Command ACONVERT

PURPOSE Convert an array of one-dimensional analyzers into a two-dimensional analyzer and vice versa

PARAMETERS

ANLID
Name of an array of one-dimensional analyzers, given by name with asterisk extension (e.g. “Q(*)” or one two-dimensional source analyzer, given by name (e.g. “A2”)).

/INTO(anl)
Target analyzer identifier, may be a name or – for an already existing analyzer – a number.
For an array of one-dimensional source analyzers, one two-dimensional analyzer must be given (e.g. “B2”).
For a two-dimensional source analyzer, an array of one-dimensional analyzers must be given (e.g. “R(*)”).
If the target analyzer (array) does not exist, it will be created with the attributes derived from the source analyzer(s).

/DIMENSION(d)
For an array of one-dimensional source analyzers only: Direction in which the data of each one-dimensional source analyzer are inserted in the two-dimensional target analyzer.
Possible values for “c” are “**x**” (horizontal, 0°), “**y**” (vertical, 90°), “**x+y**” (135°), and “**x-y**” (45°). “x” and “y” may be replaced by “1” and “2”, respectively.

/PROJECTION(d)
For two-dimensional source analyzer only: Selected dimension of the source analyzer onto which is to be projected.
Possible values for “d” are “**x**” (horizontal, 0°), “**y**” (vertical, 90°), “**x+y**” (135°), and “**x-y**” (45°). “x” and “y” may be replaced by “1” and “2”, respectively.

/CUTS(c)
For two-dimensional source analyzer only: Direction of cuts in which the data are extracted from the source analyzer.
Possible values for “c” are “**x**” (horizontal, 0°), “**y**” (vertical, 90°), “**x+y**” (135°), and “**x-y**” (45°). “x” and “y” may be replaced by “1” and “2”, respectively.

/LIMITS(l)
Limits for projection, specified by a number list of lower and upper channel number, given in each dimension ($l = x_{min}, x_{max}, y_{min}, y_{max}$).
This keyword is only valid for a two-dimensional source analyzer.

/WINDOW(w)
Limits for projection ,specified by
letter : display window identifier
one number : analyzer condition number
This keyword is only valid for a two-dimensional source analyzer.

FUNCTION For an array of one-dimensional source analyzers:
The array of source analyzers is interpreted as a two-dimensional array and stored in a two-dimensional analyzer. The direction of each one-dimensional source analyzer with respect to the two-dimensional target analyzer is taken from the “/DIMENSION” keyword.

For a two-dimensional source analyzer:
The analyzer spectrum is cut in “slices” in the direction given by the “/CUTS” keyword and stored in an array of one-dimensional target analyzers. The channels of the target analyzers are derived according to the “/PROJECTION” keyword. Data are considered only inside limits selected by “/LIMITS” or “WINDOW”.

REMARKS

The target analyzer(s), if existing, may have any type; the bin size(s) must correspond to the bin size(s) of the source analyzer(s) in the corresponding dimension(s) according to the operation. Diagonal projections are only allowed, if the bin sizes of the two-dimensional source (or destination) analyzer in x and y are equal.

The increment of the index of an array of one-dimensional analyzers on output is taken as one unit, independently of the channel numbers of the two-dimensional source analyzer.

If the directions of CUTS and PROJECTION are identical, it is sufficient to specify one of these.

The command AOPER provides an alternative simple possibility for converting arrays of one-dimensional analyzers into one two-dimensional analyzer (AOPER NZ = N(*)) and to convert one two-dimensional analyzer into an array of one-dimensional analyzers (AOPER N(*) = NZ), see documentation of the command AOPER for details.

EXAMPLE

For illustration we give some examples how to convert nuclear production cross sections given in different forms:
Assume that the 2-dim. analyzer NZ contains nuclide cross sections as a function of neutron number (x axis) and atomic number (y axis).
To produce an array N_PER_Z(*) of analyzers (neutron number on x axis, proton number as index of the analyzer array) with the isotopic cross sections of all elements:
ACONVERT NZ / INTO(N_PER_Z(*)) CUTS(X) PROJ(X)

To produce a series of element distributions with fixed mass (proton number on x axis, mass number as index of the analyzer array):
ACONVERT NZ / INTO(Z_PER_A(*)) CUTS(X-Y) PROJ(Y)

To produce a series of element distributions with fixed values of N-Z (proton number on x axis, neutron excess as index of the analyzer array):
ACONVERT NZ / INTO(Z_PER_NEXC(*)) CUTS(X+Y) PROJ(Y)

To convert an array N_PER_Z(*) of isotopic cross sections into a 2-dim. analyzer in form of a chart of the nuclides:
ACONVERT N_PER_Z(*) / INTO(NZ) DIM(X)