Command ADECONVOLUTE

PURPOSE Deconvolute a displayed analyzer spectrum with a given response matrix

PARAMETERS

NAME	Name or number of a one- or two-dimensional analyzer containing the spectrum to be deconvoluted.
/DIMENSION(di)	In case of a two-dimensional input analyzer, "di" denotes the dimension, in which the deconvolution must be performed. "1" stands for horizontal (x) and "2" for vertical (y) direction.
/RESP(ar)	"ar" specifies the name and qualifier name (or number) of a two-dimensional analyzer containing the response matrix elements. A floating point analyzer with equal limits and bin sizes in both dimensions is required. The response is given in x direction, sorted according to the "true" signal height in y direction. In the specific case, in which one response function just scales with the height of the signal, it is sufficient to give the response function with a one-dimensional analyzer. The response matrix is then constructed internally. An example of this case is given in the tutorial below.
/NONORM	The response matrix is not normalized. If this keyword is not specified, all rows of the response matrix are normalized.
/DESTINATION(de)	"de" specifies the name (or number) of a one-dimensional analyzer for the deconvoluted result. It must be a floating point analyzer. The output analyzer which will be created if not existing. If no name is given, the results are written to the analyzer "@RESULT".
/CHECK(ac)	As a check for the quality of deconvolution, the unfolded output spectrum is reconvoluted. The result is returned in the analyzer "ac" for comparison with the input spectrum. If the no name is given for this analyzer, the reconvoluted spectrum is written to the analyzer "@CHECK".
/ITERATION(i)	Maximum number of iterations. Replaceable default is "I = 30".
/ACCURACY(e)	Accuracy parameter. The iteration is terminated if the relative change in chi-square of two successive iterations is less than "e". Replaceable default is "e" = 10^{-2}; the accuracy parameter is limited to 10^{-5}.
/RANGE(n)	Number of neighour elements on each side to be taken into account for correction of the actually processed spectrum element. "n" = 0 corresponds to the quotient method and is appropriate for spectra containing many peaks. For "n" > 0 weighting is in effect working best for continuous spectra. Replaceable default is "n" = 2.
/NOLIST	If specified, control output (e.g. chi-square) is only listed for the last iteration. If omitted, it is listed for all iterations.

FUNCTION The experimental analyzer spectrum “name” is expected to be a convolution of an ideal spectrum with an already calculated response function, which must be available in “ar”.
ADECONVOLUTE performs a deconvolution of the measured spectrum within the specified limits. The result is stored in “de”. If error data are available in an attached error analyzer, an error analysis is performed. Then the error data for the deconvoluted spectrum are also stored in an error analyzer attached to “de”.

REMARKS The input spectrum must be displayed before.

EXAMPLE
```
GDISP EXP
ADECON EXP / RESP(DET86)  DEST(EXPDECON)
```
After displaying the spectrum of analyzer “EXP” is deconvoluted by the response matrix “DET86” using the response weighted method. The result is stored into the analyzer “EXPDECON”.

TUTORIAL We describe the application of the deconvolution procedure to a specific problem, with a one-dimensional response function.
The distribution of zirconium (Z=40) isotopes produced in the fission of 245Cm is measured. This distribution, including the errors is stored in the analyzer NSEC40, written to the dump file NSEC40.DMP. However, these isotopes do not represent the situation directly after fission, because the excited “primary” fission products have already emitted some neutrons. The measurement corresponds to the “secondary” fission fragments after neutron evaporation.

It is the aim to restore the “primary” isotopic distribution. For this purpose, the probabilities for the emission of neutrons as a function of the number of emitted neutrons has been estimated theoretically. The result of this estimation is stored in the analyzer RESP40, written to the dump file RESP40.DMP. (The probabilities are 30%, 40%, 20%, and 10% for the emission of zero, one, two, and three neutrons, respectively.)

An estimate of the primary isotopic distribution is obtained by deconvolution, performed by the command list DECON.SCOM. After the execution of DECON.SCOM, the following analyzers exist:

NSEC40	the input analyzer
ERRNSEC40	the attached error analyzer
RESP40	the 1-dimensional response function
CHECK	the re-convoluted check analyzer
NPRIM40	the deconvoluted spectrum
ERRNPRIM40	the attached error analyzer
@RESP_2D	the 2-dimentional response matrix,

constructed from the 1-dimensional response function.

On the following pages, we list the input files and show all analyzers.

DATASET "NSEC40.DMP"

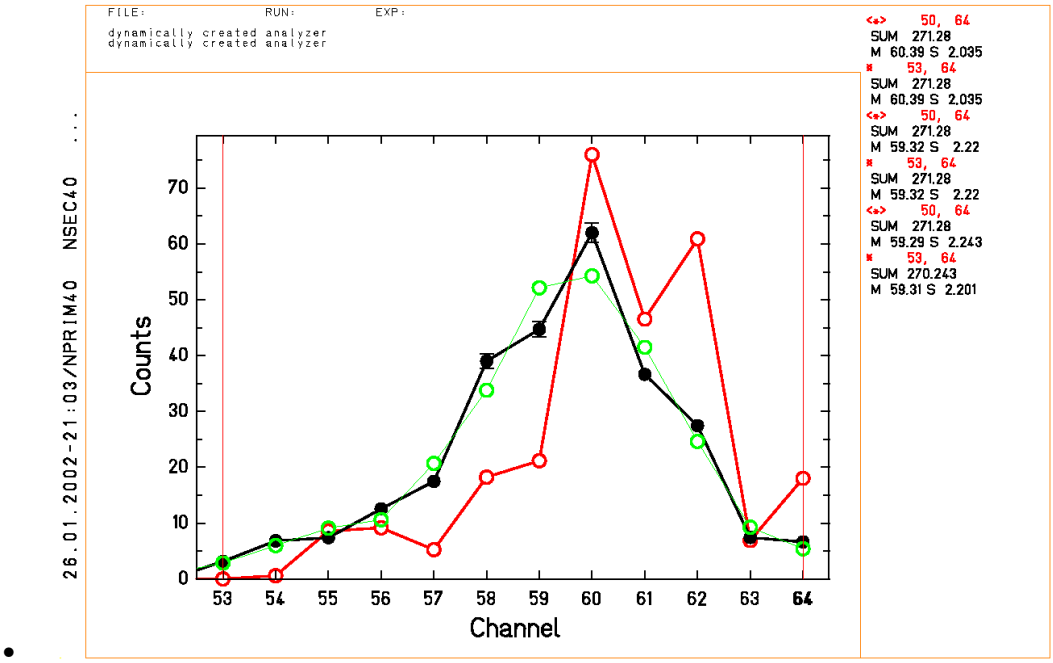
```
Isotopic distribution of secondary fragments for Z = 40
S: ANALYZER(NSEC40)
X = Neutron number
Y = Yield

A: X-40    Y,LT11    D%
   93       3.15     4.79
   94       6.82     2.75
   95       7.38     3.07
   96      12.55     2.81
   97      17.48     3.02
   98      39.01     3.33
   99      44.71     3.03
  100      62.00     2.76
  101      36.65     2.85
  102      27.46     3.08
  103       7.43     2.86
  104       6.64     2.59
```

DATASET "RESP40.DMP"

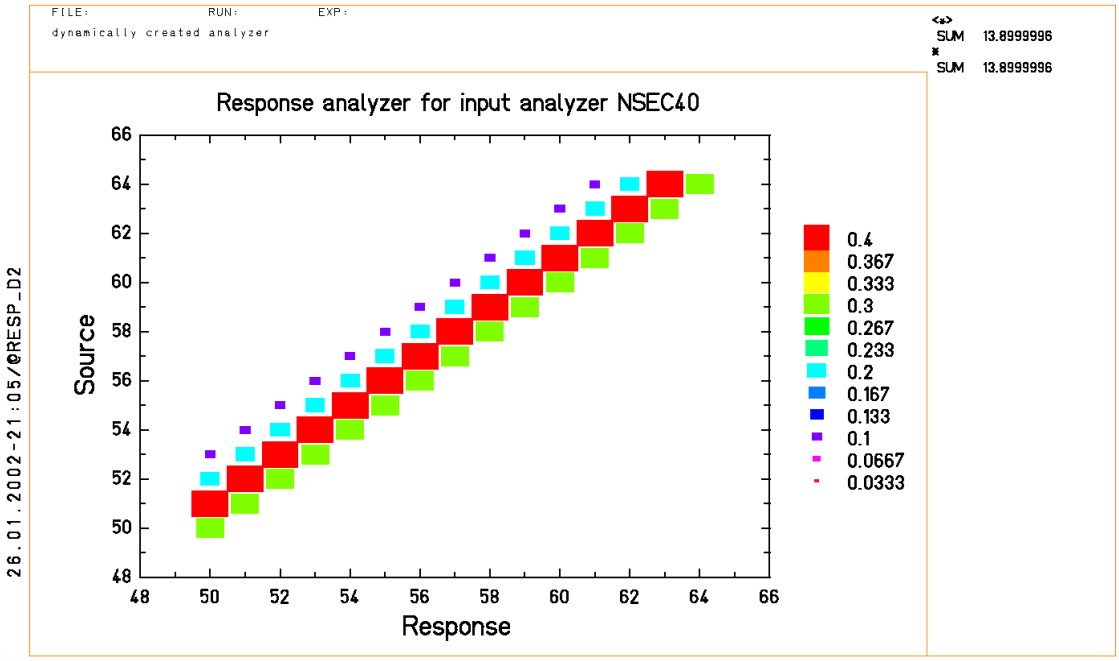
```
Response function
S: ANALYZER(RESP40)
X: Mass loss by neutron evaporation
Y: Probability

A: X     Y,LT1
  -3      0.1
  -2      0.2
  -1      0.4
   0        0.3
```

DATASET "DECON.SCOM"

```
* Application of the command ADECON

ADES * / NOCON
* Destroy all existing analyzers to get clear initial conditions.

AFETCH * / DSN(NSEC40)
* Fetch the spectrum to be deconvoluted

AFETCH * / DSN(RESP40)
* Fetch the response function

AMOD NSEC40 / LIMITS(50,64)
* Extend the limits to provide the desired range for the output analyzer

ADECON NSEC40 / DEST(NPRIM40) RESP(RESP40) CHECK(CHECK)
* Deconvolution with check option

AMOD NPRIM40 / LINES(RT1)
* Specify the graphic presentation of the result (red line and open circle)
```



Black: Input analyzer NSEC40
Red: Output analyzer NPRIM40
Green: Reconvoluted analyzer CHECK



Analyzer @RESP_D2, containing the response matrix. The two-dimensional response matrix is constructed from the one-dimensional response function stored in RESP40.