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## Procedure IMPR\_GENE

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### 1 Goal

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To write the result of a dynamic calculation in variables generalized on a file, with the format 'RESULT'.

Currently this procedure makes it possible to write results in generalized variables resulting from the following concepts:

- tran\_gene ,
- vect\_asse\_gene ,
- harm\_gene,
- mode\_gene.

## 2 Syntax

```

IMPR_GENE (
  ◊ FORMAT      = / 'RESULT',           [DEFECT]
  ◊ UNIT        = / links,              [I]
  / 8,          [DEFECT]
  ◆ GENE       = _F (
# If RESU_GENE = [vect_asse_gene]
  / ◆ RESU_GENE = tg,                   [vect_asse_gene]
  ◊ / TOUT_CMP_GENE = / 'YES',         [DEFECT]
  / 'NOT',
  / NUME_CMP_GENE = lordre,           [l_I]
# If RESU_GENE = [harm_gene] or [mode_gene]
  / ◆ RESU_GENE = tg,                   ~ [harm_gene]
  ~ [mode_gene]
  ◊ / TOUT_CHAM   = / 'NOT',           [DEFECT]
  / 'YES',
  / NOM_CHAM     = l_cham,             [l_Kn]
  ◊ / TOUT_PARA   = / 'YES',           [DEFECT]
  / 'NOT',
  / NOM_PARA     = lnomsymb,           [l_Kn]
  ◊ / TOUT_CMP_GENE = / 'YES',         [DEFECT]
  / 'NOT',
  / NUME_CMP_GENE = lordre,           [l_I]
  ◊ / ◊ / TOUT_ORDRE = 'YES',          [DEFECT]
  / NUME_ORDRE   = lordre,            [l_I]
  / LIST_ORDRE   = slow,              [listis]
  / ◊ / TOUT_MODE  = 'YES',           [DEFECT]
  / NUME_MODE    = lmode,             [l_I]
  / ◊ / FREQ       = lfreq,           [l_R]
  / LIST_FREQ    = lreel,             [listr8]
  ◊ CRITERION    = / 'ABSOLUTE',
  / 'RELATIVE', [DEFECT]
  ◊ PRECISION    = / prec,            [R]
  / 1.E-06,     [DEFECT]
# If RESU_GENE = [tran_gene]
  / ◆ RESU_GENE = tg,                   [tran_gene]
  ◊ / TOUT_CHAM   = 'YES',             [DEFECT]
  / NOM_CHAM     = l_cham,            [l_Kn]
  ◊ / TOUT_CMP_GENE = / 'YES',
  / 'NOT',
  / NUME_CMP_GENE = lordre,           [l_I]
  ◊ / ◊ / TOUT_ORDRE = 'YES',          [DEFECT]
  / NUME_ORDRE   = lordre,            [l_I]
  / LIST_ORDRE   = slow,              [listis]
  / ◊ / INST       = linst,           [l_R]
  / LIST_INST    = lreel,             [listr8]
  / TOUT_INST    = 'YES',             [DEFECT]
  ◊ CRITERION    = / 'ABSOLUTE',
  / 'RELATIVE', [DEFECT]
  ◊ PRECISION    = / prec,            [R]
  / '1.E-03',   [DEFECT]
  ◊ INFO_CMP_GENE = / 'YES',           [DEFECT]
  / 'NOT',
  ◊ SOUS_TITRE   = txt,                [KN]

```

# Code\_Aster

Version  
default

Titre : Procédure IMPR\_GENE  
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```
        ◇ INFO_GENE = 'YES',  
        'NOT',  
    ),
```

## 3 Keyword GENE

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This keyword factor makes it possible to specify the results to print. At least a block factor of the keyword is necessary for each result which one wishes to print.

## 4 Operand RESU\_GENE

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This keyword makes it possible to specify the name user of the concept of the type `tran_gene`, `vect_asse_gene`, `harm_gene` or `mode_gene` to print.

## 5 Variables of access if concept of the type vect\_asse\_gene

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### 5.1 Operands TOUT\_CMP\_GENE / NUME\_CMP\_GENE

The keyword `TOUT_CMP_GENE` indicate that one wants or not to print the fields for all the numbers of generalized components (except those which correspond to ddl of Lagrange).

The keyword `NUME_CMP_GENE` indicate that one wants to print the fields which correspond to a list of numbers of generalized components.

## 6 Variables of access if concept of the type mode\_gene or harm\_gene

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### 6.1 Extraction of a field of result: operands TOUT\_CHAM / NOM\_CHAM

The keyword `TOUT_CHAM` indicate that one wants to print all the actually calculated fields.

The keyword `NOM_CHAM` allows to choose a list of reference symbols of fields among the whole of the possible ones.

### 6.2 Extraction of a parameter: operands TOUT\_PARA / NOM\_PARA

The keyword `TOUT_PARA` indicate that one wants or not to print all the values of the parameters attached to the concept considered.

The keyword `NOM_PARA` allows to choose a list of reference symbols of parameters among the whole of the possible ones.

These keywords are available only for the concept of the type `mode_gene`.

### 6.3 Operands TOUT\_CMP\_GENE / NUME\_CMP\_GENE

The keyword `TOUT_CMP_GENE` indicate that one wants to print the fields for all the numbers of generalized components (except those which correspond to ddl of Lagrange).

The keyword `NUME_CMP_GENE` indicate that one wants to print the fields which correspond to a list of numbers of generalized components.

## 6.4 Operands TOUT\_ORDRE / NUME\_ORDRE / LIST\_ORDRE

The keyword `TOUT_ORDRE` indicate that one wants to print the fields for all the sequence numbers.

The keyword `NUME_ORDRE` and `LIST_ORDRE` allow to print only the fields corresponding to a list of sequence numbers `lordre` or `slow` defined by `DEFI_LIST_ENTI` [U4.34.02] (`slow` is thus a concept of the type `listis`).

## 6.5 Operands TOUT\_MODE / NUME\_MODE

The keyword `TOUT_MODE` indicate that one wants to print the fields for all the numbers of mode.

The keyword `NUME_MODE` indicate that one wants to print the fields corresponding to a list of numbers of mode `lmode`. These numbers are those affected by the calculation algorithm.

This keyword is usable only for one concept of the type `mode_gene`.

## 6.6 Operands FREQ / LIST\_FREQ

The keyword `FREQ` indicate that one wants to print the fields corresponding to a list of frequency `lfreq`.

The keyword `LIST_FREQ` indicate that one wants to print the fields corresponding to a list of frequencies `lreel`, defined by the operator `DEFI_LIST_REEL` [U4.34.01] (`lreel` is thus a concept of the type `listr8`).

This keyword is usable for a concept of the type `harm_gene`, and possibly `mode_gene`.

## 6.7 Operands CRITERION / PRECISION

The keyword `PRECISION` indicate with which precision one must carry out the research of the frequency of calculation.

The keyword `CRITERION` indicate with which type of interval of precision the research of the frequency of interpolation must be carried out:

`'ABSOLUTE'` : interval of research [`Fr-prec`, `fr+prec`]  
`'RELATIVE'` : interval of research [(`1-prec`) `Fr`, (`1+prec`) `Fr`]

## 7 Variables of access if concept of the type `tran_gene`

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### 7.1 Extraction of a field of result

- Operands `TOUT_CHAM / NOM_CHAM`  
See [§6.1].
- Operands `TOUT_CMP_GENE / NUME_CMP_GENE`  
See [§6.3]
- Operands `TOUT_ORDRE / NUME_ORDRE / LIST_ORDRE`  
See [§6.4].

### 7.2 Operands `INST / LIST_INST / CRITERION / PRECISION`

The keyword `INST` indicate that one wants to print the fields corresponding to a list of moments `linst`.

The keyword `LIST_INST` indicate that one wants to print the fields corresponding to a list of moments `lreel`, defined by the operator `DEFI_LIST_REEL [U4.34.01]` (`lreel` is thus a concept of the type `listr8`).

For `CRITERION / PRECISION` to see [§6.7] (by replacing frequency per moment).

## 8 Parameters of impression of the results

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### 8.1 Operand `SOUS_TITRE`

This argument makes it possible to print a title of comments.

### 8.2 Operand `FORMAT`

Format of impression of the results in the output file.

For the moment only the format `RESULT` is available.

### 8.3 Operand `INFO_GENE`

During the impression of a generalized concept, one can have forgotten the exact contents of the structure of data. The operand `INFO_GENE` allows to print these contents (many sequence numbers, list of the reference symbols of the actually calculated fields, list of the reference symbols of the actually calculated parameters,...).

### 8.4 Extraction of a genealogy of the generalized model: operand `INFO_CMP_GENE`

This keyword indicates that one wants or not to print for each generalized component the name of the concept `base_modale` or `mode_meca` from which the mode corresponding to this component is resulting, its type (clean or constrained), its frequency and the node of application of this mode if it is constrained.

## 8.5 Production run

For the concepts `tran_gene` and `harm_gene`, it is checked that the moments (frequencies) of extraction requested by the operands `NUME_ORDRE`, `LIST_ORDRE`, `INST`, `LIST_INST`, (`FREQ`, `LIST_FREQ`) are in the field of definition of the concept. It is also checked that the fields stipulated by the keywords `TOUT_CHAM`, `NOM_CHAM`, were indeed calculated.

For the concept `mode_gene`, it is checked that the names of the parameters specified by the keyword `NOM_PARA` are quite acceptable. If the number of the mode is selected by the operand `NUME_MODE`, it is checked that this number is lower than the full number of modes which define it `mode_gene`.

## 9 Examples

### 9.1 Impression of one `vect_asse_gene`

```
IMPR_GENE (GENE = _F ( RESU_GENE = fgen,
                        NUME_CMP_GENE = 'YES' ),
           _F ( RESU_GENE = fgen,
                INFO_CMP_GENE = 'NOT',
                NUME_CMP_GENE = 1 )
          )
```

The following impression is obtained:

CONCEPT	FGEN	OF TYPE VECT_ASSE_GENE				
NUME_CMP	VALUE	BASE_MODALE	TYPE_MODE	FREQUENCY	APPLICATION	
1	1.00000E+00	BAM01_CL	CLEAN	2.25079E-01		
2	5.00000E-01	BAM01_CL	CONSTRAINED	0.00000E+00	N03	DX
3	0.00000E+00	BAM02_CL	CLEAN	2.25079E-01		
4	0.00000E+00	BAM02_CL	CONSTRAINED	0.00000E+00	N01	DX

  

CONCEPT	FGEN	OF TYPE VECT_ASSE_GENE				
NUME_CMP	VALUE					
1	1.00000E+00					

### 9.2 Operand UNIT

```
◇ UNIT = / links, [I]
        / 8, [DEFECT]
```

The results are written, by default, on the logical file of unit 8. The user can define another output file of which it indicates the logical unit.

### 9.3 Impression of one `mode_gene`

```
IMPR_GENE (GENE = _F ( RESU_GENE = resgen,
                        INFO_GENE = 'YES',
                        NUME_ORDRE = 1,
                        NOM_PARA = ('FREQ', 'MASS_GENE',
                                   'RIGI_GENE' ),
                        INFO_CMP_GENE = 'NOT' ),
           _F ( RESU_GENE = resgen,
```

```
NUME_CMP_GENE = (1, 3),  
NUME_ORDRE = 1,  
NOM_PARA = ('FREQ', 'MASS_GENE',  
'RIGI_GENE'),  
INFO_CMP_GENE = 'YES' )  
)
```

The results are written, by default, on the file associated with the logical unit 8. But the user can define another output file of which it indicates the logical unit. [U4.12.01].