
Operator POST_GENE_PHYS

1 Goal

To restore in the physical base of part of the results in generalized coordinates.

This operator allows to restore in the physical space of the results got on a frame of reference generalized by methods of modal recombination. Unlike the operator `REST_GENE_PHYS`, this operator allows to limit the restitution while filtering on:

- One or more groups/lists of nodes or meshes
- One or more fields with the nodes or the elements, for all the components or only those of interest
- A list of frequency, sequence numbers, or moment according to the type of generalized result

Moreover, the operator automatically takes into account the static correction during the restitution. He also makes it possible to extract displacements and absolute velocities for the systems in multi-supports and to calculate absolute acceleration into mono like in multi-supports.

The produced concept is of type `table`. It could be handled by the classical operators of postprocessing in *Code_Aster* (`RECU_TABLE`, `RECU_FONCTION`, `IMPR_TABLE`).

2 Syntax

```
table = POST_GENE_PHYS (
    ♦ RESU_GENE = res_gen, / [tran_gene]
                        / [harm_gene]
    ◇ MODE_MECA = mode, [mode_meca]

    ♦ OBSERVATION = _F (
        ♦ NOM_CHAM =
            ! Filtering on the name of the field to be restored
            ! Computed field with the nodes
                / 'DEPL', [DEFECT]
                / 'QUICKLY',
                / 'ACCE',
                / 'DEPL_ABSOLU',
                / 'VITE_ABSOLU',
                / 'ACCE_ABSOLU',
                / 'FORC_NODA',
            ! Computed field with the elements
                / 'EFGE_ELNO',
                / 'SIPO_ELNO',
                / 'SIGM_ELNO',
                / 'EFGE_ELGA',
                / 'SIGM_ELGA',

            ! Filtering on the names of components to be restored
            ◇ NOM_CMP = lcomp, [l_K]

            ! Filtering on the group/list of nodes or meshes
            ♦ / GROUP_NO = lgrno, [l_noeud]
              / GROUP_MA = lgrma, [l_gr_ma]

            ! Filtering on the num. of order, moments, or fréqs
            ◇ / TOUT_ORDRE = 'YES', [DEFECT]
              / NUME_ORDRE = num, [l_I]
              / TOUT_INST = 'YES',
              / INST = inst, [l_R]
              / LIST_INST = list, [listr8]
              / FREQ = freq, [l_R]
              / LIST_FREQ = list, [listr8]

            ! Selection criteria if list of moments or frequencies
            ◇ CRITERION = / 'ABSOLUTE',
              / 'RELATIVE', [DEFECT]
            ◇ PRECISION = / prec, [R]
              / 1.E-06, [DEFECT]

            ! If NOM_CHAM = 'ACCE_ABSOLU', in mono-support
            ◇ | ACCE_MONO_APPUI = gamma, [function]
              | DIRECTION = (dx, Dy, dz), [l_R]
        ),
    ◇ TITLE = title, [l_Kn]
)
```

3 Operands

3.1 Operand RESU_GENE

- ◆ RESU_GENE = res_gen
 - / concept of the type tran_gene containing for various moments of the vectors generalized of standard displacement, speed and acceleration.
 - / concept of the type harm_gene containing the vectors generalized of standard displacement, speed and acceleration of the harmonic answer of a structure calculated after a projection on a modal basis

Notice : Restitution of the results by the operator POST_GENE_PHYS is not available for calculations in dynamic under-structuring.

3.2 Operand MODE_MECA

- ◇ MODE_MECA = mode

Concept of the type mode_meca containing a base of clean modes of the structure.

In the absence of this operand, the base of restitution for the modal recombination is recovered automatically starting from the generalized result res_gen at the entrance of the operator.

3.3 Keyword OBSERVATION

This keyword factor can be repeated as many times as there are restitutions. For each observation, the user is free to choose the name of the field and his components, the sequence numbers, and the geometrical support of the restitution.

In the produced table, each occurrence of the keyword OBSERVATION is indexed by the parameter NUME_OBS table.

3.3.1 Filtering by the name of the field and its components

- ◆ NOM_CHAM =/ 'DEPL' , [DEFECT]
 - / 'QUICKLY' ,
 - / 'ACCE' ,
 - / 'DEPL_ABSOLU' ,
 - / 'VITE_ABSOLU' ,
 - / 'ACCE_ABSOLU' ,
 - / 'FORC_NODA' ,
 - / 'EFGE_ELNO' ,
 - / 'SIPO_ELNO' ,
 - / 'SIGM_ELNO' ,
 - / 'EFGE_ELGA' ,
 - / 'SIGM_ELGA' ,

This keyword defines for the observation in progress, the name of the field to be restored. It should be noted that for the fields of force and constraints, it is to the user to make sure that the latter were indeed calculated on the basis of modal projection with the operator CALC_CHAMP. Before calculation, the operator POST_GENE_PHYS check the existence of these fields in the base of projection.

- ◇ NOM_CMP = lcomp, [1 K]

List of the names of components of the field to be restored.

This keyword is optional. If it is absent, all the components of the field are recovered and taken into account. If the user specifies a list of components, the operator POST_GENE_PHYS check initially the existence of these components in the field requested before carrying out calculation.

3.3.2 Filtering by selection of the geometrical support of restitution

```
◆ / GROUP_NO = lgrno, [l_noeud]
  / GROUP_MA = lgrma, [l_gr_ma]
```

It is obligatory to specify one of these 2 keyword. That makes it possible to define the geometrical support for the restitution of the required field (list of the groups of nodes/meshes).

Note:

*For the restitution of an elementary field (**** _EL **), it is essential to specify keyword GROUP_MA to find the groups of elements.*

For a field with the nodes, the user is free choice to define is the nodes directly by the keyword GROUP_NO, or meshes carrying the nodes of interest for the restitution by the keyword GROUP_MA.

3.3.3 Filtering by the sequence numbers, moments, or frequencies of calculation

```
◇ / TOUT_ORDRE = 'YES', [DEFECT]
  / NUME_ORDRE = num, [l_I]
  / TOUT_INST = 'YES',
  / INST = inst, [l_R]
  / LIST_INST = list, [listr8]
  / FREQ = freq, [l_R]
  / LIST_FREQ = list, [listr8]
```

By default, the restitution takes place on the totality of the sequence numbers stored in the result, i.e. for every moment for a transitory calculation and all the frequencies for a harmonic calculation.

It is possible for the user to limit his restitution on part of calculation: a list of sequence numbers (NUME_ORDRE), moments (INST, LIST_INST), or of frequencies (FREQ, LIST_FREQ). It is nevertheless important to note that no interpolation of the results is possible. The moments or frequencies required must obligatorily correspond to moments or frequencies of calculation in the concept tran_gene or harm_gene as starter. The operands following make it possible to regulate the selection criteria of the moments and frequencies.

```
◇ CRITERION = / 'ABSOLUTE',
              / 'RELATIVE, [DEFECT]
◇ PRECISION = / prec, [R]
              / 1.E-06, [DEFECT]
```

3.3.4 Catch in account of an acceleration of training in mono-support

```
◇ | ACCE_MONO_APPUI = gamma, [function]  
  | DIRECTION      = (dx, Dy, dz), [l_R]
```

In mono-support, to restore an acceleration in the absolute reference mark (`ACCE_ABSOLU`), it is necessary to specify the function giving the magnitude of the acceleration of the supports as well as the direction of their movement.

Notice 1:

In multi-support, the calculation of displacements, speeds, and accelerations absolutes does not require an extra information. It is enough to specify one `NOM_CHAM` among `DEPL_ABSOLU`, `VITE_ABSOLU`, and `ACCE_ABSOLU`. Information on the absolute movements of the supports is already stored in the generalized concept.

Notice 2:

If a static correction with the loadings were considered beforehand during calculation on generalized basis (`CORR_STAT=' OUI '` in `DYNA_VIBRA`), this correction is automatically taken into account in the restitutions of `POST_GENE_PHYS`.

3.4 Operands **TITLE**

```
◇ TITLE = title
```

Title attached to the concept produced by this operator [U4.03.01].