
Procedure IMPR_GENE

1 Goal

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]

```

```
        ◇ INFO_GENE = 'YES',  
        'NOT',  
    ),
```

3 Keyword GENE

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

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

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

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`

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

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 `UNIT`

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

8.4 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,...).

8.5 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.

8.6 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 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') ),
           _F ( RESU_GENE = resgen,
                NUME_CMP_GENE = (1, 3),
                NUME_ORDRE = 1,
                NOM_PARA = ('FREQ', 'MASS_GENE',
                             'RIGI_GENE') ),
           INFO_CMP_GENE = 'YES' )
          )
```