

## Data format sd\_nume\_ddl\_gene, sd\_vect\_asse\_gene and sd\_matr\_asse\_gene

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### Summarized:

This document describes data structures associated with projection on a modal base of the mode\_meca type or established 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

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

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

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

The generalized matrixes 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 symmetric in its object ".VALE").

## 2 Tree structure

```
NUME_DDL_GENE (K14):: =record
(O) ".NUMÉRIQUE" : PROF_GENE
(O) "$VIDE" : STOCKAGE
(F) ".ELIM" : ELIMINATION
(O) ".NSLV" : OJB S V K8 length = 1

PROF_GENE (K19):: =record
(O) ".DESC" : OJB S V I long = 1
(O) ".NEQU" : OJB S V I
(O) ".REFN" : OJB S V K24
(O) ".DEEQ" : OJB S V I
(O) ".DELG" : OJB S V I
(O) ".LILI" : OJB S N K24
(O) ".NUEQ" : OJB S V I
(O) ".PRNO" : OJB XC V I NOM ($.LILI) LONG (2)
(O) ".ORIG" : OJB XC V I NOM ($.LILI) LONG (2)

STOCKAGE (K14):: =record
(O) ".SLCS" : STOC_LCIEL (see D4.06.07)
(O) ".SMOS" : STOC_MORSE (see D4.06.07)

ELIMINATION (K19):: =record
(O) ".BASE" : OJB S V R
(O) ".NOMS" : OJB S V K8
(O) ".TAIL" : OJB S V I

VECT_ASSE_GENE (K19):: =record
(O) ".DESC" : OJB S V I
(O) ".REFE" : OJB S V K24
(O) ".VALE" : OJB S V R

MATR_ASSE_GENE (K19):: =record
(O) ".DESC" : OJB S V I
(O) ".REFE" : OJB S V K24
(O) ".VALE" : OJB S V R
```

## 2.1 NUME\_DDL\_GENE

### 2.1.1 ".NSLV" S V K24 long = 1

V (1) : name of the *sd\_solvor* associated with *NUME\_DDL\_GENE*

## 2.2 PROF\_GENE

### 2.2.1 ".DESC" S V I long = 1

V (1) : 2

### 2.2.2 ".LILI" S N K24 long = 2

It is the pointer of names of ".PRNO". It contains the *ligrels* of substructures and connections "&SOUSSTR" and "CONNECTIONS". If generalized classification is associated with a projection base of the *mode\_meca* type, it is considered that there is only one substructure and no connection.

Collection ".PRNO" thus contains 2 objects:

- PRNO (1) : numbers of the first modes of substructures of name "&SOUSSTR"
- PRNO (2) : numbers of the first Lagranges of connections of name "CONNECTIONS"

### 2.2.3 ".PRNO" XC V I NOM (\$.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 names "&SOUSSTR" and "CONNECTIONS". That is to say:

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

.imod is the number of the first mode of the *isstième* substructure.

.nb\_mod is the number of modes of *isstième* substructure.

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

.ilag is the number D" equation of the first lagrange of the *iliaième* substructure.

.nb\_lag is the number of lagranges of the *iliaième* connection.

### 2.2.4 ".ORIG" XC V I NOM (\$.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 imodième mode.  
.ilia is the number of connection of the ilagième lagrange.

## 2.2.5 ".NEQU" S V I long = 1

V (1) : nombre total of equations ( neq )

## 2.2.6 ".NUEQ" S V I long = 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 long = 2\*neq

If ieq is a number of equation (i.e addresses in 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 the imodième mode with isstième substructure . If
- imod = 1 and STI < 0 nueq  
is an equation of the isstième connection . "

## 2.2.8 "DELG" S V I long = neq V

(ieq) : 0 This  
object is useless. "

## 2.2.9 ".REFN" S V K8 length = 4 V (

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

2) : "DEPL\_R" V (

3,4) : 'ELIMINATION

## 2.3 It

acts of a set of objects optional, created when NUME\_DDL\_GENE is called with method "ELIMINE". One created and one store the objects for the assembly of the matrixes generalized, and the restitution on physical base. .BASE

Stamps		making it possible to carry out the elimination of the stresses (cf the section dedicated in R4.06.02 documentation of reference) .NOMS
Names		of under structures, classified in the order corresponding to storage in matrix .BASE .TAIL
Number of D.O.F.		generalized of under structures, in the order given by .NOMS For example

, if one have 3 pennies named structures "ST 1", "ST 2" and "ST 3", counting N1 respectively, N2 and N3 degrees of freedom, matrix .BASE will have N1+N2+N3 lines, and as many columns as of independent degrees of freedom. The N1 first lines are associated with under structure "ST 1", N2 following lines with under structure "ST 2", and the N3 last lines with under structure "ST 3". VECT\_ASSE\_GENE

## 2.4 .REFE

(1	) (2) nam e	of projection base: standard mode <code>_meca</code> name of the numerical concept <code>_ddl_gene</code> having been useful for projection .DESC
(1	) (2) (3) ) =	1 because vecteurnombre of vectors used in the base: <code>n_vect</code> standard of storage: = 1 so diagonal, = 2 so full .VALE
S		V I dim = <code>n_vect</code> .VALE
(I	) valu e	of the <code>ième</code> term stored MATR_ASSE_GENE

## 2.5 .REFE

(1	) (2) nam e	of projection base: standard mode <code>_meca</code> name of the numerical concept <code>_ddl_gene</code> having been useful for projection .DESC
(1	) (2) (3) ) =	2 because matricenombre of vectors used in the base: <code>n_vecttype</code> of storage: = 1 so diagonal, = 2 so full .VALE
S		V I dim = <code>n_termes</code> , <code>n_termes</code> are worth <code>n_vect</code> if diagonal storage and <code>n_vect* (n_vect + 1)/2</code> if storage full .VALE
(I	) valu e	of the <code>ième</code> stored term