QuantaSmart™ For The TriCarb® Liquid Scintillation Analyzer Reference Manual

Release History

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Safety

Electrical Safety

WARNING

Use proper plugs and good earth ground connections.

WARNING

For systems operating at voltages other then 115 volts AC or 220 volts AC, a locally approved 3-prong plug may be required to correctly power the system.

CAUTION: *Do not move the fully assembled unit. Use both hands when lifting or moving any part of the system. Carry each part from the bottom.*

Wiring Specifications

Live	(L) Brown lead
Neutral	(N) Blue lead
Earth	(E) Green/yellow lead

Cleaning the System

Clean the outer surfaces of the system by wiping them with a damp cloth and common laboratory cleaner.

System Ventilation

For adequate ventilation of this equipment, a distance of 15cm must be kept from this unit and any other surfaces.

Explanation of Symbols

You may find one or more of the following symbols used on labels on your system.

Symbol	Explanation	L'explication	Erklarung
	Alternating Current	Courant alternatift	Wechselstrom
	Protective Earth Ground	Mise a la terre	Schutz -Erdun
	On (Supply)	Marche (alimentation)	Ein
	Off (Supply)	Arret (alimentation)	Aus
	Caution-Attention: Risk of Electrical Shock	Attention Risque de choc	Vorsicht Spannug Gefahrliche
	Caution (refer to accompanying documents)	Attention: Voir les documents cijoints	Vorsicht Siehe Begleitinformation
	Serial Out	Sortie serie	Serieller Ausgang
	Printer	Imprimante	Drucker
	Monitor	Moniteur	Bildschirm
	Fuse Label 1 Current Warning	Etiquette d'advertissement relatif au type et au courant du fusible	Sicherung/Stromstarke

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Chapter 1

Specifications

All instrument specifications are developed using sources whose activity is referenced to NIST source activity and PerkinElmer Life and Analytical Sciences reference methods.

System Control

The system is controlled by an IBM-compatible Pentium computer. The standard computer is configured with one floppy disk drive, a CD-drive and one hard drive. The computer contains a serial RS-232 communications port, a parallel printer port, and a graphics adapter for the color monitor. All RS-232 communication occurs through communications port one. Communications port two is used for proprietary purposes and cannot be used in conjunction with any peripheral devices.

Note: The system can be attached to a network using an Ethernet Adapter kit option. For further information on this kit, contact your PerkinElmer representative.

Energy Range

This table represents the preset regions for the following nuclides:

Preset Regions (keV)	
Tritium	0-18.6
Carbon-14	0-156
Phosphorus-32	5-1700
Iodine-125	0-70

Figure 1-1 Energy Range

You can define preset regions for any nuclide in the Sample Nuclides Library.

Efficiency

For Tritium in the range 0-18.6 keV, the minimum acceptable efficiency is 60% (58% for 3170TR/SL). For Carbon-14 in the range 0-156keV, the minimum acceptable efficiency is 95% (94% for 3170TR/SL). These values were generated by PerkinElmer Life and Analytical Sciences at our Downers Grove, Illinois facility. The exact values obtained at other instrument locations may vary. Counting Efficiency is a parameter measured as part of Instrument Performance Assessment (IPA). IPA is an option on the TriCarb® 2800TR and 2900TR.

Chi-Square

Chi-Square acceptable range: 7.63 to 36.19, performed as 20, 0.5 minute repeat counts and tested at the 99% confidence limits. Chi-Square is a parameter measured as part of Instrument Performance Assessment (IPA). IPA is an option on the Tri-Carb 2900TR

Physical Dimensions

The following table displays the physical dimensions of all TriCarb models:

Parameter	Size
Height	19" (48cm)
Width	40.6" (103cm)
Depth	32.36" (82cm)
Weight, with refrigeration	515lbs (234kg)
Weight, without refrigeration	470bs (214kg)

Figure 1-2 Physical Dimensions

Detectors

Two diametrically opposed high performance photomultiplier tubes (PMTs) are coupled to a light-tight, reflective optical chamber. The detectors are located below the sample changer at the rear of the instrument.

Environmental Requirements

The recommended operating ambient temperatures are 59°F to 95°F (15°C to 35°C).

The recommended operating relative humidity is 30% to 85% non-condensing humidity (the system is for indoor use only).

The Pollution Category is number two.

The instrument should be located away from all sources of radiation (X-ray equipment, radiation storage vaults, etc.). The instrument should be positioned such that direct sunlight or unscreened fluorescent light will not enter the sample changer. Direct light may affect the optical sensors within the sample changer, causing erratic operation. Direct light may also induce fluorescence within your samples, causing erratic results.

The system must be connected to a stable power source, through the use of proper plugs and good earth grounding. The system provides automatic recovery after a power failure. Power to the temperature control unit should not be supplied through a power strip.

Varisette™ Sample Changer (optional on 2800TR, 2900TR)

The sample changer automatically moves the samples into position and loads them down into the detector for counting. After the count is completed, the sample is automatically unloaded and the next sample is loaded.

The sample changer typically moves the cassettes in a forward (counterclockwise) direction using a pair of synchronously driven transport belts. If necessary, these belts can run in the reverse (clockwise) direction (such as during recovery from a power failure).

The instrument can hold up to:

- 408 large vials
- 720 small vials
- 720 4ml vials

Electrical Requirements

The following table represents the electrical requirements for all Tricarb models.

	Instrument		Refrigeration Unit	
	60Hz	50Hz	60Hz	50Hz
Voltage (VAC)	100-130	200-240	117	240
Amperage (Amps)	2.5	1.8	2.5	1.5
	Overpollution Category I Pollution Degree 2			
Fuse (Amps)	4.0 (type S) (5 x 20mm)	2.5 (type T) (5 x 20mm)	Circuit Breaker	Circuit Breaker
Wattage (Watts)	500	500	500	500

Figure 1-3 Electrical Requirements

External Standard

^{133}Ba, nominal less than 20µCi (for all models except the TriCarb 3170TR/SL).

^{133}Ba, nominal less than 1µCi (for the TriCarb 3170TR/SL).

Observed Background

Average values for Normal Count Mode:

Tritium:17.3 CPM

Carbon-14:24.3 CPM

These values were generated by PerkinElmer Life and Analytical Sciences at our Downers Grove, Illinois facility. The exact values obtained at other instrument locations may vary.

Sample Cassettes

Cassettes are the plastic racks which hold sample vials and allow them to be moved on the sample changer deck. Samples are placed into cassettes that accommodate either standard or small vials without adapters (4ml vials require cassettes with adapters). The standard vial cassette can accommodate up to 12, 15-20ml vials and the mini-vial cassettes up to 18, 6-7ml mini-vials. A protocol flag, which you attach to the cassette, identifies the protocol and assay conditions that you have defined for use with your samples. The individual cassettes are identified by unique numbers (cassette IDs) located at the end of each cassette. The protocol flag and cassette ID are automatically read by the instrument to provide Positive Sample Identification (PID) when using Worklists.

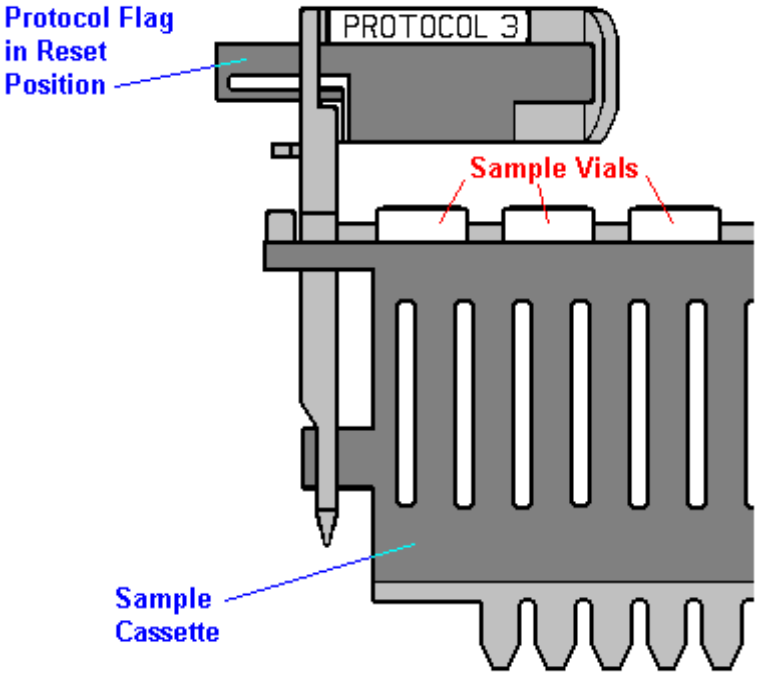

Figure 1-4 Sample Cassette

Shielding

The detector assembly is surrounded by a minimum of 2 inches of lead.

Sample Vials

Vials and caps must conform to the following sizes. Caps must not exceed the diameter of the vial.

Large Vials	Minimum	Maximum
Vial Height:	58.4mm	63.0mm
Vial Diameter:	26.0mm	28.1mm
Cap Diameter:	22.0mm	≤ vial diameter
Small Vials	**Minimum**	**Maximum**
Vial Height:	53.0mm	58.0mm
Vial Diameter:	14.5mm	17.8mm
Cap Diameter:	13.0mm	≤ vial diameter
4ml Vials	**Minimum**	**Maximum**
Vial Height:	53.0mm	58.0mm
Vial Diameter:	12.7mm	14.5mm
Cap Diameter:	12.0mm	≤ vial diameter

Figure 1-5 Vial Sizes

Chapter 2

How To...

This chapter presents a quick overview of common tasks performed with the QuantaSmart™ software.

How to Get Started

When you are ready to begin a counting procedure, you will need to perform the following tasks:

1. Calibrate and Normalize the instrument.
2. Select an assay type: Alpha Beta, Alpha Beta Standards, CPM Assay, DPM Single, DPM Dual, DPM Triple, FS DPM, Direct DPM, Quench Standards, Single Photon Counting. Note: DPM Dual is optional on 2800 series instruments. DPM Triple is optional on 2800 and 2900 series instruments.
3. For any DPM assay except Direct DPM, create quench data.
4. Define and save the new assay parameters.
5. Associate (link) the assay parameters to a protocol.
6. Attach the correct protocol flag to the first cassette to be counted and load the cassette(s) with samples.
7. Begin sample counting. Do not use the system's CD writer while the instrument is counting.

How to Perform the SNC (Self-Normalization and Calibration)

SNC for an Instrument without Super Low Level Counting Ability

1. Define the IPA parameters in the IPA Definition window.

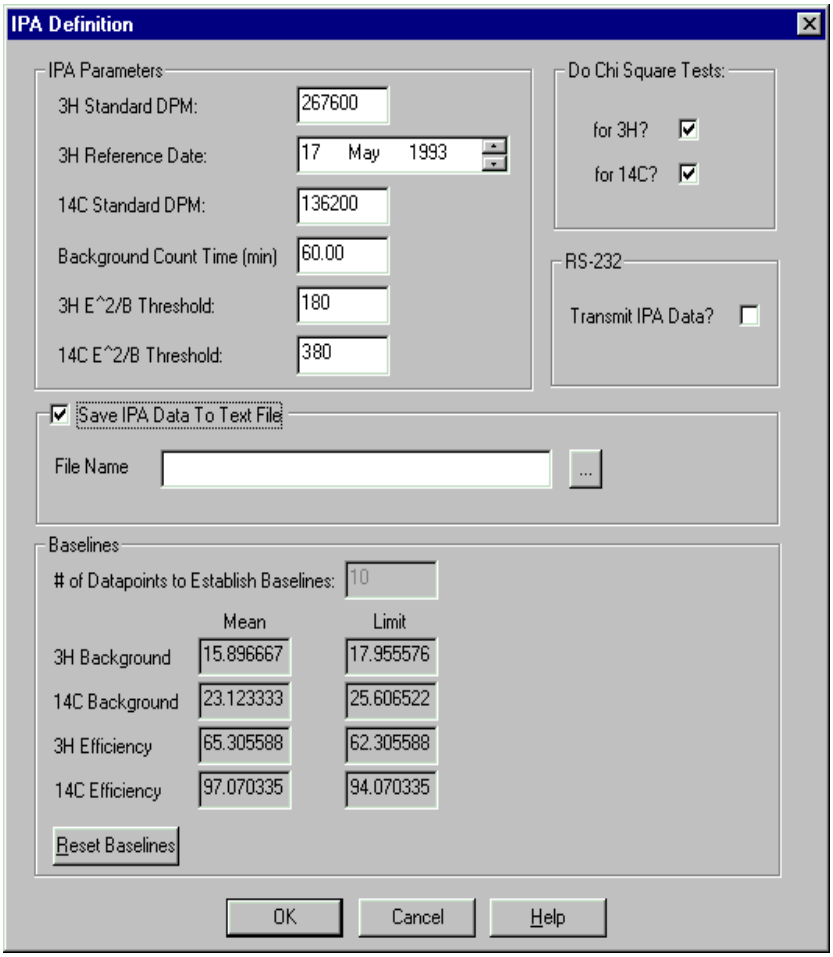

Figure 2-1 IPA Definition Window.

2. Reset the SNC protocol flag to the reset position (the flag is all the way to the left when the plug is on the left end of the cassette).
3. Load the purged, unquenched Carbon-14 standard into the first position of the cassette (this is at the same end as the protocol plug).

Caution: Do not use the unpurged, Low Level standards to calibrate the instrument, even if the instrument is to be used in Low Level, High Sensitivity or Super Low Level count mode.

4. Load the purged, unquenched Tritium standard into the second cassette position.
5. Load the purged background standard into the third cassette position.
6. Load the instrument with cassettes.
7. Press the  green flag start button to begin counting. Do not use the system's CD writer while the instrument is counting.

SNC for an Instrument with Super Low Level Counting Ability (with BGO Detector Guard)

1. Define the IPA parameters in the IPA Definition window.
2. Reset the SNC protocol flag to the reset position (the flag is all the way to the left when the plug is on the left end of the cassette).
3. Load the purged, unquenched Carbon-14 standard into the first position of the cassette (this is at the same end as the protocol flag).
4. Load an empty vial into the second cassette position.
5. Load the purged, unquenched Tritium standard into the third cassette position.
6. Load the purged background standard into the fourth cassette position.
7. Load the instrument with cassettes.
8. Press the  green flag start button to begin counting. Do not use the system's CD writer while the instrument is counting.

Steps in Performing an Assay

1. Select the File-Open Assay menu option. The Open Assay window is displayed.

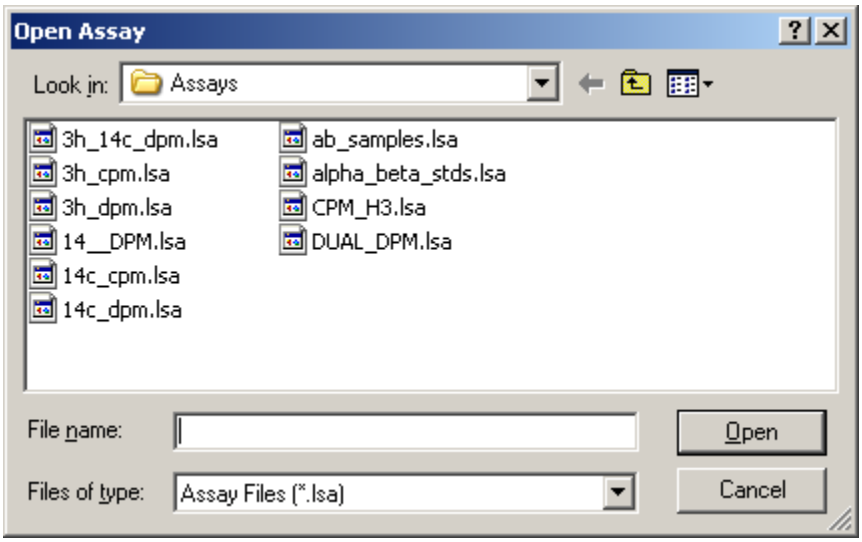

Figure 2-2 Open Assay Window.

2. In the Open Assay window, select the assay for which you would like to create a password. Click the Open button. The Assay Definition window is displayed.

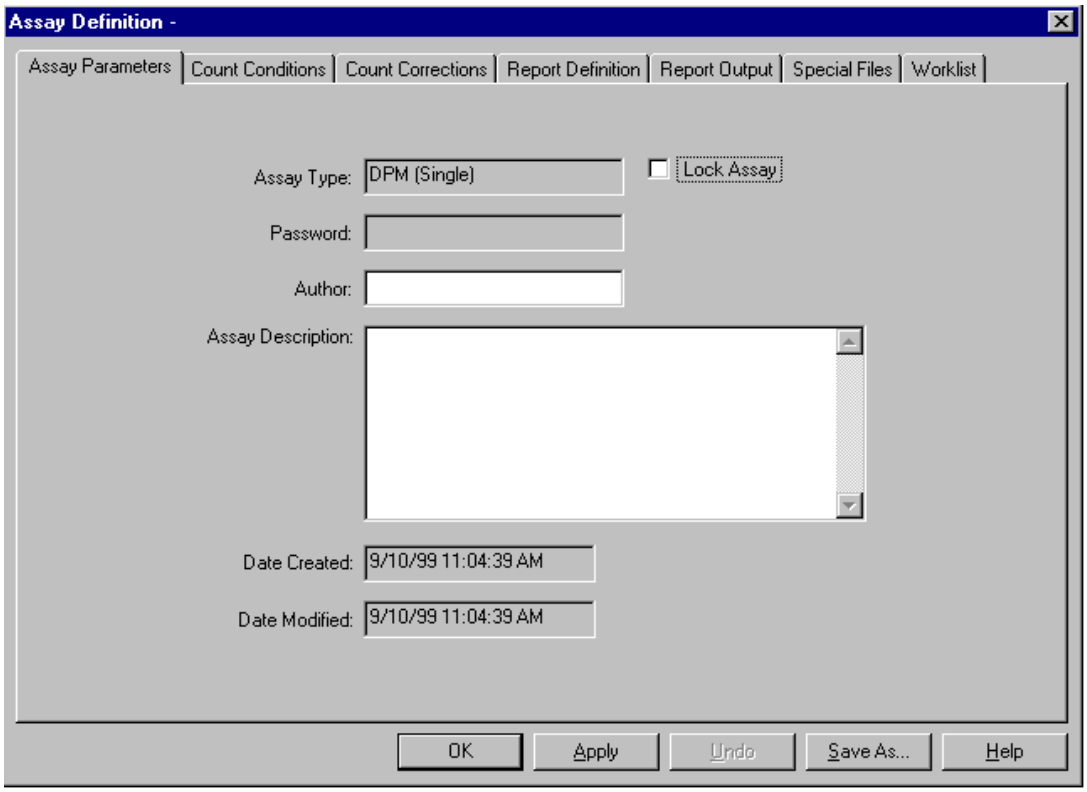

Figure 2-3 Assay Definition Window.

3. In the Assay Parameters tab, mark the Lock Assay box. The Password field becomes enabled.
4. Enter a descriptive password in the Password field.
5. When you have finished editing, save the assay. The password must be used to edit the assay after it is saved.
6. In the Sample Nuclides Library, define an appropriate nuclide for the assay, if one does not already exist.

How to Perform an Assay

1. Select the File-New Assay menu option.
2. Select an assay type in the Select Assay Type window.

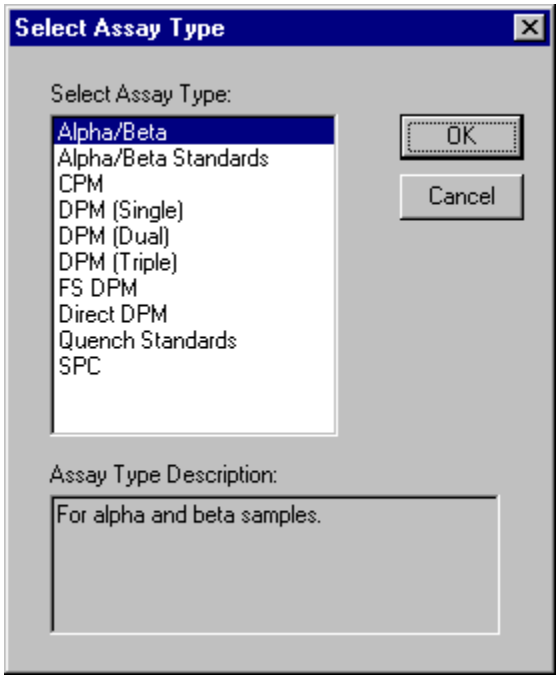

Figure 2-4 Select Assay Type Window.

3. In each of the seven tabs of the Assay Definition window, define the individual assay parameters, as needed.
4. Save the assay using a descriptive name.
5. In the Protocols Tree of the main window, select the protocol to which you would like to associate an assay.
6. Right click on that protocol flag number.
7. From the menu that is displayed, select Associate Assay. The Associate Assay window is displayed.

Note: You can also associate an assay to a flag using the File menu.

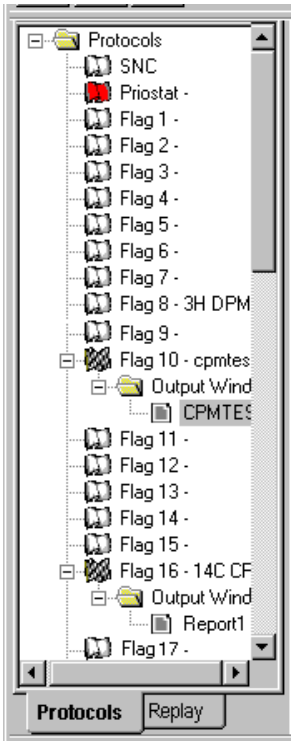

Figure 2-5 Protocol Tree.

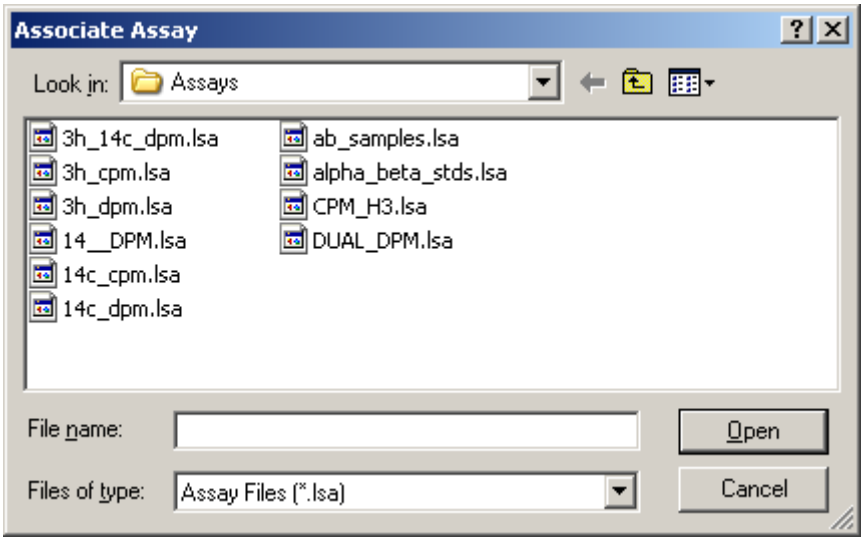

Figure 2-6 Associate Assay Window.

8. Select the Assay that you would like to associate to a protocol flag number. Click the Open button. The Data Paths window is displayed.

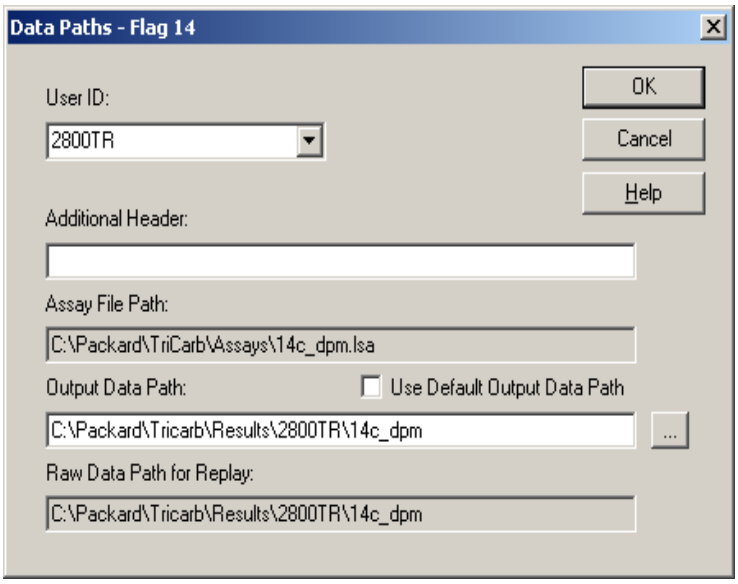

Figure 2-7 Data Paths Window.

9. In the Data Paths window, enter a User ID for the assay.
10. Enter an Additional Header, if necessary.
11. Enter an Output Data Path, if you would like the data to be saved in a directory other than the default.

In the following example, the default path is:
C:\Packard\TriCarb\Results\2800TR\14c_cpm

12. Attach the appropriate protocol flag in reset position.
13. Load the cassette(s) with samples.
14. Load the instrument with cassettes.
15. Press the  (green start flag) button to begin counting. Do not use the system's CD writer while the instrument is counting.

How to Create a Password

1. Select the File-New Assay menu option. The Select Assay Type window is displayed.

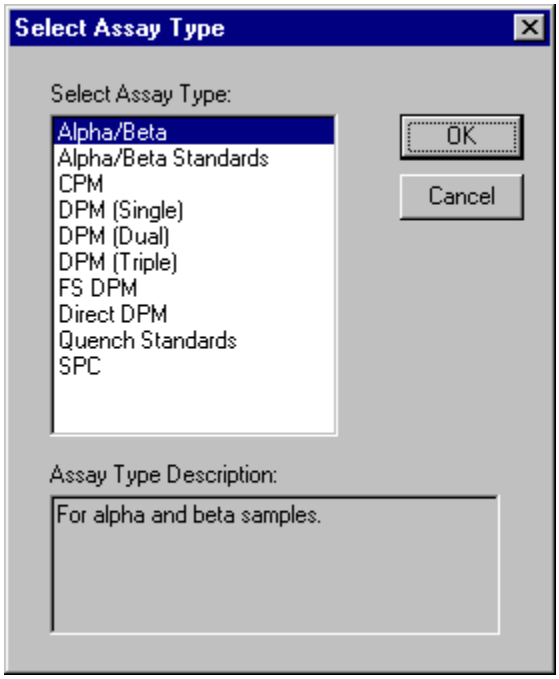

Figure 2-8 Select Assay Type Window.

2. In the Select Assay Type window, select the type of assay you would like to

create. The Assay Definition window is displayed.

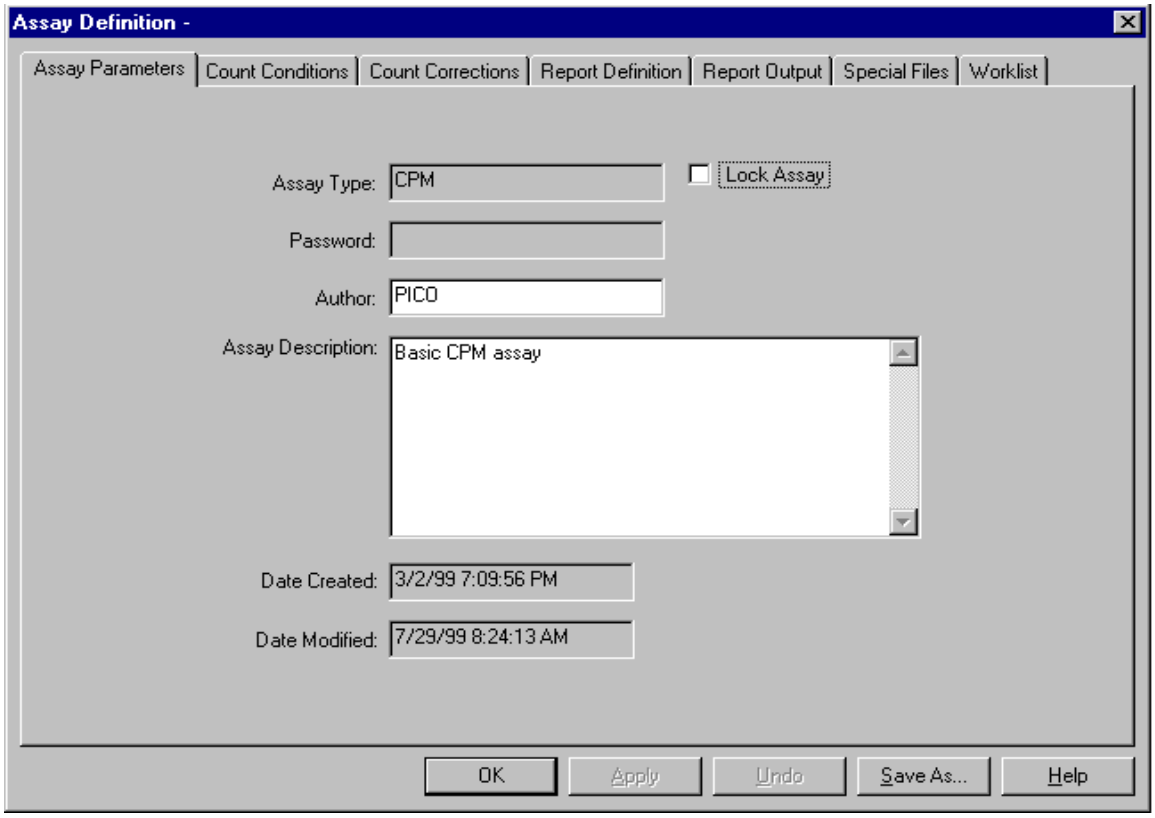

Figure 2-9 Assay Definition Window.

3. In the Assay Parameters tab, mark the Lock Assay box. The Password field becomes enabled.
4. Enter a descriptive password in the Password field.
5. When you have completed the assay definition process, save the assay. The password must be used to edit the assay after it is saved.

How to Associate an Assay to a Protocol

1. Select the protocol to which you would like to associate an assay.

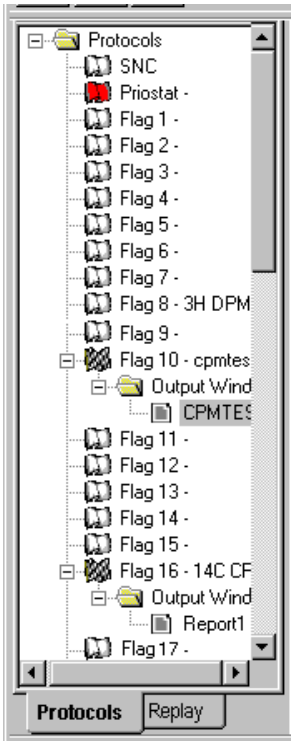

Figure 2-10 Protocol Tree.

2. Right click on that protocol flag number.
3. From the menu that is displayed, select Associate Assay. The Associate Assay window is displayed.
4. Select the Assay that you would like to associate to a protocol flag number. Click the Open button. The Data Paths window is displayed.
5. In the Data Paths window, enter a User ID for the assay.
6. Enter an Additional Header, if necessary.

7. Enter an Output Data Path, if you are generating either an RTF or Delimited Text file for the assay and would like the data to be saved in a directory other than the default. Check the Use Default Output Data Path box if you would like the data to be saved in the default directory.

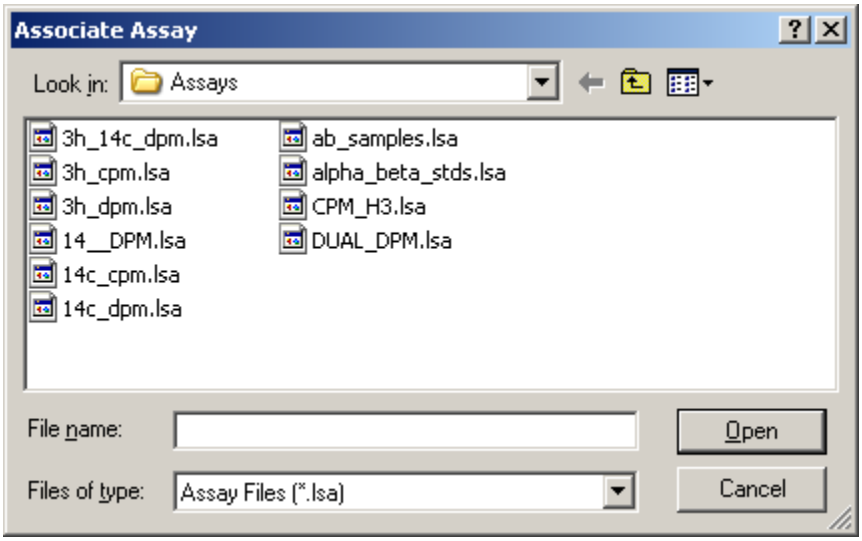

Figure 2-11 Associate Assay Window.

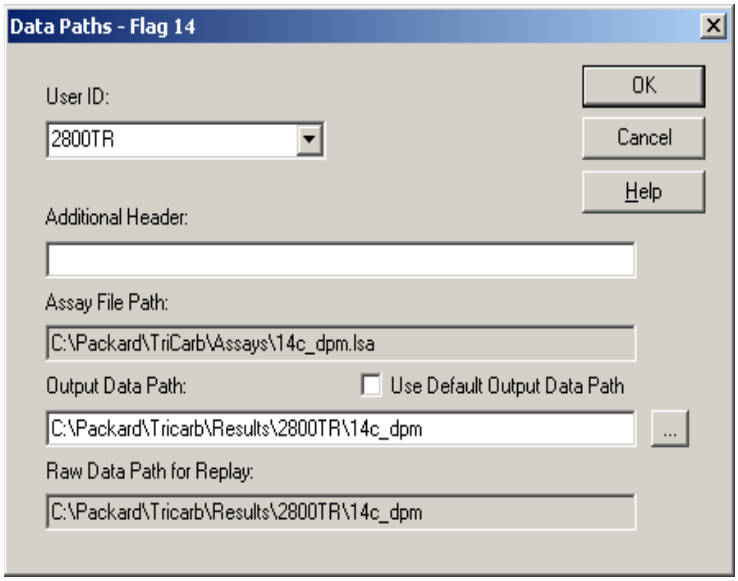

Figure 2-12 Data Paths Window.

How to Count Samples

1. Attach the protocol flag with the number matching the protocol flag to which you have associated the assay.
2. Reset the protocol flag by moving the plastic arm all the way to the left. The flag is all the way to the left when the flag is on the left end of the cassette.

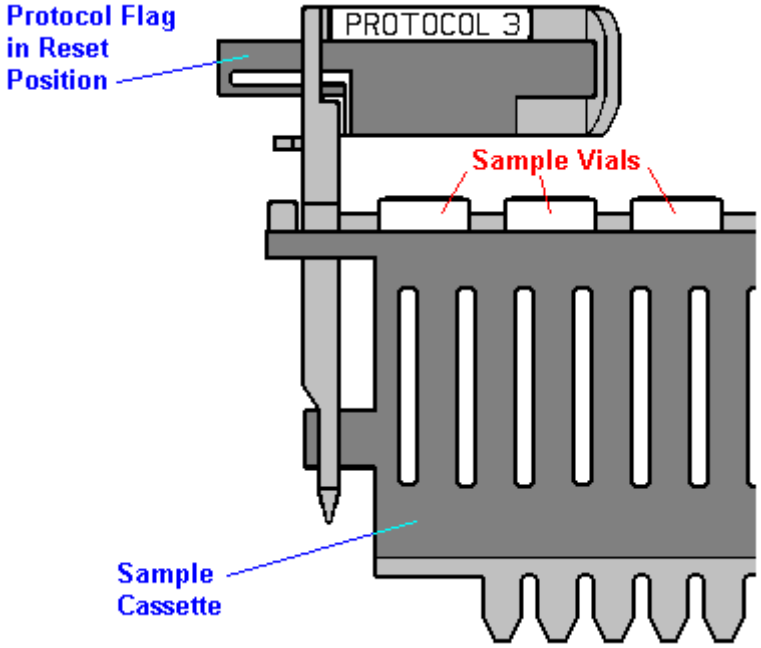

Figure 2-13 Cassette.

3. Place all of the background, reference and sample vials into the appropriate cassette positions.
4. Place the cassette(s) in the sample changer deck so that the protocol number on the flag is facing you. The cassette should be positioned on the right side along the far wall of the sample changer deck or after the last set of cassettes already on the sample changer deck if the machine is in use.
5. Press the  button to begin counting. **Note**: Do not use the system's CD writer while the instrument is counting.

How to Disassociate an Assay from a Protocol

1. In the Protocols Tree of the main window, select the assay you would like to disassociate from a protocol number.

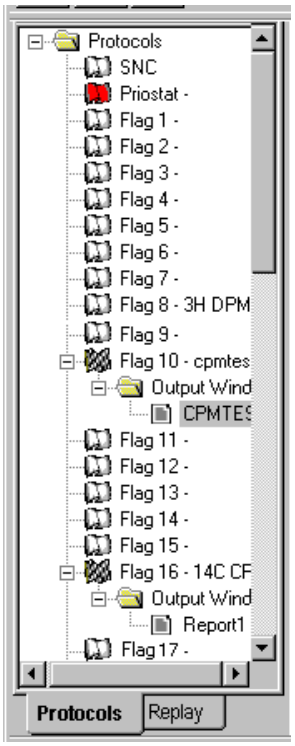

Figure 2-14 Protocol Tree.

2. Right click on that assay.

Note: You can also disassociate an assay from a flag using the File menu.

3. From the menu that is displayed, select Disassociate Assay.

How to Edit an Assay

1. Select the File-Open Assay menu option. The Open Assay window is displayed.

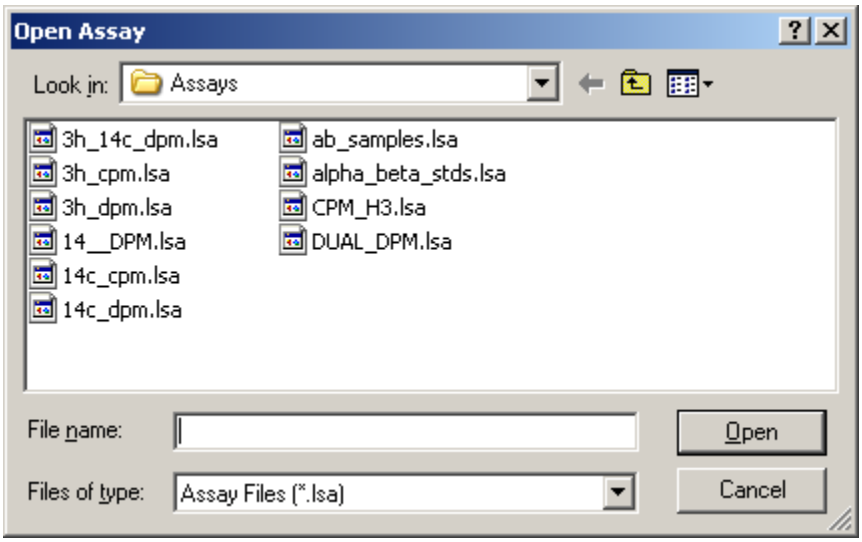

Figure 2-15 Open Assay Window.

2. In the Open Assay window, select the assay you would like to edit. Click the Open button. The Assay Definition window is displayed.

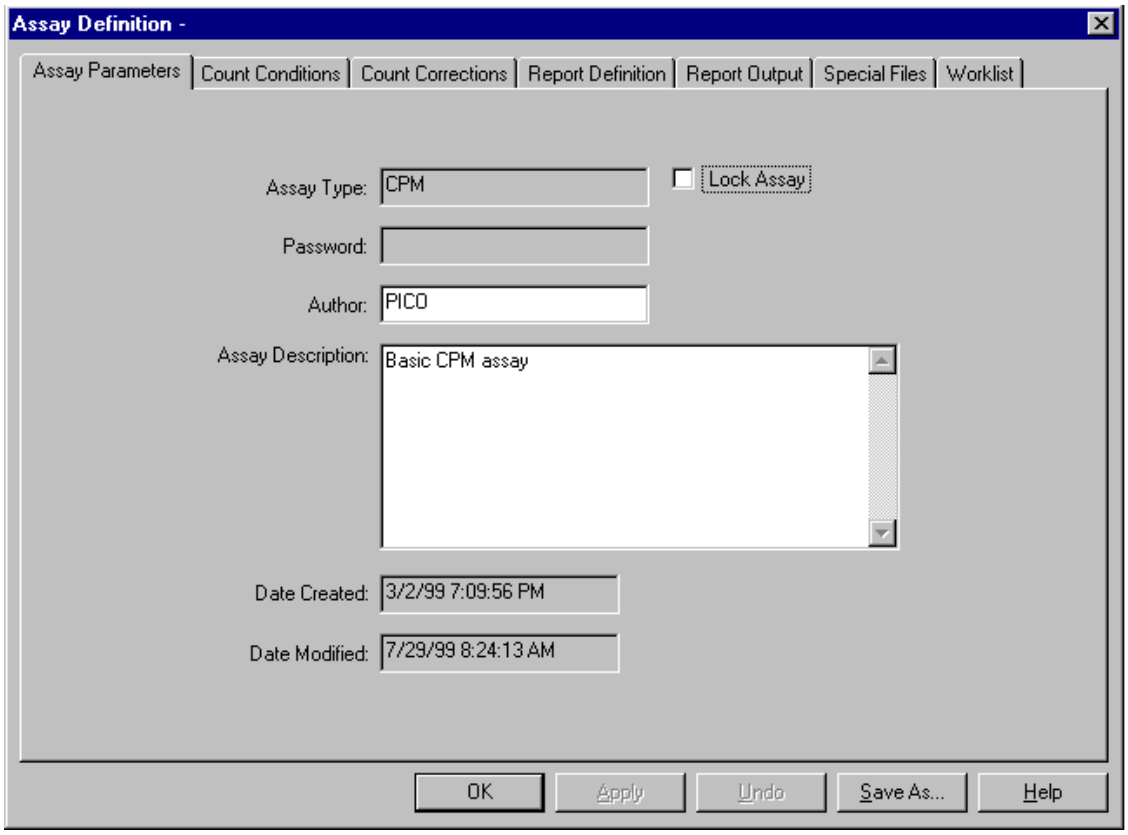

Figure 2-16 Assay Definition Window.

3. In each of the seven tabs of the Assay Definition window, change the assay parameters, as needed.
4. If you would like to save the assay with the same name, click the OK button.
5. If you would like to save the assay using a different name, click the Save As button. The Save As window is displayed.
6. Enter an appropriate name for the assay and click the Save button.

How to Print an Assay

1. Select the File-Print Assays Main menu option. The Select Assays to Print window is displayed.

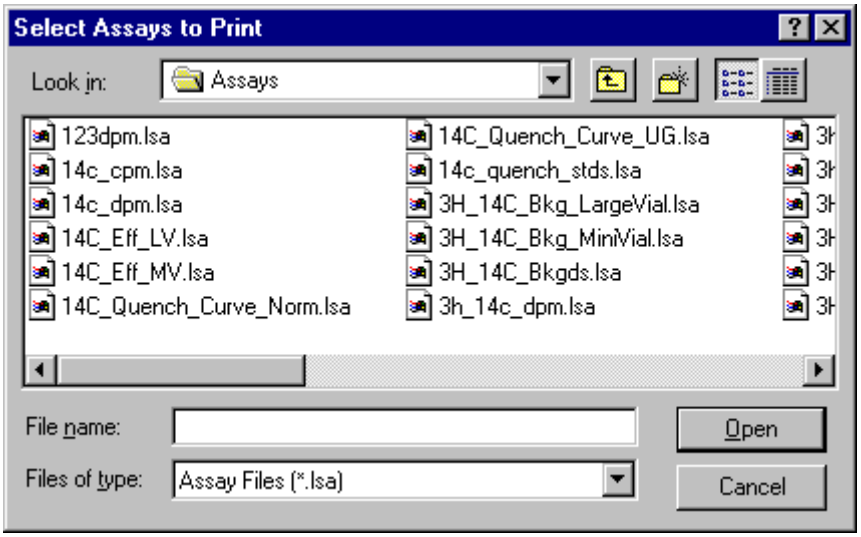

Figure 2-17 Select Assays to Print Window.

2. Select the assay you would like to print and click the Open button. The Print window is displayed.
3. In the print window, select the appropriate print parameters and click the OK button. A list of the Assay Parameters, Count Conditions, Count Corrections and Reports defined for the assay will print.

How to Manually Print a Report

1. In the Protocols Tree of the main window, select the report icon ( ) that you would like to print. The Output window is displayed.
2. In the Output window, select the print icon( ). The report of interest will print once the icon is selected.

How to Link a Quench Set to a Sample Nuclide

Note:Refer to page 26 on how to set up a quench set standards assay. This requires the single/dual/color DPM option on the 2800TR.

1. Select the Libraries-Sample Nuclides Main menu item. The Sample Nuclides window is displayed.

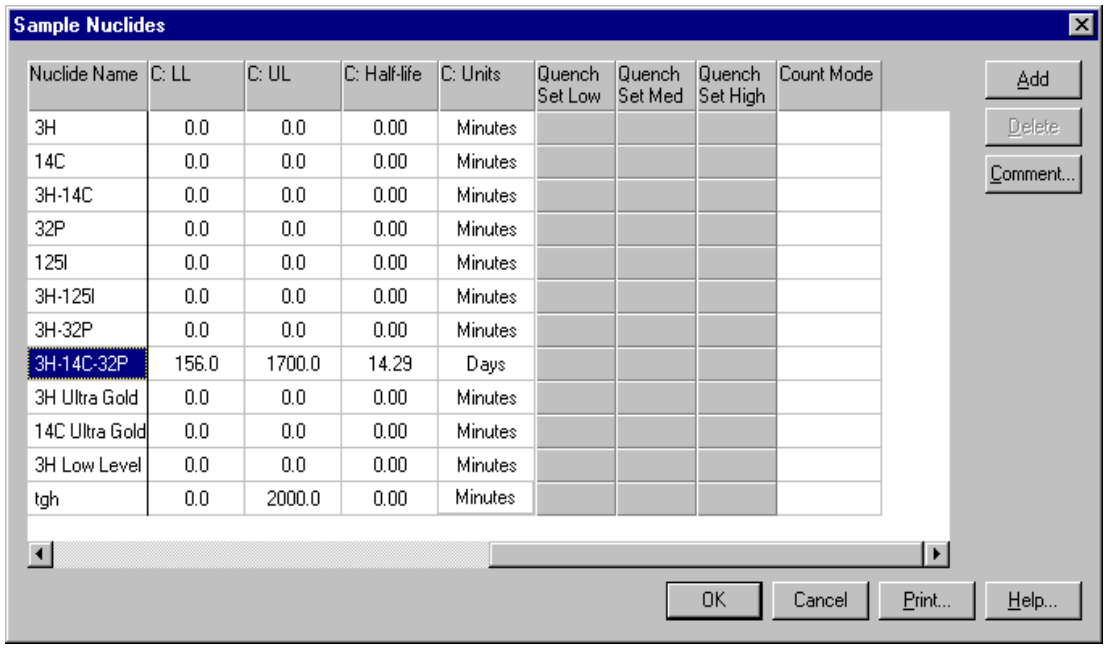

Figure 2-18 Sample Nuclides Window.

2. Click one of the Quench Set buttons. The Quench Standards window is displayed.

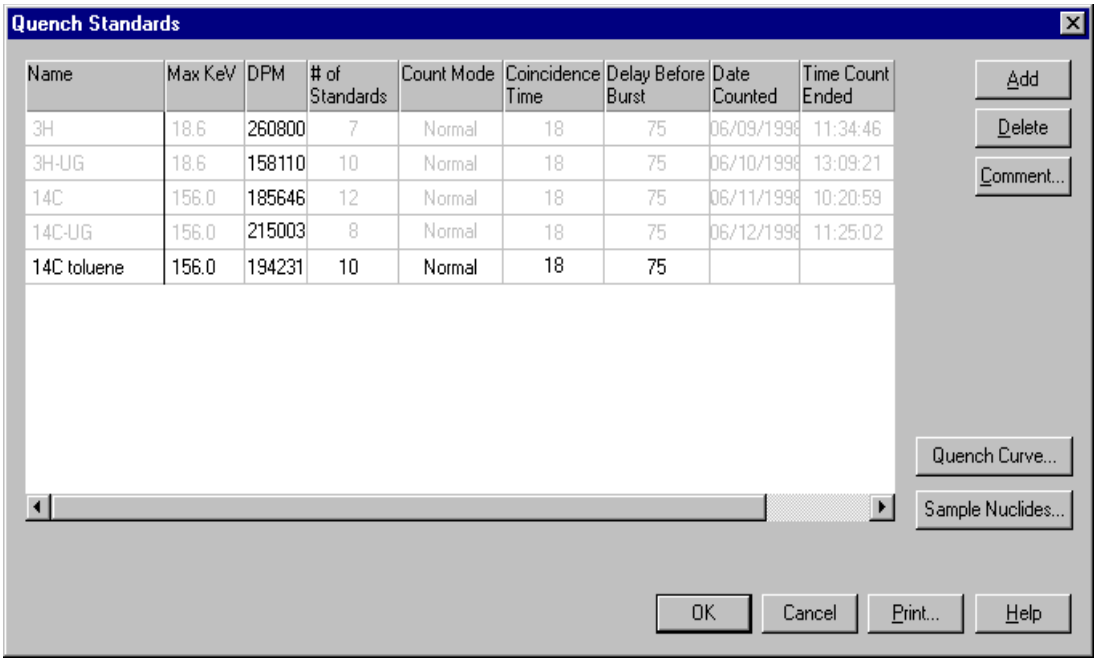

Figure 2-19 Quench Standards Window.

3. Select the Quench Set Low if you are counting one nuclide in one counting region, the Quench Set Medium if you are counting a second radionuclide in a separate region and the Quench Set High if you are counting a third radionuclide in a third region.
4. Select the name of the quench set you would like to link to the sample nuclide.
5. Click OK. The name of the quench set(s) you selected should appear in the Sample Nuclides Library window on the Quench Set buttons.

How To Set Up a Quench Standards Assay

The following tasks are required when performing a Quench Standards Assay. This requires the single/dual/color DPM option on the 2800TR.

1. Calibrate the instrument, if necessary.
2. Create a new assay, choosing Quench Standards as the assay type and define the new assay parameters.

   Or

   Open an existing Quench Standards Assay and edit or review if necessary.
3. Save the assay in the Assays folder of the Packard\TriCarb directory.
4. Associate (link) the assay parameters with a protocol and attach the corresponding protocol flag to the first cassette to be counted.
5. Load the cassette(s) with vials and load the instrument with cassettes.
6. Start the instrument.

Note:When using the Low Level count mode (if available), you must NOT use quench standards which have been purged free of oxygen with an inert gas. The oxygen quenching in unpurged standards facilitates discrimination between background and true beta events. Unpurged standards are available from PerkinElmer Life and Analytical Sciences.

How To Run an Alpha Beta Assay not available on the 2800TR; optional on the 2900TR and 3100TR series

The following tasks are required when performing an Alpha Beta Assay.

1. Calibrate the Instrument, if necessary.
2. Define and run an Alpha Beta Standards Assay (page 28), if necessary, to establish the optimal pulse decay discriminator value.
3. Define an alpha beta nuclide in the Alpha Beta Nuclide Library. Choose the Standards Set from the Alpha Beta Standards Library to use the discriminator setting from the Standard Set.
4. Create a new assay by choosing Alpha Beta as the assay type. On the Count Conditions tab, select the desired alpha beta radionuclide name from the Alpha Beta Nuclide Library. Define the remaining new assay parameters.

   Or

   Open an existing assay and edit or review if necessary.
5. Save the assay in the Assays folder of the Packard\TriCarb directory.
6. Associate (link) the assay parameters with a protocol number in the protocol tree and attach the corresponding protocol clip to the first cassette to be counted.
7. Load the cassette(s) with vials and load the instrument with cassettes.
8. Click the green start button at the top of the main window.
9. Start the instrument.

How To Run an Alpha Beta Standards Assay not available on the 2800TR; optional on the 2900TR and 3100TR series

The following tasks are required to run the Alpha Beta Standards Assay. Two standards are required, a pure beta emitter and a pure alpha emitter.

1. Choose the Alpha Beta Standards selection from the Libraries menu.
2. Click the Add button and enter the name for a new Alpha Beta Standard Set.
3. Choose **Automatic** for the Discriminator Type if your pure alpha and pure beta standards have an activity of at least 50,000 CPM each. If the activity in either standard is less than 50,000 CPM, choose **Manual** as the Discriminator Type by clicking on it.
4. The remaining fields are for information only. They are either default values or values computed by the instrument.
5. Choose **File-New** and select Alpha Beta Standards as the assay choice from the drop down menu.

   OR

   Open an existing assay and edit or review if necessary.
6. Click the Name button on the Count Conditions Tab to choose from the list of Alpha Beta Standard names in the Alpha Beta Standards Library. Define the other available parameters as desired.

Note:High Sensitivity or Low Level Count mode are not available when counting Alpha Beta Standards, but will be available when counting samples in an Alpha Beta assay

7. When the assay definition is complete, name and save the assay.
8. Associate (link) the assay parameters with an available protocol flag in the protocol tree. Place the numbered protocol clip on a cassette.
9. Place the pure beta emitter standard in cassette position 1 and the pure alpha emitter standard in cassette position 2.
10. Load the cassette onto the instrument and click the green start button at the top of the main window.
11. After counting is complete, the misclassification (or spillover) curve and the optimum discriminator value will be stored for the Standard Set. Review the curve and discriminator setting, if desired, from the Alpha Beta Standards Library.

How to Use the Replay Feature (optional on TriCarb 2800, standard on 2900/3100 series)

1. In the main window, click on the Replay™ tab.
2. Select the results file that you would like to analyze. A listing of the results files is displayed in the Replay Tree using file names with the following syntax:

   User id | *assay_name* | yyyymmdd_militarytime
3. Right click on the selected file name.
4. Select Open for Replay. The Replay window is displayed.

Note:Use the View menu and select Refresh to verify that you have the latest view of the Replay files.

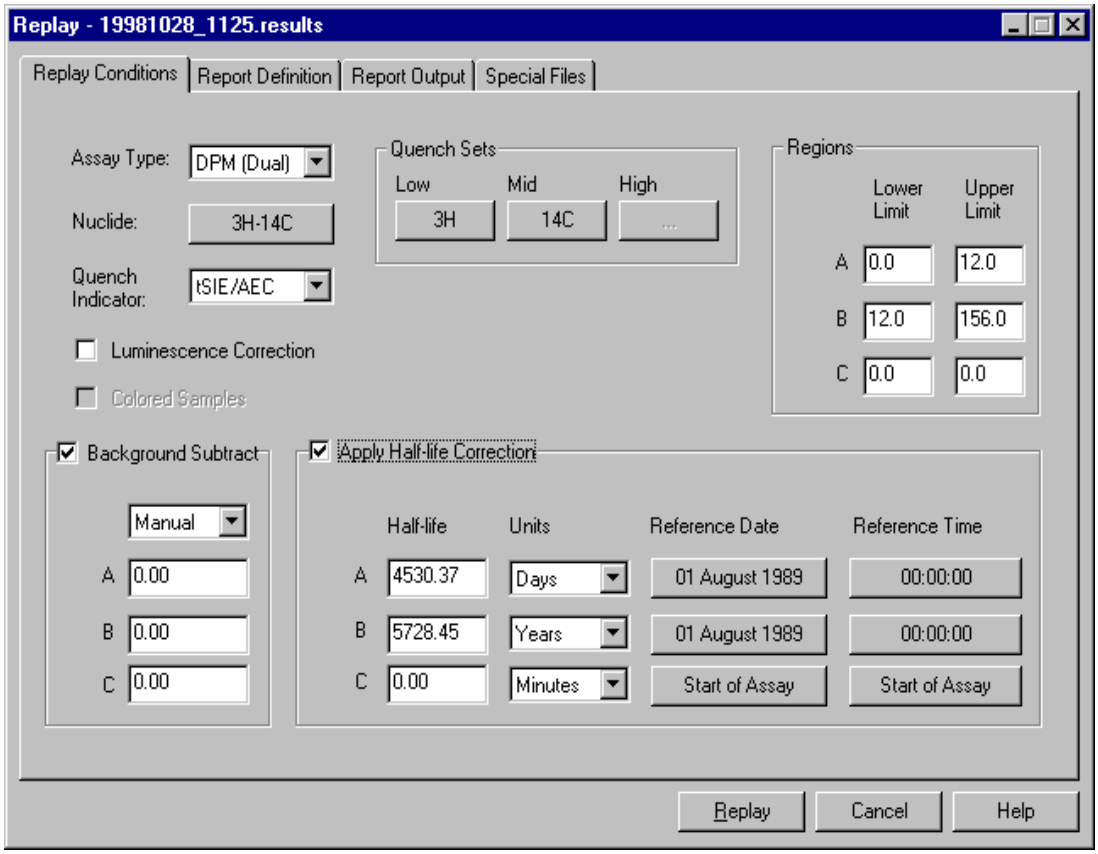

Figure 2-20 Replay Conditions Window.

5. In the Replay Conditions tab, define the parameters, as needed for reanalysis of sample data.
6. In the Report Definition tab, define any printed or electronic reports you would like to generate for the reanalysis of sample data.
7. Click the Replay button. Any reports that you defined are generated after the reanalysis of data occurs.

Note: Data processed with Replay does not change the original data. All Replay changes are temporary.

How to Calculate Radioactive Decay

1. Select the Tools-Nuclide Decay menu option. The Radionuclide Decay window is displayed.

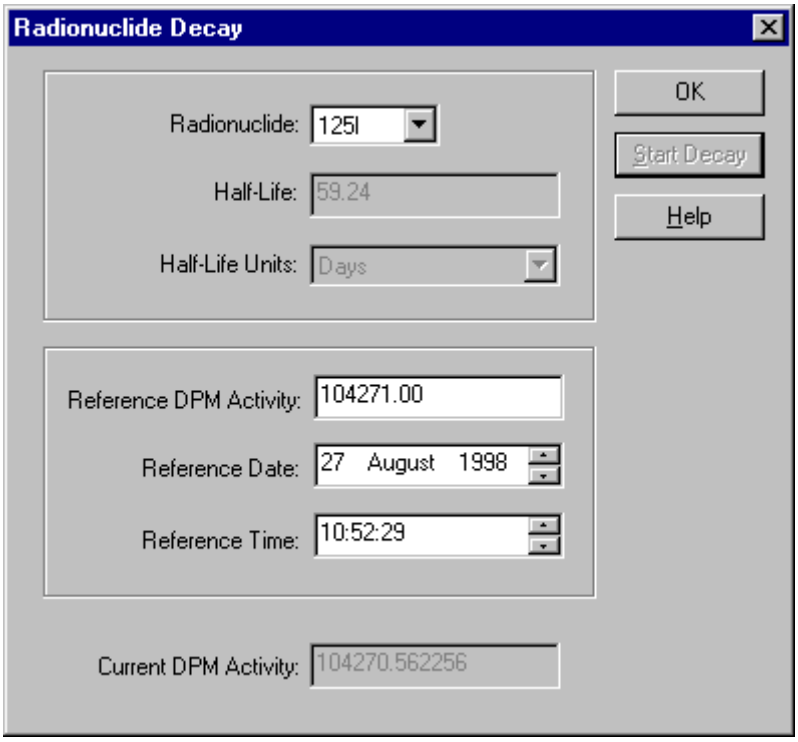

Figure 2-21 Radionuclide Decay Window.

2. From the drop-down list in the Nuclide field, select the nuclide of interest if it appears in the list; select manual if you would like to manually enter the nuclide half-life information.
3. Enter Reference Activity, Date and Time.
4. Click the Start Decay Button.
5. The current DPM for the nuclide is displayed in the Current DPM Activity field.

How to Change the Time and Date

Double click on the date and time on the task bar. The Date/Time Properties window will display. Use this window to change the date and time.

Note: If an error message displays stating that the user has insufficient rights to change the date and time, follow the procedure below.

1. On the Windows NT screen, go to **Start**, **Shutdown**, click on **Restart the computer?**, and then click on **Yes**.
2. When the Windows NT logo displays, press Shift steadily until the Logon Information window displays. Type *Administrator* in the **User:** field. Leave the **Password:** field blank. Click **OK**.

The system will start NT and you will be logged on as Administrator.

3. On the Windows NT screen, go to **Start**, **Programs**, **Administrative Tools (Common)**, and the click on **User Manager**.
4. Click on the **Policies** menu and select **User Rights**. The User Rights Policy window will display. In the **Right:** field, use the drop down list to select **Change the system time**. Click **Add...** The Add Users and Groups window displays. In the **Names:** field, select QuantaSmart User. Click **Add....** Click **OK.** Click **OK.**
5. Exit out of the User Manager program.
6. Go to **Start**, **Shutdown**, click on **Restart the computer?**. Click on **Yes**.
7. When the Windows NT logo displays, press Shift steadily until the Logon Information window displays. Type *QuantaSmart* in the **User:** field. Type *QS* (this is case sensitive) in the **Password:** field. Click **OK**.

Note: You can also access the Date/Time Properties window by going to **Start**, **Settings**, **Control Panel**, and then double clicking **Date/Time**.

Double click on the date and time on the task bar. The Date/Time Properties window will display. Use this window to change the date and time.

Chapter 3

The System Computer

The system is controlled by an IBM-compatible Pentium® computer. The standard computer is configured with one floppy disk drive, a CD-drive and one hard drive. The computer contains a serial RS-232 communications port, a parallel printer port, and a graphics adapter for the color monitor. All RS-232 communication occurs through communications port one. Communications port two is used for proprietary purposes and cannot be used in conjunction with any peripheral devices.

Attaching To A Network

The system can also be attached to a network. We sell a networking kit to attach the system to a network. For additional information on the networking kit, contact your PerkinElmer representative.

Chapter 4

The System Software

The QuantaSmart™ program is the Windows XP® interface for the TriCarb Liquid Scintillation Analyzer series of instruments. This innovative tool allows you to take advantage of all the instrument features via a main software window. The main window uses standard Windows® conventions and allows you to easily access and control all the system features and capabilities. It also provides you with graphical representations of existing assay associations in the Protocols Tree and data analyses in the Output Report and SpectraView windows. Any assay data that is collected may be reanalyzed, without recounting samples using the system's optional Replay feature.

The system utilizes a set of Libraries to store standard and sample information. For systems equipped with the single/dual label DPM feature, the Nuclide Library allows you the flexibility of selecting and using the same standards sets in any number of different assays. It also provides you with a convenient means of saving and reusing specific nuclide parameters and sample counting regions.

Software Security

Security is built-in to QuantaSmart. The same software cannot be loaded on multiple systems due to this security feature.

Main Window

The main software window is comprised of several functional elements which provides you with a means of accessing all instrument features.

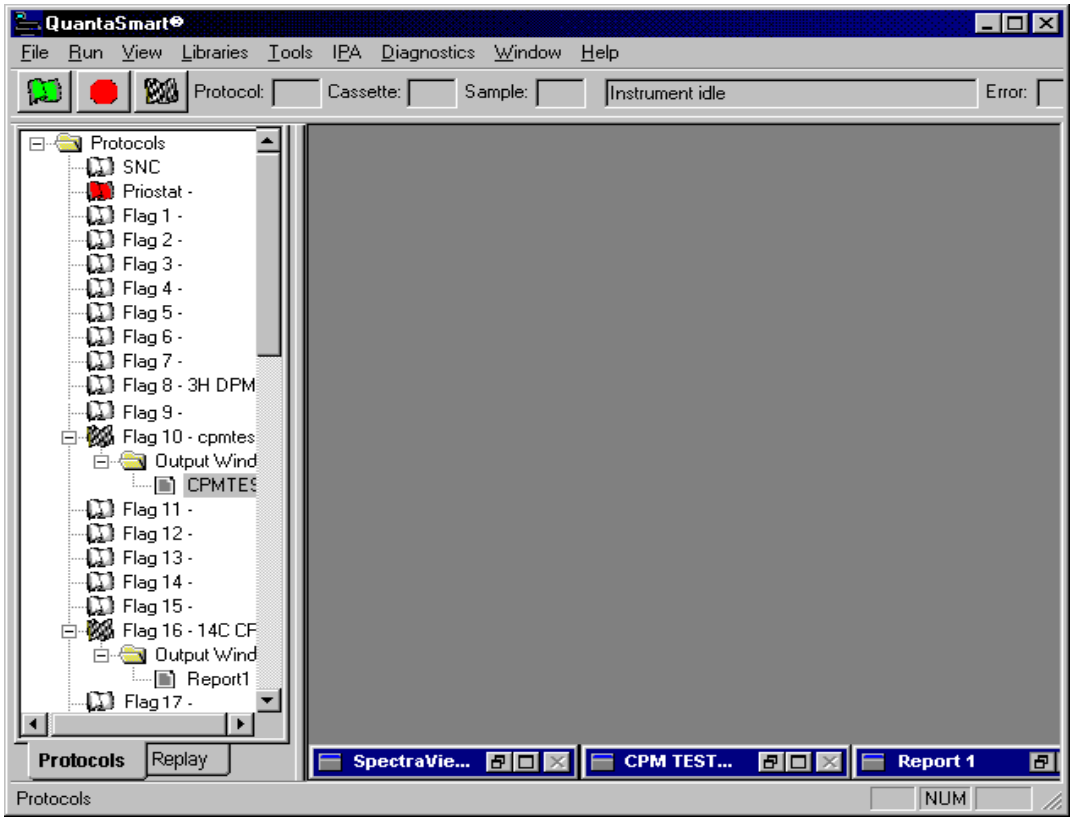

Figure 4-1 Main Window

Output Window

The Output Window is a multipurpose window which displays various data items and assay parameters. It is a copy of the printer report if one is selected. The output is defined in the Report Output window.

The following is a typical Output Window display:

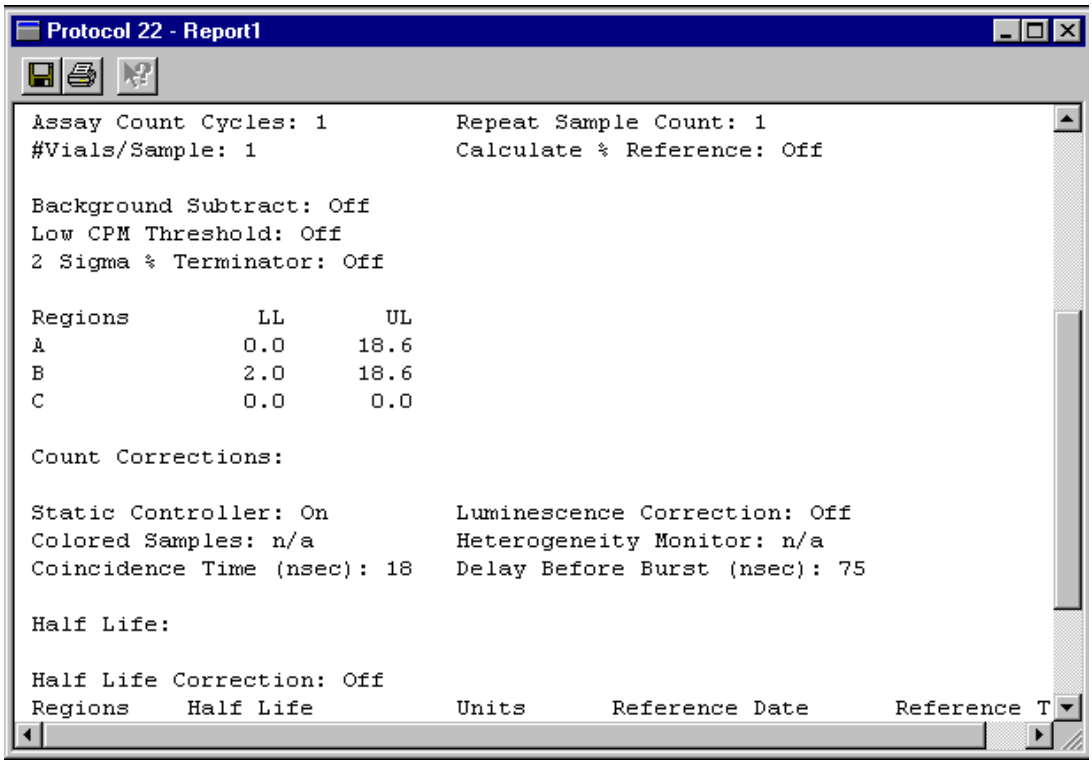

Figure 4-2 Output Window

The SpectraView Window

The SpectraView window is part of the main window. It displays a two-dimensional, real-time view of the spectrum for the current sample. The spectrum is updated every six seconds and can be displayed using either linear or logarithmic axes. It provides you with information about the status of a sample count and the region settings used in the counting procedure. A number of display options are available for the spectrum and are defined in this window.

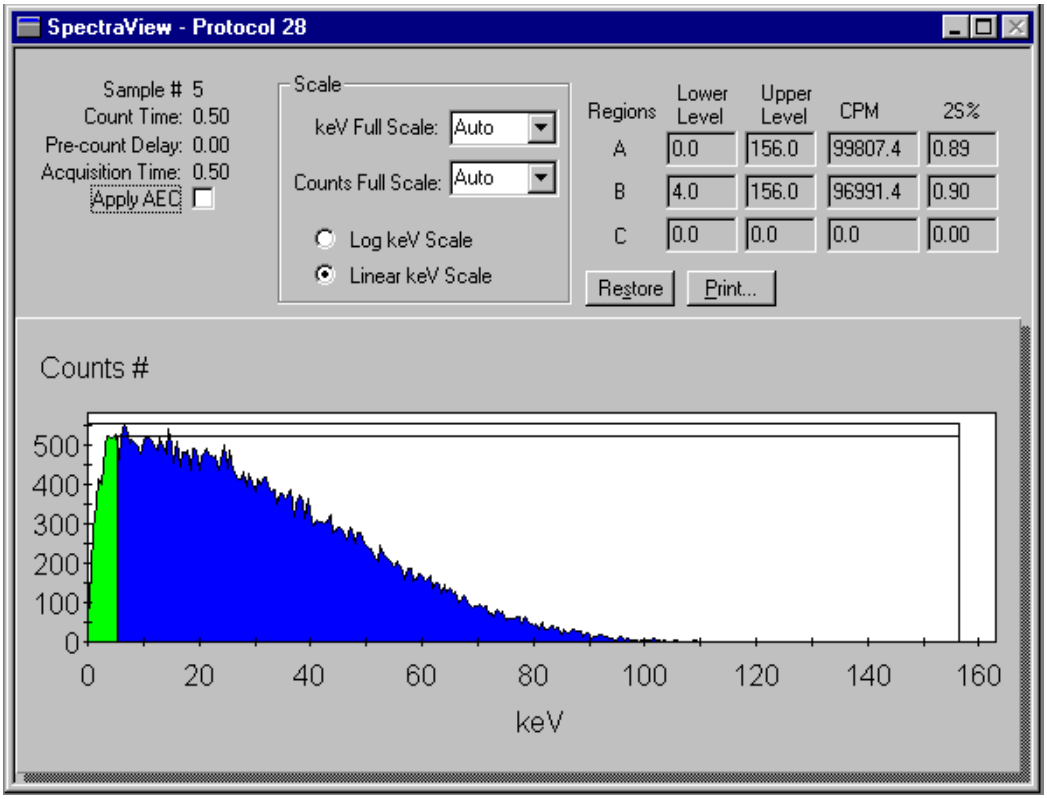

Figure 4-3 SpectraView Window

The SpectraView window is typically used for the following:

1. Monitoring sample counting.
2. Detecting spectral distortions or compressions resulting from sample quench.
3. Observing the effect of altering the counting region settings.
4. Viewing the spectrum in linear or logarithmic scale.

The Instrument Status Bar

The Instrument Status Bar contains a series of graphical buttons which allows you to Stop and Start the instrument and end a current protocol. It also provides you with information regarding the status of a current protocol and displays instrument messages.

Figure 4-4 Instrument Status Bar

The buttons in the Instrument Status Bar of the main software window allow you to start, stop and end a counting procedure.

Stop Button

Click this button to end the current protocol and stop the instrument.

Count Button

Click this button to begin a counting protocol.

End Protocol Button

Click this button to end a counting protocol and continue counting the next protocol.

The Protocols Tree

The Protocols Tree displays up to sixty available protocol flag numbers and the assay names that you have associated to flag numbers. Existing reports are also shown in this view. During protocol execution, this window uses different symbols to provide a visual indication of which protocol is being executed, which protocols have remaining cycles, and which protocols have been completed.

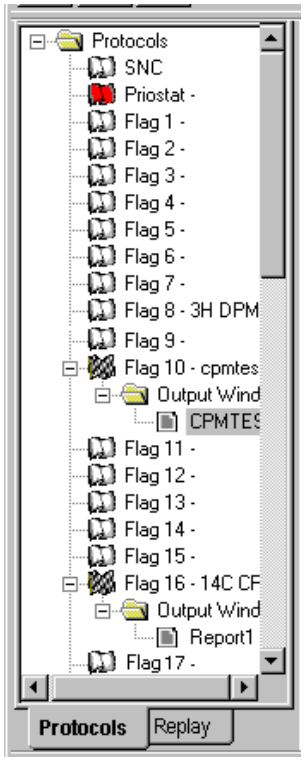

Figure 4-5 Protocol Tree

Symbols Used in the Protocols Tree

When a sample counting cycle begins, the protocol flag associated with this assay will change from white or yellow to green.

Figure 4-6 Protocol Tree Symbols

The Priostat flag is the only flag in the Protocols Tree that is normally red. It will turn from red to green when the Priostat protocol begins.

Figure 4-7 The Priostat Flag

A yellow flag in the Protocols Tree indicates that at least one count cycle for this assay has been completed but that the protocol has remaining count cycles. This yellow flag will also appear if you interrupt the protocol for a Priostat operation.

Figure 4-8 The Yellow Flag

A checkered flag is displayed when all the count cycles for the assay are completed.

Figure 4-9 The Checkered Flag

A red prohibitory symbol indicates that a protocol cannot be counted. Typically, this will result when no assay is associated with a protocol flag number that the instrument has detected. This symbol could also indicate that an assay file has been deleted.

Figure 4-10 The Red Prohibitory Symbol

A yellow prohibitory symbol indicates that data analysis cannot be performed. Typically, this will result when an appropriate standard set is missing from the

Nuclide Library, or it has been modified in the Library but not recounted after the changes were made.

Figure 4-11 The Yellow Prohibitory Symbol

The page symbol indicates that a report has been defined for this assay. The report name appears next to this symbol in the Protocols Tree.

Figure 4-12 The Page Symbol

A white flag indicates an inactive protocol. If no assay name appears adjacent to this flag, it is available to be associated to an assay.

Figure 4-13 The White Flag

The Replay Tree

Replay (optional on 2800; standard on 2900, 3100 and 3170) displays a directory of folders containing previously collected data which can be reanalyzed using different data reduction conditions, without recounting the samples.

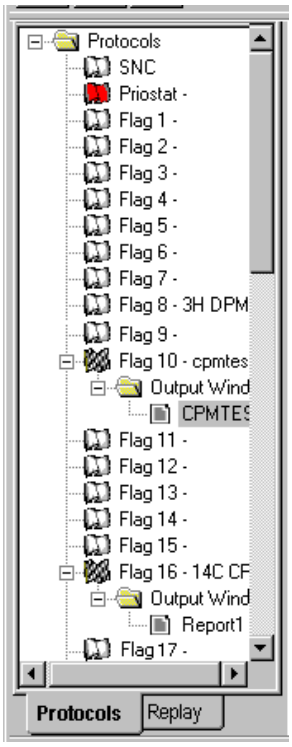

Figure 4-14 Replay Tree

Note: Clicking twice on the Results folder will bring up the Replay tree.

The Replay files have a fixed data storage path, but it can be changed in the Report Output window. The default filename is autoincrementing.

Menus

At the top of the QuantaSmart main window is the Menu Bar. The Menu Bar consists of the File, Run, View, Libraries, Tools, IPA, Diagnostics, Window and Help menus, each of which offers a variety of selections and commands. Make menu selections by using the mouse pointer to select a menu bar item. Click on an item to display a list of options within that menu. Note: Some menu items represent optional features. If your instrument is not equipped with the optional features, the corresponding menu items will be disabled.

Figure 4-15 Menu Bar

Individual menus can also be displayed by using the Alt-key in conjunction with the underlined character shown with each menu in the menu bar. Once a menu is displayed, you may display a menu item by pressing the underlined character key indicated. For example:

Use the Alt-T keys to display the Tools menu:

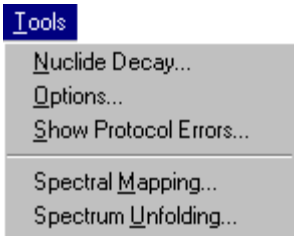

Figure 4-16 Tools menu

File Menu

Display the File menu by selecting File from the Menu Bar.

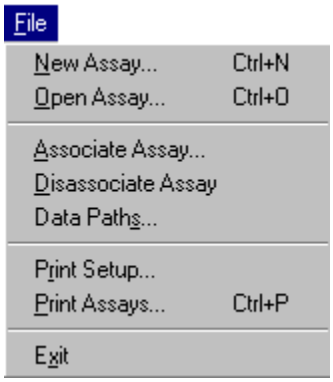

Figure 4-17 File Menu

New Assay

This menu item allows you to define a new assay.

Select Assay Type

Before defining the new assay, you must select an assay type in the Select Assay Type window.

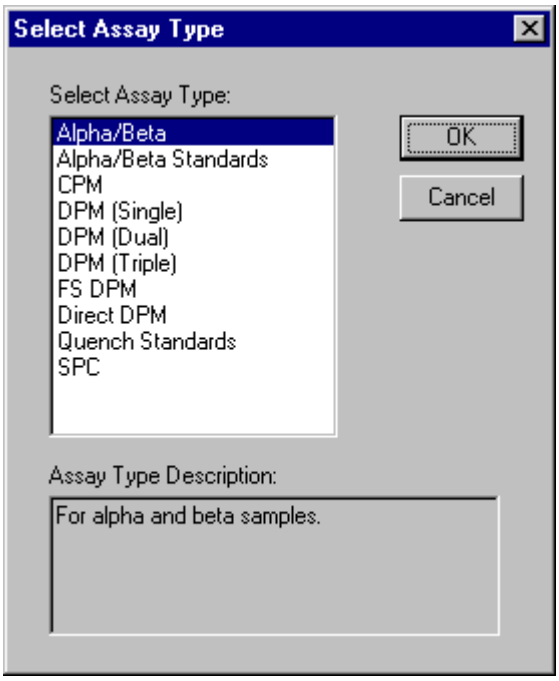

Figure 4-18 Select Assay Type

Open Assay

Select this menu option to open an existing assay.

Associate Assay

This menu item allows you to Associate (link) an assay that you have defined to a protocol number.

Disassociate Assay

You can disassociate an assay from a protocol flag number by selecting the assay you would like to disassociate in the Protocols Tree of the Main Window. Then select Disassociate Assay from the File menu. The name of the assay should disappear from the Protocols Tree. You may also right click on the assay and select Disassociate Assay from the menu that is displayed.

Data Paths Window

The Data Paths window allows you to control the location for storing data files generated by the assay. You may choose this location based on additional applications that you want to use to process the data or simply to comply with a data storage strategy in your facility. You can choose to save data to the default directory by checking the Use Default Output Data Path box.

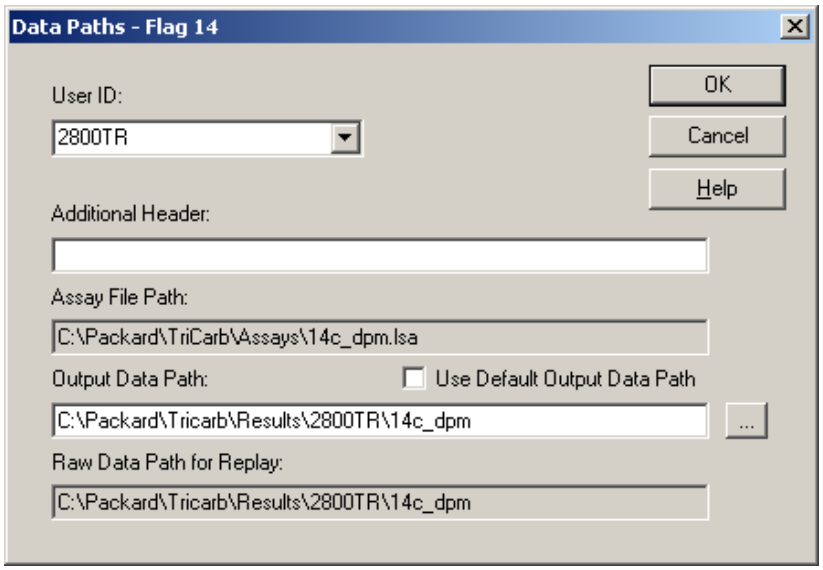

Figure 4-19 Data Paths Window

Note: This information is stored on a per protocol basis, as indicated in the Windows title bar of the window.

Print Setup

This menu item allows you to define print parameters.

Print Assays

To print a list of parameters defined for an assay, select the Print Assays item from the File menu. Select the assay you would like to print from the Select Assays to Print window and click Open.

Exit

This menu item allows you to close the QuantaSmart program.

Run Menu

Display the Run menu by selecting Run from the menu bar.

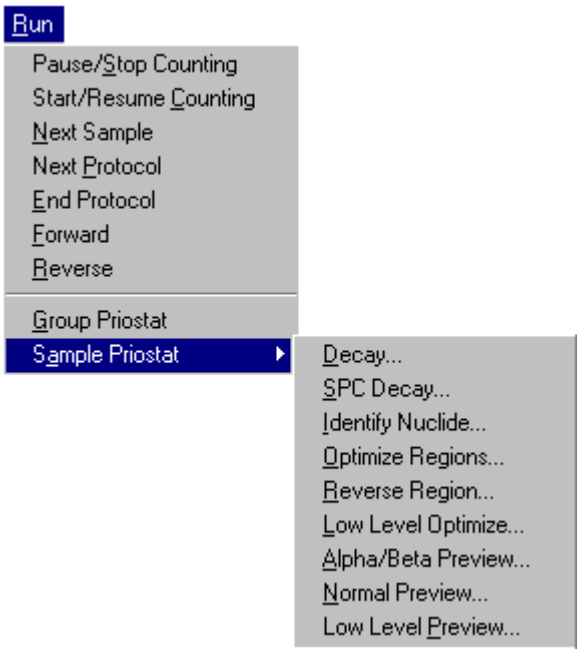

Figure 4-20 Run Menu.

The Run menu can also be displayed by selecting the Alt-R keys. Each item in the menu can be displayed by selecting the underlined character indicated.

Stop Counting

This menu item ends the current protocol and stops the instrument. This command is also available via the red button on the Instrument Status Bar.

Start/Resume Counting

This menu item loads the sample currently at the detector position and begins counting. This command is also available via the green button on the Instrument Status Bar.

Next Sample

This menu item unloads any sample in the detector, moves the next sample into the detector and starts counting.

Next Protocol

This menu item unloads any sample in the detector and aborts the current protocol. The instrument searches for the next cassette with an active protocol flag and begins running that protocol.

End Protocol
This menu item unloads any sample in the detector and ends the protocol; data reduction continues until data from the last counted sample is reported. The system begins counting the next protocol. This command is also available via the checkered button on the Instrument Status Bar.

Forward
This menu item unloads any sample in the detector and moves the sample changer in a counterclockwise direction.

Reverse
This menu item unloads any sample in the detector and moves the sample changer in a clockwise direction.

Group Priostat
This menu item allows you to count a set of high priority samples immediately, while temporarily interrupting the current protocol.

Stop Group
This menu item terminates counting of the Priostat (priority) samples; and resumes counting of the interrupted samples.

Sample Priostat (not available on the 2800, optional on the 2900 TriCarb)
This is a special interrupt mode which allows you to: Preview sample count rates, determine optimal counting conditions for variable and constant quench samples, identify an unknown nuclide in a sample and determine the duration of luminescence. This menu has the following options.

Decay
This menu item allows you to assess the duration of luminescence in a radioactive sample via a decay histogram.

SPC Decay
This menu item allows you to assess the duration of luminescence in a non-radioactive, luminescent sample via a decay histogram.

Identify Nuclide
This menu item allows you to identify an unknown nuclide in your sample using the Quench Indicating Parameters SIS and tSIE.

Optimize Regions
This menu item allows you to optimize sample counting regions to provide the highest figure of merit for Normal count mode.

Reverse Region
This menu item allows you to re-optimize sample counting region settings for a sample and determine the equivalent unquenched region settings for variable quench samples.

Low Level Optimize
This menu item allows you to optimize sample counting regions to provide the highest figure of merit for Low Level count mode.

Alpha Beta Preview
This menu item allows you to view the sample spectrum in the Alpha/Beta mode and approximate the activity for a sample containing both an Alpha and a Beta emitting nuclide.

Normal Preview
The menu item allows you to view the sample spectrum and approximate the activity for a sample using Normal count mode.

Low Level Preview
This menu item allows you to view the sample spectrum and approximate the activity for a sample using Low Level count mode.

View Menu

The View menu can also be displayed by selecting the Alt-V keys. Each item in the menu can be displayed by selecting the underlined character indicated. View has the following options.

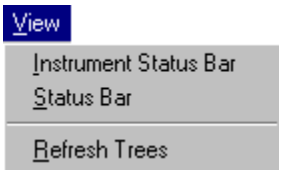

Figure 4-21 View Menu.

Instrument Status Bar
This menu item allows you to view or hide the Instrument Status Bar and its buttons. The Instrument Status Bar is located underneath the Menu Bar in the main window.

Status Bar
This menu item allows you to view or hide the Status Bar located at the bottom of the main window.

Refresh Trees

This menu item allows you to update the Protocols and Replay trees in the main window. The Replay tree is automatically updated whenever a new assay is counted. Refresh Trees is only necessary to clear report entries from the tree displays.

Libraries Menu

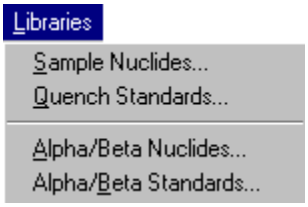

Figure 4-22 Libraries Menu

The Library Concept

Radionuclide information is stored and accessed in the Nuclide Library. The Nuclide Library consists of the Quench Standards and Sample Nuclides Libraries. If your instrument is equipped with an Alpha Beta option, an Alpha Beta Standards and an Alpha Beta Nuclides Library will also be included.

The Quench Standards Library (requires single/dual/color DPM option on the 2800TR) is comprised of quench sets, with each quench set containing individual quench standards. The data from the quench standards is used to construct quench curves for calculating DPM (Disintegrations Per Minute) in DPM Assays. Quench Standards are counted once and the entire spectrum for each quench standard is stored independent of assay information. This allows you to select and use the same quench set in any number of assays and construct a quench curve for each sample at the time the sample is counted.

The Sample Nuclides Library allows you to specify and save nuclide names, counting region limits and quench sets for sample nuclides. Up to three nuclides can be defined for each entry to support the counting of multiple nuclides. These sample nuclide parameters are typically specified as part of the assay definition process and may be edited as needed.

The Alpha Beta Standards and Alpha Beta Nuclides Libraries (not available on the 2800TR) are used in the same manner as the Quench Standards and Sample Nuclides Libraries. The information stored in these libraries is relevant only when performing Alpha Beta Assays, where both an Alpha-emitting and a Beta-emitting radionuclide are quantified independently within the same sample vial.

Sample Nuclides

This menu item allows you to display the Sample Nuclides Library window. The Sample Nuclides Library is a repository of information regarding sample nuclides.

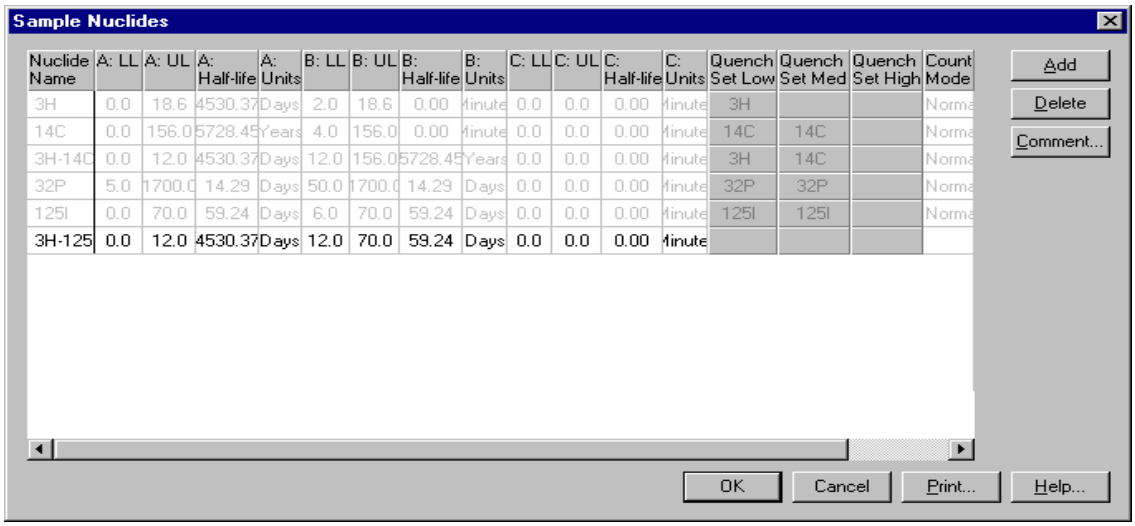

Figure 4-23 Sample Nuclides window

The Sample Nuclides window allows you to enter information into and retrieve information from the Sample Nuclides Library.

For assays, use the Sample Nuclides Library to define and save nuclide names and counting region limits for radionuclides. You can also select a quench set for each sample nuclide using the Quench Set buttons in this window.

In Replay, use the Sample Nuclide Library to select a radionuclide for the purpose of reanalyzing sample data.

Note: The fields that are enabled in the Sample Nuclides Library will be different when accessed from different locations within the software. The list of nuclides that is displayed is dependent on the assay type, the nuclide and the number of quench sets associated with the nuclide. See the Libraries chapter for information on adding a sample nuclide name.

Quench Standards

The Quench Standards window allows you to define a new quench set to be stored or select a quench standards set for DPM assays or data reanalysis in Replay. The data from these quench sets is used to construct quench curves for determining sample DPM (Disintegrations Per Minute).

Note: Name, max keV and DPM are the only entries required when entering a new quench set. The remaining parameters stored in the library are retrieved from the assay parameters chose in defining an assay. The number of standards (up to twenty) is determined automatically during counting.

For additional information, refer to the Libraries chapter.

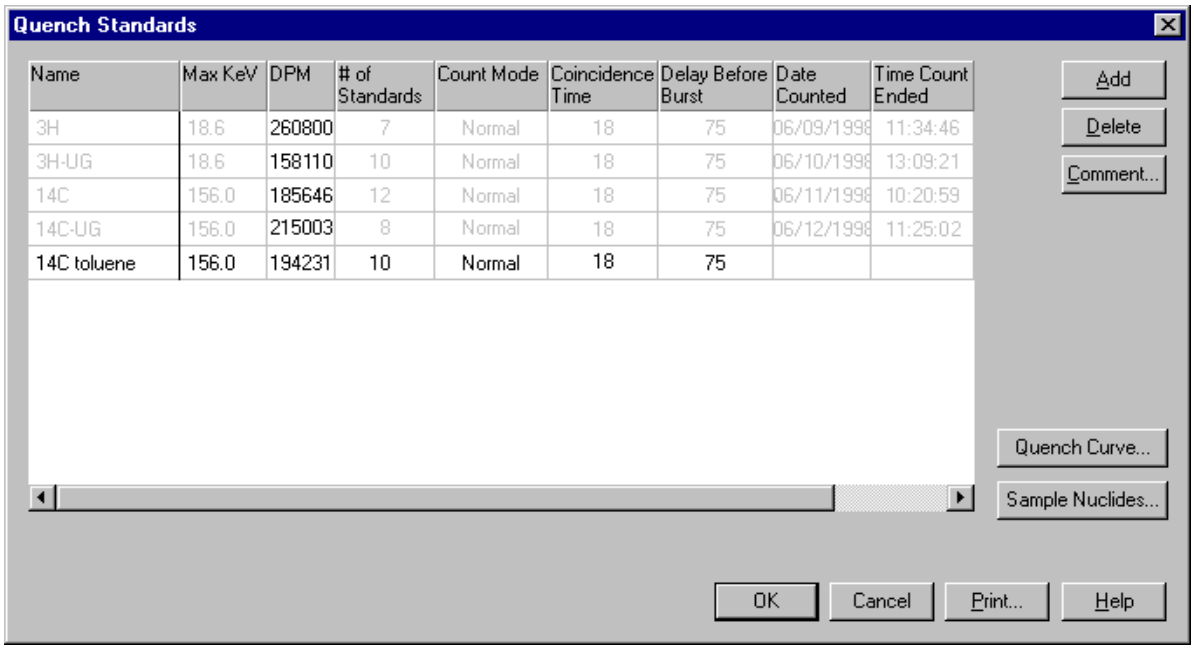

Figure 4-24 Quench Standards Window

Alpha Beta Nuclides (not available on the 2800TR)
This menu item allows you to display the Alpha Beta Nuclides Library window. The Alpha Beta Nuclides Library is a repository of information regarding previously defined Alpha and Beta emitting nuclides counted in Alpha Beta Assays.

For additional information, refer to the Libraries chapter.

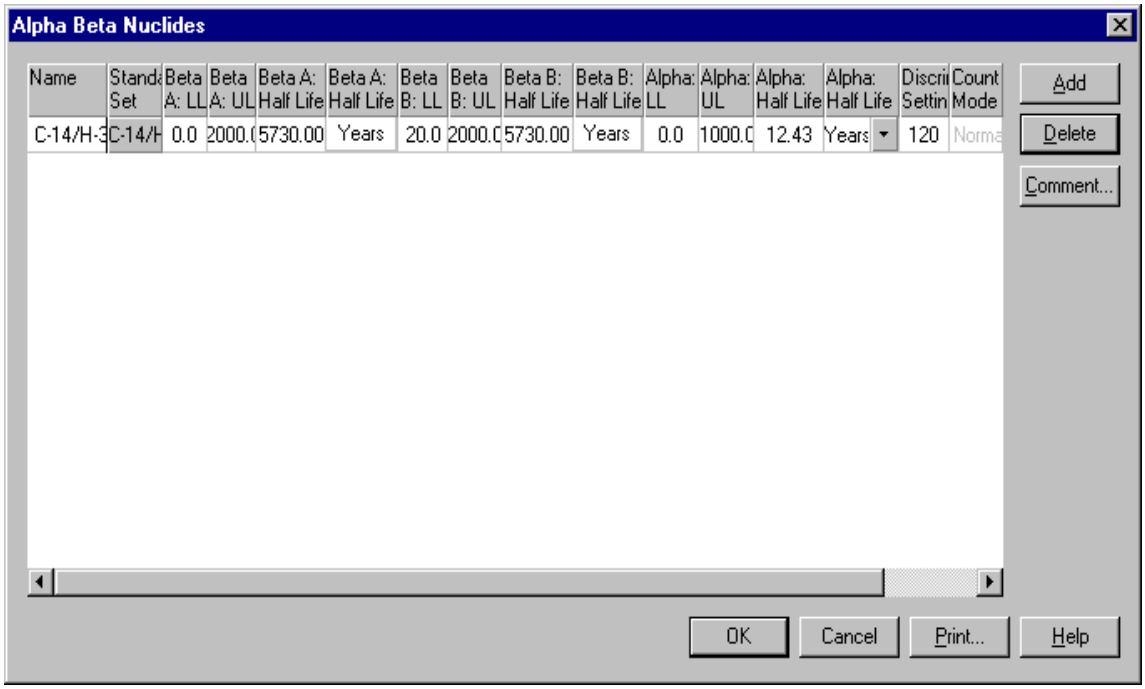

Figure 4-25 Alpha Beta Nuclides Library Window

Alpha Beta Standards

This menu item allows you to display the Alpha Beta Standards Library window. The Alpha Beta Standards Library is a repository of information regarding previously defined standards used in Alpha Beta Assays.

For additional information, refer to the Libraries chapter.

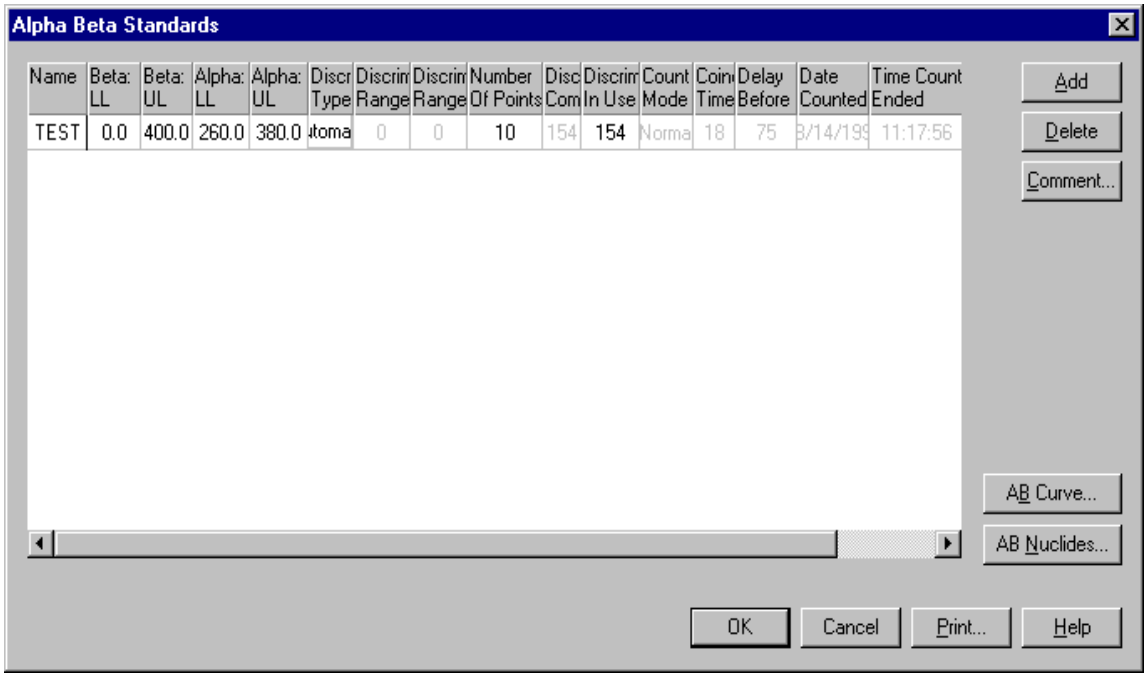

Figure 4-26 Alpha Beta Standards Library Window

Tools Menu

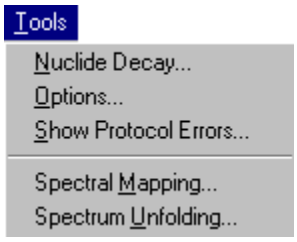

Figure 4-27 Tools Menu.

Nuclide Decay

Select this menu option to display the Radionuclide Decay window for calculating the Disintegrations Per Minute (DPM) of radionuclides.

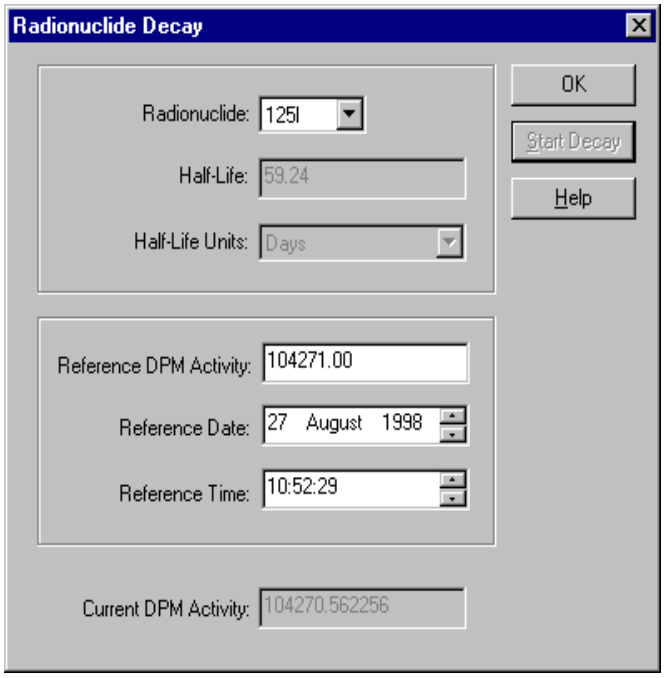

Figure 4-28 Radionuclide Decay Calculator

Options

Select this menu option to display the Options window. The Options window allows you to select a format for the Spectrum Files created in High Sensitivity and Low Level Count Modes and activate the feature which allows negative CPM and DPM reporting.

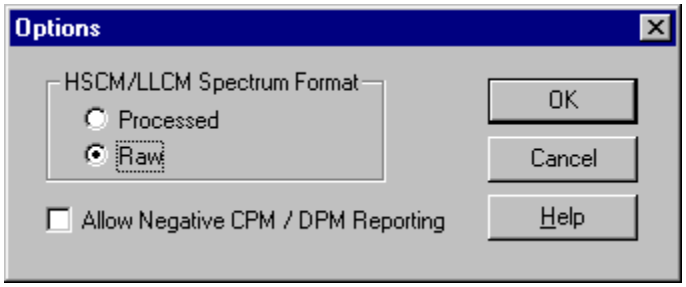

Figure 4-29 The Options Menu

Show Protocol Errors

Use this menu item to display certain error messages that are associated with an assay.

Figure 4-30 Show Protocol Errors

Spectral Mapping

The Spectral Mapping menu item allows you to view a three-dimensional spectral map for a sample and quench standards. This option is used for single-label DPM samples.

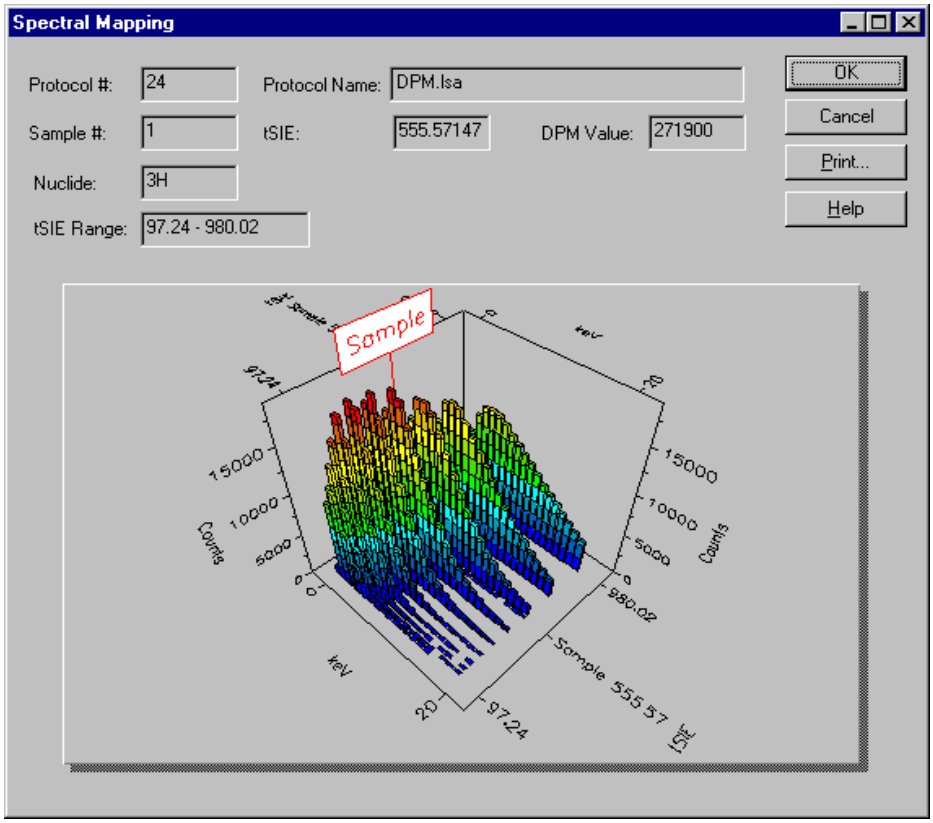

Figure 4-31 Spectral Mapping

Spectrum Unfolding

The Spectrum Unfolding menu item allows you to view a three-dimensional display of the separated, individual spectra for each nuclide in a Dual-label or Full Spectrum (FS) DPM sample counting procedure.

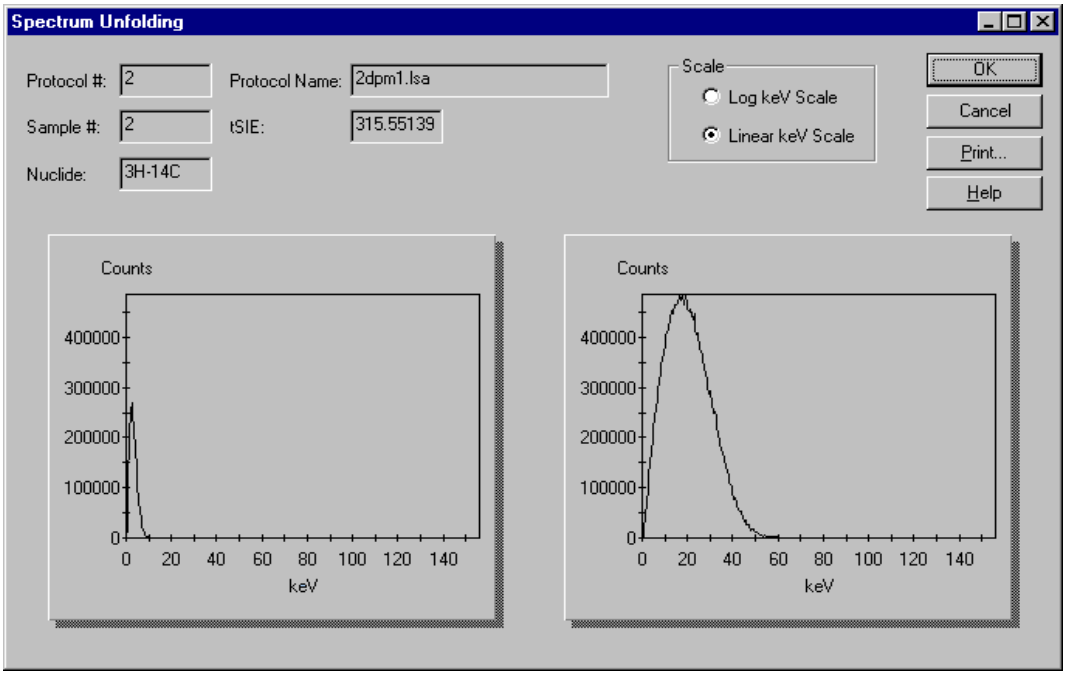

Figure 4-32 Spectrum Unfolding.

IPA Menu

Display the IPA™ (Instrument Performance Assessment) menu by selecting IPA from the menubar.

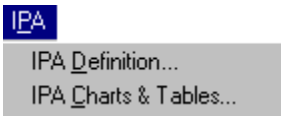

Figure 4-33 IPA Menu

The IPA menu can also be displayed by selecting the Alt-P keys. Each item in the menu can be displayed by selecting the underlined character indicated.

IPA Definition

This menu item allows you to define the parameters used to assess instrument performance.

IPA Charts &Tables

This menu item allows you to view, edit and print all instrument performance assessment parameters in chart or tabular form.

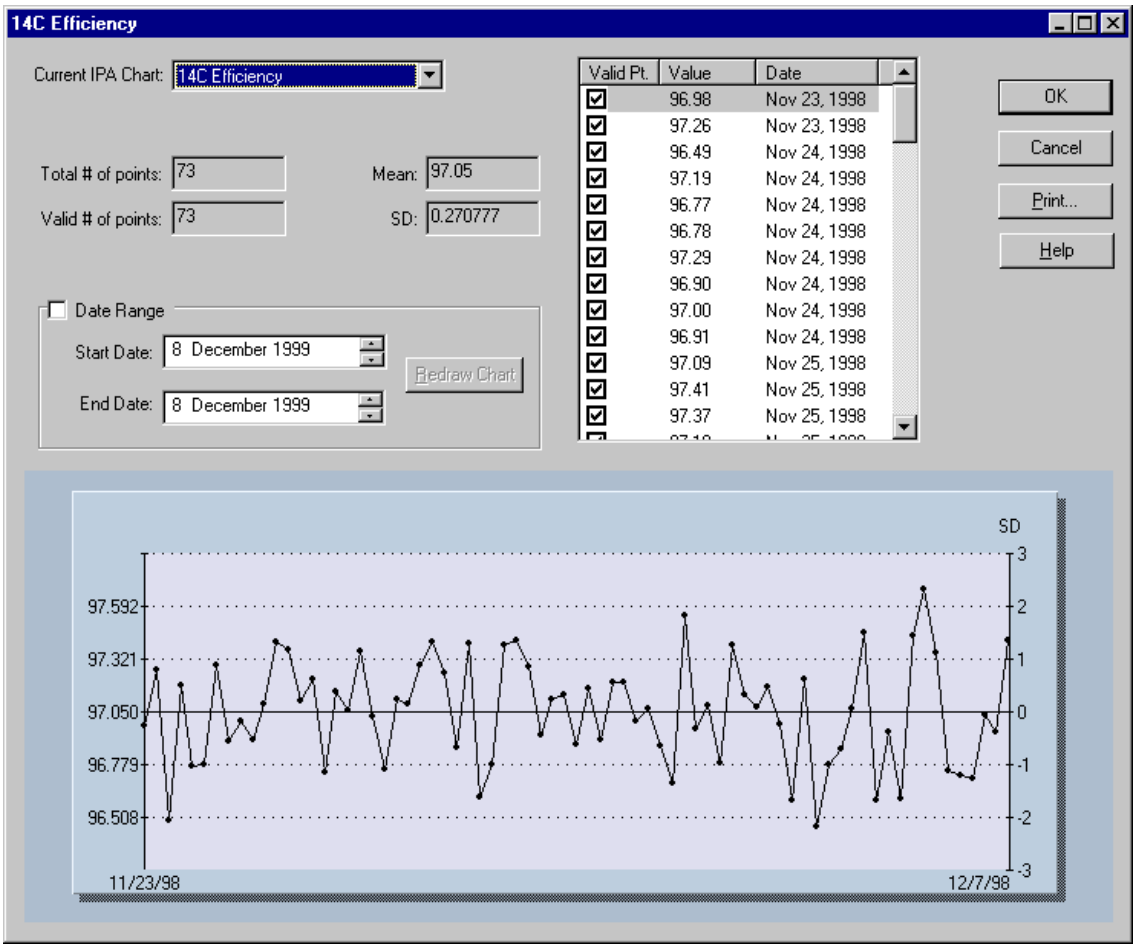

Figure 4-34 IPA Charts & Tables.

Diagnostics Menu

Display the Diagnostics menu by selecting Diagnostics from the menubar. The TSE Diagnostics item in the Diagnostics menu is for the use of a PerkinElmer Service Engineer to view the system's diagnostic screens and assess the system's functional status. A password is required.

The Diagnostics menu can also be displayed by selecting the Alt-D keys. The item in the menu can be displayed by selecting the underlined character indicated.

Window Menu

Display the Window menu by selecting Window from the menu bar. This menu allows you to define a format for the window display on the monitor and restore the SpectraView window.

Figure 4-35 Window Menu

Cascade

This menu item displays the open windows in the following fashion:

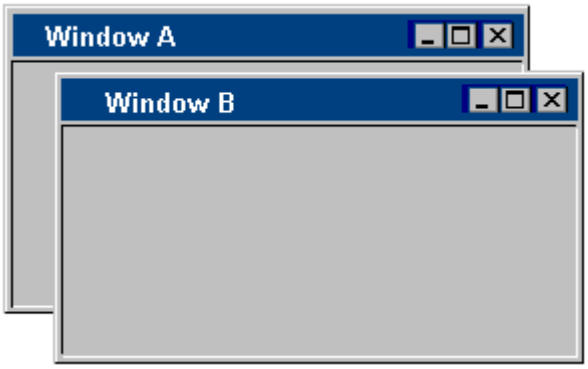

Figure 4-36 Cascaded Windows

Tile

This menu item displays the open windows in the following fashion:

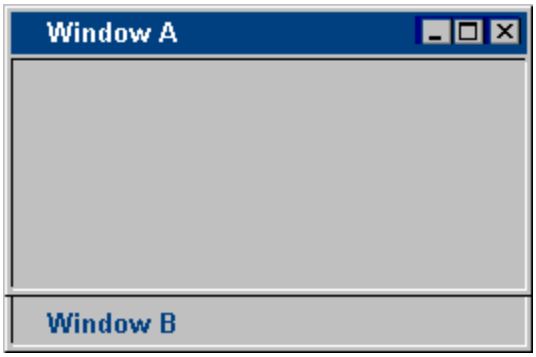

Figure 4-37 Tiled Windows

SpectraView

SpectraView is a window in the QuantaSmart program which displays a two-dimensional, real-time view of the spectrum for the current sample.

Help Menu

Display the Help menu by selecting Help from the menu bar.

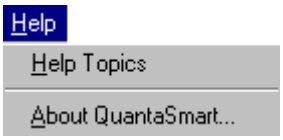

Figure 4-38 The Help Menu.

Help Topics

This menu item will launch the On-Line Help documentation with the Table of Contents initially in view.

About QuantaSmart

This menu item indicates the version of the QuantaSmart software you are using and the date and time of its creation.

Spectral Displays

Spectral Mapping

During a single-label DPM sample count, the Spectral Mapping window can display the sample and quench standards spectra in a three-dimensional view. The X-axis of the map represents the energy in keV, the Y-axis represents the counts and the Z-axis represents the quench indicating parameter, tSIE. The spectral map can be used for the following:

- Comparing a sample spectrum to the quench standard spectrum.
- Checking for spectral anomalies.

Display a spectral map by selecting the Tools-Spectral Mapping menu option.

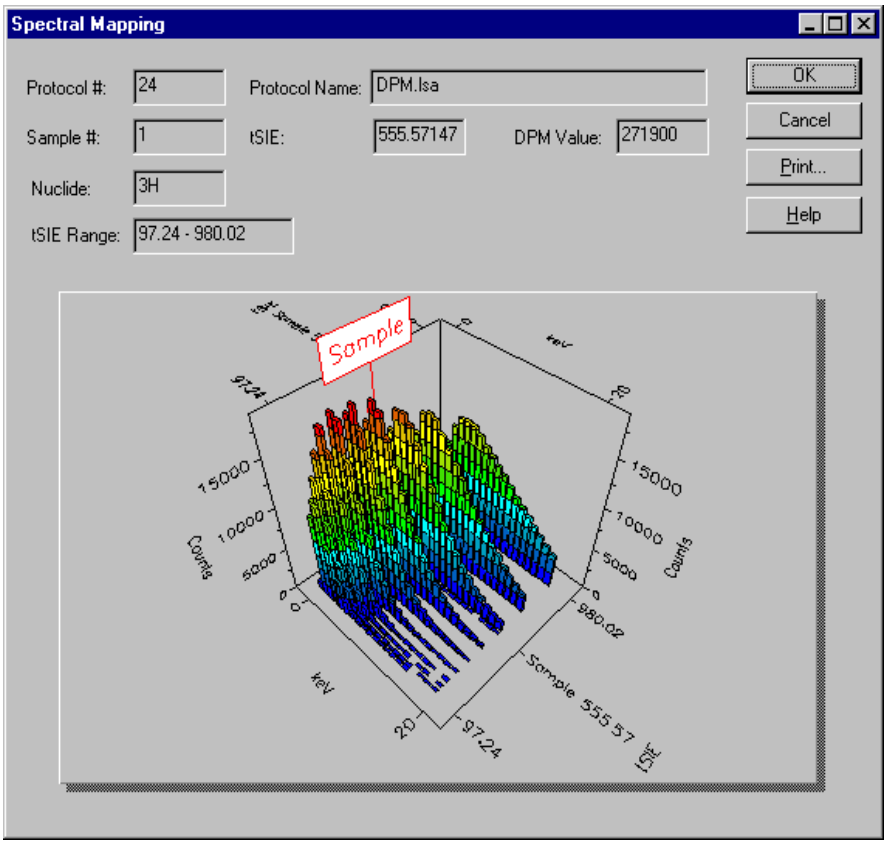

Figure 4-39 Spectral Mapping Window

A sample with a quench level exceeding the limits of the quench standards will have its position on the map determined by extrapolation. The lower limit of extrapolation is the tSIE plus 10% of the least quenched standard; the upper limit of extrapolation is the tSIE minus 10% of the most quenched standard.

Spectrum Unfolding

During a Dual-label DPM or Full Spectrum DPM sample count, the Spectrum Unfolding window can display three dimensionally, the composite nuclide spectrum as individual, separate spectra for each nuclide. The X-axes of the spectral displays represent the energy (in keV) for each counting channel up to the defined endpoint of the sample spectrum. The Y-axes represents the gross counts for the current sample. Spectrum Unfolding is often useful for the following:

- Visualizing the relationship of the individual nuclide spectra.
- Approximating the ratio of lower energy nuclide to higher energy nuclide.
- Display the unfolded spectra by selecting the Tools-Spectrum Unfolding menu option.

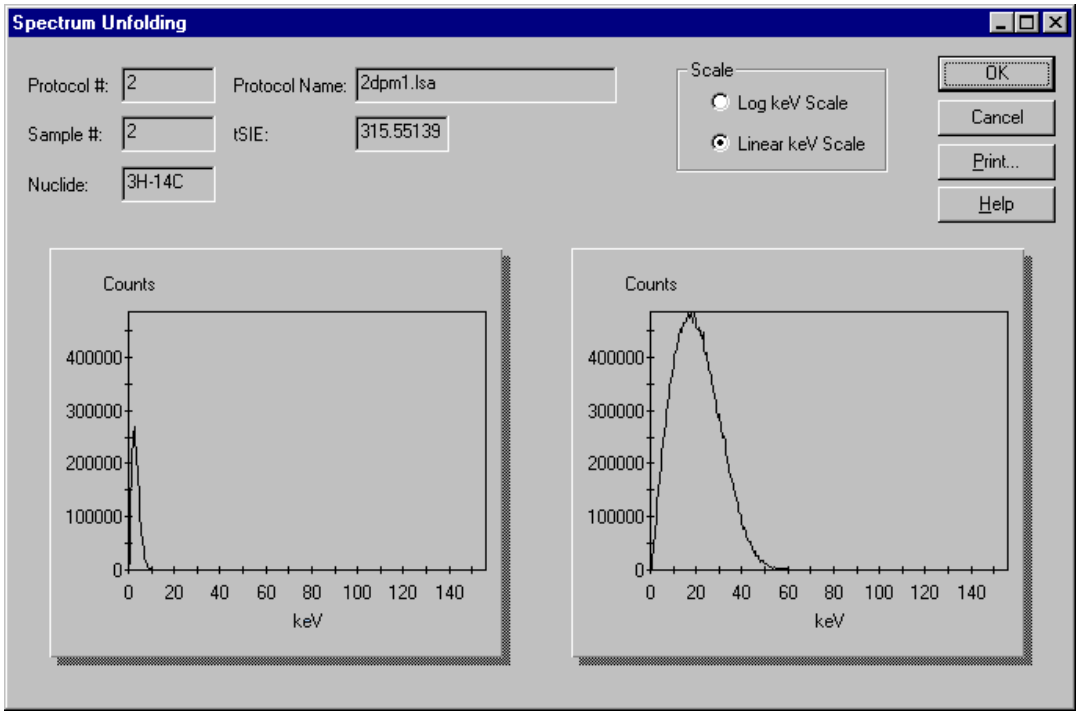

Figure 4-40 Spectrum Unfolding Window.

The SpectraView Window

The SpectraView window is part of the main window. It displays a two-dimensional, real-time view of the spectrum for the current sample. It provides you with information about the status of a sample count and the region settings used in the counting procedure. A number of display options are available for the spectrum and are defined in this window.

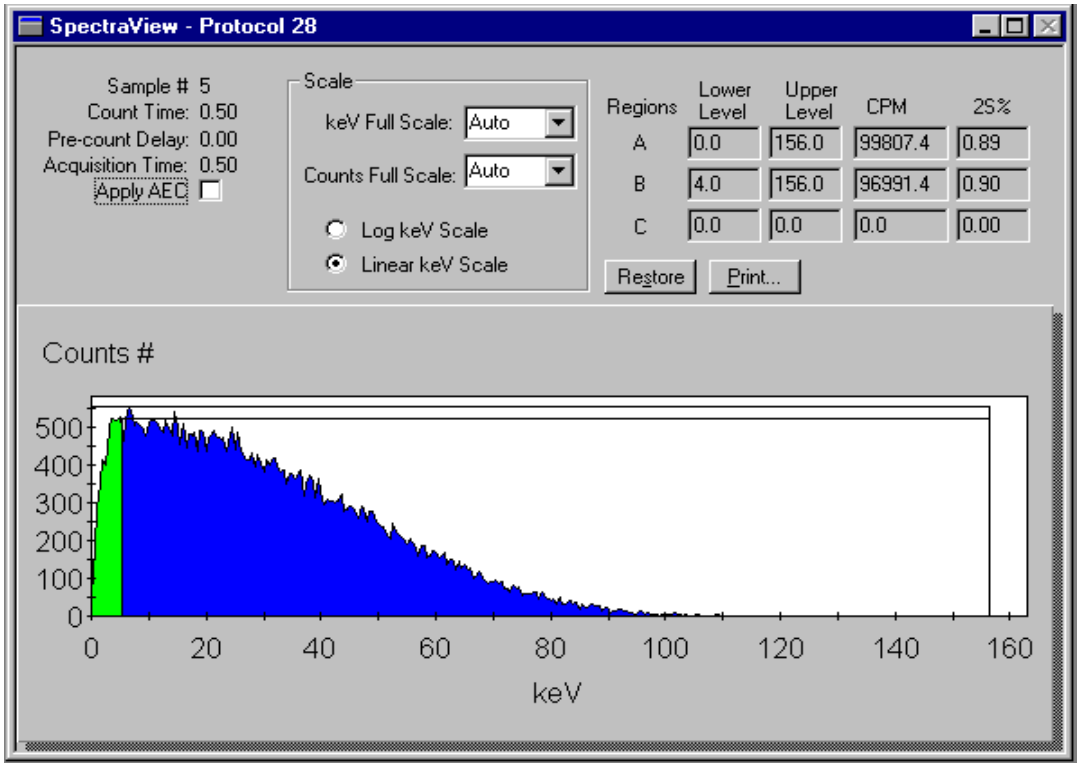

Figure 4-41 The SpectraView Window.

The SpectraView window is typically used for the following:

- Monitoring sample counting.
- Detecting spectral distortions or compressions resulting from sample quench.
- Observing the effect of altering the counting region settings.
- Viewing the spectrum in linear or logarithmic scale.

The X-axis of the spectral display represents the energy (in keV) for each counting channel up to the defined endpoint of the sample spectrum. The Y-axis represents the gross counts for the current sample. The regions settings are graphically displayed using solid line boxes. This window is updated every six seconds.

Reports

There are a variety of reports that you can generate using the QuantaSmart system, either printed or electronic. On the **Report Definition** tab of the **Assay Definition** window, first define the content and name the report(s) that you need. After creating one or more named reports, go to the **Report Output** tab to choose how each named report is to be generated.

Printed Reports

There are a variety of reports that you can print using the QuantaSmart™ system. On the **Report Definition** tab of the **Assay Definition** window, first define a named report with the information that you need. On the **Report Output** tab, select the desired named report and mark the **Output to Printer** check box. The printed report(s) you define for an assay will automatically print after the assay is completed.

To print additional reports, select the report you would like to print from the Protocols tree in the main window. Click the **Print** button to print the report when the **Output** window is displayed.

To print a list of the parameters you have selected for an assay, select the File-Print Assays menu option. The Select Assays to Print window is displayed. Select an assay that you would like to print and click OK.

Electronic Reports

There are a variety of electronic reports that you can generate using the QuantaSmart™ system. On the **Report Definition** tab of the **Assay Definition** window, first define a named report with the information that you need. On the **Report Output** tab, select the desired named report and indicate what type of electronic report that want to generate. The electronic output formats include:

- Rich Text Format (RTF)
- Delimited Text (ASCII)
- RS232 (cabled transmission, not a file format)

Other, predefined sets of data can also be selected for output using the **Special Files** tab of the **Assay Definition** interface. This other data includes:

- Composite Spectra File
- Individual Spectrum Files
- IPA™ Data
- Protocol Data (PROT.DAT)
- Protocol Data (2000CA.DAT)

All of the data files are stored to the location that you define for each protocol. When you associate an assay with a protocol flag for the first time, you will be prompted for data path information. The **Data Paths** window appears so that you can identify information specific to this protocol (not the assay) for data storage. You can also view or modify this information for existing protocol associations by choosing the **Data Paths** item on the **File** menu.

Chapter 5

Assays

CPM Assays

A CPM assay provides you with information regarding the total quantity of radioactivity within a sample, in one, two or three predefined counting regions. The data generated is expressed in CPM (Counts Per Minute). CPM reflects only the activity that is detected, without regard to counting efficiency or sample interference, such as quench.

Performing a CPM Assay

The following tasks are required when performing a CPM Assay.

- Calibrate the instrument, if necessary.
- Create a new assay, choosing CPM as the assay type and define the new assay parameters, OR open an existing CPM assay and edit or review if necessary. Save the assay in the Assays folder of the Packard\TriCarb directory.
- Associate (link) the assay parameters with a protocol and attach the corresponding protocol flag to the first cassette to be counted.
- Load the cassette(s) with vials and load the instrument with cassettes.
- Start the instrument.

DPM Assays

A DPM assay allows you to quantitate a nuclide or nuclides within a sample. The data is expressed as DPM (Disintegrations Per Minute). When DPM are being calculated, the sample must be checked for quench. If a sample is not corrected for quench, erroneous DPM results may be reported.

For each sample in a DPM assay, the instrument:

- Measures the activity in a sample vial in Counts Per Minute (CPM).
- Determines the level of quench via one of the Quench Indicating Parameters (QIPs).
- Interpolates the counting efficiency from a quench curve (plots % Efficiency vs. QIP).
- Calculates DPM, where DPM=CPM/Efficiency.

Depending on the TriCarb model, four different DPM assays are available:

Single, Dual and Triple DPM Assays allow you to count one, two or three nuclides in a sample using one, two and three defined counting regions.

FS DPM (Full Spectrum DPM) Assays allow you to count two nuclides in a sample using the full spectrum of the sample (no defined counting regions).

Performing a DPM Assay

The following tasks are required when performing a DPM Assay.

- Calibrate the instrument, if necessary.
- Define and run a Quench Standards Assay so that counting efficiency and DPM can be determined for the samples.
- Create a new assay choosing DPM Single, Dual or Triple as the assay type and define the new assay parameters.
- Save the assay, OR open an existing DPM assay and edit or review if necessary.
- Select a quench standards set for use with the sample nuclide(s).
- Save the assay in the Assays folder of the Packard\TriCarb directory.
- Associate (link) the assay parameters with a protocol and attach the corresponding protocol flag to the first cassette to be counted.
- Load the cassette(s) with vials and load the instrument with cassettes.
- Start the instrument.

Quench Set

The Quench Set field is displayed only in DPM Assays. This field displays the quench set you selected for the Sample Nuclide in the assay. When using a quench set, counting efficiency is determined for each sample in the assay. By selecting the Constant Quench option in this field, counting efficiency will only be determined for the first sample in the assay. The counting efficiency for this sample is used to calculate DPM for all the samples in the assay. The Constant Quench option is advantageous since it results in a reduction in the amount of time required to count the samples in an assay.

FS DPM Assay

The Full Spectrum DPM method is used for regionless counting of dual label samples. It uses the Quench Indicating Parameters, Spectral Index of the Sample (SIS) and transformed Spectral Index of the External standard (tSIE), as well as a spectral unfolding technique to separate the composite spectrum of the sample. The composite spectrum is separated into two component spectra, each of which is the result of a different nuclide. Spectrum unfolding yields the actual CPM for each nuclide and a quench correlation curve comparing SIS vs. tSIE and Efficiency vs. tSIE is used to determine the DPM of the unknown samples.

Maximum accuracy with this method is obtained when the concentration of nuclides in the sample falls in the range of 50:1 to 1:8 (low energy to high energy nuclide). The quench standards used for FS DPM should be of the same chemistry and geometry as your unknown samples.

Performing an FS DPM Assay

The following tasks are required when performing an FS DPM Assay.

- Calibrate the instrument, if necessary.
- Define and run a Quench Standards Assay so that counting efficiency and DPM can be determined for the samples.
- Create a new assay choosing FS DPM as the assay type and define the new assay parameters.
- Associate (link) the assay parameters with a protocol and attach the corresponding protocol flag to the first cassette to be counted.
- Load the cassette(s) with vials and load the instrument with cassettes.
- Start the instrument.
- Save the assay.

Or

- Open an existing FS DPM assay and edit or review if necessary.
- Select a quench standards set for use with the sample nuclide(s).
- Save the assay in the Assays folder of the Packard\TriCarb directory.
- Associate (link) the assay parameters with a protocol and attach the corresponding protocol flag to the first cassette to be counted.
- Load the cassette(s) with vials and load the instrument with cassettes.
- Start the instrument.

Direct DPM Assays

The Direct DPM Assay

The Direct DPM Assay is a predefined assay which performs the DPM calculation based on the Quench Indicating Parameter, SIS (Spectral Index of the Sample). Since this assay comes pre-installed as part of the system, there is no need to define individual assay parameters. This assay will calculate accurate DPM values for single label beta or beta/gamma nuclides, including Tritium. Single-label samples containing different beta nuclides may be counted in the same cassette.

When using the Direct DPM method, samples are evaluated as follows:

- If the SIS value is greater than or equal to 40, then the DPM is reported with no message on the printout.
- If the SIS value is between 20 and 40, then the DPM is reported and the sample is designated as indeterminate (I) on the printout.
- If the SIS value is less than or equal to 20 and the sample is determined to contain Tritium, the DPM is reported with no message on the printout.
- If the SIS value is less than or equal to 20 and the sample is determined not to contain Tritium, then the DPM is not reported and the sample is designated as indeterminate on the printout.

Note: When a sample is designated as indeterminate on a printout, the DPM reported may be valid if the sample is not heavily quenched. Check the tSIE value of the sample to determine the level of quench. If the tSIE is greater than 200, the DPM reported is most likely accurate, within statistical counting error. The accuracy is independent of cocktail density variation, vial size or type, sample volume, color and chemical quench. Direct DPM is not recommended for any background level samples counted for a short time.

Performing a Direct DPM Assay

The following tasks are required when performing a Direct DPM Assay.

- Calibrate the instrument, if necessary.
- Create a new assay, choosing Direct DPM as the assay type.
- If you are counting samples using PerkinElmer Ultima Gold™, scintillation cocktail, you must indicate this in the nuclide library. Doing so will ensure that the appropriate quench curve will be used to calculate DPM for 3H.

Save the assay in the Assays folder of the Packard\TriCarb directory.

- Associate (link) the assay parameters with a protocol and attach the corresponding protocol flag to the first cassette to be counted.
- Load the cassette(s) with vials and load the instrument with cassettes.
- Start the instrument.

Alpha Beta Assays (not available on the 2800TR)

An Alpha Beta assay allows you to simultaneously count alpha and beta emitting nuclides in the same sample vial. In some cases, the emission energies for alpha and beta nuclides may overlap, making discrimination between the nuclides difficult. To separate alpha and beta nuclide energies, you must take advantage of their differing pulse decay times. The TriCarb instruments equipped with the Alpha Beta feature use the Pulse Decay Analysis (PDA) method of nuclide discrimination. A time-based Pulse Decay Discriminator (PDD) is used to optimize the separation of alpha and beta pulses. The optimum PDD value minimizes the likelihood of alpha events being counted as beta events, and vice versa. To optimize this setting, you must count a pure alpha and a pure beta standard source. The optimum discriminator value is where the misclassification of alpha and beta events is at a minimum. Once the optimum PDD value is established, you may use this information to count alpha beta assays by referencing the Standard Set name in the Alpha Beta Nuclide Library. When an alpha beta nuclide name is chosen in an assay, the referenced Alpha Beta Standard Set name and its corresponding optimum discrimination is applied in the assay. The data generated from your sample protocol is expressed in CPM (Counts Per Minute) and reflects only the activity in the vial without regard to counting efficiency or sample interference (quench).

Performing an Alpha Beta Assay

The following tasks are required when performing an Alpha Beta Assay.

- Calibrate the Instrument, if necessary.
- Define and Run an Alpha Beta Standards Assay (page 75) to establish the optimal pulse decay discriminator value.
- Define an alpha beta nuclide in the Alpha Beta Nuclide Library. Choose a Standards Set (second column in the table) from the Alpha Beta Standards Library to use the discriminator setting from the Standard Set. If you do not choose a Standard Set, manually enter a discriminator setting directly in the Alpha Beta Nuclide Library.
- Open an existing assay or create a new assay by choosing Alpha Beta assay type. Select the desired alpha beta radionuclide name on the Count Conditions tab and define the remaining assay parameters
- Save the assay in the Assays folder of the Packard\TriCarb directory.
- Associate (link) the assay parameters with a protocol number in the protocol tree and attach the corresponding protocol clip to the first cassette to be counted.
- Load the cassette(s) with vials and load the instrument with cassettes.
- Start the instrument.

Tips and Techniques for Performing Alpha Beta Assays

1. Several factors influence the discrimination of alpha from beta activity in a mixed sample. First and foremost is quenching. Alpha beta discrimination degrades in heavily quenched samples. For best performance, it is recommended to minimize quench, if possible, by either using smaller sample volumes or eliminating interferences with sample purification techniques.
2. Alpha Beta standards are counted with a wide open 0-2000 region for beta activity and 0-1000 region for alpha activity. Optimize counting regions in the Alpha Beta Nuclide Library for counting unknown samples, if desired.
3. Count the alpha and beta standards used to generate the misclassification curve in your assay to either confirm the misclassification established when the Alpha Beta standards were counted or to determine the revised misclassification that results from using optimized region settings. The new misclassification must be calculated manually from the observed counts for both alpha (CPMa) and beta (CPMA or CPMB).

   Note:Only one region of interest (CPMa) is defined for alpha activity. This field is automatically included by default in alpha beta assays. Beta activity can be reported in 2 regions, CPMA and CPMB. CPMA is always included by default in the report.

4. High sensitivity (HSCM) or Low Level Count mode (LLCM) can be used in an alpha beta assay. In this case, DO NOT link an Alpha Beta Standard Name to an Alpha Beta Nuclide Name in the Alpha Beta Nuclide Library. Since all Alpha Beta Standards are always counted with normal count mode by design, linking an Alpha Beta Standard to the Alpha Beta Nuclide name will automatically choose normal count mode.

   Note:High Sensitivity or Low Level count mode is applied only to the beta counting and not alpha. Alpha background reduction is achieved with alpha beta discrimination (Pulse Decay Analysis).

5. To use High Sensitivity or Low Level count mode in an assay, define the Alpha Beta Nuclide in the library and do not link an Alpha Beta Standard set. Again the Alpha Beta standards should be counted in the assay to determine the alpha and beta misclassification.

   Note:When counting high energy beta emitters in low level count mode, it may be advantageous to change the Delay Before Burst value on the Count Corrections tab (default is 75ns). Adjusting the value, you can optimize the background reduction for the highest sensitivity. A value between 150 and 300 is typical. The optimum must be empirically determined with a representative background and sample.

Alpha Beta Standards Assay

An Alpha Beta Standards Assay allows you to count pure beta and pure alpha standard sources. By counting the beta and alpha standards, you can establish the optimal Pulse Decay Discriminator value, where misclassification of the beta and alpha events is at a minimum. Establishing this value allows the instrument to discriminate between alpha and beta emitting nuclides in your samples in Alpha Beta Assays.

Performing an Alpha Beta Standards Assay

The following tasks are required to run the Alpha Beta Standards Assay. Two standards are required, a pure beta emitter and a pure alpha emitter.

- Choose the Alpha Beta Standards selection from the Libraries menu.
- Click the Add button and enter the name for a new Alpha Beta Standard Set.
- Choose **Automatic** for the Discriminator Type if your pure alpha and pure beta standards have an activity of at least 50,000 CPM each. If the activity in either standard is less than 50,000 CPM, choose **Manual** as the Discriminator Type by clicking on it.
- The remaining fields are for information only. They are either default values or values computed by the instrument.
- Choose **File-New** and select Alpha Beta Standards as the assay choice from the drop down menu.
- Click the Name button on the Count Conditions Tab to choose from the list of Alpha Beta Standard names in the Alpha Beta Standards Library. Define the other available assay parameters as desired.

Note:High Sensitivity or Low Level Count mode are not available when counting Alpha Beta Standards, but will be available when counting samples in an Alpha Beta assay

- When the assay definition is complete, name and save the assay.
- Associate (link) the assay parameters with an available protocol flag in the protocol tree. Place the numbered protocol clip on a cassette.
- Place the pure beta emitter standard in cassette position 1 and the pure alpha emitter standard in cassette position 2.
- Click the green start button at the top of the main window.
- After counting is complete, the misclassification (or spillover) curve and the optimum discriminator value will be stored in the Alpha Beta Standards Library.

Quench Standards Assay

A Quench Standards set is composed of a series of vials, each containing the same amount of nuclide with varying amounts of quenching agent. Using the data from the quench standards, a quench curve is generated to determine the counting efficiency for a sample and calculate DPM (Disintegrations Per Minute), where DPM=CPM/Efficiency. The system stores the spectrum of each standard in the quench standards set. The quench standards set needs to be counted one time only, as the quench data is available for use with any protocol.

To accurately assess the level of quench within a sample, the nature and composition of the quench standards should reflect the matrix and environment of the samples you would like to count.

Performing a Quench Standards Assay

The following tasks are required when performing a Quench Standards Assay.

- Calibrate the instrument, if necessary.
- Create a new assay, choosing Quench Standards as the assay type and define the new assay parameters, OR Open an existing Quench Standards Assay and edit or review if necessary. Save the assay in the Assays folder of the Packard\TriCarb directory.
- Associate (link) the assay parameters with a protocol and attach the corresponding protocol flag to the first cassette to be counted.
- Load the cassette(s) with vials and load the instrument with cassettes.
- Start the instrument.

Note:When using the Low Level count mode, you must **not** use quench standards which have been purged free of oxygen with an inert gas. The oxygen quenching in unpurged standards facilitates discrimination between background and true beta events. Unpurged quench standards are available from PerkinElmer Life and Analytical Sciences.

SPC Assay

A Single Photon Counting Assay is an assay which measures the photons emitted from non-radioactive, luminescent samples. To detect scintillation, modern Liquid Scintillation Counters use two photomultiplier Tubes (PMTs) to collect virtually all of the light produced within a sample vial. Each pulse that occurs during the sample counting time is registered and expressed as Counts Per Minute (CPM). Events are considered true decay events from the sample if they occur within a specified coincidence time. If these events do not occur in coincidence, they are considered random (background) and are not counted.

In an SPC Assay, only one PMT is used. As a result, coincidence cannot be used as a means of excluding background. Therefore, it is often important to reduce the instrument background to its lowest possible level. Lowering the high voltage supplied to the photomultiplier tube typically decreases background and increases sensitivity in SPC Assays.

Performing an SPC Assay

The following tasks are required when performing an SPC Assay.

- Calibrate the instrument, if necessary.
- Create a new assay choosing SPC as the assay type and define the new assay parameters.
- Associate (link) the assay parameters with a protocol and attach the corresponding protocol flag to the first cassette to be counted.
- Load the cassette(s) with vials and load the instrument with cassettes.
- Start the instrument.

Or

- Open an existing SPC assay and edit or review if necessary. Save the assay in the Assays folder of the Packard\TriCarb directory.
- Associate (link) the assay parameters with a protocol and attach the corresponding protocol flag to the first cassette to be counted.
- Load the cassette(s) with vials and load the instrument with cassettes.
- Start the instrument.

Single Photon HV DAC %

The Single Photon HV DAC % field is displayed only in SPC Assays in the Count Conditions tab in the Regions section. The high voltage supplied to the instrument's Photomultiplier Tube is adjustable. Lowering the high voltage supplied to the PMT typically decreases background counts and increases sensitivity. The default setting for this device is 70%. The optimum setting will need to be determined empirically.

The setting is found in the Radionuclide section in the Count Conditions menu.

Defining an Assay

The process of assay definition is central to the use of the instrument software. Assays are defined using the seven Assay Definition tabs: Assay Parameters, Count Conditions, Count Corrections, Report Definition, Report Output, Special Files, and Worklist. Using these seven tabs, for each assay that you define, you will:

- Enter descriptive information about the nature of the assay and the author of the assay.
- Define a sample nuclide in the sample nuclides library if one does not already exist.
- Link the nuclide to the assay.
- Link standards to the assay, if necessary.
- Specify the appropriate count conditions and count correction factors that the instrument will use to analyze the samples.
- Define the reports you would like the system to generate.
- Output desired report options.
- Define an optional worklist to designate Positive Identification numbers and sample names that correspond to sample numbers on a printout, if desired.

The parameters defined within the context of these seven tabs can be saved and used or edited at your discretion. All of the assay information that you define and save becomes a functional entity only after it is associated to a protocol number. These protocols are recognized by the instrument via a protocol flag. This device contains an encoded, reflective metal which the instrument uses to identify the protocol number and sample counting parameters that you have defined and elected to use. The QuantaSmart program enables you to define an unlimited number of assays and associate them with up to sixty protocols by enabling the Lock Assay feature.

Assay Parameters

The Assay Parameters tab in the Assay Definition window allows you to designate an author and provide descriptive information for an assay. You may also prohibit the editing of assay parameters using this window.

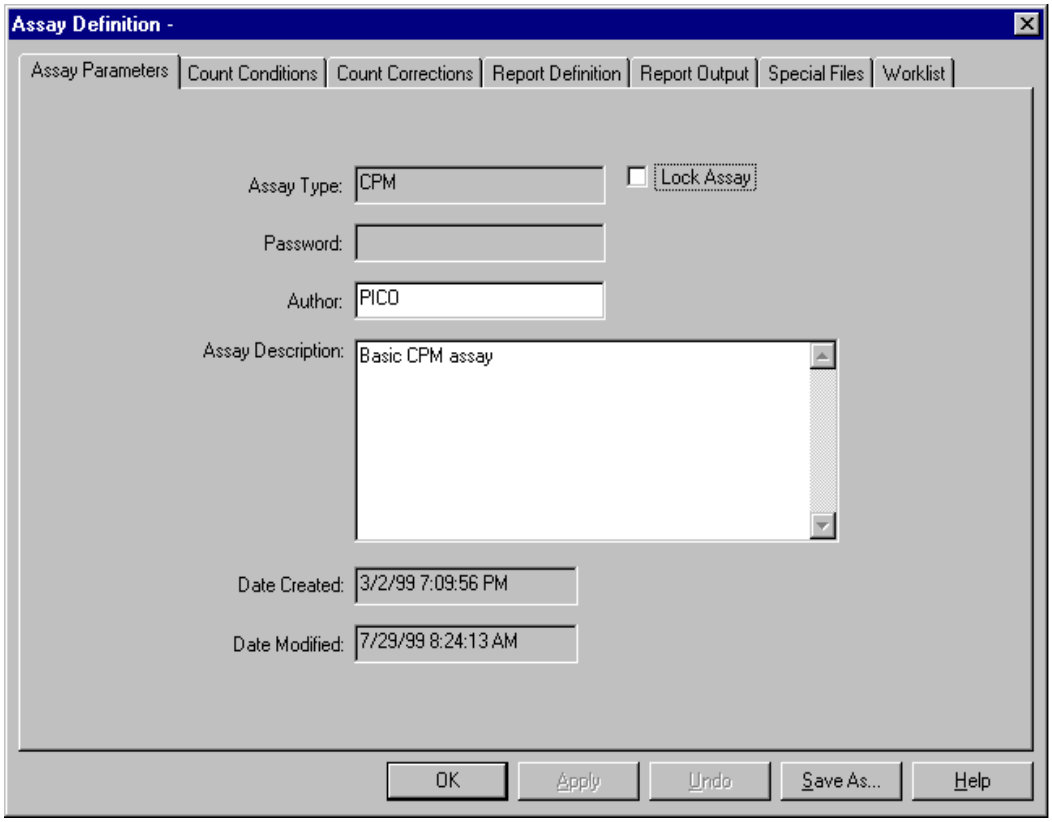

Figure 5-1 Assay Definition - Assay Parameters Tab.

Save As

Click this button to save any changes made in the Assay Definition tabs using a different filename or file location on the disk.

Password

Enter a password if you would like to restrict editing functions for this assay. You must check the Lock Assay box before you can enter a password in this field.

Author

Enter your name or other identification as the author of the assay. This is an optional entry.

Assay Description
Enter descriptive information about the assay. This information is for future reference.

Date Created
This field represents the date the assay was created.

Date Modified
This field represents the date the assay was last modified.

Lock Assay
Mark this box if you would like to restrict editing functions for this assay. You must enter a password in the Password field if you would like to lock the assay.

Assay Type
The Assay Type reflects the selection that you made in the Select Assay Type window.

Count Conditions

The Count Conditions tab in the Assay Definition window allows you to define specific counting parameters for an assay.

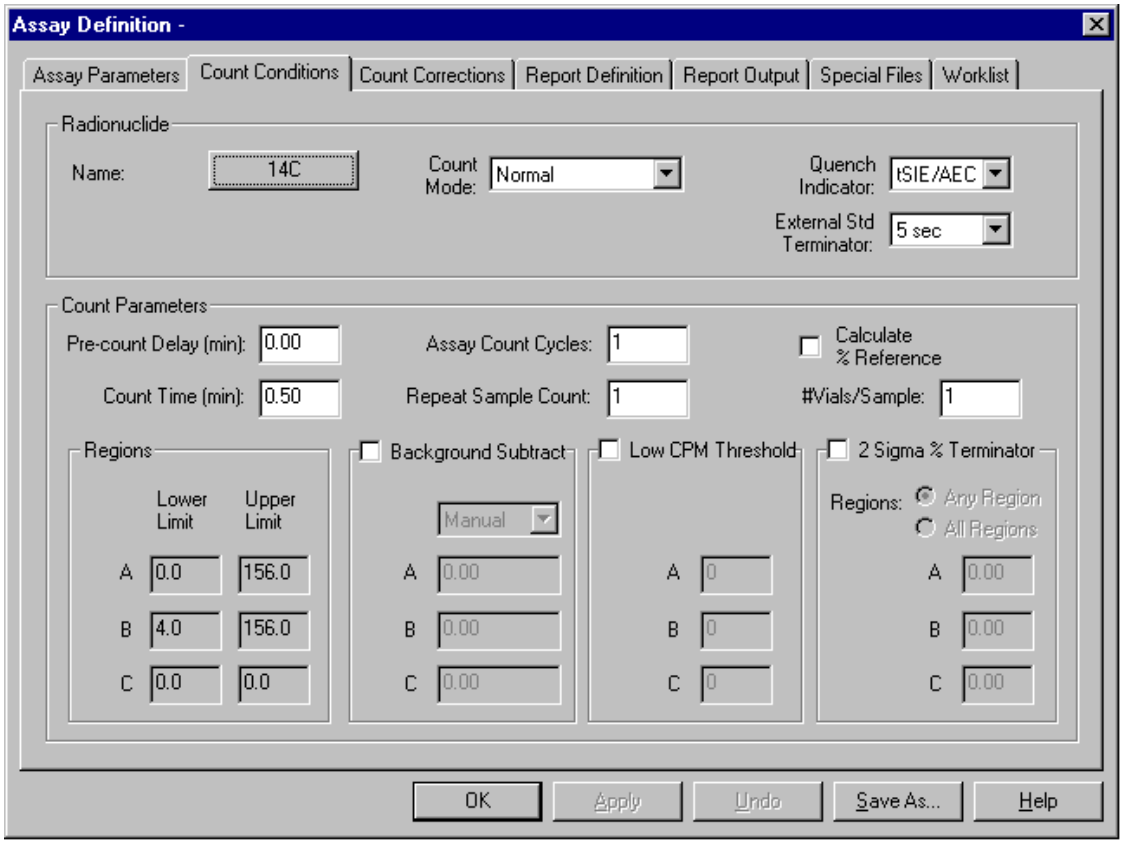

Figure 5-2 Assay Definition - Count Conditions Tab.

Radionuclide: Name

Clicking on the Name button brings up the Sample Nuclide window allowing you to select a different sample nuclide.

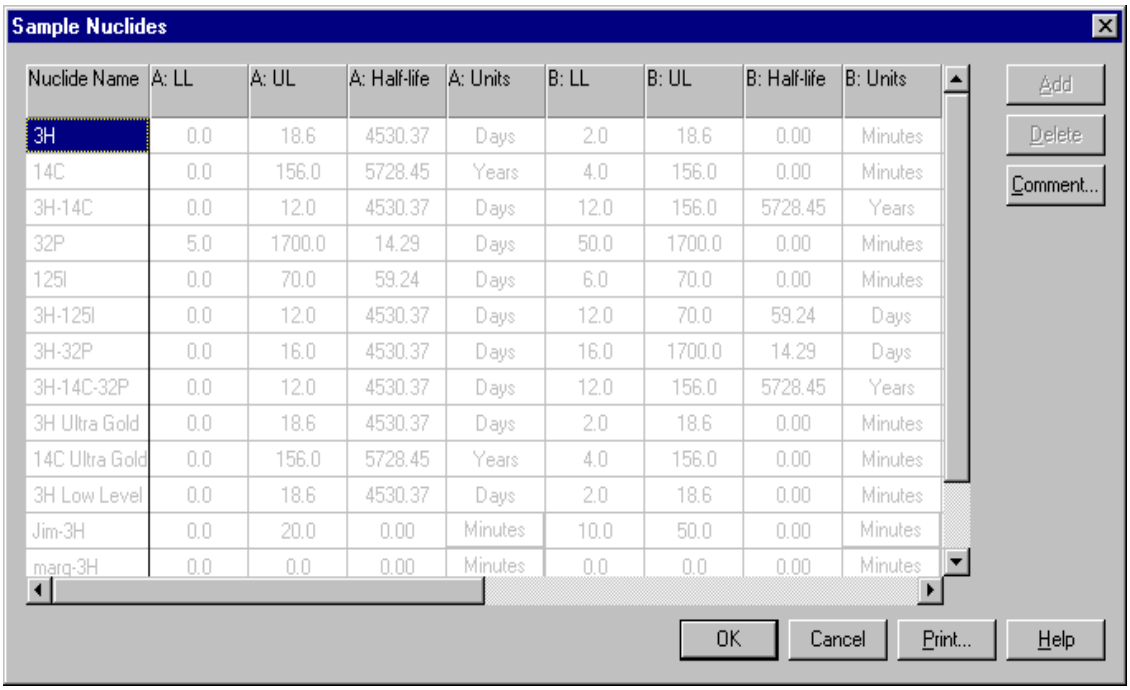

Figure 5-3 Sample Nuclide Window

Count Mode

Select either Normal, High Sensitivity or Low Level from the drop-down list. Depending on the TriCarb model you are using, the list of available count modes will be different. Normal mode is the default and works well for most samples. High sensitivity provides higher sensitivity as a result of the strict criteria used to exclude background interference. Low Level provides the highest sensitivity counting for low activity samples due to even stricter criteria for the exclusion of background interference (with a minimal compromise in counting efficiency).

Quench Indicator

Quench indicators available are: tSIE, tSIE/AEC or SIS. These parameters measure chemical quenching in your sample.

tSIE
(transformed Spectral Index of the External Standard). Using an external Barium-133 standard source, this method assigns a numeric value to the quench associated with a sample. This determination is independent of the quantity of radioactivity in the sample and its count rate. The lower the tSIE value, the more the sample is being quenched. A tSIE value of 1000 represents a completely unquenched sample. Accurate DPM values can be determined for samples with tSIE values as low as 10. To ensure good count statistics, the external standard is typically counted to a 0.5% two sigma counting error, where the gross counts equal 160,000. tSIE is the most accurate of the quench indicator options and is typically used for low count rate, variable quench, single label samples.

tSIE/AEC
(transformed Spectral Index of External standards coupled to Automatic Efficiency Correction). tSIE assigns a numeric value to the quench associated with a sample. As quench varies, the AEC automatically monitors and adjusts the counting region to exclude unwanted background. This setting is typically used for dual and triple label experiments with variable quench samples where optimal region settings are desired.

SIS
(Spectral Index of the Sample) SIS assigns a numeric value to the quench associated with a sample. The SIS is determined from the spectral shape of the sample and is based on actual sample counts. The SIS setting is typically used to monitor the quench level in single label, high count rate samples for CPM assays or in single label Cherenkov counting.

Note**:** By using one of the count termination parameters, this count time may be shortened.

External Standard Terminator
Select a length of time the external standard is counted for calculating the quench index. Selecting 0.5 2s% instead of an increment of time will allow counting to occur until gross counts of 160,000 are measured. This provides statistical accuracy of 0.5% (at 95% confidence) for the tSIE parameter. You may elect to use the External Standard Terminator only if tSIE or tSIE/AEC are chosen as quench indicators.

Pre-count Delay
Enter the length of time you would like the samples to sit in the closed detection chamber prior to counting. This process is “dark adaption”; it will reduce luminescence originating from the samples. Luminescence can distort the count statistics of the sample and is particularly problematic with low count rate samples and long count times.

Count Time
Enter the maximum length of time that the samples will be counted. For low activity samples, longer count times provide better count statistics and more accurate sample results. Changes to this parameter for an active assay will be implemented immediately.

Assay Count Cycles
Enter the number of times you would like the assay to count. The assay is recounted after it has moved one complete cycle around the sample changer deck. Any samples on the sample changer deck will be counted prior to your samples being recounted.

Repeat Sample Count
Enter the number of times you would like each sample counted while in the detector. This differs from Assay Count Cycles, where samples are unloaded from the detector and make a complete cycle around the sample changer deck prior to recounting.

Calculate Percent Reference
Activate the percent reference calculation by marking this box. The instrument reports the value of each sample as a percentage of a reference vial. The reference vial should be the first non-background vial loaded in the cassettes.

Number of Vials per Sample
Enter the number of replicates of each sample being counted. The data output will report the average value of the replicates.

Lower Limit Regions A, B, and C
These fields represent the lower counting limit for regions A, B, and C, measured in keV.

Note: This field will only be enabled for Single Label DPM Assays where tSIE is selected as the Quench Indicating Parameter. The system uses the tSIE and the sample spectrum endpoint to determine sample heterogeneity.

Background Subtract
Mark this box to subtract background CPM from all samples. The background value is established in one of three ways and is selected from the following:

1st Vial
The instrument counts the first vial in the cassette for either ten minutes or the defined protocol count time (whichever is greater) and establishes a CPM value for each region; these are the background values subtracted from each sample within each region of the assay.

IPA
The instrument subtracts the background values established during the calibration and Instrument Performance Assessment (IPA) procedures from the entire spectrum of the samples. The background spectra are stored during these procedures and are available for any counting region.

Manual
Enter the CPM values you would like the instrument to subtract from the entire spectrum of the samples.

Note: In Quench Standards assays, the 1st Vial background subtraction option is not available. Background subtraction is only applied to the reported data for quench standards and has no impact on the spectrum for each standard. Any background subtraction that occurs in DPM assays will apply to the quench standards used for the purpose of recalculating the quench curve in the DPM assay.

Two Sigma Percent Terminator

Mark this box to activate count termination from statistical accuracy. Two options are available:

Any region

Enter the level of statistical accuracy for each region (as a percent value) that you would like to achieve before counting terminates. Counting terminates when the sigma value of any one region is reached. Using this feature, counting may terminate before the specified count time elapses.

All regions

Enter the level of statistical accuracy for each region (as a percent value) that you would like to achieve before counting terminates. Counting terminates when the sigma value for each region is reached. Using this feature, counting may terminate before the specified count time elapses.

Changes to this parameter for an active assay will be implemented immediately.

Low CPM Threshold

Mark the check box to activate low CPM count termination. You can enter CPM values for each counting region to have counting terminate if these values are not reached. The sample count terminates if any one of the regions does not meet the specified minimum CPM threshold within the first 30 seconds of counting.

Count Corrections

The Count Corrections tab in the Assay Definition window allows you to define specific count correction parameters for an assay.

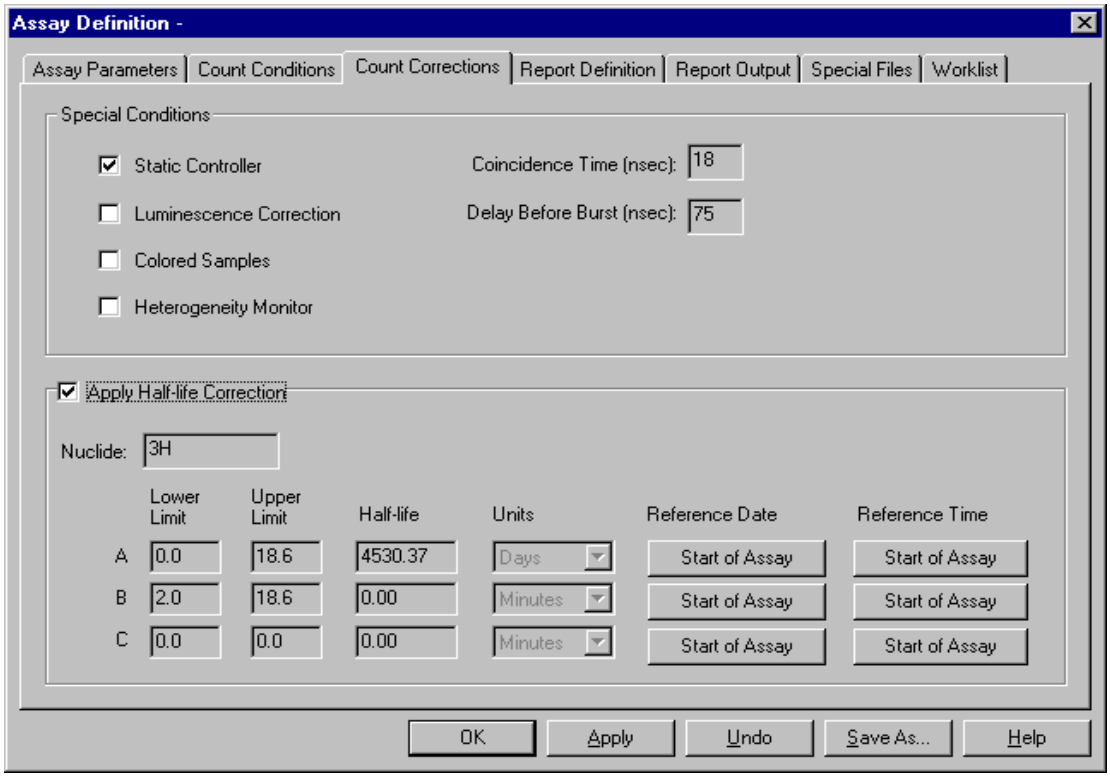

Figure 5-4 Assay Definition - Count Corrections Tab.

Static Controller

Mark this box to activate the instrument's static-controlling device, which is designed to reduce static originating on the sample vial. Static discharge can falsely elevate sample counts by producing non-beta pulses. This device should be activated in most cases. It's default value is On. It is especially important in low humidity conditions, when using plastic vials and when handling vials with latex gloves. To further reduce the likelihood of generating static:

- Maintain a relative humidity level above 40%.
- Wipe latex gloves with anti-static wipes before handling vials.
- Use the Pre-count delay timer. It delays the counting of each sample allowing time for static-induced pulses to dissipate.

Note: The Static Controller can cause a decrease in the signal to noise ratio in SPC Assays. Therefore, it is typically not used in this assay type. It is especially important in SPC Assays to employ the above mentioned techniques to minimize the likelihood of generating static.

Luminescence Correction

Mark this box to activate luminescence correction. The instrument corrects the data for counts resulting from sample luminescence. This feature is optional on 2800 and 2900 series instruments.

Colored Samples

Mark this box to activate color correction. The instrument will correct the data for color quench. Typically, this is only required if samples are highly colored. Note: This field will be enabled only for DPM Assays.

Heterogeneity Monitor

Mark this box to activate a device that monitors and flags heterogeneous samples (such as samples with phase separation). This feature is not available on the 2800TR. It is optional on the 2900TR.

Note: This field will only be enabled for Single Label DPM Assays where tSIE is selected as the Quench Indicating Parameter. The system uses the tSIE and the sample spectrum endpoint to determine sample heterogeneity.

Coincidence Time

Specify the length of time (10-200 nanoseconds) that both PMTs must detect scintillation events. If scintillation events occur “in coincidence (both events must occur within the specified coincidence time), these events are considered to be true decay events from the sample. If these events do not occur in coincidence, they are considered random (background) and are not counted.

Note: When using solid scintillators, the coincidence time may need to be extended. The optimal setting must be determined empirically.

Delay Before Burst

Specify the length of time (75-800 nanoseconds) after the initial pulse (prompt pulse) that the detector looks for additional pulses (afterpulses). Afterpulses, which occur after the prompt pulse and delay time interval, indicate that a scintillation event is due to background. Some scintillators (e.g. PerkinElmer Ultima Gold) produce slower decaying pulses which may require longer delay times. When using these scintillators, it is advisable to lengthen the delay time to retain high counting efficiencies. This is especially important when counting high energy beta-emitting nuclides. The default setting for this parameter is 75.

Note: This parameter is only accessible with high sensitivity and low level count modes.

Apply Half-life Correction

Mark this box to activate half-life correction. This feature is typically used when working with short half-life nuclides. The instrument corrects the sample counts for half-life decay of the nuclide(s) being counted. The Reference Date and Time are used to make the decay calculation. The default settings for the Reference Date and Time correspond to the start of an assay.

Note: In Quench Standards assays, activate this feature only if the DPM value entered into the Quench Standards Library for the nuclide has not been corrected for decay. If the DPM value entered in the library for the standards has been corrected for decay, the half-life correction feature should not be activated.

Report Definition

The **Report Definition** tab allows you to custom design a report.

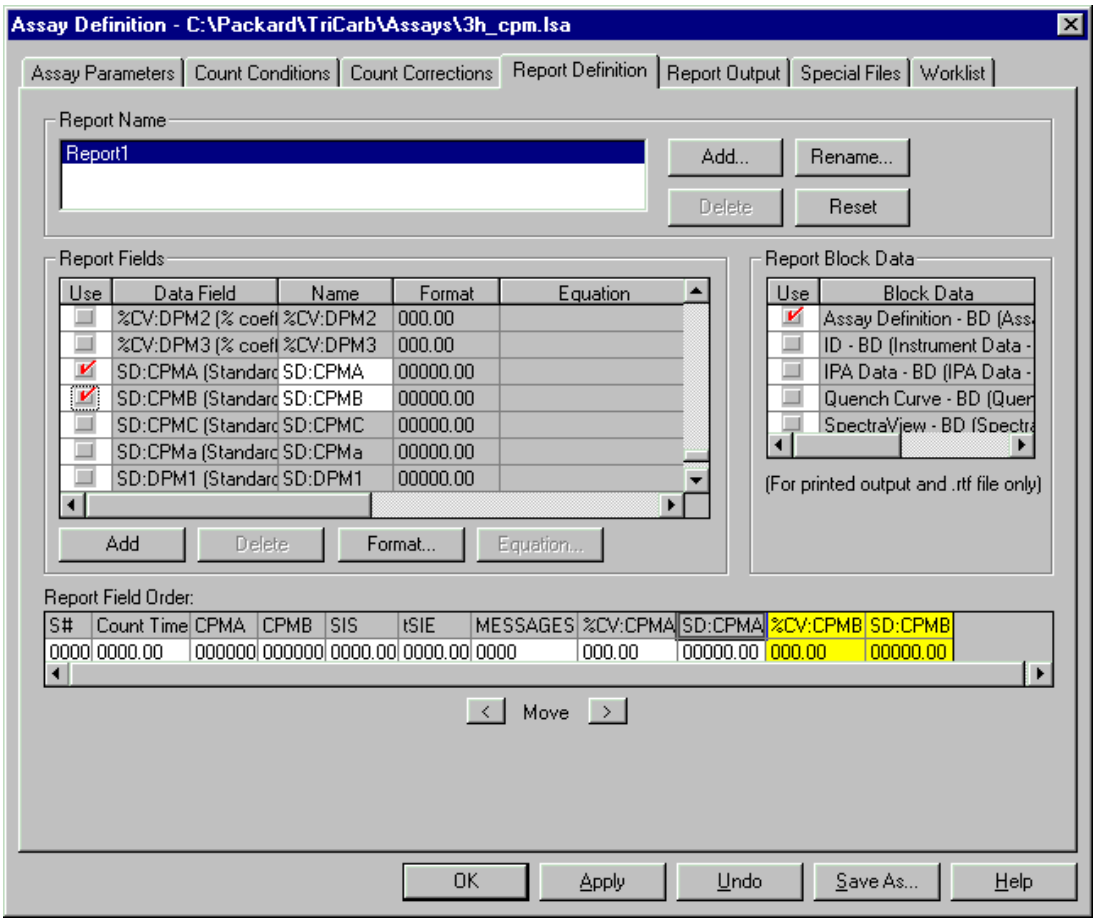

Figure 5-5 Assay Definition - Report Definition Tab.

Report Name

The Report Name field allows you to assign a descriptive name to a report.

Add Report

Click this button to define a new report for the assay. You can choose to use any of the named report formats in the list for the different output types identified on the Report Output tab. You can use a different report format for each of the output types (Printer, Data File, RS232, Rich Text Format), if desired.

Rename
Click this button to rename the report. After clicking this button, the following window appears:

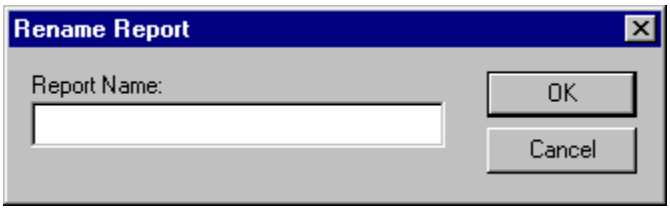

Figure 5-6 Rename Report Window

Type in the new name for the report.

Note: If you type in a name that already exists, or a name that has invalid characters / \ ? “ | < > a warning prompt will appear.

Delete
Click on this button to delete a report. First, select the report by highlighting it in the Report Name box. Then click on **Delete**.

Reset
Click this button to restore the default list of Report Fields for the selected Report.

Use
Checking the Use field selects the corresponding custom or data field to appear on the report.

Note: Any changes to the format or equation of custom fields will be saved when the Assay Definition window is closed whether or not the Use field is checked.

Data Field
A series of pre-defined Data Fields are provided for many of the report fields that you may wish to see in your reports. These fields include typical result values such as CPM, DPM, quench parameters, count time, statistical calculations, etc. In addition, you can also define your own Custom fields to report special calculations or formats for your application. These Custom Fields are automatically titled Custom1, Custom2, and so on when you create them. You can name these custom fields anything appropriate. If you decide to delete a custom field, QuantaSmart will not reuse the title in this assay.

Equation Field
This field displays an equation if one is defined. To enter an equation or edit an existing one, click on the **Equation...** button. A dialog box will appear so that you can define the information that will appear in this field.

Equation
This column displays an equation defined for the corresponding Custom Field.

Add
Click this button to add a new field to the list of available output fields for your reports. You can define the name, format and content of each custom field that you create. Content of Custom fields can be defined to be a specific value, copy of a field FOR THE SAME SAMPLE, or a formula using mathematical operands on other field values and/or constants.

Only one operation per Custom Field may be defined. For complex operations, you may find the need to create several Custom Fields to generate intermediate values, which can then be combined together in another Custom Field for the final result. Calculated Custom Fields do NOT have to be included in the final output, so your intermediate results can be hidden if desired.

Custom Fields are stored with the individual named reports. Custom Fields in one report are not available in other reports, even in the same assay.

Delete
Clicking the Delete button discards the custom field.

Note: You cannot delete a custom field if it is referenced by an equation in another field. Delete or modify any field(s) that reference the one you want to delete, so that you can then delete the desired field.

Format

The Format button allows you to define the format for reporting the currently selected data field. To define the data format, select a field that is already marked for **Use** in the report and click the Format button. The Format Field window is displayed.

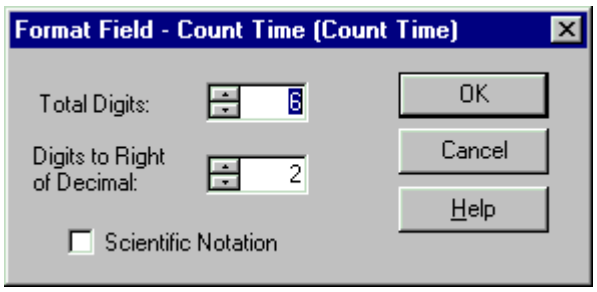

Figure 5-7 Format Field Window

The total number of digits can be specified using the spin buttons or by typing a number in this field. This represents the overall width of the field, including decimal space, integer space and the padding (spaces inserted in front of the value) necessary to fill any unused space. The decimal point (if appropriate) is NOT counted as a digit for this purpose.

The number of digits to the right of the decimal point can also be defined in the same manner. Click OK to save any changes.

For fields that may result in very large or very small numbers, you may choose to report them in Scientific Notation by marking the indicated check box. The following examples indicate the format of this standard notation:

Examples:3.123e+006 is equivalent to 3.123×10^{6} (3,123,000)

3.123e-003 is equivalent to 3.123×10^{-3} (0.003123)

The Format column shows a sample of the format that you have selected for the associated field. The sample is intended to show the number of digits and decimal places that will be used to report this field. The zero character is used to represent a digit that can take on any value appropriate for the field type (alpha and/or numeric).

Equation… button

Click on the **Equation...** button to enter an equation that defines the value reported by the selected Custom Field. The following window will appear:

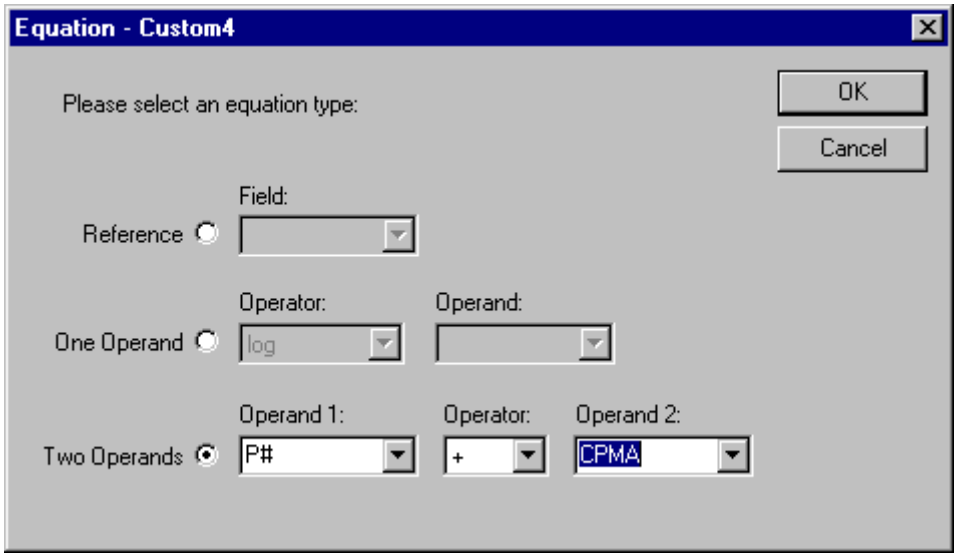

Figure 5-8 Equation Dialog Box

Reference

Click on the Reference (radio) button if you want to select a single value for this Custom Field. The value may be a constant value that you enter or the value from some other defined field in the drop-down list marked Field.

One Operand

Click on the One Operand (radio) button to select from a list of unary operators (operators that work on a single operand) and a single field from the drop-down listed marked **Operand**.

Operator

This drop down box contains the unary operators (operators that work on a single operand): **log** (common logarithm), **exp** (inverse natural logarithm) and **sqrt** (square root).

Operand

This drop-down box contains the defined report fields that yield a numeric value. You can type a numeric constant (either an integer or a floating point number) into this field or select one of the entries from the drop-down list.

Two Operands
Selecting this (radio) button allows you to select two data fields (operands) from drop-down lists of defined report fields and a binary operator to perform the desired calculation.

Operand 1
This drop-down list box contains the defined report fields that yield a numeric value. No alphabetic standard or blank custom fields are available.

You can type in a numeric constant (either an integer or a floating point number) into the field or select from the entries in the drop-down list.

Operator
This drop-down allows you to select the following binary operators:

+ addition

-subtraction

/division

*multiplication

Operand 2
This drop-down list contains the defined report data fields that yield a numeric value. No alphabetic standard or blank custom fields are available.

You can type in a numeric constant (either an integer or a floating point number) into the field or select from the entries in the drop-down box.

Report Block Data

When defining reports for your assay, you can choose to include Block Data Items, as well as the individual fields related to the sample counting. Block Data Items are comprised of a predetermined set of data about the system, the assay or the samples. These Block Data Items are included in printed reports and Rich Text Files (RTF). The other output types, Data Files and RS-232, will NOT include the selected Block Data Items.

Note:Some of the information available in the Block Data Items may also be included in the RS-232 output by marking appropriate check boxes when choosing the RS-232 output type. This is NOT controlled through the use of Block Data Item mechanism described here.

Available Block Data Items include:

- SpectraView Block Data
- IPA Data-Block Data
- Assay Definition
- Quench Curve-Block Data
- I.D. (Instrument Data) Block Data

Block Data items can also be used to send files to an external device via the RS-232 communications port. All data sent via this method will be in ASCII format. IPA data can be transmitted through the RS-232 communications port by selecting this option in the IPA Definitions window.

Assay Definition - Block Data

Select this Block Data Item to include information regarding the parameters used to count the assay in your printed (or RTF) report. These parameters include those defined on the Assay Parameters tab, Count Conditions tab and Count Corrections tab when defining an assay.

IPA Data-Block Data

Select this Block Data Item to include information from the last set of acquired IPA data in your printed (and RTF file) reports. This Block Data Item contains information regarding efficiency, background, figure of merit and Chi-square for the Tritium and Carbon-14 performance of the system.

Instrument Data-Block Data

If you would like for certain instrument related data to be included in your printed (or RTF file) reports, select this Block Data Item from the list. This block of data contains information about the instrument and software. The following keywords and values are contained in the Instrument Data-Block Data Item.

Keyword	Value
MACHINE=	Instrument model number
VERSION=	Software version
MAXP#=	Number of available protocols
CRT=	Type of video (monochrome or color)
LPT=	Printer port
\EOF=	End-Of-File

Figure 5-9 Instrument Data-Block Data Item Keywords

SpectraView-Block Data

This Block Data item allows you to print a graphical display of the spectrum for each sample.

Report Field Order

Displays the order and format in which the report fields will be output. Fields highlighted in yellow will not fit on a single sample line when printing the report. These fields will be wrapped to a second line for printed and RTF reports. The data output window does NOT wrap on the screen. This highlight is the only indication of how the sample lines in your printed reports will be formatted.

Move Report Field Order

Use the button to move a selected field to the left.

Use the button to move a selected field to the right.

Report Output

The Report Output tab allows you to customize the output of the report.

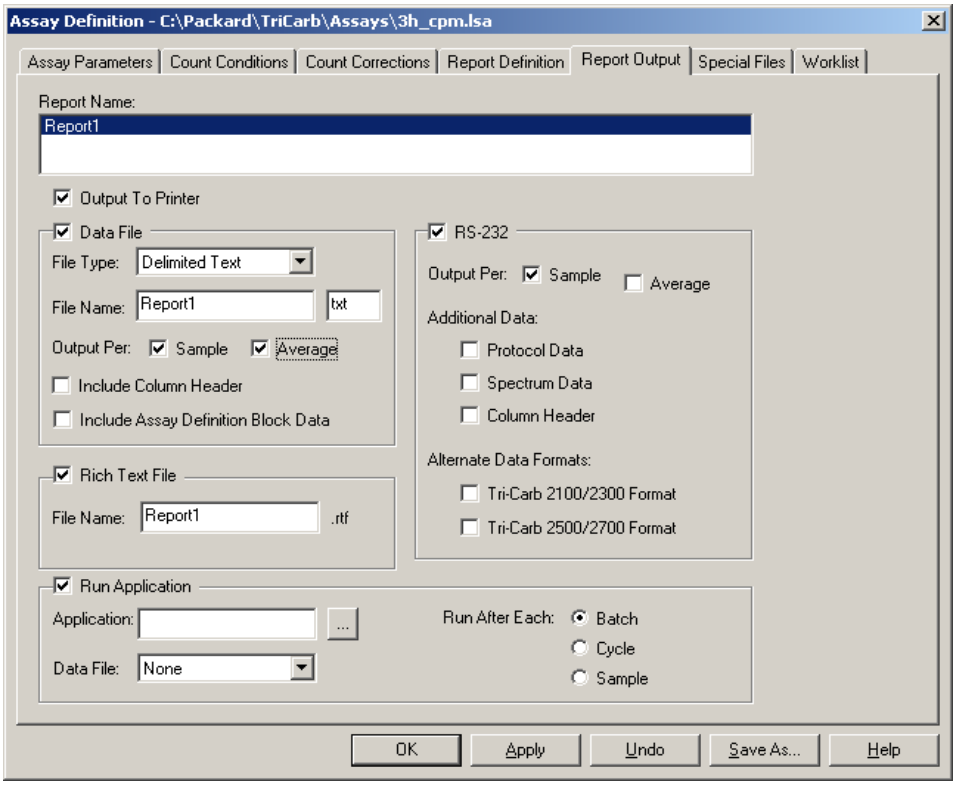

Figure 5-10 Assay Definition - Report Output Tab.

Report Name

This box allows you to select a named report for output.

Output To Printer

Select this to send the report to the printer. Data from an assay will automatically print once an assay count cycle is completed.

Data File

Check this to output the data for the specified type of file.

File Type

QuantaSmart automatically saves data for internal use and Replay (if available) as dated Results files. These files are completely separate from the data files that you are defining here. This data file provides count data to other programs or archival facilities. You can select the ASCII file type for this auxiliary data file using the drop down list. The data fields that will be included in the file are defined by the Report Definition.

Auto Incrementing - The file is named by automatically incrementing a numerical extension each time that QuantaSmart generates the file. This prevents the data from being overwritten from one run to the next.

Delimited Text - Generates data as delimited ASCII text. If you enter a numerical extension, this selection is identical to the Auto Incrementing selection described above.

Excel - Generates data compatible with Microsoft® Excel.

Lotus - Generates data compatible with Lotus® 1-2-3.

Note: The field delimiter is defined by the Windows NT operating system, using the LIST SEPARATOR field on the NUMBER tab of the REGIONAL SETTINGS PROPERTIES window accessed from the CONTROL PANEL.

File Name

Enter the desired name for your data file in this field. If you choose the Delimited Text type, you can also enter any file extension that you want to use for the name. All other file types have the extension predefined by convention. These predefined extensions are:

Excel - csv

Lotus - 123

Auto Increment - ### (incrementing numeric)

Delimited Text - txt (default, user selectable).

Output per Sample and/or Average

Select Sample and/or Average to indicate the type of data to be included in the output. **Average** allows the data file to contain one line of data for each average data line in the output window. **Sample** allows the data file to contain one line of data for each sample data line in the output window. Checking both Sample and Average allows the data file to contain one line of data for each average data line and one line of data for each sample data line.

Include Column Header

Check this box if you want headers included at the beginning of the data file for each data field.

Include Assay Definition Block Data

Check this box if you want the Block Data information included in the data file output.

RS-232

Check this to allow QuantaSmart to transmit lines of sample data via the RS-232 port.

Choose either Output per: Sample and/or Average.

Output per Average: allows QuantaSmart to transmit one line of data for each average data line in the output window.

Output per Sample: allows QuantaSmart to transmit one line of data for each sample data line in the output window.

The default selection is Sample.

Additional Data

Mark the appropriate check boxes for additional information that you would like included in the RS-232 output. You can choose any combination of the following three data items as desired.

	2800/2900/3100 Format	**2500/2700 Format**	**2100/2300 Format**
Protocol Data	Before First Sample	Before First Sample	Before First Sample (after Spectrum Data, if enabled.
Spectrum Data	After All Samples	After All Samples	Before Each Sample
Column Headers	Before First Sample	Before First Sample	Before First Sample

Alternate Data Formats

Mark one of the check boxes for an alternate RS-232 format. You can choose to emulate the format from either a Model 2100 / Model 2300 TriCarb liquid scintillation analyzer or a Model 2500 / Model 2700 Tri-Carb LSA. If you choose not to emulate either of these alternate formats, your RS-232 data will appear as defined by the selected Report Definition. You may NOT choose to emulate both alternate data formats simultaneously.

Rich Text File

Enter a descriptive filename for the rich text file. QuantaSmart will automatically assign an extension of RTF, the standard extension for a rich text file. The RTF file is essentially a carbon copy of the output window.

Run Application

Select this to use the Tandem Processing feature of the system. This will cause an external program to further process your data. If information is entered in any of the fields, but the Run Application checkbox is unchecked, the information in the fields is retained, but they are “grayed out.”

Application

When you mark the Run Application check box on the Report Output tab, you can enter the name and location of a particular Tandem Processing application that you want to run. If necessary, you can use the button to “browse” for the application.

Application Browse Button

Click this button to display the browse window. Tandem processing allows the instrument to analyze samples, perform data reduction and automatically pass the data to an application program.

Data File

Select the type of data file to be processed by the application. The appropriate filename will be “passed to the application” as a “command line parameter”.

Options in the drop down list are:

Data File - the file defined in the Data File section above is used

Rich Text File - the file defined in the Rich Text File section above is used.

None - No specific data file is identified for use.

Run After Each Batch, Cycle, or Sample

Click on a (radio) button to specify when the application is to be run.

Batch – the application program will run once at the end of the protocol.

Cycle – the application program will run at the end of each cycle.

Sample – the application program will run after each sample.

Special Files

The Special Files window allows you to select and configure information regarding files pertinent to the assays.

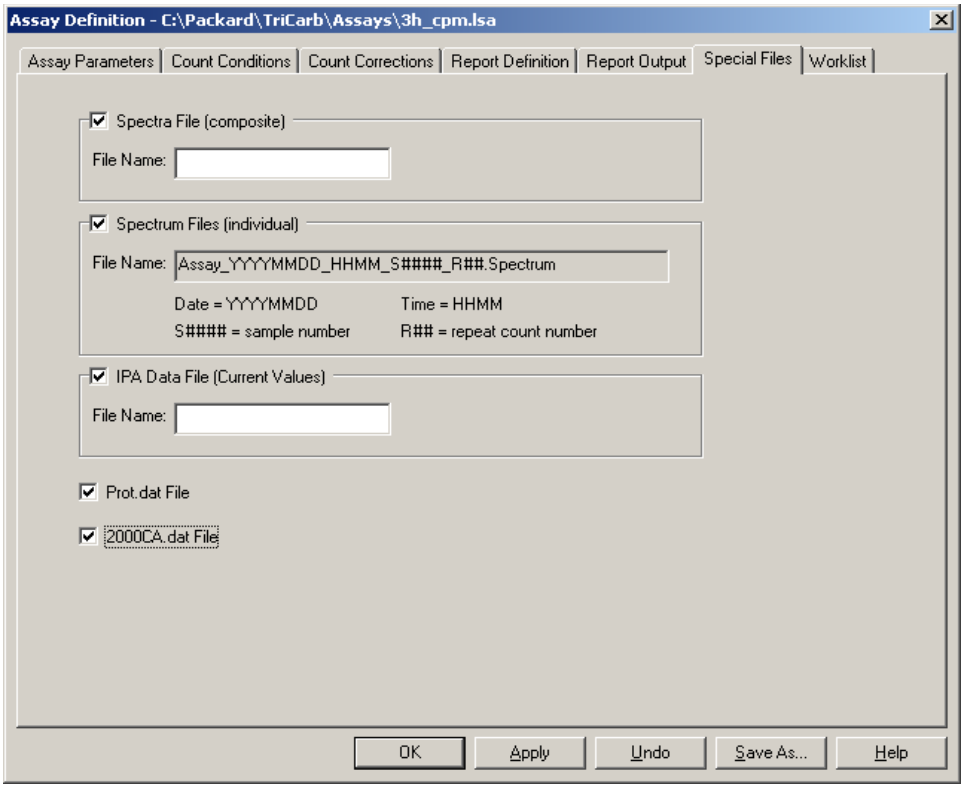

Figure 5-11 Assay Definition - Special Files Tab.

Spectra File (composite)

Selecting this checkbox causes QuantaSmart to generate a single, composite, ASCII spectra file that contains all of the samples counted in the assay. Each individual sample spectrum is appended to the end of this composite file as it is counted so that you end up with all of the sample data in it.

The data file format is similar to that created for individual spectrum files as shown in, with count parameters for a single sample in a header and the channel data listed serially after it. The protocol number, sample number and sample repeat value precede each parameter header to identify the individual sample spectrums within the file.

Enter a name for the file in the box. The composite spectra file will be created in the **Output Data Path** (**Raw Data Path for Replay** if used from Replay) identified in the Data Paths window.

Keywords	Values
CTIME=	Sample count time defined in protocol
TSIE=	Quench Indicating Parameter defined in protocol
LLA=	Lower counting limit for region A
ULA=	Upper counting limit for region A
LLB=	Lower counting limit for region B
ULB=	Upper counting limit for region B
LLC=	Lower counting limit for region C
ULC=	Upper counting limit for region C
COIN_TIME=	Coincidence Time defined in protocol
DELAY_BEFORE_BURST	Delay Before Burst defined in protocol
COUNT_MODE=	Count Mode defined in protocol
COMMENTS:	Comments
COUNTS	List of counts/channel (1 channel/line)

Figure 5-12 Spectrum File Format.

Spectrum Files (individual)

If you are performing a Tandem Processing application that requires Spectrum files, you must check this box to create the individual sample spectrum data files in the Output Data Path directory for the assay. A Spectrum file is an ASCII text file that contains the spectral data for a single sample (a separate file is created for each sample). The spectral data is reported in 0.5keV increments, up to the highest endpoint of the defined regions being counted (one channel is reported per line).

Spectrum Filename

Spectrum data files are created with a filename that corresponds to the following structure.

3HCPM_20040511_1024_S0001_R01.Spectrum

where 3HCPM = protocol name;

20040511= the year, month and day;

1024= the hour and minute;

S0001= the sample number;

R01=the sample repeat count number;

.Spectrum= the file extension.

Note: In the Alpha/Beta count mode, the alpha spectrum is stored to a separate file with a similar naming convention. The alpha spectrum file is identified in the extension with an "_A" following the repeat count value. From the example above, the alpha spectrum file would be named:

3HCPM_20040511_1024_S0001_R01_A.Spectrum

IPA Data File (Current Values)

Selecting this checkbox causes QuantaSmart to generate an IPA data file containing the most recent IPA parameter values.

Enter a name for the file in the box.

Prot.dat File

Selecting this checkbox causes QuantaSmart to generate a Prot.dat file containing information regarding the protocol. The Prot.dat file is an ASCII text file that contains information regarding a protocol. The following keywords and values are contained in the Prot.dat file.

2000CA.dat File

Selecting this checkbox causes QuantaSmart to generate a 2000CA.dat file, an ASCII, comma-delimited text file that contains information about a protocol.

Worklist

The Worklist tab in the Assay Definition window allows you to designate Positive Identification numbers and sample names that correspond to sample numbers on a printout or electronic report. You may also create a Sample List Library of frequently used sample names. The Worklist feature is optional on 2800 and 2900 series instruments.

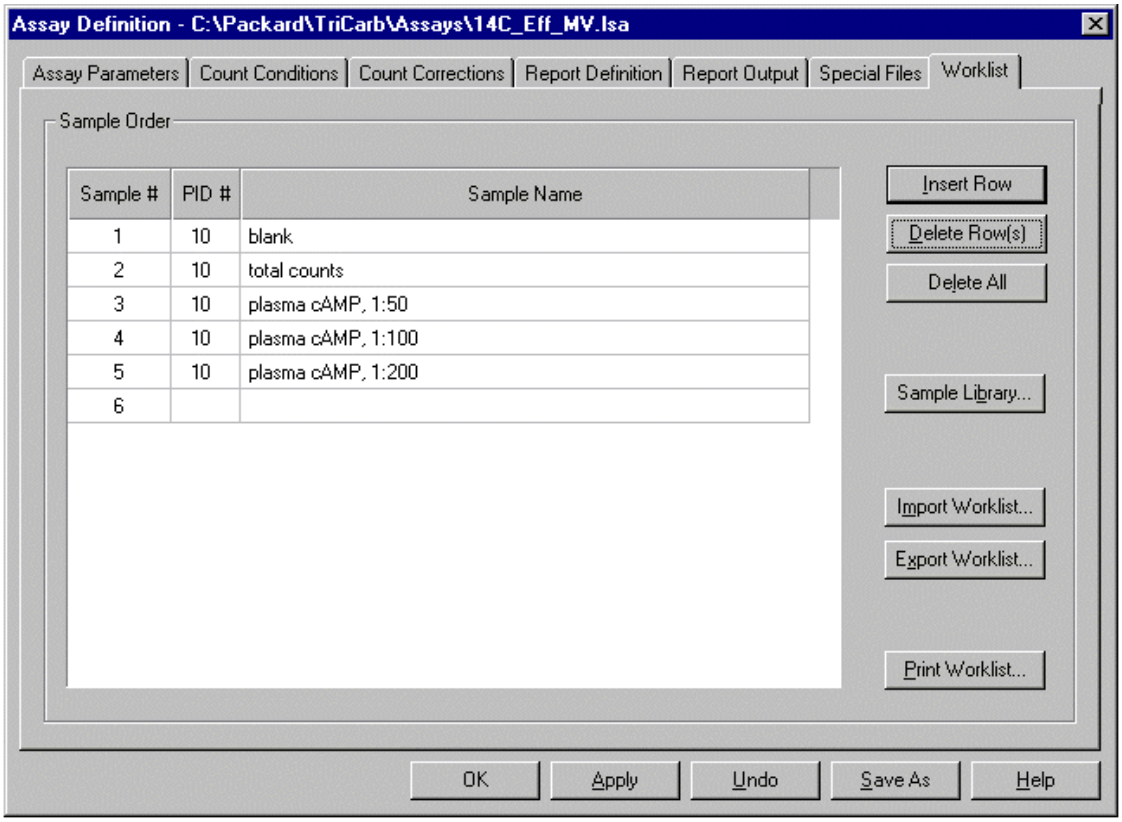

Figure 5-13 Assay Definition - Worklist Tab.

Sample

This represents the sample number on the printout or electronic report.

PID#
This is the Positive (Sample) Identification number. Enter the cassette number (located on the end of each cassette) that is used to hold each sample. Position one in the cassette corresponds to Sample #1 in the worklist.

Note: If you have empty cassette positions, the corresponding sample in the Worklist should be left blank.

Sample Name
Enter descriptive names for each sample number. The maximum characters entered is twenty-five.

Insert Row
Click this button to add a blank row to the Sample Order table.

Delete Row
Click this button to delete selected rows from the Sample Order table.

Delete All
Click this button to delete all rows from the Sample Order table.

Sample Library
Click this button to display the Sample Library window. This window is used to create lists of frequently used sample names for the Sample List Library.

Import Worklist
Sample ID names that have been saved in ASCII format may be imported into Worklist. Click this button if you would like to import a worklist. The Import Worklist window is displayed. Select the file you would like to import as a worklist and click Open.

About the imported file: The file must have the exact header with the exact case and punctuation as shown in the example below. This is the format used by the Export Worklist function.

Export Worklist

Sample ID names can be exported from Worklist for future used. Any files that you export will be saved in ASCII format. Click this button to export a Worklist. The Export Worklist window is displayed. Enter a descriptive name for the Worklist and click Save.

The exported worklist file is saved in the required format so that you can later use the Import Worklist function to reuse it if desired.

Note: The default folder for exporting Worklists is the Libraries folder. Worklists can be saved to other folders, as necessary.

Print Worklist

Click this button to print a Worklist.

Chapter 6

Libraries

Radionuclide information is stored and accessed in the Nuclide Library. The Nuclide Library consists of the Quench Standards and Sample Nuclides Libraries. If your instrument is equipped with an Alpha Beta option, an Alpha Beta Standards and an Alpha Beta Nuclides Library will also be included.

The Quench Standards Library is comprised quench sets, with each quench set containing individual quench standards. The data from the quench standards is used to construct quench curves for calculating DPM (Disintegrations Per Minute) in DPM Assays. Quench Standards are counted once and the entire spectrum for each quench standard is stored independent of assay information. This allows you to select and use the same quench set in any number of assays and construct a quench curve for each sample at the time the sample is counted.

The Sample Nuclides Library allows you to specify and save nuclide names, counting region limits and quench sets for sample nuclides. Up to three nuclides can be defined for each entry to support the counting of multiple nuclides. These sample nuclide parameters are typically specified as part of the assay definition process and may be edited as needed.

The Alpha Beta Standards and Alpha Beta Nuclides Libraries are used in the same manner as the Quench Standards and Sample Nuclides Libraries. The information stored in these libraries is relevant only when performing Alpha Beta Assays, where both an Alpha-emitting and a Beta-emitting radionuclide are quantified independently within the same sample vial.

Sample Nuclides Library

The Sample Nuclides window allows you to enter information into and retrieve information from the Sample Nuclides Library.

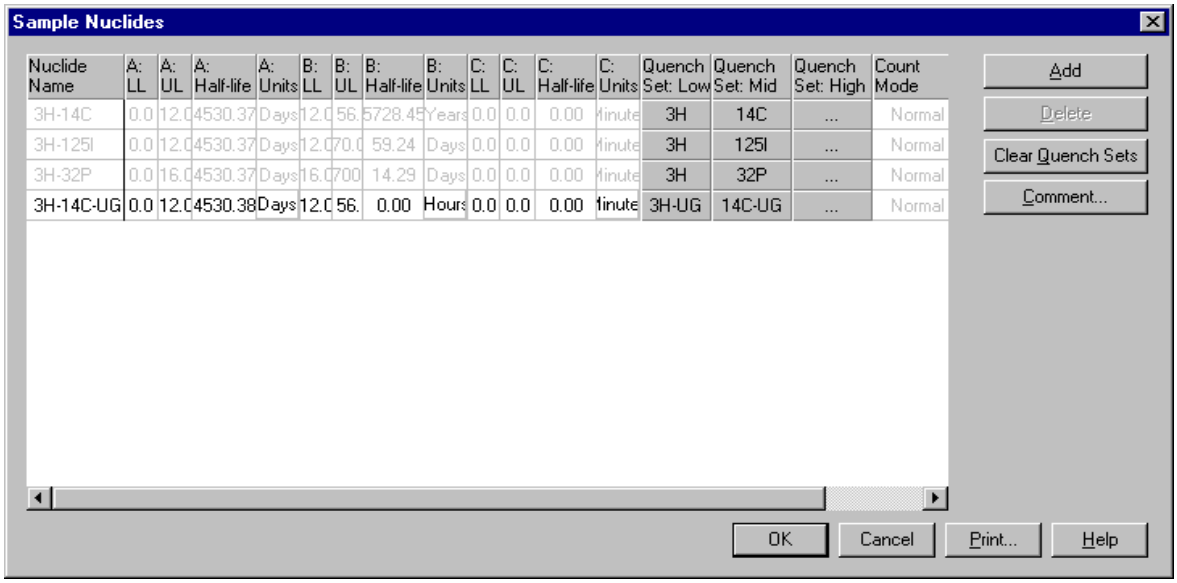

Figure 6-1 Sample Nuclides Library Window

For assays, use the Sample Nuclides Library to define and save nuclide names and counting region limits for radionuclides. You can also select a quench set for each sample nuclide using the Quench Set buttons in this window.

In Replay, use the Sample Nuclide Library to select a radionuclide for the purpose of reanalyzing sample data.

Note: The fields that are enabled in the Sample Nuclides Library will be different when accessed from different locations within the software. The list of nuclides that is displayed is dependent on the assay type, the nuclide and the number of quench sets associated with the nuclide.

Nuclide Name

Select the appropriate nuclide(s) for your assay from the list and click OK. If you would like to define a different nuclide, click the Add button and type the name of the nuclide you would like to count. Define the parameters in the fields displayed in the new row in the table and click OK. To delete a nuclide from the list, select that nuclide, click the Delete button and click OK.

A:LL - Lower Limit Region A

This field represents the lower counting limit for region A, measured in keV.

A:UL - Upper Limit Region A
This field represents the upper counting limit for region A, measured in keV.

A:Half Life - Half Life of Nuclide A
This field represents the half-life of nuclide A.

A:Units - Units for Region A
This field represents the units for the half-life of nuclide A.

B:LL - Lower Limit Region B
This field represents the lower counting limit for region B, measured in keV.

B:UL - Upper Limit Region B
This field represents the upper counting limit for region B, measured in keV.

B:Half Life - Half Life of Nuclide B
This field represents the half-life of nuclide B.

B:Units - Units for Region B
This field represents the units for the half-life of nuclide B.

C:LL - Lower Limit Region C
This field represents the lower counting limit for region C, measured in keV.

C:UL - Upper Limit Region C
This field represents the upper counting limit for region C, measured in keV.

C:Half Life - Half Life of Nuclide C
This field represents the half-life of nuclide C.

C:Units - Units for Region C
This field represents the units for the half-life of nuclide C.

Quench Set:Low, Mid, High - Quench Sets
Select a quench set by clicking one or more of the quench set buttons. Select the Quench Set Low set if you are counting one nuclide in one counting region, the Quench Set Medium if you are counting two nuclides in two counting regions and the Quench Set High if you are counting three nuclides in three counting regions. The Quench Standards Library window is displayed. Select the name of the quench standards you would like to use for calculating DPM values. The names of the quench sets selected should appear on the Quench Set buttons. Note: Depending on the DPM options installed, you may not have access to all three quench sets.

Add
Click this button to add a line to the table and enter the new nuclide name. Manually enter regions A, B, and C.

Delete
Click this button to delete a selected entry from the table.

Clear Quench Sets
Click this button to unlink all of the quench sets that are linked to the selected sample nuclide. To unlink individual quench sets from a sample nuclide, right-click on the corresponding quench set button in the Sample Nuclides table and select Clear Quench Set.

Comment
Click this button if you would like to enter descriptive comments. The Comment window is displayed.

Count Mode (Normal, High Sensitivity, Low Level, Ultra Low Level)
This field is for display purposes only. It represents the Count Mode used to count the quench standards which was defined in the Quench standards assay.

Note:The count mode associated with the Quench standards will be used in DPM assays when linking the Quench set(s) to the sample nuclides.

Quench Standards Library

The Quench Standards window allows you to enter information into and retrieve information from the Quench Standards Library.

The data from these quench sets is used to construct quench curves for determining DPM (Disintegrations Per Minute) in DPM Assays. Use the Quench Standards Library to define and save the name, maximum energy value and the number of standards for each quench set for Quench Standards Assays. Quench standards are counted once and the entire spectrum for each quench standard is stored in the Quench Standards Library. This allows you to select and use the same quench set in any number of assays.

In Replay, the Quench Standards window allows you to select a quench standards set for the purpose of reanalyzing sample data. The data from these quench sets is used to construct quench curves for determining sample DPM (Disintegrations Per Minute).

Note: The fields that are enabled in the Quench Standards Library will be different when accessed from different locations within the software.

To count a new quench curve, the following needs to be entered in the quench standards library:

- Add a name
- Max keV
- DPM value

# of Standards, Count Mode, Coincidence Time, Delay Before Burst, Date Counted, and Time Counted will be filled after quench standards is counted.

Alpha Beta Nuclide Library (not available on the 2800TR)

You can use the Alpha Beta Nuclides Library to define and save Alpha and Beta nuclide names, their associated counting regions, the instrument's discriminator setting (this allows discrimination between alpha and beta events). Using the Standard Set button located in (column 2) of this library, you can reference parameters established for an existing Standard Set.

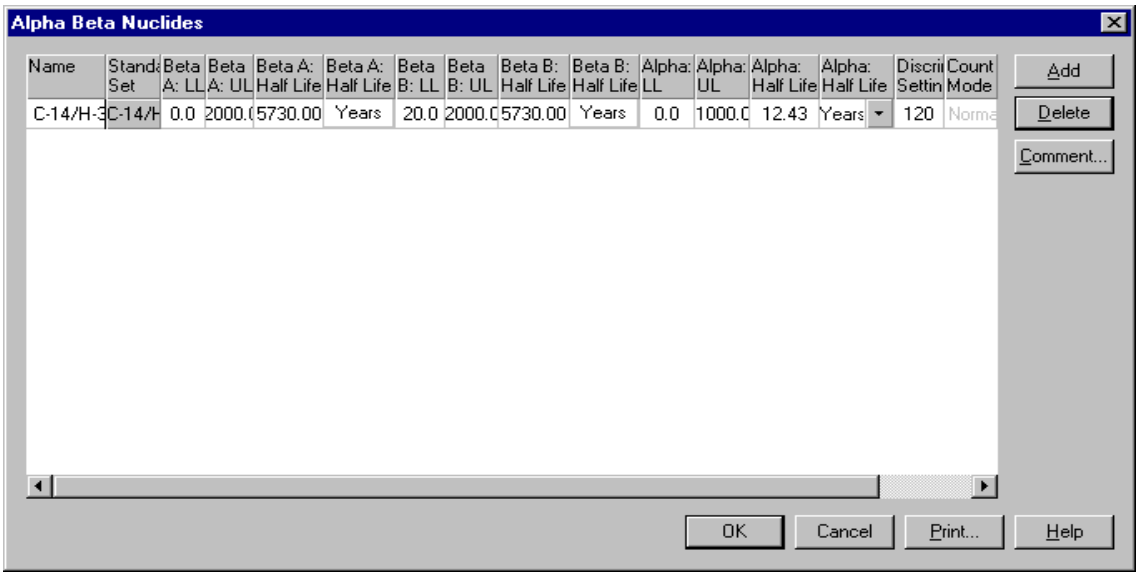

Figure 6-2 Alpha Beta Nuclide Library Window.

Name

This is the name given to the alpha beta nuclide. To type in a new name click on the ADD button. This will create an additional row to define a new nuclide. Type in the desired name to be used in an alpha beta assay.

Standard Set

This is the name of the Alpha Beta Standard set that will be linked (associated) with the Alpha Beta Nuclide name. Clicking on this field displays the entire Alpha Beta Standards library. In the Alpha Beta Standards Library, highlight the desired standard set you wish to link to the nuclide and press OK. That name will now appear next to the Alpha Beta Nuclide name.

Beta A:LL

This is the lower limit of the counting region for the Beta nuclide in Region A, in keV.

Note:This value cannot exceed 2000

Beta A:UL
This is the upper limit of the counting region for the Beta nuclide in Region A, in keV.

Note:This value cannot exceed 2000.

Beta A Half life
For Region A, enter the numeric value for half-life correction, if desired. See the next entry.

Beta A Half Life Units
For Region A, select the appropriate units to apply to the numeric half-life value. Clicking on the field displays a drop down box of available units: minutes, hours weeks, days, or years. Highlight and mouse click on the desired unit.

Beta B:LL
This is the lower limit of the counting region for the Beta nuclide in Region B, in keV.

Note:This value cannot exceed 2000.

Beta B:UL
This is the upper limit of the counting region for the Beta nuclide in Region B, in keV.

Note:This value cannot exceed 2000.

Beta B Half Life
For Region B, enter the numeric value for half-life correction, if desired. See the next entry.

Beta B Half Life Units
For Region B, select the appropriate units to apply to the numeric half-life value. Clicking on the field displays a drop down box of available units: minutes, hours weeks, days, or years. Highlight and mouse click on the desired unit.

Alpha:LL
This is the lower limit of the counting region for the Alpha nuclide, in keV.

Note:This value cannot exceed 1000.

Alpha:UL
This is the upper limit of the counting region for the Alpha nuclide, in keV.

Note:This value cannot exceed 1000.

Alpha: Half Life
Enter the numeric half life value. See the next entry.

Alpha: Half Life Units
Click on the field to display the available units to apply to the numeric half-life value. Highlight and mouse click on the desired unit.

Discriminator Setting
This is the discriminator value corresponding to the Alpha Beta Standards Set linked (associated) with this nuclide, if any. If no Alpha Beta Standard set is linked, then you can enter the discriminator value manually.

Count Mode
If an Alpha Beta Standard Set is referenced by the nuclide, then Normal (Count Mode) is displayed. If no Alpha Beta Standard set is linked then this field remains blank.

Alpha Beta Standards Library
The Alpha Beta Standards window allows you to define an Alpha Beta Standard Set for use with Alpha Beta Assays. Once the information is entered in the Alpha Beta Standards Library, an Alpha Beta Standards Assay can be run to establish the instrument's optimum pulse discriminator value. This value is then used to discriminate between Alpha and Beta nuclides in Alpha Beta Assays.

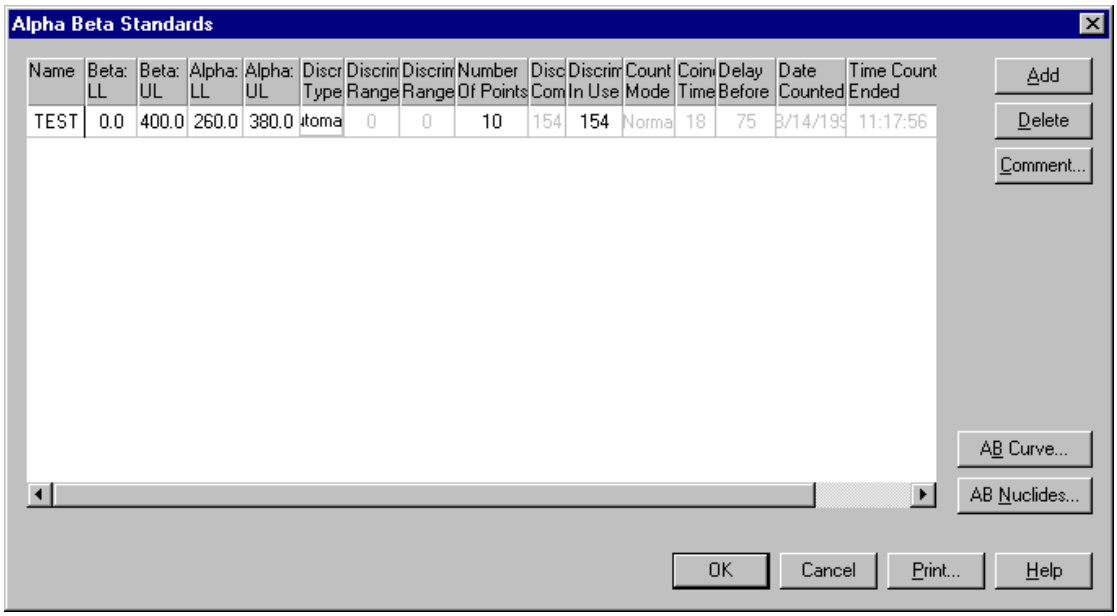

Figure 6-3 Alpha Beta Standard Library Window.

Name
This is the name of the Alpha Beta Standards set. To add a new standards set to the library, click the Add button. A blank line appears in the table. Type in the desired name for the Alpha Beta Standard Set.

Beta:LL
This is the lower limit of the counting region for the Beta nuclide, in keV.

Note: This field is for information only in this library.

Beta:UL
This is the upper limit of the counting region for the Beta nuclide, in keV.

Note: This field is for information only in this library.

Alpha:LL
This is the lower limit of the counting region for the Alpha nuclide, in keV.

Note: This field is for information only in this library.

Alpha:UL
This is the upper limit of the counting region for the Alpha nuclide, in keV.

Note: This field is for information only in this library.

Discriminator Type
Select either Automatic or Manual from the drop-down list. Selecting Automatic allows the instrument to determine the pulse decay discriminator range. Selecting Manual allows you to enter the upper and lower limits for the pulse decay discriminator.

Note:When using Automatic mode, each pure standard source must generate a minimum of 50,000 CPM (Counts Per Minute). There is no activity requirement when using Manual mode.

Discriminator Range: LL
If you selected Manual as the Discriminator Type, you may enter a value between 0 and 255 for the lower limit of the Pulse Decay Discriminator Range.

Discriminator Range: UL
If you selected Manual as the Discriminator Type, you may enter a value between 0 and 255 for the upper limit of the Pulse Decay Discriminator Range.

Number of Points
Enter the number of points you would like to use to manually generate the Alpha and Beta misclassification curves. This is not required if Automatic is chosen in the Discriminator Type. Ten points are used if Automatic is chosen. Up to 15 points can be used if Manual is chosen.

Discriminator Computed
This field represents the optimal Pulse Decay Discriminator value, as determined by the instrument.

Discriminator in Use
This value represents the Pulse Decay Discriminator value currently in use.

Count Mode
Normal is the Count Mode used to count the Alpha and Beta Standards.

Note: This field is for information only.

Coincidence Time
This field represents the Coincidence Time of 18 ηs used when counting the Alpha Beta Standards Assay.

Note: This field is for information only in this library.

Delay Before Burst
This field represents the Delay Before Burst time of 75 ηs used when counting the Alpha Beta Standards Assay.

Note: This field is for information only in this library.

Date Counted
This field represents the date on which the Alpha Beta Standard Assay was counted.

Note: This field is for information only.

Time Count Ended
This field represents the time at which the Alpha Beta Standard Assay was completed.

Note: This field is for information only.

Add
Click this button to add a line to the table and enter a new Alpha Beta Standard Set.

Delete
Click this button to delete a selected entry from the table.

Comment
Click this button if you want to enter descriptive comments. The Comment window will appear.

AB Nuclides
Click this button to display the Alpha Beta Nuclides Library.

AB Curve

Click this button to display the stored Alpha Beta Standard misclassification (spillover) curve for the Standard Set selected in the table.

The Alpha/Beta Standard Curve window shows the data used to calculate the optimal discriminator setting for the Standard Set. This data is generated from counting an Alpha Beta Standards assay. The data points for the curve are shown in a table and are also plotted graphically.

The calculated optimum discriminator setting appears as the Computed value in this window. If you want to further minimize misclassified events for one of the nuclides, you can enter your own discriminator setting for the In Use value instead of using the optimum setting determined by the instrument. Higher values will favor alpha counting and lower values will favor beta counting.

Spillover percentages are shown for both the Computed and In Use values. The In Use setting is reported and used as the Discriminator Setting in the Alpha Beta Standards Library.

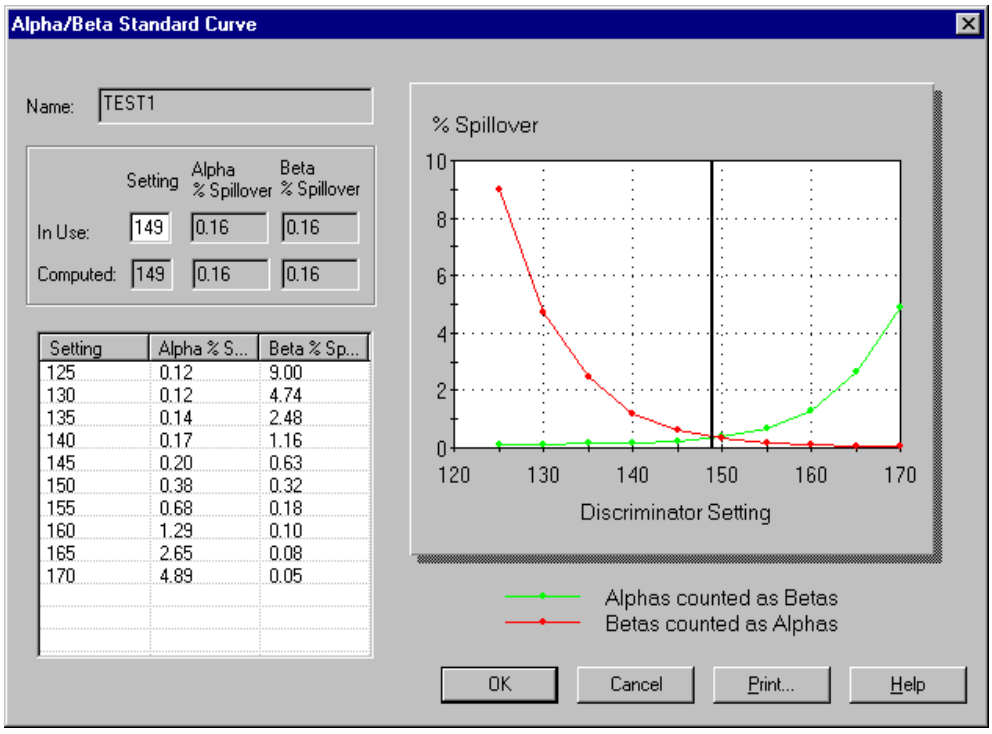

Figure 6-4 Alpha Beta Standard Curve Window.

Chapter 7

Calibration and Normalization

Before any samples are counted, you should calibrate and normalize the system (**S**elf **N**ormalization and **C**alibration - SNC) and assess the performance of the instrument (**I**nstrument **P**erformance **A**ssessment - IPA) The SNC/IPA protocol requires a special protocol flag and cassette loading that depends on your instrument model.

Calibration/Normalization

During the calibration and normalization portion of the SNC, the voltage applied to each of the two Photomultiplier Tubes (PMTs) is adjusted until the tubes have been synchronized in their response to a Carbon-14 standard. Then, the high voltage to both PMTs is adjusted simultaneously until the endpoint of the 14C spectrum falls at the appropriate position in the Spectralyzer (on-board 4000 channel) multi-channel analyzer. This process is designed to ensure that the instrument accurately quantifies the energy from all beta-particle emissions.

IPA

During Instrument Performance Assessment (IPA), the instrument measures background, counting efficiency, sensitivity (Figure-of-Merit) and the reproducibility of sample counting (Chi-Square test). Note: IPA is an optional feature on the 2800 and 2900 series instruments.

When to Perform these Procedures

The calibration, normalization and IPA procedures occur automatically by leaving the Self-Normalization and Calibration (SNC) and IPA cassette (containing the Carbon-14 calibration standard, unquenched Tritium standard and background standard) on the instrument counting deck at all times. Whenever the SNC protocol flag is read by the instrument, a 23-hour timer is checked (this timer only applies to instruments without a BGO detector guard). If 23 hours have elapsed since the previous calibration and normalization, the instrument will perform the SNC/IPA procedure. If 23 hours have not elapsed since the previous calibration and normalization, the SNC/IPA cassette is bypassed and this procedure is not performed. Ideally, the instrument Calibration, Normalization and Instrument Performance Assessment should be performed on this timed, 23-hour (~ daily) cycle. SNC is only initiated if the sample changer is moving. It will not start up at the 23 hour mode. Certain IPA parameters will need to be defined prior to the machine performing the assessment procedures. You may perform instrument calibration, normalization and IPA manually (not using the 23-hour timer) by “resetting” the protocol flag on the cassette.

An IPA report is generated after each IPA procedure is completed. To access the data generated from all IPA runs, select IPA Charts & Tables from the IPA menu.

Instrument Performance Assessment

Instrument Performance Assessment (IPA) is an optional feature on the 2800 and 2900 series instruments.

IPA Definition

Before performing any Instrument Performance Assessment (IPA) you must define the parameters that the instrument will use in the assessment process. To define these parameters, select IPA Definition from the IPA menu. The IPA Definition window is displayed.

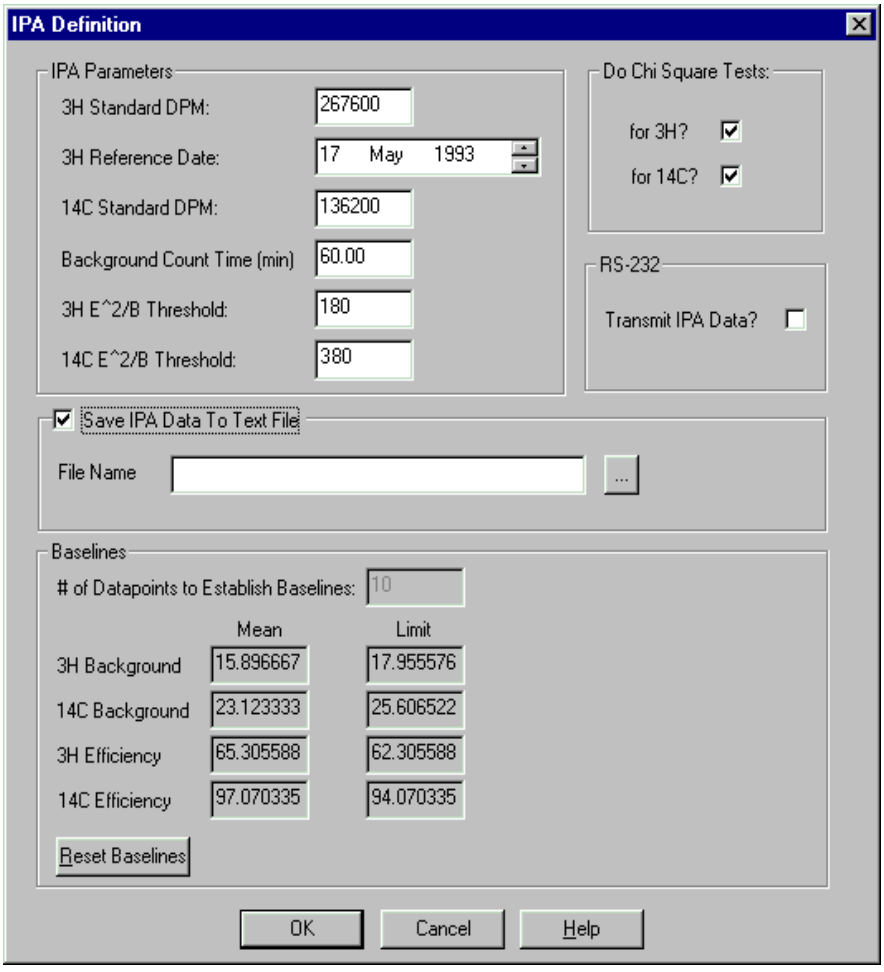

Figure 7-1 IPA Definition Window

Following is a brief description of the IPA Definition fields.

3H (Tritium) Standard DPM

Enter the DPM value for the unquenched, sealed Tritium standard (supplied). The DPM values for standards purchased from PerkinElmer Life and Analytical Sciences are printed on the vial.

3H (Tritium) Reference Date

Enter the reference (calibration) date for the unquenched Tritium standard. This is the date on which the standard has the specified amount of activity. You must enter this value for half-life correction to occur. The reference date for standards purchased from PerkinElmer Life and Analytical Sciences are printed on the vial.

Carbon-14 Standard DPM

Enter the DPM value for the unquenched, sealed Carbon-14 standard (supplied). The DPM values for standards purchased from PerkinElmer Life and Analytical Sciences are printed on the vial. No reference date is required due to the long half-life of Carbon-14.

Background Count Time

This is the length of time (in minutes) the instrument will measure the background counts. The background for both Carbon-14 and Tritium are collected simultaneously. Typically, a 60 minute count time is used to assess background.

Tritium Figure of Merit Threshold

This is the lower limit for the calculated Tritium Figure of Merit value. If the figure of merit value falls below the defined threshold, a message is displayed in the main window. If this occurs, it indicates either an increase in background or a decrease in efficiency. Typically, the default threshold can be used until sufficient IPA data for this parameter is collected and an alternate threshold is established.

Carbon-14 Figure of Merit Threshold

This is the lower limit for the calculated Carbon-14 Figure of Merit value. If the figure of merit value falls below the defined threshold, a message is displayed in the main window. If this occurs, it indicates either an increase in background or a decrease in efficiency. Typically, the default threshold can be used until sufficient IPA data for this parameter is collected and an alternate threshold is established.

Do Chi-Square Test for Tritium?

Mark this box to enable a test that measures the degree of reproducibility for sample counting for Tritium. If the Chi-Square value for a Tritium standard counted 20 times falls within an acceptable range of values, the variation in individual sample counts is a result of the count statistics of the sample, as opposed to an instrument problem.

Do Chi-Square Test for Carbon-14?

Mark this box to enable a test that measures the degree of reproducibility for sample counting for Carbon-14. If the Chi-Square value for a Carbon-14 standard counted 20 times falls within an acceptable range of values, the variation in individual sample counts is a result of the count statistics of the sample, as opposed to an instrument problem.

Note: The range of acceptable values for the Chi-Square test is based on a 95% confidence level. Therefore, statistically, one out of every twenty Chi-Square tests could fail.

RS-232 Transmit IPA Data?

Mark this box if you would like to transmit the IPA data to an external device, via the RS-232 communications port.

Save IPA Data to Text file

Check this box and then enter a filename in the box below to save Instrument Performance Data to a file.

of Datapoints to Establish Baselines

Enter the number of IPA runs you would like to use to generate baselines for Tritium and Carbon-14 background and efficiency. The range for this value is between five and 99. The default setting is five.

Tritium Background Mean and Limit

The instrument calculates the mean value for Tritium background from the number of IPA runs (datapoints) specified. The limit is calculated as the baseline + 4 standard deviations. When the limit is reached, a message is displayed in the main window.

Carbon-14 Background Mean and Limit

The instrument calculates the mean value for Carbon-14 background from the number of IPA runs (datapoints) specified. The limit is calculated as the baseline + 4 standard deviations. When the limit is reached, a message is displayed in the main window.

Tritium Efficiency Mean and Limit

The instrument calculates the mean value for Tritium efficiency from the number of IPA runs (datapoints) specified. The limit is calculated as 3% below the baseline, or less than 58% efficiency. When this limit is exceeded, a message is displayed in the main window.

Carbon-14 Efficiency Mean and Limit

The instrument calculates the mean value for Carbon-14 efficiency from the number of IPA runs (datapoints) specified. The limit is calculated as 3% below the baseline. When this limit is exceeded, a message is displayed in the main window.

Reset Baselines

Click this button to delete the current baselines. The instrument will establish new baselines from the number of datapoints indicated in this window.

Not Processed

This message indicates that Chi-Square data has never been collected. To acquire Chi-Square data for Tritium or Carbon-14, check the corresponding boxes in the IPA Definition window. This window is accessible via the IPA-IPA Definition menu option.

IPA Charts & Tables (optional on TriCarb 2800 and 2900TR)

The following window displays a typical IPA chart and table for Carbon-14 Efficiency:

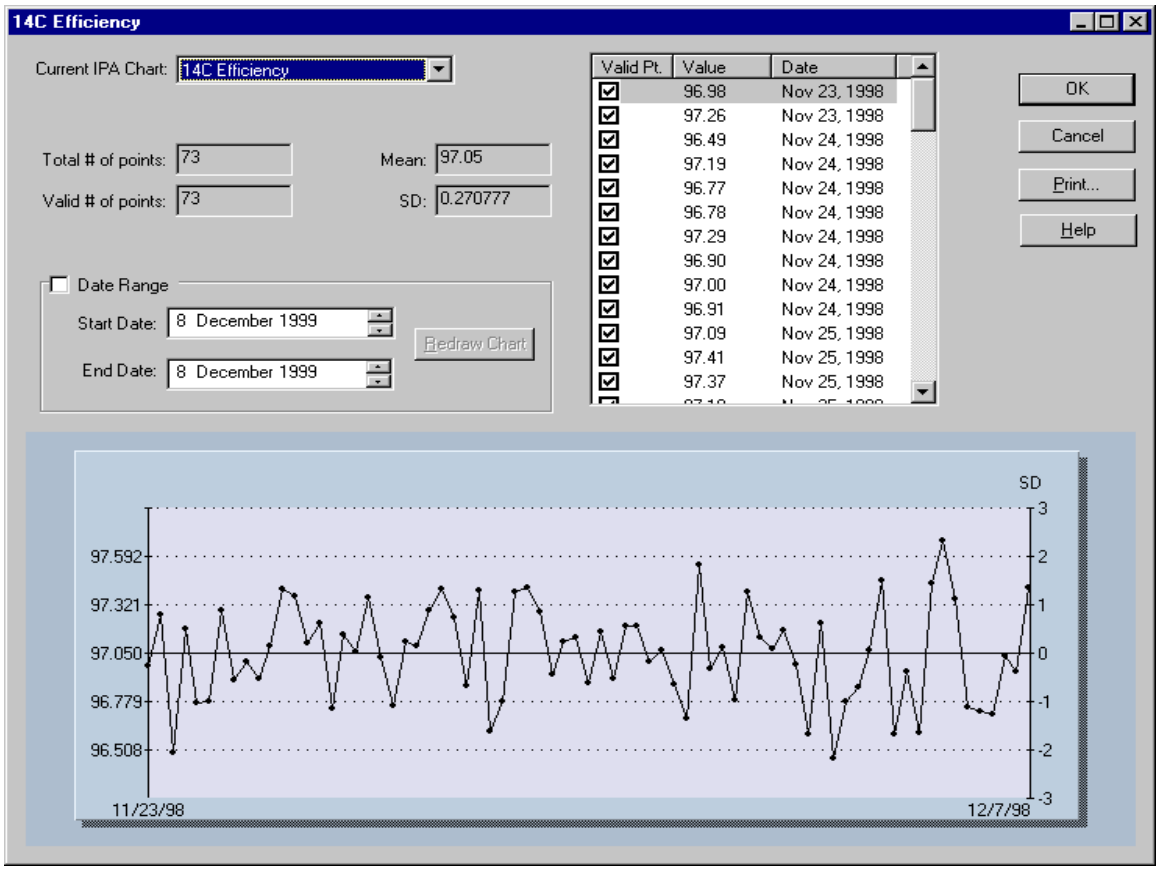

Figure 7-2 IPA Charts & Tables Window

The IPA Charts & Tables window allows you to view, edit and print data for individual IPA parameters in chart or tabular form. When the data is displayed as a table, points can be included or excluded from the data set. The axes on the chart represent the Mean and Standard Deviation values for the selected IPA parameter. Using the Print button, you may print an individual IPA chart or table, or you may print all the IPA charts and tables.

All of the available IPA charts have similar graphical displays and include the same data items.

Current IPA Chart

Select from the drop-down list an IPA parameter that you would like to view in chart or tabular form.

The following IPA Charts are available:

Carbon-14 Background

This chart displays the results of the IPA test for Carbon-14 background counts. This test checks for detector contamination or light leaks. The limit for this parameter is > baseline + 4 standard deviations. The mean and SD for this parameter are recalculated as new IPA data are generated.

Carbon-14 Background Baseline

This chart displays the Carbon-14 background data based on a fixed baseline value. The number of values used to generate the baseline is defined in the IPA Definition window. The default for this setting is five.

Carbon-14 Chi-Square

This chart displays the results of the IPA test that measures the reproducibility of sample counting for Carbon-14. The test is performed by counting a single sample in the detector 20 consecutive times with a count time of 30 seconds for each repeat measurement. The normal range for this value is 7.63 to 36.19. with 95% confidence. A properly performing instrument may generate Chi-Square values outside this range 2% of the time, due to the statistical nature of the test. The mean and standard deviation for this parameter are recalculated as new IPA data are generated.

Carbon-14 Figure of Merit

Figure of Merit (FOM) is a measure of the sensitivity of the instrument for Carbon-14 based on the Carbon-14 background and the instrument's counting efficiency. The mean and standard deviation for this parameter are recalculated as new IPA data are generated.

Carbon-14 Efficiency

This chart displays the results of repeated Carbon-14 efficiency determinations. The mean and standard deviation for this parameter are recalculated as new IPA data are generated.

Carbon-14 Efficiency Baseline

This chart displays the Carbon-14 efficiency data based on a fixed baseline value. The number of values used to generate the baseline is defined in the IPA Definition window. The default for this setting is five.

Tritium Background Baseline
This chart displays the Tritium background data based on a fixed baseline value. The number of values used to generate the baseline is defined in the IPA Definition window. The default for this setting is five.

Tritium Chi-Square
This chart displays the results of the IPA test that measures the reproducibility of sample counting for Tritium. The test is performed by counting a single sample in the detector 20 consecutive times with a count time of 30 seconds for each repeat measurement. The normal range for this value is 7.63 to 36.19. with 95% confidence. A properly performing instrument may generate Chi-Square values outside this range 2% of the time, due to the statistical nature of the test. The mean and standard deviation for this parameter are recalculated as new IPA data are generated.

Tritium Efficiency
This chart displays the results of repeated Tritium efficiency determinations. The mean and standard deviation for this parameter are recalculated as new IPA data are generated. The limit for this parameter is < baseline minus 3%.

Tritium Efficiency Baseline
This chart displays the Tritium efficiency data based on a fixed baseline value. The number of values used to generate the baseline is defined in the IPA Definition window. The default for this setting is five.

Tritium Figure of Merit
Figure of Merit (FOM) is a measure of the sensitivity of the instrument for Tritium based on the Tritium background and the instrument's counting efficiency. The mean and standard deviation for this parameter are recalculated as new IPA data is generated.

Tritium Background
This chart displays the results of the IPA test for Tritium background counts. This test checks for detector contamination or light leaks. The limit for this parameter is > baseline + 4 standard deviations. The mean and SD for this parameter are recalculated as new IPA data are generated.

Total # of Points
This field indicates the total number of data points available for the selected IPA parameter.

Mean
This field displays the Mean value of the selected IPA parameter as calculated from all the included data points. A deleted data point is not used to determine the mean value of the IPA parameter.

Valid # of Points

This field indicates the number of points used to generate the selected chart.

SD

This field displays the Standard Deviation of the selected IPA parameter as calculated from all the included data points. A deleted data point is not used to determine the Standard Deviation of the IPA parameter.

IPA Reports

The following display shows the IPA Report window with no current warning messages. Any performance parameter that fails to meet specification will generate a warning message at the top of the report. Any IPA or calibration operation that fails to complete satisfactorily will result in an error message reported for this run.

Any IPA errors or warnings displayed at the bottom of the report represent the most recent status of any given IPA parameter that generated a message during an IPA run. The dates for each error or warning may vary to reflect the most recent date on which data for that individual IPA parameter was acquired.

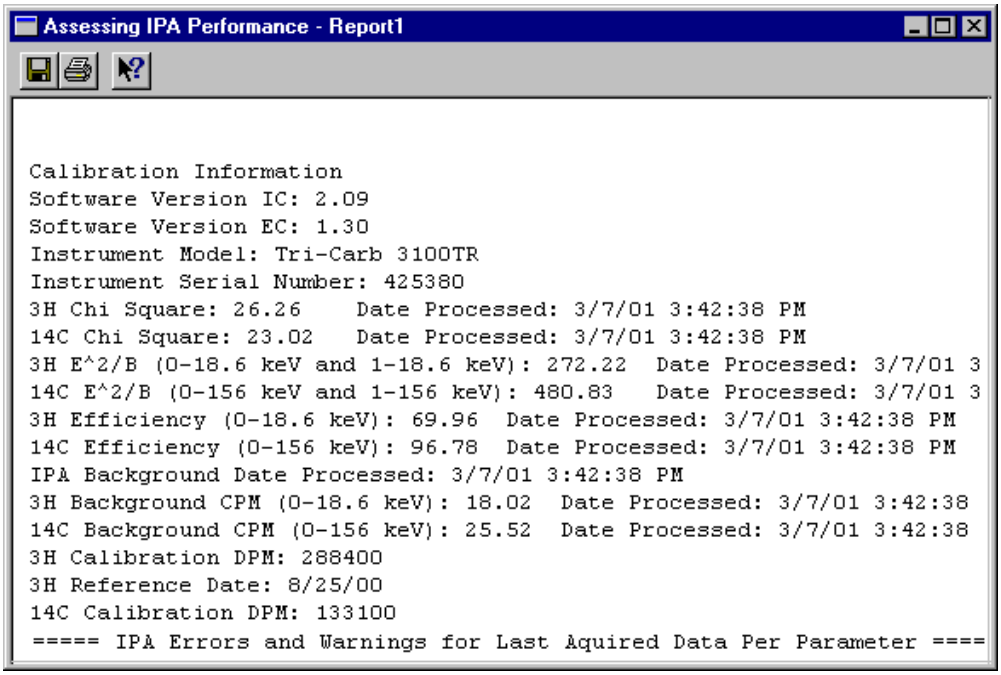

Figure 7-3 An IPA Report

This IPA report will print after the IPA procedure is completed.

SNC for an Instrument without Super Low Level Counting

This procedure is intended for those systems that DO NOT have the BGO detector guard. After defining the IPA parameters:

To run the SNC/IPA protocol, regardless of how long it has been since it last ran, reset the SNC protocol flag to the “reset position (the flag is all the way to the left when the flag is on the left end of the cassette). If the protocol flag is not “reset”, the SNC/IPA protocol will only run if 23 hours have elapsed since the last time that the protocol was run.

Note: The cassette must be loaded in the following order:

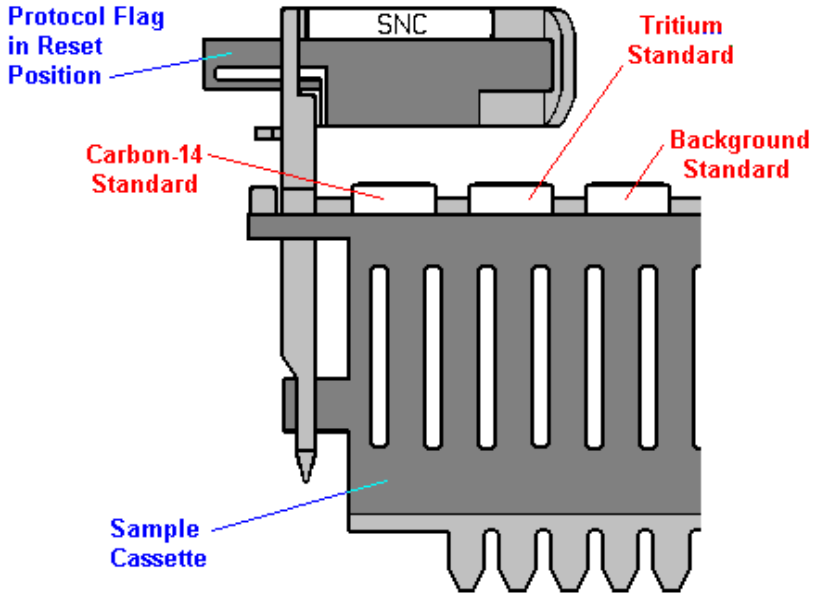

Figure 7-4 Standard SNC/IPA Cassette Loading.

8. Load the purged, unquenched Carbon-14 standard (supplied) into the first position of the cassette (this is at the same end as the protocol flag).

Caution: Do not use the unpurged, Low Level standards to calibrate the instrument, even if the instrument is to be used in Low Level, High Sensitivity or Super Low Level count mode.

9. Load the purged, unquenched Tritium standard (supplied) into the second cassette position.
10. Load the purged background standard (supplied) into the third cassette position.

If the instrument is IDLE (not counting):

11. Load the calibration cassette on the right-hand side of the sample changer deck such that you can read the protocol flag.

    Press the **Start** button to begin counting.

If the instrument is currently counting a sample:

Load the calibration cassette after the last cassette belonging to the current protocol. When the current protocol is completed, the calibration cassette will automatically move into the counting position. After the SNC flag is read by the instrument, the calibration, normalization and IPA procedure begins and the flag is automatically returned to the “non-reset” position.

To access the data generated from the IPA runs, select IPA Charts & Tables (optional on the Tri-Carb 2900TR) from the IPA menu.

SNC for Super Low Level Counting (with BGO detector guard)

This procedure is intended for those systems that are equipped with the BGO detector guard (Tri-Carb® 3170TR/SL). After defining the IPA parameters:

1. The SNC/IPA protocol will run every time that the protocol plug is recognized, regardless of the state of the protocol flag or how long it has been since it was last run.

Note: The cassette must be loaded in the following order:

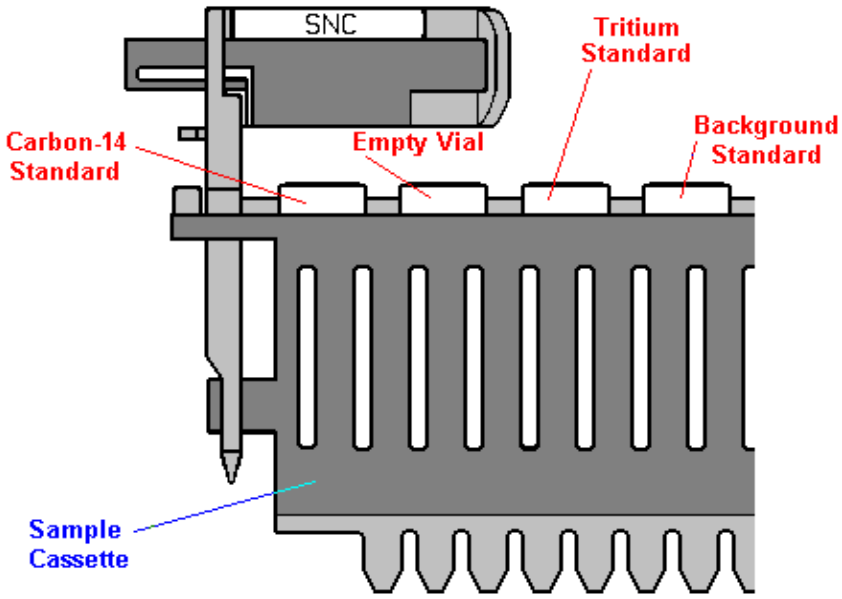

Figure 7-5 Super Low Level SNC/IPA Cassette Loading.

2. Load the purged, unquenched Carbon-14 standard (supplied) into the first position of the cassette (this is at the same end as the protocol flag).

Caution: Do not use the unpurged, Low Level standards to calibrate the instrument, even if the instrument is to be used in the Super Low Level count mode.

3. Load an empty vial into the second cassette position. This is used to establish the normalization spectrum for the BGO detector guard.

Note:The empty vial must be of the same type and material that will used to count low level samples.

If you wish to re-normalize the system for a different sample counting vial, rerun SNC with only the new vial in position two of the SNC cassette. An SNC cassette with an appropriate vial in position two may precede any assay using different vial types.

4. Load the purged, unquenched Tritium standard into the third cassette position.
5. Load the purged background standard into the fourth cassette position.

If the instrument is IDLE (not counting):

Load the calibration cassette on the right-hand side of the sample changer deck such that you can read the protocol flag.

Press the **Start** button to begin counting.

If the instrument is currently counting a sample:

Load the calibration cassette after the last cassette belonging to the current protocol. When the current protocol is completed, the calibration cassette will automatically move into the counting position. After the SNC flag is read by the instrument, the calibration, normalization and IPA procedure begins.

Once you have defined the IPA parameters and performed IPA, you can access the data generated from the IPA runs by selecting IPA Charts & Tables from the IPA menu.

Chapter 8

Advanced Features

Priostat

Priostat allows you direct control over several sample analysis features. Two different types of Priostat counting are available:

Group Priostat

This method allows you to count a set of high priority samples immediately, while temporarily interrupting the current protocol. Group Priostat allows you to select any existing assay for the purpose of data reduction.

To use this feature:

1. Load the samples into cassettes and attach the Priostat flag to the first cassette to be counted.
2. Select Group Priostat from the Run menu. The Associate assay for Priostat window is displayed.
3. Select the assay you would like to use to count the samples.

Note: The interrupted protocol number cannot be selected to count the Group Priostat samples.

The instrument will search for the Priostat flag and begin counting the samples. Once the Group Priostat samples are counted, the instrument automatically resumes executing the interrupted protocol with the sample it was counting when the Group Priostat counting commenced. The results of the Group Priostat counting will be displayed in the Output window.

4. Print the results of the Group Priostat results by selecting the print icon in the Output window.

Note:To end the Group Priostat protocol prior to counting all of the samples, select End Group Priostat from the Run menu.

Sample Priostat

This method allows you to count individual samples using a number of different analysis options without the need for defining an assay. It is a high priority interrupt mode, operating similarly to Group Priostat. Note: The Sample Priostat feature is not available on the 2800 series instrument. It is an optional feature on the 2900 series instrument.

The following items are available via the Run-Sample Priostat menu option:

- Decay allows you to assess the duration of luminescence in a radioactive sample via a decay histogram.
- SPC Decay allows you to assess the duration of luminescence in a non-radioactive, luminescent sample via a decay histogram.
- Identify Nuclide allows you to identify an unknown nuclide in your sample using the Quench Indicating Parameters SIS and tSIE.
- Optimize Regions allows you to optimize sample counting regions to provide the highest figure of merit in Normal count mode for samples with constant quench.
- Reverse Region allows you to optimize sample counting region settings for a sample and determine the equivalent unquenched region settings for variable quench samples.
- Low Level Optimize allows you to optimize sample counting regions to provide the highest figure of merit for Low Level count mode.
- Alpha Beta Preview allows you to view the sample spectrum and approximate the activity for a sample containing both an Alpha and a Beta emitting nuclide.
- Normal Preview allows you to view the sample spectrum and approximate the activity for a sample using Normal count mode.
- Low Level Preview allows you to view the sample spectrum and approximate the activity for a sample using Low Level count mode.

Sample Priostat is a manual process; you must select Count from the Run menu to initiate sample counting. To move to the next sample in the cassette, you must select Next Sample from the Run menu. To stop the counting of a sample, you must select Stop from the Run menu. To end the Sample Priostat counting session, you must select End Sample Priostat from the Run menu.

The data that is generated during any of the Sample Priostat options are not saved. You can print the data by selecting the print button in the Report window.

Decay

The Decay feature allows you to confirm the existence of sample luminescence and determine the rate of decay of luminescence for a radioactive sample. Using this mode, samples are recounted until the counting procedure is manually halted. If the counts collected decrease with each successive count (assuming the half life of the nuclide is long in relation to the total count time), the radioactive sample is luminescent. You can view either the sample spectrum or the results plotted as a histogram. The histogram displays the rate at which luminescence is decaying from the sample. This process is useful in establishing an appropriate Pre-Count Delay Time for samples in an assay.

To count samples using the Decay mode:

1. Load your sample(s) into a cassette. Attach the Priostat flag in the reset position to the cassette.
2. Select Decay from the Run menu. The Sample Priostat window is displayed.

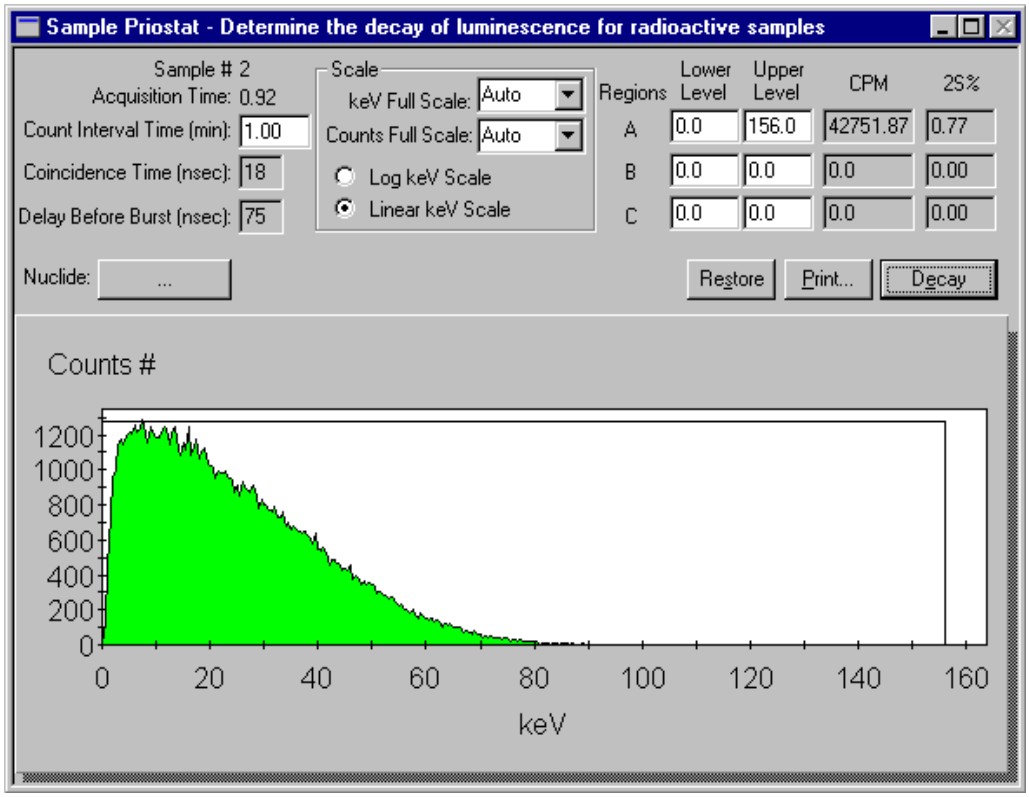

Figure 8-1 Decay Window

3. Select Count from the Run menu. The sample counting will commence after the instrument identifies the Priostat flag.
4. Stop the counting of a sample by selecting Stop from the Run menu.
5. Select Next Sample followed by Count from the Run menu if you would like to count additional samples.
6. Stop the sample counting procedure by selecting End Sample Priostat from the Run menu.

SPC Decay

The SPC (Single Photon Counting) feature allows you to measure the rate of decay of luminescence for a nonradioactive sample. In SPC counting, a single photomultiplier tube is used to collect counts for nonradioactive, luminescent samples. Using the SPC Decay mode, samples are recounted until the procedure is manually halted. The rate at which counts decrease with each successive recount determines the rate of decay of the sample. You can view either the sample spectrum or the results plotted as a histogram. The histogram displays the rate at which luminescence is decaying from the sample.

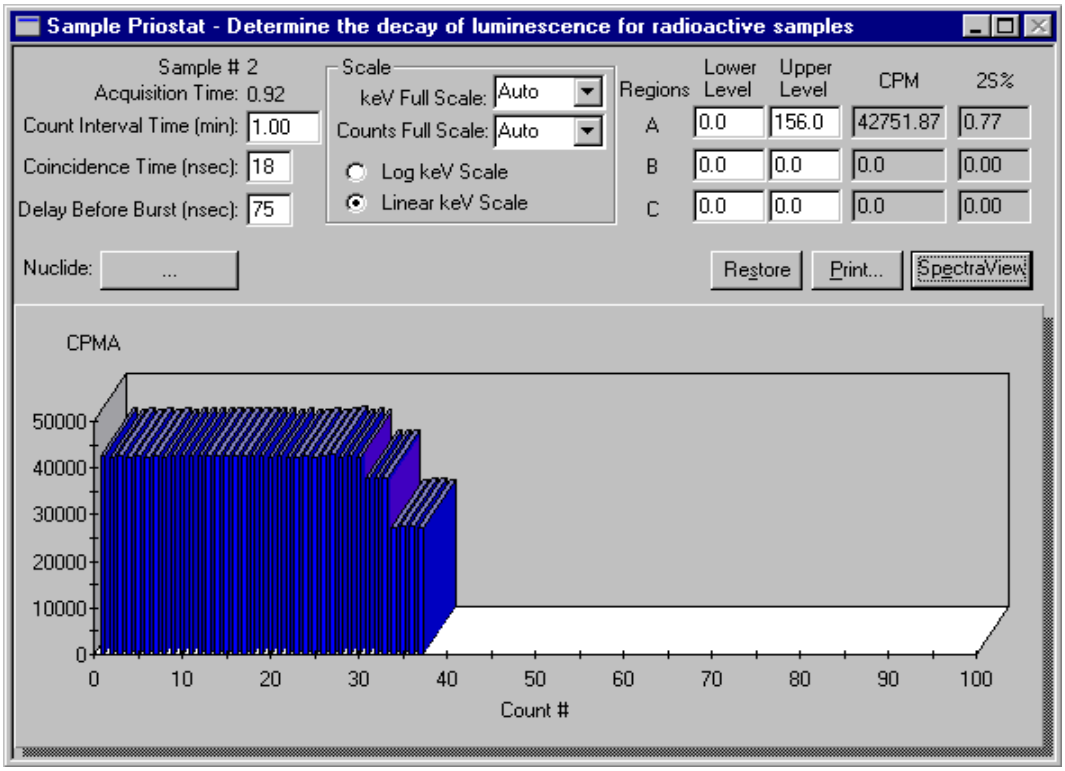

Figure 8-2 SPC Decay Window

To count samples using the SPC Decay mode:

1. Load your sample(s) into a cassette. Attach the Priostat flag in the reset position to the cassette.
2. Select SPC Decay from the Run menu. The Sample Priostat window is displayed.
3. Select Count from the Run menu. Sample counting commences immediately after the instrument identifies the Priostat flag.
4. To stop the counting of a sample, select Stop from the Run menu.
5. Select Next Sample followed by Count from the Run menu if you would like to count additional samples.
6. Stop the sample counting procedure by selecting End Sample Priostat from the Run menu.

Identify Nuclide

Several nuclides display a characteristic relationship between their calculated SIS and tSIE Quench Indicating Parameters. As a result of this relationship, the Identify Nuclide feature allows you to identify any of the following nuclides in a single-label sample:

- Carbon-14 or Sulphur-35 (these nuclides cannot be differentiated).
- Chlorine-36
- Iron-55
- Nickel-63
- Phosphorus-32
- Tritium

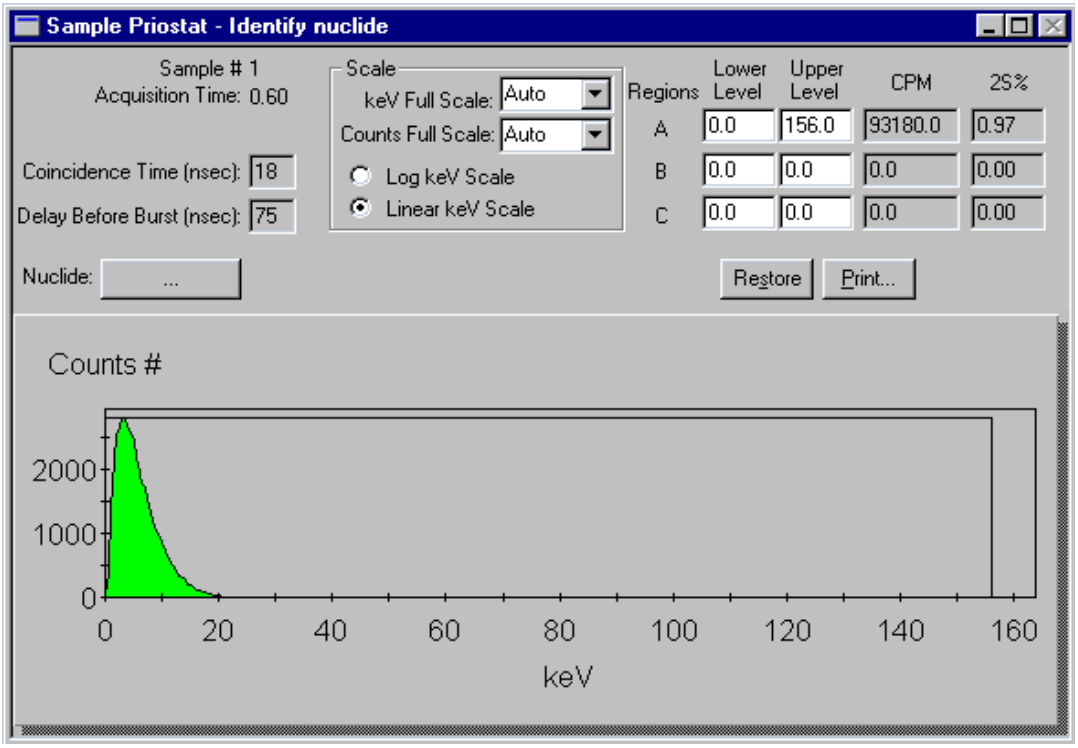

Figure 8-3 Identify Nuclide Window

To identify an unknown nuclide in your sample:

1. Load your sample(s) into a cassette. Attach the Priostat flag in the reset position to the cassette.
2. Select Identify Nuclide from the Run menu. The Sample Priostat window is displayed.
3. Select Count from the Run menu. Sample counting will commence immediately after the instrument identifies the Priostat flag.
4. Stop the counting of a sample by selecting Stop from the Run menu.
5. Select Next Sample followed by Count from the Run menu if you would like to count additional samples.
6. Stop the sample counting procedure by selecting End Sample Priostat from the Run menu. An output window is displayed which provides you with the identity of the nuclide.

Optimize Regions

The Optimize Regions function allows you to eliminate a portion of the background counts and thus increase the overall Figure of Merit for a counting procedure for samples with constant quench using Normal count mode.

If you would like the instrument to automatically optimize the sample counting regions with respect to the chemical environment of the sample, you can perform the Reverse Region compensation procedure prior to region optimization. The Reverse Region compensation feature is typically used for samples with variable quench; it allows the instrument to determine what the endpoint equivalent for the nuclide spectrum would be if the sample was not quenched.

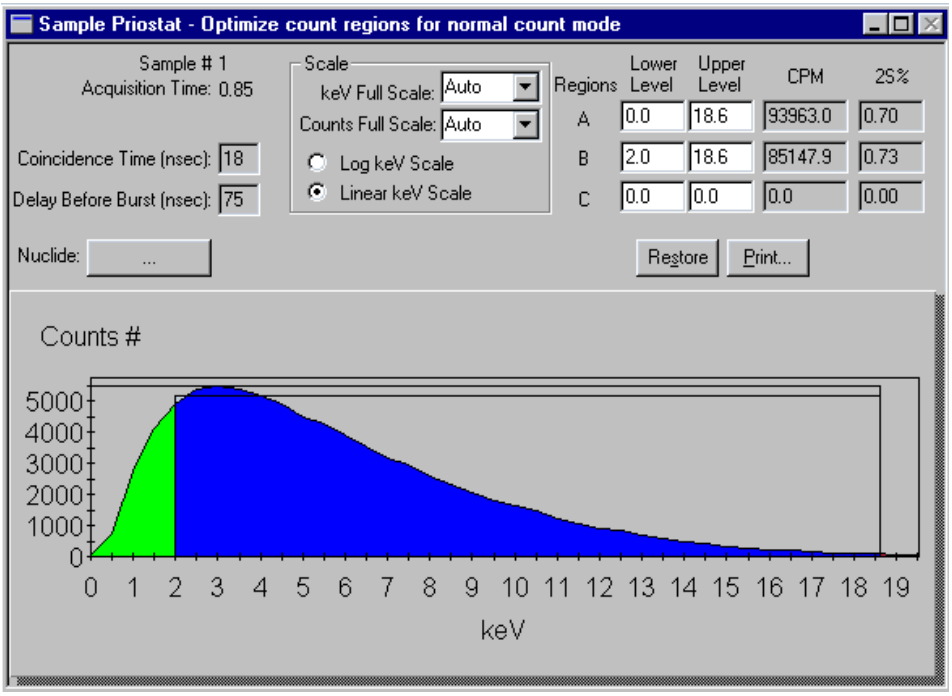

Figure 8-4 Optimize Regions Window

To establish the optimal region settings for a nuclide using the Optimize Regions feature, you will need to perform the following tasks:

1. Load the background vial in an odd numbered cassette position and the sample vial in even numbered cassette positions.

   Note: A background vial must be counted for each sample vial.
   Attach the Priostat flag in the reset position to the cassette.

2. Select Optimize Regions from the Run Menu. The Sample Priostat window is displayed.
3. Select Count from the Run menu. Counting will commence immediately after the instrument identifies the Priostat flag.
4. Allow the samples to count long enough to reach statistical accuracy (2S%) of 2.00 (equivalent to 10,000 gross counts) before terminating the counting procedure. The recommended minimum count time for a background sample is ten minutes.
5. Stop the counting of a sample by selecting the Run-Stop menu item.
6. Select Next Sample from the Run menu, if you would like to count additional samples.
7. Stop the Optimize Region counting procedure by selecting the Run-End Sample Priostat menu item. An output window is displayed which provides you with the optimal region settings for the sample nuclide.
8. Add this nuclide with the optimized region settings into the Sample Nuclide Library for later use in various assays. Any quench standards sets defined for use with this nuclide will automatically use the new region settings. No new quench standards need to be counted as long as the nuclide is the same.

Notes: Enter values in the Region Fields to change the axes and counting regions for Regions A, B and C. To restore the counting region limits defined for the nuclide in the Nuclide Library, click the Restore button. If no nuclide exists, or one is not available, the region default setting for the Lower Level is 0.0 and the Upper Level is 2000.0

Reverse Region

To optimize the counting region settings such that they take into account your sample's chemical environment, Reverse Region compensation should be used. Reverse Region determines region settings using a factor based on the tSIE and the observed spectral endpoint of the sample.

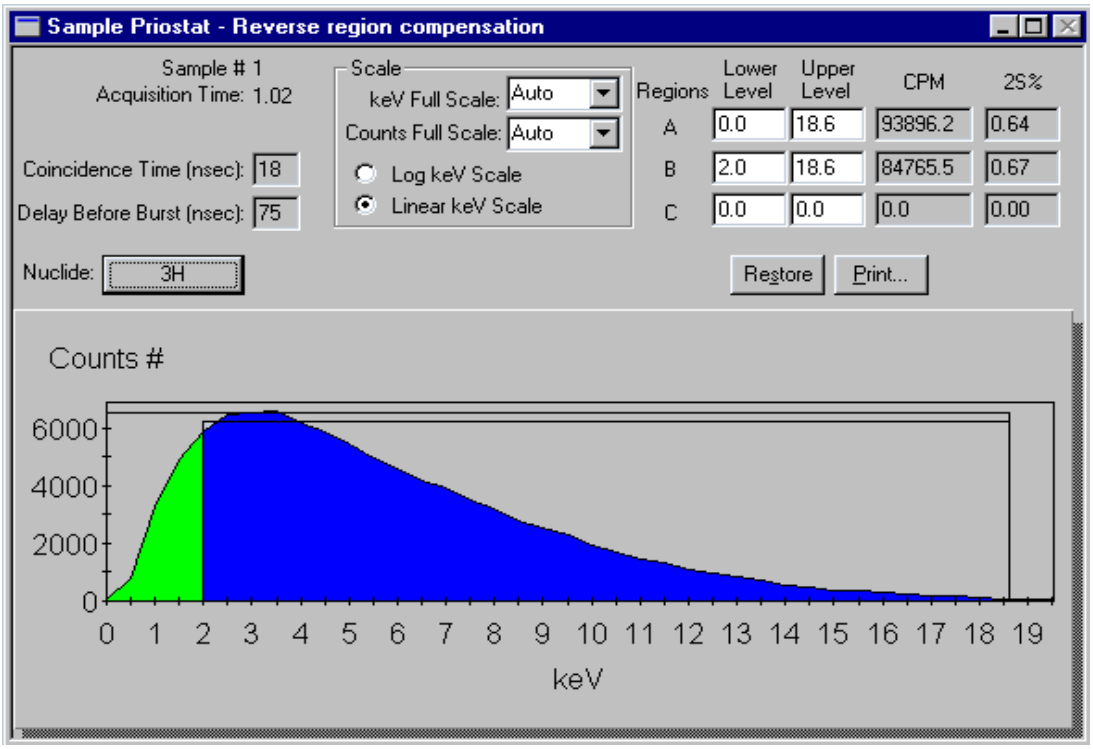

Figure 8-5 Sample Priostat Window

To establish the optimal region settings using the Reverse Region option, you will first need to approximate these settings using the Sample Priostat Preview function:

1. Load your sample(s) into a cassette. Attach the Priostat flag in the reset position to the cassette.
2. Preview your samples using one of the Sample Priostat Preview options (Normal, Alpha Beta or Low Level). The appropriate option corresponds to the count mode that will be used to count the samples. All of these options are available via the Run-Sample Priostat menu option. The Sample Priostat window is displayed.
3. Select Count from the Run menu. Counting will commence after the instrument identifies the Priostat flag.
4. Allow the samples to count to a statistical accuracy (2S%) of 1.0 (equivalent to 40,000 gross counts). While previewing the sample, determine the lower level and upper level region settings by observing the sample spectrum.
5. Stop the Sample Priostat count via the Run-Stop menu option. Select Next Sample from the Run menu, if you would like to count additional samples.
6. Select Reverse Region from the Run menu. The Sample Priostat window is displayed. Enter the region settings established during the preview count.
7. Select Count from the Run menu.
8. Stop the Reverse Region sample counting using the Run-Stop menu item.
9. Select Next Sample followed by Count from the Run menu, if you would like to count additional samples.
10. Stop the Reverse Region sample counting by selecting the End Sample Priostat menu item. An output window is displayed which provides you with the Equivalent Unquenched Settings for Regions A, B and C for the sample nuclide.
11. Add this nuclide with the optimized region settings into the Sample Nuclide Library for later use in various assays. Any quench standards sets defined for use with this nuclide will automatically use the new region settings. No new quench standards need to be counted as long as the nuclide is the same.

Low Level Optimize

The Optimize Regions function allows you to eliminate a portion of the background counts and thus increase the overall Figure of Merit for a counting procedure using the Low Level count mode.

If you would like to also optimize the sample counting regions with respect to the chemical environment of the sample, you can perform the Reverse Region compensation procedure prior to Low Level region optimization.

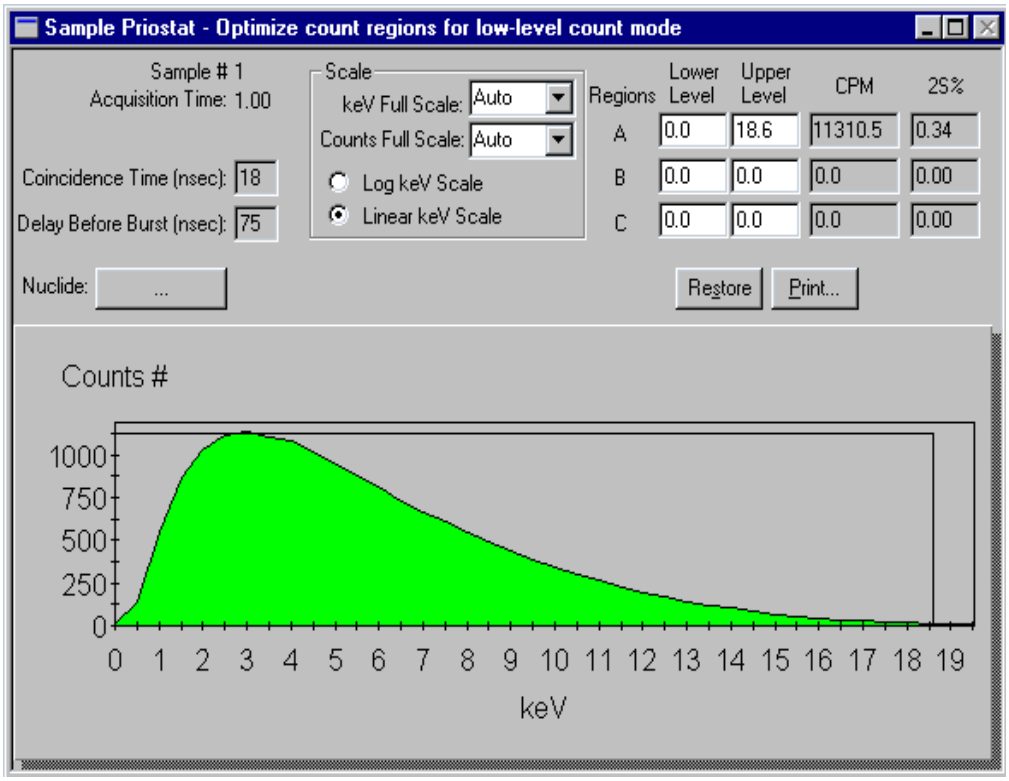

Figure 8-6 Sample Priostat Optimize Window

To establish the optimal region settings for a nuclide, you will need to perform the following tasks:

1. Load the background vial in an odd numbered cassette position and the sample vial in even numbered cassette positions.

   Note:A background vial must be counted for each sample vial.
   Attach the Priostat flag in the reset position to the cassette.

2. Select Low Level Optimize from the Run Menu. The Sample Priostat window is displayed.
3. Select Count from the Run menu. Counting will commence immediately after the instrument identifies the Priostat flag.
4. Allow the samples to count long enough to reach statistical accuracy (2S%) of 2.00 (equivalent to 10,000 gross counts) before terminating the counting procedure. The recommended minimum count time for a background sample is ten minutes.
5. Stop the counting of a sample by selecting the Run-Stop menu item.
6. Select Next Sample followed by Count from the Run menu, if you would like to count additional samples.
7. Stop the Low Level Optimize counting procedure by selecting the Run-End Sample Priostat menu item. An output window is displayed which provides you with the optimal region settings for the sample nuclide.
8. Add this nuclide with the optimized region settings into the Sample Nuclide Library for later use in various assays. Any quench standards sets defined for use with this nuclide will automatically use the new region settings. No new quench standards need to be counted as long as the nuclide is the same.

Alpha Beta Preview

The Alpha Beta Preview function is a Sample Priostat option available via the Run menu. This feature allows you to observe the sample spectrum and approximate the count rate of a sample containing an Alpha and Beta emitting nuclide in the same vial.

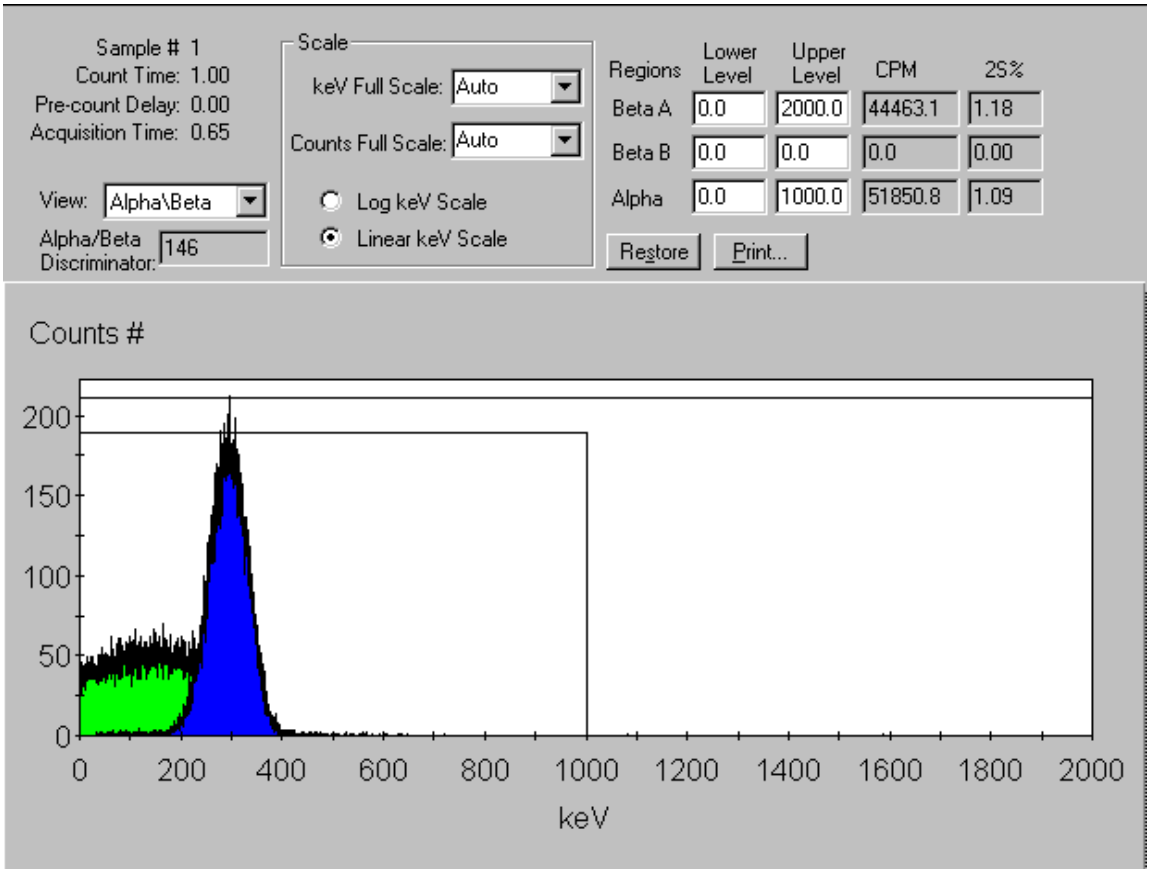

Figure 8-7 Alpha Beta Preview Window

To preview sample counting using the Alpha Beta Preview feature, you will need to perform the following tasks:

1. Load your sample(s) into a cassette. Attach the Priostat flag in the reset position to the cassette.
2. Select Alpha Beta Preview from the Run menu. The Sample Priostat window is displayed.
3. Select Count from the Run menu. Sample counting will commence immediately after the instrument identifies the Priostat flag.
4. Stop the counting of a sample by selecting Stop from the Run menu.
5. Select Next Sample followed by Count from the Run menu if you would like to count additional samples.
6. Stop the sample counting procedure by selecting End Sample Priostat from the Run menu.

Normal Preview

The Normal Preview function is a Sample Priostat option available via the Run menu. This feature allows you to observe the sample spectrum and approximate the count rate of a sample using Normal count mode.

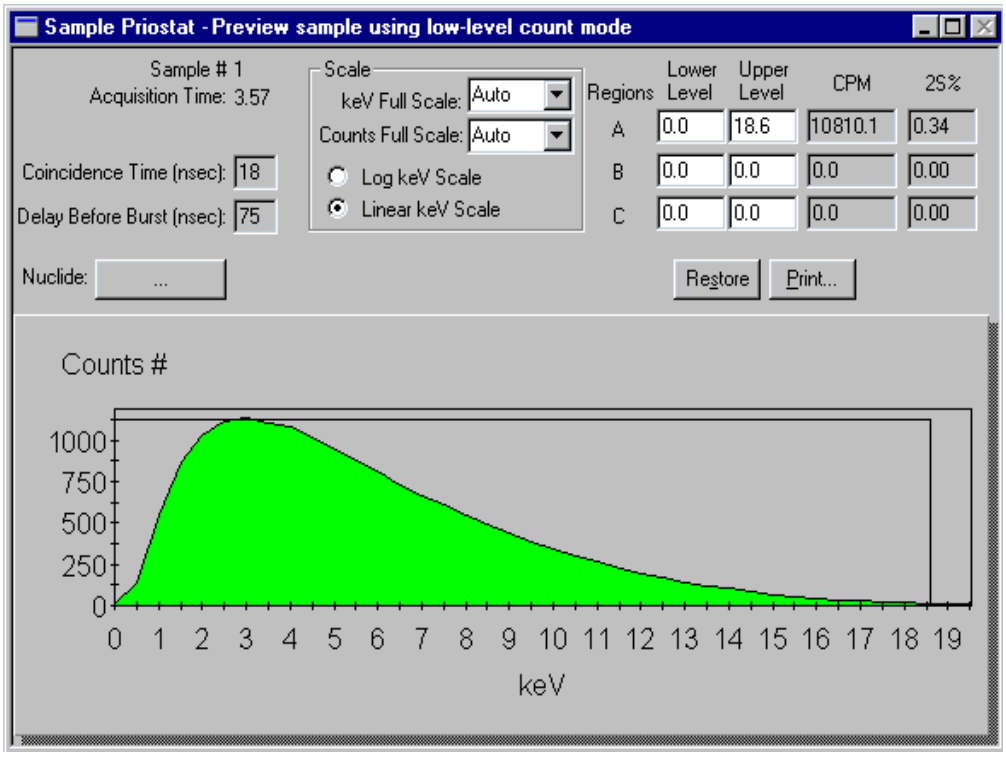

Figure 8-8 Normal Preview Window

To preview sample counting using the Normal Preview feature, you will need to perform the following tasks:

1. Load your sample(s) into a cassette. Attach the Priostat flag in the reset position to the cassette.
2. Select Normal Preview from the Run menu. The Sample Priostat window is displayed.
3. Select Count from the Run menu. Sample counting will commence immediately after the instrument identifies the Priostat flag.
4. Stop the counting of a sample by selecting Stop from the Run menu.
5. Select Next Sample followed by Count from the Run menu if you would like to count additional samples.
6. Stop the sample counting procedure by selecting End Sample Priostat from the Run menu.

Low Level Preview

The Low Level Preview function is a Sample Priostat option available via the Run menu. This feature allows you to observe the sample spectrum and approximate the count rate of a sample using Low Level count mode.

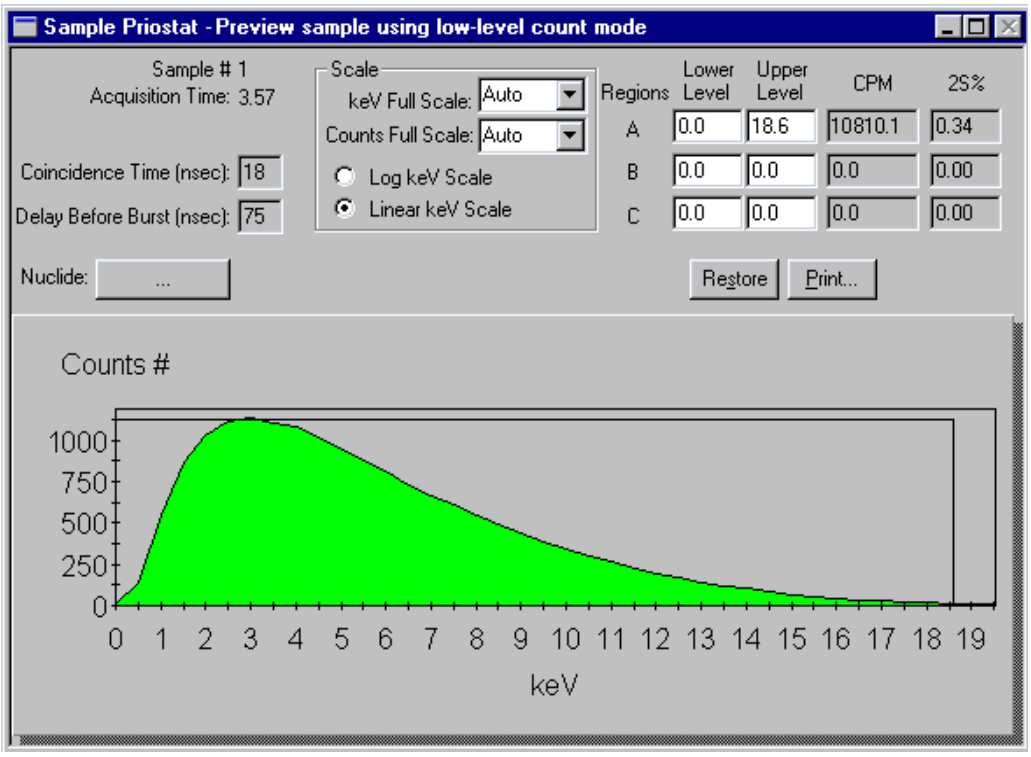

Figure 8-9 Sample Priostat Window

To preview sample counting using the Low Level Preview feature, you will need to perform the following tasks:

1. Load your sample(s) into a cassette. Attach the Priostat flag in the reset position to the cassette.
2. Select Low Level Preview from the Run menu. The Sample Priostat window is displayed.
3. Select Count from the Run menu. Sample counting will commence immediately after the instrument identifies the Priostat flag.
4. Stop the counting of a sample by selecting Stop from the Run menu.
5. Select Next Sample followed by Count from the Run menu if you would like to count additional samples.
6. Stop the sample counting procedure by selecting End Sample Priostat from the Run menu.

The Replay Feature (optional on 2800TR, standard on 2900/3100/3170TR)

The Replay feature allows you to analyze previously collected data under a variety of data reduction conditions. Since the spectrum of each sample is saved, you can reanalyze data using different data reduction parameters without recounting samples. The data reduction protocols listed in the Replay tab of the main window are the same as those listed in the Protocols tab. Any modifications made to protocols during Replay do not affect the original acquisition parameters. To access this function, select the Replay tab in the main window. Select a data file for which you would like to reanalyze data. Right click on that item and select Open for Replay. The Replay window is displayed.

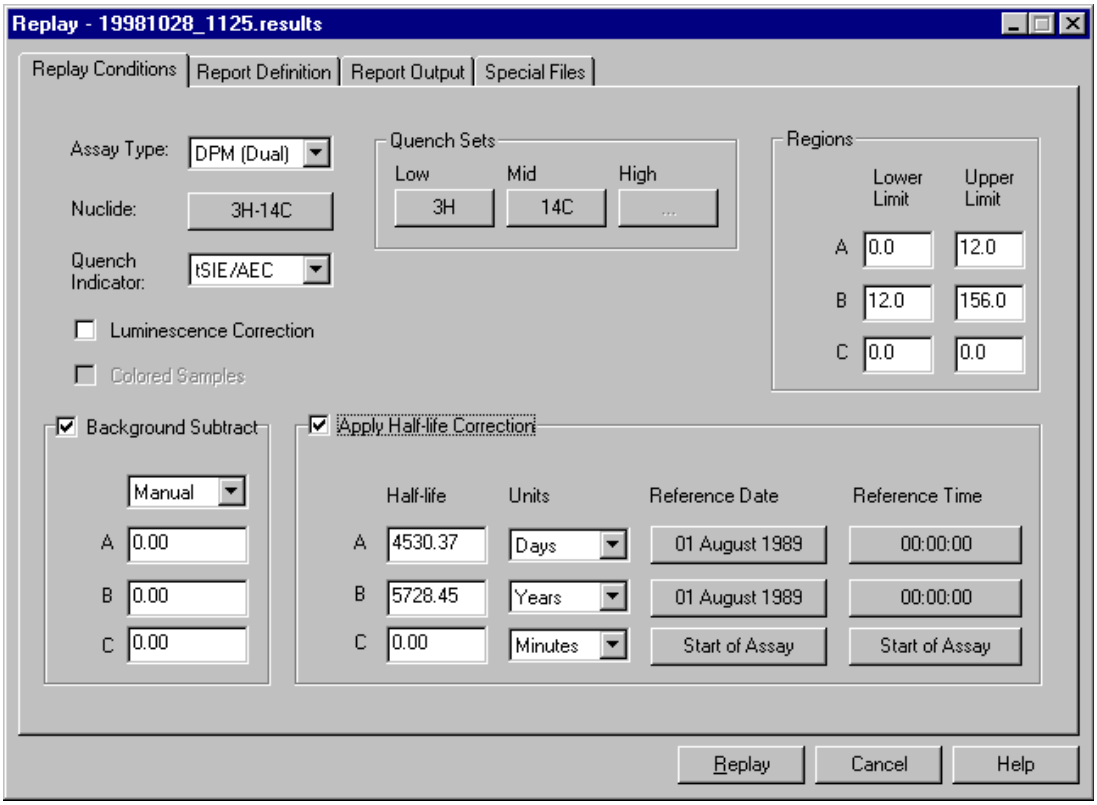

Figure 8-10 Replay Conditions Window

Assay Type

Select the type of data (CPM or DPM) you would like the instrument to calculate from the stored sample data and spectra.

Nuclide

Click this button to display the Sample Nuclides Library for informational purposes.

Quench Indicator

Select one of the following Quench Indicating Parameters (QIPs) from the drop-down list. These parameters are used to calculate DPM using the instrument's Replay feature:

- **tSIE** (transformed Spectral Index of External standard) assigns a numeric value to the quench associated with a sample. This is independent of the quantity of radioactivity in the sample and its count rate. tSIE is the most accurate of the quench indicator options and is typically used for low count rate, variable quench, single label samples. You may select this Quench Indicator only if the samples were originally counted using tSIE.
- **tSIE/AEC** (transformed Spectral Index of External Standard coupled to Automatic Efficiency Correction). tSIE assigns a numeric value to the quench associated with a sample. As quench varies, the AEC automatically monitors and adjusts the counting region to exclude unwanted background. This setting is typically used for dual and triple label experiments with variable quench samples where optimal region settings are desired. You may select this Quench Indicator only if the samples were originally counted using tSIE.
- **SIS** (Spectral Index of the Sample) assigns a numeric value to the quench associated with a sample. The SIS is determined from the spectral shape of the sample and is based on actual sample counts. The SIS setting is typically used to monitor the quench level in single label, high count rate samples for CPM assays or in single label Cherenkov counting.

Luminescence Correction

Mark this box to activate luminescence correction. During Replay, the instrument will correct the data for counts contributed by luminescence. Note: This feature is optional on the 2800 and 2900 series instruments.

Regions

Enter upper and lower limits for any of the three regions, A, B and C if you would like to redefine these limits for Replay analysis of data.

Background Subtraction

Mark this box if you would like to activate the Background Subtraction feature. When this feature is activated, the instrument subtracts background values from sample data prior to reanalysis in Replay. Choose a background source from the drop down list.

- **Manual -** You can manually define background values for each of the three regions, A, B, and C.
- **1st Vial -** The instrument counts the first vial in the cassette for either ten minutes or the defined protocol count time (whichever is greater) and establishes a CPM value for each region; these are the background values subtracted from each sample within each region of the assay.

Apply Half-life Correction

Mark this box if you would like to activate the Half-life Correction feature. When this feature is activated, the instrument corrects the sample data for half-life decay of the nuclide(s) being reanalyzed in Replay. The Reference Date and Time are used to make the decay calculation. The default settings for the Reference Date and Time correspond to the start of an assay.

Replay

Click on Replay. The following Replay output windows are displayed in the main window immediately after the data is reanalyzed.

If Quench Curves - Block Data is selected during Replay processing, only the curve will be initially displayed. Double-click on this curve to view the Expanded Quench Curve with the standard points and efficiency displayed.

Replay Output Window

The Output Window displays various assay parameters and data items. You may customize the information that is displayed in this window by defining the Output Window/Printer report. This report is defined in the Reports tab of the Replay window.

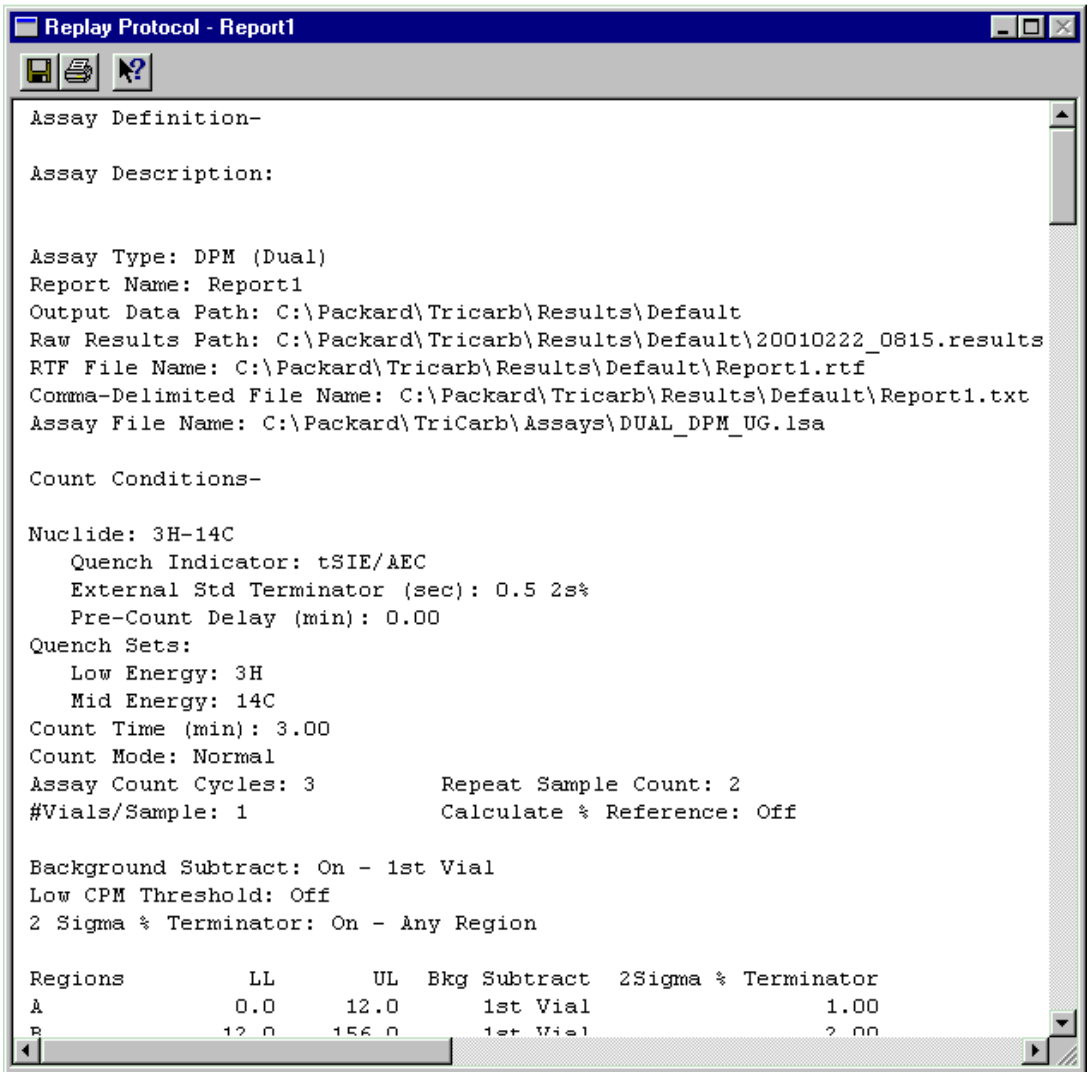

Figure 8-11 Replay Output Window

High Sensitivity and Low Level Counting

In liquid scintillation counting, the limits of detection are dependent on an instrument's detection efficiency and it's ability to detect background counts. The TriCarb line of instruments uses Time Resolved Liquid Scintillation Counting (TR-LSC™), an electronic background discrimination technique (burst counting circuitry), to enhance background discrimination and thus increase sensitivity. Sensitivity may be further enhanced through the use of the optional BGO (Bismuth Germanium Oxide) detector guard (available on the TriCarb 3170TR).

The following table describes the differences between the counting modes available on the TriCarb line of instruments:

Type of Counting	Background Discrimination	Instrument Count Mode	Typical Count Rate	Availability
Normal	Minimal	Normal	>500 CPM	Standard
Low Activity	Intermediate	High Sensitivity	50-500 CPM	Optional
Ultra Low Level	High	Low Level	1-20 CPM above background	Optional
Super Low Level	Maximum	Low Level	1-20 CPM above background	Optional with BGO Detector Guard only

Note: Do NOT use High Sensitivity or Low Level Count Modes to count alpha samples in normal CPM or DPM counting assays. These TR-LSC discrimination modes are not appropriate for counting alpha samples. Extremely low alpha count rates will be observed.

The increase in sensitivity obtained with the various counting modes is the result of varying the amount of electronic background discrimination. For High Sensitivity and Low Level Count Modes, the criteria employed for discriminating true Beta counts from background counts becomes more stringent. Some loss of counting efficiency may occur as background discrimination is increased. The reduction in background, however, is usually far greater than the loss of counting efficiency, resulting in an increase in counting efficiency as measured by E^2/B (Efficiency^2/Background). Counting high energy beta emitters like ^{90}Sr or ^{90}Y in High Sensitivity or Low Level Count Mode requires optimization of TR-LSC parameters. This is accomplished by changing the Delay Before Burst value in the Count Corrections tab of Assay Definition. The Delay Before Burst feature works by delaying the time that afterpulse discrimination begins. The effect of this delay is to preserve high beta counting efficiency at the lowest possible background.

Super Low Level Counting

The TriCarb instrument with Super Low Level Counting capability uses a slow, scintillating, Bismuth Germanium Oxide (BGO) detector guard. The BGO detector guard is a special assembly that surrounds the sample. The BGO detector assembly replaces the conventional sample changer and provides an increase in the Figure of Merit performance compared to the standard counting system alone.

With the exception of the Calibration, Normalization and IPA procedures, operation of TriCarb models equipped with a BGO detector is the same as the standard TriCarb models.

The following information is relevant when performing Low Activity, Ultra Low Level or Super Low Level Counting:

- Low potassium glass vials are recommended when counting low levels of Tritium or Carbon-14 since they enhance discrimination between Beta and background pulses. Certain plastic vials may be suitable for measuring Tritium in water.
- The source of water used for making background determinations must be free of contamination by radionuclides. When counting very low levels of radionuclides, especially Tritium, even the smallest amount of contamination will increase the count rate of the background sample. Therefore, it is necessary to secure a source of water for the background samples which is “dead”, or free of radioactivity.
- Samples must be free of extraneous sources of radionuclides, such as that which may be found in scintillators or any reagents used in their preparation.
- Glass vials should be washed and rinsed with a dilute (0.1M) ethylene diamine tetraacetic acid (EDTA) solution, followed by a “dead deionized water rinse. This will reduce background and surface contaminants which could contaminate either the detector guard or sample chamber.
- All vials used with this instrument should be sealed with Teflon cap liners and screw caps to prevent leakage.
- Maximum vial dimensions are as follows: small vials must not exceed 17.8mm in diameter and 58.0mm in height (including the cap); large vials must not exceed 28.1mm in diameter and 63.0mm in height (including the cap).
- The maximum sample activity is 100,000 Counts Per Minute (CPM). If a sample exceeds this count rate, the system will automatically switch to the Normal Count Mode. This is particularly important when purchasing or preparing quench or reference standards for use in High Sensitivity or Low Level Count Mode.
- The luminescence correction feature is typically not used when counting very low CPM samples. It is preferable to dark adapt samples before the counting begins. The instrument provides a protocol specific pre-count delay of up to 99.99 minutes. With a pre-count delay, a sample is lowered into the detection

chamber and allowed to dark adapt for the specified delay time. Dark adaption will allow luminescence emanating from the sample vial to dissipate.

Cautions and Limitations

It is important to note that background radiation varies throughout the world, and will be a factor in determining background. Higher elevations and geological areas where Uranium and its decay products tend to concentrate will most likely experience higher background levels. The exact instrument background and performance for a given location must be determined at the site of the installation.

Caution:When using the High Sensitivity or Low Level Count Modes, you MUST NOT use quench standards which have been purged free of oxygen with an inert gas. The oxygen quenching in unpurged standards facilitates discrimination between background and true beta events. Unpurged standards are available from PerkinElmer Life and Analytical Sciences. For best DPM performance, it is recommended that the quench standards match your unknown samples as closely as possible in terms of cocktail, vial type and sample volume.

Note: Do NOT use the Low Level (LL) standards to calibrate (SNC/ IPA) the instrument. It is always calibrated with the unquenched, purged ^{14}C calibration standard.

Alpha Beta Counting

Alpha Beta Discrimination is an optional feature on TriCarb Liquid scintillation analyzers that provides the ability to discriminate between the gross alpha and gross beta activity in a mixed sample. Results are reported as CPM alpha (CPMa) and CPM beta (CPMA and CPMB).

In liquid scintillation counting, emission energies for alpha and higher energy beta radionuclides such as $^{90}Sr/^{90}Y$ will overlap, making discrimination between the nuclides impossible on the basis of energy discrimination. However, alpha induced pulses in a scintillation cocktail have a longer duration than beta induced pulses. Pulse shape and duration are used to effectively discriminate between alpha and beta activity.

TriCarbs equipped with the alpha/beta discrimination use Pulse Decay Analysis (PDA), a form of pulse shape analysis, to perform the separation of alpha and beta events. PDA uses a time based Pulse Decay Discriminator (PDD) to evaluate the pulse duration of scintillation events and categorize the events as either alpha or beta. Resolution of individual alpha or individual beta radionuclides is not performed.

A misclassification (spillover) curve is created automatically by varying the PDD values when counting a pure beta and a pure alpha standard. An instrument determined optimum PDD value is established at the crossover point of the two curves where there is minimal alpha and beta misclassification. The misclassification curve information and its associated optimum PDD value is stored in a library of such curves called the Alpha Beta Standards Library.

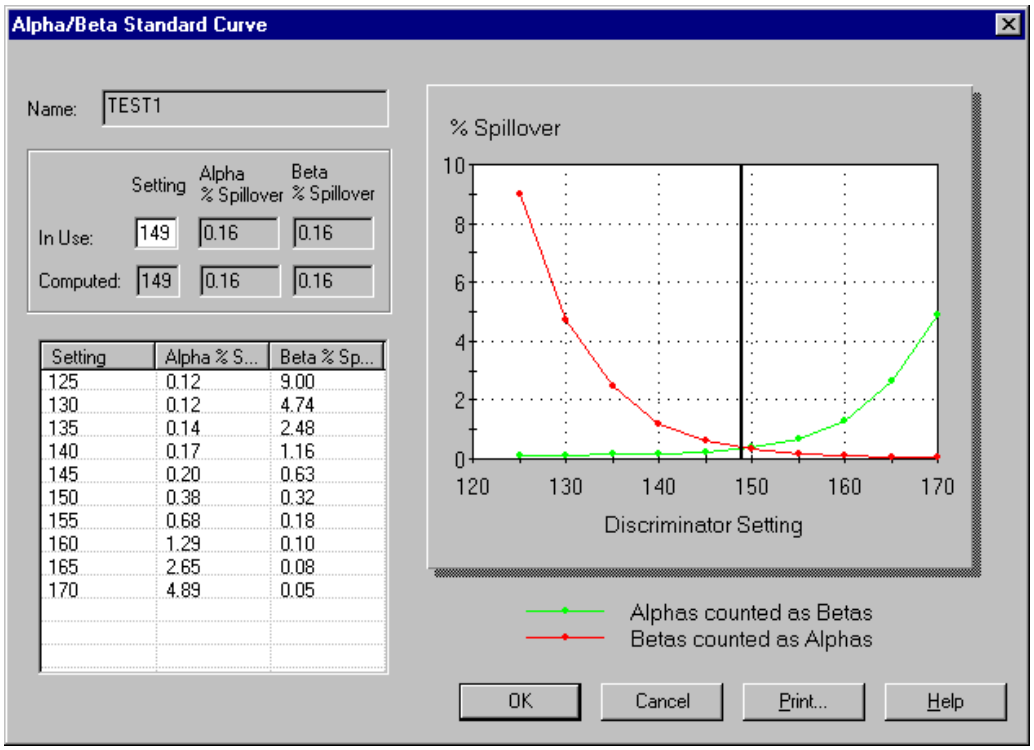

Figure 8-12 Alpha Beta Standards Curve

A specific misclassification curve can be associated for use with an alpha beta radionuclide in the Alpha Beta Nuclide Library. By selecting the appropriate alpha beta radionuclide in an assay, the PDD from the Alpha Beta Nuclide Library is used by the assay as the criterion for alpha/beta separation.

Note: Alpha and beta standards are not mandatory in order to use the alpha beta discrimination feature. You can enter a PDD value manually for an alpha beta radionuclide. In this case, no alpha beta misclassification curve is associated with the alpha beta radionuclide. The PDD value is empirically determined. This capability is useful when no alpha and beta standards are available or it is not possible to obtain a pure beta and alpha standard as is the case when counting ^{222}Rn which decays by both alpha and beta emission.

Note: For alpha beta discrimination to be successful, the quench level of the alpha and beta standards (if used) should closely approximate the quench level of the unknown samples to be assayed. Increased quenching adversely affects alpha beta discrimination. The primary effect is increased misclassification of alpha events.

Tandem Processing

Tandem Processing allows the instrument to pass data from an assay to an application program. Application programs can provide various features, including data manipulation (data reduction, graphing, etc.). Suitable application programs are commercially available or can be written and compiled by you. The instrument can store the appropriate data from an assay to a disk file, where the application program can access it without your intervention. These data files are generated if you:

- Create a report that includes the desired data fields.
- Specify that a data file of the desired format be created.
- Select any appropriate special files that may be required by your application. **Prot.dat** and **2000ca.dat** are special files necessary for certain PerkinElmer application programs, but additional data from spectrum files or IPA information may also be required.
- Check **Run Application** in the Report Output tab. Specify the name of the application program, the type of program and when the application should be run with respect to the assay.

In the Report Output window, Indicate that you would like to perform Tandem Processing. The Report Output window allows you to specify the location of the application program executable file and the name of the data file required by this program.

Specify the location of the data files in the Data Paths window so that they area accessible to your application program.

Run Application

Select this box if you would like to perform tandem processing.

Batch

Select this button if you would like to run the application program after the entire set of sample data is collected.

Cycle

Select this button if you would like to run the application program after the samples in the assay have counted the specified number of cycles.

Note: This option does not apply to Tandem Processing in Replay.

Sample

Select this button if you would like to run the application program after the data for each sample is collected.

Note: Each time the application program is run, it must be loaded into memory. Whenever possible, run the application program after a batch or cycle, since it is more efficient and faster than running the program after each sample.

Chapter 9

Maintenance and Troubleshooting

Preventative Maintenance

With the exception of inspection and cleaning, there are no preventative maintenance procedures that you should perform. Normal system preventative maintenance can be performed on a prescribed basis under a PerkinElmer Maintenance Agreement. Contact your PerkinElmer district office or official PerkinElmer distributor for information concerning the availability of a maintenance agreement.

Inspection

The following should be inspected on the TriCarb system at least once per week or whenever a system malfunction occurs:

1. Check that the cassettes and sample changer surfaces are free of dirt.
2. Cassette movement should be smooth with no excessive vibration.
3. Check for loose electrical or mechanical connectors. DO NOT PERFORM ANY DISASSEMBLY.
4. Ensure that all controls and indicators are working.

Cleaning

The sample changer lid should be cleaned occasionally using a soft cloth moistened with a mild soap and water solution. The system sample changer should be cleaned occasionally using a soft cloth moistened with PicoClean-N (PerkinElmer Life and Analytical Sciences, PPN:6013814) or an appropriate commercial cleaning agent.

If the system has the refrigerated sample changer option installed, check (monthly) that the filter is free of dust and dirt, and clean the filter as required.

Storing Data

Back Up the Hard Drive

To safeguard against the loss of data due to hard drive failure, periodically back up all files in the Packard folder. The Packard folder is automatically created when the QuantaSmart software is installed. This folder contains the TriCarb folder, which contains several sub-folders for the organization of various program and data files.

You can back up the contents of the hard drive using the CD writer that is installed in the system computer. **Note**: you can only use the CD writer when the instrument is not acquiring data.

Folder Contents

TriCarb
The TriCarb folder contains several sub-folders, each of which contains different types of program or data files. Note: Because the system requires that certain program files are located in specific folders, the files in the sub-folders should not be moved.

Assays
The files in this folder contain information regarding the assay parameters you have specified during the assay definition process.

Bin
The files in this folder contain information regarding the execution of the QuantaSmart™ program.

Help
The files in this folder contain information regarding the Help system for the QuantaSmart program.

IPA Results
The files in this folder contain information regarding IPA data.

Libraries
The files in this folder contain information regarding the Libraries used in the QuantaSmart program.

QuenchStdResults
The files in this folder contain information regarding Quench Standards.

Results
The files in this folder contain the sample data generated from the assays.

CPM Assays
This is an example of a results folder.

Examples
The files in this folder contain examples of sample data.

Operational Errors

Troubleshooting Operational Problems

These problems may occur during normal system operation.

Erratic Sample Changer Motion

1. Check that the instrument lid is closed. The sample changer optical sensors are affected by bright light.
2. Look for an obstruction in the sample changer.
3. Confirm that the Varisette cassette is properly labeled with a protocol flag.

No Display

1. Confirm that the computer and video monitor power switches are in the ON position.
2. Reboot the computer by simultaneously pressing the control (Ctrl), alternate (Alt) and delete (delete) keys.

No Printout

1. Confirm that the printer switch is in the ON position.
2. Verify that the ON-LINE indicator light is ON.
3. Confirm that the printer has sufficient paper.
4. Reset the printer by switching it from the ON to the OFF position and switching back to the ON position.

Protocol Flag Bypassed

1. Verify that an assay has been defined and associated with a protocol.
2. Check to see that the protocol flag is active.
3. Determine if all sample counting cycles have completed.

Sample Changer Fails to Respond to Sample Changer Commands

1. Confirm that the instrument power switch (located at the bottom right side near the front of the instrument) is in the ON position.
2. Verify that the sample changer deck contains the appropriate number of cassettes. Push all the cassettes on the deck toward the detector chamber. If any cassettes remain in the “Clear Zone” (at the front of the deck), there are too many cassettes on the sample changer deck.
3. Determine if the instrument has initiated Priostat recovery.
4. Check if an error message is displayed in the Status Bar of the Main Window.
5. Reset the instrument by turning the power switch OFF for ten seconds and switching back to the ON position.

Sample Changer Idle

1. Confirm that the instrument power switch is in the ON position.
2. Determine if all sample counting cycles have completed.
3. Check for an error message in the Status Bar of the main window and on the printout.
4. Determine if a sample is counting.

Samples Fail to Load

1. Verify that an assay has been defined and associated with a protocol.
2. Determine if all sample counting cycles have completed.
3. Check the vial dimensions. See Specifications for sample vials.

System Lock-up

1. Reboot the computer by simultaneously pressing the control (Ctrl), alternate (Alt) and delete (Delete) keys.
2. Turn the instrument power switch OFF, wait 10 seconds and switch back ON.

Diagnostics

The Diagnostics windows are typically used by PerkinElmer Technical Service to assess the system’s functional status. The TSE Diagnostics item in the Diagnostics menu would allow you to view the system’s diagnostic screens if you could log on to the system with the TSE rights.

IPA Errors

Troubleshooting IPA Parameters

These problems occur when the IPA parameters are outside of the specified limits.

High Carbon-14 Background

1. Check for contaminated detector by counting an empty vial and displaying the spectrum via the SpectraView window. If the detector is contaminated, call PerkinElmer Technical Service.
2. Check for increased environmental radiation; determine if high energy sources are stored near the instrument.
3. Check for electrostatic discharge; use static controller.
4. If gamma sources are used in the lab, perform a wipe test to check for gamma nuclide contamination on the vial.
5. Check for electronic noise; use a separate power line for the instrument or call PerkinElmer Technical Service.

High Chi-Square

- Problem with high voltage power supply or the photomultiplier tubes. Call PerkinElmer Technical Service.

Note: A properly performing instrument may exceed the 7.63 to 36.19% limit 2% of the time. This is a result of the statistical nature of the Chi-Square test.

High Tritium Background

1. Check for contaminated detector by counting an empty vial and displaying the spectrum in the SpectraView window. If the detector is contaminated, call PerkinElmer Technical Service.
2. Check for increased environmental radiation; determine if high energy sources are stored near the instrument.
3. Check for electrostatic discharge; use the static controller.
4. If gamma sources are used in the lab, perform a wipe test check for gamma nuclide contamination on the vial.
5. Check for electronic noise; use a separate power line for the instrument or call PerkinElmer Technical Service.

Low Carbon-14 Figure of Merit

1. Verify that the previous efficiency measurement is within ± 2% when using the same standard. If not, clean the outside of the vials and rerun.
2. Check that the Carbon-14 background and efficiency values are within specification (when using unquenched standards). If so, the integrity of the IPA standards is suspect.

Low Chi-Square

- Check for electronic noise. This typically creates spurious pulses of uniform rate. Use a separate power line for the instrument, or call PerkinElmer Technical Service.

Note: A properly performing instrument may exceed the 7.63 to 36.19% limit 2% of the time. This is a result of the statistical nature of the Chi-Square test.

Low Tritium Efficiency

1. Verify that the instrument has been calibrated. If not, perform an SNC calibration.
2. Confirm that the correct standard (unquenched and purged of oxygen) is being used.
3. Confirm that the tSIE value of the standard is in the range of 950-1050. If not, check the expiration date of the standard.
4. Confirm that the efficiency is ± 2% of the previous measurement using the same standard. If not, clean the outside of the vial and rerun.

Low Tritium Figure of Merit

1. Verify that the previous efficiency measurement is within ± 2% when using the same standard. If not, clean the outside of the vials and rerun.
2. Check that the tritium background and efficiency values are within specification (when using unquenched standards). If so, the integrity of the IPA™ standards is suspect.

Warnings and Messages

System Messages

The following system messages are presented in alpha-numerical order.

2000CA File Error

The system encountered an error while writing the 2000CA.DAT file. This file is needed by PerkinElmer application programs. Rerun the assay. If the error recurs, call you PerkinElmer Technical Service.

? (message column)

If this character appears in the **Messages** column of a report, a math error occurred when calculating the result for the sample.

< (message column)

If this character appears in the **Messages** column of a report, the sample was rejected due to low count rate within the first 30 seconds of the sample count.

(message column)

If this character appears in the **Messages** column of a report, the sample was determined to be heterogeneous. Typically, this is due to phase separation in the sample vial.

* (message column)

If this character appears in the **Messages** column of a report, the sample counts exceeded 100,000 in either High Sensitivity or Low Level count mode. The instrument automatically switched to Normal count mode.

A (message column)

If this character appears in the **Messages** column of a report, this data line represents an Average value for replicate sample vials.

A quench set associated with this assay's nuclide was modified after being run.

Information for a quench set has been changed in the Quench Standards Library, but the standard set has not been recounted after the changes were made.

Recount the Quench set.

A quench set associated with this assay's nuclide was not counted with a sufficient number of samples.

A sample nuclide has been defined in the library, but the quench set selected for the nuclide has not been counted. A minimum of two quench standards must be counted for each quench set.

Count the appropriate quench standards.

An active protocol is invalid for group priostat.

An active protocol was selected as a Group priostat protocol.

Select a different protocol or wait until the active protocol is completed.

B (message column)

If this character appears in the **Message** column of a report, this data line represents data about a Background Subtraction vial.

BACK PIN JAM FWD

A Sample changer error has occurred.

No action is required unless a message is printed. If this message appears on a printout, call PerkinElmer Technical Service.

BACK PIN JAM REV

A Sample changer error has occurred. No action is required unless a message is printed.

If this message appears on a printout, call PerkinElmer Technical Service.

BAD ELEV/EXT STD

A Sample changer error has occurred. No action is required unless a message is printed.

If this message appears on a printout, call PerkinElmer Technical Service.

Bad shutter.

A Sample changer error has occurred. No action is required unless a message is printed.

If this message appears on a printout, call PerkinElmer Technical Service.

BGO spectrum not present

External standard counting was attempted on an instrument with a BGO detector guard before the SNC/IPA calibration was performed.

Perform the SNC/IPA calibration.

C (message column)

If this character appears in the **Message** column of a report, this indicates that the color quench correction for this sample is suspect (tSIE < 100).

The reported sample results may be invalid.

Cannot associate an assay with the priostat flag while that assay is active.

An assay cannot be associated with the priostat flag while priostat is active.

Allow the current set of priostat samples to finish counting before changing the assay that is associated with the priostat protocol flag.

Cannot associate another assay to this flag while the current assay associated with this flag is active.

Multiple assays cannot be associated to the same protocol flag number.

Allow the instrument to complete the current assay. Once the assay is completed, you can disassociate the assay from the protocol flag and associate a different assay to it.

Cannot change priostat flag association while priostat is active. Stop priostat first.

The assay that is associated with the priostat flag cannot be changed while priostat is active.

Allow the current set of priostat samples to finish counting before changing the assay that is associated with the priostat protocol flag.

Cannot disassociate assay from this flag while the assay is active.

The protocol flag for the assay that is currently counting cannot be disassociated from the assay while it is active.

Allow the instrument to complete the current assay before disassociating it from the protocol flag.

Cannot find the protocol associations file.
An assay file has been moved from the Assays folder, or it has been deleted.

Call PerkinElmer Technical Service.

Cannot open serial port. Make sure that it is configured and not in use by some other program.
A multiple instance of the QuantaSmart program may be running.

Close any multiple instances of the program.

Cannot read results file.
A results file may have been moved from the Results folder or deleted.

Call PerkinElmer Technical Service.

Cannot replay assays.
The assay type cannot be used in Replay.

Only CPM, Single, Dual, Triple and FS DPM assays may be used in Replay.

Can’t drop vial.
A Sample changer error has occurred. No action is required unless a message is printed.

If this message appears on a printout, call PerkinElmer Technical Service.

Can’t raise vial.
A Sample changer error has occurred. No action is required unless a message is printed.

If this message appears on a printout, call PerkinElmer Technical Service.

Check the assay file: either the assay file does not exist or the assay file format is corrupted.
Either an assay file is corrupted or a standard that was associated with an assay has been deleted.

Call PerkinElmer Technical Service.

Communications Interrupted.
An RS-232 failure has occurred.

Restart the QuantaSmart program.

D5:Unable to open file filename because of error: A Hardware I/O error was reported while accessing filename.

The assay is set up to save data to drive A, but there is no disk currently in the drive. This disk check is performed when the protocol flag is first recognized. Ensure that there is a formatted disk in the drive and then click the OK button. The error message will continue to appear until the drive requirement is satisfied.

E (message column)

If this character appears in the **Message** column of a report, this indicates that the quench indicating parameter (SIS or tSIE) value was extrapolated from a portion of the quench curve beyond one of the end data points.

Depending on how good your curve has fit the standard data points, the extrapolated quench value for the sample may not be accurate.

Elevator down.

A Sample changer error has occurred. No action is required unless a message is printed.

If this message appears on a printout, call PerkinElmer Technical Service.

Elevator up.

A Sample changer error has occurred. No action is required unless a message is printed.

If this message appears on a printout, call PerkinElmer Technical Service.

Error in BGO spectrum determination.

An error was encountered during the acquisition of the BGO detector guard spectrum while counting the SNC/IPA protocol.

Rerun the SNC/IPA calibration procedure. If the problem persists, call PerkinElmer Technical Service.

EXT STD IN.

A Sample changer error has occurred. No action is required unless a message is printed.

If this message appears on a printout, call PerkinElmer Technical Service.

EXT STD OUT.

A Sample changer error has occurred. No action is required unless a message is printed.

If this message appears on a printout, call PerkinElmer Technical Service.

Fatal SC error.
An unrecoverable sample changer error has occurred.

Call PerkinElmer Technical Service.

FRONT PIN JAM FWD
A Sample changer error has occurred. No action is required unless a message is printed.

If this message appears on a printout, call PerkinElmer Technical Service.

FRONT PIN JAM REV.
A Sample changer error has occurred. No action is required unless a message is printed.

If this message appears on a printout, call PerkinElmer Technical Service.

I (message column)
If this character appears in the **Message** column of a report, this sample has been determined to be *Indeterminate* in a Direct DPM assay. This means that the system could not reliably determine the DPM value for this sample.

When a sample is designated as indeterminate, the DPM reported may be valid if the sample is not heavily quenched. Check the tSIE value of the sample to determine the level of quench. If the tSIE is greater than 200, the DPM reported is most likely accurate, within statistical counting error. The accuracy is independent of cocktail density variation, vial size or type, sample volume, color and chemical quench.

Internal error.
A system error (such as file mismatch) has occurred on the instrument.

Perform a COLD START of the instrument. If the error message reappears, call PerkinElmer Technical Service.

Instrument off line.
The instrument is not responding to the computer.

Check that the instrument power is on.

IPA error C-14 chi-square.
The Chi-Square test failed while counting the Carbon-14 source.

Rerun the Chi-Square test. If the test fails again, call PerkinElmer Technical Service.

IPA error C-14 LCR.
The Carbon-14 source does not contain enough activity.

Check that the correct source is being used. Use a new source, if necessary.

IPA error-H-3 chi-square
The Chi-square test failed while counting the Tritium source.

Rerun the Chi-Square test. If the test fails, call PerkinElmer Technical Service.

IPA error-H-3 LCR.
Tritium source does not contain enough activity.

Check that the correct source is being used. Use a new source, if necessary.

LOST PIN POS.
A Sample changer error has occurred.

No action is required unless a message is printed. If this message appears on a printout, call PerkinElmer Technical Service.

Missing Vial
This message indicates that a vial is missing from the cassette.

No Quench sets specified.
No quench set has been selected for the assay.

Select the appropriate quench set from the Quench Standards Library. If an appropriate standard set does not exist, you must perform an appropriate Quench Standards assay.

No quench standard is defined for this assay.
A standard that is being used by a sample nuclide in an assay has been deselected.

Re-select the standard for the assay.

Normalization error-both tubes LCR.
The count rate in both photomultiplier tubes is too low.

Check that the unquenched Carbon-14 source is in sample position 1 in the cassette. Call PerkinElmer Technical Service.

Normalization error-both tubes SIS.
The count rate in both photomultiplier tubes is too low.

Check that the unquenched Carbon-14 source is in sample position 1 in the cassette. Call PerkinElmer Technical Service.

Normalization error-EXT STD.
The external standard is not loading properly.

Call PerkinElmer Technical Service.

Normalization error-left PMT LCR.
The count rate in the left photomultiplier tube is too low.

Check that the unquenched Carbon-14 source is in sample position 1 in the cassette. Call PerkinElmer Technical Service.

Normalization error-left PMT SIS.
The left photomultiplier tube detected inappropriate beta energy.

Check that the unquenched Carbon-14 source is in sample position 1 in the cassette. Call PerkinElmer Technical Service.

Normalization error-right PMT LCR.
The right photomultiplier tube detected inappropriate beta energy.

Check the unquenched Carbon-14 source is in sample position 1 in the cassette. Call PerkinElmer Technical Service.

Normalization error-right PMT SIS.
The right photomultiplier tube detected inappropriate beta energy.

Check the unquenched Carbon-14 source is in sample position 1 in the cassette. Call PerkinElmer Technical Service.

Not normalized.
The instrument has not been normalized.

Perform the calibration procedure before counting any samples.

Power fail.
The system has recovered from a power failure.

Check your sample results for missing data.

Power recovery.
Power to the instrument was lost.

The instrument should resume the function it was performing when the power failure occurred.

Priostat ready to count.
A Priostat sample has been loaded into the detection chamber. Sample counting has not been initiated.

To start the counting of the sample, your must select the Start button on the toolbar.

Priostat SC NO ACK.
The selected sample changer control command was not accepted by the instrument during Priostat counting mode.

Check the instrument State field in the main window for an INSTRUMENT OFF-LINE message. If this message is displayed intermittently, shut down Windows, and then turn the instrument power off and back on. If this message is not displayed, wait and periodically retry the sample changer commands.

Priostat search.
The instrument is searching the sample changer deck for the Priostat cassette.

Verify that the Priostat cassette is on the sample changer deck.

R (message column)
If this character appears in the **Message** column of a report, this report line represents data about a Reference standard vial, used for calculating% Ref.

S (message column)
If this character appears in the **Message** column of a report, this report line represents data about a Quench standard vial, used for generating quench curves.

Shutter close.
A Sample changer error has occurred.

No action is required unless a message is printed. If this message appears on a printout, call PerkinElmer Technical Service.

Shutter open.
A Sample changer error has occurred.

No action is required unless a message is printed. If this message appears on a printout, call PerkinElmer Technical Service.

Skipped cassette with no label.
A cassette on the sample changer deck is without an ID label.

Attach an ID label to the cassette.

The instrument encountered a protocol flag for which there is no assay associated. This protocol was not counted.
There is a cassette on the instrument's sample changer deck with a protocol flag to which no assay has been associated.

Remove the cassette from the sample changer deck, or associate an assay to the protocol flag number.

The nuclide associated with this assay has an incorrect number of Quench sets.
One or more quench sets associated with a multiple label sample nuclide has been deselected from the assay or deleted from the library.

Re-select the appropriate quench sets for the sample nuclides. Recount quench set, if necessary.

The nuclide associated with this assay was not found in the nuclide library. Unable to retrieve nuclide information.
The sample nuclide defined for the assay was deleted from the library.

Re-enter the sample nuclide information in the nuclide library.

The quench standard associated with this assay's nuclide was not found in the Quench standard library.
A quench set that was associated with a sample nuclide in an assay has been deleted from the library.

Re-enter the standard information in the library and recount the standards.

The standard associated with this assay has not been counted.
The standard that is selected for the assay has not been counted prior to performing the assay.

Count the standards and restart the assay.

Vial release close.
A Sample changer error has occurred.

No action is required unless a message is printed. If this message appears on a printout, call PerkinElmer Technical Service.

Vial release open
A Sample changer error has occurred.

No action is required unless a message is printed. If this message appears on a printout, call PerkinElmer Technical Service.

W (message column)
If this character appears in the **Message** column of a report, this indicates that the Positive ID (PID) that was entered in the worklist does not match the PID read from the cassette.

Verify that the PID number that you used in the worklist matches that found on the appropriate cassette.

Warning: C-14 Normalization DPM not defined.
The C-14 Normalization DPM has not been defined.

In the IPA Definition window, enter a DPM value for the C-14 Standard.

Warning: H-3 Normalization DPM not defined.
The H-3 Normalization DPM has not been defined.

In the IPA Definition window, enter a DPM value for the H-3 Standard.

Warning: IPA background data not available.
No IPA background values are available for background subtraction.

Perform the IPA procedures.

Warning: questionable C-14 background value-please view historic data.
The background source failed the IPA check in the Carbon-14 region.

If Carbon-14 background is high and Tritium background is normal, there may be an increase in environmental radiation. The detector may be contaminated, or light is leaking into the detector. Check the background spectrum via the SpectraView window. Review the historic IPA data. Call PerkinElmer Technical Service.

Warning: questionable C-14 chi-square value-please view historic data.
The Chi-Square result is outside the range of 7.63 to 36.19.

Verify the integrity of the Carbon-14 spectrum via the SpectraView window. Repeat the Chi-Square test. If the result falls outside the range on the repeat test, call PerkinElmer Technical Service.

Warning: questionable C-14 figure of merit value-please view historic data.
Check the Figure-of-Merit threshold value. Clean the Carbon-14 and background sources and repeat the test. Check the efficiency and background values for Carbon-14. If these values are within specifications, call PerkinElmer Technical Service.

Warning: questionable H-3 background value-please view historic data.
Check that the correct background sample is in cassette position number 3. The detector may be contaminated, or light is leaking into the detector. Review the historic IPA data. Call PerkinElmer Technical Service.

Warning: questionable H-3 chi-square value-please view historic data.
The Chi-Square result is outside the range of 7.63 to 36.19.

Verify the integrity of the Carbon-14 spectrum via the SpectraView window. Repeat the Chi-Square test. If the result falls outside the range on the repeat test, call PerkinElmer Technical Service.

Warning: questionable H-3 efficiency value-please rerun quench curves and view historic data.
The Tritium source failed the IPA check and the tSIE value for the source is less than 950.

Check that the correct source is being used in sample position 2 of the SNC/IPA cassette. Check for dirt on the Tritium standard. Check the DPM value entered in the IPA Definitions window. Review the historic IPA data. Rerun the quench curve. Call PerkinElmer Technical Service.

Warning: questionable H-3 efficiency value-please view historic data.
The Tritium source failed the IPA check.

Check that the correct source is being used in sample position 2 of the SNC/IPA cassette. Check for dirt on the Tritium standard. Check the DPM value entered in the IPA Definitions window. Review the historic IPA data. Call PerkinElmer Technical Service.

Warning: questionable H-3 figure of merit value-please view historic data.

The Figure-of-Merit value for Tritium is below the threshold entered in the IPA Definitions window.

Check the Figure-of-Merit threshold value. Check the efficiency and background values for Tritium. If these values are within specifications, call PerkinElmer Technical Service.

Warning: system not normalized.

The instrument is not normalized.

Perform the instrument Calibration and Normalization procedures.

Warning: User Has Modified Count Conditions

Changes have been made to the assay that is currently counting.

Allow the current assay to finish counting prior to making changes.

You cannot exit the application because the instrument is counting a protocol.

The QuantaSmart program cannot be closed while the instrument is counting samples.

Allow the instrument to finish counting prior to closing the program.

You cannot exit the application because the instrument is counting group priostat.

The QuantaSmart program cannot be closed while the instrument is counting samples.

Allow the instrument to finish counting prior to closing the program.

You cannot exit the application because the instrument is engaged in a sample priostat activity.

The QuantaSmart program cannot be closed while the instrument is counting samples.

Allow the instrument to finish counting prior to closing the program.

Chapter 10

Calculations

The instrument performs the following calculations:

Background Correction

The background correction process subtracts background from sample nuclide activity. The background correction is performed before any other calculations (such as half-life correction) are performed. The correction of the sample count for background is calculated as:

$$CPM_{corrected} = CPM_{sample} - CPM_{background}$$

Background Threshold

The background threshold value is expressed as Counts Per Minute (CPM) and is calculated from the Instrument Performance Assessment (IPA) background value.

$$BKG_{threshold} = \overline{BKG}_{IPA} + \frac{4 \times \sqrt{\overline{BKG}_{IPA} \times CT}}{CT}$$

where:

$BKG_{threshold}$ = Background threshold in CPM

$\overline{BKG}_{IPA}$ = Mean of first five IPA background values in CPM

CT = Background count time for IPA

Chi-Square Calculation

The Chi-square test is a measure of reproducibility of sample counting. The test is performed by counting a single sample in the detector 20 consecutive times with a count time of 30 seconds for each repeat measurement.

$$X^2 = \frac{\sum (CNT_1 - \overline{CNT})^2}{CNT}$$

where :

$\overline{CNT}$ = mean of the repeat measurements

CNT_i = gross count of each repeat measure

This test is not a measure of detector accuracy.

DPM (Disintegrations Per Minute)

Disintegrations Per Minute (DPM) is an expression of radionuclide activity. DPM are calculated as follows:

$$DPM = \frac{\text{Counts Per Minute}}{\text{Efficiency}}$$

Efficiency

Counting efficiency is a measurement of the instrument's ability to quantify radionuclide activity. This value is calculated as follows:

$$\text{Efficiency} = \frac{\text{Counts Per Minute}}{\text{Disintegrations Per Minute}}$$

Figure of Merit Calculation

Figure of Merit (FOM) is a measure of the sensitivity of the instrument based on the instrument's counting efficiency. This value is calculated as follows:

$$FOM = \frac{(\text{Efficiency})^2}{\text{Background}}$$

Half-life Correction

The process of half-life correction recalculates sample CPM or DPM and accounts for the half-life decay of the sample nuclide. This calculation is performed as follows:

$$\text{Activity}_{\text{current}} = \text{Activity}_{\text{initial}} \times e^{-0.693t/T(\text{hl})}$$

where :

$\text{Activity}_{\text{current}}$ = the current remaining activity

$\text{Activity}_{\text{initial}}$ = the starting activity of the nuclide

T(HL) = the half - life of the radionucli de, in hours

e = 2.71828 (base of natural logarithmi c scale)

t = time interval in hours, from the reference date to the current date

The half-life correction is performed after the background correction.

IPA Background

The IPA background may be subtracted from all samples. The background value is established as the mean of the first five background values collected via the SNC (Self-Normalization and Calibration) protocol.

$$\overline{\text{BKG}}_{\text{IPA}} = \sum_{1}^{5} \text{BKG}_{\text{i}}$$

LCR (Low Count Reject)

Low Count Reject (LCR) is a means of rejecting samples if the sample nuclide activity doesn't meet a minimum specified criterion. Samples are rejected and flagged if they do not reach the specified count level within the first 30 seconds of the sample count.

LUM (% Luminescence)

This value represents the % luminescence of a sample and is calculated as follows:

$$\text{LUM} = \frac{\text{chance coincidence events}}{\text{true coincidence events}} \times 100$$

Radioactivity Units

The Curie and the Becquerel represent different units of measure for radioactivity. The Becquerel is the International System (SI) unit of activity.

$$\text{One Becquerel} = \text{One Disintegration Per Second (DPS)}$$

$$\text{One Curie} = 3.7 \times 10^{10} \text{ Becquerels}$$

2 Sigma % (%2s)

This value represents the percent of uncertainty in a gross count value (with 95% confidence limits). It is calculated as:

$$\%2s = \frac{200}{\sqrt{\text{accumulated counts}}}$$

The following table indicates the total accumulated counts necessary to achieve the corresponding 2% Sigma:

Uncertainty 2 Sigma %	Total Accumulated Counts
0.4	250,000
0.5	160,000
0.8	62,500
1.0	40,000
1.5	17,778
2.0	10,000
2.5	6400

Figure 10-1 Gross Count Equivalents for 2 Sigma Percent Values

Radionuclide Decay Calculator

The Radionuclide Decay calculator allows you to conveniently calculate the Current DPM Activity for common nuclides.

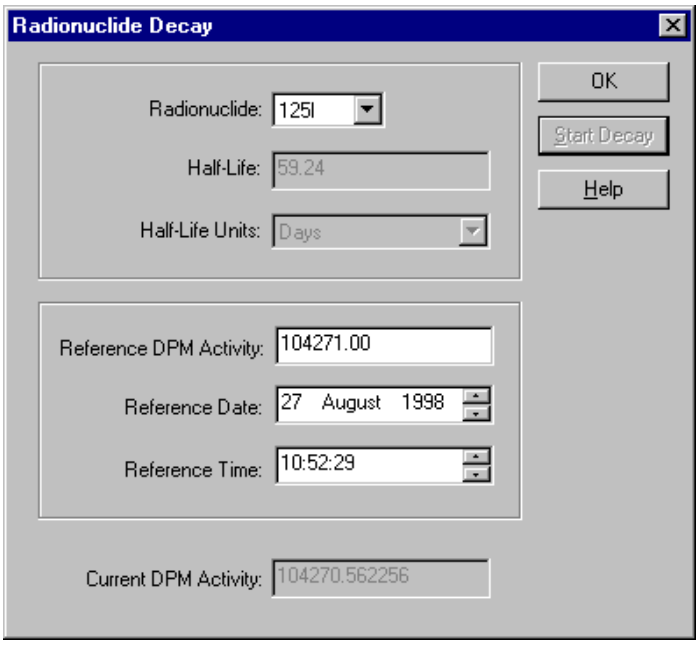

Figure 10-2 Radionuclide Decay Calculator

% Reference (% Ref)

This value represents the percent of a reference standard and is calculated using the CPM of the unknown sample and the CPM of the reference standard. The reference standard is typically the first vial counted in the assay, unless the first vial is being used to measure background. In this case, the second vial is used as the reference standard.

$$\%\text{Ref} = \frac{\text{CPM}_{\text{sample}}}{\text{CPM}_{\text{reference}}} \text{ x } 100$$

Chapter 11

Glossary

2S%
This value represents the percent of uncertainty in a gross count value.

Acquisition Time
This is the amount of time a sample has been counting.

Automatic Efficiency Correction (AEC)
This is a method used to adjust counting region settings to compensate for the effect of quenching on a sample spectrum.

Background Radiation
This is environmental radiation such as cosmic rays from space, and the radionuclides present in metals, glasses, ceramics and concrete.

Becquerel (Bq)
The Becquerel is the International System of Units basic unit of radioactivity.

One Becquerel=One Disintegration Per Second

One Curie=$3.7x10^{10}$ Becquerels

The calculation for Bq is (DPM for nuclide 1, 2, or 3)/(60DPM/Bq).

For uCi = DPM(nuclide 1, 2, or 3) / (2.22* e6 DPM/ uCi);

For pCi = DPM(nuclide 1, 2, or 3) /(2.22DPM/pCi)

Block Data Items
Block data items, which are comprised of several data items are used for the purpose of defining reports. The most common usage for Block Data items is in printing reports. By selecting certain Block Data items, the instrument is able to create reports that include instrument, protocol, spectrum or performance (IPA) information.

Calibration
Calibration is a process by which the voltage applied to each of the two Photomultiplier Tubes (PMTs) in a liquid scintillation counter is adjusted until the tubes have been synchronized in their response to a standard. This process is designed to assure that the instrument accurately quantifies the energy from all beta-particle emissions.

Cassettes
Cassettes are the plastic racks which hold sample vials and allow them to be moved on the sample changer deck.

Chemical Quenching
Chemical quenching is the reduction in the scintillation intensity seen by the photomultiplier tubes of a liquid scintillation counter due to materials present in the scintillation solution that interfere with the processes leading to the production of light. The result is fewer photons per keV of beta particle energy and usually a reduction in counting efficiency.

Chemiluminescence
Chemiluminescence involves random single photon events which are generated as a result of the chemical interaction of sample components. The coincidence circuit used in the TriCarb instruments excludes most chemiluminescent events except when they occur at high rates.

Chi-Square Test
The Chi-Square test is a general procedure for determining the probability that two different distributions are actually samples of the same population. In scintillation counting, this test is frequently used to compare the observed variations in repeat counts of a radioactive sample with the variation predicted by statistical theory.

Cocktail
A cocktail is the solution in which samples are placed for measurement in a liquid scintillation counter. Solvents and scintillators are the major components of a scintillation cocktail.

Coincidence
Coincidence refers to a system that uses a special circuit which acts to reject pulses that are not received from the scintillation counter's two photomultiplier tubes within the specified coincidence time. If scintillation events occur "in coincidence" (both events must occur within the specified coincidence time), these events are considered to be true decay events from the sample. If events do not occur in coincidence, they are considered random (background) and are not counted.

Color Quenching
Color quenching is the reduction in the scintillation intensity seen by the photomultiplier tubes of a liquid scintillation counter due to the presence of colored materials in the scintillation solution that interfere with the detection of light. The result is fewer photons per keV of beta particle energy and usually a reduction in counting efficiency.

CPM
Counts Per Minute. CPM are an expression of radionuclide activity. The gross counts per channel cumulatively equal the counts per region. The gross counts per counting region are divided by the count time to calculate CPM (Counts Per Minute) for each region.

Curie (Ci)
A basic unit of radioactivity named for Marie and Pierre Curie, who discovered Radium in 1898.

One Curie=$3.7x10^{10}$ Becquerels

One Becquerel=One Disintegration Per Second

Decay, radioactive
Decay is the spontaneous transformation of one nuclide into a different nuclide or into a different energy state of the same nuclide. This process results in a decrease over time of the number of original radioactive atoms in a sample. It involves the emission from the nucleus of alpha particles, beta particles, gamma rays or the nuclear capture or ejection of orbital electrons (fission). Also called radioactive disintegration.

Delay Before Burst
This is the length of time after the initial pulse (prompt pulse) that the detector of a liquid scintillation analyzer looks for additional pulses (afterpulses). Afterpulses, which occur after the prompt pulse and delay time interval, indicate that a scintillation event is due to background.

Delimited Text File
Mark this box to create a delimited text. Delimited Text is a file format in which each data item is separated by a defined delimiting character. This is a common format for transferring data between applications since database systems are able to import and export this type of file.

Note:The field delimiter is defined by the Windows NT operating system, using the LIST SEPARATOR field on the NUMBER tab of the REGIONAL SETTINGS PROPERTIES window accessed from the CONTROL PANEL.

Detector
This is a device that is sensitive to radiation and can produce a response signal suitable for measurement or analysis. In a liquid scintillation counter, this device measures the light emitted as a result of the interaction between a scintillation cocktail and an alpha or beta-emitting nuclide.

Discriminator
This is an electronic circuit which distinguishes signal pulses according to their pulse height or voltage. It is used to exclude extraneous radiation counts or background radiation. It is also used as the basis for pulse height analysis.

DPM
Disintegrations Per Minute. DPM are an expression of radionuclide activity. DPM are calculated as follows:

$$\text{DPM} = \frac{\text{Counts Per Minute}}{\text{Efficiency}}$$

Dual Label
This refers to a sample that contains two different radionuclides.

Efficiency
Efficiency is the ratio of measured counts to the number of decay events which occur during a measurement interval. It is usually expressed as a percentage.

External Standard
An external standard is a radioactive source that is placed adjacent to a sample to produce scintillation in the sample for the purpose of monitoring the sample's quench level. The TriCarb instruments use a Barium-133 source for this purpose.

Figure of Merit
Figure of merit is a term applied to a numerical value used to characterize the performance of a system.

Flags, protocol
Protocol flags are numbered, plastic devices that contain an encoded, reflective metal that the instrument uses to identify the appropriate assay counting parameters for a set of samples. Physically place an appropriately numbered flag on the first vial cassette of a group to identify the protocol that associates the desired assay parameters.

Half-Life
Half-Life is the time in which one-half the atoms of a radioactive substance disintegrate to another nuclear form.

IPA (Instrument Performance Assessment)
IPA is a process by which a TriCarb instrument measures background, counting efficiency, sensitivity (Figure-of-Merit) and the reproducibility of sample counting (Chi-Square test).

Isotope
This refers to atoms of the same element that have the same atomic number with different atomic weights.

keV (kiloelectron Volt)
One thousand electron volts. This is the unit used to express the energy associated with radioactive decay.

Library
In the QuantaSmart program, a library is a repository of data regarding sample nuclides or standards.

Luminescence
This is a general term applied to the emission of light that cannot be attributed to the radioactivity of the sample. It is typically due to a chemical reaction between the sample and the emulsifier (detergent) containing cocktails. Luminescence is most often caused by alkaline pH and peroxides in the sample.

Normalization
Normalization is a process used to establish a lower limit of measurement for quench.

Nuclide
This is a general term applicable to all isotopes, stable and radioactive, of all elements. Frequently, the term “isotope” is erroneously used to mean nuclide.

Photomultiplier Tube (PMT)
A PMT is a device capable of converting low levels of light into electrical energy (photoelectrons). Photoelectrons generated in a PMT are multiplied to facilitate their detection.

Photon
In the quantum theory of electromagnetic radiation, light is emitted in discrete units of energy called photons.

Priostat
This is a set of capabilities on the TriCarb instrument which allows for the interruption of a current protocol to count a set of high priority samples or perform specialized counting functions.

Pulse
A pulse is an electrical signal resulting when photons are detected by a PMT.

Pulse Decay Analysis (PDA)
PDA is a technique by which nuclide pulses are sorted into separate multichannel analyzers for analysis and quantitation. Pulse Decay Analysis relies on the differences in pulse duration to classify the types of radioactive emissions (alpha, beta or gamma) from a nuclide.

Quench
Quench results in the reduction in the scintillation intensity seen by the photomultiplier tubes of a liquid scintillation counter as a result of materials present in the scintillation solution that interfere with the processes leading to the production or detection of light. The result is fewer photons per keV of beta particle energy and usually a reduction in counting efficiency.

Quench Curve
A quench curve is a mathematical graph which correlates the counting efficiency to a quench indicating parameter (QIP). The QIP for a sample is determined during sample counting. This value is used to interpolate the counting efficiency for a sample from the quench curve (where %Efficiency is plotted vs. the QIP). The interpolated efficiency value is used to calculate the DPM (Disintegrations Per Minute, where DPM=CPM/Efficiency).

Quench Indicating Parameter (QIP)
A QIP is a numerical value used to express the level of quench in a sample. SIS, tSIE and tSIE are quench indicating parameters used in the TriCarb system.

Reference Date
This is the date on which a radio-labeled material has the specified amount of activity.

Reference Time
This is the time at which a radio-labeled material has the specified amount of activity. Typically, this parameter is described only for radionuclides with very short half-lives.

Region
This is the range of energy over which counts are measured for a nuclide in a liquid scintillation counter. Also referred to as “window” or “channel”.

Replay
Replay is a feature available on the TriCarb instrument which allows for the reanalysis of previously collected data under a variety of data reduction conditions, without recounting samples.

Rich Text Format
This is a common ASCII file type. These files have special commands which specify document formatting information, such as fonts and margins. This type of output is particularly useful if you want to bring your data into a word processing software package to perform additional formatting for more formal reports.

RS-232
This is a standard interface for connecting serial devices to a computer.

Sample List Library
The Sample List Library is a function available in the Worklist portion of the QuantaSmart program. It is used to create a Sample List Library of frequently used sample names.

Scintillation
Scintillation is a flash of light produced in a scintillator by an ionizing event. The scintillation is the sum of all photons produced by the decay event.

Shielding
Shielding is a process used to reduce the amount of ionizing radiation that reaches a physical area through the use of a shield, such as lead.

SPC (Single Photon Counting)
A method used on the TriCarb instrument for counting luminescent samples, using only one PMT (Photomultiplier Tube).

Specific Activity
This is the quantity of radioactivity per unit mass, e.g. DPM/g or Ci/g.

Spectral Index of the Sample (SIS)
SIS is a number obtained from the spectrum analyzer of a liquid scintillation counter that is calculated from the spectral distribution of the sample; this is used as an index for the level of quench in a sample.

Spectral Mapping
Spectral Mapping is a technique used during single-label DPM sample counting for displaying the sample and quench standards spectra in a three-dimensional view.

SpectraView
SpectraView is a window in the QuantaSmart program which displays a two-dimensional, real-time view of the spectrum for the current sample.

Spectrum Unfolding
Spectrum Unfolding is a technique which separates a composite spectrum of a dual-label sample into individual components.

Spillover
Spillover is a term used to describe the situation in dual-label counting where a portion of the spectrum from one radionuclide is included in the region used to count the other radionuclide.

Static
Static refers to the accumulation of electric charge on an insulated body such as a scintillation vial. In liquid scintillation counting, a discharge of static may result in spurious pulses from the PMT.

Tandem Processing
Tandem Processing is a process which allows a TriCarb instrument to pass data from a protocol to an application program.

TR-LSC
Time Resolved Liquid Scintillation Counting is a process patented by PerkinElmer Life and Analytical Sciences which allows for the detection of low levels of background counts. The result of this process is enhanced sensitivity through the discrimination of true beta from background counts.

Transformed Spectral Index of the External Standard (tSIE)
tSIE is a number obtained from the spectrum analyzer of a liquid scintillation counter that is calculated from the spectral distribution of the external standard and is used as an index for the level of quench in a sample.

Worklist
Worklist is a function in the QuantaSmart program which is used to designate Positive Identification numbers and sample names that correspond to sample numbers on a printout.

Chapter 12

Theory

This chapter contains supplementary information regarding the theory of the Low Level Counting mode and the Alpha Beta Counting mode.

Low Level Counting Theory

In liquid scintillation counting, the limit of detectability is a function of detection efficiency and background noise. By increasing the efficiency of detection, reducing the background, or both, the sensitivity is enhanced. This enhanced sensitivity yields lower limits of detection. In practical terms, this means accurate measurements are achieved in less time with much smaller samples. This is particularly important in measuring environmental samples for radioactive contamination from nuclear power plants, dump sites and naturally occurring radiation. In radiocarbon age dating, to determine the age of archaeological artifacts, only the smallest sample may be spared for measurement without sacrificing the specimen. In medicine and biomedical research, improved sensitivity facilitates the use of less test substance to determine metabolic pathways.

Most approaches to background reduction employ massive amounts of heavy lead shielding, expensive secondary detection circuits, or both. Such systems are very expensive and, because of their design, have very limited utility beyond low level counting. In 1985, however, Packard Instrument Company developed the first electronic burst counting circuitry to be used in a commercial liquid scintillation counting system. This patented development is the basis of TR-LSC (Time Resolved Liquid Scintillation Counting) in PerkinElmer TriCarb liquid scintillation analyzers. In the TriCarb Model 3170 TR/SL analyzer, the burst counting circuitry is further enhanced through the use of a slow scintillating, Bismuth-Germanium Oxide (BGO) detector guard, thereby yielding even higher sensitivity.

Burst Counting

The TR-LSC burst counting circuitry employs a background discrimination technique which differentiates the characteristics of beta scintillation pulses from non-quenchable background scintillation pulses. A typical beta scintillation event is composed of at least two components as a function of time. There is a fast, or prompt, component due to the fluorescence of the scintillator(s), and there is a slower, or delayed, component due to the annihilation of the triplet excited molecules (200-900 nanoseconds). The slow component is present only in the absence of quenching agents, particularly oxygen. When oxygen or other quenching agents are present in the sample, which is the most common case for routine laboratory samples, the slow component is reduced. This means that in routine samples prepared in ambient laboratory air, there is little or no slow component or afterpulses originating from the sample itself.

TR-LSC increases counting sensitivity by reducing the non-quenchable component of instrument background that is caused by interaction of high energy cosmic radiation with the sample vial and photomultiplier (PMT) glass face. Other non-quenchable background interferences including PMT afterpulsing and natural radiation in the PMT and vial construction materials are also reduced by TR-LSC. Approximately 68% of the observed total background is non-quenchable and therefore can be greatly reduced by this technique.

Non-quenchable background events can be distinguished from true beta events since they are characterized by a series of low amplitude afterpulses that follow the initial prompt pulse. True scintillation pulses have fewer afterpulses associated with them. The figures below show a graphical representation of a background pulse and ^{3}H beta pulse. Note that the background pulse has more prominent afterpulse characteristics that extend over time. TR-LSC is designed to evaluate each event for the presence of these afterpulses as one criteria to reduce background. When a series of afterpulses is detected, TR-LSC characterizes the event as background and rejects it. The efficacy of this rejection can be increased when a bismuth germanium oxide (BGO) detector guard is used in conjunction with TR-LSC electronics. The BGO guard completely surrounds the sample vial and acts as a cosmic guard to further increase afterpulse rejection, thus reducing

the background.

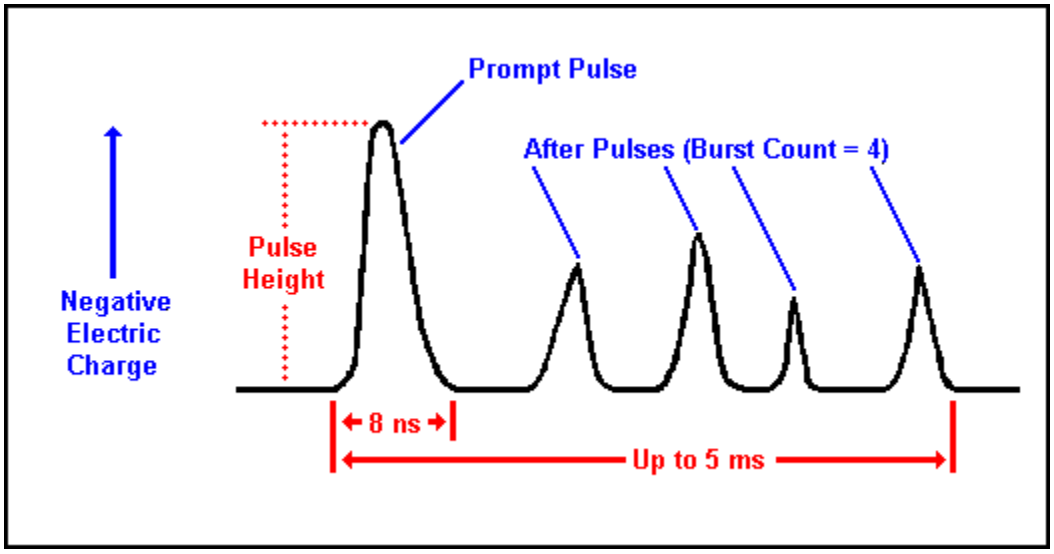

Figure 12-1 Liquid Scintillation Background Pulse.

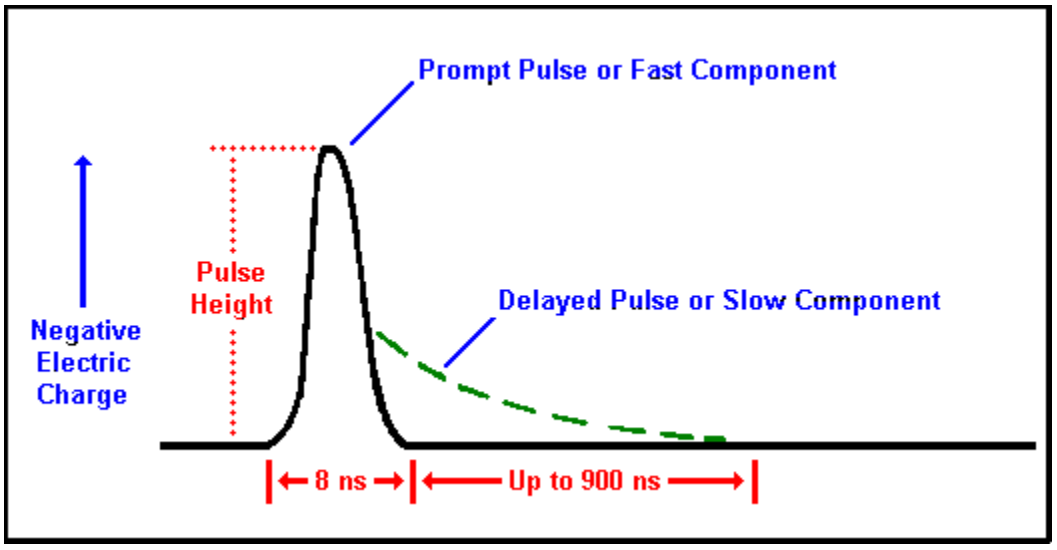

Figure 12-2 Liquid Scintillation True Beta Pulse.

TR-LSC can be optimized for the latest generation of safer cocktail formulations and for higher energy beta emitters. This is easily accomplished through the instrument software by modifying the Delay Before Burst parameter on the Count Corrections tab in Assay Definition. The Delay Before Burst feature functions by implementing a time delay before afterpulse discrimination is enabled. This is necessary because:

- Scintillation cocktails that contain solvents based on di-isopropyl naphthalene (DIN) and 1-phenylxylylethane (PXE) have long scintillation decay constants, i.e. produce light pulses of longer duration.
- Higher energy beta emitters produce longer duration pulses.

These phenomena must be considered in order to minimize the misclassification of beta and background events, since the longer duration pulses arising from either of these conditions mimic background pulses and may be eliminated by TR-LSC. By increasing the time delay before afterpulse discrimination begins, counting efficiency losses are minimized and sensitivity is increased.

High Sensitivity and Low Level Counting

In the PerkinElmer TriCarb series of liquid scintillation analyzers, the patented TR-LSC burst counting circuitry quantitates the number of afterpulses following a coincident event. This information is then used to discriminate background pulses from pulses arising from actual scintillation events in the sample. Thresholds have been established and are used to reject events which produce significant numbers of afterpulses. The thresholds vary with the energy of the coincident pulses due to the afterpulsing phenomena in the photomultiplier tubes. Since the Photomultiplier tubes can produce energy-dependent afterpulses, this must be factored into the discrimination of background noise from sample activity.

The PerkinElmer Tri-Carb series liquid scintillation analyzers use this time-resolved discrimination of afterpulses at three levels. These levels are:

Normal Count Mode. This mode employs a minimum amount of discrimination.

High Sensitivity Count Mode (HSCM). This mode applies an intermediate amount of discrimination.

Low Level Count Mode (LLCM). This mode provides maximum discrimination.

Progressing from NCM to LLCM yields increasing efficiency to background ratios (E^2/B). The improvement is demonstrated in the table of ^{14}C data below.

PerkinElmer also offers the Tri-Carb Model 3170TR/SL analyzer, which achieves super low level sensitivity through use of a slow scintillating BGO detector guard. In the 3170TR/SL analyzer, this special material surrounds the sample in the form of a special detector assembly to further increase the number of photons in the trailing burst from background radiation. The detector assembly replaces the conventional sample changer and provides a considerable increase in E^2/B performance as compared to the burst counting system alone. This configuration is referred to as the Super Low Level Count Mode (SLLCM).

For environmental water samples, it is generally necessary to count as much water as possible, since the amounts of ^3H found are extremely low and the larger volume permits shorter counting times. Typical water samples are made up using from 9mL to 12mL of water in a total volume of 20mL to 22mL.

Radiocarbon dating samples are generally made up of pure benzene from the conversion of the raw sample through a benzene synthesis procedure. Such samples are generally only 3mL to 5mL total volume. Comparative data are shown in the following tables for ^{14}C samples and ^3H water samples.

TR-LSC Count Mode	Sample Configuration	Energy (keV)	^{14}C % Efficiency	BKG CPM	E^2/B Ratio
None	Sample Only	20.0-113.0	64.99	3.62	1167
NCM	Sample Only	20.5-101.5	64.03	3.28	1250
HSCM	Sample Only	21.5-95.5	61.22	1.36	2756
LLCM	Sample Only	19.5-95.5	54.05	0.76	3844
LLCM (SLLCM)	Sample+BGO Detector	10.0-75.0	70.70	0.54	9256

Example of ^{14}C in Benzene Sample Performance.

The samples were ^{14}C toluene in benzene cocktail (PPO 6 grams/ liter POPOP 0.2 grams/liter). Total sample volume was 3.5mL in standard low 40K 7mL vials, prewashed with 0.1M EDTA, and Teflon® cap liners were used.

TR-LSC Count Mode	Sample Configuration	Energy (keV)	^{3}H % Efficiency	BKG CPM	E^2/B Ratio
None	Sample Only	0.0-18.6	34.2	22.3	52
NCM	Sample Only	0.0-18.6	33.8	17.8	64
HSCM	Sample Only	0.0-18.6	33.9	12.8	90
LLCM	Sample Only	0.0-18.6	29.4	6.2	139
LLCM (SLLCM)	Sample+BGO Detector	0.0-18.6	26.7	2.8	255

Example of Large Volume ^{3}H in Water.

TR-LSC Count Mode	Burst Discrimination Modes
None	Equivalent to conventional LSC systems.
NCM	Minimum or Normal Count Mode.
HSCM	Intermediate or Low Activity, High Sensitivity Count Mode.
LLCM	Maximum or Ultra Low Level Count Mode

Burst Discrimination Modes.

The performance in any given laboratory will depend on many factors. First, in counting environmental water, the source of water used for the background sample is extremely important. The water must be free of contamination by radionuclides, especially ^{3}H. When counting very low levels of ^{3}H, even the smallest amount of contamination will increase the count rate of the background sample. This cannot be discriminated out since the contamination comes from the sample itself. Therefore, it is necessary to secure a source of water for the background samples which is “dead’’ in terms of radioactivity.

For radiocarbon dating samples, it is important to ensure that the reagents used in the process of sample preparation are free from contaminating ^{14}C. This includes the actual scintillators and any reagents used to convert the sample into benzene.

Overall, the preparation of samples for extremely low level counting must be conducted with extreme care to provide contamination free samples for counting. If the background samples or the unknown samples contain extraneous sources of radionuclides, performance will be degraded.

In Super Low Level counting as in other low level count modes, it is important to tailor the scintillation fluor (scintillator) to the counting conditions. Secondary scintillators produce significantly higher counting efficiencies than are possible using only a primary scintillator. These secondary scintillators include BBOT, DPA, POPOP, Me2POPOP, and bis-MSB.

Although there are many potential combinations of primary and secondary scintillators which are suitable for use with the TR-LSC, a combination of 6 grams per liter PPO and 0.2 grams per liter bis-MSB works well for many sample types and can be used reliably. This is the commonly used combination of scintillators for a wide variety of counting applications.

Operational Considerations

The operating procedures for the Tri-Carb 3170TR/SL liquid scintillation analyzer are described in the appropriate areas of this documentation. Aside from the count rate limitations and differences in the SNC/IPA procedures, operation of the Model 3170TR/SL analyzer is exactly the same as other Tri-Carb 3100 analyzers.

The selection of counting vials for low level counting is very important to assure low background and high sample counting sensitivity. Low potassium glass vials are recommended when counting low levels of ^{3}H or ^{14}C. Certain plastic vials may also be used for large or small samples measuring ^{3}H in water.

It is recommended that all glass or plastic vials used for low level counting be carefully sealed. Teflon cap liners for the screw caps of the vials improve the seal against leakage.

Glass vials should be washed, then rinsed in a dilute ethylene-diamine-tetraacetic acid (EDTA) solution, followed by a “dead” deionized water rinse and allowed to air dry. This will help reduce background and further reduce surface contaminants which could contaminate the detector guard.

Maximum vial dimensions are as follows: small vials must not exceed 17.8mm diameter and 58.0mm height (including cap); large vials must not exceed 28.1mm diameter and 63.0mm height (including cap).

High Sensitivity/Low Level Count Mode Setup

When operating the system in the High Sensitivity or Low Level Count Modes, remember that the maximum sample activity is 100,000 CPM. If a sample exceeds this count rate, the system will automatically switch to the Normal Count Mode. Therefore, when purchasing or making quenched standards or reference standards, this limitation must be observed for proper operation.

When defining a protocol, either the High Sensitivity (HSCM) or Low Level Count Mode (LLCM) must be selected in the Count Conditions window. Selecting LLCM will automatically cause the instrument to operate at that level of afterpulse discrimination. This will enable the TR-LSC background discrimination.

Note:The luminescence correction feature is not recommended for use when you are counting very low CPM samples. For such samples, the Luminescence Correction check box in the Count Corrections window should be NOT be marked.

Note:Do NOT use High Sensitivity or Low Level Count Modes to count alpha samples in normal CPM or DPM counting assays. These TR-LSC discrimination modes are not appropriate for counting alpha samples. Extremely low alpha count rates will be observed.

Frequently, it is preferable to allow samples to dark adapt before actual counting commences. The Tri-Carb analyzer provides sample counting delays up to 99.99 minutes. With a sample counting delay selected, the sample is lowered into the counting chamber and allowed to dark adapt for the specified delay time before counting for the indicated counting time. The Pre-Count Delay is selected in the Count Conditions window and is specific for the assay.

Precautions and Limitations

It is important to note that background radiation varies throughout the world, and will be a factor when determining the instrument background. Higher elevations and areas where the geology tends to concentrate uranium and its decay products will most likely yield higher backgrounds. The exact instrument background and performance for a given location must be determined at the site of the installation.

Alpha Beta Counting Theory

Alpha and beta emitting radionuclides may be counted simultaneously in the same liquid scintillation sample. Some alpha and beta nuclide energies may overlap in the LSC environment, and their spectra are not resolvable with simple energy discrimination. To separate alpha and beta nuclide energies, you must take advantage of their differing pulse decay times. The pulse decay analysis (PDA) method of discrimination is used by the Tri-Carb instruments equipped with the Alpha/Beta capability.

Pulse Decay Analysis (PDA)

A scintillation (light) pulse consists of a prompt (initial) component and delayed (slow) component. Each component contributes to the total amount of light which makes up the pulse, and determines the pulse decay time. Beta nuclides typically produce a minimal slow component leading to a fast decay time. Alpha nuclides produce a significant slow component which increases their overall decay time. Pulse Decay Analysis uses the differences in pulse duration to discriminate between alpha and beta nuclide pulses. The pulses are sorted into separate multichannel analyzers for subsequent analysis and quantitation.

A time-based Pulse Decay Discriminator (PDD) is used to optimize the separation of alpha and beta pulses. The PDD may be adjusted by the operator, or the system, to determine the optimum setting for specific sample conditions.

The optimum PDD is influenced by sample chemistry, vial type, geometry and degree of quenching. To obtain the best results, it is necessary to determine the optimum PDD for each type of sample.

Refer to page 159 for more information regarding Alpha Beta counting.

Optimum Pulse Decay Discriminator

The optimum pulse decay discriminator minimizes the misclassification of alpha events being counted as beta events, and vice versa. If the discriminator is set too low, beta events are erroneously counted as alpha events. If the discriminator time is set too high, alpha events are erroneously counted as beta events. An optimum Pulse Decay Discriminator is established when counting an Alpha Beta Standard Set.

To optimize the pulse discriminator setting, you must perform an Alpha Beta Standards assay to count two standard sources, a pure beta emitter and a pure alpha emitter. The composition of the standards must be as close as possible to the chemistry and volume of the subsequent samples to be counted. When counting the pure beta emitter source, the percent of beta events counted as alpha events is plotted (and stored) as %Spill versus Discriminator value (misclassification curve). When counting the pure alpha emitter source, the percent of alpha events counted as beta events is also plotted. The optimum discriminator value is where the spillover for both radionuclides is at a minimum.

Note:After counting the two standards, the optimum computed discriminator setting is determined (minimal spill for both alpha and beta events). You can manually adjust this setting to favor either the alpha or the beta nuclide by entering the desired discriminator setting for In Use.

Refer to page 156 for more information.