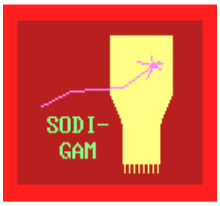
Guide to

Gamma-W, Sodigam and Alps

for Windows

Addendum to the original manuals for
Gamma-W, Sodigam and Alps



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Dr. Westmeier GmbH
Manuals QA Sheet

Description	This manual describes the features and operation of the software package Gamma-W, Sodigam & Alps for Windows

Software version	Manual last updated	Edited by
	Manual file/s location	

Comments:

The manuals for the original DOS Versions of Gamma-W, Sodigam and Alps remain an excellent reference manual with detailed explanations of the CODEWORDs used in Gamma-W, Sodigam and Alps for Windows.

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Foreword

Gamma-W, Sodigam and Alps for Windows are developed, maintained and ©copyrighted by:

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SOFTWARE from the Dr. Westmeier GmbH

Gamma-W is a high sensitivity, high precision code for the analysis of gamma ray spectra from almost all producers - including 16K spectra in ASCII and Ortec format - from Ge(Li) and HPGe detectors. Peakareas are determined through the fitting of mathematical shape functions to experimental counts after subtraction of the analytical background distribution. Up to 30 peaks can be fitted simultaneously to one spectral region, thus allowing the analysis of complex overlapping multiplets.

The code is either manually operated by the user or automatically controlled through the use of batch files. It uses **CODEWORDs** with associated parameters as elements of a highly flexible meta-language. This allows the user to tailor extremely simple and fast analysis sequences as well as very complex and detailed analyses.

For example, the codeword **CALC** is used to instruct the program to carry out an "automatic high precision spectrum analysis". Each codeword may be followed by up to three variables which serve as parameters to further define the codeword function. For example, `CALC 100 400 1´ means that a Region of Interest (ROI) should be set for automatic spectrum analysis between channels 100 and 400, and the fit results should be shown in the spectrum graphics window.

Batch files allow the user to automate the analysis for groups of samples or repetitive measurements. A batch file is an ASCII file which contains codewords and their parameters or even other batch files as sub-routines. For example, the following batch file

```
READ
/ ... / TESTSPEC.SPM
FILE
/ ... / TESTSPEC.ENE
CALC  450  750   0
```

instructs Gamma-W to read the spectrum **TestSpec.spm** from a directory /.../ along with the energy calibration file **TestSpec.ene** and carry out a peak analysis between channels 450 and 750. The results are automatically written in an ASCII-formatted output file called **Output.txt**.

Gamma-W for Windows encompasses all scientific capabilities of **Gamma-W** and includes many new possibilities. There are new spectrum handling features; a management hierarchy for the administration of routines and datafiles and personnel accessibility; and, software for the control of **target MCAs** (ISA, TISA, TMCA II, dMCA-pro and scintiSPEC).

☞ Gamma-W for Windows supports the analysis of 16K spectra with up to 2000 peaks and with external background correction data for 500 peaks.

In addition to the Gamma-W and Gamma-W for Windows codes, the Dr. Westmeier GmbH provides the following programs for PC systems:

Sodigam High precision analysis of gamma ray spectra from NaI(Tl), CsI, or similar detectors. Sodigam is also suitable for the analysis of x-ray spectra measured with proportional counters.
Sodigam for Windows is now available.

Alps High precision analysis of alpha particle spectra from semiconductor detectors or gridded ionization chambers.
Alps for Windows is now available.

The Dr. Westmeier Gesellschaft für Kernspektrometrie mbH also develops customized scientific software on request.

Introduction

A complete guide to the structure and functions of **Gamma-W**, **Sodigam and Alps** as well as detailed examples of typical spectrum analysis sequences including the use of batch files are given in the original DOS manuals for the software.

This manual describes the developments and the new features in **Gamma-W, Sodigam and Alps for Windows,** and presents typical analysis sequences which will enable you to use the software fast and easy.

Gamma-W screens and files are used in the examples, however, the operations are almost identical in **Sodigam and Alps**, the main difference being that the screens and file names are then pertinent to the program Sodigam or Alps**.**
Some CODEWORD features will of course be specific to one or the other of the three programs.

It will be helpful if you already have some familiarity with Windows, Gamma-W, Sodigam, Alps and where applicable with **target** software. However, even if you don´t, you will be able to learn to use Gamma-W, Sodigam and Alps for Windows quickly and efficiently.
You may increase your knowledge of the capabilities of the software by referring to the original manual, in particular the section CODEWORDs. There are several examples of analysis sequences in the manual which will help to use the more advanced codeword and batch file options.

This ***Guide to Gamma-W, Sodigam and Alps for Windows*** is divided into six main sections :

Section I : The hardware requirements, installation and initial start-up of the software.

Section II : The Windows handling features that are directly related to the codeword and batch file modes of operation of the DOS version of Gamma-W, Sodigam and Alps.

Section III : A completely new management capability for the setting up and automatic application of "Analytical **Procedures**".

Section IV : A User Management System

Section V : An overview of the direct control of hardware settings and MCA manipulation of **target MCA**s (e.g. ISA, TISA, TMCA II, dMCA-pro and scintiSPEC).

Section VI : A list of Hotkey functions.

The software package **Gamma-W, Sodigam and Alps for Windows** encompasses all scientific capabilities of the DOS versions of **Gamma-W**, **Sodigam and Alps** and the operation of the code is very similar. However, standard handling capabilities of the Windows platform have replaced and simplifies some features of the original software.
For example, the codeword **COLO** (for setting the display mode for graphics) is no longer necessary because MS Windows Application Programming Interface (API) routines are used in Gamma-W, Sodigam and Alps for Windows. Nevertheless, most of the codewords are functional and can be used in **batch files** or from the **Codeword Terminal** dialog window.

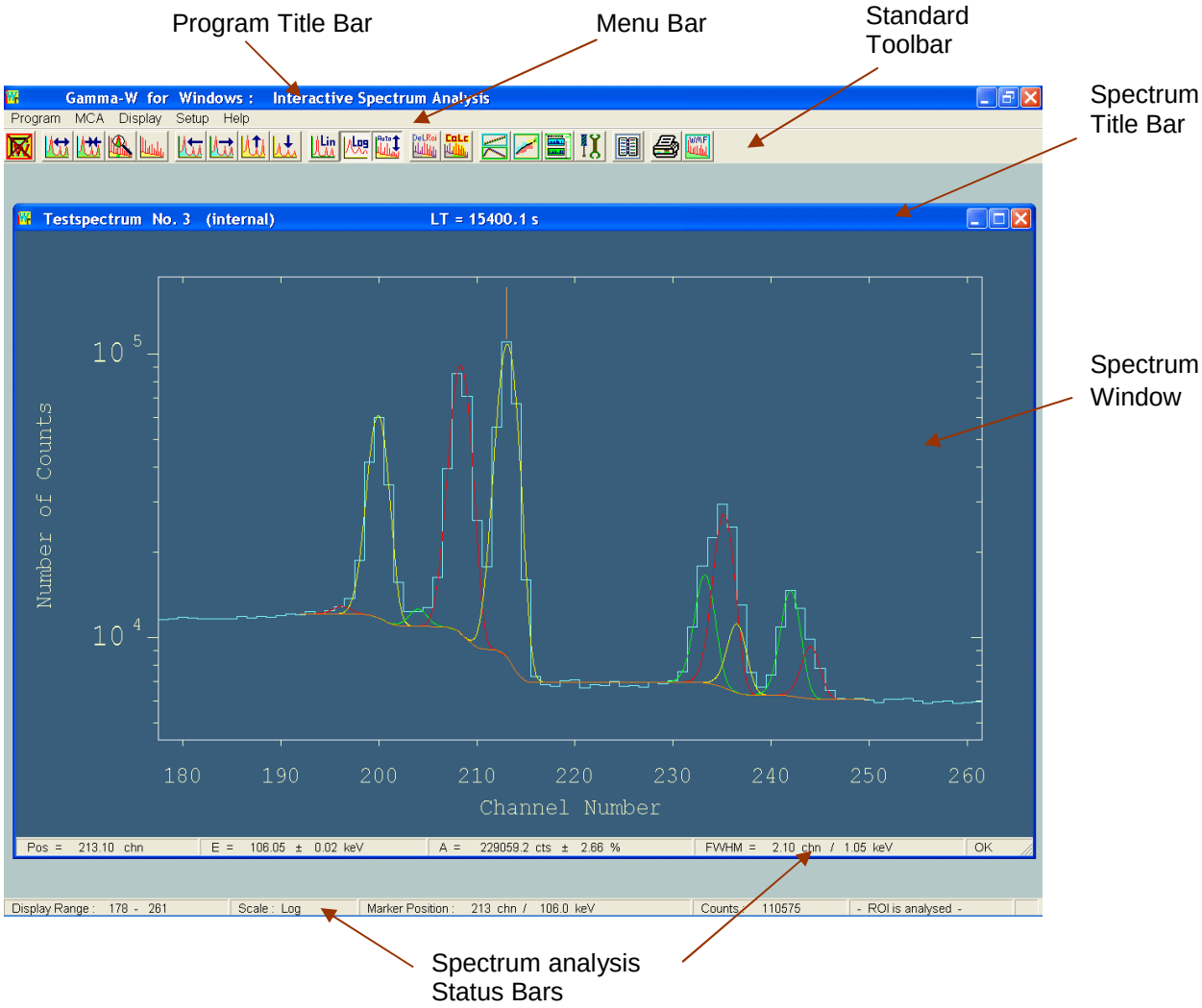
Please contact us if you wish to use a codeword that is presently deactivated.

♦ Structures and Conventions

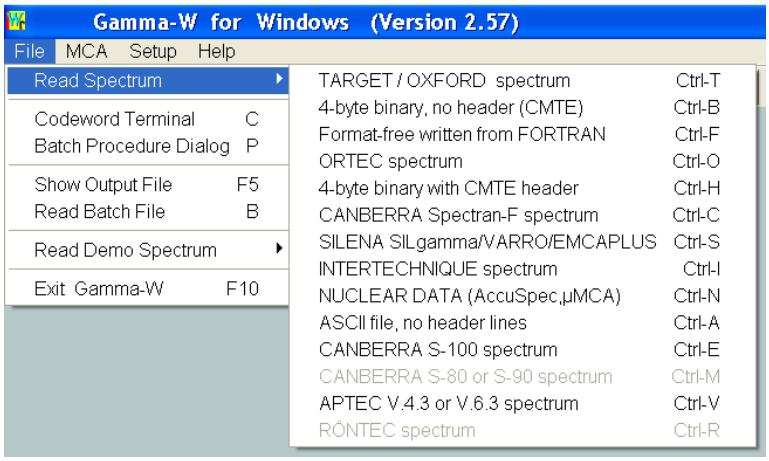
Gamma-W, Sodigam and Alps for Windows uses Menus and Dialog Boxes to call the commands and set the parameters for operations. The menu structures and controls that you will use are very similar to those usually found in other MS Windows applications and will not be described here. However, an overview of the program structure is given here.

In a simplified language the verb "to click" is frequently used in this manual. The term actually means: move the mouse pointer onto an item and then click a mouse button.

The Gamma-W, Sodigam and Alps for Windows Spectrum *Screen*



Controls

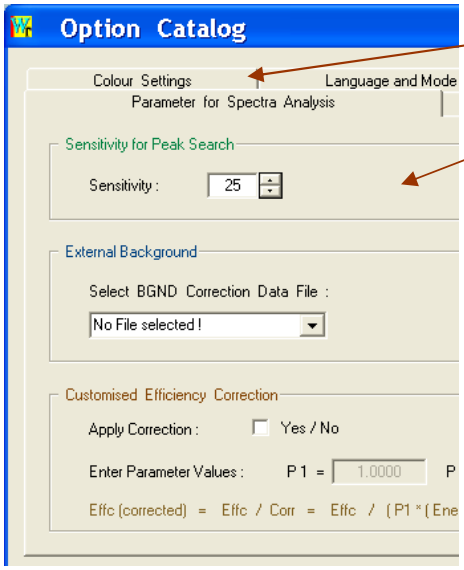


Menus with commands and fly-outs:

Click a menu title in a Menu Bar to open the menu to access commands, fly-outs and dialog boxes.

Click on the ▸ arrow to open a fly-out.

A menu item with an ellipsis (...) means that this item will open a dialog box.



Tab

Tab page

Dialog boxes with tab pages:

Click on a tab to access a page.

The pages are organized by category and contain commands and options that pertain to the title of the tab page.

Text boxes and spin buttons:

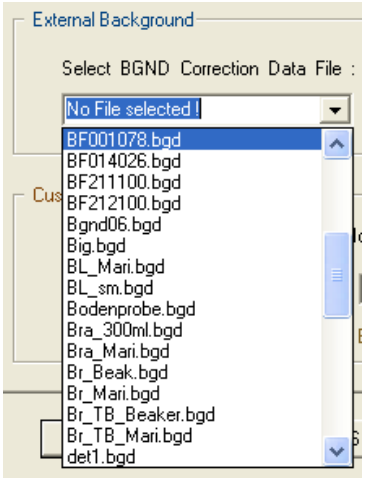
You can enter text or numbers in text boxes. Spin buttons are used to increase or decrease integer numbers.

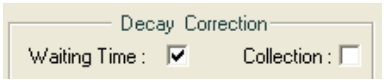
To increase a number, click the ↑ arrow; to decrease a number, click the ↓ arrow.

Drop-down lists:

Drop-down lists present a selection of items from which you may choose one.

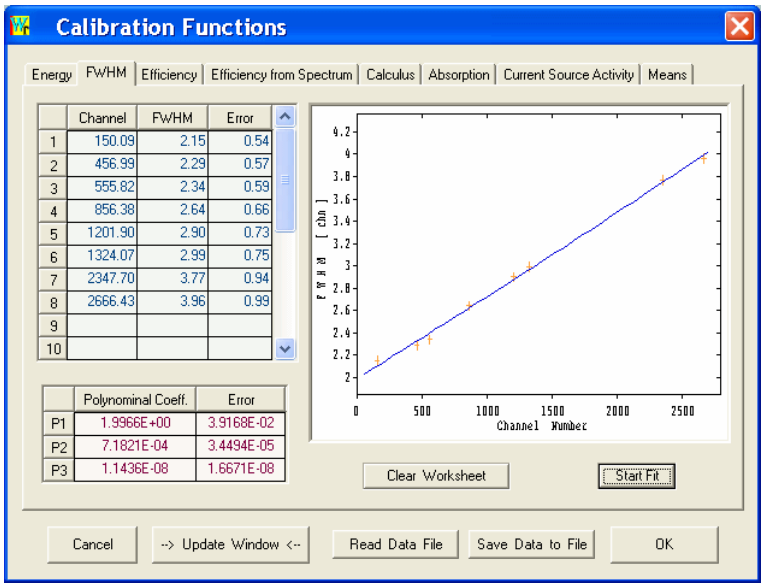
To open the list, click the ▾ arrow to the right of the list box.

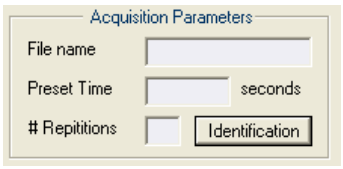




Check boxes:

Click a check box to turn an option on or off. A ✓ in the box indicates that the option is active.



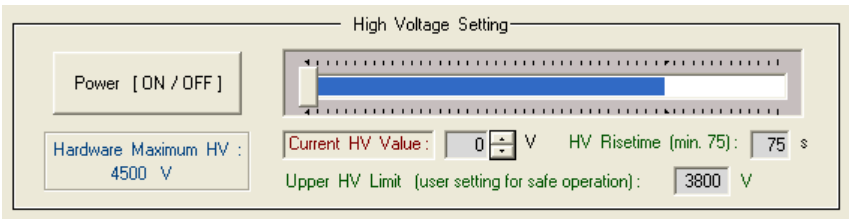


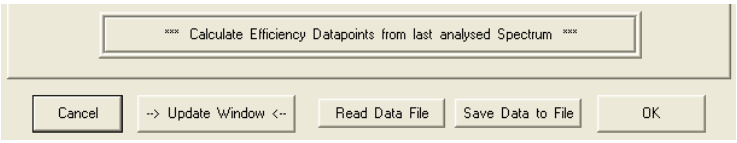
Data entry fields and tables:

Click with the left mouse button in the designated area and type in the required information or data.

Sliders:

Sliders let you increase or decrease an integer numerical setting. To move the slider, position the mouse over the slider bar. Press the left **mouse** button and drag right and left or up and down to increase or decrease, respectively.





Execute buttons and bars:
Simply click with the left mouse button on the bar or button to have the command executed which is written there.

Conventions

Hints given throughout the manual are prefaced with a ☞.

Main Menu commands are written in bold in a way similar to how they will appear in Gamma-W, Sodigam and Alps for Windows,
e.g. **Setup** or **Batch Procedure Dialog**.

The names of tab pages are marked 🗁 to remind you to click on the tab at the top of the page in order to open the dialog box.

The names of execute buttons and bars on tab pages and keyboard commands are in **bold** and enclosed in <...>.

Directories and file names are written in **bold**.

Section I

In this section, you will find information about the system requirements for running Gamma-W, Sodigam and Alps for Windows, and how to install and get started with the software.

For simplicity, references will be made to **Gamma-W for Windows** and to **Gamma-W** features, but as mentioned before, **Sodigam and Alps for Windows** handling is almost identical.

♦ Hardware Requirements

The Gamma-W, Sodigam and Alps for Windows code is developed and tested to run under all 32 bit and 64 bit version of MS Windows (Windows 95/ 98/ ME or Windows NT/2000/ XP, Win7).
It is optimized to run with **XGA** (1024x768 pixel) resolution, and at least 256 colors, (better with 64K colors, i.e. high color, 15, 16 or 24 bit), and using MS Windows *"Large Fonts"* setting.

☞ Because of MS Windows peculiarities the size of all secondary or pop-up windows is dependent on the font size setting chosen under the Windows system set-up menu (*to access this menu and change settings, select: Start, Settings, Control Panel, Display, Settings, Advanced, General, Font Size*).

☞ If your monitor cannot display XGA resolution, you can run Gamma-W, Sodigam and Alps for Windows at **SVGA** (800x600 pixel) or standard **VGA** (640x480 pixel) resolution without any problems except for the *'Procedures Management'* features. There you have to use in addition the "*Small Fonts*" setting !

☞ You may have problems running other software when the "*Large Fonts*" option is chosen. Should this be the case, then select the *User-defined* or *Other* options for font sizes and set the *Custom Fonts Size* to 120% of normal.

There are three different versions of **Gamma-W, Sodigam and Alps for Windows** available :

The ***Standard Version*** , and *two* ***Extended Versions*** with support for **target MCA**s.

☞ The two extended versions of Gamma-W, Sodigam and Alps for Windows uses either 32 bit or 16 bit DLLs to operate the **target MCA** hardware (**16 bit:** TMCA II, ISA, TISA plug-in cards, **32 bit:** dMCA-Pro card or scintiSPEC).
The 16 bit Version does not run under Windows NT, 2000, XP, or Win7 !

A fully functioning licensed version of Gamma-W, Sodigam and Alps requires a **Hardlock** connected to any **USB port** or to the **parallel port** (CENTRONICS).

At start-up of Gamma-W, Sodigam and Alps the license information is read from the Hardlock to start the Gamma-W, Sodigam and Alps for Windows program in "Gamma-W"- or "Sodigam"- or "Alps"-Mode.

Licenses for all possible **combinations** of Gamma-W, Sodigam and Alps for Windows are available, so that one will not need to have various Hardlocks when running several softwares on one computer.

The Hardlock can also be programmed to provide **runtime limited licenses** of Gamma-W, Sodigam and Alps for Windows. Please ask the Dr. Westmeier GmbH for details.

Without a Hardlock Gamma-W, Sodigam and Alps for Windows is restricted to run in a **demo mode** i.e. the user can carry out all quantitative analytical functions, but *only* with the **demo spectra** included in the software.

Without a Hardlock the reading of spectra from files or analyzing of already read spectra is denied.

The Management of Nuclide Libraries and calibration functions is not restricted in the demo mode.

☞ **Do not disconnect the Hardlock** while running Gamma-W, Sodigam and Alps for Windows.

☞ A pure **demo version** of Gamma-W, Sodigam and Alps for Windows is available **free of charge** and can be downloaded from our website (the web-link will be sent to you on request by e-mail).

The **demo version** of Gamma-W, Sodigam and Alps for Windows is the ***Standard Version*** which does not support **target** MCA hardware handling and which runs on all 32 bit or 64 bit MS Windows platforms.

♦ Installing Gamma-W, Sodigam and Alps for Windows

Installing Gamma-W, Sodigam and Alps for Windows is very fast and simple :
You will be provided with a DVD/CD-ROM *or* an USB Flash-Memory-Stick *or* the required files will be e-mailed to you (Zip-File) *or* the installation package can be downloaded from our Webserver at www.Westmeier.com, so that you can install the software from the installation files on your harddisk.

Installation of Gamma-W, Sodigam and Alps for Windows from DVD/CD-ROM or Harddisk or Flash-Memory-Stick :

The following self-extracting files are provided:

GW_Win_1.exe and **GW_Win_2.exe**, respectively;
(or **SodiWin_1.exe** and **SodiWin_2.exe**)
(or **AlpsWin_1.exe** and **AlpsWin_2.exe**)

as well as an **Install.bat** file.

The installation is started by double-clicking on the **Install.bat** file in Windows Explorer.

Alternatively, you can start the installation by clicking on the <**Start**> bar in the Windows Taskbar and select the command <**Run**...>.
In the command line type:

X:\...\Install.bat <↵>

where "X:\...\" is the path where the installation files are located (i.e. on the Harddisk, CD-ROM etc.).

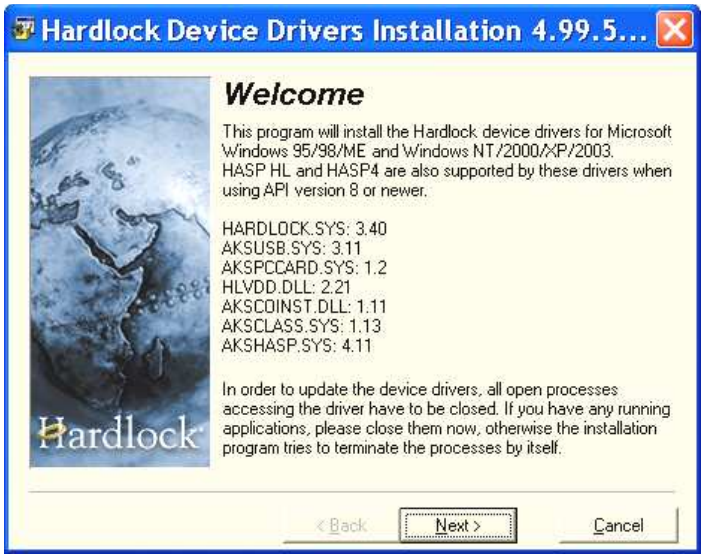
Gamma-W, Sodigam and Alps for Windows will be installed in an automatically created directory :

C:\Gamma-W.Win or **C:\Sodigam.Win** or **C:\Alps.Win**

When the **Install.bat** routine asks for the second disk, just press <↵>. Finally, please remember to close the DOS box (by clicking on the **X** in the uppermost right corner of the window) when the installation process is completed.

Installation of the Hardlock driver:

Before starting the licensed software one has to install the Hardlock driver.
The driver software is delivered either on a diskette labeled "Hardlock" or on the Gamma-W, Sodigam and Alps for Windows distribution (DVD/CD-ROM or USB Flash-Memory-Stick) under the sub-directory \..**Hardlock_Driver**.
There is an **.exe** file that must be executed.



If the **Hardlock driver** which comes with your Gamma-W, Sodigam and Alps for Windows distribution (e.g.: \..\hardlock) does not work with your MS Windows Version, i.e. due to most recently released MS Windows Service Packs or other updates, you may look at www.westmeier.com\download\HlDrv32.zip section: "Support/Download" -> "Hardlock Support" for the latest driver version.

♦ Some start-up options

The color settings (i.e. the RGB values), the language of *choice (english, french or german*), the *linear or logarithmic* y-axis display scaling, the *histogram or dot* spectrum display mode and other options are stored in a "**start-up definition file**". This file is called **Start_up.def** by default. The file is created by pressing the <**Save as Startup Options**> button in the **Option Catalog** folder under the **Setup** Menu.

The **Start_up.def** file is stored in the main directory (e.g. C:\Gamma-W.Win, C:\Sodigam.Win or C:\Alps.Win) and will be read automatically at every program start. If this file does not exist, Gamma-W, Sodigam and Alps for Windows will start with *english* as the language setting. Internally defined default settings for colors and spectrum display modes will be used.

The last used window-size dimensions (**Window (X,Y,W,H)**) for the Gamma-W, Sodigam and Alps for Windows screen and the coordinates for its position in the monitor screen are also stored in the file. As shown in the example below, the program mode currently being used (**GammaW/Sodigam/Alps**) is also indicated.

```
GammaW/Sodigam/Alps :     common start-up settings
Language            :     english
Colour Section      :      R    G    B
Main Window Colour  :     180  200  200
Spectrum Window     :      56   94  124
Peak Sum-Function   :     255  255  255
ROI Background      :     255  128    0
ROI Highlight       :     255  255    0
Spectrum Cursor     :     255  140   26
Spectrum Dot/Hist   :     128  255  255
Peak Marker Line    :       0  255    0
Fit Function Peak 1 :     255    0    0
Fit Function Peak 2 :     255  255    0
Fit Function Peak 3 :       0  255    0
Label and Numbers   :     255  255  196
Y-scaling Spectrum  :     log
Y-scaling PRC-Sp_1  :     log
Y-scaling PRC-Sp_2  :     log
Histogram or Dots   :     his
GammaW/Sodigam/Alps :     Alps
Window (X,Y,W,H)    :         0    0    0    0
End of data section to be read at start-up.
Lines #1 to #3 may be used as comment lines.
```

Start_up.def is an ASCII formatted file that can be edited with any standard ASCII editor software, e.g. MS Notepad. However, it is easier to use the <**Save as Startup Options**> button because then you won´t need to be concerned with proper data format and column alignments.
The **Start_up.def** file may contain some user's comments in lines 1, 2 and 3.

You can very conveniently setup Gamma-W, Sodigam and Alps for Windows to run with your personally preferred 'look and feel' settings. On the 🗁 **Color Settings** page of the **Option Catalog**, one may for example, specify the preferred color settings for the axes numbering and labels of the Spectrum Window.

When a very dark background color for the Spectrum Window is used the axes, labels and notation will be displayed in white. If the background color of this window is very bright, the color for the axes, labels and notation will automatically be switched to black.

♦ Hints and Remarks

☞ Installation of Gamma-W, Sodigam and Alps for Windows results in absolutely no changes in your MS Windows Registry Database !
Files are only written to the directory **C:\Gamma-W.Win**
(or **C:\Sodigam.Win** or **C:\Alps.Win)** and its sub-directories.

☞ The program does not need to be uninstalled - it can be removed from your PC by just deleting the program directory with its sub-directories.

☞ If you do not want to keep the program in the default installation directory, you may move all files and folders to any other drive or even rename the main program directory.
However, the sub-directory names structure (Bgnd, Calib, Library, Process, Source, Spectra) must be maintained within the new directory !

☞ You can start the program by a double-click on the **Gamma-W.exe** or **Sodi_Gam.exe** or **Alps.exe** file in MS Windows Explorer. For ease of access it is recommended that you link the program icon to your desktop or to the MS Windows "Start" menu. To do so :
Look for the **Gamma-w.exe** or **Sodi_Gam.exe** or **Alps.exe** file in the program´s main directory **c:\Gamma-W.Win** or **c:\Sodigam.win** or **c:\Alps.win**. Click on the file name with the right mouse button, hold down the button and drag to the desktop, and finally release the button.
A Menu with various options will appear. Choose the option `Make Link...´. Now you can start the software by double-clicking on the icon on the desktop.

☞ Gamma-W, Sodigam and Alps for Windows can also be started with a "**start-up argument**" indicating that the program should be started with a spectrum or a batch file. This is useful when you start the program from other MS Windows applications, e.g. the WinTMCA32 software from **FLIR** (former **icx**, former **target**).

You must give the full path and file name of an ASCII formatted spectrum or batch file. ***The filename extensions must be *.spc, *.asc or *.dat for a spectrum or *.fil for a batch file.***
For example, you can use the "run" command in the Windows "Start" menu. The following command will start Gamma-W and read the spectrum file **Testspec.dat** :

c:\gamma-w.win\gamma-w.exe c:\gamma-w.win\spectra\testspec.dat

☞ Gamma-W, Sodigam and Alps for Windows are supplied with either of two Hardlocks. Connect the software protection (**E-Y-E**) unit to either a USB port or a parallel (CENTRONICS) port.
If you have the parallel port version of Hardlock, plug the male connector side into the PC and connect your printer to the other side (connection in line).
If a printer is connected to your computer it has to be turned on.

You may connect several different Hardlock **E-Y-E** units in line.
If you have a USB Hardlock, just plug it into any appropriate USB slot.

☞ The file **Start_up.ini** has the same function as the **gammawst.fil** in the **DOS version of Gamma-W** (**sodigast.fil** for the DOS version of **Sodigam** and **alpsst.fil** for the DOS version of **Alps**).
The start-up file is located in the main directory of the program.
An example is given below :

```
! 'Start_up.ini'
!
! Initialization Batch File will be read at
! Gamma-W / SODIGAM / Alps  Startup  -or-  on [RESET] command.
!
! *** Lines starting with '!' are Comment Lines ***
!
! For meaning of Definitions (Codewords) and
! appropriate Parameter Values see Codeword References
! for Gamma-W, Sodigam or Alps.
!
! Set Printout Parameter (0=standard, 1= extensive Printout)
PRIN  1  1  0
!
! Set default Energy Calibration
ENER 1
    0.00000E+00    0.50000E+00    0.00000E+00
!
! Set upper Limit for Area in Peak Tailing (%)
! -or- thin/thick Source (0/1) for Alps
TAIL  10
!
! Set Detection Limit (x * Sigma, Min. Counts, Type 2 error,
!                      -1= read Data only)
DETL 2.0 4 0.10 -1
!
! Set Sensitivity (x/10 Sigma, 25/10 is default)
SENS  30
!
! Specify Nuclide Library (full Path & Filename)
LIB
C:\Gamma-W.Win\Library\Nuclides.lib
!
! Set Specific Activity Unit (1=Bq/kg,...)
UNIT  1
!
! Set default Spectra Path
PATH  0
C:\Gamma-W.Win\Spectra
!
! Set P1: default Spectrum Format (here 9=ASCII)
!     P2: = -1  --->  no READ, just set Spectrum Format
!     P3: Spectrum Type (0=no change): HPGe=1,NaI(Tl)=2,Alpha = 3
READ 9 -1 0
!
! Set default FWHM for NaI(Tl) Detectors in % (7.5 % default)
! NB: this has to be done AFTER Spectrum Type Selection !
FWHM 70
!
! Set Energy Window Width for Nuclide Assignment (keV)
NUCL 8 2.5
```

☞ **Start_up.ini** is an ASCII formatted file that contains initialization definitions, file names for default calibrations, libraries, default parameters for codewords and it even may call other batch files.

☞ You may edit this file with any ASCII editor software and enable or disable command lines in the file by deleting or inserting a " **!** " at the beginning of the line.
As shown in the example, comment lines are especially useful to help keeping codeword parameters and their meanings in mind.

☞ Not all codewords from the DOS version of Sodigam and Alps have been activated in Sodigam and Alps for Windows.

☞ Gamma-W, Sodigam and Alps for Windows are provided in three languages :

German, English and **French**.

You can select the language of your preference from the **Setup** drop-down menu under **Options Catalog** on the 🗁 **Language and Mode Setting** tab page.

☞ If you have installed the **16 bit *Extended Version*** of Gamma-W, Sodigam or Alps for Windows then, BEFORE STARTING the software, you MUST first check to ensure that the **TmcaInit.txt** file has been correctly edited and set up as described in **Section V**.

The **16 bit *Extended Version*** of Gamma-W, Sodigam and Alps for Windows will crash if you try to run the software without properly defining the installed hardware in the **TmcaInit.txt** file.

The 16 bit hardware (TMCA II, ISA, TISA plug-in cards) **MUST** match exactly the settings given in the **TmcaInit.txt** file !

☞ If you have installed the **32 bit *Extended Version*** of Gamma-W, Sodigam or Alps for Windows the 32 bit hardware (dMCA, dMCA-pro, scintiSPEC) will automatically be detected by the associated 32 bit DLL (Tmcadrv32wdm.DLL). Therefore the file **TmcaInit.txt does not have to exist** in your program directory.

Section II

The handling of Gamma-W, Sodigam and Alps for Windows is described below. Remember that although the examples and screens being used are shown with Gamma-W, the operations described are almost the same for Sodigam and Alps.
The user will quickly become familiar with

- operating the program with the mouse, pull-down menus, icons, and through the keyboard
- loading and analyzing a spectrum in the spectrum display mode
- performing energy, FWHM and efficiency calibrations
- performing an analysis of a spectrum
- using the Nuclide Library facility
- printing out a results file
- carrying out spectrum background corrections

♦ Getting started with Gamma-W, Sodigam and Alps for Windows

It is best to work through this section step by step with Gamma-W for Windows up and running on your computer.

When Gamma-W for Windows is first started, the program opens a start-up window, checks the software protection Hardlock, reads the start-up file **Start_up.ini** and checks for the presence of the default Nuclide Library **Nuclides.lib** (**Alpha.lib** for Alps).

On the start-up screen click on the <**OK**> button or just wait for some seconds for automatically closing the start-up window. The **Main Screen** of the program will be displayed, as shown in the following picture.

From now on the program can be operated through the pull-down menus, through icons, through shortcut keys, or through batch files.

In the following examples showing the handling of the program, you will often be given several possibilities to carry out a particular command.

☞ The Function Key assignments in the Main and Spectrum Window (see ***Section VI:*** *Hotkeys*) are different from those in the DOS versions of **Gamma-W, Sodigam and Alps**.

☞ **Online help** for the user is integrated into the software. Bubble help exists for all buttons in the icon bars giving short descriptions of the assignments of the Function Keys.

Keyboard shortcut keys and mouse operations are also explained in the bubble help.

A User's Manual in html format (not yet complete) is available in the **Help** menu.

☞ **Codeword help** from the printed manual for Gamma-W, Sodigam and Alps is available through the **Codeword Terminal** window of the program.
You may access this window from either the Main Window under the Menu **File** or from the Spectrum Window under the Menu **Program** or by just pressing the character **"c"** on the keyboard.

If you enter a "**?**" on the command line, you will be given information on how to use the **Codeword help.**
Entering the word "CODE**"** will give you a list of the codewords in Gamma-W, Sodigam and Alps.
Codewords that are not active in Gamma-W, Sodigam or Alps for Windows are marked with an **" * "**.

If you type a codeword with a question mark, e.g. *"CALC ?",* you will see a short on-screen description of this codeword and its **parameters**, as given in the original manual.

♦ The icons of the Main Window

provides information on the software version and on the Dr. Westmeier GmbH.

reads in an implemented demo spectrum (various spectra are available for Gamma-W, for Sodigam and for Alps).

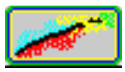
opens the "**Read Spectrum**" dialog box.

switches the program to the "**Batch Procedure Dialog**" window.

calls the "**Read Batch File**" window for more advanced operation of Gamma-W, Sodigam and Alps for Windows.

restarts the program. The results file, all previous parameters and calibrations are preset to start-up condition as defined in the **Start_up.ini** and **Start_up.def** files.

opens the "**Calibration Functions**" window (Energy, FWHM and Efficiency, Absorption, Calculus, Means, etc.).



opens the "**Nuclide assignment & Reus/Westmeier - Nuclide Library**" window to select a new library and make quantitative peak assignments.

opens the "**Options Catalog**" window.

opens the output and result file **Output.txt** with the integrated editor.

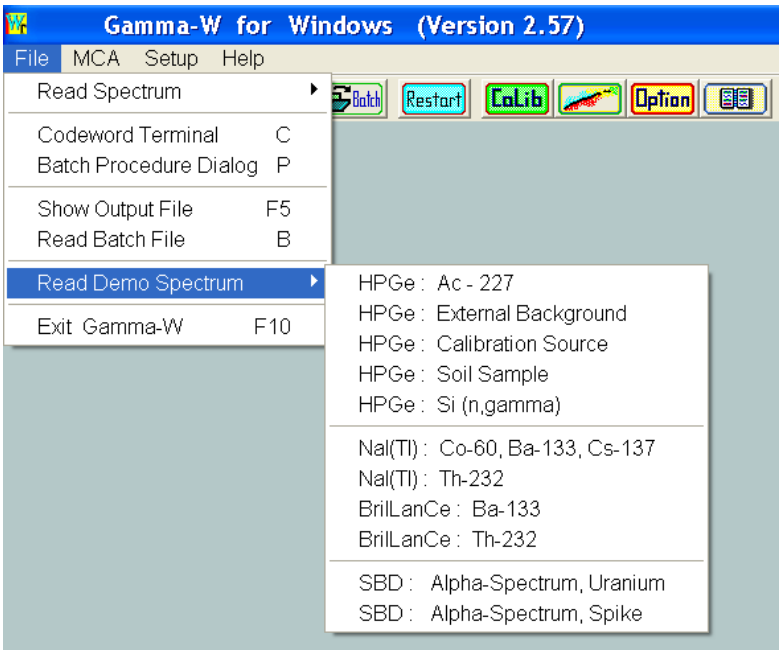
You will become familiar very fast with the use of these icons as you work your way through the examples in the section below.

♦ The Demo Spectra

Gamma-W, Sodigam and Alps for Windows is provided with eleven internal demo spectra labeled **Testspectrum No. 1** to **Testspectrum No. 11**. Nine of these spectra are gamma-ray spectra five of which have been measured with HPGe-detectors and four with scintillation detectors. The last two spectra are alpha-spectra that have been measured with surface-barrier detectors (SBD). See screenshots of all these spectra in the **Appendix** section.

The first four spectra are **1**: ^{227}Ac spectrum; **2**: an external background spectrum; **3**: a mixed calibration standards spectrum and **4**: a soil sample spectrum.

Testspectrum No. 5 is a special case in that it is a 16K spectrum: ***Si (n,γ)***. The energy range extends up to 14 MeV and there are many single and double escape peaks.



You may choose a spectrum from the menu shown above (**File** pull-down menu and selecting **Read Demo Spectrum)** or you may toggle through these eleven spectra: by clicking on the 

icon or press **F9**.

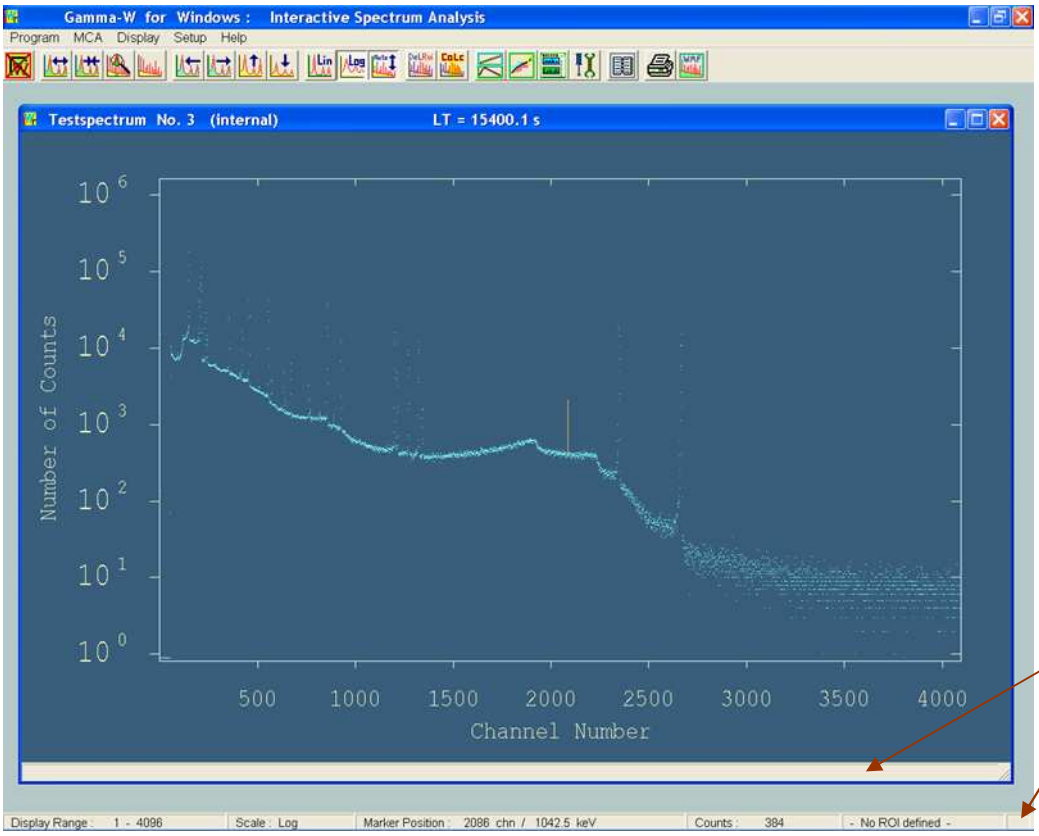
Test spectrum No. 6 and **Test spectrum No. 7** have been measured with a NaI(Tl) detector, and therefore these test spectra are relevant to Sodigam.

Testspectrum No. 8 and **Test spectrum No. 9** have been measured with a BrilLanCe detector. These test spectra are relevant to Sodigam, too.

Test spectrum No. 10 and **Test spectrum No. 11** were measured with a Silicon semiconductor detector, and therefore these test spectra are relevant to Alps for Windows. It is worthwhile to work with other software modes and types of spectra when testing and learning to do spectrum analysis, because the handling of Gamma-W for Windows, Sodigam for Windows and Alps for Windows is almost identical.

After selecting one of the demo spectra the program will open a "**Spectrum Display**" window and a new menu structure and button bar will appear as shown in the following screenshot.

All the icons and their functions will be presented in the following examples.



The upper one of the two spectrum analysis status bars is empty at start. The lower status bar contains the *'Display Range'* in channels, *'Y-Scale'* (*'Log'* or *'Lin'*), *'Marker Position'* in channel number and energy, *'Counts'* in the cursor channel and other additional comments or information.

After an analysis procedure, the upper status bar shows defined ROIs, areas of ROIs with associated uncertainties, etc. The title and status bars are updated during your working session in Gamma-W for Windows.

Please note that the `*spectrum name*´ and `*live time*´ (LT) are given in the top title bar of the Spectrum Window.
If you wish to load another demo spectrum, then close the Spectrum Window by clicking on the **Program** menu, choose the option **Exit (Clear Spectrum and close Window)** or click on the icon  or press **F10**.

Then choose the next spectrum from the pull-down menu as described above or press  once more to load the next consecutive demo spectrum.

☞ The default spectrum type with **Read Spectrum** is an ASCII formatted file (as defined in the Start_up.ini file: "**READ 9 -1**").
However, during a running session Gamma-W for Windows "remembers" the last selected spectrum type and the directory path selected by the user and retains this information as the new default.

Each time a new spectrum type is read using **File**, **Read Spectrum** , this new spectrum type and path are stored as the current default.

☞ If you use the codeword **READ N** in the **Codeword Terminal** to read a spectrum, this spectrum will automatically be displayed in the Spectrum Window when you exit the **Codeword Terminal**.

♦ Some hints on Spectrum Graphics

The spectrum display format may be altered from "Histogram" to "Dot" with the **Toggle Display : Histogram / Dots** command in the **Display** pull-down menu from the Spectrum Window, or (simpler) with the keyboard key **H**.

The dot size is automatically adjusted in three steps according to the display range. If less than 150 channels are displayed the dots are large, and they become progressively smaller as more channels are shown.

When using the "**Spectrum Live Display**" feature (only available in Gamma-W, Sodigam and Alps for Windows versions with **target** MCA support) during a running measurement "Dot" display is selected to avoid screen flickering.

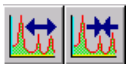
♦ A quick analysis of a Region of Interest (ROI)

To get started with the software, the setting and analysis of a **Region Of Interest (ROI)** around a peak between channels 1650 and 1690 in a demo spectrum is described. This shall, as an example, illustrate various handling possibilities which are available in Gamma-W, Sodigam and Alps for Windows for this purpose.

Load **Testspectrum No. 1**. with the "**Demo**" icon or via menu **File, Read Demo Spectrum, HPGe: Ac-227**.
Point and click the mouse cursor (i.e. *cross-hairs*) to approximately channel 1650 which moves the spectrum cursor (i.e. *red line cursor*) to that position or use the ***left and right arrow*** *keys* to move the spectrum cursor.
Note that the position of the spectrum cursor is written in the status bar at the bottom of the screen.

Expand the view by clicking on the expand icon  in the icon bar or use the ↓ arrow key or **<space bar>** to expand the spectrum around the cursor or double-click with the left mouse button at the cursor position (there are 4 ways to expand).

To **show the whole spectrum**, use the ↑ arrow key or **<space bar>** *(refer to the icons´ bubble help for other shortcut keys, e.g.* ***F3*** *and* ***F4****).*

Adjust the expansion by **holding down the *right* mouse button and moving the mouse up and down** or use the expand and contract icons  in the button bar.
You can also use the keyboard commands **<Ctrl>+↑** and **<Ctrl>+↓** or **F1** and **F2**.

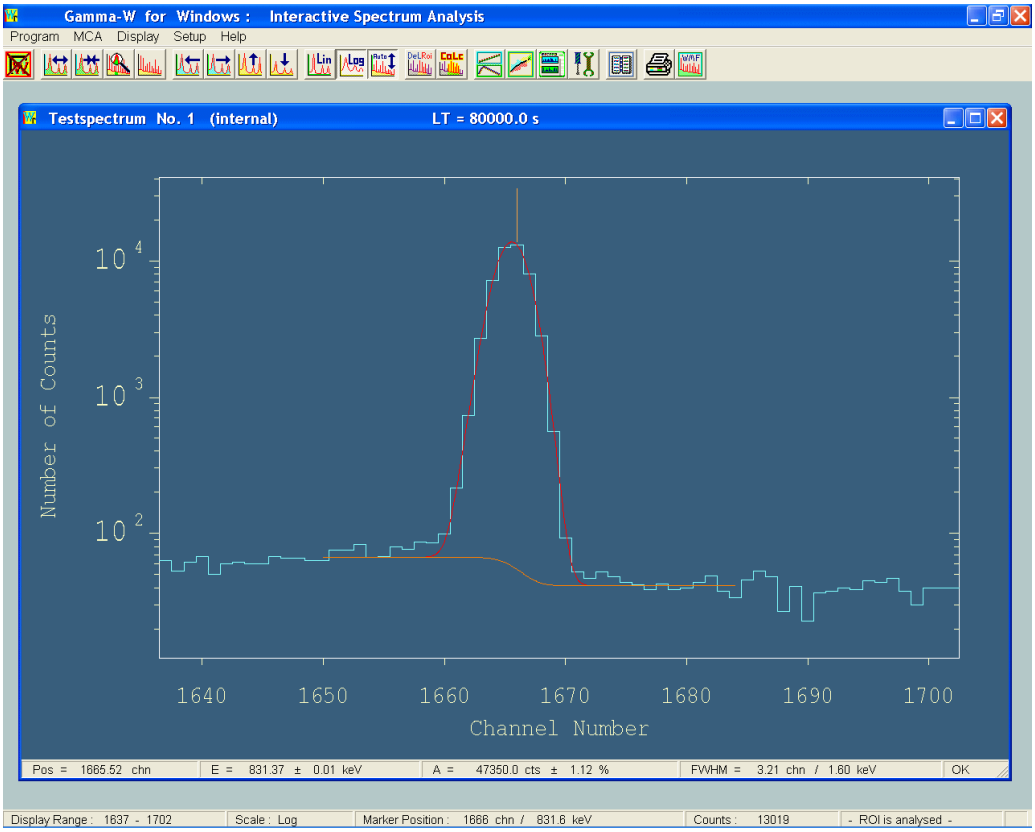
Use the left and right arrow keys to move the spectrum cursor in the field of view or point & click with the mouse. Set the spectrum cursor to approx. channel 1647.

Now **hold the *left* mouse button down and drag** the spectrum cursor over the peak to the end of the required region of interest at channel 1684. Release the mouse button.

The ROI is now highlighted in yellow.

Click with the left mouse button on the calculate  icon or just press **<CR>** or **F8**.

The fitted peak is now outlined in red, the baseline is brown and some associated information is given in the spectrum status bar i.e. the position and energy of the peak, the area and FWHM together with their uncertainties.



☞ The **ROI can also be set with the arrow keys**. Move the spectrum cursor with either the arrow keys or with the mouse to approx. channel 1647 as before. Now *hold down the* ***<shift>*** *key and using the* ***right arrow*** *key (* → *)* move the spectrum cursor to channel 1684. The region is highlighted (i.e. in yellow) as before.

☞ You can **extend** or **shrink the ROI** with the mouse: when the mouse cursor is in the left half of the ROI, drag the cursor left or right to move the left border of the ROI.

The same applies to the right border of the ROI when the mouse cursor is placed in the right half of the ROI.

Using the ***<shift>*** key together with ***left*** or ***right arrow*** keys works also for modifying the **ROI**.

☞ While the ROI is being marked, the ***total integral*** **counts** in the marked region is constantly updated in the fourth segment of the Main Window Status Bar.

☞ The "**n**" key (for "net") toggles between the **integral counts** and the ***background corrected*** **counts** (only for Gamma-W and Sodigam). The type of background can be selected with the codeword BGND (see the codeword BGND).

☞ In a marked region one can mark the **approximate position of a peak** with a green line. Move the cursor with the arrow keys to a position somewhere on the top of the peak and press the "**y**" key to **mark a peak position** or **double-click with the left mouse button**. Many peaks can be marked to define a multiplet.
The **<↵>** key or **F8** start the peak analysis routine.

☞ If you wish to **delete the ROI** without carrying out an analysis (CALC), simply use the **<Esc>** key or click on the `Delete ROI´ 

icon.

The peak analysis results are stored in the default output file **Output.txt** which can be opened with an ASCII editor through the  icon or **<Ctrl>+F1** or via pull-down menu : Program, Show Output File.

This short example shows how easily Gamma-W for Windows is operated (and how similar it is to the DOS version).

☞ The **automatic analysis of peaks** is even easier to perform (= no marking of a ROI is needed):
Choose and display the section of the spectrum that shall be analyzed and then click the 'Calc' 

icon or press **F8**.

Each fitted sub-region is shown and one activates the next peak analysis with the **<↵>** key. The fitted data are shown in the status bars under the spectrum.

☞ You may also place the mouse pointer somewhere near the top of an analyzed peak within a ROI and click to set the cursor. The **fitted data for this peak** will be displayed in the status bar.

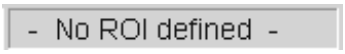
☞ *Note* that while you are analyzing peaks and jumping from peak to peak to see the fitted data in the status bars, you cannot exit the Spectrum Window with the **X** or the  icon.

☞ To **quit the ROI analysis** and return to normal spectrum display mode use the <**Esc**> key or click the `Delete ROI´  icon.

A message on the right of the lower status bar instructs you to enter **<↵>** until the ROI is completely analyzed : 

.

If you wish to exit the Spectrum Window during a ROI analysis you must use the <**Esc**> key or the `Delete ROI´  icon.

After the ROI analysis has been completed or has been interrupted by the user the status bar message will show : 

.

☞ You can analyze up to **2000 peaks** from one single spectrum.

☞ If you press the "**5**" key while working in the Spectrum Window, Gamma-W for Windows will display two additional spectrum markers.

These are the Escape-Peak Markers at 511 keV distances each.
The **green** marker indicates the location of an associated ***Single-Escape-Peak*** at an energy **of 511 keV below** the channel in which your original spectrum marker (orange-red) stands, while the **yellow** marker shows the location of the ***Double-Escape-Peak*** at **1022 keV below** your marked energy.

Note: escape peak marking is only active when the spectrum marker is placed in a channel with associated energy greater than 1022 keV.

The "**5**" key **toggles** the "Escape-Peak-Marker" display **On** and **Off**. Reading in a new spectrum will reset the "Escape-Peak-Markers" display to Off.

Use the "**s**" (**S**ingle-Escape-Peak) and the "**d**" (**D**ouble-Escape-Peak) keys to zoom into an automatically adjusted region around the single- and double-escape peaks, respectively.
Press these keys again to return to your previously displayed spectrum region.

♦ A quick analysis of a spectrum

We will use **Test spectrum No. 3** (the mixed calibration source) to carry out the following:

- An energy calibration
- Check the automatic FWHM calibration
- Carry out an efficiency calibration
- Store the calibration data to files
- Perform nuclide assignment and calculate activities
- Printout the Results File

At first open **Test spectrum No. 3** by using the pull-down menu commands **File, Read Demo Spectrum, 'HPGe: Calibration Source'** to display this spectrum in the Spectrum Window.

➢ *Energy calibration*

Move the cross-hair cursor with the mouse into the region around the second peak of ^{60}Co (the peak is in channel 2666), set the cursor with the left mouse button and then expand the region by pressing the ↓ arrow key (or use the  icon or **F3).**

Move the cursor with the arrow keys onto the peak or point & click channel 2667 and press **E**. This automatically opens the Calibration Functions window and selects the tab:

🗁 Energy

The *peak center position* is written in the first column (*'Channel'*) of the next empty row of the energy calibration table. The cursor sits in the second column (*'Energy'*) of the current row.

Now enter the correct energy in keV of the peak **1332.5**.

Click the <**Update Window**> button and the point is plotted in the graph box.

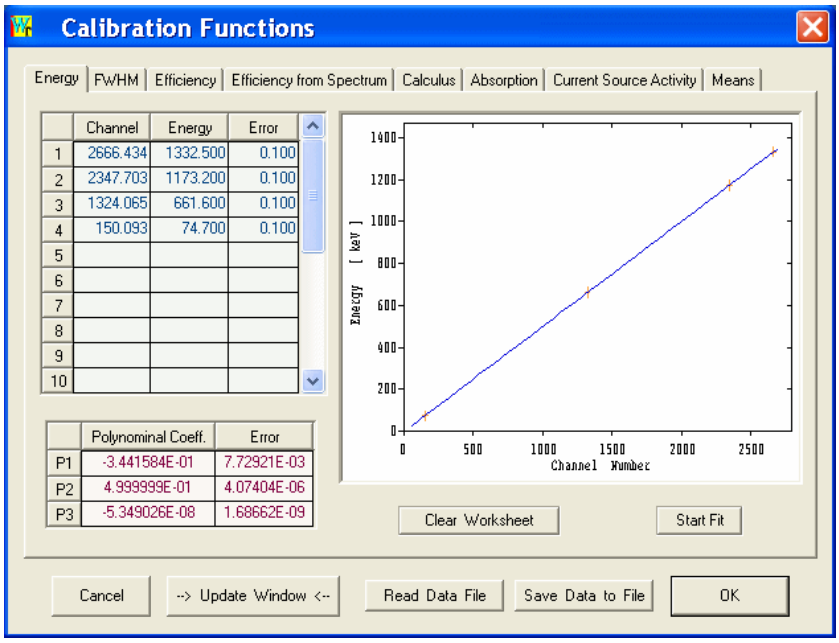
Press the <**Start Fit**> button to obtain the best fit for the existing data points. The coefficients (seven significant figures) of the fitted polynomial function will be displayed in the lower left box and the fit will be drawn in the graphics box. This preliminary fit will help you to identify other peaks in the spectrum.

Press <**OK**> to store this energy calibration to the internal variables of the program.

Return to the full spectrum display via the  icon or F4.

Repeat the process for three other peaks with the data from the table below. You can jump from cell to cell with **<Tab>** and **<Shift> + <Tab>**.

Nuclide	**Channel** #	**Energy** / keV
Co-60	2666	1332.5
	2348	1173.2
Cs-137	1324	661.6
Am-243	150	74.7



To **store the calibration data**, click the **<Save Data to File>** button and enter a file name, e.g. "**Testcal**".
The **filename extension** is automatically set to ***.ene** for energy calibration data.
The **default directory** for calibration files is **\..\Calib**.

You may now close the **Calibration Functions** tab pages by clicking the <**OK**> button.

As shown in the example "**Testcal.ene**" below, the channel numbers, energy data points and uncertainties are stored, read and displayed from file with three decimal figures.
The polynomial parameters of the fitted energy equation are stored and read to seven significant figures.

```
ENER 2
   2666.434   1332.500      0.050
   2347.703   1173.200      0.050
   1324.065    661.600      0.050
    150.093     74.700      0.050
      0.000      0.000      0.000
      0.000
ENER 1
 -3.441584E-01   4.999999E-01  -5.349026E-08
```

➢ *FWHM calibration*

Open the **Calibration Functions** pages via the  icon and select from the tabs:

🗁 FWHM

In **Gamma-W** a FWHM function is automatically calculated from each new spectrum. The function coefficients are written in the lower part of the worksheet and the function is plotted in the graphic box. The data points for the most prominent peaks in the spectrum are plotted as red crosses.

Click on any value in the data table. The according data point will be highlighted in green in the graphics box. You may move through the data points by moving the cursor in the data table with the arrow keys.

☞ You may delete or edit any of the data in either of the data columns (*'Channel'* or *'FWHM'*) for the selected peak.
Click the <**Update Window**> button to see the edited results.

Click on the <**Start Fit**> button (with or without removing or editing data points), to obtain the best fit to the current dataset.

☞ If you make a mistake or if you are simply exploring the program´s fitting routines, click on the <**Cancel**> button. You can re-enter the **Calibration Functions** as before.

FWHM in Sodigam: For proper peak analysis with the Sodigam program it is important to provide the program with the correct energy calibration and the specified resolution value for the detector used, i.e. the FWHM in percent specified for the 661.6 keV peak of ^{137}Cs. This value should be entered in the $\mathbf{p_2}$ position in the spreadsheet on the 🗁 **FWHM** tab page.
The $\mathbf{p_1}$ and $\mathbf{p_3}$ values have to be set to "**0**". The default value of $\mathbf{p_2}$ for NaI(Tl) detectors is 7.5%.
From the Codeword Terminal or in batch files you can use the codeword "**FWHM x**", where x is the FWHM given in percent.

☞ If $\mathbf{p_2}$ is <5% Sodigam automatically switches from NaI(Tl) mode to BrilLanCe mode. The latter having a significantly better resolution (compare Demo Spectra No. 7 and 9 in **Appendix I**) a different polynomial function is fitted to the channel/energy data points.

FWHM in Alps: For many applications in Alps it is recommended to use a constant FWHM function ($\mathbf{p_1}$ = FWHM in channels). The $\mathbf{p_2}$ and $\mathbf{p_3}$ values should be set to "**0**".

➢ *Efficiency calibration*

To calculate an efficiency function from **Testspectrum No. 3** we will return to the spectrum window (close the **Calibration Functions** pages by clicking on <**OK**>) and select the **command line mode** of the program by clicking on the **Program** pull-down menu and choosing the option **Codeword Terminal** (or press "c").

At the prompt in the newly opened window, type:

"calc" and < ↵ >

The program will perform a precision analysis of the entire spectrum (identical to "CALC 0 0 0" in **Gamma-W** for DOS).

Close the **Codeword Terminal** with the codeword :

"exit" < ↵ > or just "e" < ↵ >

[Alternatively to the automatic spectrum analysis with the 'calc' command in the Codeword Terminal, you may click on the "Calc" Icon, while the full range of the spectrum is displayed. The automatic analysis will start immediately and the peakfit results are shown for each peak in the spectrum.
Press the < ↵ > key repeatedly until the analysis of the whole spectrum is done and the full spectrum range is displayed again.]

Return to the **Calibration Functions** pages (e.g. press **F5**) and switch to the tab:

🗁 Efficiency from Spectrum

Define the *'Start Spectrum Date and Time'* as:

Date : 28 08 1995 *Time* : 18 35 56

The reference information for the measured calibration source (nuclide names, calibration date, reference activities A_0 and their uncertainties) is given in a "**Source Description File**" named **Mpsand.src**.

Click on the <**Open Source Description File**> button and open this file from the File Management window that comes up.

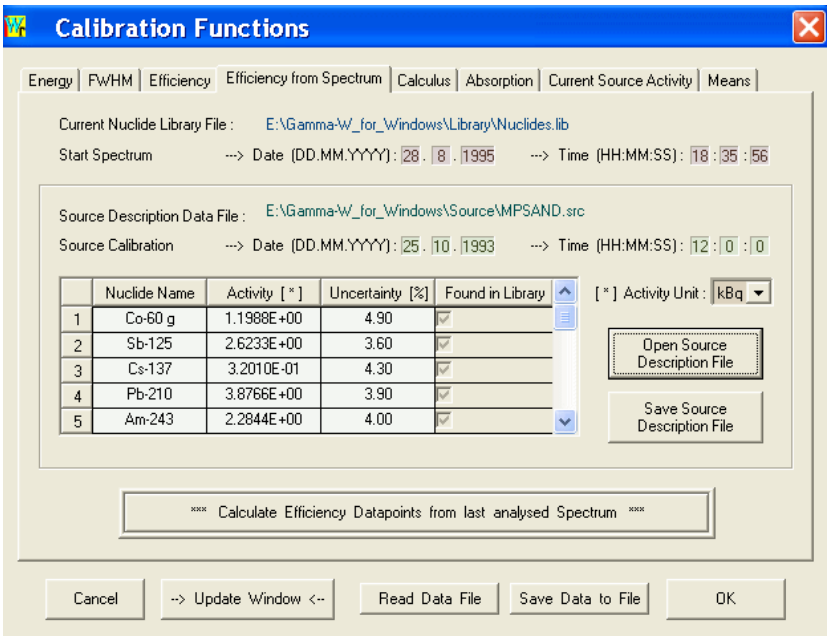
☞ "Source Description Files" contain all relevant data of your standard calibration sources, like calibration data, nuclide inventory, reference activities together with their uncertainties; one file must be created for each source.

This is very convenient, because you need to enter these data only once and for all.

☞ When a "Source Description File" is opened, Gamma-W, Sodigam and Alps for Windows check that the nuclide names referenced in the file are found in the current Nuclide Library in order to have access to the relevant decay data (halflives, γ-energies and their intensities).

☞ If there is NO checkmark ✓ in the **Found in Library** column for a given nuclide i.e. the nuclide is not in the library, then the efficiency data for lines from this nuclide cannot be calculated.
Note! Some nuclides are listed in the library as “ground state”, e.g. Co-60 g

Now click on <**Calculate Efficiency Datapoints from last analyzed Spectrum**>.



☞ The Nuclide Library currently in use is shown in the first line of the tab page.

☞ For Gamma-W and Sodigam for Windows the default Nuclide Library is **Nuclides.lib** (**Alpha.lib** for Alps).

☞ You may save an edited "Source Description File" from the 🗁 **Efficiency from Spectrum** tab page using the **<Save Source Description File>** button.

After you have clicked the <**Calculate Efficiency Datapoints from last analyzed Spectrum**> bar, the program will switch to the tab page:

🗁 Efficiency

Here you will see the most recently calculated efficiency datapoints with their uncertainties.

Gamma-W´s special fitting routine (*'Number of Coefficients'* = 0)[1] will be used by default to create an efficiency function. However, you may also select the power of a polynomial function that you wish to be fitted in the log-*y* vs. log-*x* data display.

You may delete incorrect data points or edit data. To delete a data point, just delete the value in the 'Efficiency' column by typing the "del" key on your keyboard. Click the <**Update Window**> button to see the results.

☞ To fit just a constant function, e.g. when using Alps for Windows with an energy independent efficiency, you set the power of the polynomial function (*'Number of Coefficients'*) to 1.

---

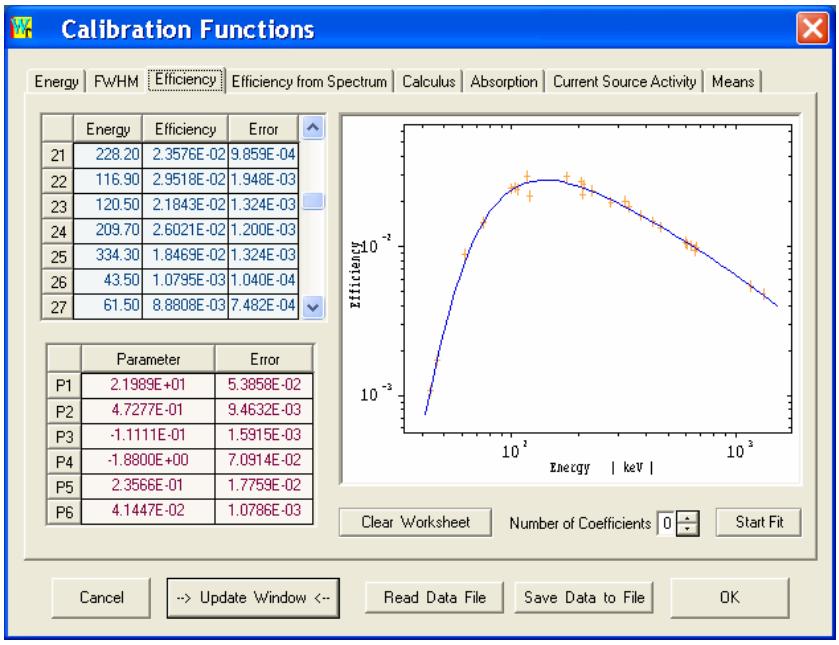
[1] B. Jäckel, W. Westmeier and P. Patzelt, "On the photopeak efficiency of germanium detectors", Nucl. Instr. Meth. A261 (1987) 543.

The intrinsic efficiency curve is empirically described with the equation:

$$\ln \varepsilon(x) = (EF_1 + EF_2 \cdot z + EF_3 \cdot z^2) \cdot 2/\pi \cdot \arctan\left(\exp[EF_4 + EF_5 \cdot z + EF_6 \cdot z^3]\right) - 25$$

where EF_n are polynomial coefficients, $z = \ln(E\gamma/keV)$ and $x = E\gamma/keV$

You may now click on <**Start Fit**> to fit a function to the datapoints.



Save the efficiency calibration data to a file, e.g. named "**Test3.eff**" by clicking on the <**Save Data to File**> button.

General information on Calibration and the *Calibration Functions* pages

The **Calibration Functions** pages are called from the **Setup** Menu with the **Calibration Window** command or with the  icon (or via F1 or via the  icon from the Main Window).

☞ The first ten channels of a "Gamma-W, Sodigam and Alps for Windows - ASCII formatted spectrum file" are reserved for measuring time information (LT, RT, DT), for energy calibration parameters (p_1, p_2, p_3, p_4) and three extra channels for user-specific information.

It is therefore best to load, make an energy calibration and re-save as ASCII spectra using Gamma-W, Sodigam and Alps for Windows via **<Ctrl> + <↵>** to ensure that the correct information is written to these reserved channels.

☞ If no energy calibration comes along with a spectrum file, the former energy calibration given by a previously read spectrum or data set (like defined in the Start_up.ini file) is retained.

☞ If there is no existent calibration, then the parameters for the default calibration function i.e. channel number ≡ energy in keV are shown in the energy calibration parameter worksheet.
The same method is applied to the FWHM and efficiency calibration.

☞ Suitable default start-up values for NaI(Tl) detectors (e.g. FWHM = 7%) and for SBD detectors are taken in SODIGAM and ALPS, respectively.

☞ The program will not accept the use of very small and statistically not well-defined peaks for energy calibrations. An example would be the peak in channel 333. The program prints a message to this effect on the screen.

☞ There are special applications where the polynomial function

$$\text{Energy} = p_1 + p_2\,\text{chn} + p_3\,\text{chn}^2$$

for energy calibration does not provide the best fit to the experimental data. One such possibility has been specifically included in the programs. The function used for this special mode is:

☞

$$\text{Energy} = p_1 + p_2\,\text{chn} + p_3\,\text{chn}^2 + p_4\,\text{chn}^{-1}$$

The parameter p_4 is stored in channel 7 of the ASCII spectrum file, for example with an editor program.

☞ You may store all calibration data (identical as in **Gamma-W** for DOS, codeword '**STOC**') in one file having extension ***.ene**, ***.fwh**, ***.eff** or ***.cal**.
Indeed, do just this right now as you will need the files in Section III. Store three separate calibration files as 'Test3.ene', 'Test3.fwh', and 'Test3.eff'

☞ All calibration files (***.ene**, ***.fwh**, ***.eff** and ***.cal** in the default directory for calibration files **\..\Calib**) are **ASCII formatted** and can be edited with any ASCII editor of your choice.

☞ One can make energy calibration using the strongest lines of nuclides and library information. Place the cursor on top of the main peak of a nuclide, for example the 661.6 keV peak of Cs-137, and then enter the **Codeword Terminal** with a “c”. The nuclide name Cs-137 is now keyed in followed by <CR> and the energy of the most intensive transition (first line of this nuclide in the Nuclide Library) is assigned to the current cursor position in the spectrum for energy calibration.
This mode is particularly useful in Alps for Windows.

☞ When the printout parameter PRIN is set to **extended printout** (*see* codeword "PRIN 1" or see "Enable extensive Documentation" in the 🗁 **Input / Output Definitions** tab of the **Option Catalog**), the output file which you can view by pressing the  icon, will contain a very detailed output of efficiency data.
These data are the parameters for the efficiency function, a peak list with the efficiency data calculated from the relevant certificate, the efficiency data calculated from the fitted function, and the difference between these two columns with corresponding uncertainties.

☞ In all calibration tables single columns, single rows or even whole worksheets (Ecal, FWHM, Effc,...) can be marked by clicking with the left mouse button into the worksheet header line.
If you now click with the right mouse button within the selection, a pop-up menu (cut, copy, paste, delete) will appear and you may copy the contents to the clipboard and paste them into another application.

☞ If you wish to copy and paste only a section of the worksheet, use the <Shift-Key> + <Left Mouse Button> simultaneously to mark the corner-cells of the required rectangle in the worksheet.

☞ Several tab pages have been added to the Calibration Functions window to assist with calculations.

🗁 Calculus :

Here one can easily calculate the energy and FWHM for a given channel number, or the efficiency with uncertainty for a given energy in gamma-ray spectra, or the **geometric efficiency for an alpha detector** where the detector diameter, distance and sample diameter must be given (see Section VIII: Miscellaneous).

🗁 Absorption :

This tab page allows the calculation of self-absorption. The user may load experimental datasets of absorption functions (via <Read Data file>), i.e. the attenuation as a function of gamma-ray energy. As attenuation depends on sample density various absorption functions must be given for different densities (typically in the range from 0.42 g/cm^3 to 1.6 g/cm^3). When one defines the density of the actual sample (see Chapter: *Nuclide assignment*) Gamma-W will find the correction values for self absorption through interpolation and correct calculated activities in the *Nuclide assignment* window (see below).

Please contact us for further information on this feature!

🗁 Current Source Activity :

This tab page allows the calculation of the decay corrected activities of your calibration standard sources for any given date and time.
By default the results are written in the **Output.txt** file and can additionally be stored in a ***.txt ASCII file** in the **\..\Calib** directory. This is a very useful feature for fast decay calculation.

🗁 Means :

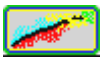
Calculation of the "**Weighted Mean Value**", its "**Internal Consistency**" and "**External Consistency**" and the "**Reduced Chi-Square**" (Fit-Parameter).

In addition to the "Weighted Mean" calculation of up to 20 data sets rows (1) and (2) in the worksheet have a special meaning. These two data pairs will be taken to calculate the "Ratio" (1)/(2), "Product" (1)x(2), "Sum" (1)+(2) and the "Difference" (1)-(2) of the values with uncertainties **(Error Propagation)**.

Data from the two worksheet columns ('**Data**' and '**Error**') can be saved to a file by clicking on the <**Save Data to File**> button. The filename extension will automatically set to ***.txt**.
Data files can be re-read by clicking on the <**Read Data File**> button.

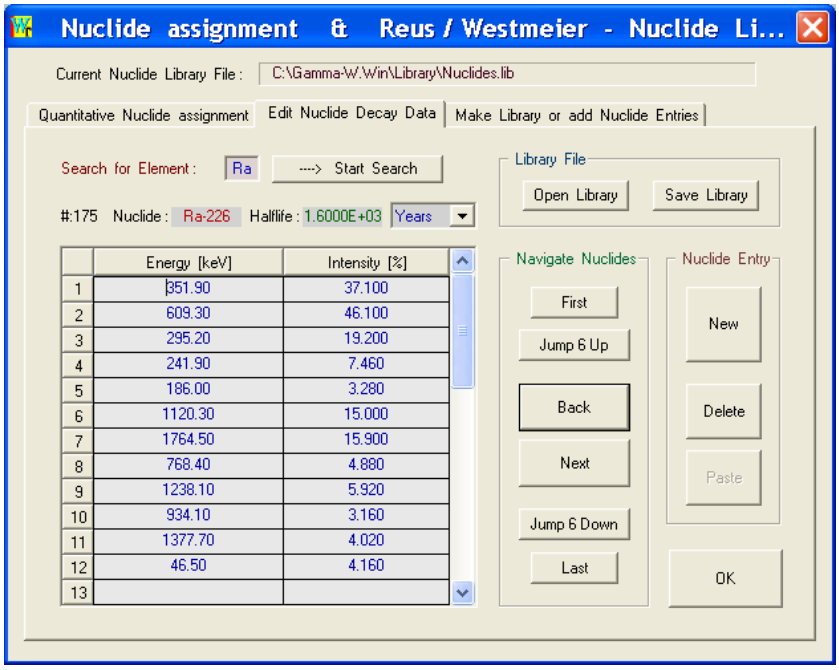
➢ *Perform a nuclide assignment and calculate activities*

Load Test spectrum No. 4 "**HPGe: Soil Sample**" as described above.
Analyze the spectrum from the **Codeword Terminal (type "c"**, then the codewords **CALC + <↵>** and **EXIT + <↵>**).

Select the Nuclide Library for nuclide assignment by clicking on the  icon in the icon bar or by choosing **Nuclide Library** in the **Setup** drop-down menu or by pressing **F6**. Go to the 🗁 **Edit Nuclide Decay Data** tab page.

🗁 Edit Nuclide Decay Data

Now click on the <**Open Library**> button in the **'Library File'** section of the page. When you are asked to "Save the current Library", answer <No>.
Select the library **Nature.lib** from the MS Windows File Management window and click the <**Open**> button.

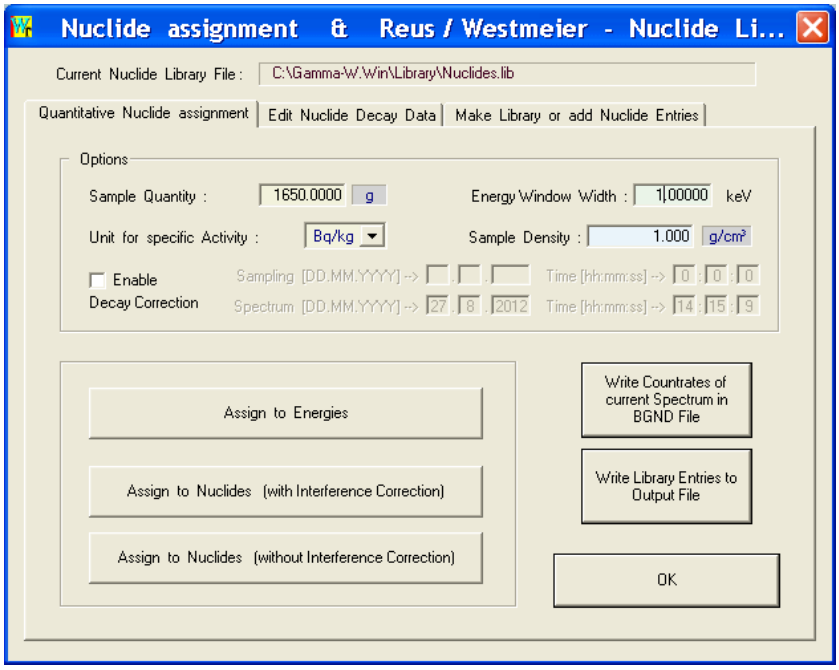


Now click the 🗁 **Quantitative Nuclide assignment** tab.

🗁 Quantitative Nuclide assignment

As an example define the *'Sample Mass'* as 1650.0 g and the *'Window Width'* as 1 keV which means that peaks within ±1 keV around a library energy will be accepted as candidates for this nuclide in the assignment.
[The default value for *'Window Width'* is zero. In this case, **Gamma-W or SODIGAM for Windows** automatically calculate a reasonable search window width which is dependent on the resolution of peaks in the spectrum.]

Press the <**Assign to Nuclides (with Interference Correction)>** bar (which is the same as using the codeword "NUCL 5" in the **Codeword Terminal**). No confirmation window or message will appear.



Press <**OK**> to exit the pages and return to the spectrum display.

The nuclide assignment is done and all results are written in the output file **Output.txt**.

☞ All data stored in a Library for the nuclides can be written to the output file. Click on the <**Write Library Entries to Output File**> button on the 🗁 **Quantitative Nuclide assignment** tab or use the codeword "**NUCL 3**" in the **Codeword Terminal**.
You may also use "NUCL 3" for this purpose in a batch file. When using very large Nuclide Libraries the printout may take some time.

☞ *Note*: All Nuclide Library entries can be automatically written to the output file when a Nuclide Library file is read in. To activate this function, you must set the printout parameter to at least 3, e.g. with the codeword "**PRIN 3**" in the Codeword Terminal.

☞ **<Ctrl>+<backspace>** writes the current list of peaks from former analyses with CALC, REGI, CALF or hand controlled analyses that will be used for the calculation of activities into the output file **Output.txt**. Details on the sub-regions used by the program and the Gaussian parameters from peak fitting are also included.

☞ The Nuclide Library files are packed; they are the only files used by Gamma-W, Sodigam and Alps for Windows which are not ASCII formatted and which cannot be edited with an editor of your choice.

☞ The Nuclide Library format of Gamma-W, Sodigam and Alps holds up to **2000** nuclide entries (DOS version 400 entries) with up to **32** lines for each nuclide (12 in DOS version).

Due to the change in file format, Nuclide Libraries from the DOS version of Gamma-W, Sodigam and Alps can be read by Gamma-W, Sodigam and Alps for Windows, but a Nuclide Library which was edited and saved with a Windows version cannot be used by the DOS version of Gamma-W, Sodigam and Alps.

☞ Each time a Nuclide Library is used by Gamma-W, Sodigam and Alps the current system date is written in its header to make a very simple check for correct system date, e.g. for proper decay calculations no "backwards running clocks" are allowed.
A Nuclide Library containing a more advanced date than the current system clock will not be accepted by Gamma-W, Sodigam and Alps.

☞ If a Nuclide Library has been corrupted by a wrong system date it can be repaired via the start-up argument "repair" (e.g.: "c:\gamma-w.win\gamma-w.exe repair" which writes the actual system date into the library Nuclide.lib).

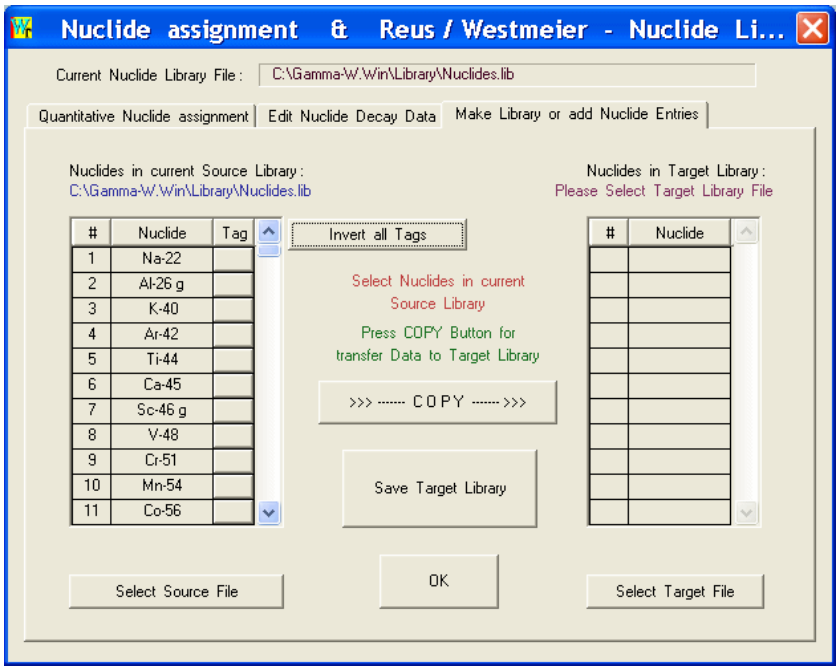
➢ *Short excursion: how to manage nuclides in libraries and how to edit nuclide data*

In the following the handling of libraries and nuclide data in Gamma-W, Sodigam and Alps for Windows is briefly explained.

We will focus on the two tab pages indicated by the indexing labels
🗁 **Make Library or add Nuclide Entries** and 🗁 **Edit Nuclide decay Data**.
On entering the Gamma-W, Sodigam and Alps for Windows library section the 🗁**"Quantitative Nuclide assignment** tab is active with the Nuclides.lib (Gamma-W and Sodigam) or with the Alpha.lib (Alps) loaded.
Click on the 🗁 **Make Library or add Nuclide Entries** to bring this page to the front.

🗁 Make Library or add Nuclide entries

Basically the page consists of two scroll boxes, one for a "**Source Library**" on the left and the other for a "**Target Library**" on the right, plus several buttons to operate these two libraries.



You may select another source library with the <**Select Source File**> button on the left side under the box listing the nuclides. The standard MS Windows file handling window will then open and you can select a source library from any desired unit and path.

The name of the current (source) library file is listed in the top line of the window under the window identification bar.
The names of nuclides in that library are listed in the scroll box on the left and you can browse through the sequentially numbered list by pulling the scroll button, by clicking the up/down arrows in the window or by using the keyboard via <Arrow up> and <Arrow down> or the <Page up> and <Page down> keys.

Creation of new libraries

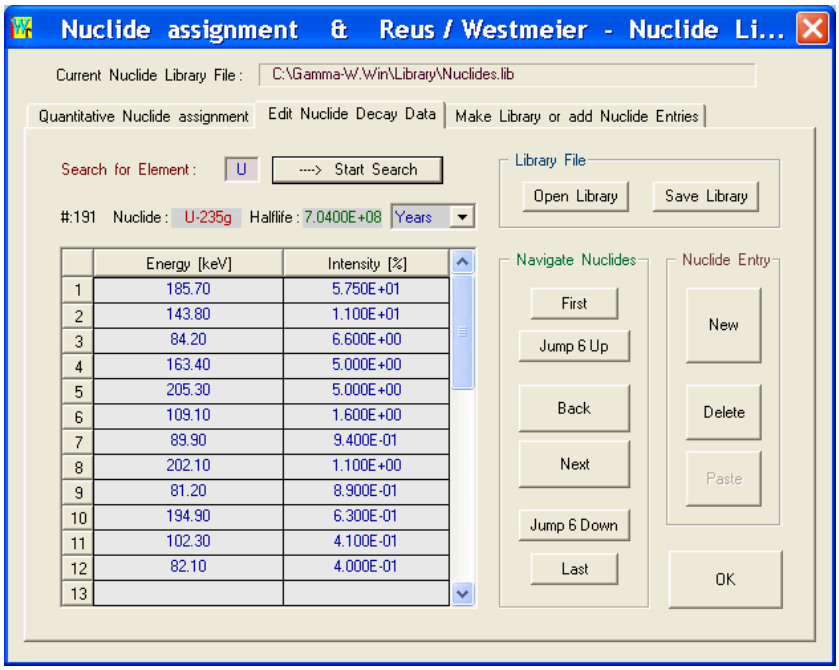
You may create a new user (target) library from data in any other source library. On the right of each nuclide name in the source library is a toggle button called "Tag" which is activated when clicked, i.e. the button is white, and deactivated with the second click. You may activate buttons from all nuclides that you want to transfer into the new user library. Then click the <**COPY**> button and data for all activated nuclides are copied into the target library.
You will see the names of the copied nuclides in the right (target) scroll box. If you want to add nuclides from another source library you may click on the <**Select Source Library**> button, open another library, tag the required nuclides and copy to the target library.

All nuclides that exist in a target library will be automatically tagged in the source library as well.
When the target library is complete it is saved with the <**Save Target Library**> button which will again open the MS Windows file handling window. You may also select any existing library file as the target library with the <**Select Target Library**> button and extend this library from other source libraries.

When you exit the **Nuclide assignment & Reus/Westmeier - Nuclide Library** Window with the <**OK**> button the program will for safety reasons always ask if one wants to save the target library.

Viewing and editing of data

The 🗁 **Edit Nuclide decay Data** tab serves for viewing and editing of data in a library. In this folder one can see the data for one nuclide at a time where the gamma-ray energy (or alpha energy) and intensity data are listed in a scroll box.



On top of the box on the left one will see the index number ("#:..") of this nuclide in the library, the Nuclide name and the halflife.

The name of the currently active library is listed in the top line of the page.
The active library in the 🗁 **Edit Nuclide decay Data** tab is the same as the source library in the 🗁 **Make Library or add Nuclide Entries** page.

Below the name are buttons for saving the current library file or opening a new library for editing.

The buttons in the "**Navigate Nuclides**" section are used to:

- select the first or last nuclide in the library (<**First**> and <**Last**> button)
- select the following (<**Next**>) or preceding (<**Back**>) nuclide or
- jump through the library in bigger steps (<**Jump Up**> or <**Jump Down**>).

For the Jump function the library is divided into 30 steps of equal length, thus in a library containing 121 nuclides one will jump in steps of 4 nuclides.

The buttons in the "**Nuclide Entry**" section serve for the re-ordering of nuclides or for deleting complete data sets.

- To edit data of a nuclide you just click into the respective data field and erase or modify the data as desired. There is no check as to whether the new data are meaningful or not. The unit for the halflife is selected from the drop-down box.

- To delete a line from the list just delete the energy value, i.e. blank the energy field; the line will be deleted when the next nuclide is selected or when the library is saved.

- To delete a nuclide from the library use the <**Delete**> button. The data set is then taken out of the library and stored in an internal one-nuclide buffer for retrieval. When you delete a second nuclide the data from the first deleted nuclide are overwritten in this buffer and completely lost.

- To move a nuclide entry to another place within the library you must first delete this nuclide. You may note that the <**Paste**> button is activated when a nuclide was deleted. Then select the nuclide after which you want to place the nuclide and click the <**Paste**> button. The retrievable nuclide is now inserted behind the selected nuclide.

- To create a new nuclide entry in the library select that nuclide after which the new entry shall be inserted and press the <**Insert**> button. The program will create empty space for one nuclide which can be filled with data as described above under "To edit data".

- To save the library use the <**Save Library**> button and define the file name and destination for the file in the MS Windows file managing window.

Another useful feature for scanning larger libraries is "**Search for Element**".
One enters the symbol for an element in the box over the nuclide name (e.g. am, not case sensitive) and search for the next following nuclide of this element in the library with the <**Start Search**> button.
When the end of the library is reached during the search, the program will wrap around and continue searching from the beginning of the library.

➢ *How to view, edit and print out the Results-Output-File (Output.txt)*

One may open the output file with the built-in text editor by clicking the  icon and have a look at the results.

☞ Using MS Windows "**Copy and Paste**" functions, one can transfer results or fractions of the printout to any other application e.g. MS Word, MS Excel, Microcal Origin etc..

☞ For **quality assurance** one can save the whole output file or just a selection of your interest to another file.
All relevant information needed for reviewing the results like date and time, spectrum names and comments, ROIs, batch-, calibration files and Nuclide Libraries used, are stored in the Output.txt file.

☞ While having the output file opened with the program´s built-in text editor one can print results by selecting **Print Output File** from the **Miscellaneous** pull-down menu. One can also print from the Main Screen and from the Spectrum Window by pressing **<Crtl>+<P>**.

☞ **Long file names** are supported for many file types in Gamma-W, Sodigam and Alps for Windows, such as spectra, Nuclide Libraries, calibration files, batch files etc…
To maintain compatibility with the Gamma-W, Sodigam and Alps DOS version and many older MS DOS or MS Windows software, we strongly recommend that one should use the short "8+3" characters file naming convention **without any special characters**; in particular **do NOT use BLANK characters** (space) in file names.

☞ The customized printout of the output file is described in the next Section III under ➢**Custom-made Printing of Batch Procedures results** (see page 69).

➢ *Printout parameters*

The codeword **PRIN** enables one to set up the printout length of the result files. It is recommended to try out which PRIN parameter setting is best for your purpose. Almost every action that one takes in Gamma-W/Sodigam/Alps (e.g. read a spectrum, calibrate, execute a batch-file etc.) produces a more or less extensive amount of data (and maybe helpful error messages). The PRIN-parameters determine to which degree these details are listed in the output file. Some important results may not appear in the output file if the print parameter “ipr” is small like 0 or 1. On the other hand the output file will become excessively large and confusing if you choose a high “ipr” value like 5 or 6.

PRIN ipr, tab Set the printout control parameters:

ipr determines the amount of printout produced in each spectrum analysis

tab selects a table format for the peak analysis results

ipr = 0 Minimum printout of controls, dialogue and final results.

ipr = 1 Extended printout of fitted results with uncertainties.

ipr = 2 Information about the region search algorithm, from the subroutines which make a sub-division of the spectrum into regions for analysis. This information includes region search limits and advance criteria.

ipr = 3 Information from the subroutines which find peakpositions, make the subdivision of sub-regions into finally analyzed fractions, make the multifold analysis of the region, and which control the peak insert and throw-out logic.

ipr = 4 Listing of counts in the sub-region after the background subtraction. These counts constitute the final spectrum to be submitted to the fitting section.

ipr = 5 Parameters and corrections during the iterative fitting process.

ipr = 6 Listing of the spectrum after the codeword READ. The whole spectrum will be listed after reading, provided that "PRIN 6" was given before the codeword READ. After confirming this command a DOS-Window will open. DO NOT close this window as this will

completely shut down Gamma-W (Sodigam/Alps)! Minimize the window. It will disappear when Gamma-W is closed.

☞ Each printout level (1 to 6) includes the printout of all lower levels; thus the codeword "PRIN 5" requests all possible printouts except the spectrum listing. *Usually all printout levels in excess of 1 are used for diagnostic purposes only.*

tab = 1 Standard peak table containing the columns :
#, Position, Energy, E-Error, Area, A-Error, FWHM, FIT, Quality information

tab = 2 Alternate peak table containing the columns:
#, Position, Gross Area, Net Area, A-Error, Energy, Efficiency, Gammas/s

tab = 3 The same as tab = 1 but with the **Position**, **Energy**, **E-Error** and **Area-Error** given with more decimal points.

tab = 4 The peak table includes "**Bgnd Area**" (calculated number of count from an analysis of an external background spectrum using the codeword BGND) along with the "**Net Area**" calculated after background subtraction.

See **Appendix II** for **examples** how the file output.txt looks like, depending on the PRIN parameters.

When the Gamma-W, Sodigam and Alps for Windows code is started, the control parameters are preset to ipr = 0, tab = 1, unless default values are otherwise specified, e.g. in the **Start_up.ini** file.

➢ *Saving spectrum graphics (WMF file or printout)*

The currently displayed spectrum graphics (with fit-functions if applicable) can be saved to a graphics file which is formatted as ***.WMF** (Windows Meta File).

This is done by clicking on the  icon in the Spectrum Window icon bar.

The name of this WMF file is identical to the name of the currently loaded spectrum (up to 20 characters; special characters are replaced by "_"). The WMF file is stored in the same directory where the spectrum file is located and its filename extension is automatically set to **.WMF**.

Note: If a the second picture is saved from the same spectrum, i.e. with an already existing file name, the old WMF file will be overwritten without a warning.

Clicking the  icon sends the spectrum directly to the printer as black and white printout. At the top of the spectrum is a title line with the full path & spectrum name and with the livetime (LT) and realtime (RT) printed.

♦ External Background Correction

Gamma-W does not carry out direct channel for channel subtraction of an external background spectrum from a given spectrum (pro rata subtraction), since this tends to alter the peak shapes (Gamma-W, Sodigam and Alps are extremely sensitive peak-fitting programs) and it destroys the statistical significance of resulting countrates.

Gamma-W rather generates a **background reference file** by analyzing the background spectrum and creating an ASCII file of **peak countrates** with their associated uncertainties. The reference file may contain up to 500 background peaks. This file is then used to correct the corresponding countrates in the sample spectrum and to calculate proper uncertainties for the corrected countrates.

To carry out a background correction for your sample spectra, you must **first load and analyze your external background spectrum**, i.e. you have to create an ASCII data file in which the countrates of all peaks occurring in the external background spectrum are stored.

Load the internal **Test spectrum No. 2**. from the Main Window using the menu **File, Read Demo Spectrum, "HPGe: External Background"**.

Then go to the 🗁 **Parameter for Spectra Analysis** page in the **Options Catalog** in the **Setup** menu or click on the  icon.

Click on the <**Write countrates of current spectrum in BGND file**> button and enter the desired file name of the new background file.

The spectrum is then automatically analyzed (via codeword "**CALC**") and the count rates and uncertainties for all peaks in the spectrum are written into the specified file.

The **background reference files** are stored in the subdirectory **\..\BGND**.

One will also find the same <**Write countrates of current spectrum in BGND file**> button on the 🗁 **Quantitative Nuclide assignment** page of the **Nuclide Assignment & Reus/Westmeier - Nuclide Library** folder.

In the **Options Catalog**s 🗁 **Parameter for Spectra Analysis** tab one can now select the **.bgd** file (**.bdf** in french language setting) as the file to be used for external background corrections by choosing the data file from the dialog box.

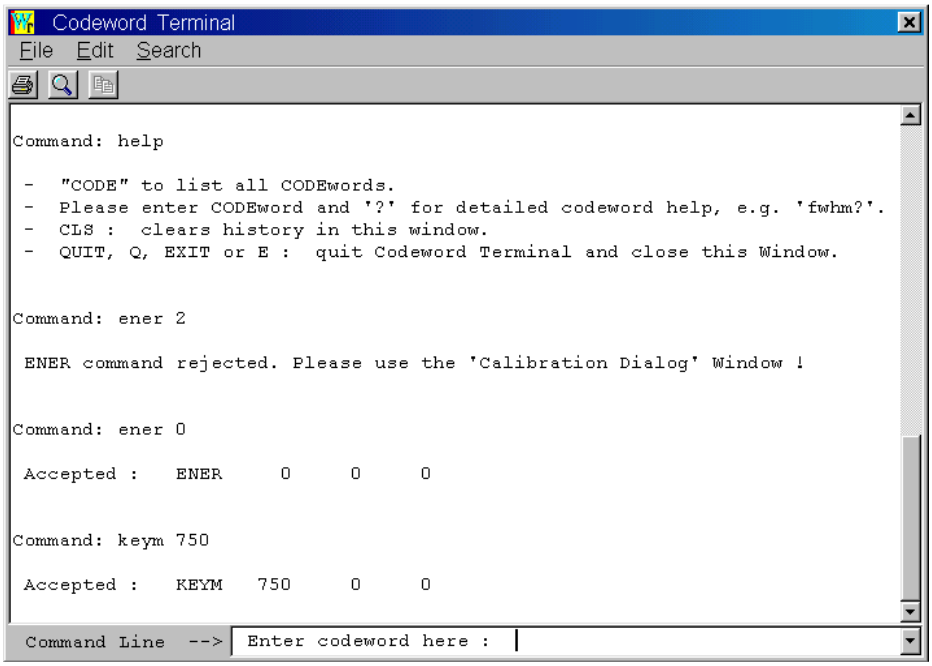
Select the relevant .bgd file **before** analyzing a sample spectrum.

All these steps can be included in a **batch file** using the codewords READ, **BGPI** and CALC.

♦ How to enter and use the Codeword Terminal

The built-in **Codeword Terminal** offers a fast and easy way to enter codewords and their parameters without using the Windows Grafic-User-Interface.

You may access the Codeword Terminal window from
either the Main Window under the Menu **File** or
from the Spectrum Window under the Menu **Program** or
by simply pressing **"c"**.



The Codeword Terminal in Gamma-W, Sodigam and Alps for Windows works very similar to the "command line interface" known from the DOS versions of Gamma-W, Sodigam and Alps.

After typing in the codeword together with its parameters and pressing the <↵> key the **Codeword Terminal Interpreter** reads the **Command Line** and checks for a valid codeword and correct syntax.

A message is displayed in the Codeword Terminal window whether the codeword with its parameters has been accepted or not.

☞ If a codeword **requires additional data input** (e.g. "ENER 2", DETL, "SPIK 1", DECA) exceeding a single line, it cannot be used from the codeword terminal but the **codeword must be used in a batch file**.

☞ On-line **Codeword help** for Gamma-W, Sodigam and Alps is also available. If you enter a "**?**" on the command line, you will receive information about how to use the **Codeword help.**
Entering the word "CODE**"** will provide a long list of codewords available in Gamma-W, Sodigam and Alps.

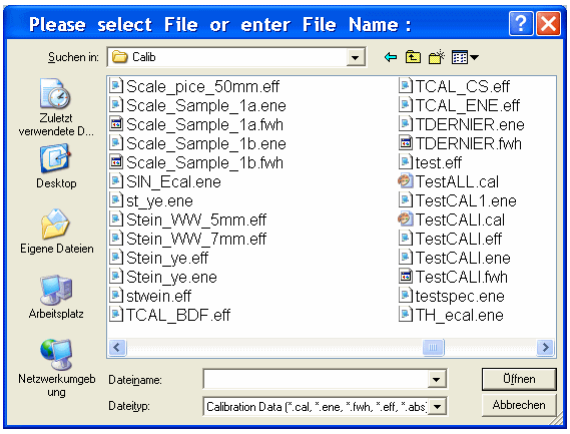
Codewords which are not active in the Windows versions of Gamma-W, Sodigam or Alps are marked with an **" * "**.

☞ If one types a codeword with a question mark, e.g. *"NUCL ?",* one will get a short on-screen description of the codeword and its **parameters**.

☞ The Command Line has a **history function** which can be accessed by clicking the "down arrow" at the end of the Command Line. The history holds all codewords and parameter values which have been entered since the Codeword Terminal window was last opened.

When closing the Codeword Terminal window the history is cleared.

☞ Using the codeword FILE, batch files can also be accessed from the Codeword Terminal. A MS Windows File Management window is opened, where the batch file can be selected. The file may be located on any available storage device (Harddisk, DVD/CD drive, Memory Stick or even Network).



Before running a batch file it can be viewed or even edited while the File Management window is still opened. To do so, select the file by clicking on its name with the right mouse button.
A MS Windows pop-up menu is opened. Now you may click "Open" to open the selected file with that editor which has been associated with the filename extension.

For a detailed description of all CODEWORDs see :

- Online help in the **Codeword Terminal**, e.g. type "calc ?" in the command line or
- printed DOS manuals Gamma-W, Sodigam and Alps or
- **electronic versions of the DOS manuals** (.pdf files or MS Word files), which you will find on your Gamma-W, Sodigam and Alps for Windows distribution in the directory **\..\Documentation** :

- Gamma-W_Codeword_Reference_English.pdf
  (or Gamma-W_Codewort_Referenz_Deutsch.pdf)

- Sodigam_Codeword_Reference_English.pdf
  (or Sodigam _Codewort_Referenz_Deutsch.pdf)

- Alps_Codeword_Reference_English.pdf
  (or Alps_Codewort_Referenz_Deutsch.pdf)

♦ Notes on CODEWORDs

➢ *ADDI*

The codeword **ADDI** is used to add the contents of two or more adjacent channels (determined by the first codeword parameter). You can use this codeword to compress a spectrum from 8k to 4k or from 4k to 2k, respectively, and then save the new compressed spectrum. This feature is helpful for the enhancement of the statistical significance of small peaks, for the calculation of detection limits, and for saving spectrum space and calculation times.
The polynomial parameter values for the energy calibration (if present) and for the FWHM calibration are recalculated automatically.

➢ *REGI*

The codeword **REGI** gives the user the possibility to define a region in units of channels or energy and to define the positions of known peaks. The region length must not exceed 200 channels in Gamma-W, or 300 channels in Sodigam or 400 channels in Alps. When the region limits are defined in terms of energy, the program calculates the corresponding channel numbers and checks that the length conditions given above are fulfilled.

➢ *ROIS*

The codeword **ROIS** is used to calculate the sum of all counts in a defined channel range. Furthermore, this sum is used to calculate the dose equivalent rate deposited in the detector by the gamma radiation. The calculation is based on physical data of the nuclide assigned to the integrated photopeak and the measuring time as well as the volume and mass of the detector crystal.
The detector mass can be directly entered via a codeword parameter. For NaI detectors with standard sizes of 2”x2” and 3”x3” the masses are stored in the program and they can be retrieved by special codeword parameters (see codeword help or manual).

Section III

In many standard applications the same detector and geometry are used to measure many samples with similar matrices. This analytical procedure will then routinely call for the same energy and efficiency calibration, the library, and even the background correction file.

Gamma-W, Sodigam and Alps for Windows provides a new platform for easy repetitive analyses through its **Batch Procedure Dialog (BPD)** Window.

♦ The Batch Procedure Dialog (BPD)

A ***'Batch Procedure'*** is defined and stored containing file names with calibration information (energy, efficiency, library, external background etc.) for a given setup and other definitions that are relevant for spectrum analysis.

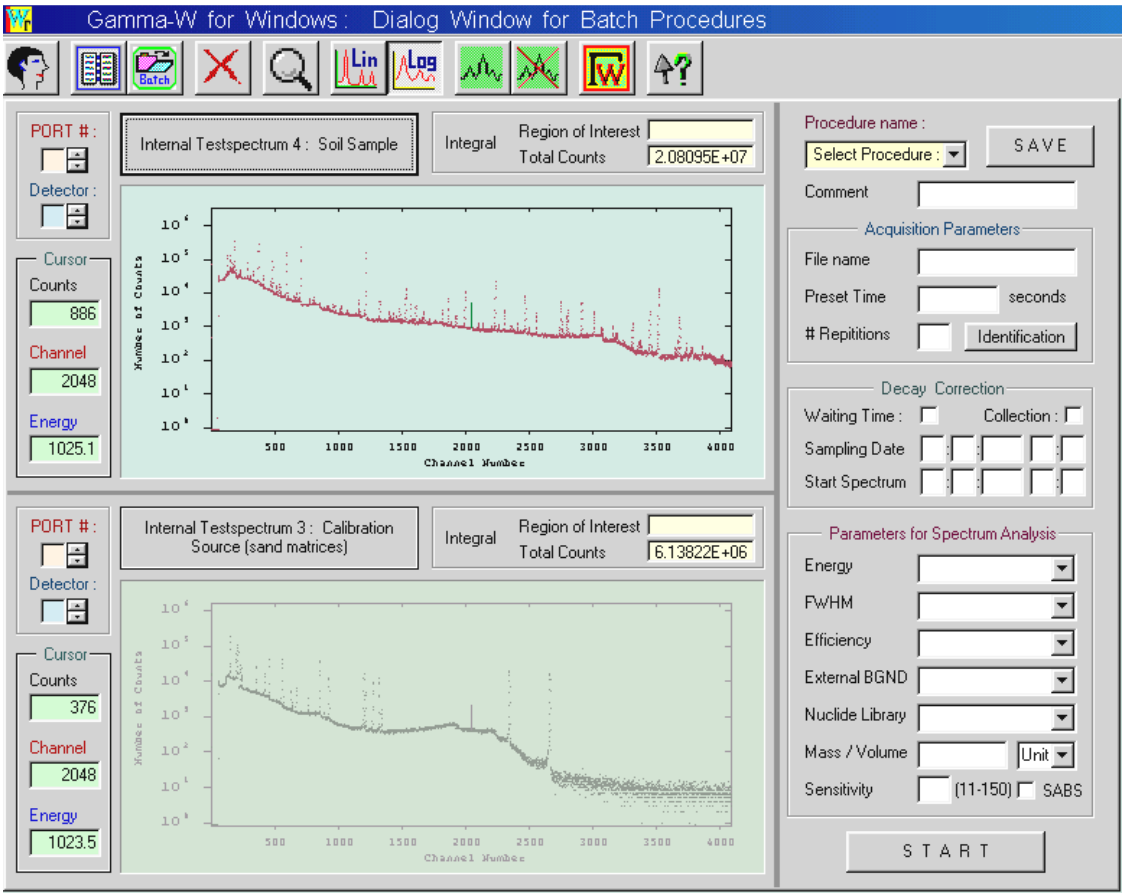
➢ *To enter the Batch Procedure Dialog :*

Start **Gamma-W, Sodigam or Alps for Windows**, and in the Main Window of the program choose the **File** pull-down menu and then **Batch Procedure Dialog** or press the  icon in the icon bar or simply press <**P**>.

The following screen will appear with typical Windows features such as drop-down boxes, fields and buttons for secondary windows, etc. which have been described in the introduction to this manual.

You should find it very straightforward to become familiar with and to use BPD.

☞ When the BPD is called from the Spectrum Window with a spectrum in the display, then this spectrum will be copied into the upper spectrum frame of the BPD.



♦ Operations in the Batch Procedure Dialog

As a quick exercise to illustrate some of the functions available under the BPD you may now

- define a ROI
- create a procedure
- use this procedure to analyze **Testspectrum No. 4**
- export the data to other Applications

If you have a Demo version of **Gamma-W for Windows, Testspectra No. 4 and 3** will be automatically loaded into the two spectrum windows.

If you are running a licensed version, then the two spectrum boxes will be empty and you may read in an ASCII formatted spectrum by clicking on the large <**Channel 1: empty spectrum**> button. (For other formats, see below.)

The Standard Toolbar contains features that you are already familiar with from the **Gamma-W, Sodigam and Alps for Windows** Main Window and Spectrum Window.

☞ Bubble Help is also available for these buttons. There is a lot of built-in feedback and helping pop-up boxes to assist the user in setting up meaningful procedures.

☞ The two spectral windows can be independently manipulated and controlled. One may select either spectrum by clicking with the left mouse button in the spectrum area. The active screen is highlighted in blue and the other one in grey.

☞ You may activate the **Codeword Terminal** for entering codewords with the **F1** key.
This provides the full power of Gamma-W, Sodigam and Alps for Windows, including the capability of **reading all spectrum formats** into the Batch Procedure Dialog Window.

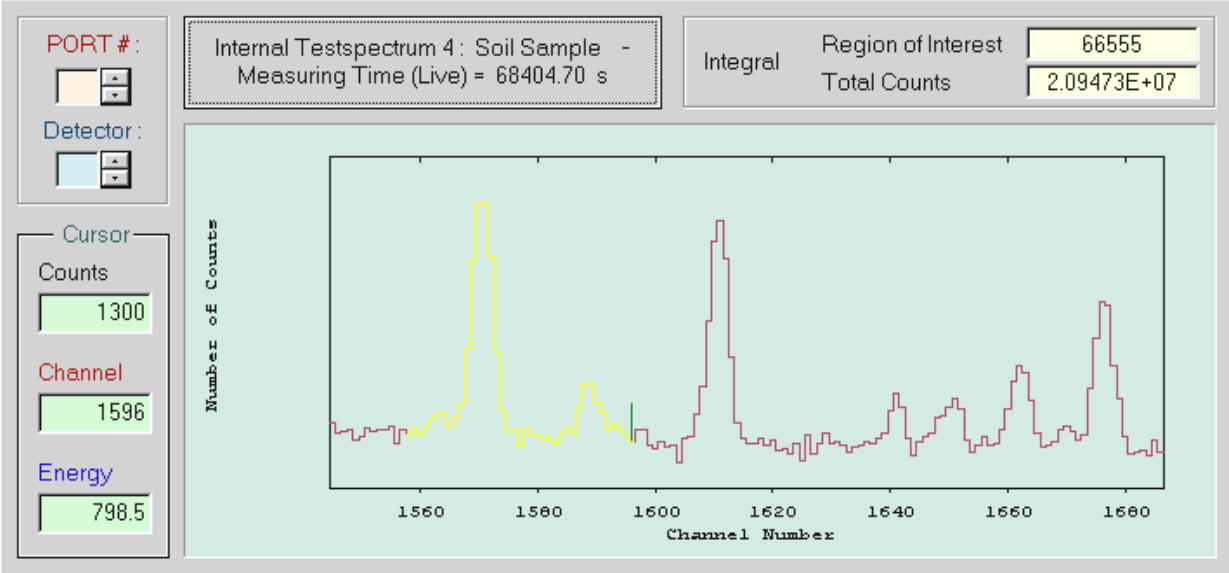
➢ *Define and highlight a Region of Interest*

Use the mouse to move the cursor to a position of interest in the **Testspectrum No. 4**. *(Point with the arrow and click with the left mouse button in the required region of the spectrum, and the cursor will jump there).*

Now click on the magnifying glass  icon and the spectrum will be expanded around the cursor. A second click will toggle the display to full spectrum.

Note that the cursor channel number, the corresponding energy and counts in the channel are shown in the data fields to the left of the spectrum.

☞ In the expanded mode the display can be further manipulated with the mouse. Holding down the **right mouse button** and pushing the mouse **up and down expands and contracts** the spectrum display, while moving **left and right scrolls** through the spectrum.



Point with the mouse cursor to the starting channel of a required ROI, hold down the left mouse button and drag the mouse to the end channel of the required ROI. This section of the spectrum will now be highlighted in yellow.
You will notice that you can adjust the extent of the region like in the Spectrum Window with your movements of the mouse. That is, when the mouse cursor is in the left section of the ROI, you may enlarge or decrease the ROI on this side by dragging the cursor left or right respectively. The same applies to the right section of the ROI when the mouse cursor sits in this section of the ROI.

The **total number of counts in the ROI** is given at the top right of the spectrum window.

You may mark the ROI by clicking on the  icon. It will then be highlighted in green.
You may delete a ROI with the  icon or highlight additional regions of interest.

The  icon takes you **directly to the Spectrum Window** of Gamma-W, Sodigam and Alps for Windows.
You will note that a **green ROI is transferred** when you switch windows.

The  icon returns the user from the Spectrum Window to the BPD Window.

☞ To **close** the BPD Window and return to the Main Window, you must click on the **X** in the uppermost right corner of the window (i.e. "Close" Icon) or close by pressing the **<Esc>** key twice or the <Alt>+<F4> keys simultaneously.

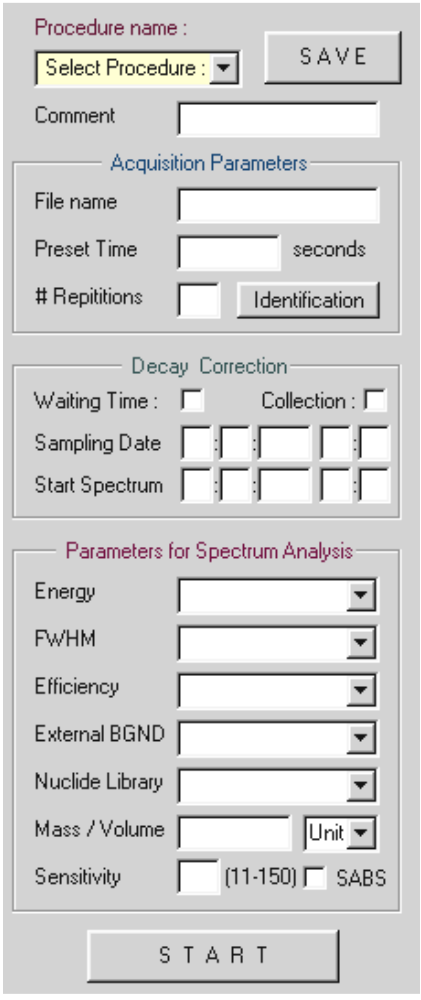
The  icon takes the user to another feature called the **'User Management'** facility which is described in **Section IV**.

The **Procedure Management section** of the BPD Window appears to the right of the spectra display area. This part is used for fast automatic "standard" analyses of spectra with predefined batch files. The top drop-down list contains a list of all **procedures** that are stored in the default directory, i.e. :

\..\ Gamma-W.Win \ Process \ *.prc

At present the drop-down list boxes contain example files.

When a procedure has been selected, the names of the associated energy-, resolution-, efficiency-files etc. for the procedure will automatically appear in the respective boxes.



➢ *How to create a Batch Procedure*

One may set up a new procedure using the calibration files you saved while analyzing **Test-spectrum No. 3** in **Section II**.

In the `**Parameters for Spectrum Analysis**´ section, click on the *'Energy'* drop-down list (▾ arrow) and select **Test3.ene**. Click on the *'FWHM'* drop-down list (▾ arrow) and select **Test3.fwh**. Click on the *'Efficiency'* list (▾ arrow) and select **Test3.eff**.
Select **Nuclides.lib** from the `*Nuclide Library*´ list. Put the cursor in the `*Mass/Volume*´ text box and type **1650** and select the `*unit*´ **g**.

Put the cursor in the *'Sensitivity'* text box and type **35** *(The default value is 25).*

One may now enter a description of your procedure in the field labelled **Comment**.

Now press the <**SAVE**> button at the top of the page. Type the name of the procedure, for example, ***'ProcTest'*** in the appropriate area of the File Management Window.

The names of the procedures in the **'Procedure name:'** drop-down list will be automatically updated and you can now select your just created Batch Procedure.

The procedure file is saved as ASCII text file which you can view and edit at any time. You will find these files in the sub-directory:

C:\Gamma-W.Win\Process
(or C:\Sodigam.Win\Process or C:\Alps.Win\Process)

See next chapter (page 67) on ***how to use batch procedures*** for spectrum analysis.

There are two other features that we will not use in this example but which you may find useful: *Sample Identification* and *Decay Correction*.

Sample Identification

Using a Sample Identification file one can enter details e.g. about the sample preparation, the detector or special acquisition conditions. For quality assurance (QA) this information will be copied together with the Batch Procedure´s peak fit results into the output files (Output.txt and Batch Procedure output file, see below).

You may edit these **ASCII formatted** files by pressing the <**Identification**> button in the field for **Acquisition Parameters**.

When using the Standard Version of Gamma-W, Sodigam and Alps for Windows, i.e. when **no MCA hardware** is present, the name of Sample Identification file stored in the main directory **C:\Gamma-W.Win** (or C:\Sodigam.Win or C:\Alps.Win) is

SampleID.txt

When using the Extended Version of Gamma-W, Sodigam and Alps for Windows the Sample Identification files for each hardware controlled MCA port are called

Port_*n*ID.txt

where *n* = 1,..,4 is the number of the currently selected port.

☞ There are three additional ways to create a sample description file:

1) in the Options catalogue on the 🗁**Parameter for Spectra Analysis** tab page using the <**Sample ID**> button,

2) under **target MCA Control Panel** on the 🗁 **Select Port and Setup Spectrum** tab page and

3) by using any ASCII editor of your preference.

Decay Correction

There are two modes of decay correction provided in the BPD Window under the section **Decay Correction.**

The first mode "**Waiting Time"** (with the "**Collection" check box empty**) makes the same calculation as the codeword **DECA** in Gamma-W, Sodigam and Alps, i.e. the calculated **activities are corrected for decay between sampling and counting**.
As an alternative you can use the codeword DECA within a batch file.
An example is given in the batch file C:\Gamma-W.Win\Process\Dec_Corr.fil

When the check box **"Collection"** is selected and marked with a ✓ (with the "**Waiting Time" check box empty**), you may enter the start and end dates of sample collection.
Gamma-W, Sodigam and Alps for Windows will then calculate a decay correction for this period of time. This feature is useful for the analysis of samples that were accumulated for a long period of time, e.g. filters or moss.

Note: The correction for **decay during counting is always calculated** in Gamma-W and Sodigam; it can be activated in Alps.

Note: **using both decay correction modes** in the BPD at the same time will be supported in the future. For the time being one can make the "Collection" correction in the Batch Procedure Dialog and use a batch file with the codeword DECA for the "Waiting Time" correction.

➢ *Analyze a spectrum with a Batch Procedure*

Please load the **Testspectrum No. 4 "HPGe : Soil Sample"** from the Main Window.

Open the BPD Window and click in the top spectrum window where the **Testspectrum No. 4** is shown.

Now select the just created procedure ***'ProcTest'*** to analyze Testspectrum No. 4.

Check the settings of the procedure and click on the <**START**> button.

Then **Gamma-W and Sodigam for Windows will analyze the entire spectrum** (like doing by codeword 'CALC 0 0 0').
Alps for Windows will switch to the Spectrum Window for manual spectrum analyses because for detection and unfolding of α-peaks user's attention is needed (manually or by batch-file defined ROIs and start-up values for the peak positions).

☞ In both cases the peakfit results are written into a special internal result file, the Batch Procedure Output File, which can be copied into the Output.txt file by pressing <Strg> and <Backspace> simultaneously.

After the spectrum analysis is finished the results will be automatically assigned to nuclides from the selected Nuclide Library.

☞ This corresponds to using the codewords '**NUCL 0**' (**Energy-oriented overview mode**) and '**NUCL 5**' (**Nuclide-oriented mode**) or clicking the "Nuclide Assignments Button" in the 🗁 **Quantitative Nuclide assignment** tab of the "Assign Nuclides & Manage Nuclide Library" Window.

All results of the procedure are printed to the **Output.txt** file which is opened and shown automatically in the "Output File Browser" every time after a Batch Procedure is finished.

Of course you may view the results at any time by pressing the  icon.

☞ The printout parameter for all Batch Procedure outputs written into the Output.txt file is automatically set to "extensive printout" (codeword 'PRIN 1').

☞ For **quality assurance** the Output.txt file contains, complementary to the procedure results, the **complete procedure setup** used for spectrum analysis and for running the procedure.

☞ In addition to the Output.txt file the complete Batch Procedure section starting from

```
**************************************************************************

**       B A T C H  -  P R O C E D U R E    S T A R T E D        **

**************************************************************************
```

until

```
**************************************************************************

**       B A T C H  -  P R O C E D U R E    C O M P L E T E      **

**************************************************************************
```

is written into a separate "**Batch Procedure Output File**".

The name of this file is the same as the name of the analyzed spectrum and its filename extension is set to *.txt.

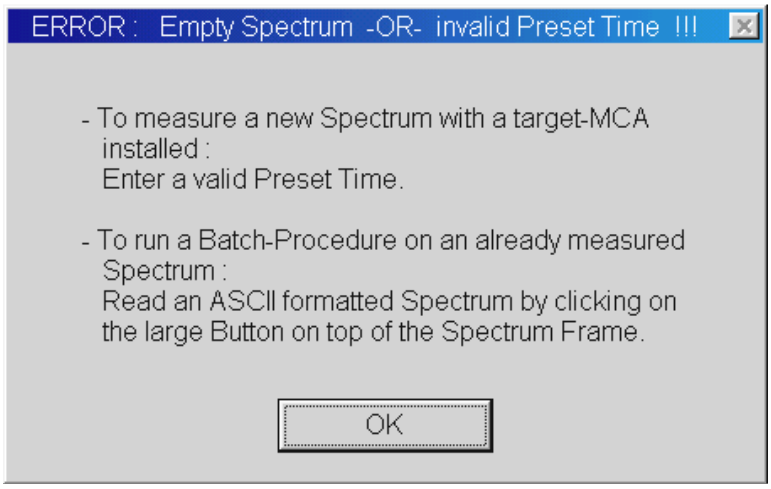
The "**Batch Procedure Output File**" file is stored in the **current spectrum directory**. If it already exists, it will not be overwritten but the name of the new file is extended with an increment running from "_001" up to "_999".

☞ **For all parameters** (energy-, fwhm-, efficiency-, absorption-calibration, decay correction, correction data for external background, sample mass and density, if absorption correction is requested,

Nuclide Library, energy window width for nuclide assignment, unit for activity, sensitivity, background type, tailing) **which are not explicitly specified in the Batch Procedure the currently defined values are adopted**.

☞ Remember that you may activate the **Codeword Terminal** with the **F1** key for entering codewords and to complete the parameter setup before starting a Batch Procedure.

☞ The message below illustrates another application of the BPD, namely, if you have **target** hardware installed, you may start the ADC with a preset **Live Time** from this Window *(see Section V).*



➢ *Custom-made printing of Batch Procedures results*

One may wish to print results in a specific format, for example for publishing or for filing. This feature is provided by Gamma-W, Sodigam and Alps for Windows, too.

When doing an analysis through a Procedure job, results are written to both the **Output.txt** and a file called **Outp_Exp.txt**.

If one wants to extract custom-made information from the **Outp_Exp.txt** file, one may write one's own printout generation program.

When this program has the dedicated name **Outp_Exp.exe** and it is found in Gamma-W´s, Sodigam´s or Alps´s main directory, Gamma-W, Sodigam and Alps for Windows will **automatically start and execute** this program, **seamlessly creating the desired printout** from the **Outp_Exp.txt** file.

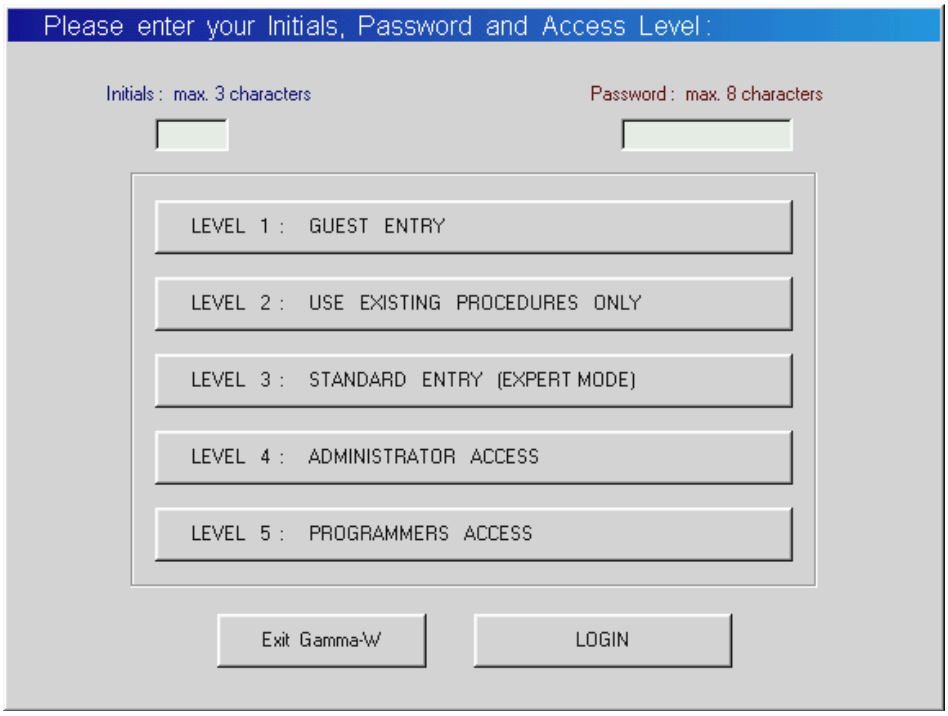
☞ After a Batch Procedure is finished, Gamma-W, Sodigam and Alps for Windows will automatically copy the contents of the Output.txt File to the Outp_Exp.txt file, will run Outp_Exp.exe and will open the Output-File-Browser/Editor.

Section IV

Gamma-W, Sodigam and Alps for Windows can also be pre-programmed by an Administrator to check access via a **User Management System (UMS)**.

Access to the capabilities of the software package will be regulated by a hierarchical system based on the user´s qualifications as defined by the Administrator.

When the UMS is in place, and Gamma-W, Sodigam and Alps for Windows is started, the user is asked to enter his **three characters identifier** in the **Initials** box, enter the **password** and **select the level** to which he has been assigned.



When these data are correctly entered, the program starts directly in the Batch Procedure Dialog (BPD) window.

If the log-in data do not match any valid entry in the **UserDat.bin** file (see below) access to Gamma-W, Sodigam and Alps for Windows is denied :

♦ The User Management System

There are five levels of users. A user has access to the full capabilities of Gamma-W, Sodigam and Alps for Windows only if he is assigned to Level 3 or higher.
Quantitative spectrum analysis is possible on all levels, but data interference is progressively restricted.

Level 1: *Guest Entry* (*view only mode)*

This is seen primarily as a **training mode**. The user is directly routed to the BPD and has no access to the interactive facilities of Gamma-W, Sodigam and Alps for Windows.
No calibrations can be performed and no data can be changed or transferred to the network. He may however recover spectrum analysis results from the Output.txt file.

Level 2: *Standard mode (use existing Procedures only)*

The user has **access to the Batch Procedure Dialog** and may use any of the stored procedures (containing energy, efficiency, library, etc. information) in the network.
He may transfer his results to the network, but he is not allowed to edit or change any procedures.

Level 3: *Expert mode (access to **Gamma-W, Sodigam and Alps for Windows**)*

The user may modify a given procedure to suit his immediate purposes and he may transfer results to the network. He can **store modified procedures**.
The user has full access to the program´s **calibration functions and Nuclide Library set-up**. He may carry out energy, resolution, efficiency, background calibrations and he may store this information in a new or modified procedure.

Only at this level 3 and higher does a user have access to the full capabilities of Gamma-W, Sodigam and Alps for Windows.
*For example, one may access the Codeword Terminal with the **F1** key.*

Level 4: Administrator Access

The user has all the privileges of the previous level and in addition he is allowed to alter all **settings for the TMCA hardware** operation management, like spectrum length, high voltage setting, gain, fine gain, ADC mode, BLR mode etc.

Level 5: *Programmer Access*

This user has the responsibilities of managing the hierarchy of users. He may enter new users and define their user levels and passwords.

♦ Setting up a User Management System

The files that a Programmer will need in order to set up a UMS are found in the root directory of the Program **C:\Gamma-W.Win**
(or **C:\Sodigam.Win** or **C:\Alps.Win**):

UserDat.txt
UserMan.exe (and **UserDat.bin** after running **UserMan.exe**)

The **UserDat.txt** file is an ASCII file that contains the instructions that you need to create and assign the levels of accessibility to your various users. This information is saved directly to this file (some comments and examples of the formats used to set up the information in this file are given in the distributed **UserDat.txt** file itself).
Run the program **UserMan.exe** and it will automatically use the **UserDat.txt** file to create an encoded **UserDat.bin** file, which actually is the UMS database for your system.

Administrative user control is **disabled** when the file **UserDat.bin** is renamed (e.g.: UserDat.bin.disabled) or deleted from your computer.

For safety reasons the Administrator should remove the **UserDat.txt** and **UserMan.exe** files from the computer after putting the UMS into effect.

It is recommended to discuss the UMS feature with the Dr. Westmeier GmbH before implementation.

Section V

Direct control of ***four*** independent hardware ports is supported under Gamma-W, Sodigam and Alps for Windows for **target** TMCA, TISA and ISA plug-in cards (16 bit) and for dMCA, dMCA-pro and scintiSPEC MCAs (32bit).

♦ Hardware Operation

The ***Extended Versions*** of Gamma-W, Sodigam and Alps for Windows provide support for the 16 bit ISA computer slot plug-in MCAs,

i.e ISA, TISA and TMCA plugin cards

and the 32 bit PCI and USB computer slot MCAs,

i.e. scintiSPEC, dMCA and dMCA-pro

If your system is running 16 bit **target** hardware, then a copy of the start-up file **TMCAINIT.txt** must exist in **C:\Gamma-W.Win** (or C:\Sodigam.Win or C:\Alps.win). This file defines the system, i.e. the number of active ports and the types of TARGET plug-in cards attached.

☞ The **TMCAINIT.txt** start-up file MUST be absent from the **C:\Gamma-W.Win** (or C:\Sodigam.Win or C:\Alps.win) for the 32 bit version or else the system will not run.

The parameter **r** in the **TMCAINIT.txt** gives the number of ports installed and it must define a number between 1 and 4.

r = 1 means that there is only one port installed

r = 3 means that three ports are installed

The parameter **p** in the **TMCAINIT.txt** defines which hardware is attached to which port.

A ≡ TMCA, T ≡ TISA, I ≡ ISA

p = 2, I means that an ISA card is installed on port No. 2.

The definition **h=1** is used only for ISA cards and means that the High Voltage setting remains active even when Gamma-W, Sodigam and Alps for Windows is ended. This is to safeguard against damage to the FET of the pre-amplifier.

For every **target** MCA hardware there is a s**tart-up file** for initialization of the hardware:

Tmca_*N*.ini
Tisa_*N*.ini
Isa_*N*.ini for 16 bit MCAs

and

Scinti_*N*.ini
DMCA_*N*.ini for 32 bit MCAs

where *N* specifies the port number.

These are ASCII files which can be edited with MS Notepad or MS Write, etc..

These files are set up for each individual system, whereby values of given specifications may be changed.

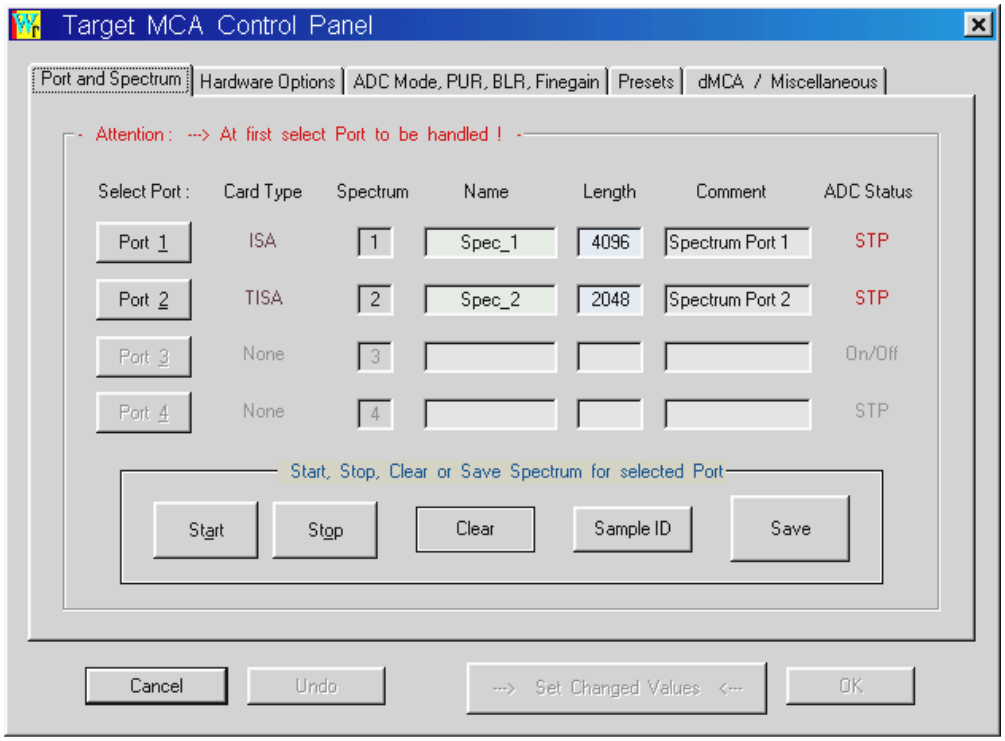
A sample file (e.g. for an ISA PC plug-in card) **Isa_1.ini** looks as follows :

```
Start-up initialisation File for ISA target MCA (KS 11/02)|
ISA Card at Port 1,     SN: xxx xxx xxxxx - 8K            |
Settings made for:  xx-TPxxxxxx (30% PopTop with xCooler) V
-  Spectrum Length  [max. 8192 channels]          :    4096
-  Optional User HV Limit         [0 V - 4500 V]  :    2600
-  Fix Ramping Time for HV Register [ms, 0=HPGe]  :       0
-  Input Polarity Register      [0=neg., 1=pos.]  :       1
-  Coarse Gain Register Value          [1,..,15]  :       4
-  Lower Level Discriminator         [0,..,255]   :       0
-  Upper Level Discriminator         [0,..,255]   :     255
-  Conversion Gain Register Value    [0,..,255]   :       0
-  Noise Filter Register Value       [0,..,255]   :      20
-  Pile Up Rejector                [0=off, 1=on]  :       1
```

Lines #1 to #3 are identifying comments.

The voltage and gain settings, the MCA control functions, etc. are accessed through the **MCA** menus from both the Main Window or the Spectrum Window under the option **target MCA Control Panel**. Most of the manipulations available through the original **target** Software are also available on one of the five tab pages:

- **Port and Spectrum**
- **Hardware Options**
- **ADC Mode, PUR, BLR and Finegain**
- **Presets**
- **dMCA / Miscellaneous**



*If you are not familiar with **target hardware***, it would be advisable to have a look at the manuals which describe the various functions of the optional settings.

The main points to note here are:

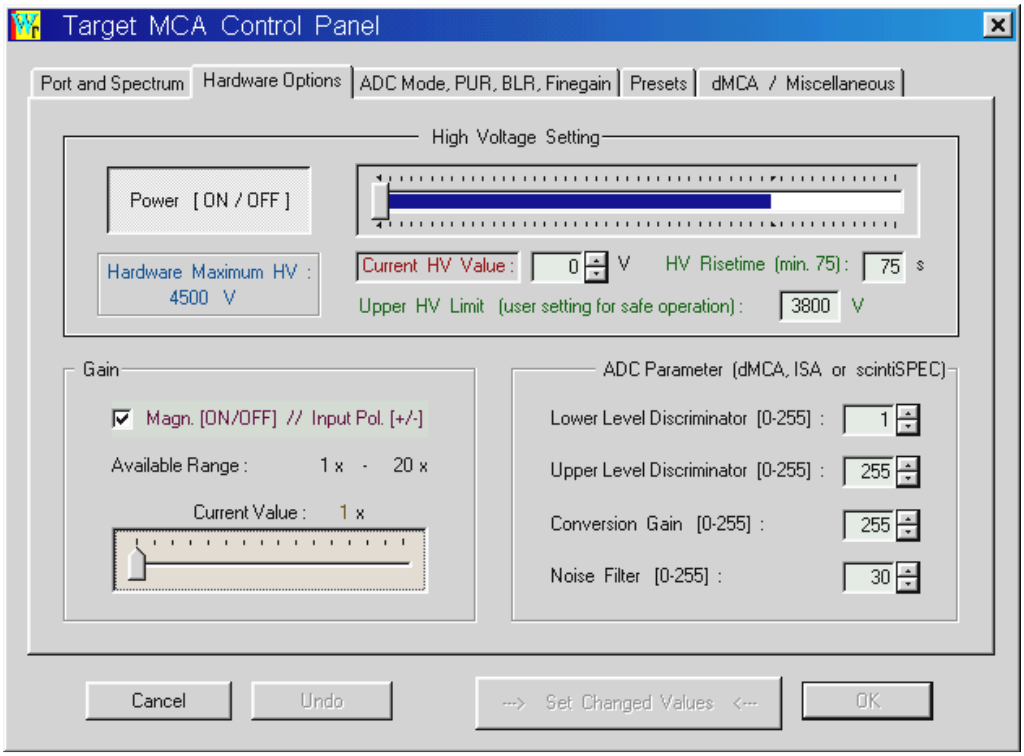
- The very first thing that you MUST do if you have more than one plug-in card installed, is to **select the active port**.
- The port selection is done automatically when only one MCA is installed.

☞ The Power <**ON/OFF**> button on the 🗁 **Hardware Options** tab page *must* be toggled to **ON** so that the Hardware settings can be defined.

☞ The <**Set Changed Values**> button must be pressed to activate any settings e.g. the High Voltage or Gain.
This is a protection feature. It is always necessary to activate the settings as the keyboard entries are not immediately accepted by the program.
You may also use the <**OK**> button to make the settings active, but then you will switch back to the former window.

☞ As in the WinTMCA16 and the WinTMCA32 software, the <**STABILIZATION Mode**> must be selected on the 🗁**ADC Mode, PUR,…** tab page before the box for the fine gain setting is activated.

☞ The ADC Parameter section of the tab page 🗁**Hardware Options** shown below can only be set for the ISA card, scintiSPEC and dMCA-pro and only when Power is `ON´

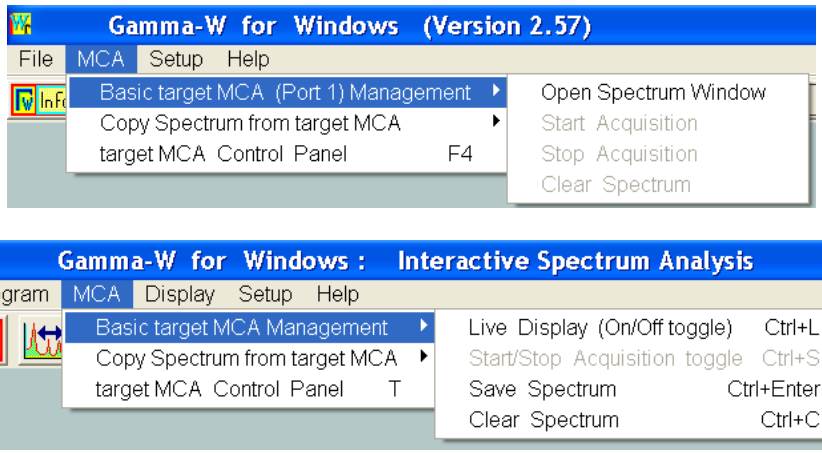


☞ The high voltage step width is 17.5 V for the ISA card, 5.0 V for the TISA and 6 V for the scintiSPEC.

☞ There is a **Risetime Register Ramping** option with a default value of 0 ms for the normal (slow) step-wise **ramping up and down** of the high voltage for ISA and TISA cards. When a value is defined it will be used for the ramping speed; a higher value means a slower ramp.
If you want to be most careful then you may use a very large value of e.g. 5000 ms.

♦ MCA control

The MCA controls are accessed either from the Main Window or the Spectrum Window, respectively, as shown in the next two figures below or through the designated shortcut keys. You will see the display from the MCA Port 1 as default.



You can load spectra into the spectrum screen of Gamma-W, Sodigam and Alps for Windows from any of the four MCA ports by pressing **<Ctrl>+<n>** where **n** is the required port number **1 - 4**.

For a convenient handling of an acquisition the following shortcut keys are of special interest:

<Ctrl> + <n>	selects the active MCA (Portnumber **n** = 1,.., 4)
<Ctrl> + <c>	**c**lears the Spectrum in the active MCA buffer
<Ctrl> + <s>	toggles the acquisition status ON (**s**tart) and OFF (**s**top)
<Ctrl> + <l>	toggles the **L**ive Display mode ON and OFF (switching the Live Display mode on turns the ADC on if it was in stopped condition)
<Ctrl>+<↵>	save the currently selected spectrum

☞ There is a **Live Display Simulation** of six internal demo spectra in the software. This feature is only available in the Gamma-W, Sodigam and Alps for Windows version without MCA support (Standard Version).
To access this feature select ***'Basic target MCA (Port 1) Management'*** from the pull-down menu **MCA** in the Main Window of the program, and then ***'Open Spectrum Window´*** in the fly-out menu that appears.

The following message will appear:

Click on the <**OK**> button and then the live display simulation of **Testspectrum No. 1** will be automatically started in the Spectrum Window.

You may use the shortcut key **<Ctrl>+<C>** to toggle through the six demo spectra.

Each time you restart the live display simulation with **<Ctrl>+<C>**, the next demo spectrum will be used for the simulation.

Pressing **<Ctrl>+<L>** will stop the "acquisition" at the simulated port, so you can work with the current spectrum.

You can "acquire" spectra with the Live-Display Simulation using any of the demo spectra.
With **<Ctrl>+<↵>** you can save any of the intermediate stages of the acquisition simulation as ASCII files. This provides you with spectra with different counting statistics which may be used for teaching laboratory exercises.

☞ The ASCII spectrum files saved by Gamma-W, Sodigam and Alps for Windows have real-, live- and dead- times stored in channels 1-3 and energy calibration polynomial parameters in channels 4-6.

♦ Linking Gamma-W, Sodigam and Alps for Windows to target WinTMCA software

By using the batch structure integrated in target WinTMCA16 or WinTMCA32 software you can link Gamma-W, Sodigam and Alps for Windows in such a way that spectra which are measured in the WinTMCA software can seamlessly be analyzed with Gamma-W, Sodigam and Alps for Windows.

This is very convenient, because one has the best choice of handling the target MCA hardware, such as a "Signal Monitor" for dMCA-Pro cards and one can have as many MCAs connected as being supported by the target WinTMCA software.

☞ There is no interference between data acquisition and spectrum analysis.

To link Sodigam/Gamma-W/Alps to WinTMCA one must first install the appropriate target WinTMCA software. The choice of WinTMCA16 (16 bit) or WinTMCA32 (32 bit) version depends on the installed target MCA hardware (16 bit for TMCA, ISA or TISA plug-in cards, 32 bit for dMCA, dMCA-pro and scintiSPEC).

The **installation path name must not contain blanks** or special characters and should not be longer than 32 characters, e.g. the installation directory **C:\WinTMCA32_scintiSPEC** for a scintiSPEC installation would be fine.

Second, install the ***Standard Version*** (without MCA support) of Gamma-W, Sodigam or Alps for Windows in its default directory, e.g. **C:\Sodigam.Win** (or **C:\Gamma-W.Win** or **C:\Alps.Win**).

After the installation is done one moves (or copies) the complete directory structure of Gamma-W, Sodigam and Alps for Windows to a subdirectory in the WinTMCA software, e.g. to **C:\WinTMCA32_ScintiSPEC\Sodigam.Win**

Third, one has to extend the WinTMCA pull-down menu structure to be able to invoke Gamma-W, Sodigam and Alps for Windows via a WinTMCA batch file.
Look in the WinTMCA subdirectory **\..\config** for a file named **Menu.def**. This is an ASCII file in which the pull-down menu entries of the WinTMCA software are defined.

Insert the line :

```
6.9 "Spectrum analysis: Sodigam" "winproc Sodigam -p=1"
```

after the already existing command line: **`6.8 PEAKSEARCH_S PEAKSEARCH`**.

The text **"Spectrum analysis: Sodigam"** is the character string to be displayed in the pull-down menu. You may modify this line according to your needs, e.g. replace **"Sodigam"** by **"GammaW"** or **"Alps"**.

The command **"winproc Sodigam -p=1"** will execute a WinTMCA batch file, here it is named **Sodigam,** with the default extension **.WPB**.

Finally one has to provide the WinTMCA batch file **Gamma-W.wpb**, **Sodigam.wpb** or **Alps.wpb** in the WinTMCA subdirectory **\..\config**.

An example for **Sodigam.wpb** is given below:

```
GetActualSpectrum Spec
GetSpectrumPath Path $Spec
Strcat GammaWPath $WinTMCADir "\Sodigam.win"
Strcat GWSpecpath $WinTMCADir "\Sodigam.win\Spectra"
SetSpectrumPath $Spec $GWSpecpath
GetSpectrumName SPCName $Spec
if $SPCName=""
{
  SetPar SPCName "Noname.spc"
  SetSpectrumName $Spec $SPCName
}
FileExists $Spec $SPCName Res
if $Res=1
{
  ShowQuestion Res Dummy 0 "Spectrum name exists. Overwrite"
  if $Res<>0
  Goto End
}
SaveSpectrum $Spec $SPCName
SetSpectrumPath $Spec $GWSpecpath
Strcat CMDLine "Sodi-Gam.EXE " $GWSpecpath "\" $SPCName
WinExec $GammaWPath $CMDLine SHOWNORMAL
SetSpectrumPath $Spec $Path
:End
Variables
GammaWPath %s
GWSpecpath %s
Spec %d
Path %s
CMDLine %s
SPCName %s
Res %d
```

☞ Examples for *.wpb files can be found on the Gamma-W, Sodigam and Alps for Windows distribution in the directory : **\.._Target_MCA\Copy_to_WinTMCA_directory**.

☞ For a detailed description of the batch file structure, definition and handling of variables and their parameters refer to the manual of the target WinTMCA software.

By executing the WinTMCA batch file shown above the spectrum of the currently (in the WinTMCA software) selected MCA will be saved to the harddisk. The file name will be the same name which was set in the WinTMCA software.

After the spectrum is written to the harddisk Gamma-W, Sodigam and Alps for Windows is automatically started with the name of the saved spectrum as a start-up argument.

Due to this start-up argument Gamma-W, Sodigam and Alps for Windows will read the spectrum file and open the Spectrum Window. The spectrum is displayed and is ready for manual analysis, calibrations, applying the Batch Procedure Dialog facility, or any other operation.

☞ The spectrum can be analyzed while the acquisition in the WinTMCA software continues. When closing the Spectrum Window Gamma-W, Sodigam and Alps for Windows will be terminated and the WinTMCA display comes to the front again.

☞ You may also switch between the Gamma-W, Sodigam or Alps for Windows process and the WinTMCA software while the spectrum analysis is running and the acquisition in the WinTMCA software is still active.

☞ An existing energy calibration in the WinTMCA will be stored in the ASCII formatted spectrum file header. After reading the spectrum in Gamma-W, Sodigam or Alps for Windows these polynomial energy calibration parameters will be used.

☞ As a second start-up argument the command may contain a procedure name. Gamma-W will then switch to the BPD after starting. The procedure has to be located in the "\..\Process" sub-directory.

Section VI

H O T K E Y S

(for Gamma-W, Sodigam and Alps)

*** Main Window ***

[F1]	Calibration Functions (Energy, FHWM, Efficiency, Calculus, Decay, Means)
[F2]	Nuclide Library Manager (editing Nuclide Data, making and editing Libraries)
[F3]	Options, Colors, Mode (Gamma-W, Sodigam, Alps) and Language setting
[F4]	MCA Hardware Control (version with 16- or 32-Bit MCA support or ISA/TISA Simulation)
[F5]	Open Output File (Output.txt) with built-in ASCII Editor
[F6]	Read Batch File
[F7]	Read Spectrum File (ASCII Format or as defined by "READ 9 -1 n", n=Type)
[F8]	HTML Codeword Help (not fully implemented)
[F9]	Read internal DEMO Spectrum
[F10]	Exit Program
[Ctrl] + c	Read Spectrum File c = Format, see Hotkey Definitions in Pull Down Menu: File | Read Spectrum
[Ctrl]+[P]	Print Output File
[Esc]	Exit Program (press [Esc] twice for fast Exit)
[B]	Read Batch File
[C]	Codeword Terminal
[P]	Procedure Dialog Window

Version with 16- or 32-Bit MCA support only:

[Ctrl]+[1]	Select MCA, open Spectrum Window and read Spectrum from Port 1
[Ctrl]+[2]	Select MCA, open Spectrum Window and read Spectrum from Port 2
[Ctrl]+[3]	Select MCA, open Spectrum Window and read Spectrum from Port 3
[Ctrl]+[4]	Select MCA, open Spectrum Window and read Spectrum from Port 4

*** Spectrum Window ***

[F1]	Expand Spectrum Display
[F2]	Contract Spectrum Display
[F3]	Zoom in at Spectrum Marker Position
[F4]	Show full Spectrum
[F5]	Calibration Functions (Energy, FHWM, Efficiency, Calculus, Decay-Corr, Means)
[F6]	Nuclide Library Manager (editing Nuclide Data, making and editing Libraries)
[F7]	Options, Colors, Mode (Gamma-W, Sodigam, Alps) and Language setting
[F8]	Spectrum analysis (i.e. Peak-fitting in already marked ROI or Display Range)
[F10]	Close Spectrum Window and return to previous Screen (Main or Procedure Window)
[F12]	Print Spectrum (current Display Range)
[Ctrl]+[F1]	Open Output File (Output.txt) with built in ASCII Editor
[Ctrl]+[F8]	Clear Peaklist
[Ctrl]+[F12]	Save Spectrum graphics to File (WMF format)
[Ctrl]+[Up]	Expand Spectrum Display
[Ctrl]+[Down]	Contract Spectrum Display
[Ctrl]+[Left]	Move Spectrum Display to left
[Ctrl]+[Right]	Move Spectrum Display to right
[Ctrl]+[CR]	Save Spectrum to File (ASCII format)
[Ctrl]+[Back]	Copy Procedure Peak Listing into Output File
[Ctrl]+[P]	Print Output File
[Ctrl]+[I]	Open/Close Programmers Info Window
[Ctrl]+[W]	Toggle: SPC -> Cts*Chn -> Cts*Energy -> Cts sorted -> SPC
[Shift]+[Up]	Increase vertical Scaling
[Shift]+[Down]	Decrease vertical Scaling
[Shift]+[Left]	Move Spectrum Cursor to left and mark ROI
[Shift]+[Right]	Move Spectrum Cursor to right and mark ROI
[Ctrl]+[L]	Switch Live Display for Spectrum Simulation ON or OFF [Ctrl]+[C] clears Spectrum and selects next Demo-Spectrum

[Up]	Show full Spectrum
[Down]	Expand around Spectrum Marker Position
[Left]	Move Spectrum Marker left
[Right]	Move Spectrum Marker right
[Page Up]	Increase vertical Scaling
[Page Down]	Decrease vertical Scaling
[Pos1]	Set Spectrum Marker to the very left Channel
[End]	Set Spectrum Marker to the very right Channel
[Space]	Zoom in at Spectrum Marker Position or show full Spectrum (toggle)
[Esc]	Clear ROI, Clear Display with Fit-Results, interrupt ROI analysis
[Back]	Force Histogram Mode for Display Range greater than 2K Channels (caveat!)
[-]	Subtract Sum-Fit-Function from Spectrum Data
[CR]	Show next Fit (when ROI was split into Sub-regions)
[A]	Automatic horizontal Scaling (on/off toggle)
[B]	Read Batch File
[C]	Codeword Terminal
[H]	Histogram or Dot Display (toggle)
[L]	Vertical Scaling: linear or logarithmic (toggle)
[M]	Show Spectrum Marker (on/off toggle)
[N]	Brutto or netto Counts in marked ROI (toggle, Gamma-W and Sodigam only)
[P]	Procedure Dialog Window
[S]	Display Sum-Fit-Function (on/off toggle)
[Y]	Set Peak Marker Line in defined ROI
[5]	Display Markers for Single- and Double-Escape-Peaks
[D]	Expand around Double-Escape-Peak (if Escape-Peak Markers are shown)
[S]	Expand around Single-Escape-Peak (if Escape-Peak Markers are shown)
[I]	Open Sample Description File (SampleID.txt) with built in ASCII Editor

Version with 16- or 32-Bit MCA support only:

[Ctrl]+[1]	Select MCA and read Spectrum from Port 1
[Ctrl]+[2]	Select MCA and read Spectrum from Port 2
[Ctrl]+[3]	Select MCA and read Spectrum from Port 3
[Ctrl]+[4]	Select MCA and read Spectrum from Port 4

[Ctrl]+[C]	Clear Spectrum Data in currently selected MCA
[Ctrl]+[H]	Force Histogram Mode for Display Range greater then 2K Channels (cave!)
[Ctrl]+[L]	Switch Live Display Mode ON or OFF
[Ctrl]+[S]	Switch ADC ON or OFF ("ON" starts Live Display simultaneously)
[T]	Open MCA Hardware Control (version with 16- or 32-Bit MCA support only)

*** Calibration Function Windows ***

[Tab]	If cursor in data input table: jump to next cell
[Shift]+[Tab]	If cursor in data input table: jump to previous cell
[Del]	Delete selected value

*** Procedure Window ***

[F1]	Codeword Terminal
[ESC]	Close Procedure Window and return to previous Screen (Main or Spectrum Window)

Section VII

Changes and Enhancements in Codeword usage

GENERAL:

Detection limit and decision threshold

Codeword DETL

Syntax:

DETL Sigma, Mincount, Type2, Mode

General:

- The Codeword can only be used in a batch-file.
- The Codeword calculates detection limits according to KTA 1503.1 as well as decision thresholds according to DIN/ISO 11929.
- Before proper calculations of decision thresholds according to DIN/ISO 11929 can be carried out all peaks in a spectrum must have been analyzed. Prior to spectrum analysis one must define the statistical significance, normally with the Codeword DETL in the Start-up.ini file, e.g.: DETL 2 4 0.12 -1 (2 sigma, 4 counts minimum, 12% Type 2 uncertainties)
- For proper calculation of detection limits and decision thresholds the spectrum must have a correct energy calibration.

Parameters:

Sigma:

gives the statistical significance in multiples of standard deviations (sigma). Supported values are: 1, 2 or 3 sigma (only integer values are accepted).

Mincount:

is the minimum number of counts that is accepted as count rate. This parameter is mainly used in alpha-spectrometry.

Type2:

defines the sum of all "Typ 2" uncertainties (total uncertainty). The total uncertainty is calculated via the square sum of all relative individual uncertainties, e.g.:
Weighing error = 4%; single uncertainty = 0,04.
Sampling error = 5%; single uncertainty = 0,05.
Operator error = 3%; single uncertainty = 0,03.

Total uncertainty = SQRT ($0,04^2$+$0,05^2$+$0,03^2$) = 0,0707.

Mode:

defines the working mode:

Mode = -1 parameters **Sigma, Mincount** and **Type2** are entered only, no calculation. This mode is most commonly used in the start-up.fil

Mode = 0 calculation of limits is carried out. In this case the command is followed by data input lines:

1. First input line : sample mass or volume in the previously chosen unit (see codeword UNIT or drop down menu in the Nuclide Assignment window). If a "0" is entered as sample mass the actual mass (e.g. if it has previously been entered in the Nuclide Assignment window) is retained. If the actual mass **is** 0 it is set to 1000 g.
2. Second input line : energy value (in keV) for which limits are to be calculated, e.g.: 661.6. If a nuclide name like Cs-137 is given instead, the dominant gamma-line of that nuclide is searched from the library. The KTA detection limit and DIN/ISO 11929 decision threshold are then calculated for this gamma-ray energy.
3. An undefined number of input lines can be entered. The calculation of limits is terminated with an energy ≤ 0 or a nuclide name that does not exist in the library.

- Codeword CALC/CALF

"CALC jp1 jp2 jp3" :

Parameter jp3 is interpreted in the same way as that of codeword REGI, i.e.:

jp3 = 0 jp1 and jp2 are given in channels

jp3 = 10 jp1 and jp2 are given in channels and all peak-fits are displayed in the spectrum

jp3 = 1 jp1 and jp2 are given in energy

jp3 = 11 jp1 and jp2 are given in energy and all peak-fits are displayed in the spectrum

Note: There is NO Fit display for the Codeword CALF.

- Codeword EFFC

When reading efficiency data via EFFC 2, uncertainties having a value > 2 are interpreted as an error in %.

- Codeword FWHM

"FWHM jp1" :

jp1 > 2 FWHM is given in % * 10 (e.g.: 7.5 % is given as jp1 = 75)

jp1 = 2 read 3 polynomial coefficients (in next line)

jp1 = 1 read up to 20 data points (Energy!,FWHM,dFWHM)

- Codeword FIXP

"FIXP jp1 jp2" :

jp1 = [0,1] peak position parameters free or fixed

jp2 = [0,1] FWHM parameter free or fixed

- Codeword NUCL

"NUCL 5" and "NUCL 6" :

The energy window width for nuclide assignment is now 20 keV for Sodigam and 30 keV for Alps (i.e. the according widths indicated in the Codeword Manual are no longer valid).

- Codeword RESF

Start date and start time of the measurement of a spectrum are listed in the output file. If the file names of the output files are automatically generated the last five files are saved before overwriting (ex.: Output.**00x**.txt, where x = 1-5).

- Codeword STOP

Terminates the program and creates a file named 'StartupINI.fil'. This file contains codewords and parameters with the actual settings for: ENER, TAIL, SENS, PRIN, FIXP, LIB, DOKU, UNIT, BGPI, PATH. The settings can be transferred into the 'Start_up.INI' (not to be confused with 'Start_up.def'; see page 15) via Windows Clipboard **or** the 'StartupINI.fil' can be read as a batch file at the end of the 'Start_up.INI'.

ALPS:

- *Quick and simple energy calibration in ALPS*
  - set the cursor onto the main peak of a nuclide
  - start codeword terminal with “c”
  - enter the nuclide name for this main peak (e.g. “U-238”)
  - call the Calibration Functions window (**F5** or icon) and start energy fit **or**
  - enter more nuclides in the same way and then start fitting

  NOTE:
  1. Alpha.lib has to be the active library (usually is chosen when ALPS is started)
  2. No ROIs must be marked (keep an eye on the status bar when selecting peak maxima).

- Nuclide assignment using "NUCL 5" and "NUCL 6": only nuclides are assigned whose main peak is found in the spectrum.

- Codeword SPIK

  "SPIK -1" :

  Restores the efficiency function that was valid before a spike-calculation was carried out (only for polynomial functions of a degree of 0). The process and the efficiency values are written into the output file.

  "SPIK 1" :

  The nuclide name that is used with the codeword "SPIK 1" can be followed by a commentary, e.g. the reference number of the spike-solution. After the nuclide name (8 characters) 72 characters are read from the 9^{th} column on. This text is written to the output file together with the other spike solution data.

  If "PRIN ipr" with ipr ≥ 2, decay correction data for the spike-solution are written to the output file.

  Calculation of chemical yields: if possible an overall activity is used. The overall activity results from the sum of all transitions of the according nuclide.

- Codeword AREA
  "PRIN ipr" :
  If ipr ≥ 2, for each peakfit the peakarea within the ROI is compared to the integral area. The result is written to the output file.
  If ipr ≥ 4, the function values and their integral for each channel are written to the output file.

- When a **geometrical efficiency** has been calculated ("Calibration Functions", "Calculus") the resulting data can be transferred directly to the efficiency dialogue. Click on "Update Window" after pressing the "CALC" button. Existing calibration data are overwritten after a confirmation request and ALPS automatically switches to the efficiency tab page.

- Parameters for the Codewords "AREA", "NOBA", "GIC" and "TAIL" can be entered under "Options" | "Special Settings" (alternatively to the Codeword Terminal).

SODIGAM:

- Test function for ScintiSpec-timing, count rate and sum of all events in the spectrum (<Ctrl>+<i>). Codeword "NOBA n" with n>10 can be used to increase the number of measurements (10 by default). Only available in the version with 32-Bit hardware support.

- Codeword FWHM
  "FWHM P1 P2 P3":
  If P1 ≠ 0 the automatic calculation of the FWHM function (based on P2) is disabled. Instead, the FWHM function is calculated using the polynomial parameters P1, P2 and P3.

- Creating a correction file for external background:
  - Codeword Terminal: "BGPI 1", enter file name (EXAMPLE.BGD),
  - Spectrum analysis via batch file or manually in spectrum window using codeword REGI,
  - Codeword Terminal: "BGPI -1" to close .BGD file.

GAMMA-W:

- Energy calibration parameter E4.
  The energy function is then calculated as follows:
  Energy = E1 + E2×channel + E3×channel×channel + E4/channel

Section VIII

Miscellaneous

- Codeword Terminal:
  Energy calibration (in a previously defined ROI) can be done by entering a nuclide name in the Codeword Terminal.
  Definition of peak positions (peak marking lines) in a previously marked ROI by entering one or more nuclide name(s) in the Codeword Terminal. The nuclide names must be entered in the format "NN-XXXX" (e.g.: Ba-137m) and may **not** contain blanks (e.g.: Tc-99 m). If more than one nuclide name is entered the names have to be separated by comma, semicolon or blank. NOTE: only works if the currently active nuclide library (open Nuclide Assignment window with **F6**, see first line) contains the entered nuclide names.

- The energy window width for nuclide assignment can be entered at:
  Nuclide Assignment, tab page "Quantitative Nuclide Assignment, data field Energy window width **or** via "NUCL 8 x" (x = window width/keV).
  The energy window width is used when nuclides are assigned to the peaks previous to the calculation of efficiency data points from the last analyzed spectrum.
  If x = 0, predefined values are used (Gamma-W: ± 1 keV, Sodigam: ± 15 keV, Alps: ± 25 keV).

- When the start files "Start_up.DEF" and "Start_up.INI" have been processed the program automatically searches for the file "Service.FIL" in the main directory. This file may contain codewords or may call further batch-files. In case the "Service.FIL" file exists this is reported in the output file.

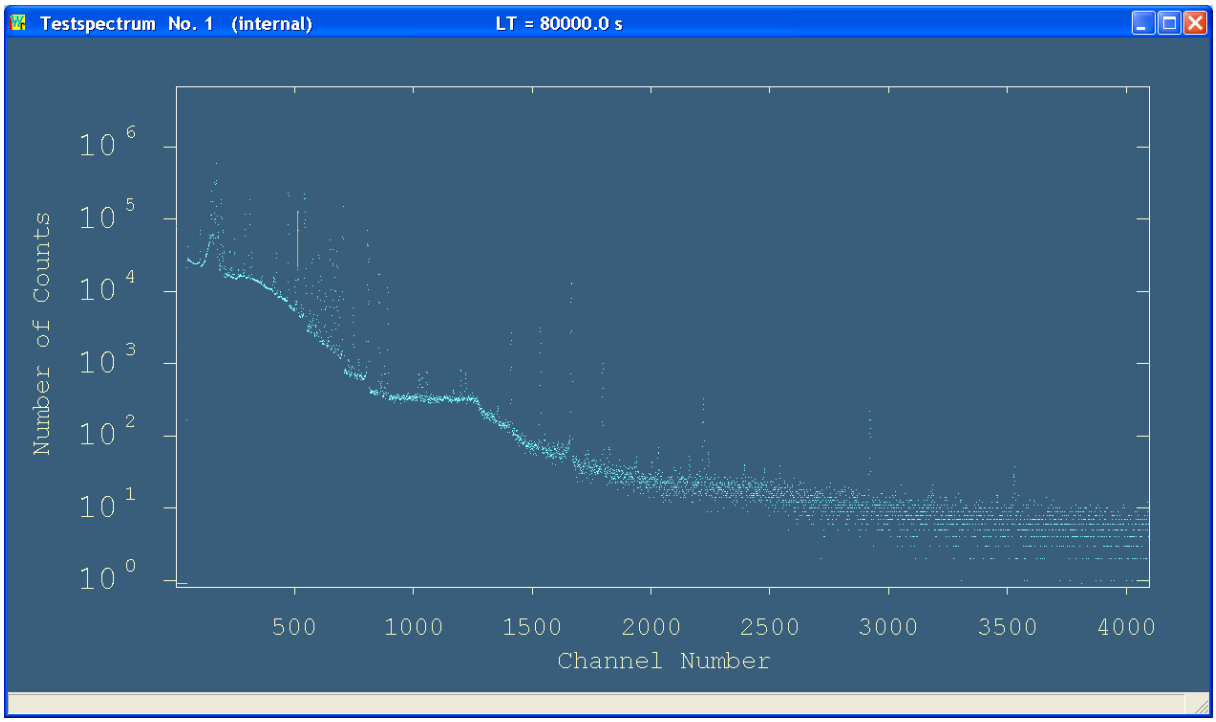
- When a nuclide library is read the following information are written to the output file depending on "PRIN ipr":
  for ipr ≥ 1 : 'Reading Nuclide Library :'
  for ipr ≥ 2 : 'Number of Nuclides in Library :'
  for ipr ≥ 3 : 'Last opened on :' + complete list of nuclides in the library.

- A second user defined function for efficiency correction is available in the Option Dialogue, Tab page Parameter for Spectra Analysis, Customized Efficiency Correction: EffcKorr = Effc / P1

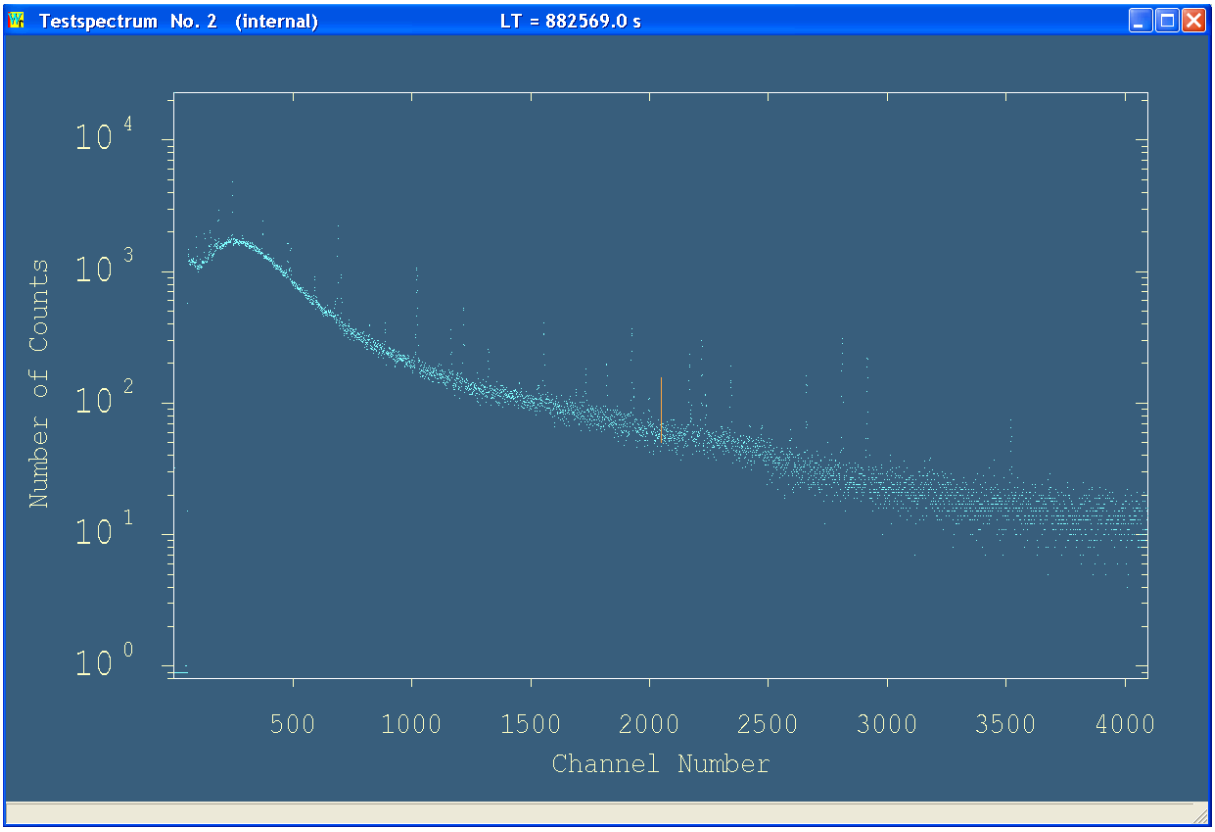
Appendix I

Demo Spectra

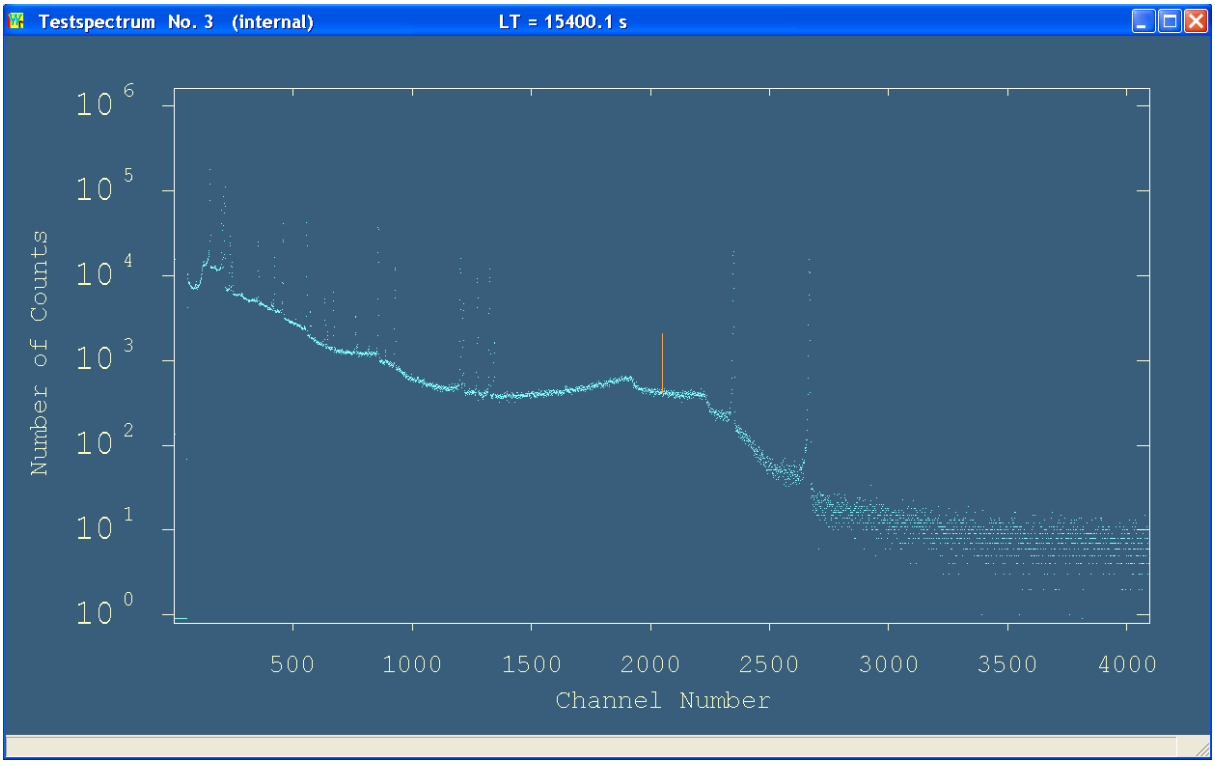
No. 1 : HPGe detector; Ac-227



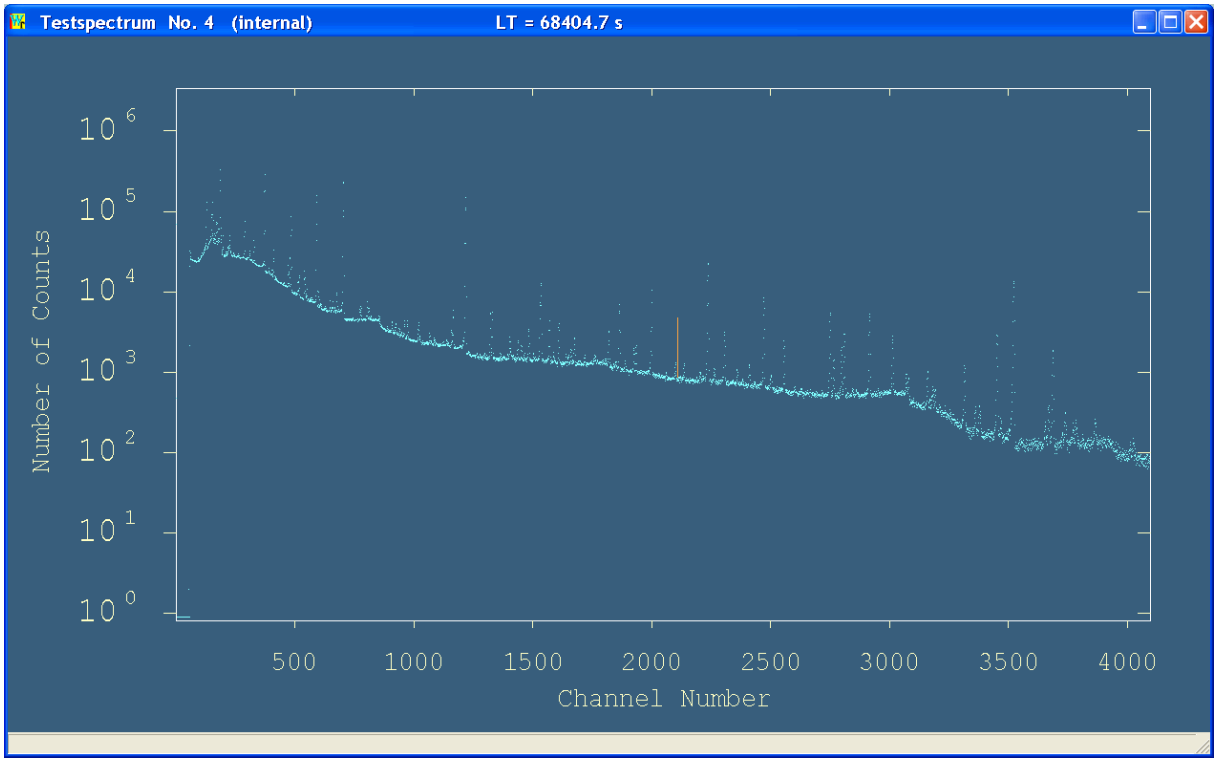
No. 2 : HPGe; background spectrum



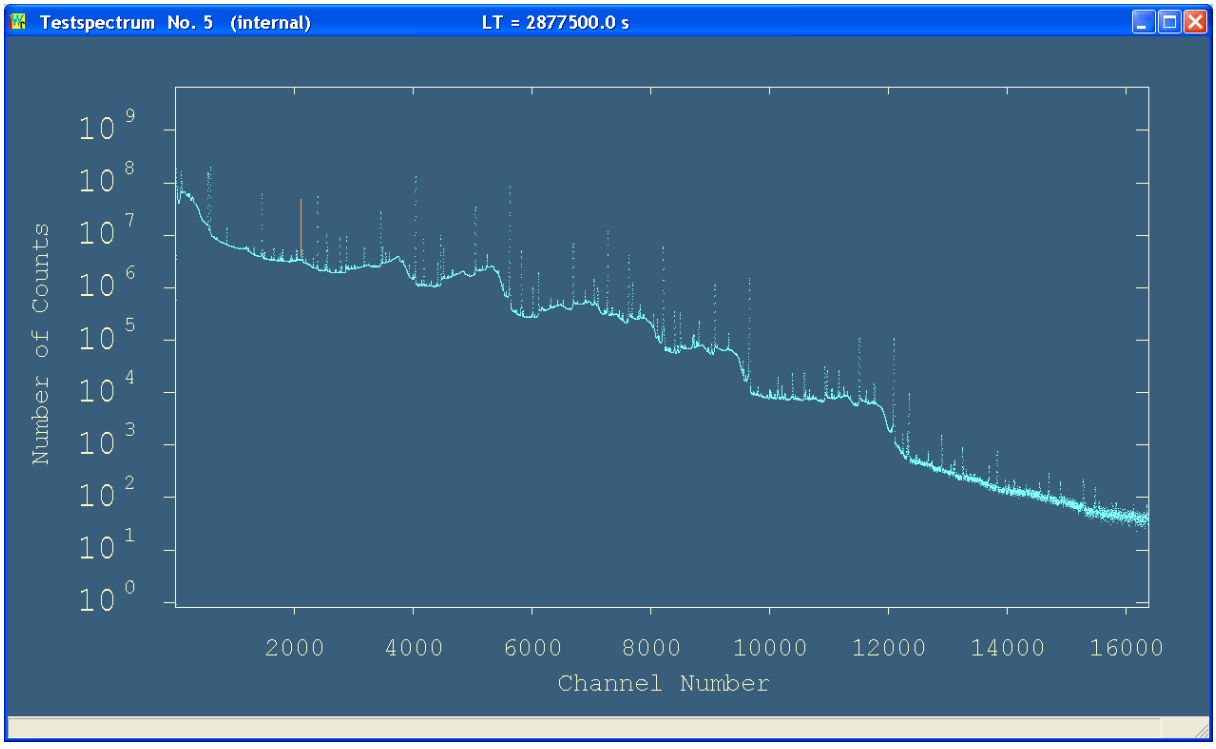
No. 3: HPGe; calibration source (optimized Marinelli, nuclides: Co-60, Sb-125, Cs-137, Pb-210, Am-243)



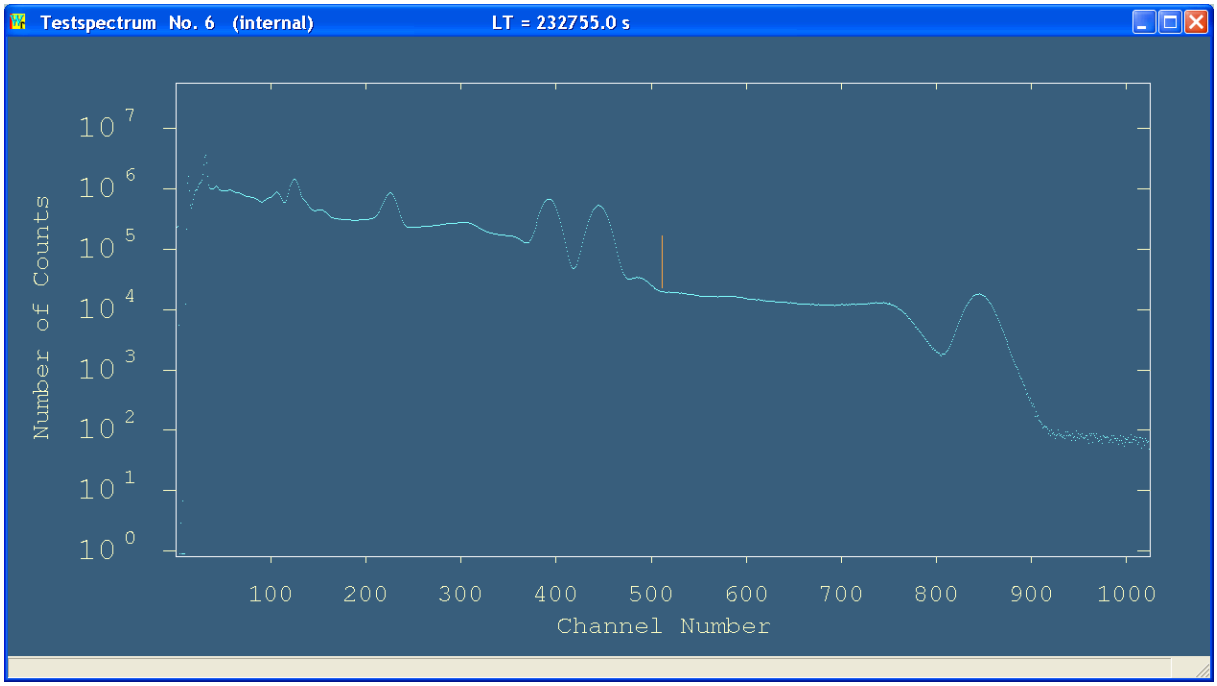
No. 4: HPGe; soil sample



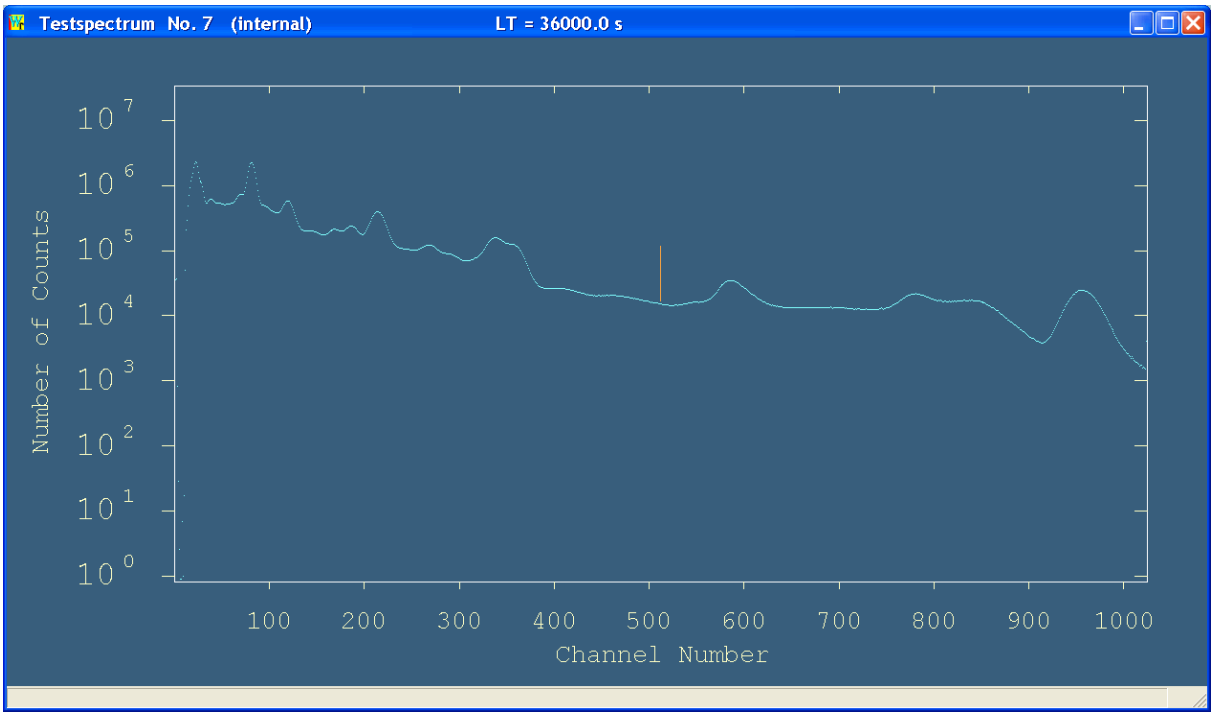
No. 5: HPGe; Si (n,γ) reaction



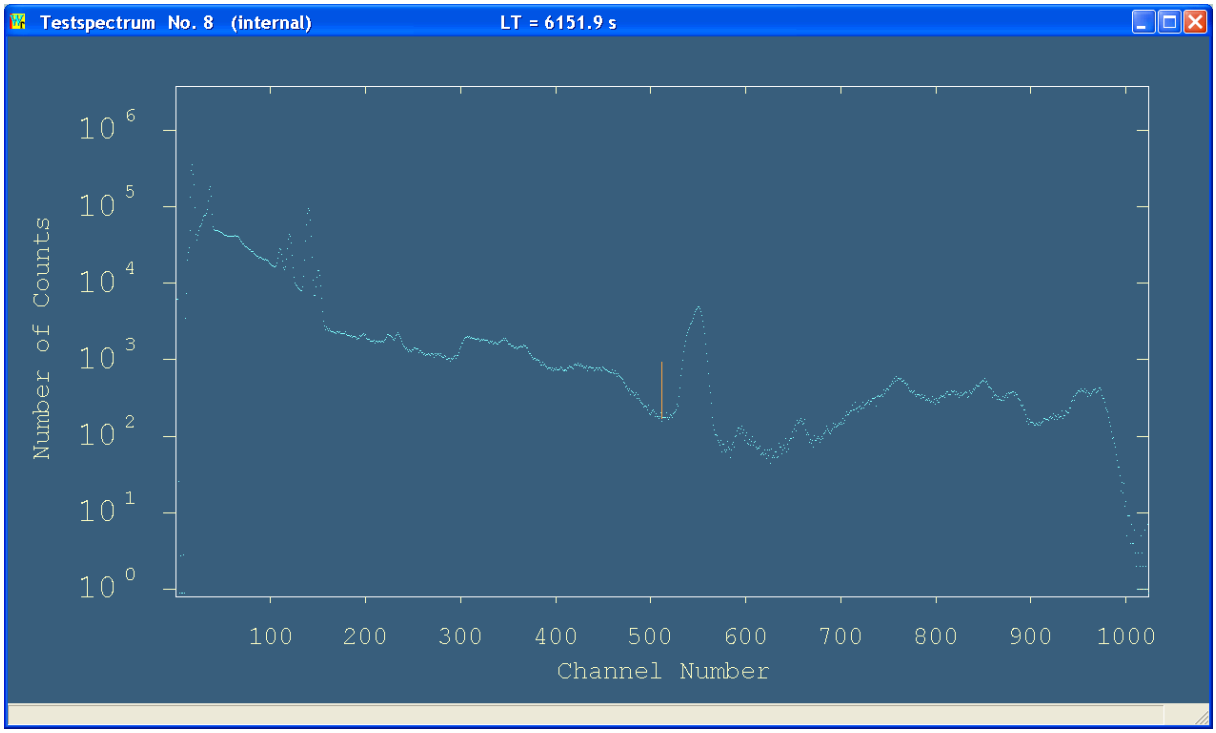
No. 6: NaI(Tl) detector; Co-60, Ba-133, Cs-137



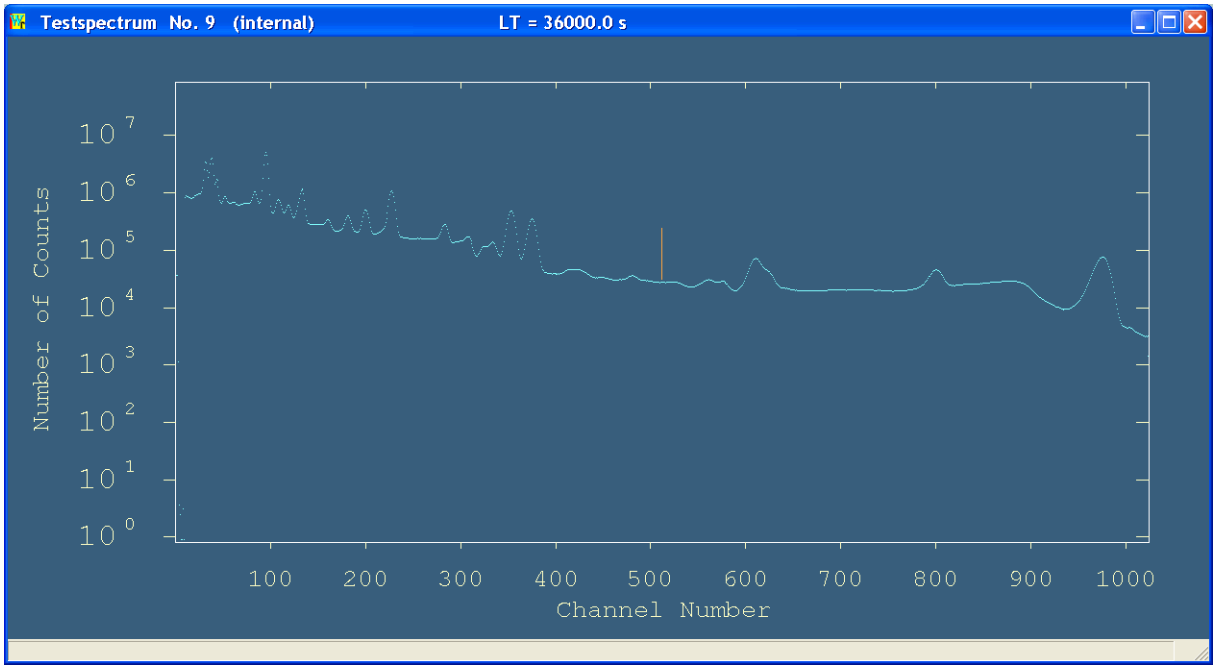
No. 7: NaI(Tl); Th-232



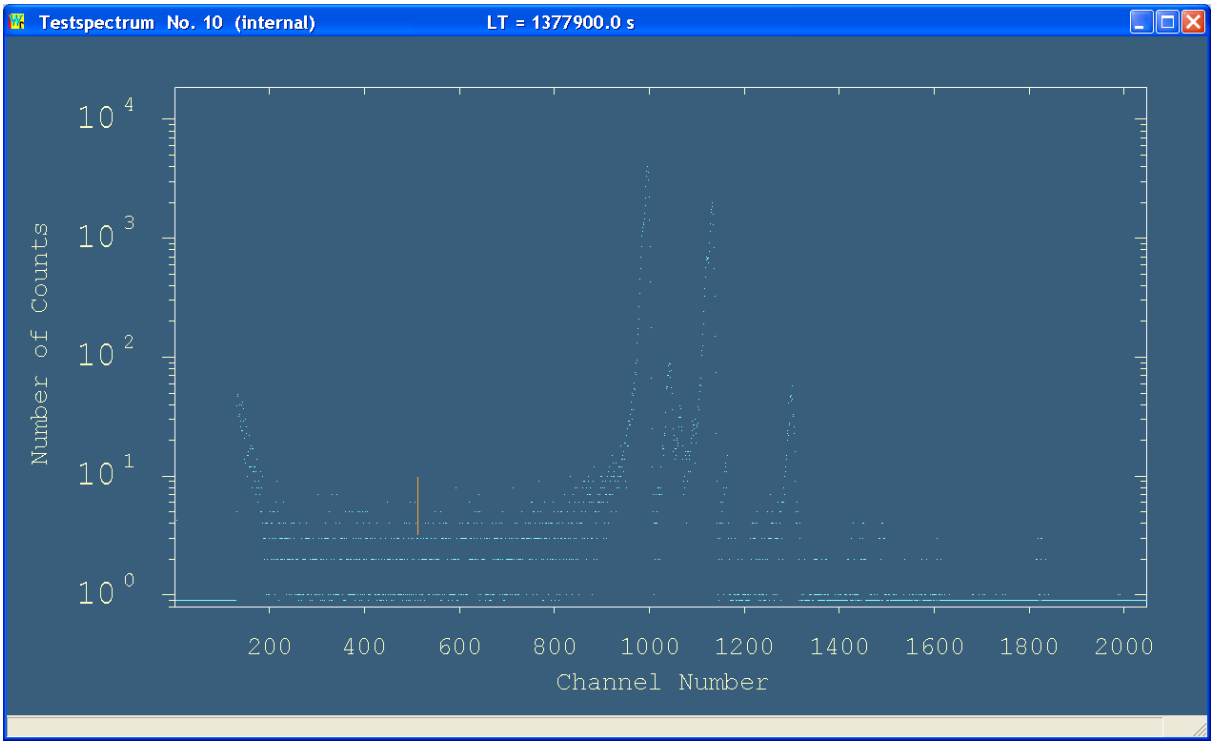
No. 8: BriLanCe detector; Ba-133



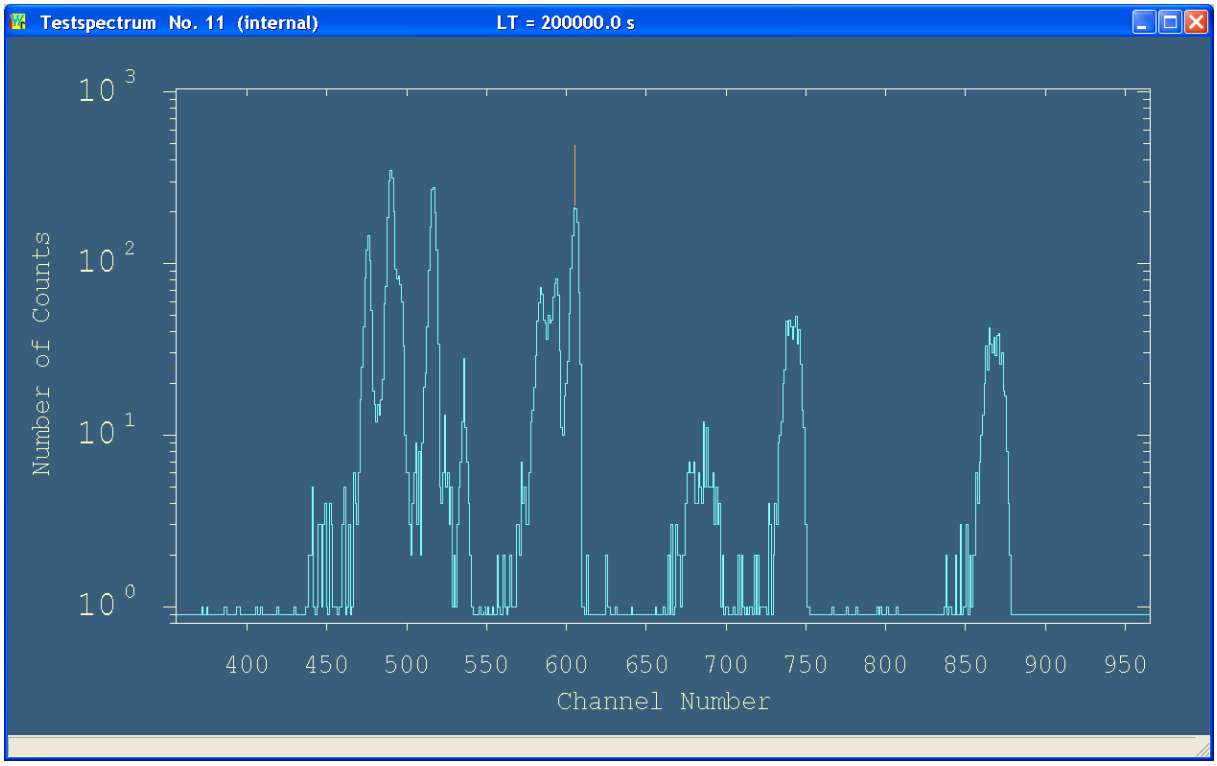
No. 9: BriLanCe; Th-232



No. 10: SBD (surface barrier detector); alpha-Spectrum of Uranium



No. 11 (enlarged): SBD; alpha-Spectrum of a spiked Plutonium-238 and Thorium-228 sample; spike: Uranium-232 and Plutonium-236



Appendix II

Printout Examples

PRIN 0 1

```
  *** Reading Internal DEMO Spectrum 3 ***

 SPECTRUM : SandCal.spc
 stored on AUG 28 1995 at 18:35:56 AM Time  15400.1 seconds (live)
 ID: Marinelli - Sandmatrix  (M.Pütz)


 FWHM coefficients  :
 F1 =  1.9966E+00   F2 =  7.1821E-04   F3 =  1.1436E-08

 Spectrum: Testspectrum  No. 3   (internal)              21.09.2012   10:37:08
 Measuring time :   15400 seconds
 Channel  1317 to  1332    SENS 25  FIXP 0 0  SMOO 0           BGND 0
 ================================================================================
   # Position  Energy   DE         Area        DA(%) FWHM/keV  FIT  POFIF QUAL
   1   1324.1   661.5  0.0        37716.4         1.2   1.49   0.65    000
 ================================================================================
```

PRIN 0 2

```
*** Reading Internal DEMO Spectrum 3 ***

 SPECTRUM : SandCal.spc
 stored on AUG 28 1995 at 18:35:56 AM Time  15400.1 seconds (live)
 ID: Marinelli - Sandmatrix  (M.Pütz)


 FWHM coefficients  :
 F1 =  1.9966E+00   F2 =  7.1821E-04   F3 =  1.1436E-08

 Spectrum: Testspectrum  No. 3   (internal)              21.09.2012   10:44:50
 Measuring time :   15400 seconds
 Channel  1317 to  1331    SENS 25  FIXP 0 0  SMOO 0           BGND 0
 ================================================================================
 | N°| Channel| Gross area |   Net area | Err-% |  Energy|Efficiency| Gammas/s|
 |---+--------+------------+------------+-------+--------+----------+---------|
 |  1|  1324.1|     44043.0|     37594.8|   0.67|   661.5|1.0000E+00|     2.44|
 ================================================================================
```

PRIN 0 3

```
*** Reading Internal DEMO Spectrum 3 ***

 SPECTRUM : SandCal.spc
 stored on AUG 28 1995 at 18:35:56 AM Time  15400.1 seconds (live)
 ID: Marinelli - Sandmatrix  (M.Pütz)


 FWHM coefficients  :
 F1 =  1.9966E+00   F2 =  7.1821E-04   F3 =  1.1436E-08

 Spectrum: Testspectrum  No. 3   (internal)              21.09.2012   10:46:57
 Measuring time :   15400 seconds
 Channel  1317 to  1331    SENS 25  FIXP 0 0  SMOO 0           BGND 0
 ================================================================================
   #  Position    Energy     DE         Area    DA(%) FWHM/keV  FIT POFIF QUAL
    1  1324.09   661.5474  0.0069      37594.8  0.6669  1.48   0.28   000

 ================================================================================
```

PRIN 0 4

```
 *** Reading Internal DEMO Spectrum 3 ***

 SPECTRUM : SandCal.spc
 stored on AUG 28 1995 at 18:35:56 AM Time  15400.1 seconds (live)
 ID: Marinelli - Sandmatrix  (M.Pütz)


 FWHM coefficients  :
 F1 =  1.9966E+00   F2 =  7.1821E-04   F3 =  1.1436E-08

 Spectrum: Testspectrum  No. 3   (internal)              21.09.2012   10:51:57
 Measuring time :   15400 seconds
 Channel  1317 to  1331    SENS 25  FIXP 0 0  SMOO 0           BGND 0
 ================================================================================
   # Position  Energy   DE      Area  DA(%)   Bgnd  DB(%) FWHM/keV FIT POFIF QU
   1   1324.1   661.5  0.0    37594.8   0.7     0.0   0.0   1.48  0.28   000
 ================================================================================
```

PRIN 0 5

```
*** Reading Internal DEMO Spectrum 3 ***

 SPECTRUM : SandCal.spc
 stored on AUG 28 1995 at 18:35:56 AM Time  15400.1 seconds (live)
 ID: Marinelli - Sandmatrix  (M.Pütz)


 FWHM coefficients  :
 F1 =  1.9966E+00   F2 =  7.1821E-04   F3 =  1.1436E-08

 Spectrum: Testspectrum  No. 3   (internal)              21.09.2012   10:50:23
 Measuring time :   15400 seconds
 Channel  1317 to  1332    SENS 25  FIXP 0 0  SMOO 0           BGND 0
 ================================================================================
   # Position  Energy   DE      Area  DA(%)     BGND  DB(%) FWHM   FIT POFIF QU
   1   1324.1   661.5  0.0    37716.4  1.2     2553.1  2.0  1.49  0.65   000
 ================================================================================
```

Conclusion

You should now have a decent understanding of the structure and capabilities of **Gamma-W, Sodigam and Alps for Windows.** You should be able to continue exploring the program on your own and to use it for your own applications.

Refer to the original (i.e. MS DOS version) manual for more detailed information about **Gamma-W and Sodigam and Alps**, particularly the use of CODEWORDs for operation of the program in the Codeword Terminal and the use of batch files.

And finally, if you have any problems or questions or comments, please contact us.

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