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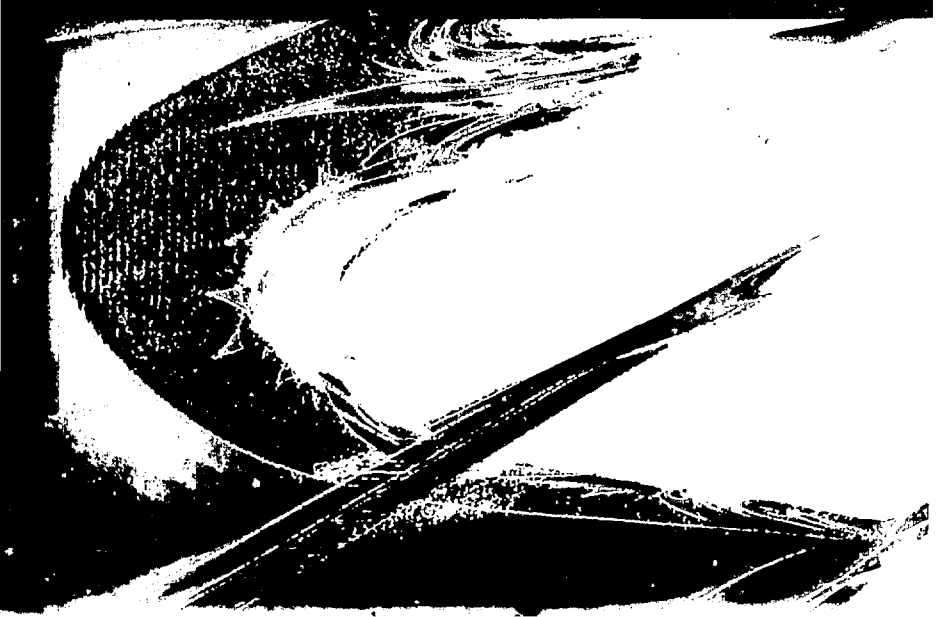

MAMA Version 3.0

Matrix Manipulation Program

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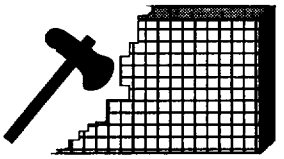
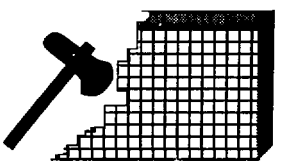


M A M A (Version 3.0)

Matrix Manipulation Program



Oslo Cyclotron Laboratory
Magne Guttormsen
February 1994

1. Introduction

The program MAMA is an analyzing tool for experimental nuclear data. The data is represented in the form of one and two dimensional spectra (matrices). Totally, there exist about 80 commands which allow you to read/write spectra, apply arithmetic operations on spectra, peak fit routines, smoothing procedures, (un)folding with the detector response functions and so on.

The package contains modules from the GF2 (ver. 6.4) program written by D.C. Radford and R.W. Macleod and the KELVIN (ver. 1.0) program written by M. Guttormsen. This version of MAMA is implemented on the SPARCstation 10/512 (called lynx) at the Oslo Cyclotron Laboratory. The program can be accessed either from the lynx console or from X-terminals (or emulated X-terminals on Mac or PC). Also, a stripped version (MIMA) without display and peak fit facilities has been implemented.

In order to set up and run, you have to add to the **.cshrc** file in your home directory the things underlined below:

```
.
set path = ( $lpath ~/bin /usr/bin /usr/local /usr/local/bin  /usr/ccs/bin /usr/ucb  /usr/etc
/d2/fys/mama/bin  .)
.
.
#set lcd = ( )  #  add parents of frequently used directories
#set cdpath = (.. ~ ~/bin ~/src $lcd)
source  /d2/fys/mama/.radwarerc
.
Remember the space before "." in  "/d2/fys/mama/bin  ." !
```

In addition to the environment set up file *.radwarerc* in the mama folder, you also find folders like *bin, demo, doc, font, icc* and *resp*. There also exist many other programs in the *mama/bin* folder as: *decay, zigzag, kin, scatter, range , vigs, autofit, mama2pc* - and many more is to come...

When you start a MAMA session, you should be located in the same directory as your data files (spectra) are stored. Use the **cd** UNIX command to walk to the proper directory. Type **mama,** and you are up running.

The best way to learn how the program works is to use it. There exist on-line help by typing **HE** (for HElp). To end your MAMA session, simply type **ST** (for STop).

If you have problems, please contact:
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2. Data Structure and Display Window

MAMA can handle two matrices of maximum dimension 2048x512 in the X and Y directions, respectively, and two singles spectra of dimension 8192. In addition, there exists a matrix housing the response matrix with 512x512 and an 8192 channel long singles spectrum housing the data to be displayed or processed by the GF2 part of the program. The way to shuffle data back and forth is shown in Fig.1.

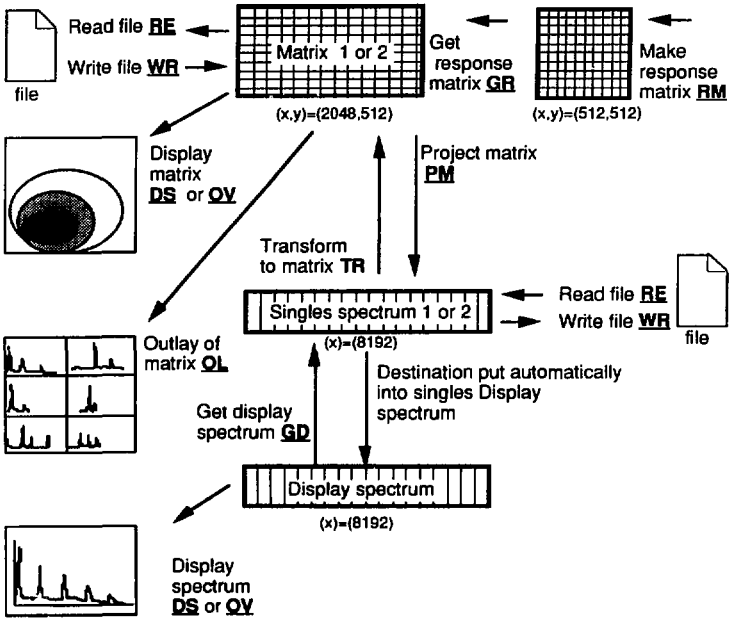

Figure 1: Input and output commands to the various matrices, spectra and displays.

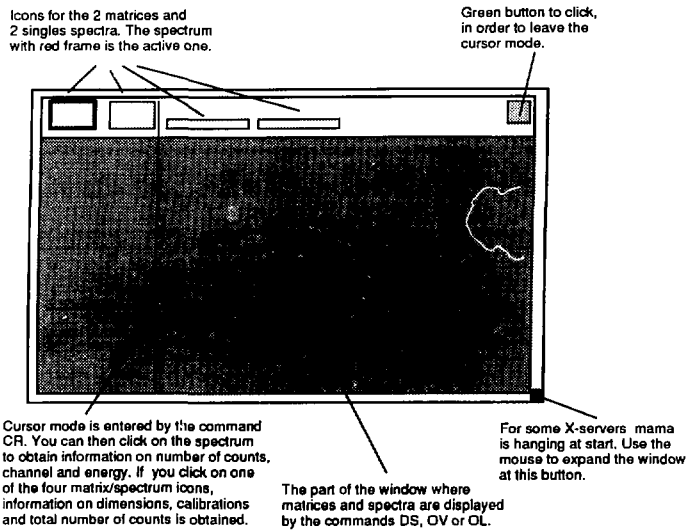

Figure 2: The objects of the mama spectrum/matrix window.

As default, the mama commands act on the matrix or spectrum currently activated. The active spectrum is indicated by a thicker red frame, as illustrated in the left upper corner of Fig.2. If another matrix or spectrum should have to be activated, type CR (CursoR) and click with the mouse on the proper icon.

3. Quick Menu Description

read/write

RE Read matr./spc. **WR** Write matr./spc.

modify spectrum

AR ARithmetic on mat./spc. **CO** COmpress matr./spc.
CU CUt in matrix **EL** ELastic stretch/compress
PM Project Matrix **PC** Put Constant in matr./spc.
PA PArtition of matr./spc. **NO** NOrmalize along X-axis in matr.
FN Fill Neg.'s from Neighbs. **RN** Replace Neg.'s with 0's
SM Smooth matr./spc. **TR** Transform spc. to matrix
XY Interchange XY axis

display

DS DiSplay matr./spc. **OV** OVerlay matr./spc.
DF Display Fit **OL** OutLay matrix in spectra
DM Display Markers **HC** Hard Copy of screen
SH SHow counts of matr./spc.

modify display

EX EXpand display. w/curs. **DX** Low/high for Disp. of X
DY Low/high for Disp. of Y **DZ** Low/high for Disp. of Z
SC Type of scale for Y axis **CC** Change Colour Map

folding

RM Make Response Matr. **UN** UNfold matrix
FO FOld matrix **GR** Get Response matrix

fit

NF Set-up new Fit **FT** Do FiT
RF Reset Free param. **AP** Add Peak
DP Delete Peak **LP** List Parameters
FF New Fit File (.gf2) **SF** Store Fit in .gf2 File
EF Edit Fit file (.gf2) **NU** Nuclear Temperature
AN Fit (A,N) separately **TF** Total Fit (a,n) of matrix
FG First Generation matr. **SA** Store Areas & Centroids
PO POlynom fit of data

modify peak fit

FX Fix Parameter(s) **FR** FRee parameter(s)
RP Fix/free Rel. Pos. **RW** Fix/free Relative Widths
MA Change MArkers **SW** Change Starting Widths
WM Change Weight Mode

info

CR Call CursoR **CA** CAlibrate mat./spc.
HE Help **LS** LiSt files (UNIX)
PF Peak Find on display **SU** SUm counts
UX UniX command

exit/misc

CF Execute Command File **CF** END Close Command File

CF Create Command File **CF** CHK Command File Check
CF CON Continue Command File
ST STop and exit mama

fix/free parameters

<rtn>	RW	RP	A	B	C
R	Beta	Step	P1	W1	H1
P2	W2	H2	P3	W3	H3
P4	W4	H4	P5	W5	H5
P6	W6	H6	P7	W7	H7
P8	W8	H8	P9	W9	H9
PA	WA	HA	PB	WB	HB
PC	WC	HC	PD	WD	HD
PE	WE	HE	PF	WF	HF

Commands not in use

(These commands reads/writes etc. spectra with format not used at the Oslo Cyclotron Laboratory. The commands are not tested, and might not work in this version of MAMA.)

SP Read SPectrum
WS Write Spectrum
DW Display Windows
WI Add WIndows
DE Divide by Efficiency
LU Create Look-Up table
GD Get Display spectrum
DU DUmp set-up
IN INdump set-up
CT Set CounTs with cursor
RD Re-Draw spectra
SL Open Slice File

4. Menu Description

AN Fit A and N separately
The level density parameter *a* (1/MeV) and the exponent *n* of E_γ are used as fitting parameters to the 2-dimensional landscape of (E_γ, E_X) obtained from the first generation gamma-spectra.

AP Add a new Peak to the fit set-up
If you have a peak fit set up, but wish to add a peak to this fit, use the command AP. You will be prompted for the position of the new peak. The width of the new peak will be set to its initial starting value, so if the widths are free, but relative widths fixed, you will be given the option of resetting all non-fixed widths to their initial values also. If the new peak is not higher in energy than the previous last peak, you may also select to re-order the peaks in order of increasing energy.

AR ARithmetic operations +, -, /, and * on matrix/spectrum
You can add matrix/spectrum, multiply by factors etc. The operations possible are listed below:

adding spectra:	1=1+2
adding constant:	2=1+120.0
subtracting spectra:	2=1-2
subtract constant:	2=1-120.0
multiply spectra:	2=1*2
multiply by const:	1=2*1.17
divide spectra:	2=1/2
divide by constant:	2=2/1.17

NOTE: Integer numbers mean spectra, and real numbers mean constants.

CA Get CAlibration and dimension info, and ev. change these
The command tells what is the current energy calibration and dimension of matrix/spectrum. These values can be changed by you.

CC [N1,N2...] Change Color map to N1,N2...
The program uses a "color map" to display spectra in different colors according to the value of the parameter I in the DS command. Thus, for example, DS 1 4 will display the spectrum in color 1, DS 3 5 in color 3, etc. In order to overlay spectra in the same region but in different colors, use the CC command to change the color map. The old map will be listed, and the new map requested. You need provide only those values you wish to change; the other values will remain at their old values.

CF Execute/create Command File
CF filename take commands from disk command file
CF CHK : check whether to proceed with command file
CF END : end of command file
CF YN : continue with present command file
CF INI : log all typed input to create a new command file
CF END : close new file

[illegible] commands within Mama is achieved through the

use of the command CF to execute command files. The default extension for these files is .cmd. They may be written using the system editor utility, and can include any valid Mama commands. Be sure, however, to include valid responses to any prompts or questions the program may ask, since while the command file is being executed, it will replace the keyboard as the source of all user responses, with the exception of those involving the graphics cursor. If the program reads a command it does not recognize, you will be informed of this and asked if you wish to continue with the file execution.

If you put CF CHK (Command File CHecK) as a command entry in your file, execution will be interrupted at that point, and you will be given the option of continuing or stopping execution. This may be used, for example, to verify the quality of fits while the command file is being used to automate the fitting of a series of related spectra. If you elect to stop the execution of the file, you may resume at the same point in the same file at a later time by typing the command CF CON (Command File CONtinue). In addition, the window may be cleared from within the command file by use of the command CF ERA (Command File ERAse).

You may create command files directly in Mama, without using the system editor, by typing CF LOG. This will cause all typed commands and responses to be logged to a new command file, with a *filename* specified by you. You may enter the commands CF CHK and CF ERA into the file simply by typing them, and the commands CF END, CF *filename* and CF LOG will all close the new file. NOTE that these last commands will also be entered into the file, and executed when the file is called.

CO COmpress matrix/spectrum by integer value

This command contracts the current spectrum by the integer factor n. Channels 0 through n-1 will be summed into channel 0, etc. The program automatically calculates the new calibration for the matrix/spectrum.

If you need to stretch/compress or turn over the direction of axis, use the EL command (ELastic massage).

CR [N] Call CursoR and get info, or activate matrix/spectrum

This command causes the cursor to be called. By positioning the cursor and typing any character other than X (e.g. a space, or the mouse button), the co-ordinates of any point in the presently displayed axes may be determined. The counts in the channel is also given, and the energy is listed as well.

If you point on the matrix/spectrum icon at the top of the window, you get info on the matrix/spectrum: Energy calibration, dimension and number of counts. If you want to change these values, use CA (CAlibrate).

In order to leave the cursor mode of operation, click on the green button in the upper right corner or type X.

If followed by an integer will cause a marker to be displayed in the channel corresponding to that integer, and the counts and energy for that channel to be listed.

CT Set CounTs per channel using cursor
This command operates just on the display spectrum. Use instead PC (Put Content).

The CT command enables the user to alter the counts per channel over a selected range of the display spectrum, by specifying the required contents. This may be done either through the cursor or by typing the desired value. If the spectrum is displayed, the cursor will be called up repeatedly. Each pair of entries through the cursor specifies a straight line between the cross-hair positions; the spectrum counts will be set to correspond to this line. To exit from the CT routine, simply type X. If, at either cursor entry, you type the character T (for Type), you will asked to type limiting channel numbers and the required counts per channel for that range.

CU Cut in matrix
The X and Y axis can be transformed to a new set of axis by defining $X_{new}=X_{old}+F1*Y_{old}$ and $Y_{new}=Y_{old}+F2*X_{old}$. The calibration (keV/ch) is conserved in the transformation.

DE Divide spc. by det. effic.(from an EFFIT .eff file)
Divides the display spectrum by a detector efficiency. The parameters defining this efficiency should have been stored in an .eff file from program EFFIT. See also HElp EFFit.

DM Display Markers
DF Display Fit
These commands simply display the marker positions and fit, as currently defined, on top of the most recent display of the spectrum. The limits of the fit are shown as the vertical lines from the X axis to the spectrum, and the vertical arrows with numbers below them are peak position markers. The difference between the data and the fit (in counts per channel) is shown halfway between the spectrum and the X axis. The vertical offset is added to the difference to separate it from the X axis for reasons of visibility.

DP [N] Delete a Peak [peak no. N] from the fit set-up
Use this command to delete a peak from a fit you have set up, if you wish to have fewer peaks. If you do not provide the number of the peak you want deleted, the program will prompt you for it.

DS Display Spectrum
OV OVerlay spectrum
The commands DS and OV are used to display the current spectrum or matrix. DS causes the window to be cleared before the spectrum is displayed. OV, which does not clear the screen, allows different spectra or portions of spectra to be displayed simultaneously. OV accepts the same integer arguments as DS, so that the spectra may be either overlapped or drawn on different parts of the window.

[illegible] spectrum with the parameters DS [I,J[,K]] and OV [I,J[,K]] means [illegible] [illegible] parts of the window. If the third parameter K is given [illegible] the first parameter then I gives full scale and J autoscale.

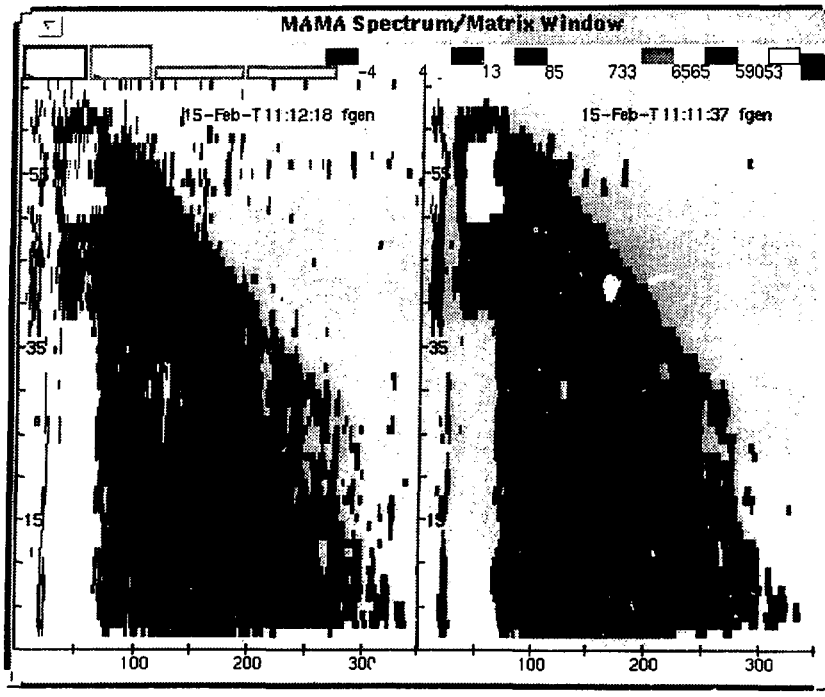

Figure 3: The display of the first generation matrix (left) and after smoothing (right), see the SM command. The commands used for display: DX 1 2 (left) and DY 2 2 (right). The DX and DY commands are also used.

By default, the whole window will be used to display the part of the spectrum between channel limits previously defined using the DX, DY, DZ and EX, commands. However, by following the command with up to three integers, you may select a certain portion of the window for the display, and still display the entire spectrum. In general, DG n m will select the nth part of the screen for the display, while a trailing 1 displays the full spectrum. Thus DG 1, for example, will display the entire spectrum in the whole screen, DG 1 4 will display the expanded part of the spectrum in the upper left quarter of the screen, while DG 1 will display

entire spectrum in the middle third.

The last display drawn is always considered to be the current display for the purposes of the cursor, summing of counts, multiplication etc.

DU DUmp program set-up
IN IN-dump program set-up
These commands are used to dump (write) and in-dump (read) the current peak fit status to and from disk files. The default extension for dump files is .dmp. All relevant information is stored in these files, including:

i) the current parameters for the fit, and which parameters are fixed
ii) the specified initial estimates for R, BETA, STEP and peak FWHM
iii) the display parameters (X0, NX, Y0, NY etc, and the CC and PF values)
iv) the energy calibration
v) any fitted areas and centroids that have been saved using the SA command, but not yet written to disk (see HELP SA - Store Areas and centroids from fit). These data are always written to the dump file; however, when reading the file (in-dumping), you will be given the option of reading them from disk or disregarding them, thus leaving the current stored areas and centroids unchanged.

The only things not stored and restored are the spectrum itself, and the weight-spectrum, if any.

Dump files are very useful, since they save fits for later reference, use and/or improvement. For example, during the analysis of a series of spectra, it is often a good idea to fit the sum of all the spectra initially, followed by individual fits to each spectrum with the (relative or absolute) positions and widths fixed from the fit to the sum spectrum. Dump files may then be used to verify that the proposed fit is satisfactory for all of the individual spectra. The series of individual fits may be done using a command file; see HELP CF (execute/create Command File).

DW Display Windows as they are presently defined (not Oslo format)
Displays the ranges and window labels of the currently defined window file (either SLice or Look-Up). For slice files, a background calculated from the stored peak-to-total ratio is also displayed.

DX M1 M2 Low/high markers for Display of X axis
DY M1 M2 Low/high markers for Display of Y axis
DZ M1 M2 Low/high markers for Display of Z axis
These commands are used to define the limits of display. Using the display commands DS, OV or OL, the matrix/spectrum is displayed with the markers defined by DX, DY and/or DZ. These limits will not be active if you apply e.g. DS 1 (full scale) or DS 2 (auto scale).

EF *filename* **Edit Fit parameters (.gf2)**
This is a simple editor that allows you to List, Print and/or Delete fit segments from a .gf2 file. Only the limits of the segment, and the peak positions are listed; however, all parameters of the fit are saved in the .fit file.

EL ELastic stretch/compress giving new a0,a1 and a2 calibration
This command work either on X or Y axis. You type the a0,a1 and a2 of the old and new calibration. The program then changes the matrix/spectrum to give the wanted calibration. If e.g. the new a1 is not a multiple of the old one, the counts in one channel before, will be distributed on two or more channels afterwards. Thus, be aware of that a certain smoothing (usually just over two channels) might take place.

You can also use the EL command to change the direction of the e.g. X axis. Let us say the spectrum has 1000 channels. Type then 0,1,0 for the old calibration and 1000,-1,0 for the new one.

If you simply want a compression of e.g. 3 and 3 channels, use instead the CO (COmpress) command.

EX EXpand display using cursor (mouse)
RD [1] Re-Draw and display spectra
The lower and upper limits of the X axis (channels) may be changed by using the EX command. To change both limits, type EX. The cursor will be called, and you must position it and reply with a character, once for each of the lower and upper limits. You may enter them in either order. You will be asked to provide either the new lower limit or new upper limit using the cursor.

The EX command works also on matrices. The rectangular region to expand is defined by the hair-cross of the cursor. Click the mouse at lower left corner and then click on higher right corner to define the region.

If you wish to redraw singles spectra for any reason, you may also use the RD (ReDraw) command. For example, if you have displayed a set of several gamma-gamma gates on different parts of the window, and now wish to see a different range of channels, you may use the DX and DY commands to select the range and then redisplay by typing RD. If you wish to view the entire X range, you may type RD 1.

For all these commands, ALL display spectra shown since the last DS command will be redrawn, using the same new X axis limits. The Y axis (or axes) will be left unchanged, except possibly in the case of auto scaling. The screen will be automatically cleared before the display is redrawn.

FF *filename* Open new .gf2 Fit File
SF *filename* Store Fit parameters in .gf2 file
The SF command is used to save fit parameters in .gf2 files, for later use by the program MATFIT. After fitting a number of peaks, you can save the parameters for (a segment of) the fit by typing SF *filename*. MAMA will ask for new limits if you have fitted more than six peaks, and it may warn you when there is a peak overlapping the upper limit. You can only save up to six peaks per region, so large fits must be stored as several segments. The segments must also be at most 128 channels wide. (NOTE: The previous filename is the default *filename*.)

To open a new .gf2 fit file use the FF command then use SF to write your fit to this file.

FG Make First Generation matrix from experimental particle-gamma coincidences

This is a relative complicated procedure and you should read the paper in Nucl. Instr. and Methods: M.Guttormsen et al. NIM A255(1987)518.

You need a set of unfolded gamma (NaI) spectra representing various excitation energies. You also need to know the intensity (counts) N(Ex) in the corresponding particle spectrum at these excitation energies. Alternatively, you may use the gamma-multiplicity M(Ex). To get an idea of what is needed of inputs, just run the command (without writing spectra to disk) and find what is needed.

FN Fill channels with Negative counts from neighbour chs.
RN Replace Negative counts with 0's

The FN command looks first for channels with negative counts in the matrix/spectrum. Then it searches the channels around if there are positive channels to take counts from and put into the negative channels. In this way the holes might be totally or partially filled up (=0). The FN command conserves the total number of counts.

The region for search is given by a 1 (or 2) dimensional Gaussian described by FWHM in X (and Y) direction by the user. The channels most close to the negative counts will then be used in the filling procedure.

The RP command is much more brutal and simply takes away all negative counts, and should be used after FN. The number of counts increases in the matrix/spectrum.

FO FOld matrix/spectrum with NaI or Gaussian response matrix
UN UNfold matrix/spectrum with NaI or Gaussian response matrix

FO (and UN) (un)folds the gamma-ray spectrum with the NaI response function. It is also possible to use a Gaussian response which is suitable for particle spectra. The command requires that the response matrix has been created first by the command RM (Response Matrix). The response function must (of course) have the calibration of the matrix/spectrum which you wish to fold or unfold.

FX [P] Fix additional param. P or change fixed value(s)
FR [P,Q..]Free additional parameters P,Q..

These commands are used to fix or free (i.e. unfix) additional parameters, or to change the values of parameters already fixed. If the command is not followed by a parameter name or number, the parameters will be listed, with asterisks indicating any fixed parameters, and you will be asked which parameters you wish to fix or free. If you wish to fix or free just one parameter, you may do so by typing the name or number of that parameter following the command. For FX, you will also be asked for the fixed parameter value. <Rtn> to this question indicates that the parameter should remain at its current value.

In addition, you may fix or free the RELATIVE widths and/or peak positions by giving FW (Relative Widths) or FP (Relative Positions) as the parameter name. You may fix as many parameters as you wish, provided that at least two independent parameters are left to vary in the fit. See also HELP FW or HELP

RP - relative widths/positions.)

FT FiT spectrum
NF New Fit

FT [N] N=1-15: set-up for N peaks and do fit
[N=0] : do fit using present parameter values
N=-1 : recalculate initial param. estimates and do fit

Before typing these commands, you should first display the portion of the spectrum which you wish to fit. The FT command has three slightly different functions, depending on whether it is followed by an integer:
(a) >0,
(b) non-existent (or 0), or
(c) -1.
These are discussed below. An example of a fit is shown in Fig.4.

When the command FT is followed by an integer between one and fifteen, this integer is taken to be the number of peaks required in the fit, and the program will proceed to set up for a new fit. You will be prompted with "Limits for fit? (hit T to type)", and the cursor will appear on the screen. You may then enter the boundaries of the spectrum region you wish to fit by positioning the cursor at the required channels and typing any character other than T (e.g. the mouse button or the space bar), once for each limit. The prompt "Peak positions? (hit T to type, R to restart)" will then appear, and you should respond by using the cursor to give an approximate position for each peak. If there are limit channels or peak positions that you would like to have given a special value, you may type the character T in response to the cursor when asked for that position; you will then be prompted to type the value. Limits should be given as integers, but peak positions may be real numbers. If you wish to restart the limit and/or peak position definition, type R at one of the peak positions; the program will then return to requesting the fit limits.

The NF command is equivalent to the FT n command except that you do not have to specify the number of peaks that you wish to fit. You just choose the fit limits and then indicate the peak locations until you have entered as many peaks as you wish (up to the maximum of 15). Then, type X or hit the third mouse button and the fit will proceed as described below.

The parameters of the fit will then be written on the screen, together with the "parameter number" that identifies it. An asterisk in place of the parameter number will denote any parameter that is already fixed at its initial estimate; that is, will not be varied in the chi-squared minimization. You will be prompted to type the name or number of any (additional) parameters that you wish to fix, one per line. Each time you fix a parameter, you will also be asked for the value you wish it to be fixed to. <Rtn> to this question indicates that the parameter should remain at its current value (in this case, at the initial estimate). Note that you may fix any parameter you wish, by giving either its number or its name (e.g. 7 or P1). In addition, you may fix the RELATIVE widths and/or peak positions by responding with RW ("Relative Widths") or RP ("Relative Positions"). In this way you may fix as many parameters as you wish, provided that at least two are left to vary in the fit.

When you have finished fixing parameters, hit <Rtn> if you do not wish to fix any, type <Rtn>. You will then be prompted for a maximum number of iterations to

```
cmdtool (CONSOLE) - /bin/tcsh
mama fr 2
   Limits for fit?  (hit T to type)
  Peak positions? (hit T to type, R to restart)
     1   2   3   4   5   6   7   8   9  10  11  12
     A   B   C   R  BTA STP P1  W1  H1  P2  W2  H2
 Parameters to be fixed =? (one per line,RTN to end)
3
Value=?(rtn for present value)0
4
Value=?(rtn for present value)
5
Value=?(rtn for present value)
6
Value=?(rtn for present value)

 Max. no. of iterations=?(rtn for 50)
 File eu152                              Spectrum eu152        15-Feb-T 11:38:46
 Fitted chs  167 to  239       2 Peaks
   8 indept. pars     65 degrees of freedom     weighted with fit.
  12 iterations,  Chisq/d.o.f.= 2.682
 Background: A=  1644.31 +-   12.71      B=  -22.3277 +-  0.3626      C=    0.0000 +-  0.0000
      Shape: R=    10.00 +-    0.00   Beta=   12.000 +-   0.000   Step=    0.2500 +-  0.0000
 Peaks:      position              width              height              area      centroid          energy
  1   190.417 +-  0.078  13.339 +- 0.091   2162.20 +-   27.31    34918 +-  485   187.912   954.549 +- 0.397
  2   216.804 +-  0.055  17.723 +- 0.069   3534.62 +-   23.41    73149 +-  546   214.649  1090.741 +- 0.281
Print parameters? (Y/N)
mama>
```

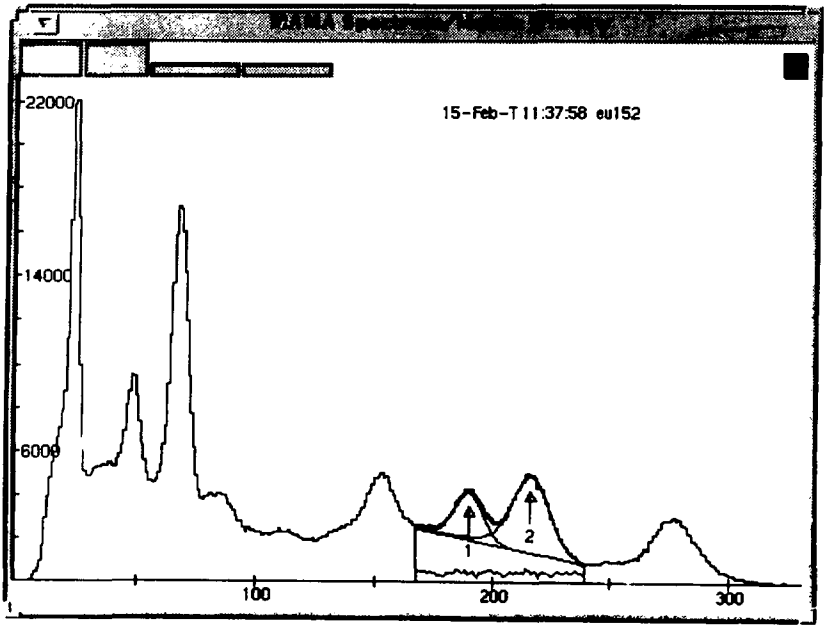

Figure 4: Fit to peaks in a NaI ^{152}Eu gamma-source spectrum. The results are also shown graphically.

be performed. If the fitting algorithm has not converged before this number of iterations has been completed, the fit will be aborted. If you are unhappy with the way the parameters or markers have been set up (e.g. if you would like to fit more peaks, or free parameters etc.), answer 0 to this question, and no iterations will be performed. A <rtn> in response to the prompt will select the default of 50 as the maximum number of iterations.

Once you have defined the maximum number of iterations, the fit will begin. When the fit has been completed such information as the limits, number of peaks and iterations, and chi-square will be listed on the terminal. Provided that the fit converged, these data will also be written to the print file. You will then be asked if you wish to type and/or print the parameters; that is, have a listing of the parameter values sent to the screen and/or print file. This print file is labelled GF2.OUT, and may be saved, deleted, or printed and then deleted, on exiting the program.

FT

If you type simply FT, without a following number, the program will return to the point where it asks you for the maximum number of iterations, and then proceeds to do the fitting with the present parameter values as the new initial estimates. This command is used, for example, when the fit has previously failed to converge, or you have read in a new spectrum.

FT -1

FT -1 has the same effect as the above (FT), except that before the fitting is begun the non-fixed parameters will first be reset to their original initial estimates.

GD Get Display spectrum into singles spectrum 1 or 2

This command allows the use of file formats different from the Oslo format. Use first the SP command, which brings the spectrum to the display buffer. The spectrum can then be transferred (GD) into one of the two singles spectra, and can be written out in Oslo format (WR). In this way several of the ASSociated programs can be used, which apply another input/output file format than the Oslo format.

GR Get Response matrix into working matrix 1 or 2

The command copies the response function into one of the working matrix/spectrum. In this way one can inspect the matrix, make laser print, etc.

HC Hard Copy of screen

The command uses the snapshot utility of the OpenWindow 3.0 to make either a laser plot of window, screen, or region. Normally, you make a copy of the mama window. The snapshots take a few seconds, so be patient.

HE **Prints commands and other HElp-topics on TTY**
HE/P **Send this output to the laser printer**
HE <TOPIC> Help on command or topic <TOPIC>
(2 or 3 letters needed)

The command HE or HE TOPics lists the topics with help information available in Mama, and prompts for a topic to be explored. The command HE Summary writes a summary of the valid commands to be listed on the terminal screen. The command HE P causes the same listing to be printed on the laser printer.

IN IN-dump program set-up
See the DU command.

LP List Parameter values
This command simply causes all the present limits, peak position markers and parameter values to be listed on the TTY.

LS LiSt files in current directory
This command corresponds to the ls UNIX command. Files in your current directory are listed on the screen. For more sophisticated UNIX commands, like "ls -a" or "pwd", type the UX command which allows you to send a text string to the UNIX shell.

LU *filename* Create Look-Up table file (not Oslo format)
This command allows the user to create a look-up file of numerically labelled regions (gates), that can be used in tape replay tasks (e.g. MATLUHK, MATTRIP, and MATBGO). Windows can be added to the file, or overwritten, through the use of the command WI. If the *filename* does not exist, a new look-up table, initially containing only zeroes, is created. If it does exist, the user is allowed the option of reading and modifying it.

MA [N] Change limits for fit and/or peak positions
N=1-17 : change MArker no. N
The MA command is used to change the limits for the fit and/or the peak positions. If followed by an integer N, it will be assumed that you wish to change only one marker. Here N=1 and 2 for the lower and upper limits, respectively, and N=n+2 for the position of peak number n. If there is no integer on the command line, you will be asked if you wish to change the limits and/or peak positions, at which time you will be prompted with the cursor for the new positions. Again, you may hit T to type specific values. After the markers have been changed, you will be asked if you wish to reset the free parameters to their new initial estimates.

NF New Fit
See the FT command.

NO NOrmalize to 100000 along X axis in matrix
The total number of counts are normalized to 100000 along the X axis. If you instead want the Y axis, you have first to type XY (interchange X and Y axis, max 512x512 matrix).

NU Extract NUclear temperature from exp. first-gen. matrix
First an unfolded first generation NaI matrix have to be read in. The procedure finds then the nuclear temperature as a function of excitation energy.

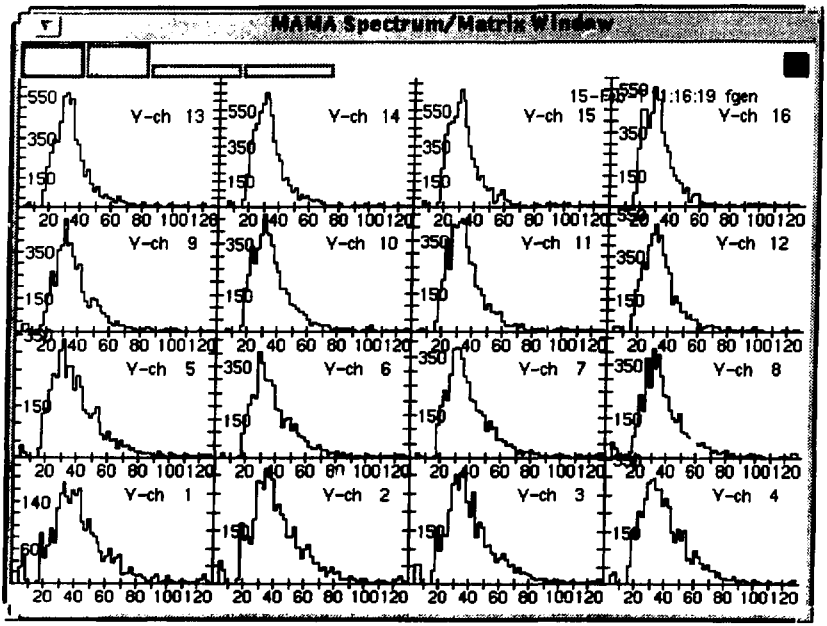

Figure 5: An outlay of 16 rows of a matrix using the OL 2 command.

OL OutLay matrix in spectra
The command helps you displaying a number of rows or columns from a matrix as multiple singles spectra. OL 1 gives full scale. We recommend the OL 2 alternative, which gives auto scale. Up to 8x8 spectra can be shown simultaneously. If you wish to display singles spectra of the whole matrix with more then 64 rows (columns), you should first compress (CO) the matrix one or more times. See Fig.5.

OV OVerlay spectrum
See the DS command.

PA PArtition of matrix/spectrum

You can choose a new origo for the matrix/spectrum. The linear transformation of the axis is in units of channels (see Fig.6).

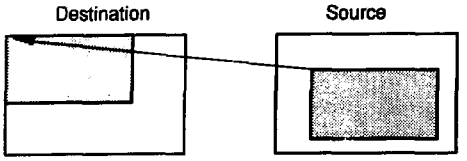

Figure 6: A region of the matrix can be shifted to a new origo.

PO POlynom fit to data set

This command fits the coefficients of a polynom up to third order to the data given as x and y values. E.g. x values can be channels and y is corresponding energies in keV. For a ^{152}Eu calibration source you should type channels and energies in free format, and end with a character:

240.1	121.78
480.3	244.69
700.2	344.27
830.7	411.11
890.4	443.97
1400.2	688.67
1500.9	778.90
1900.3	964.13
2300.9	1112.11
2900.6	1408.01

x

Then, the three polynoms are fitted:

$y=a_0+a_1x$

$y=a_0+a_1x+a_2x^2$

$y=a_0+a_1x+a_2x^2+a_3x^3$

and the X^2-value for the various polynoms are given. It is assumed an error in y's of 1 (sigma=1), so that X^2 is normalized accordingly. The number of freedoms is taken into account for X^2.

You should take one set of coeff. a_0, a_1,... and calibrate your spectrum by using the CA (CAlibrate) command. Be careful to use the highest order polynom in energy calibrations. In the example shown in Fig.7, the best fit is probably the linear one.

```
mama>
mama>
mama>po

Type pairs of x and y values for the data set.
The numbers in a pair should be separated with space,
and each pair should end with RETURN. Type characters
instead of numbers to terminate the inputs
Example:
1.2 5.7
2.6 9.7
3.1 8.5
x
(Maximum 100 pairs)
Type x y pair (character for stop):1.2 4.6
Type x y pair (character for stop):1.5 8.0
Type x y pair (character for stop):3.0 9.0
Type x y pair (character for stop):4.0 11.
Type x y pair (character for stop):8.0 15.0
Type x y pair (character for stop):4. 7.2
Type x y pair (character for stop):x

   Pair no.          X            Y
      1          1.20000      4.60000
      2          1.50000      8.00000
      3          3.00000      9.00000
      4          4.00000     11.00000
      5          8.00000     15.00000
      6          4.00000      7.20000
Average:         3.61667      9.13333

Are values OK <Y>:

Pair no.    X        Y      Linear   Quadratic   Cubic
   1     1.200    4.600     6.003       6.000    5.417
   2     1.500    8.000     6.392       6.390    6.857
   3     3.000    9.000     8.335       8.337    9.622
   4     4.000   11.000     9.630       9.633    8.950
   5     8.000   15.000    14.811      14.807   15.009
   6     4.000    7.200     9.630       9.633    8.950
Chisquare (sigma=1):         3.126       4.135    4.590
Linear: a0=    4.4489 a1=    1.2952
Quadr.: a0=    4.4397 a1=    1.3008 a2= -.603580E-03
Cubic : a0=   -4.4561 a1=   11.3843 a2= -.289752E+01 a3= 0.22232834E+00
mama>
```

Figure 7 : The result of a polynom fit through 6 points.

PC Put Constant in matrix/spectrum

You can put in a constant value of counts in a part of the matrix/spectrum. If you just answers with defaults (RETURNs) the data are zeroed (=0).

PF Activate Peak Find when displaying

You may use this command to set up a peak find routine to list the energy (or channel) of significant peaks when you display spectra. The energy or channel is given above a marker on the screen, indicating the position of

the found peak. Parameters requested by the program are:

FWHM : an estimate of the width (in channels) of the peaks in the region of the spectrum that you wish to display,

SIGMA : a threshold for the peak find in standard deviations, and

% : a threshold for listing of the peak in percent height of the strongest peak found.

PM Project Matrix down on X or Y axis

The rows or columns are summed up and put into singles spectrum 1 or 2.

RD [1] Re-Draw and display spectra

See the EX command.

RE Read matrix or spectrum from disk

The procedure make an auto-check of the file you want, and decides what kind of matrix/spectrum you ask for. Spectra can be

- Singles spectra (one dimensional)
- Matrices (two dimensional)
- A set of singles spectra labelled e.g. spec-1, spec-2, spec-3,..

The calibration and dimensions are read. These properties are glued to the matrix/spectrum throughout the Mama session. By writing (WR) the manipulated matrix/spectrum is written back to disk. You get qualified suggestions for the calibrations and dimensions to be written away.

RF Reset Free parameters to their original value

RF causes the non-fixed peak fit parameters to be reset to their original initial estimates.

RM Make Response Matrix of NaI or Gaussian shape

Before folding (FO) or unfolding (UN) spectra, the response matrix have to be created. The inputs needed are the energy calibration, dimension and FWHM values. For each Y channel (full-energy) a spectrum is created which describes the detector response function for that energy. Thus, the response matrix covers a triangle of a quadratic matrix with dimension up to 512x512. The response matrix can be inspected by the GR (Get Response matrix) command.

RN Replace Negative counts with 0's

See the FN command.

RP N Free (N=1) or fix (N=0) relative peak positions

RW N Free (N=1) or fix (N=0) relative widths

RP [0] and RP 1 fix and free, respectively, the relative peak positions, for those peaks whose position is not fixed. Similarly, RW [0] and RW 1 fix and free, respectively, the relative peak widths, for those peaks whose width is not fixed. The same effect may be achieved using the FX and FP commands, with RP or RW as a parameter name.

Fixing the relative positions and or widths is very useful in analyzing a series of spectra in which there may be slight gain shifts, so that the

peaks may move slightly in absolute position but have a constant spacing. Fixing the relative widths from the start of a fit also has the effect of fitting one common width to all peaks in the fitted region. This is usually an excellent approximation, and has the additional advantage of decreasing the uncertainties on the peak areas, especially for weak peaks.

SA N N=1-20: store fitted centr. and areas as 1 of 20 data sets
N=-1 : write stored values to disk file gf2.sto

This command may be used to build a file of peak centroids and areas for later analysis, using for example the programs SOURCE, ENCAL, EFFIT, ENERGY, RDMFIT and/or LEGFT; see HELP ASSociated programs. When you have a satisfactory fit to a spectrum segment, and wish to store the areas and centroids, type SA followed by an integer in the range 1 to 20. This will save the areas and centroids in the program's memory, but not yet write them to disk. You may then fit the same peaks in a second and third, etc., spectrum, up to a maximum of twenty, saving the areas and centroids each time by using a different integer after the SA command. Once all required spectra have been fitted and the results saved, type SA-1 to write all of the saved data to the disk file gf2.sto. If this file exists, the new data will be appended to the end of it; otherwise, a new file will be created. The numbers used in the previous SA commands will also appear in the file, to help identify the respective spectra.

This procedure, of not writing the results to disk immediately following the fit, is followed to allow a re-ordering of the data in the gf2.sto file. It is usually advantageous to have the results for all spectra listed together for each peak (rather than all peaks together for each spectrum). However, it does have the disadvantage of requiring an additional command to write the spectra to disk, so that even if only one spectrum is being analysed, the results must be saved using the TWO commands SA 1 and SA 1.

SC N Scale for Y axis

The command can make three types of scaling for singles spectra:
N=-1 linear scale
N=-2 square-root scale
N=-3 logarithmic scale
Default is linear scale

SF *filename* Store Fit parameters in .gf2 file

See the FF command.

SH SHow counts

The command lists on the TTY the counts in of matrix or spectrum around a given channel.

SL *filename* Create SLice input file

The SL command works on GF2 files and not on files with the Oslo format. The command allows the user to create a gate file for use by the program [illegible], or set gates on 2-dimensional matrices. Windows can be [illegible] with the use of the command WI. If the file does not exist, a new [illegible] will be created. If it does exist, the user is allowed the [illegible] deleting and adding [illegible]. Windows saved in the file specify both

the upper and lower limits, and a peak-to-total ratio. The user specifies the background used to calculate this ratio by the vertical position of the cursor when adding windows.

SM Smooth matrix/spectrum
The command smooths the matrix/spectrum with a Gaussian weighting function, as indicated in Fig.8. The inputs needed are FWHMx (and FWHMy) values at two different channels. The results of a smoothing procedure is shown in Fig.3.

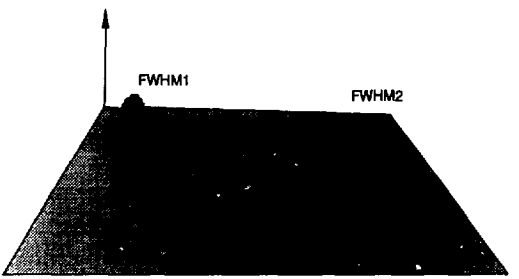

Figure 8: The weighting functions have a FWHM depending on the (x,y) positions.

SP *filename* Read in new spectrum (not Oslo format)
[SP-1 asks for new initial estimates etc. for R, Beta, Step]
SP/C Read in spectrum from matrix w/cursor for limits
This command is used to read a new spectrum from disk. The default extension for spectrum filenames is .spc, which corresponds to the GF2 format. The CRL version can also read spectra from ORNL .SPK files, and from Chalk River style .mat and .spn files. For these latter formats, you need to specify the *filename* extension. If the last spectrum you read was from a .SPK, .mat or .spn file, and you wish to read a different spectrum from that same file, there is no need to retype the *filename*; simply give the number(s) corresponding to the desired spectrum or range of y-channels. In these cases, the program will read from the last file opened.

SP/C (SPectrum using Cursor) will assume that you are reading from, or intend to read from, a matrix (.mat) file. The cursor will be called, and you can use it to enter two gate limits from previously displayed spectra. If the last spectrum was not read from a matrix, you will then be prompted for the matrix file name.

The command SP-1 allows you to change the initial estimates of, or by default fix at fixed, the parameters R, Beta and Step. SP-1 will have this effect regardless of whether you previously used the file gfinit.dat or ginit.ini to initialize these parameters. You can also type SP-2 to re-

execute the file gfinit.dat and/or gfinit.cmd. See also HElp INIt files.

ST STop and exit from Mama
After checking that you do indeed wish to stop the program execution, this command will cause Mama to terminate.

SU [I,J] SUm counts between channel I and J using cursor
The commands SU may be used to sum over a range of channels, with and without background subtraction, respectively. By default, the cursor will be called up, and you use it to enter the channel limits, in either order. The subtracted background is taken as the straight line joining the positions of the horizontal cross-hair at the two limiting channels. In each case, the centroid and area are computed.

You may also sum over a selected range of channels by entering the command SU <lim1> <lim2>, where <lim1> and <lim2> are the limiting channel numbers. This form of the command does not require the current spectrum to be displayed on the screen.

SW Change Starting Widths FWHM parameters, etc.
This command may be used to change the parameters defining the starting FWHM of the peaks, and whether the absolute and relative widths are fixed by default. After the starting width has been changed, you will be asked if you wish to reset the free parameters to their new initial estimates.

TF Total Fit with (a,n)
The command makes a fit of the total landscape of the 2-dimensional experimental first-generation matrix. The level density parameter a (1/MeV) and the exponent n of Egamma are used as fitting parameters.

TR Transform spectrum to one or many rows in a matrix
The command puts a singles spectrum into a matrix. The same spectrum can be copied to one or many rows in the matrix.

UN UNfold matrix/spectrum with MaI or Gaussian response matrix
See the FO command.

UX Type in your UniX command
The UX command allows you to send a text string to the UNIX shell. However, to make "cd" to another directory, will not change your working directory (the directory were you started Mama).

WI Add WIndow to look-up table or slice file using cursor
The command works on GF2 files (not Oslo format). The command adds a window to the currently defined file (Look-up or Slice). The cursor is called, and is used to specify the upper and lower limits of each window. For each window, in LU mode, the user is also asked for a look-up value to be inserted in the table for the appropriate range of channels. In SLice mode,

the y position of the cursor is used to define a background for the gate, used to calculate the peak-to-total ratio.

WM [N] Change Weighting Mode (i.e. error bar)
N=1/2/3: weight with fit/data/another spectrum

This command lets you select the algorithm to be used in determining the weight to be applied to each channel in the fit. The integer n is by default one, so that the standard deviation assigned to the counts in a given channel is taken as the result of the fit, as calculated using the current parameter values for each iteration. This option removes excessive weighting of channels which have lower counts because of statistical fluctuations, and is generally to be preferred. If n is given as 2, the standard deviation is taken as the square root of the number of counts in the data itself. The third option, n = 3, is used in fitting a subtracted spectrum. Let us suppose, for example, that you are fitting a spectrum A, which is computed by subtracting a spectrum C, multiplied by a factor x, from spectrum B. That is,

$$\text{counts}(A) = \text{counts}(B) - x*\text{counts}(C)$$

then

$$\text{sigma}^2(A) = \text{sigma}^2(B) + x^2*\text{sigma}^2(C)$$
$$= \text{counts}(B) + x^2*\text{counts}(C)$$

Thus the correct weighting spectrum may be obtained by computing a fourth spectrum which is the sum of B and x^2 times C, and weighting according to (the square root of) the counts in this fourth spectrum. After typing WM 3 you will be asked for the *filename* of this weighting spectrum.

WR Write matrix/spectrum to disk

The command ask you for the type (1,2,3) of matrix or spectrum that you wish to write on disk. Furthermore, you have to give the calibration(s), dimension(s) and *filename*. The procedure gives adequate defaults for these values.

WS *filename* Write Spectrum

This command write gf2 files (not Oslo format). Use instead WR for Oslo format. The WS command writes the current spectrum to a disk file. If the file name is omitted from the command line, the program will prompt for it. You will also be asked for a spectrum name, or title, which will be written to the file along with the data. The output file always has the default extension .spc.

Note that WS cannot write to .SPK, .mat, .spn or Oslo files.

XY Interchange X and Y axis

The command puts the counts in (x1,y1) into the position (y1,x1). This corresponds to a reflection about the diagonal of the matrix. Note that the maximum dimension of the matrix after the XY command is 512x152.

4. Various Topics

4.1 Peak Find

Mama contains a least-squares peak fit program designed primarily for use in analyzing gamma-ray spectra from Germanium detectors. However, it can also be used to analyze other types of spectra, such as those from Si(Li) electron detectors and silicon surface barrier detectors, and under some circumstances may even be used to extract lifetimes from time spectra.

This is a program to fit portions of spectra with up to fifteen peaks on a quadratic background.

The fitted parameters are :

A,B and C :	Background = A + B*X + C*X*X where X is the channel number minus an offset.
R,BETA, STEP :	These define the shape of the peaks. The peak is the sum of a gaussian of height H*(1-R/100) and a skew gaussian of height H*R/100, where BETA is the decay constant of the skew gaussian (in channels). STEP is the relative height (in % of the peak height) of a smoothed step function which increases the background below each peak.
Pn,Wn AND Hn :	The position (centroid of the non-skew gaussian), width and height of the nth peak.
Initial estimates	of A,B and C are taken to give a straight line between the limits for the fit.
Initial estimates	for Pn and Hn are taken from the given peak positions (Hn = counts at peak position - background)
Initial estimate	for R is taken as R = A + B*X (X = ch. no.)
Initial estimate	for BETA is taken as BETA = C + D*X (X = ch. no.)
Initial estimate	for STEP is taken as STEP = E

FWHM = SQRT(F*F + G*G*x + H*H*x*x) (x = ch. no. /1000)
Default values are: F = 3.00, G = 2.00, H = 0.00

Mama fits a portion of the spectrum using the sum of up to fifteen peaks on a quadratic background. Each peak is composed of three components:

(1) a Gaussian,
(2) a skewed Gaussian, and
(3) a smoothed step function to increase the background on the low-energy side of the peak. Components (2) and/or (3) can easily be set to zero if not required.

Component (1), the Gaussian, is usually the main component of the peak, and in Ge detectors, physically arises from complete charge collection of a photoelectric event in the detector.

Component (2), the skewed Gaussian, arises from incomplete charge collection, often due to "trapping" of charge at dislocations in the crystal lattice caused by impurities or neutron damage. If the detector and electronics had infinite resolution, component (1) would be a delta-function and component (2) would yield an exponential tail on the low-energy side. The convolution of this exponential tail with a Gaussian resolution function yields the functional form:

* EXP((x-c)/beta)
* ERFC((x-c)/(SQRT(2)*sigma) + sigma/(SQRT(2)*beta))

where ERFC is the complement of the error function, x is the channel number, c and sigma are the centroid and standard deviation of the Gaussian in component (1), and beta is the decay constant of the exponential. Beta now corresponds to the "skewedness" of the skewed Gaussian.

Component (3) arises mainly from Compton scattering of photons INTO the detector and from escape of photoelectrons from the Ge crystal, which result in a slightly higher background on the low-energy side of the peak. The functional form used in mama is:

y = constant * ERFC((x-c)/(SQRT(2)*sigma))

which is produced by the convolution of a step function with a Gaussian of width sigma.

When both R and Beta are allowed to vary during a fit, component (2) will usually greatly increase the uncertainties calculated for the peak areas. This is because there is a large cross-correlation, between the heights of components (1) and (2), which is not properly taken into account in the calculation of the uncertainties. Since, if Beta is unknown, the relative height of the skewed Gaussian is not generally well-determined by the fit, the large uncertainty in the relative heights yields a large uncertainty in the area. If, however, at least one of the parameters R and Beta can be fixed at some reasonable or previously determined value, then the quoted error on the area is usually reliable.

For this reason, and for the purpose of consistency, it is suggested that at the start of the analysis of a series of spectra, at least one preliminary pass be made in the analysis of a source calibration spectrum, to determine a set of shape parameters R, Beta and Step which describe the peak shapes well, as a function of channel number. Experience shows that Beta and Step do not seem to vary appreciably with gamma-ray energy, and R can usually be approximated by a straight line (or combination of two straight lines, one at low energies and the other at higher energies) as a function of channel number. These values can then be entered as the initial estimates, and one or more of the parameters fixed, on entering the program. Initial estimates may also be entered from within the program by typing the command SP-1, or by using the initialization file gfinit.dat (see INIt files).

The limits of the fit are shown as vertical lines from the X axis to the spectrum, and the vertical arrows with numbers below them are peak position markers. The difference between the data and the fit (in counts per channel) is shown halfway between the spectrum and the X axis. The vertical offset is added to the difference to separate it from the X axis for reasons of visibility.

Once you become familiar with peak fit, you will probably want to create one of the two initialization files gfinit.dat or gfinit.cmd. The operation of these files is described under the command HE INIt files.

4.1 First Generation Gamma-Ray Spectra

In the following a very short description of the method of extracting first generation gamma-ray spectra from particle-gamma coincidences is given. You find a more detailed outline in M. Guttormsen et al., NIM A255 (1987)518.

The figure below illustrate the first generation gamma spectrum from 8 MeV of excitation energy. There exists no way to separate these transitions from transitions originating from higher order generations using timing techniques.

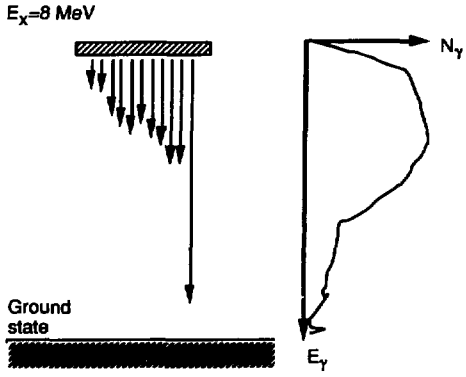

Figure 9: The first generation gamma-ray spectrum consists of the primary gammas from a certain excitation energy.

The method is based on the assumption that states populated after the first gamma-transition have the same decay properties as states populated directly in one-nucleon transfer at that energy.

The method is illustrated in Fig.10. The coefficients w_i are unknown and represent the probability of decay from bin 1 to i. In fact, the w_i values corresponds to the first generation gamma-ray spectrum. This close relation allows a determination of w_i through an iteration, as shown in the figure.

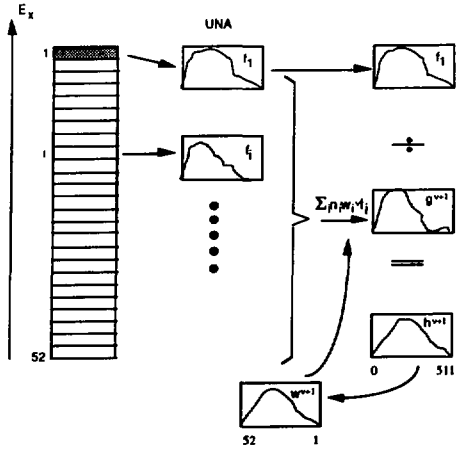

Figure 10: The iterative procedure in the extraction of first generation gamma-ray spectra from bin 1. The same procedure is then performed for all bins. An example of the results from this procedure is shown in Figs. 3 and 5.

In order to run the command, you should have a set (matrix) of unfolded gamma-ray spectra with known calibration for both gamma and particle energies. In addition you should know the counts in the corresponding singles particle spectrum, so that the program can estimate the number of populated states (and number of cascades) from each bin.

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