Code_Aster

Version default

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Responsable : Albert ALARCON

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Procedure `IMPR_GENE`

1   Drank

To write result dynamic computation in variables generalized on a file, with format "RESULTAT".

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.

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2 Syntax

```
IMPR_GENE   (
   ◊FORMAT=/              "RESULTAT",                    [DEFAULT]
   ◊UNITE=/unit              ,                          [I]
               /8,                                       [DEFAULT]
   ♦GENE=_F         (
# If RESU_GENE = [vect_asse_gene]
           /♦RESU_GENE=tg          ,                    /
   [vect_asse_gene]
           ◊/TOUT_CMP_GENE=/            "OUI',
[DEFAULT]
                           /   "NON",
             /NUME_CMP_GENE        =lordre   ,          [l_I]
# If RESU_GENE = [harm_gene] or [mode_gene]
           /♦RESU_GENE=tg          ,              ˜
   [harm_gene]
                                        ˜         [mode_gene]
           ◊/TOUT_CHAM=/              "NON",
                           /   "OUI',        [DEFAULT]
             /NOM_CHAM        =l_cham   ,       [l_Kn]
           ◊/TOUT_PARA=/              "OUI',       [DEFAULT]
                           /   "NON",
             /NOM_PARA        =lnomsymb   ,       [l_Kn]
           ◊/TOUT_CMP_GENE=/            "OUI',
[DEFAULT]
                           /   "NON",
             /NUME_CMP_GENE        =lordre   ,       [l_I]
                   ◊/◊/TOUT_ORDRE=' OUI',     [DEFAULT]
             /NUME_ORDRE        =lordre   ,     [l_I]
             /LIST_ORDRE        =lent ,       [listis]
                       /◊/TOUT_MODE=' OUI',
[DEFAULT]
             /NUME_MODE          =lmode   ,          [l_I]
           /◊/FREQ=lfreq                ,          [l_R]
             /LIST_FREQ        =lreel   ,       [listr8]
             ◊CRITERE=/           "ABSOLU",
                       /   "RELATIF",     [DEFAULT]
             ◊PRECISION=/prec         ,          [R]
                       /1.E-06   ,       [DEFAULT]
# If RESU_GENE = [tran_gene]
         /♦RESU_GENE=tg          ,
   [tran_gene]
                       ◊/TOUT_CHAM=' OUI',
[DEFAULT]
             /NOM_CHAM        =l_cham   ,          [l_Kn]
           ◊/TOUT_CMP_GENE=/            "OUI',
                       /   "NON",
             /NUME_CMP_GENE        =lordre   ,       [l_I]
                   ◊/◊/TOUT_ORDRE=' OUI',       [DEFAULT]
             /NUME_ORDRE        =lordre   ,     [l_I]
             /LIST_ORDRE        =lent ,        [listis]
           /◊/INST=linst                ,        [l_R]
             /LIST_INST        =lreel   ,       [listr8]
             /TOUT_INST        =  ' OUI',
   [DEFAULT]
```

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```
                         ◊CRITERE=/              "ABSOLU",
                                    /   "RELATIF",     [DEFAULT]
                         ◊PRECISION=/prec              ,           [R]
                                    /   "1.E-03",      [DEFAULT]

             ◊INFO_CMP_GENE=/                 "OUI',         [DEFAULT]
                                    /   "NON",
             ◊SOUS_TITER=txt          ,                      [kN]

             ◊INFO_GENE=             `OUI',
                              "NON",
          ),
    )
```

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3   Key word GENE

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

4   Operand RESU_GENE

This key word makes it possible to specify the name user of the concept of the tran_gene type, vect_asse_gene, harm_gene or mode_gene to be printed.

5   Variables of access if concept of the type vect_asse_gene

5.1   Operands TOUT_CMP_GENE / NUME_CMP_GENE

key word TOUT_CMP_GENE indicates that one wants or not to print the fields for all the numbers of generalized components (except those which correspond to d.o.f. of Lagrange).

Key word NUME_CMP_GENE indicates 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 mode_gene type or harm_gene

6.1   Extraction of a field of result: operands TOUT_CHAM / NOM_CHAM

key word TOUT_CHAM indicates that one wants to print all the actually calculated fields.

Key word NOM_CHAM makes it possible to choose a list of symbolic names of fields among all the possible ones.

6.2   Extraction of a parameter: operands TOUT_PARA / NOM_PARA

key word TOUT_PARA indicates that one wants or not to print all the values of the parameters attached to the concept considered.

Key word NOM_PARA makes it possible to choose a list of symbolic names of parameters among all the possible ones.

These key words are available only for the concept of the mode_gene type.

6.3   Operands TOUT_CMP_GENE / NUME_CMP_GENE

key word TOUT_CMP_GENE indicates that one wants to print the fields for all the numbers of generalized components (except those which correspond to d.o.f. of Lagrange).

Key word NUME_CMP_GENE indicates that one wants to print the fields which correspond to a list of numbers of generalized components.

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6.4 Operands `TOUT_ORDRE` / `NUME_ORDRE` / `LIST_ORDRE`

key word `TOUT_ORDRE` indicates that one wants to print the fields for all the sequence numbers.

Key word `NUME_ORDRE` and `LIST_ORDRE` make it possible 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 listis `type`).

6.5 Operands `TOUT_MODE` / `NUME_MODE`

key word `TOUT_MODE` indicates that one wants to print the fields for all the numbers of mode.

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

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

6.6 Operands `FREQ` / `LIST_FREQ`

key word `FREQ` indicates that one wants to print the fields corresponding to a list of frequency `lfreq`.

Key word `LIST_FREQ` by the operator indicates that one wants to print the fields corresponding to a list of `frequencies lreel` , definite `DEFI_LIST_REEL` [U4.34.01] (`lreel` is thus a concept of the listr8 `type`).

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

6.7 Operands `CRITERE` / `accuracy`

the key word `accuracy` indicates with which accuracy one must carry out the search of the frequency of computation.

Key word `CRITERE` indicates with which type of interval of accuracy the search of the frequency of interpolation must be carried out:

"ABSOLU"   :   interval of search `[Fr-PREC, fr+prec]`
"RELATIF":   interval of search `[(1-PREC) Fr, (1+prec) Fr]`

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7 Variable 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` / `CRITERE` / `accuracy`

the key word `INST` indicates that one wants to print the fields corresponding to a list of times `linst`.

Key word `LIST_INST` by the operator indicates that one wants to print the fields corresponding to a list of `times` lreel, definite `DEFI_LIST_REEL` [U4.34.01] (`lreel` is thus a concept of the listr8 type).

For `CRITERE` / `accuracy` to see [§6.7] (by replacing frequency per time).

8 Parameters of printing 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 printing of the results in the output file.

For time only result format is available.

8.3 Operand `UNITE`

the results are written, by default, on the results file . 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 printing of a generalized concept, one can have forgotten the exact contents of data structure. Operand `INFO_GENE` makes it possible to print these contents (many sequence numbers, list of symbolic names of the actually calculated fields, list of symbolic names of the actually calculated parameters,…).

8.5 Extraction of a genealogy of modele generalized: operand `INFO_CMP_GENE`

This key word 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, his type (clean or constrained), his frequency and the node of application of this mode if it is constrained.

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8.6 Stage of execution

For the concepts `tran_gene` and `harm_gene`, one checks that times (frequencies) of extraction required by 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 key words `TOUT_CHAM`, `NOM_CHAM`, were indeed calculated.

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

9 Printing

9.1 examples of a `vect_asse_gene`

```
IMPR_GENE     (GENE =      _F (          RESU_GENE= fgen,
                              NUME_CMP_GENE=    "YES"      ),
                     _F (          RESU_GENE= fgen,
                              INFO_CMP_GENE=    "NON",
                              NUME_CMP_GENE=    1         )
                 )
```

the following printing is obtained:

```
CONCEPTFGENDE              TYPE VECT_ASSE_GENE

              NUME_CMPVALEURBASE_MODALETYPE_MODEFREQUENCEAPPLICATION

   11.00000E+00BAM01_CLPROPRE2.25079E-01
   25.00000E-01BAM01_CLCONTRAINT0.00000E+00N03DX

   30.00000E+00BAM02_CLPROPRE2.25079E-01
   40.00000E+00BAM02_CLCONTRAINT0.00000E+00N01DX


CONCEPTFGENDE              TYPE VECT_ASSE_GENE

NUME_CMPVALEUR
   11.00000E+00
```

9.2 Printing of a `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=    "NON" ),
                  _F (          RESU_GENE= resgen,
                     NUME_CMP_GENE=   (1, 3),
                     NUME_ORDRE = 1,
                     NOM_PARA=  ("FREQ", "MASS_GENE", "RIGI_GENE"),
                      INFO_CMP_GENE=   "YES" )
                 )
```

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