume\_ddl\_gene, sd\_vect\_asse\_gene and sd\_matr\_asse\_gene

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### Summary:

This document describes the structures of data associated with projection on a modal basis of type `mode_meca` or established starting from a concept `modele_gene` resulting from the `sous_structuration`, i.e.: `nume_ddl_gene`, `vect_asse_gene` and `matr_asse_gene`.

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## 1 General information

One `nume_ddl_gene` is used to define the classification of the generalized coordinates of a system associated with a base with projection of the type `mode_meca` or starting from a concept `modele_gene` resulting from the `sous_structuration`.

The projection of vectors or matrices, assembled according to it `nume_ddl_gene` on the modes of the base of projection or on those of `modele_gene`, resulting from the `sous_structuration` respectively creates concepts of vectors or matrices generalized (`vect_asse_gene` resp. `matr_asse_gene`)

The number of terms or equations of the vectors or matrices generalized depends amongst modes taken into account in the concept `nume_ddl_gene`.

The generalized matrices are stored in only one block according to a diagonal storage (in this case, as many terms as of modes) or full (in this case, its terms are arranged like a half stamps symmetrical in its object `.VALM`).

## 2 Tree structure

```
NUME_DDL_GENE (K14):: =record
  (O) \'.NUMÉRIQUE' : PROF_GENE
  (O) \$.VIDE' : STORAGE
  (F) \'.ELIM' : ELIMINATION

PROF_GENE (K19):: =record
  (O) \'.DESC' : OBJ S V I length = 1
  (O) \'.NEQU' : OBJ S V I
  (O) \'.REFN' : OBJ S V K24
  (O) \'.DEEQ' : OBJ S V I
  (O) \'.DELG' : OBJ S V I
  (O) \'.LILI' : OBJ S NR K24
  (O) \'.NUEQ' : OBJ S V I
  (O) \'.PRNO' : OBJ XC V I NAME ($.LILI) LENGTH (2)
  (O) \'.ORIG' : OBJ XC V I NAME ($.LILI) LENGTH (2)

STORAGE (K14):: =record
  (O) \'.SLCS' : STOC_LCIEL (see D4.06.07)
  (O) \'.SMOS' : STOC_MORSE (see D4.06.07)

ELIMINATION (K19):: =record
  (O) \'.BASE' : OBJ S V R
  (O) \'.NOMS' : OBJ S V K8
  (O) \'.TAIL' : OBJ S V I

VECT_ASSE_GENE (K19):: =record
  (O) \'.DESC' : OBJ S V I
  (O) \'.REFE' : OBJ S V K24
  (O) \'.VALE' : OBJ S V R

MATR_ASSE_GENE (K19):: =record
  (O) \'.DESC' : OBJ S V I
  (O) \'.REFE' : OBJ S V K24
  (O) \'.VALM' : OBJ S V R
```

## 2.1 NUME\_DDL\_GENE

## 2.2 PROF\_GENE

### 2.2.1 '.DESC' S V I length = 1

V (1) : 2

### 2.2.2 '.LILI' S NR long K24 = 2

It is the pointer of names of '.PRNO'. It contains them `ligrels` substructures and connections '`&SOUSSTR`' and '`LIAISONS`'. If generalized classification is associated with a base of projection of the type `mode_meca`, it is considered that there are only one substructure and no connection.

The collection '`.PRNO`' thus contains 2 objects:

- PRNO (1) : numbers of the first modes of the substructures of name '`&SOUSSTR`'
- PRNO (2) : numbers of first Lagranges of the connections of name '`LIAISONS`'

### 2.2.3 '.PRNO' XC V I NAME (\$.LILI) LONG = 2

This collection describes the numbers of the modes (resp. lagranges) carried by the substructures (resp. connections).

It contains 2 vectors pointed respectively by the names '`&SOUSSTR`' and '`CONNECTIONS`'. That is to say:

```
V = PRNO (1)
V (2* (STI-1) +1) = imod
V (2* (STI-1) +2) = nb_mod
```

`.imod` is the number of the first mode of `STI`<sup>ième</sup> substructure.  
`.nb_mod` is the number of modes of `STI`<sup>ième</sup> substructure.

```
V = PRNO (2)
V (2* (ilia-1) +1) = ilag
V (2* (ilia-1) +2) = nb_lag
```

`.ilag` is the number of equation of the first lagrange of `ilia`<sup>ième</sup> substructure.  
`.nb_lag` is the number of lagranges of `ilia`<sup>ième</sup> connection.

### 2.2.4 '.ORIG' XC V I NAME (\$.LILI) LONG = 2

This collection describes the numbers of the substructures (resp. connections) carrying the modes (resp. lagranges).

It contains 2 vectors pointed respectively by names '`&SOUSSTR`' and '`CONNECTIONS`'. That is to say:

```
V = PRNO (1)
```

```
V (imod) = STI
V = PRNO (2)
V (ilag) = ilia
```

.isst is the number of substructure of imod<sup>ième</sup> mode.  
.ilia is the number of connection of ilag<sup>ième</sup> lagrange.

## 2.2.5 `\.NEQU'` S V I length = 1

V (1) : full number of equations ( neq )

## 2.2.6 `\.NUEQ'` S V I length = neq

It is a vector containing the numbers of the equations.

V (ieq) =ieq

This vector is "foreseeable", it is useless.

## 2.2.7 `\.DEEQ'` S V I length = 2\*neq

If ieq is a number of equation (i.e addresses in the object .VALE).

```
V ((ieq-1) *2+1) : imod
V ((ieq-1) *2+2) : STI
```

- If imod > 0 and STI > 0  
nueq is the equation associated with imod<sup>ième</sup> mode of STI<sup>ième</sup> substructure.
- If imod = 1 and STI < 0  
nueq is an equation of STI<sup>ième</sup> connection.

## 2.2.8 `\.DELG'` S V I length = neq

V (ieq) : 0

This object is useless.

## 2.2.9 `\.REFN'` S V K8 length = 4

V (1) : name of the generalized model (if it is necessary).

V (2) : 'DEPL\_R'

V (3.4) : ''

## 2.3 ELIMINATION

They are a set of objects optional, created when `NUME_DDL_GENE` is called with the method 'ELIMINATE'. One created and one store the objects for the assembly of the matrices generalized, and the restitution on physical basis.

.BASE		Matrix allowing to carry out the elimination of the constraints (cf the section dedicated in the reference material R4.06.02)
.NAMES		Names of under structures, classified in the order corresponding to storage in the matrix.BASE
.TAIL		Number of DDL generalized of under structures, in the order given par.NAMES

For example, if there are 3 pennies named structures " SST1 ", " SST2 " and " SST3 ", counting respectively  $N_1$ ,  $N_2$  and  $N_3$  degrees of freedom, the matrix.BASE will have  $N_1+N_2+N_3$  lines, and as many columns as of independent degrees of freedom.  $N_1$  first lines are associated with under structure " SST1 ",  $N_2$  following lines with under structure " SST2 ", and them  $N_3$  last lines with under structure " SST3 ".

## 2.4 VECT\_ASSE\_GENE

.REFE	(1) (2)	name of the base of projection: type <code>mode_meca</code> name of the concept <code>nume_ddl_gene</code> having been useful for projection
.DESC	(1) (2) (3)	= 1 because vector many vectors used in the base: <code>n_vect</code> type of storage: = 1 so diagonal, = 2 so full
.VALE		S V I dim = <code>n_vect</code>
.VALE	(I)	value of $I^{\text{ème}}$ stored term

## 2.5 MATR\_ASSE\_GENE

.REFE	(1) (2)	name of the base of projection: type <code>mode_meca</code> name of the concept <code>nume_ddl_gene</code> having been useful for projection
.DESC	(1) (2) (3)	= 2 because matrix many vectors used in the base: <code>n_vect</code> type of storage: = 1 so diagonal, = 2 so full, =3 so unspecified
.VALM		S V I dim = <code>n_termes</code> , <code>n_termes</code> is worth <code>n_vect</code> if diagonal storage and <code>n_vect*(n_vect+1)/2</code> if full storage
.VALM	(I)	value of $I^{\text{ème}}$ stored term