| Command | APROJECT |
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**PURPOSE**  Project the selected part of a two-dimensional analyzer spectrum on the specified dimension and store the result in a target analyzer

**PARAMETERS**

ANLID  Name of the two-dimensional source analyzer.

/ONTO(anl)  Target analyzer identifier, may be a name or – for an already existing analyzer – a number.
If the target analyzer does not exist, it will be created with the attributes derived from the source analyzer.

/DIMENSION(d)  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.

/LIMITS(l)  Limits for projection, specified by a number list of lower and upper channel number, given in each dimension ($l = x_{min}, x_{max}, y_{min}, y_{max}$).

/WINDOW(w)  Limits for projection ,specified by
          letter           : display window identifier
          one number   : analyzer condition number

**FUNCTION**  The analyzer spectrum is summed up along the dimension vertical to the one specified in the keyword "/DIM" and inside limits selected by "/LIMITS" or "WINDOW". The result is stored in a one-dimensional analyzer in direction of the "/DIM" keyword.

**REMARKS**  The target analyzer, if existing, may have any type; the bin size must correspond to the bin size of the source analyzer in the dimension specified by the "/DIM" keyword. Diagonal projections are only allowed, if the binsizes of the source analyzer in x and y are equal. Projection limits concern the dimension along which, as well as the dimension onto which, the spectrum will be projected. Only channel number limits differing from input analyzer limits must be specified.

For illustration, we give the values to be specified for the "/DIM" keyword for specific projections of data stored on a chart of the nuclides with neutron number in horizontal and proton number in vertical direction:
      x          projection on neutron number (N)
      y          projection on proton number (Z)
      x+y      projection on mass number (N+Z)
      x-y       projection on isospin (N-Z)

**EXAMPLE**  APRO A / ON(AP)  DIM(1)  W(100,300,50,70)
Get the projection of the two-dimensional analyzer  A  on dimension 1, summing up dimension 2 between channels 100 and 300 in horizontal and between 50 and 70 in vertical direction.

APRO  B  /  ON(B1)  DIM(x-y)  W(A)
Project the two-dimension analyzer  B  onto the one-dimensional
analyzer B1 by summing up under 135° and projecting on 45°. Only
the counts inside the display window A of the source analyzer are
considered.

APROJECT  NZ  /  ONTO(Z80)  DIM(X)  LIMITS(0,200,80,80)
Assume, nuclide cross sections are given in the analyzer  NZ  on a chart
of the nuclides (neutron number as x axis, proton number as y axis).
The projection extracts the isotopic cross sections of $Z = 80$ as a
function of neutron number.

APROJECT  NZ  /  ONTO(A)  DIM(X+Y)
Again NZ contains nuclide cross sections on a chart of the nuclides.
The projection produces the total mass distribution.