gamma11

GAMMA-11
Operator's Guide

January 1978

This document describes the operating procedures for GAMMA-11. For background information to this manual, refer to the *Introduction to GAMMA-11* (AA-5689A-TC).

SUPERSESSION/UPDATE INFORMATION:	This document completely supersedes the document of the same name, Order No. DEC-11-MGOGA-A-D, published August 1976.
OPERATING SYSTEM AND VERSION:	RT-11 V03
SOFTWARE VERSION:	GAMMA-11 V2C

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Operator's Guide

Order No. AA-2185B-TC

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First Printing, August 1976
Revision, January 1978

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PREFACE

The GAMMA-11 system is a computer application system designed for acquisition and analysis of gamma-camera data. GAMMA-11 has been developed for the nuclear medicine department that examines a large number of patients.

GAMMA-11 does not require you to know any computer language. However, you must have a working knowledge of nuclear medicine techniques and terminology and of the gamma camera and its related instruments. To learn more about computers in nuclear medicine, and specifically about GAMMA-11, read the Introduction to GAMMA-11 before reading the GAMMA-11 Operator's Guide.

The GAMMA-11 Operator's Guide describes the GAMMA-11 system, its operation, and use of the foreground/background (F/B) environment. All GAMMA-11 applications are illustrated by examples and photographs.

The GAMMA-11 system, running under the RT-11 F/B operating system, permits direct access to patient data files. Thus, those users who understand computer languages can perform extended analysis on data by using BASIC/RT-11, FOCAL/RT-11, or FORTRAN/RT-11.

This manual refers you (for further information) to the following other manuals.

Introduction to GAMMA-11	(AA-5689A-TC)
GAMMA-11 System Reference Manual	(AA-2186B-TC)
Introduction to RT-11	(DEC-11-ORITA-A-D)
RT-11 System User's Guide	(DEC-11-ORGDA-A-D)
RT-11 Advanced Programmer's Guide	(DEC-11-ORADA-A-D)
RT-11 System Generation Manual	(DEC-11-ORGMA-B-D)
NC11-A Camera Interface for a GAMMA-11 System	(EK-NC11A-TM-001)
NCV11 Gamma Camera Interface Technical Manual	(EK-NCV11-TM-001)
PDP-11 Processor Handbook	
PDP-11 Peripherals Handbook	

SYMBOL NAMING AND CONVENTIONS

This manual supports the VT01 storage scope as well as the VSV01 color display. Please note that all references made to the VSV01 color display also refer to the VT01 storage scope unless otherwise specified. Chapter 6 is totally devoted to the commands that you can perform on only the VSV01 color display.

In the chapters that have colored inserts, references to figures on the inserts are marked "color insert."

The symbol RET represents pressing the RETURN key on the terminal keyboard. The symbol SP represents pressing the space bar on the terminal keyboard.

The change bars in the outside margins indicate technical changes and additions to the previous edition of the GAMMA-11 Operator's Guide.

PART 1

GAMMA-11 SYSTEM OVERVIEW

CHAPTER 1

INTRODUCTION

A gamma camera records radionuclide distributions in patients. It collects this information following patient intake of a radiopharmaceutical that localizes in a particular organ or pathological lesion. The GAMMA-11 system receives information from gamma-camera data and returns information about radionuclide tests. These tests include studies of the distribution of radioactive quantities in patients. Such studies are divided into dynamic and static studies.

A static study records one or more images of an organ but does not try to capture flow or motion. A dynamic study records many images or frames of the same organ and tries to capture the motion of the organ -- as a movie does.

An example of a dynamic or flow study is the 131-I Hippuran renogram. Following intravenous injection, the 131-I Hippuran is extracted from the blood by the kidneys and excreted to the bladder. Abnormalities in kidney function show up as irregularities in the distribution and rate of movement of the radiopharmaceutical. A gamma-camera oscilloscope shows this flow distribution of radioactivity within the kidneys. The GAMMA-11 system allows this flow distribution to be taken from the camera, digitized, and stored within the computer for analysis.

An example of a static study is a liver scan using 99-mTc-Sulfur colloid. Following intravenous injection, the liver and spleen take up the sulfer colloid. The distribution of the radionuclide throughout the organ may show a malignant or pathological area. In this liver study, the static image showing the final distribution of the radionuclide is more important than the dynamic flow of the radionuclide to the liver. Separate static images of the liver can be taken to show the following:

- Position of the organ
- Size of the organ
- Distribution of the radioactivity
- Pathological lesions

However, these images are not dependent on each other as in a dynamic study.

The GAMMA-11 system allows you to manipulate the image for better visualization of such a study. When necessary, you can also extract study statistics from the raw or modified data.

1.1 GAMMA-11 AND YOU

GAMMA-11 is designed to help you, the operator, by:

- Providing an easy-to-use system for nuclear medicine
- Enabling detailed and accurate diagnostic reports
- Providing a high degree of file protection
- Providing a system capable of future expansion to meet changing needs

1.2 SYSTEM DESCRIPTION

The GAMMA-11 system is a series of programs that acquires and analyzes data from a gamma camera. The system also contains utility programs for file upkeep and system modification. GAMMA-11 runs under the RT-11 F/B operating system, or the RT-11 single-job operating system. It uses the RT-11 file structure for the patient data files. The GAMMA-11 F/B system basically consists of two independent components:

- A foreground program for data acquisition only
- A series of background programs for data acquisition, data analysis, and utility functions

The background program can collect data only if there is no foreground program or if you are running a single-job RT-11 system (where there is no foreground job). Thus, while you collect data in the foreground, you can also do one of the following:

- Analyze data in the background
- Run BASIC or FOCAL in the background
- Run any other RT-11 programs (i.e., FORTRAN, assembly language, etc.) in the background

1.3 HARDWARE REQUIREMENTS

The minimum hardware requirements (excluding the gamma camera and its related equipment) are:

- PDP-11 CPU
- 28K of memory for F/B or 16K for RT-11 single job
- Hard-copy console terminal (LA36 DECwriter)
- High-speed video alphanumeric terminal (F/B only)
- RK11/RK05 disk controller and two drives, or RK611/RK06 disk controller and drive and an additional RK06 drive, or magnetic tape drive
- BM792-YB bootstrap loader
- KW11-P real-time clock (for data acquisition)

- KW11-L line frequency clock (for RT-11 F/B)
- VSV01 color display
- NC11A or NCV11 gamma-camera interface
- AR11 A/D converter for simultaneous joystick positioning and foreground acquisition, or for gate-synchronized studies

NOTE

> The GAMMA-11 system still supports the VT01 storage scope as part of the minimum hardware requirement only if the VSV01 is not part of your system. Gate-synchronized acquisition, however, is not supported on the VT01.

The following hardware is optional:

- Additional disk drives for data acquisition and data analysis
- Any mass-storage device that is supported by RT-11 (e.g., a TU10/TM11 9-track magnetic tape)

For single-user systems only 16K of memory is required.

The video alphanumeric terminal, such as the VT52 or VT05, is used by the foreground data-acquisition program. The DECwriter keyboard and VSV01 color display are used by the background. GAMMA-11 does not normally use the LA36 DECwriter printer. It directs output to the DECwriter only when you specifically ask for hardcopy output of reports, summaries, and so forth.

1.3.1 The Gamma Camera

The gamma camera interfaces with the GAMMA-11 system by means of the gamma-camera interface (NC11A or NCV11). The gamma camera is sensitive to gamma rays and is used to visualize the distribution of radioactivity within the body of a patient who has been given a dose of a radiopharmaceutical. The gamma camera's output is displayed on an oscilloscope, which you can photograph also. There are usually two oscilloscopes:

1. A storage scope for (variable persistence) monitoring
2. A refresh scope for photographing

Depending on the organ being studied, you can take a one-time-exposure photo of the oscilloscope, or several photos, showing the distribution of radioactivity at different times. The photographs can represent either a static or dynamic study.

1.4 STUDY TYPES

The GAMMA-11 study types are:

- Static
- Dynamic
- List
- Gate-synchronized
- Gated-list
- Flood
- Predefined

These studies are described in the following sections.

1.4.1 Static Study

A static study consists of one to eight separate frames combined into one study file. You can vary the camera and collection parameters between frames. For example, you can use a multiple-frame static study to show several different views of a particular organ.

1.4.2 Dynamic Study

A dynamic study consists of a series of frames that GAMMA-11 collects at the rate you specify (comparable to a sequence of motion picture frames). Data are collected in sequential frames showing the amount of radioactivity in an organ as a function of time.

A dynamic study can consist of 1 to 512 frames.

The frame rate (frames per second) can change within a single study. Each change in frame rate constitutes a group. You can specify up to 13 groups in one dynamic study.

GAMMA-11 can calculate curves showing the rate of radioactivity within a region of interest.

1.4.3 Flood Study

The flood study is a single-frame static study that checks and corrects for a nonuniform camera response. In a flood study, you present the camera with a uniform sheet of a particular radioactive source. Variations from uniformity in the resulting image reflect irregularities of response in the camera's field. You can then use the data to create a flood-correction matrix, which in turn is used to compensate for these irregularities in other studies. No patient data is required. Of the collection parameters, you must supply only the duration of the run (in either elapsed time or in total number of counts) and the camera orientation with respect to the flood source.

1.4.4 List Study

A list study contains unstructured data. Rather than storing an image the way it looks on the camera's oscilloscope, GAMMA-11 breaks the image into a matrix with X and Y coordinates. It stores each pair of X and Y coordinates in a list, with periodic time-reference marks and optional gate marks. You instruct GAMMA-11 to restructure the raw data into a static or dynamic study at data-analysis time. GAMMA-11 uses the time marks to determine the frame duration for data formatting. The gate marks are also used for data formatting in a gated-list study.

1.4.5 Gate-Synchronized Study

In a gate-synchronized study, GAMMA-11 synchronizes the camera data acquisition to a gate signal (such as an ECG gate). Multiple frames are stored in core. When the system receives a gate signal, it begins acquiring data in Frame 1. After a short, preset time, acquisition is switched to Frame 2, then Frame 3, and continues until all the frames have been filled or until a new gate signal is received, whichever comes first. When another gate signal is received, acquisition returns to Frame 1. Thus, Frame 1 represents the sum of all the first time periods during the gate interval. (Frame 2 represents the sum of all the second time periods in the gate interval, etc.)

1.4.6 Gated-List Study

A gated-list study gathers data in the same way that a regular list study does. However, the timing marks in a gated-list study occur every 1 millisecond instead of every 10 milliseconds as in a regular list study. A gated-list study also records the gate marks along with the raw data.

1.4.7 Predefined Study

The predefined study is not really a study type, but rather an aid to acquiring data. The predefined study allows you to save time in setting up routines or often-used study plans. You can define collection parameters and other common data in advance; you need add only the specific run-time information when you use the study plan to acquire data (i.e., patient name, ID, birthdate). The use of predefined studies ensures that often-used studies are collected consistently. Predefined studies can be used with any study type except a flood study.

CHAPTER 2

GAMMA-11 SOFTWARE ENVIRONMENT

2.1 INTRODUCTION TO RT-11

The RT-11 operating system, designed for the PDP-11 computer series, provides both single-program operations and a powerful foreground/background (F/B) capability. RT-11 also offers a versatile keyboard monitor, which provides complete user control of the system from the console terminal keyboard. You direct both background and foreground operations by means of monitor commands.

In addition to the monitor facilities, RT-11 offers a full complement of system resources that allow you to develop programs using higher level languages, such as FORTRAN, FOCAL, and BASIC, or assembly language (MACRO).

The uses of a foreground/background RT-11 system and differences between this type of system and a single job RT-11 system are outlined in the following sections.

2.1.1 The Single-User Background System

The single-user background system can only run one job at a time. Consequently, the single-user system can do only one of the following at a time:

- Data acquisition
- Data analysis
- Program development

2.1.2 The Foreground/Background System

The foreground/background system greatly increases the efficiency of processor usage and system resources. For example, the central processor of a computer system may spend a large percentage of time waiting for an external event to occur, such as completion of an input/output (I/O) transfer. Programs that perform large amounts of I/O cause the computer to become idle for as much as 90 percent or more of processor intervention time.

In an F/B system the foreground job is given top priority and, whenever possible, the processor runs the foreground job. However, when the foreground job reaches a state where no more processing can be performed, or when an external event takes place, the RT-11 monitor relinquishes control to a lower priority job -- the background job.

The background job then runs until the foreground job is once again in an executable state. At this time, control is again required by the foreground program. The central processor stops running the background job and resumes executing the foreground job. This facility results in greater processor efficiency.

In GAMMA-11, data acquisition can be done in the foreground while data analysis or program development is being done in the background.

2.2 GAMMA-11 AND RT-11

The GAMMA-11 programs run under the control of RT-11 F/B or RT-11 single job. All GAMMA-11 programs run as background programs. The data-acquisition program runs as either background or foreground. The system is divided into two independent parts as follows:

1. The background, which is referred to as BGAMMA

2. The foreground, which is referred to as FGAMMA

These independent parts are further discussed in Sections 2.2.1 and 2.2.6.

2.2.1 The Single and Background User

The background programs (BGAMMA) consist of a background driver program and the individual data-acquisition, data-analysis, and utility procedures, such as study deletion, study transfer, and patient monitor.

2.2.2 Data Analysis (Background Only)

The data-analysis and review programs allow you to view the data of a patient or flood study and perform analysis of the data. Specifically you can:

1. Select a patient study from the patient index

2. View the administrative data of the selected study

3. View the frames of the study

4. Perform image enhancement of the display

    - Smooth the data (9-point)
    - Switch from color to black and white
    - Use isocontours

5. Call macro commands

6. Perform frame arithmetic (i.e., add, subtract, or divide multiple frames)

7. Define regular (i.e., rectangular) and irregular regions of interest and use these regions to calculate and display dynamic curves

8. Save frames or dynamic curves in a save area that can later be referenced by the data-analysis program or by user-supplied BASIC, FORTRAN, FOCAL, or assembly-language programs
9. Plot slice profiles
10. Flood-correct data
11. Structure list-mode data and, having done so, perform any of the above procedures, 1 through 10
12. Play back dynamic studies in a movie-like manner
13. Automatically load and execute user programs

2.2.3 Study Deletion (Background Only)

The study-deletion routine allows you to display and select those studies that are to be deleted. Specifically, the study-deletion program can do the following:

1. Display the study index
2. Select, by number, the study to be deleted
3. Delete the study selected
4. Squeeze the disk

2.2.4 Study Transfer (Background Only)

The study-transfer routine allows you to transfer patient studies between any mass-storage media (i.e., disks, magtape, DECtape, etc.).

2.2.5 System Summary (Background or Foreground)

The system-summary routine displays the available disk space for patient data files. The routine allows you to quickly determine the largest data file you can acquire on a given disk.

2.2.6 Data Acquisition Used as Foreground or Background

The data-acquisition program runs from either the foreground or the background. Using the data-acquisition program, you can set up and acquire the following types of studies:

1. Single or multiple-frame static studies
2. Dynamic studies
3. List studies (gated or ungated)

4. In-core gate-synchronized studies (in background only)
5. Flood studies

All user interaction with the foreground acquisition program is via the VT52 or VT05 terminal. The console terminal and VSV01 color display are used by the background program.

NOTE

The background data-acquisition program can be used only

1. With the single-user RT-11 monitor
2. With the F/B RT-11 monitor, if there is no foreground job running

2.2.7 Patient Monitor (Background Only)

When data is not actually being acquired in the foreground, you can use the patient-monitoring program in the background to verify that the patient positioning is correct. In the case of gated studies, the program can determine that the system is receiving a proper gate signal and can compute the gate interval. No data are stored by the computer.

CHAPTER 3

GAMMA-11 STARTING PROCEDURES

3.1 LOADING GAMMA-11 FOR THE SINGLE-JOB USERS

The operating procedures for loading and starting RT-11 and GAMMA-11 for the PDP-11/34 are outlined below. (Loading instructions for a PDP-11/40 are given in Appendixes A and B.) The disk-loading instructions given here (3 through 6) are for RK05 disks only. To load RK06 disks, see Appendix C.

CAUTION

> Whenever changing system disks, you MUST start the system again. If you do not start the system again, disk destruction results.

1. Turn the computer console power switch clockwise to the DC/ON position.
2. Turn the LINE/OFF/LOCAL switch on the terminal to be used to LINE. (Set to REMOTE if an LA30.) Also press the ON/OFF switch on the VT05 or VT52 to ON.
3. Pull the RK05 disk drive (unit 0) door down and place the removable disk cartridge in the disk drive with the metal ring on the bottom of the cartridge facing down.
4. Close the RK05 disk drive door.
5. Set the LOAD/RUN switch on the disk drive controller to RUN.
6. Make sure that the disk controller WRITE PROTECT light is off. If the light is not off, press the WRITE PROTECT switch once. This places the system in the WRITE ENABLE position.
7. When the disk READY light comes on, press and release the CNTRL button and the HALT button at the same time.
8. Then press and release the CNTRL button and the BOOT button at the same time.
9. Four numbers are printed on the terminal, followed by a $ on the next line.
10. For RK05 disks, type DK followed by a carriage return. For RK06 disks, type DM followed by a carriage return.

11. The system responds with the version number of RT-11. The system then types

    ```
    .SET TTY QUIET
    PLEASE ENTER
    TODAY'S DATE:
    ```

    and waits for you to enter the current date in the form

    ```
    dd-mmm-yy
    ```

    followed by the RETURN key, where dd-mmm-yy is the day, month, and year to be entered. dd is a decimal number in the range 1-31; mmm is the first three characters of the name of the month; and yy is a decimal number in the range 73-99.

    Example:

    To enter May 25, 1977 as the current date for the system, type:

    ```
    25-MAY-77   RET
    ```

    If the date is entered in an incorrect format, the message is repeated.

12. The system then responds with the prompt

    ```
    CURRENT TIME:
    ```

    and waits for you to respond in the form

    ```
         hh:mm:ss
    or
         hh:mm
    or
         hh
    ```

    followed by the RETURN key, where hh:mm:ss represents the hour, minute, and second.

    The time is in hours, minutes, and seconds past midnight.

    Example:

    ```
    14:48:32   RET
    ```

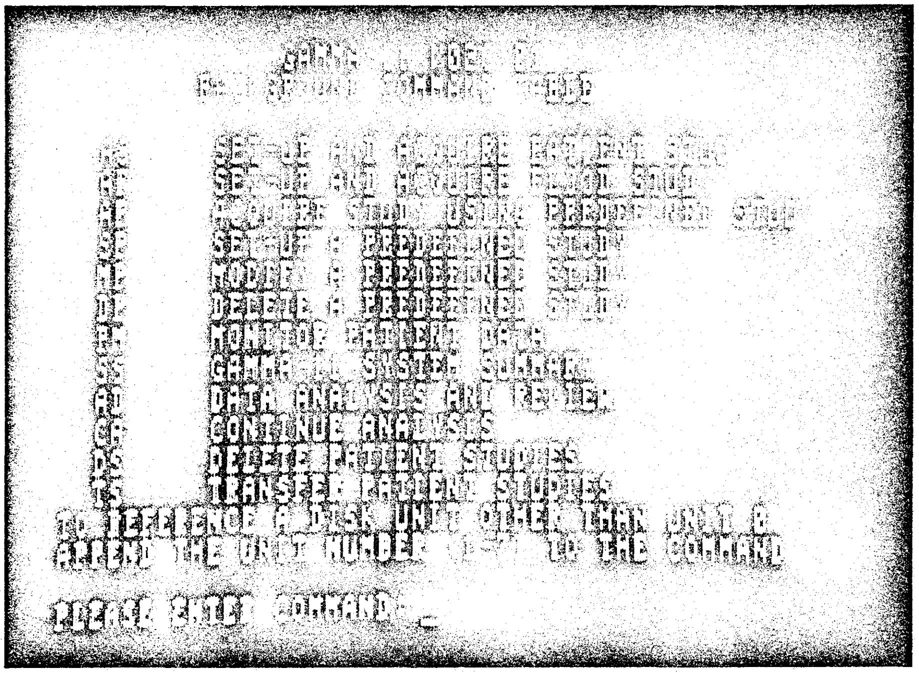
    This sets the internal clock to 14 hours, 48 minutes, and 32 seconds.

13. The system responds with the background command table on the color display (or VT01). (See Section 3.1.1.)

14. The background is now loaded and running.

3.1.1 Loading Commands

Once the GAMMA-11 software has been loaded into the system, you have the option to choose one of the GAMMA-11 programs. Figure 3-1 shows a VSV01 displaying the GAMMA-11 programs.



```
GAMMA-11 [illegible]
BACKGROUND COMMAND TABLE

[illegible]     SET-UP AND ACQUIRE [illegible] STUDY
[illegible]     SET-UP AND ACQUIRE [illegible] STUDY
[illegible]     ACQUIRE STUDY USING PREDEFINED STUDY
[illegible]     SET-UP A PREDEFINED STUDY
[illegible]     MODIFY A PREDEFINED STUDY
[illegible]     DELETE A PREDEFINED STUDY
[illegible]     MONITOR PATIENT DATA
[illegible]     GAMMA-11 SYSTEM SUMMARY
[illegible]     DATA ANALYSIS AND REVIEW
[illegible]     CONTINUE ANALYSIS
[illegible]     DELETE PATIENT STUDIES
[illegible]     TRANSFER PATIENT STUDIES
TO REFERENCE A DISK UNIT OTHER THAN UNIT 0
APPEND THE UNIT NUMBER [illegible] TO THE COMMAND

PLEASE ENTER COMMAND: _
```

Figure 3-1
Background Command Table

Make your selection by entering the two characters representing the function you wish to perform, followed by a carriage return.

3.2 LOADING GAMMA-11 FOR THE FOREGROUND/BACKGROUND USERS

The operating procedures for loading and starting RT-11 and GAMMA-11 for the PDP-11/34 are outlined below. The disk-loading procedure (steps 3 through 6) is for an RK05 disk. To load RK06 disks, see Appendix C.

CAUTION

> Whenever changing system disks, you MUST start the system again. If you do not start the system again, disk destruction results.

1. Turn the computer console power switch clockwise to the DC/ON position.
2. Turn the LINE/OFF/LOCAL switch on the terminal to LINE. (Set to REMOTE if an LA30.) Also, press the ON/OFF switch on the VT05 or VT52 to ON.

3. Pull the RK05 disk drive (unit 0) door down and place the removable disk cartridge in the disk drive with the metal ring on the bottom of the cartridge facing down.

4. Close the RK05 disk drive door.

5. Set the LOAD/RUN switch on the disk drive controller to RUN.

6. Make sure that the disk controller WRITE PROTECT light is off. If the light is not off, press the WRITE PROTECT switch once. This places the system in the WRITE ENABLE position.

7. When the disk READY light comes on, press and release the CNTRL button and the HALT button at the same time.

8. Then press and release the CNTRL button and the BOOT button at the same time.

9. Four numbers are printed on the terminal, followed by a $.

10. For RK05 disks, type DK followed by a carriage return. For RK06 disks, type DM followed by a carriage return.

11. The system responds with the version number of RT-11 and a dot on the console terminal. The system then types

    ```
    .SET TTY QUIET
    PLEASE ENTER
    TODAY'S DATE:
    ```

    and waits for you to enter the current date in the form

    ```
    dd-mmm-yy
    ```

    followed by the RETURN key, where dd-mmm-yy is the day, month, and year to be entered. dd is a decimal number in the range 1-31; mmm is the first three characters of the name of the month, and yy is a decimal number of the range 73-99.

    Example:

    If you wish to enter May 25, 1977 as the current date for the system, type:

    ```
    25-MAY-77   RET
    ```

    If the date is entered in an incorrect format, the message is repeated.

12. The system then responds with the prompt

    ```
    CURRENT TIME:
    ```

    and waits for you to respond in the form

    ```
        hh:mm:ss
    or
        hh:mm
    or
        hh
    ```

    followed by the RETURN key, where hh:mm:ss represents the hour, minute, and second.

The time is in hours, minutes, and seconds past midnight.

Example:

```
16:48:32 RET
```

This sets the internal clock to 16 hours, 48 minutes, and 32 seconds.

13. There is a slight pause, and the foreground command table is now present on the VT52. (See Section 3.2.1) The following message is printed on the console:

```
FGAMMA LOADED AND RUNNING
```

14. The system now responds with the background command table on the color display (or VT01). (See Section 3.1.1.)
15. Both the background and foreground GAMMA-11 programs are now loaded and running.

3.2.1 Foreground Commands

The foreground commands are identical to those for the background, except that AD (data analysis and review), CA (continue analysis), DS (delete patient studies), TS (transfer studies), and PM (patient monitor) are not used. With these exceptions, the foreground commands are displayed on the foreground terminal and are referenced through the foreground terminal. Figure 3-2 is an example of the foreground command table.

NOTE

If the VT52 has not been turned on, push the ON/OFF switch on the right side of the terminal forward. When the blinking cursor appears, press the RETURN key.

If the VT05 has not been turned on, turn on the power switch. After the terminal has warmed up, set the LOC/REM switch to REM and press RETURN. The foreground commands will then be displayed.

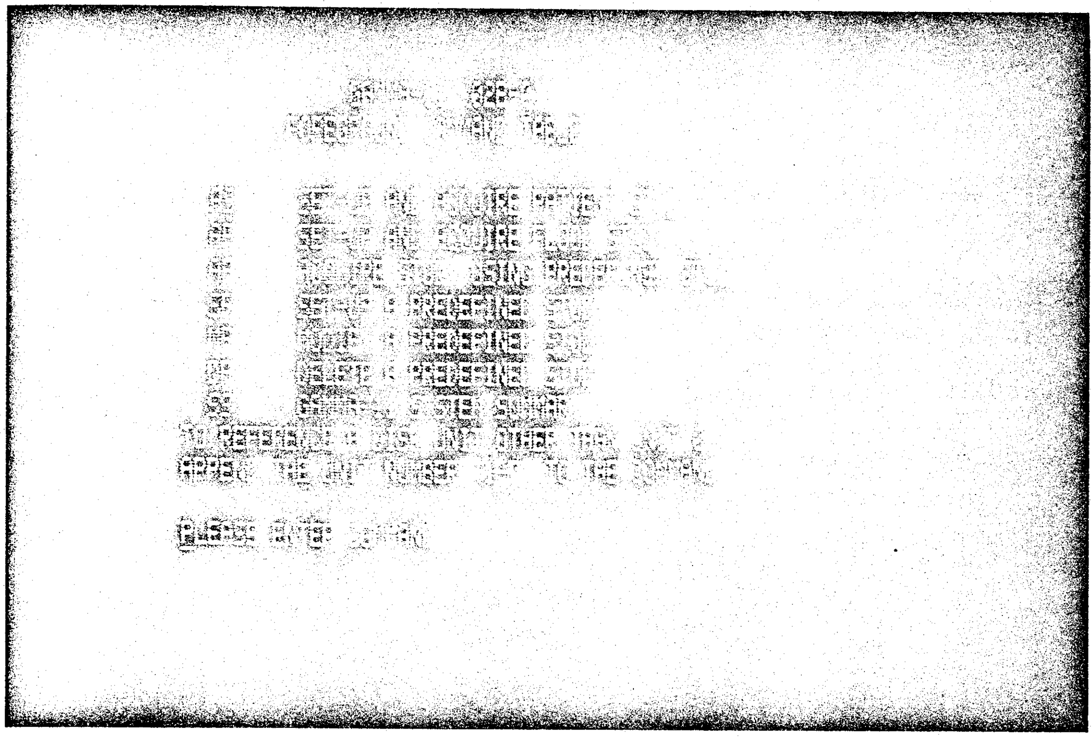


Figure 3-2
Foreground Command Table

To select a function, type the two characters of the corresponding command, followed by a carriage return.

3.3 KEYBOARD PROCEDURES AND SPECIAL CHARACTERS

Certain keyboard characters have special meaning to the system. The RT-11 operating system's keyboard characters may be different from those of other systems.

3.3.1 RT-11 Operating System Characters

Some of the keyboard characters provide communication with the RT-11 monitor. These characters are discussed in the following paragraphs.

1. Pressing the RETURN key indicates that you have completed typing a line of input and are now telling the computer to take control. Pressing RETURN also causes the console terminal to return to the left margin and space to the next line. The symbol (RET) is used in this manual to indicate pressing the RETURN key.

2. Pressing DELETE (RUBOUT) causes the preceding character (the very last one typed in) to be ignored by the computer. When you type the DELETE key, the system terminal echoes a backslash (\) plus the preceding character. The DELETE key can be used repeatedly to delete an additional character to

the left each time it is pressed. An enclosing backslash is printed when a key other than DELETE is typed. The DELETE key has no effect after all characters up to the last RETURN have been deleted.

For example, the patient name, GANEK, was mistyped as GAKNE. It can be corrected by typing three DELETEs and then NEK, as follows:

```
GAKNE\ENK\NEK
```

3. CTRL/C is typed by holding down the CTRL key while typing the C key. This echoes as ^C on the terminal. If a program is waiting for terminal input or is using the device handler TT: for input, a single CTRL/C interrupts execution and returns control to the monitor command level. Otherwise, type two CTRL/Cs in order to interrupt execution. Note that under the F/B Monitor, the job that is currently receiving input is the job that is stopped (determined by whether the last keyboard command was a CTRL/F or CTRL/B). To ensure that the command is directed to the proper job, type CTRL/F or CTRL/B first and then CTRL/C.

4. CTRL/B (for foreground/background systems only) echoes:

   ```
   B>
   ```

   on the LA36 terminal and causes all input to be directed to the background job and at least one line of output to be taken from the background job. All typed input is directed to the background job until control is redirected to the foreground job (via CTRL/F). CTRL/B has no special meaning when used under a single-job monitor.

5. CTRL/F (used for foreground/background systems only) echoes:

   ```
   F>
   ```

   on the terminal. It directs all input to the foreground job and takes all output from the foreground job. If no foreground job exists, F? is printed and control is directed to the background job. Otherwise, control remains with the foreground job until redirected to the background job (via CTRL/B) or until the foreground job terminates. CTRL/F has no special meaning when used under a single-job monitor.

6. CTRL/O echoes ^O on the terminal and causes suppression of teleprinter output while continuing program execution. Teleprinter output is re-enabled when one of the following occurs:

   a. A second CTRL/O is typed.

   b. A return to the monitor is indicated via CTRL/C.

   c. The running program issues a reset CTRL/O directive. (Some programs will reset CTRL/O if the output is extremely important. If you are interested in more details, see the Introduction to RT-11.)

7. CTRL/U deletes the current input line and echoes as ^U followed by a RETURN at the terminal. (The current line is defined to be all characters back to, but not including, the most recent line feed, CTRL/C or CTRL/Z.)

8. CTRL/S does not echo. It temporarily suspends output to the terminal until a CTRL/Q is typed. This feature allows users with high-speed terminals to fill the display screen, stop output with CTRL/S, read the screen, and then continue with CTRL/Q.

9. CTRL/Q does not echo. It causes the terminal to resume printing characters from the point at which printing previously stopped (via CTRL/S).

NOTE

> If a CTRL/S is inadvertently typed, it may appear that the system has crashed or is hung since nothing is echoed on the terminal. Type CTRL/Q once more before rebooting the system to make sure that a CTRL/S has not been typed.

The next two special characters operate for only those users who have a GT40 included in their hardware configuration.

10. CTRL/A is valid when the monitor GT ON command has been typed and the display is in use. It does not echo on the terminal. Used after CTRL/S has been typed, CTRL/A permits console output to resume until the screen is completely filled (all text previously displayed is eliminated). CTRL/A has no special meaning if GT ON is not in effect. For example, if the screen is filled with patient data, new console output is displayed, the screen is erased, and the new output is displayed.

11. CTRL/E is valid only when the monitor GT ON command has been typed and the display is in use. CTRL/E does not echo on the terminal, but causes all I/O to appear simultaneously on both the display screen and the console terminal. CTRL/E has no special meaning if GT ON is not in effect.

3.3.2 GAMMA-11 Characters

Some GAMMA-11 characters have special uses under data acquisition. These are as follows:

1. The ESCAPE (ALTMODE) key edits and verifies pages. This editing option is explicitly offered at the completion of each displayed page of the study plan, but it may be used at any time. The screen is erased, and the first question on that page, with its answer, is displayed. If a satisfactory answer is accepted, press RETURN; the next question and answer appears. To change an answer, type DELETE and proceed as described above. After the new answer has been typed, all

remaining completed questions and answers, up to the point at which you typed ESCAPE, are redisplayed. You may then finish the page, or, if errors remain, type ESCAPE again. For each use of ESCAPE, only one answer can be corrected.

2. CTRL/E is used for erasing and editing. If a number of corrections have cluttered the display, typing CTRL/E removes the debris. The screen is erased, the corrections are incorporated, and the edited page is redisplayed. If CTRL/E is typed in the middle of a response, the incomplete entry is deleted from the edited display; used in this manner, CTRL/E has the effect of a DELETE.

3.3.3 Exiting from GAMMA-11 to RT-11

To exit from GAMMA-11 background or a single-user application to the RT-11 monitor, you must type a CTRL/C on the terminal. This procedure returns control to the RT-11 monitor, which prints a dot (.), indicating that the system is waiting for an RT-11 command.

To exit from GAMMA-11 foreground, you must type CTRL/F on the console terminal. RT-11 responds with

```
F>
```

You must then type two CTRL/Cs on the terminal. To exit from the background program and return to the RT-11 monitor, type another CTRL/C, which outputs a dot (.). At this point, you must type

```
UNLOAD FG RET
```

to free the memory space used by the foreground program.

When the system is initially started up, GAMMA-11 foreground and background are automatically invoked. To run just the background, you should unload the foreground. (Otherwise the foreground will continue to take space in memory.) To run RT-11, you must exit from both the foreground and the background.

3.3.4 Reentering GAMMA-11 from RT-11

After GAMMA-11 has been exited, it can be reentered.

3.3.4.1 Reentering a Single Job or a Background Job - To reenter a single-job system, in response to the RT-11 dot type:

```
R BGAMMA RET
```

The system responds with the background command table on the color display (or VT01).

3.3.4.2 Reentering a F/B System - To reenter GAMMA-11 or a F/B system, in response to the RT-11 dot type:

```
FRUN FGAMMA RET
```

There is a slight pause, and the foreground command table is now present on the foreground terminal. The following message is printed on the console:

```
FGAMMA LOADED AND RUNNING
```

FGAMMA no longer references the DECwriter.

The system then responds with

```
B>.
```

on the DECwriter. Type

```
R BGAMMA RET
```

on the terminal to call in the background for GAMMA-11. The system responds with the background command table on the color display (or VT01).

3.4 CONTROL CHARACTERS WITHIN GAMMA-11

Two control characters aid you in interrupting, aborting, or terminating any procedure in GAMMA-11. These are:

1. CTRL/Z, which immediately displays either the background or foreground command table, depending upon the system being run.
2. CTRL/X, which immediately returns to the previous command level. For example, if you are displaying regions of interest and type CTRL/X on the terminal, control returns to review and analysis (AD). If another CTRL/X is typed at this time, the command table is displayed.

If CTRL/Z or CTRL/X is typed while the system is performing a particular operation, GAMMA-11 does not honor it until completion of the operation.

PART 2

GAMMA-11 DATA ACQUISITION

CHAPTER 4 GAMMA-11 DATA ACQUISITION

CHAPTER 4

GAMMA-11 DATA ACQUISITION

To use the GAMMA-11 system to acquire data from a gamma camera, you must perform a series of steps. The three main steps in the data acquisition process are:

1. Preparing the study plan
2. Editing and verifying the study summary
3. Initiating the collection run

You control the entire procedure from the keyboard in response to questions, instructions, or choices that appear on the display screen.

SS

4.1 GAMMA-11 SYSTEM SUMMARY

Before you begin setting up a study for acquiring data, you may want to look at a system summary. The system summary indicates the amount of disk space available for acquiring and storing patient data.

To display a GAMMA-11 system summary, type the SS command from the background or foreground command table. The form of the command is:

```
SS n(RET)
```

where n is an optional disk unit number and 0 is the default.

When you type SS, the information in Figure 4-1 appears on the display.

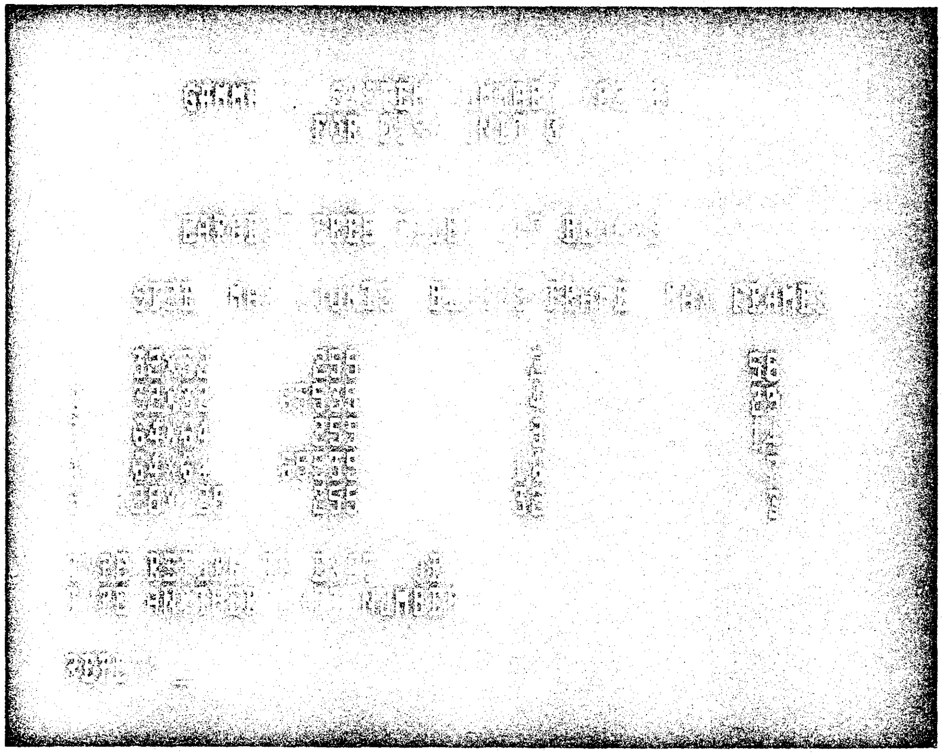


Figure 4-1
System Summary

The system summary presents several different matrix configurations for the collection of data. Your choice of matrix depends on several variables, among them the count rate and image resolution, the amount of available disk storage space, and the kinds of analysis you perform. Five standard configurations are available, differing in matrix dimension and in the maximum number of counts per cell, as shown in the following table:

CONFIGURATION	DIMENSION	MATRIX TYPE	MAXIMUM CELL COUNT
1	32x32	Byte	255
2	32x32	Word	65535
3	64x64	Byte	255
4	64x64	Word	65535
5	128x128	Byte	255

In Figure 4-1 the line that reads "LARGEST FREE FILE = xxxx BLOCKS" informs you of the largest disk file available for data acquisition. The column "BLOCKS/FRAME" informs you of the number of blocks required per frame (image) for a particular matrix size. The column "MAX FRAMES" establishes how many frames of that matrix size you can acquire on the available disk space.

For example, the RK05 disk is capable of holding approximately one million words of patient data. The system summary describes this space in terms of frames for the five standard configurations as follows (also see Section 4.9):

	MATRIX SIZE	MATRIX TYPE	BLOCKS/FRAME	MAX FRAMES OF DATA
1	32x32	Byte	2	2000
2	32x32	Word	4	1000
3	64x64	Byte	8	500
4	64x64	Word	16	250
5	128x128	Byte	32	125

If you type RETURN in response to the SS reply, the program returns to the command table. However, if you type another unit number, the system summary changes in accordance with the available disk space on that disk.

4.1.1 Matrix Sizes and Types

The preceding tables show matrix sizes and matrix types. The size indicates the number of cells in an image. Each cell represents one small area of the image and holds the number of counts received for that portion of the image.

The type of the matrix establishes the maximum number of counts each cell can hold. If the type is byte, each cell can hold a maximum of 255 counts. If the type is word, each cell can hold a maximum of 65,535 counts.

4.1.2 Insufficient Disk Space

If there is not enough disk space for the study that you want to acquire, you can squeeze the data already on the disk or delete previous patient studies and then squeeze the disk. Chapter 10 describes these operations in detail.

AS

4.2 SET-UP AND ACQUIRE PATIENT STUDY

The data acquisition command, AS (acquire study), sets up and acquires patient studies. This process, known as a study plan, consists of three display-pages of data as follows:

1. Page 1 requests administrative information about a patient. GAMMA-11 uses this information to create the patient study index entry by which you can later access the study.

2. Page 2 requests gamma camera parameters and study-type specifications. Camera parameters refer to switch settings and other operational data about the gamma camera.

3. Page 3 requests information about collection parameters. Collection parameters specify the duration of the collection run and the structure of the data.

To prepare a study plan, type the following command, where n is an optional disk unit number.

AS n(RET)

The first question of page 1 now appears on the display.

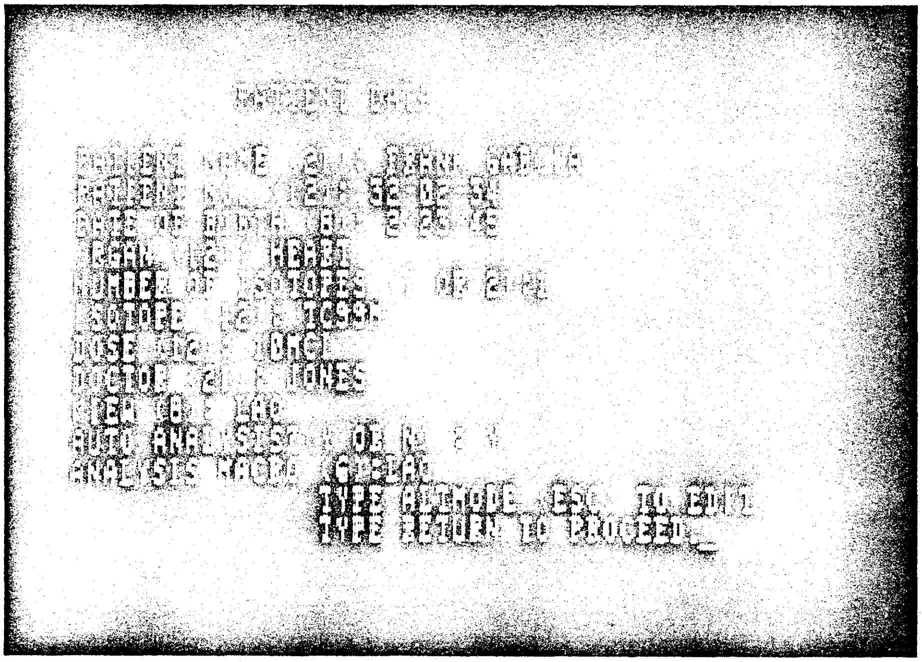
4.2.1 Study Plan Page 1: Patient Data

A complete example of Page 1 is shown in Figure 4-2. All answers except that for NUMBER OF ISOTOPES are free-field. A free-field answer can contain any printing keyboard character or characters, up to the maximum number indicated by the question. For example, the study plan question that follows expects a free-field answer of not more than 21 characters.

PATIENT NAME (21):

If an answer is too long, GAMMA-11 automatically deletes it and displays a number sign (#) and a colon (:), and waits for a new response.

Answers to PATIENT NAME and PATIENT NUMBER are required; all other responses are optional. Type RETURN to skip these optional responses. After you make each entry, you must type a RETURN to proceed to the next question.



```
TYPE ALTMODE (ESC) TO EDIT
TYPE RETURN TO PROCEED_
```

Figure 4-2
Study Plan Page 1: Patient Data

The following are the page 1 entries:

Entry	Comment
PATIENT NAME (21)	
PATIENT NO. (12)	
DATE OF BIRTH (8)	
ORGAN (12)	
NUMBER OF ISOTOPES (1 OR 2)	is a multiple choice answer requiring an entry by typing 1, 2, or RETURN. If you type in a RETURN, only one isotope is assumed.
ISOTOPE 1 (12)	
DOSE 1 (12)	
ISOTOPE 2 (12)	(only if the number of isotopes is 2)
DOSE 2 (12)	(only if the number of isotopes is 2)
DOCTOR (12)	
VIEW (8)	identifies the position of the camera relative to the body or organ. This answer is also optional.

The last two entries pertain to an automatic analysis of a macro. The first of these entries is:

AUTO ANALYSIS (Y OR N)

If you type Y, the data acquisition program automatically calls the data analysis program after it has acquired all the data. The data analysis program automatically selects and displays the first frame of the study that has just been acquired. If you specify an analysis macro name in the next question, the analysis program automatically loads and executes this macro. See Sections 5.24 through 5.24.9. If you specify auto analysis from FGAMMA (the foreground data acquisition program), the background program must meet the following conditions:

1. The GAMMA-11 program BGAMMA must be running in the background
2. The background command table must be displayed on the screen at that time

If either of the conditions is not met, auto analysis does not take place. If you specify auto analysis from the background data acquisition program, the background data acquisition program always calls the data analysis program. The last entry is:

ANALYSIS MACRO (6)

You must specify the data analysis macro file name if you want to use a macro for auto analysis. A discussion of macros and macro commands appears in Sections 5.24 through 5.24.14.

The replies to all of these page 1 entries are optional except for PATIENT NAME and NUMBER.

NOTE

Only PATIENT NAME, PATIENT NUMBER, ORGAN, DATE of acquisition, and type of STUDY (L,D, or S) become part of the study name in the patient index.

When the page is complete, the acquisition program prompts you to type ESCape, in order to verify and edit all of the answers, or to type RETURN to go on to the next page.

4.2.2 Study Plan Page 2: Camera Parameters

The first question on Page 2 of the study plan automatically appears on the display when you enter a RETURN as a reply from Page 1. The first question depends on whether your system has an NC11A or NCV11 gamma-camera interface. If your system has an NCV11 interface, the following question appears before the rest of the camera parameters.

```
CAMERA NO. (0,1,2,3):
```

Here you must enter the number of the camera that will be acquiring the data.

If your system has an NC11A interface, the questions for the camera parameters are represented in Figure 4-3. These questions are the same as for the NCV11, but the NCV11 has the additional first question described previously.

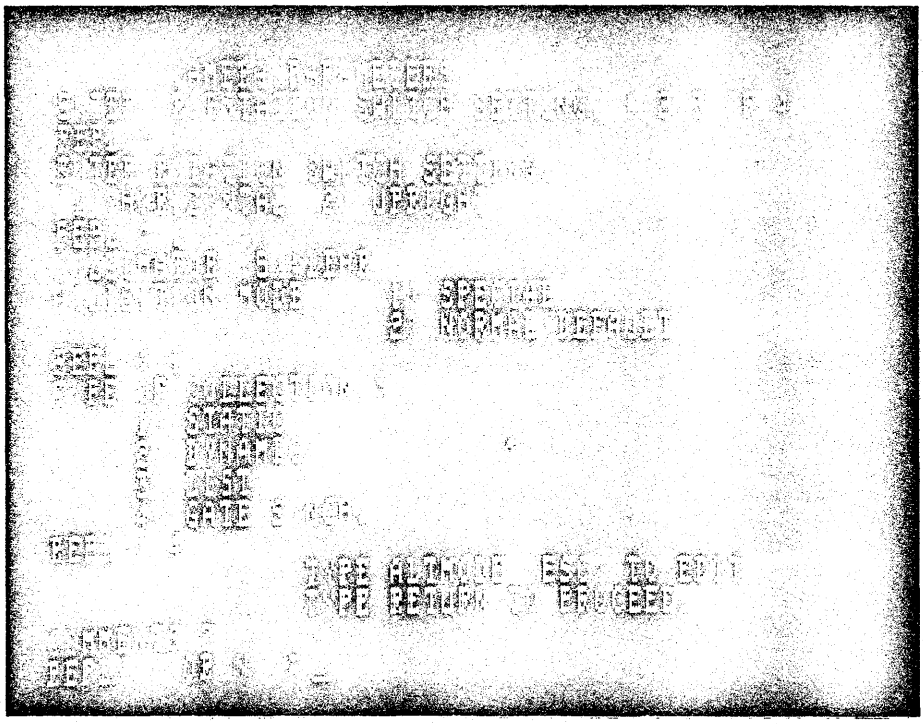


Figure 4-3
Study Plan Page 2: Camera Parameters

Notice that the first and second questions asked (repeated below) are related.

```
ENTER ORIENTATION SWITCH SETTING:  1,2,3 OR 4

ENTER ROTATION SWITCH SETTING
 1) HORIZONTAL  2) UPRIGHT
```

In both cases, the answers are required. The questions refer to switches on the gamma cameras manufactured by Searle Radiographics, Inc. (formerly Nuclear-Chicago), which together control the orientation of the camera's viewing axes.

On the Searle cameras, the 4-position Orientation switch and the 2-position Rotation switch combine to produce eight possible coordinate relationships according to Table 4-1. In this table, X and Y represent the camera's field coordinates, and X' and Y' represent the coordinates of the matrix displayed on the screen. Tables 4-2 through 4-4 show other camera settings.

Table 4-1
Orientation-Rotation Switch Position Logic Table

ORIENTATION SWITCH POSITION	ROTATION SWITCH POSITION	
	1 (HORIZONTAL)	2 (UPRIGHT)
1	X' = -Y Y' = X	X' = X Y' = -Y
2	X' = -Y Y' = -X	X' = X Y' = Y
3	X' = Y Y' = -X	X' = -X Y' = Y
4	X' = Y Y' = X	X' = -X Y' = -Y

Table 4-2
Picker Switch Settings

ORIENTATION SWITCH	ROTATION SWITCH	PICKER EQUIVALENT
1	1	270
3	1	90
2	2	0
4	2	180

Table 4-3
Ohio-Nuclear Settings

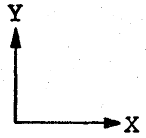
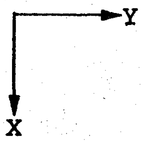
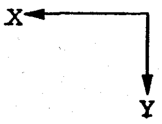
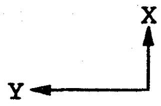
Orientation Switch	Rotation Switch	X-invert (1=On, 0=Off)	Y-invert (1=On, 0=Off)	X-y Exchange
1	1	0	1	1
2	1	1	1	1
3	1	1	0	1
4	1	0	0	1
1	2	0	1	0
2	2	0	0	0
3	2	1	0	0
4	2	1	1	0

Table 4-4
Toshiba Settings

Orientation Switch	Rotation Switch	Toshiba Equivalent
3	2	G
4	1	ᘓ
1	2	Ә
2	1	ᘎ
2	2	⅁
1	1	ᘏ
4	2	ɘ
1	1	ᘐ

If you have a camera type other than Searle, the corresponding functions of the other camera types can be matched to the settings of the two switches used by Searle. For example, given a camera that can rotate the image only clockwise (e.g., Picker), the corresponding switch settings would be as follows:

Table 4-5
Other Camera Settings

Camera X	Searle Switch Settings	
	Rotation Switch	Orientation Switch
	2 UPRIGHT	2
	1 HORIZONTAL	3
	2 UPRIGHT	4
	1 HORIZONTAL	1

After you have entered each answer followed by a RETURN, you have the option to enter the type of collimator used on the gamma camera as follows:

COLLIMATOR (5)

The answer, which is not required, is free-field. If you are ready for the next question to appear, type only RETURN.

ACQUISITION MODE 1) SPECIAL
2) NORMAL (DEFAULT)

GAMMA-11 DATA ACQUISITION

The acquisition mode refers to the two program-selectable modes of the GAMMA-11 A/D converters. These two modes of the A/D converters give you a choice of two different image sizes. Acquisition mode 1 and acquisition mode 2 are described in the following:

1. Acquisition mode 1 provides a close-up image -- that is, gives an enlarged view of a portion of the camera field. This enlarged view is called ZOOM mode (see Figure 4-4A).
2. Acquisition mode 2 provides a normal image -- that is, it covers the entire field of view (see Figure 4-4B).

If you skip the question by typing only RETURN, GAMMA-11 assumes the default (normal image size).

(Actually, you may set the acquisition modes to whatever you want by adjusting the GAIN 1 and GAIN 2 controls on the A/D converters. Refer to the NC11-A Camera Interface for a GAMMA-11 System or the NCV11 Gamma Camera Interface Technical Manual.)

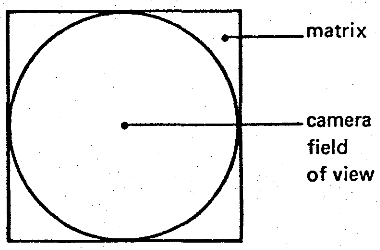


Figure 4-4A
ZOOM Mode

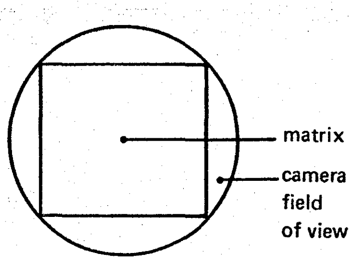


Figure 4-4B
Normal Mode

The next question the program asks is:

```
TYPE OF COLLECTION:
     1) STATIC
     2) DYNAMIC
     3) LIST
     4) GATE SYNCH.
```

This answer is required, because it determines the questions to be asked on the third page of the study plan.

When you enter the camera parameters and study type, edit them if necessary, and verify them. The program then asks for comments.

This is the first of three opportunities during an acquisition run to enter into the file any commentary about the study. Comments might include notes on patient history or conditions that might affect the interpretation of the data. If you answer Y (for YES) to the question, the program erases the screen and prepares for the text to be entered. You can type up to ten lines, each 49 characters. Use any printing character. Correct errors by using the methods described in Section 3.3.2. Terminate the text by typing a "null" line, that is, two RETURNs in a row.

NOTE

If you answer NO to the request for comments at this time, you can add comments during the review phase, but not immediately following collection.

4.2.3 Study Plan Page 3: Collection Parameters

The study plan on page 3 displays different formats for collection parameters, depending on the answer to the page 2 question TYPE OF COLLECTION. These formats are described in Sections 4.2.4 and 4.2.5.

4.2.4 Static Collection Parameters

A complete example of the static collection parameters is shown in Figure 4-5.

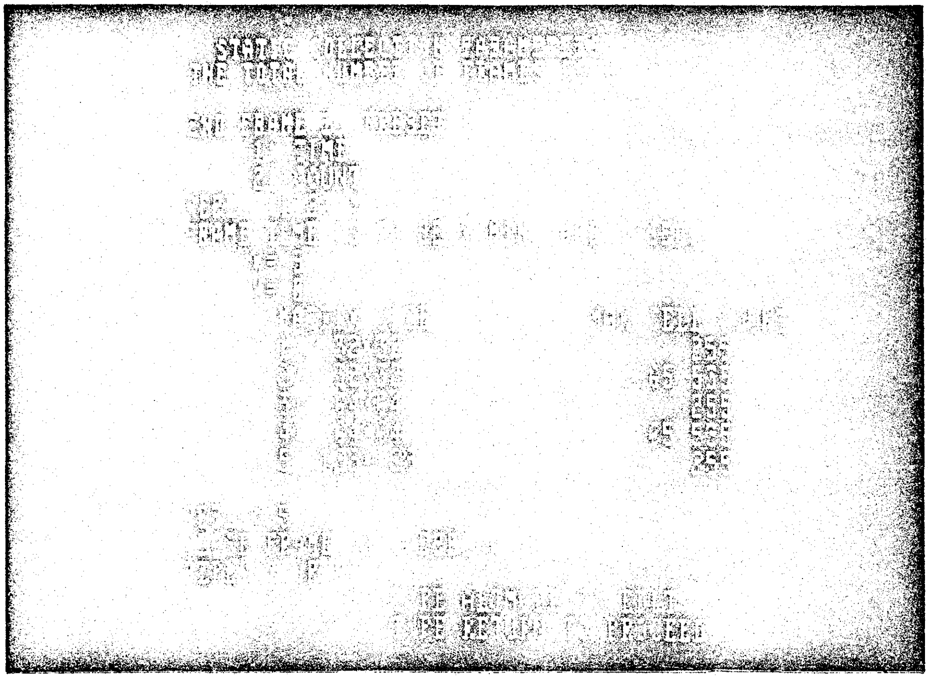


Figure 4-5
Study Plan Page 3: Static Collection Parameters

The first question the program asks is:

THE TOTAL NUMBER OF FRAMES IS

A maximum of eight frames is allowed in one study. If you enter a 1, the static study becomes a single frame study. If you enter a number in the range 2 to 8, the static study becomes a multiple frame study (i.e., more than one view is acquired). If you just press RETURN, the default is 1 (single static study).

In some cases, there may not be enough space on the disk for the number of frames you choose. If not, after you have entered all the collection parameters, the program alerts you to proceed or to edit the page and enter a new number. If you proceed, the program collects only as many frames as the disk can hold.

The next question asked is:

END FRAME BY PRESET:
    1) TIME
    2) COUNT

This question establishes the period of time or the number of counts for collection. If you choose "TIME," the following question appears:

FRAME TIME IS TO BE X MIN. AND Y SEC.
    X=
    Y=

You must enter a value for X and Y, each followed by a RETURN. The maximum for X and Y is 999. If you choose option 2, "COUNT", the following question appears:

PRESET COUNT IS

You can establish a preset count value to stop data collection. The maximum preset count that you can enter in the system is 999,999,999. (Note: do not enter the commas in response to this question; their presence here is for clarity.)

After you have entered a RETURN, the program displays a table of possible matrix configurations. Parameter or space limitations may restrict the number of choices. For example, matrix (5) is not available for dual-isotope studies (see Section 4.1).

The final question asked on page 3 is:

CLOSE FRAME ON OVERFLOW?
REPLY (Y OR N):

If you reply with a YES, the program stops collection of data as soon as any cell attempts to exceed its count capacity. Close on overflow occurs only if overflow occurs before the preset time or count limit is reached. For example, if you enter an X value of 5 and a Y value of 0 and choose matrix 5 as the size, the maximum cell count of 255 might be reached before five minutes of collection pass. In this case, the system stops collecting data.

However, if you reply with a NO, the program allows cell overflow to occur during the run. When the count capacity for an element is exceeded, the element remains at maximum count and collection continues.

This question does not need a reply. If you enter RETURN, the system automatically defaults to NO.

The usefulness of closing a frame on overflow is shown in a liver study, where the actual concentration and distribution of isotopes over the single frame are of interest. Closing the frame when a cell overflows preserves the relative count concentration. The cell-overflow limit would not be used, on the other hand, in a brain study, where the isotope concentrates most in areas that are not significant, such as the temporal muscles and salivary glands. Saturation in these areas can be ignored.

4.2.5 Static Study Summary

After you enter all of the collection parameters, the system displays a summary of the entire static study plan (except for comments), as illustrated in Figure 4-6. You can make changes to any of the entries by typing the appropriate reply from the list of choices offered at the bottom of the display. A reply of 2, 3, 4, or 5 is equivalent to typing an ESCape for the page indicated. Entries for the page appear one by one for examination. After you edit the summary, the system displays it once again for verification. To obtain a print-out of the summary, type 1. Printout is possible only in the background version.

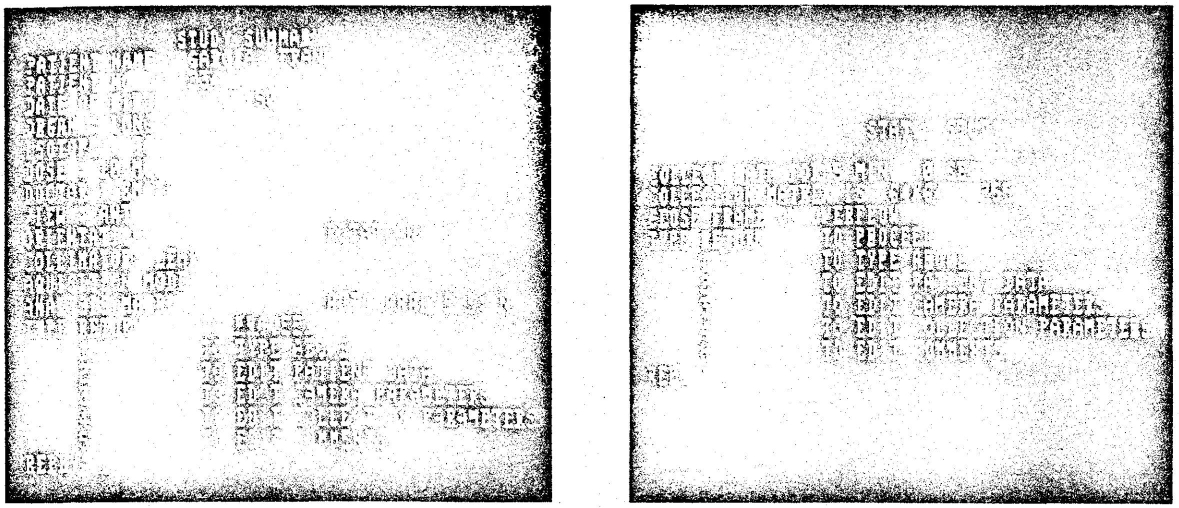


Figure 4-6
Static Study Summary: Parts 1 and 2

The example in Figure 4-6 shows a multiple-frame study. The message, FRAME 1 OF 4, establishes that this summary applies to the first frame of the study. This program conducts data collection as a separate run for each frame. You can change the static study plan between frames (see Section 4.2.7).

NOTE

> When performing a multiple-frame static study, GAMMA-11 assumes that succeeding frames are the same matrix size as frame 1. If you increase the matrix size of a frame after collecting frame 1, a DISK FULL message may appear on the terminal. The message does not indicate that the disk is actually full, but that GAMMA-11 has not allocated enough disk space for the increased matrix size.

4.2.6 Precollection Frame

When you verify the static study summary and type a RETURN, the precollection frame appears on the screen (Figure 4-7). This is a programmed pause to allow final adjustments, wait for the patient, or reconsider the entire procedure. If for any reason you do not proceed with the collection, you must type CTRL/X or CTRL/Z, and the program deletes the entire study file. Otherwise, you should proceed as directed.

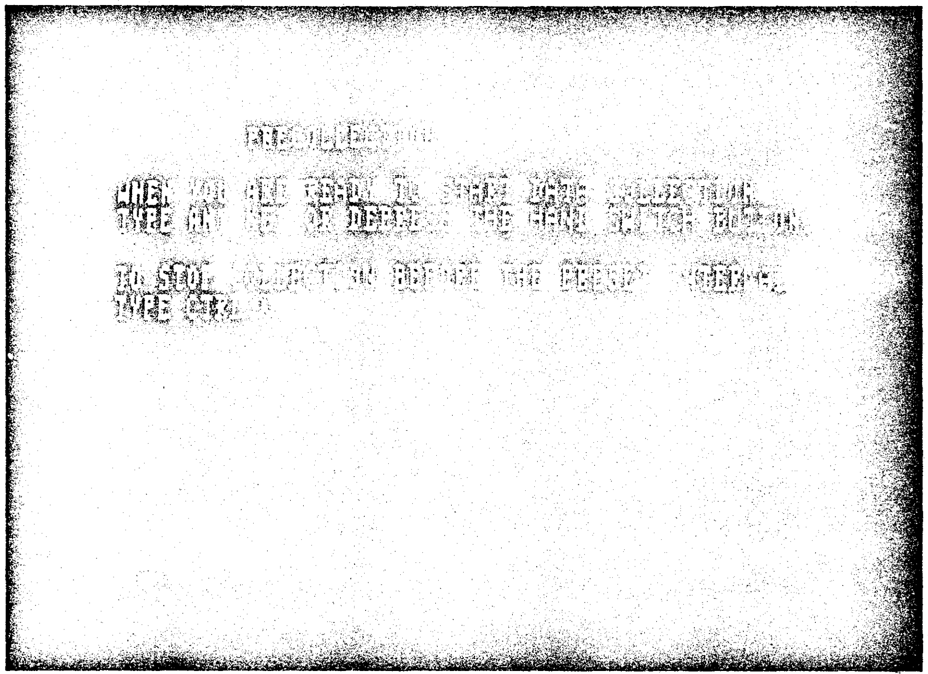


Figure 4-7
Precollection Frame

4.2.7 Data Collection

Once the collection of data has begun, a moving dot repeatedly draws a line at the bottom of the screen to indicate the passage of time. At the end of the run, GAMMA-11 closes the frame, transfers it to the disk, and sounds a beep or bell. Subsequent events depend on the specifications of the study plan as follows:

1. If the study is a single frame static study with no comments, the study file closes and control returns to the command table (background or foreground).
2. If you have included comments, GAMMA-11 gives you an opportunity to edit or add to the text. Next, the file closes and control returns to the command table. The only exception to this procedure occurs during auto analysis. The program displays the first image acquired instead of the command table.

3. If the study is a multiple-frame static study, the following request appears on the screen:

   VIEW (8)

   VIEW is the study plan entry that is most likely to require change between frames. Skipping the answer with a RETURN leaves a blank entry. If the VIEW is unchanged, you must re-enter it. When you type the answer, the program displays the entire study summary, with the new VIEW and the list of editing options. Thus, any or all of the study plan entries can be changed between frames. Note, however, that even if you change any of the items used in the index entry (patient name, patient number, organ), the original index entry name remains in effect.

For each frame, you have the option of repeating the procedures in Sections 4.2.5 through 4.2.7. After the last frame, GAMMA-11 closes the entire file and returns control to the command table.

4.2.7.1 Special Comments on Dual-Isotope Studies - If the study scans two isotopes, each collection run consists of two frames, one for each isotope. Once again, the largest matrix you can use for static dual-isotope studies is 64 x 64 x word. The dual-isotope study may be useful for collection of gated studies.

4.2.7.2 Restarting a Static Frame on Acquisition - Occasionally during a static study, the patient may move, or the image may be degraded for some other reason. You can restart a static frame by typing CTRL/R. When you type CTRL/R, the program stops acquisition; clears the data in core; and resets the time, the counts, and the precollection information. If you restart a static frame, the following message appears on the display.

RESTART

The restart option is available for both foreground and background acquisition.

The restart option works only while the program is actually acquiring data. If the frame has already ended, it cannot be restarted.

4.2.8 Dynamic Collection Parameters

In a dynamic study, each group of frames requires a separate page of collection parameters. You must specify all groups before collection begins. Each group of frames can have different frame rates, numbers of frames, and matrix configurations. A complete example of the dynamic collection parameters is shown in Figure 4-8. For example, you might change the frame rate in a renal flow study. A frame rate of one frame per second for 60 seconds is appropriate for the uptake and one frame per 30 seconds for 10 minutes for the washout.

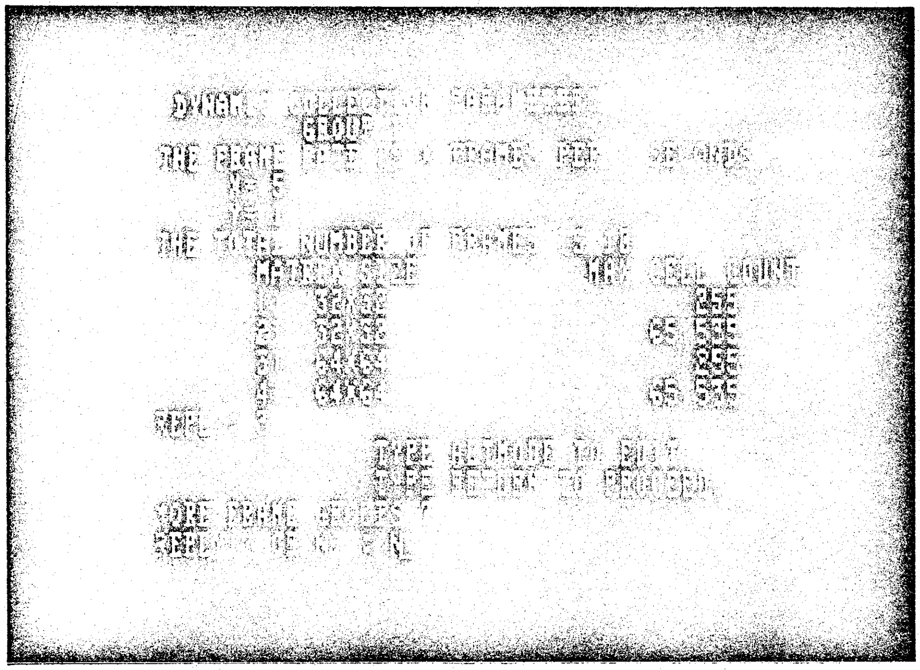


Figure 4-8
Study Plan Page 3: Dynamic Collection Parameters

Page 3 for dynamic collection parameters appears if you requested DYNAMIC under TYPE OF COLLECTION on page 2.

The first question the program asks is:

THE FRAME RATE IS X FRAMES PER Y SECONDS
X=
Y=

GAMMA-11 holds each frame open for Y/X seconds (frame rate). The maximum frame rate depends on the matrix configuration.

The next question the program asks is:

THE TOTAL NUMBER OF FRAMES IS

The number of frames in a group also depends on the matrix configuration. The following question lists the configurations identified by the number in the study summary.

MATRIX SIZE and CELL COUNT

The collection parameters for a dynamic study are subject to the following limitations:

1. Use no more than 13 groups in one study.
2. Use no more than 512 frames in the entire study.
3. Do not use the 128 x 128 matrix.
4. The number of frames per group and the maximum frame rate depend on the matrix configuration, as shown in the following table. For every group of a study except the last, the number of frames must be a multiple of the frame multiplier for that matrix. The last group is not subject to this restriction.

MATRIX	SIZE	MAXIMUM CELL COUNT	MAXIMUM FRAME RATE (frames/sec)		MULTIPLIER
			RK05	RK06	
1	32x32	255	50	80	8
2	32x32	65535	25	40	4
3	64x64	255	12	20	2
4	64x64	65535	6	10	1

After you have verified the collection parameters, another question appears on the display.

MORE FRAME GROUPS?

If you reply with a Y, the program requests a new set of collection parameters. If you respond with an N or RETURN, the program displays the study summary (see next section).

4.2.9 Dynamic Study Summary

After you enter all of the collection parameters, GAMMA-11 displays a summary of the entire dynamic study plan (except for comments), as shown in Figure 4-9. Note that each group of the dynamic study has the collection parameters listed in the summary. You can make changes to any of the entries by typing the appropriate reply from the list of choices offered at the bottom of the display. A reply of 2, 3, 4, or 5 is equivalent to typing an ESCape for the page indicated. After you edit it, the entire summary is displayed once again for verification. To obtain a printout of the summary, type 1 (background only).

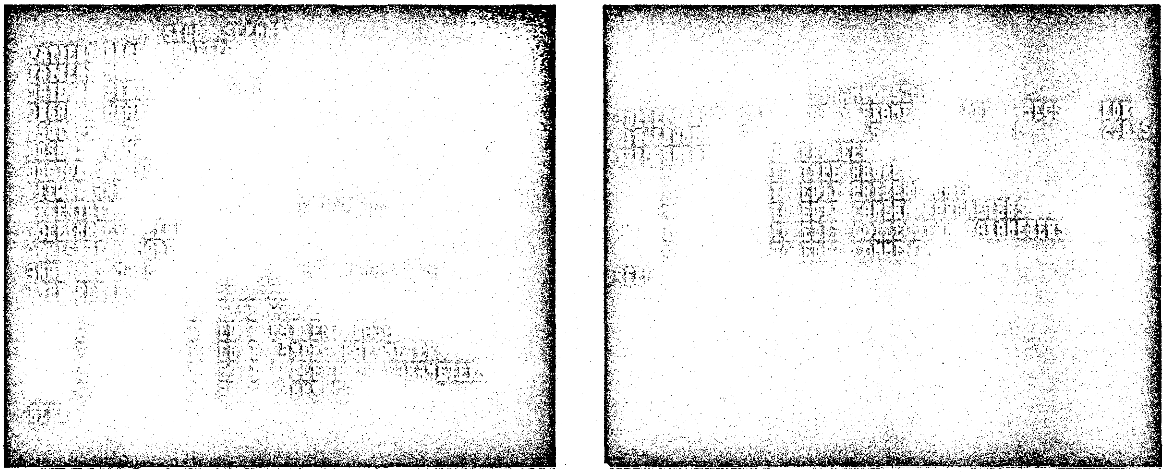


Figure 4-9
Dynamic Study Summary: Parts 1 and 2

4.2.10 Precollection Frame

When you verify the dynamic study summary, type a RETURN to bring the precollection frame to the screen (see Figure 4-7). This is a programmed pause to allow final adjustments, to wait for the patient, or to reconsider the entire procedure. If for any reason you do not proceed with the collection, you must type CTRL/X or CTRL/Z. The program deletes the entire study file. Otherwise, proceed as directed.

4.2.11 Data Collection

Once data collection begins, the collection proceeds through every group of the study. As the program starts each group, it sounds a beep and displays GROUP n (where n is the group number). When all of the groups finish, the program closes the file. Comments, if included, can be edited at this time. Control returns to the command table (except during auto analysis, when the program displays the first image acquired).

Special Comments on Dual-Isotope Studies - In a dual-isotope study, the collection parameter specifying the number of frames per group actually represents twice that number. Each frame is really two, one for each isotope. GAMMA-11 collects the frames simultaneously and stores them alternately in the study file. That is, the program stores frame 1 of isotope 1, frame 1 of isotope 2, frame 2 of isotope 1, etc. in that order. The use of dual isotopes changes some of the limitations on the collection parameters as follows:

1. Use no more than 256 frames per isotope in the study.
2. The maximum frame rates and the frame multipliers are half those given in the table in Section 4.2.8.
3. Do not use the 64 x 64 word-matrix (type 4) for dual-isotope dynamic studies.

4.2.12 Dynamic Collection Rates

Table 4-6 shows the frame rates of data collection for foreground/background (column 2) and single job (column 3) systems.

Table 4-6
Maximum Frame Rates

Matrix Size	Data Acquisition Without Suspending Background (frames/sec)		Data Acquisition In Foreground Only (or Single Job) (frames/sec)	
	RK05	RK06	RK05	RK06
32 x 32 x byte	12	24	50	80
32 x 32 x word	6	12	25	40
64 x 64 x byte	3	6	12	20
64 x 64 x word	1.5	3	6	10

If you use the foreground to collect data at a rate faster than the rates indicated in the second column of Table 4-6, the system suspends the background.

The system establishes the speed of the dynamic study through the questions you answer on page 3 of the study plan. If the system calculates those answers as a fast dynamic study (faster than the rates in Table 4-6 for data acquisition in foreground), it suspends the background when the precollection frame appears on the display. The system does not warn the background job, but it does warn the foreground job at study summary time.

NOTE

> If a background program appears to halt, make sure that the foreground is not running before rebooting the system.

When data collection completes or when the frame rate drops below the rates listed in Table 4-6, the background resumes operation where it was suspended.

If the system establishes that the speed of the dynamic study is slower than the values in Table 4-6, background execution proceeds normally.

4.3 LIST STUDY

In the list study collection mode, GAMMA-11 does not structure the data in matrices. Instead, it stores each pair of X- and Y-coordinates as an item of raw data, with a timing mark every 10 milliseconds. Consequently, the only limit on collection is the amount of disk storage space available.

In a gated list study, the program inserts the time marks every millisecond instead of every ten milliseconds. The gate signal is inserted as a gate-mark bit. (See Section 5.27 for more detail.)

4.3.1 List Collection Parameters

The page of list mode collection parameters appears only if you request LIST under TYPE OF COLLECTION on page 2. A complete page of collection parameters for a list study is illustrated in Figure 4-10.

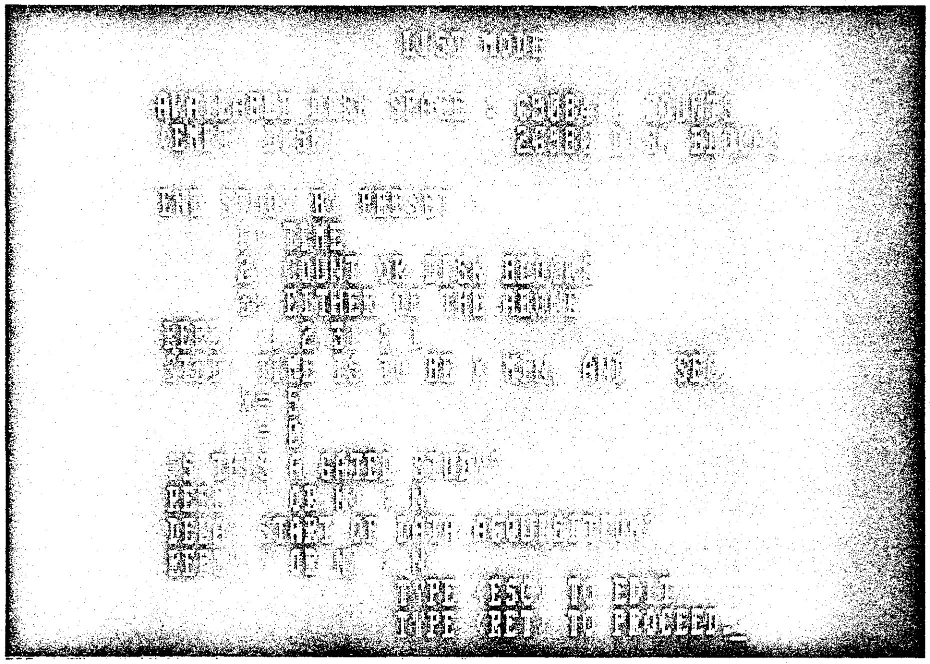


Figure 4-10
List Study Collection Parameters

The first line of the list study collection parameters is:

AVAILABLE DISK SPACE

This line represents the total number of counts and the number of disk blocks available to store these counts. You can choose the most suitable terminating limit. Each disk block has a capacity of 256 counts.

The following line allows you to choose the collection parameter that terminates collection.

```
     END STUDY BY PRESET:
          1)  TIME
          2)  COUNT OR DISK BLOCKS
          3)  EITHER OF THE ABOVE
```

If you choose option 3, you must specify both time and counts or disk blocks. The collection stops at whichever limit it reaches first.

If you choose TIME, the system displays the following question:

```
     STUDY TIME IS TO BE X MIN.  AND Y SEC.
          X=
          Y=
```

Collection stops after the specified time has elapsed.

If you choose COUNT OR DISK BLOCKS, the system displays:

```
     DO YOU WISH TO SPECIFY
          1)  COUNTS
          2)  DISK BLOCKS
```

You must choose one or the other. Also, the total number (counts or blocks) cannot exceed the limits at the top of the displayed page (Figure 4-10).

The next line requires a YES or NO answer.

```
     IS THIS A GATED STUDY? (Y OR N)
```

If you respond YES, the program looks for a gate input from the AR11. (See Section 5.27 for reframing.) The default answer is NO.

The next line also requires a YES or NO answer.

```
     DELAY START OF DATA ACQUISITION?
```

If you choose YES, the program delays the start of the collection run until it reaches a count rate you specify. The program measures the time and/or count limit parameters from the delayed starting point. The delay option is another aid in conserving storage space. You can wait until the count rate rises to a meaningful level above the background before storing the data. On the other hand, if you respond NO, no delay takes place.

The following line appears only if a delayed start has been specified.

```
     ENTER STARTING COUNT RATE AS X COUNTS/SEC
```

Collection begins as soon as the count rate reaches the given number of counts per second. After you enter a carriage return to proceed, the program displays the list study summary on the screen (Figure 4-11).

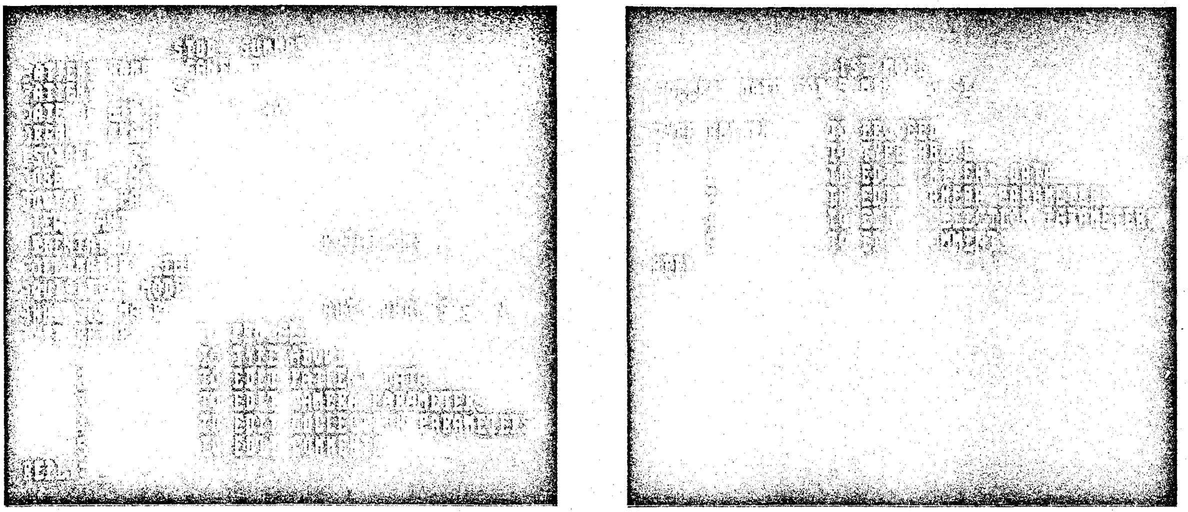


Figure 4-11
List Study Summary: Parts 1 and 2

4.3.2 Data Collection

To begin list data collection, you should follow the precollection procedure described in Section 4.2.6. At the end of the collection run, the program displays one of the following termination messages, indicating how the run was ended.

```
STUDY TERMINATED    BY PRESET TIME
  "        "        BY OPERATOR (CTRL/X)
  "        "        BY PRESET COUNT OR BLOCKS
  "        "        :DISK ERROR
  "        "        :DISK FULL
TYPE RETURN TO RETURN TO COMMAND TABLE
```

The maximum collectable data count rate is about 30,000 counts per second for the RK05 disk and 70,000 counts per second for the RK06 disk. If the rate exceeds this limit, collection continues, but data are lost. If you specify a delayed start, GAMMA-11 draws a line across the bottom of the screen until the actual collection begins. When actual collection begins, the line jumps up half an inch.

NOTE

You cannot use dual isotopes in a list study.

4.3.3 List Mode Collection Using F/B

When you use foreground programs to collect list data, GAMMA-11 always suspends background program execution.

You can perform gated-list-mode studies in either the foreground or the background. If you do them in the background, GAMMA-11 invokes the patient monitor program (see Sections 4.8.3 and 4.9) before acquisition begins. If you perform the study in the foreground, GAMMA-11 does not invoke the patient monitor program; you must run the patient monitor program (PM) in the background before acquiring the data in the foreground.

AF

4.4 FLOOD STUDY ACQUISITION

A flood study is a single-frame static study; GAMMA-11 predefines almost the entire study plan for a flood study. The only collection parameter information that is not predefined is the time and number of counts. The flood study command (AF) invokes flood study acquisition.

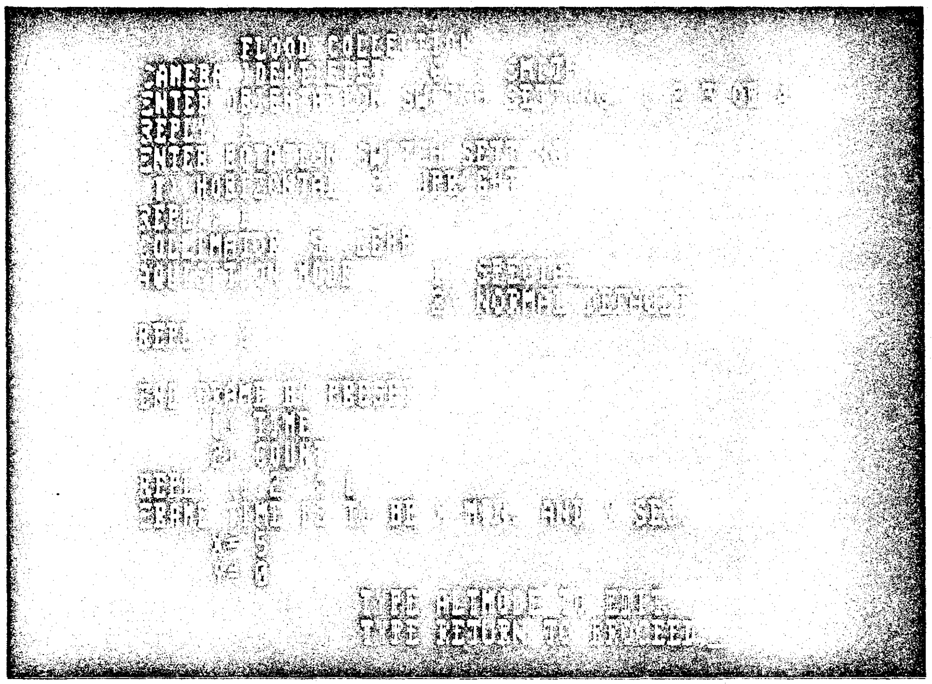
In a flood study, you must present the camera with a uniform radiation source. Variations from uniformity in the resulting matrix reflect irregularities in the camera's response.

The study plan of a flood study is shorter than previously described study plans. You need no patient data because GAMMA-11 automatically defines most of the collection parameters.

To prepare a flood study, type the following, where n is an optional disk unit number.

```
AF n (RET)
```

The information in Figure 4-12 then appears on the display.



```
FLOOD COLLECTION
TYPE ALTMODE TO EDIT
TYPE RETURN TO PROCEED
```

Figure 4-12
Flood Collection

The system asks you for only one item of administrative data, instead of the usual patient data.

CAMERA IDENTIFIER (6)

Your response is a free-field answer that corresponds to the patient name.

NOTE

> The flood study incorporates all three pages of the study plan described under the static study into one page.

The next sequence of questions GAMMA-11 asks for a flood study are:

ENTER ORIENTATION SWITCH SETTING 1, 2, 3, OR 4
ENTER ROTATION SWITCH SETTING
COLLIMATOR
ACQUISITION MODE
END FRAME BY PRESET (time or counts)

Of the collection parameters, you must supply only the duration of the run, either in elapsed time or in total counts. GAMMA-11 automatically defines all other collection parameters as follows:

Number of frames: 1
Matrix size: 64 x 64
Matrix type: word
Close frame on overflow? Yes

At this time, you can verify these parameters or proceed (by typing RETURN) and add comments.

Precollection and collection procedures are described in Sections 4.2.6 and 4.2.7. At the conclusion of the run, the system tags the study internally to identify it as a flood study for review and analysis. The file is closed, and control returns to the command table.

4.5 PREDEFINED STUDY ACQUISITION

The predefined study acquisition commands perform the following functions:

1. Set up a predefined study
2. Acquire a patient study
3. Modify a predefined study
4. Delete a predefined study

You can save much time in setting up routine or often-used study plans by creating a predefined study plan. Define collection parameters and other common data in advance, and you need add only the specific run-time information when you use the study plan to acquire data.

For example, in a routine renal-flow study, the organ (kidney), nuclide (Tc99m), dose (10MCI), view and camera parameters, and collection parameters, can all be defined in advance. At collection time, you need add only the patient (and doctor, if necessary) identification and comments.

SP

4.5.1 Set up a Predefined Study

The procedure for setting up a predefined study is similar to that for setting up a general study plan. The question and answer format and error-correcting procedures are also the same. There are only a few differences, as follows:

1. Instead of the patient name, birthdate, and patient number, GAMMA-11 asks for a STUDY NAME. This name identifies the entry in the predefined study index. The maximum number of characters allowed in the study name is 30.
2. You cannot enter comments.

3. You must define the following items in the skeleton:

   Number of Isotopes
   Type of Study
   All Collection Parameters

Orientation switches and rotation switches are optional.

To set up a predefined study, type:

```
SP (RET)
```

A complete predefined study summary is shown in Figure 4-13. When you have edited and verified the study, the system stores it in the predefined study file on the disk. GAMMA-11 creates an entry in the predefined study index which you can then display (see Figure 4-14).

NOTE

> To make GAMMA-11 ask a question during acquisition, type RETURN at that question when predefining the study. For example, by typing RETURN for the doctor's name during the predefined study, you cause the DOCTOR question to appear at acquisition. To bypass a question during acquisition, type a space followed by RETURN when predefining the study.

Static, dynamic, or list studies can be predefined. A flood study is itself a sort of predefined study that cannot be set up in the manner described here.

AP

4.5.2 Acquiring Data with a Predefined Study

To acquire data with a predefined study, you must first select the correct predefined study. All of the predefined studies are listed in an index. To display the index of predefined studies, type:

```
AP n(RET)
```

where n is an optional disk unit number. GAMMA-11 then displays the current index of predefined studies (see Figure 4-14).

You can have a maximum of twenty predefined studies in the index.

To print the index on the terminal, type:

```
P (RET)
```

If you type only a RETURN, the system returns to the command table.

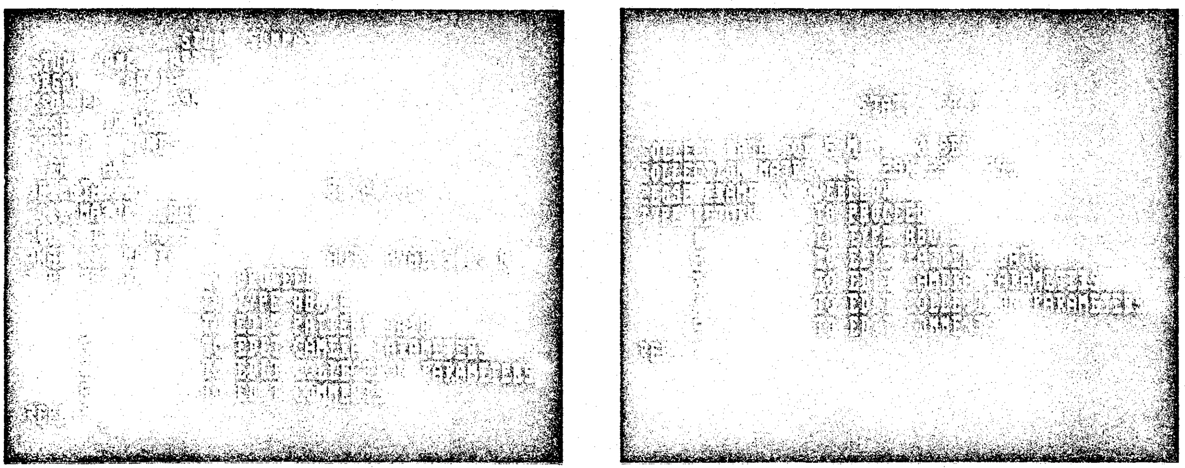


Figure 4-13
Predefined Study Summary: Parts 1 and 2

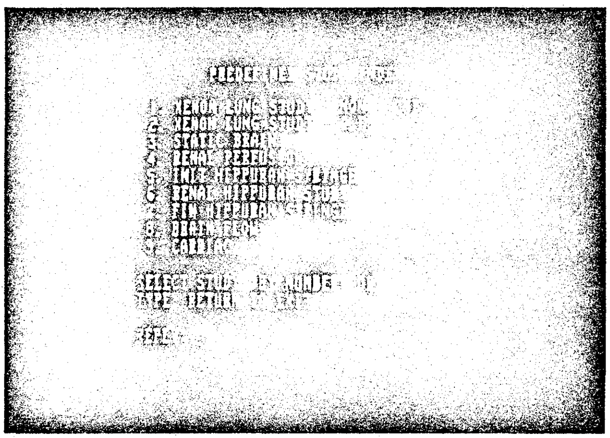


Figure 4-14
Predefined Study Index

To initiate one of the predefined studies, type the index entry number for that study followed by a RETURN. The system then asks you for the PATIENT NAME, DATE OF BIRTH, and PATIENT NUMBER. (Performing this function is like setting up pages 1, 2, and 3 of the previous studies.) The system then displays the rest of the patient data and camera parameters, stopping at each entry that is blank in the predefined study. At this point you can enter the information needed, or you can enter a RETURN to continue, leaving the question blank. You can add comments at this time. As soon as you finish entering comments or type a RETURN, the system displays the predefined study summary (Figure 4-13). The collection run proceeds as a normal study (see Section 4.2.7). At the end of the run, GAMMA-11 stores the completed study in the patient study file and updates the patient study index.

NOTE

> When you are setting up the predefined study, if you want to leave a field blank and do not want the program to stop to wait for user input, you should enter a space and a RETURN.

The predefined study is an invaluable tool when you can use it because it minimizes the chance of error, standardizes collection procedures, and ensures fast set-up time.

NOTE

> When performing a predefined study, you should not edit collection parameters to increase the number of frames or matrix size. The system allocates space on the disk only for initial collection parameters. If you increase the number or size, a DISK FULL message appears on the terminal.

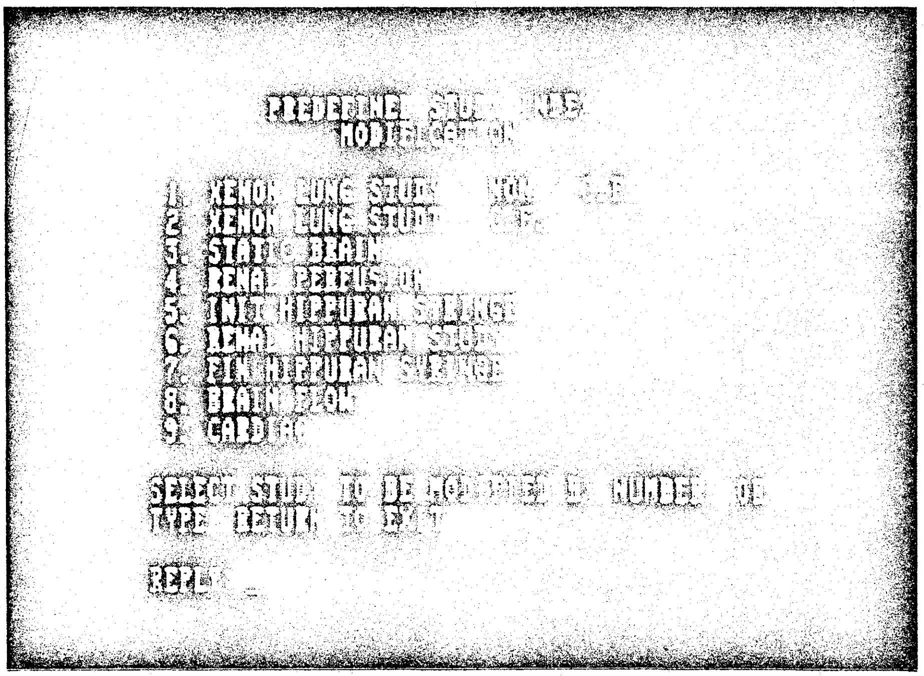
MP

4.5.3 Modify a Predefined Study

GAMMA-11 permits you to modify a selected study in the predefined study index. To modify the study, type:

```
MP (RET)
```

Figure 4-15 illustrates the information that appears on the display.



```
PREDEFINED STUDY INDEX
     MODIFICATION

1. XENON LUNG STUDY  NON C.F.
2. XENON LUNG STUDY  C.F.
3. STATIC BRAIN
4. RENAL PERFUSION
5. INIT HIPPURAN SEQUENCE
6. RENAL HIPPURAN STUDY
7. FIN HIPPURAN SEQUENCE
8. BRAIN FLOW
9. CARDIAC

SELECT STUDY TO BE MODIFIED BY NUMBER OR
TYPE RETURN TO EXIT

REPLY: _
```

Figure 4-15
Predefined Study Index Modification

To print the predefined study index on the terminal, when the index is displayed, type P followed by a RETURN. If you enter the index number, the system displays the predefined study summary giving you the usual editing options. When complete, the edited study replaces the original one in the file.

DP

4.5.4 Delete a Predefined Study

To delete a study in the patient study index, type:

```
DP (RET)
```

Figure 4-16 represents the display after you type this command.

```
PREDEFINED STUDY INDEX
DELETION

1. XENON LUNG STUDY [illegible]
2. XENON LUNG STUDY [illegible]
3. STATIC BRAIN
4. RENAL PERFUSION
5. INIT HIPPURAN STORAGE
6. RENAL HIPPURAN STUDY
7. FIN HIPPURAN STORAGE
8. BRAIN FLOW
9. CARDIAC

SELECT STUDY TO BE DELETED BY NUMBER OR
TYPE RETURN TO EXIT

REPLY _
```

Figure 4-16
Predefined Study Index Deletion

The predefined study index is displayed. At this point you can type either the number of the study to be deleted followed by a RETURN or P followed by a RETURN to print the index on the terminal. After you enter the appropriate index number, the system removes the study from the file and displays the updated index. You can delete only one index study at a time from the predefined study file.

4.6 COMMENTS ABOUT ABORTING DATA ACQUISITION

At any time during the preparation of a study plan, up to and including the precollection frame display, you can terminate the entire operation by typing CTRL/X or CTRL/Z. The system does not enter the study plan in the patient file, and control returns to the command table.

4.7 COMMENTS ABOUT MATRICES

GAMMA-11's choice of five different types of matrices gives you the flexibility to make efficient use of storage space. Careful selection of matrix size ensures that more patient data can be stored on the disk. The smaller the matrix you use, the more frames the system can hold (see Section 4.1).

A second benefit results from the use of smaller matrices -- the maximum frame rate increases. The maximum background-acquisition frame rate for each type of matrix is listed in the following table.

MATRIX SIZE	MAX CELL COUNT	FRAME RATE (frames/sec)	
		RK05	RK06
32 x 32 x byte	255	50	80
32 x 32 x word	65535	25	40
64 x 64 x byte	255	12	20
64 x 64 x word	65535	6	10

Dynamic collection does not limit you to a single matrix size. For fast studies a smaller matrix allows a faster frame rate.

For example, a renal study begins with a rapid frame rate and ends with a slow frame rate so that you can observe washout without wasting disk space. The collection parameters might be as follows:

1. Collect 60 frames of data in a 64 x 64 x byte matrix at 1 frame per second.
2. Collect 10 frames of data in a 64 x 64 x word matrix at 1 frame per minute.

4.8 IN-CORE GATE-SYNCHRONIZED STUDY

In a gate-synchronized study, GAMMA-11 monitors signals from an external gating device, such as an ECG gate, while acquiring the gamma camera data. The program synchronizes the camera data acquisition to the gate signal. Core-resident buffers store multiple frames. When the program receives a gate signal, it begins to store the acquired data into data buffer 1. After a short, preset time, the program stores the data in data buffer 2. Then after the same amount of time, acquisition is switched to buffer 3, and so forth. Thus, the program acquires data in each of the buffers for a short time until either it reaches the last buffer or it detects another gate signal.

Data acquisition stops temporarily if the program reaches the end of the buffers. When it detects another gate signal, acquisition begins again in image buffer 1. If the program detects a gate signal before reaching the end of the buffers, it switches acquisition to buffer 1.

This program adds the data for each gate cycle to the previously collected data. The in-core buffers contain data representing a composite cycle of the acquisition run.

The gate-synchronized study program is designed for cardiac acquisition but is not limited to it. For cardiac acquisition, the gate signal comes from an ECG gating device and represents the R wave.

You can acquire data in either 32 x 32 or 64 x 64 format. The in-core buffers are always byte mode while the disk-resident data is word mode. If cell-count overflow occurs, data acquisition stops, the program adds the in-core buffers (byte) to the disk data (word), zeroes core, and resumes data acquisition. The maximum number of frames that can be acquired depends on the matrix size, computer memory size, and disk type. You should use the single-job RT-11 monitor for a gate-synchronized study. The following table lists the maximum number of frames that can be in core during gate-synchronized acquisition.

Memory size	RK05 disk		RK06 disk
	28K	16K	48K
32x32 matrix	48	24	80
64x64 matrix	12	6	20

Maximum Number of Frames in Core

If your system has additional memory (than listed in the table), GAMMA-11 can hold more frames in core.

During data acquisition, the program supplies a live display of the data in a movie-like fashion. Thus, you can see the representative cycle while it is being acquired.

4.8.1 Gate-Synchronized Collection Parameters

When you do a gate-synchronized collection, you must set the specific gate-synchronized collection parameters at page 3 of the study plan. A complete example of the gate-synchronized collection parameters is shown in Figure 4-17. Page 3 for gate-synchronized collection parameters appears if you request choice 3, GATE SYNCH. under TYPE OF COLLECTION on page 2.

The program asks:

```
MATRIX TYPE 1) 32x32     nnn FRAMES
            2) 64x64     nnn FRAMES
```

Again, the matrix type is byte in core, but it is word on the disk.

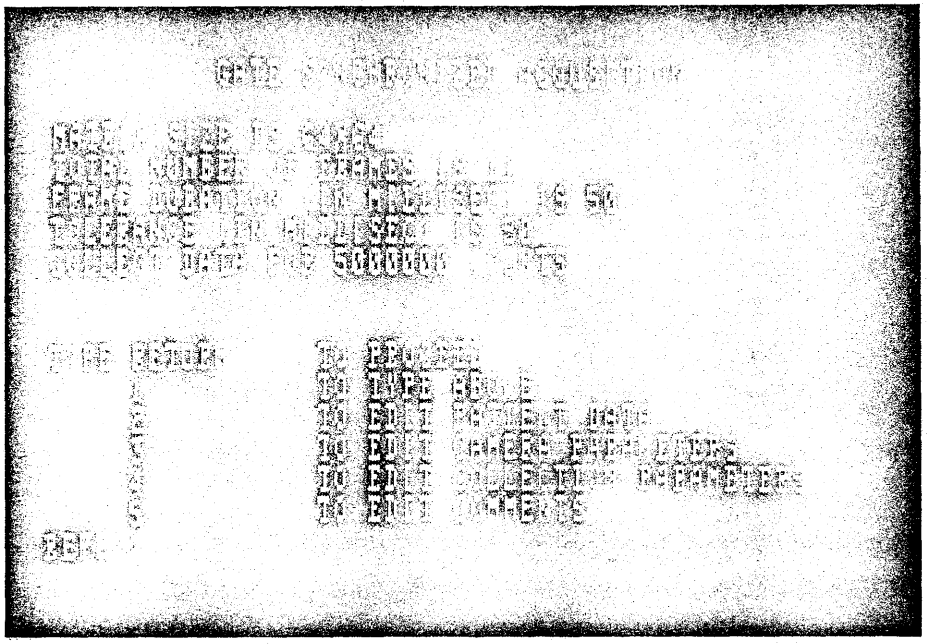


Figure 4-17
Gate-Synchronized Collection Parameters

The next question asked is:

```
     NUMBER OF FRAMES IS
```

You can specify the exact number of frames in the gated study by typing in the number. The maximum allowed is displayed with the first question. You can also default to the maximum by typing a RETURN.

The next question is:

```
     FRAME DURATION IS
```

Specify the duration of a single frame in milliseconds, or default this answer by typing a RETURN. If defaulted, the program calculates the duration from the average gate duration for the last 30 seconds prior to acquisition. If you do not default this answer, you can run the patient monitor program prior to acquisition to establish the R-R interval.

In the next question, you can specify the gate tolerance in milliseconds.

```
     GATE TOLERANCE IS
```

Gate tolerance establishes a window of acceptable heartbeats around the average heartbeat. For example, if the average heartbeat is 700 ms and the gate tolerance is 50 ms, the program accepts any heartbeat of duration 650 ms to 750 ms. Any heartbeat outside of this range is considered arrhythmic by the system. If you type a RETURN, the system performs no tolerance checking.

Next, the program asks:

```
     TERMINATE STUDY BY 1) PRESET TIME
                        2) PRESET COUNTS
                        3) PRESET CYCLES
```

You must decide how to terminate the study. If you choose 1 as the response, the following question appears:

```
     FRAME TIME IS TO BE X MIN.  AND Y SEC.
         X=
         Y=
```

You must enter values for X and Y, each followed by a RETURN. The maximum value for X and Y is 999.

If you choose 2 as the response, the following question appears:

```
     PRESET COUNT IS
```

Enter a count value at which data collection stops. The maximum preset count value is 999,999,999. (Note: do not enter the commas in response to this question; their presence here is for clarity.)

If you choose 3 as the response, the following question appears:

```
     NUMBER OF CYCLES IS
```

Enter the number of cycles in the study. The maximum number of cycles is 9999.

Next the program displays the study summary.

4.8.2 Gate-Synchronized Study Summary

After you have entered all the collection parameters, the program displays a summary of the entire gate-synchronized study plan (except for comments) as shown in Figure 4-18.

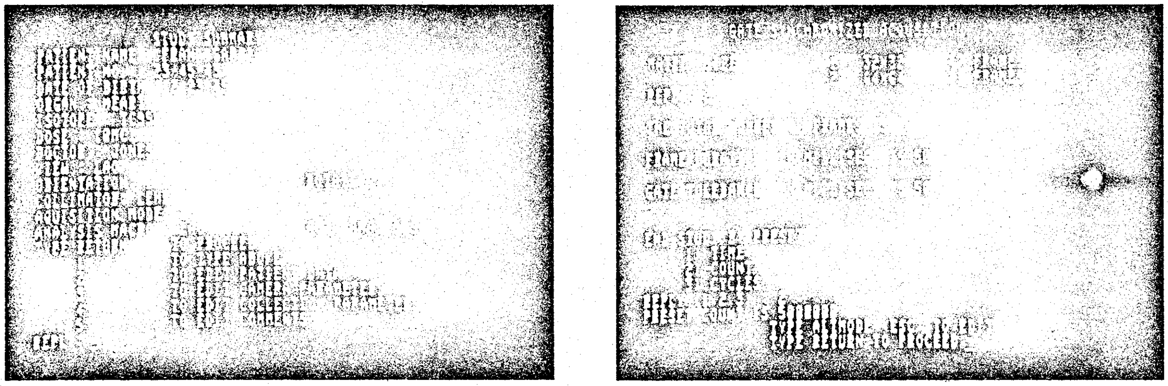


Figure 4-18
Gate-Synchronized Study Plan

4.8.3 Gate-Synchronized Study Precollection

The gated study has a special precollection monitor -- the patient monitor program (see Section 4.9). The patient monitor program displays the gamma-camera data and gate signal without storing the data. This allows you to position the patient and verify that the gate signal is being received. At this point, you can use the patient monitor program for patient positioning but not to help answer the acquisition questions. You would already have answered the questions. To aid in answering the questions, you must use the PM command prior to beginning acquisition.

Type a P to exit the patient monitor program and proceed to the precollection message shown in Figure 4-7. This is a programmed pause to allow final adjustments, wait for the patient, or reconsider the entire procedure. If for any reason you do not proceed with the collection, you must type CTRL/X or CTRL/Z. The program deletes the entire study file. Otherwise, to begin actual data acquisition, you should press the hand switch button or any key on the terminal.

4.8.4 Data Acquisition

During data acquisition, the system displays the core-resident data in a movie-like fashion. At the same time, it displays the following information:

```
TOTAL TIME           TOTAL CYCLES
TOTAL COUNTS         REJ. CYCLES (rejected cycles)
COUNT RATE           GATE INTERVAL
```

GAMMA-11 updates this information once per second. It specifies the time in seconds, the count rate in counts/second, and the gate interval in milliseconds. If ???? appears for the gate interval, the last gate interval exceeded 10 seconds. This situation usually indicates that GAMMA-11 is no longer receiving a gate signal.

The display has only a simple scaling algorithm for displaying the core-resident data. During gated acquisition, you can scale the data to a cell count maximum of 31, 63, 127, or 255. The initial scaling is 31 (2 counts/intensity level). The commands to change the scaling are 1, 2, 3, or 4 for maximum cell counts of 31, 63, 127, or 255 respectively.

CTRL/X and CTRL/Z terminate the study just as they do for other types of studies. If you type a CTRL/Z or CTRL/X any time before actual acquisition, control returns to the background command table.

If a cell overflows during acquisition, acquisition stops and the following message appears:

```
DISK UPDATE
```

The program adds the core-resident data to the disk data, zeroes core, and finally resumes acquisition. The message is erased when acquisition resumes.

NOTE

> In-core gated acquisition is available only in the background.

4.8.5 Hints on Using Gate-Synchronized Acquisition

You should use the single job RT-11 monitor during gate-synchronized acquisition to acquire the maximum number of frames. To call in the single job monitor, type CTRL/C. At the dot type the following for RK05 disks:

```
BOOT RKMNSJ RET
```

Or type the following for RK06 disks:

```
BOOT DMMNSJ RET
```

When acquisition is complete, type one of the following to return to the foreground/background monitor:

```
BOOT RKMNFB RET (for RK05 disks)

BOOT DMMNFB RET (for RK05 disks)
```

PM

4.9 PATIENT MONITORING

At times, you may need to verify that the patient positioning is correct, especially if you are going to use ZOOM mode for data acquisition. Also, with gate-synchronized acquisition, it is desirable to establish that the system is receiving the gate signals and what is the gating interval.

The patient monitor program allows you to do these processes quickly. It is a quick acquisition program that acquires data in a fixed, 64 x 64 x word format and displays the data in real time. It monitors the gate signal if there is one. The patient monitor program is also a quick test of the GAMMA-11 camera interface and real time clock.

The patient monitor program requires no setup. You need only type the following from the background command table:

```
PM RET
```

The program immediately begins to acquire data in 64 x 64 x word format and displays it on the color display. The program updates the display once every second. The program scales the data on the display in the normal manner but does not allow the display commands such as thresholding or interpolation.

Above the image, the program displays the following information:

```
TIME        nn SEC   GATE INTERVAL       nn MSEC
COUNTS      nn       FRAME DURATION (32) nn
COUNT RATE  nn       FRAME DURATION (64) nn
```

The time is elapsed time in seconds. The counts are total counts accumulated in the image. The count rate is the total counts divided by the elapsed time.

The gate interval and frame duration pertain to gate-synchronized acquisition studies which are explained in Section 4.8. The gate interval is the time between the two previous gate signals in milliseconds. If the program detects no gate signals in the last 10 seconds, it displays a "????" instead.

The frame duration is the duration of a single frame for an in-core gate-synchronized acquisition study. The system displays the frame duration for both 32 x 32 and 64 x 64 matrices. The program determines the frame duration by dividing the gate interval by the maximum number of frames that can fit in core. For a 64 x 64 matrix this is rounded up to the nearest 5 milliseconds. For example, if the gate interval is 800 ms and twelve 64 x 64 frames can fit in core, the frame duration is 70 ms (800/12=66.666, round up to 70 ms). For a 32 x 32 matrix, the frame duration is rounded up to the nearest 1 ms.

The commands for controlling the program are all immediate mode commands, except for timed restart. The commands are:

R	Zero core and restart.
Z	Change to zoom mode if in normal mode, or vice versa.
T	Timed restart, program will ask for the time in seconds. After each specified time interval, core is zeroed and data acquisition is restarted.
E	Exit timed mode.
B	Change to black and white mode if in color.
C	Change to color if in black and white.
CTRL/X	Exit to background command table.
CTRL/Z	Exit to background command table.

PART 3

GAMMA-11 DATA ANALYSIS

CHAPTER 5

GENERAL DATA ANALYSIS COMMANDS

The data analysis procedures work with the collected patient data. These procedures provide variations on displaying the data and mathematical operations and analytical tools for working with and analyzing the data. This chapter will describe the general data analysis commands that can be performed on both the VT01 storage scope and the VSV01 color display.

5.1 INITIATING AND CONTINUING DATA ANALYSIS

To initiate analysis of a patient study, use the Analyze Data command (AD) from the background command table. All of the other data analysis commands described in this chapter and Chapters 6, 7, and 8 are subsets of the data analysis program and can be invoked only after you have typed the AD command.

Occasionally, you may want to interrupt the analysis procedure, use BASIC (FORTRAN or FOCAL) for some calculations on the data, and then return to the analysis. In these instances the AD command is used to initiate the study, and the CA command (Continue Analysis) is used from the background command table to continue analysis after the interruption.

AD

5.1.1 Initiating Data Analysis

The analysis and review procedures run only as a single job under RT-11 S/J or in the background for RT-11 F/B. These procedures do not run in the foreground.

To select a study for analysis and review, type the Analyze Data (AD) command.

```
AD n(RET)
```

The disk unit number n is optional. If n is not present, the index of data on disk 0 will be displayed. If you type any number other than 0 for n, the data on that disk unit will be displayed.

The first page of the patient study index is shown on the display as shown in Figure 5-1.

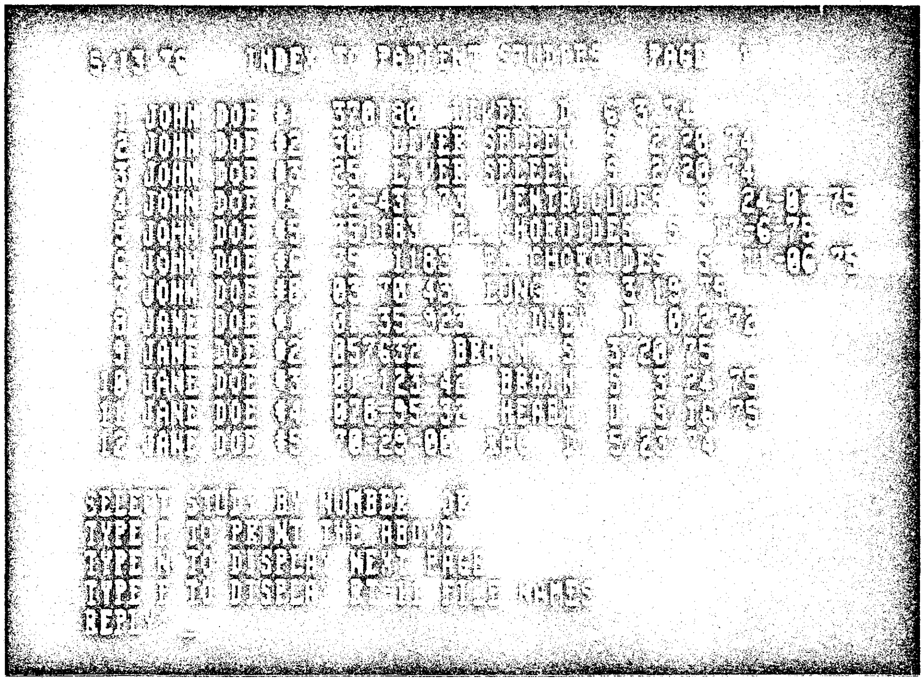


Figure 5-1
Index To Patient Studies

Each page of the index is numbered sequentially, with the entries on the first page numbered from 1-12; second page, 13-24; third page, 25-36, etc. The most recent study is displayed first on Page 1. Each entry consists of the following items:

PATIENT NAME
PATIENT NUMBER
ORGAN
STUDY TYPE (S, D, L, OR BLANK)
DATE or RT-11 FILENAME

Missing items are left blank. For STUDY TYPE, the letters S, D, L, and Blank indicate Static, Dynamic, List, and Flood studies, respectively. (Gated studies are either dynamic or list studies.)

Four procedure choices are displayed:

STUDY Enter the number of the study to be reviewed.

N The next page of the index is displayed. This choice is not offered on the last page of the index. To return to the first page, you must type CTRL/Z to obtain the background command table and again type the AD command to select analysis and review.

P The displayed page is printed on the terminal.

F Instead of the acquisition date appearing on the display, it is replaced with the RT-11 filename. The RT-11 filename is automatically created during data acquisition. Internally, the data acquisition program takes the first six characters of the patient name and creates an extension in the format of an X and a 2-digit number. For example, if there were two patients with the last name of RICHARDSON, the first RICHARDSON to have a study performed would be RICHAR.X00 and the second RICHARDSON to have a study performed would be RICHAR.X01.

To initiate analysis for a particular study, type the appropriate study number (followed by a RETURN) from the patient study index. The index is erased and the study summary of the chosen patient file appears on the display. The study summary is arranged a bit differently from the one displayed during an acquisition run, but it provides the same information. Collection parameters for each frame of a static study (Figure 5-2), or for each group of a dynamic study (Figure 5-3), appear on the display. In the latter, the matrix configuration is identified by its type number in parentheses. Five procedure choices are listed:

RET displays the first frame of a study and starts the analysis and review procedure.

P followed by a RETURN, prints the summary on the terminal.

C followed by a RETURN, displays comments, if any exist. The text cannot be edited at this time, only examined or printed.

X followed by a RETURN, returns to the index of patient studies.

N followed by a carriage return, displays the patient administrative block for the next frame. N does not apply to dynamic or list mode studies.

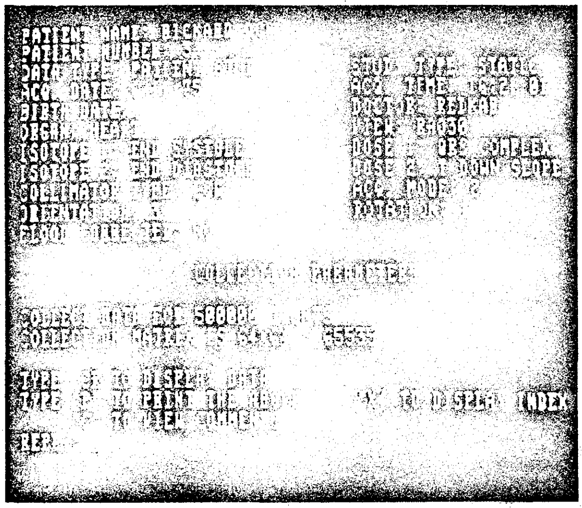


Figure 5-2
Static Patient Study Summary

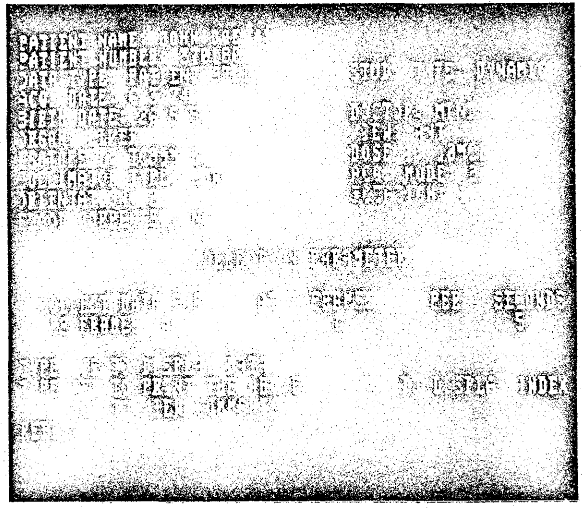


Figure 5-3
Dynamic Patient Study Summary

CA

5.1.2 Continue Analysis

You can call the Continue Analysis command (CA) only at the background command table level. The Continue Analysis routine is an alternate entry point to the data analysis program. To select a study for continuing analysis, type:

```
CA(RET)
```

When you issue the CA command, the data analysis program reads save area 0, opens the data file referenced by it for analysis, and then displays save area 0. This command causes the data analysis program to bypass the patient study index and the administrative data display. Thus, you have a direct route to enter the data analysis program and continue analysis of the last study analyzed. Users who perform data analysis with higher-level languages (FOCAL, FORTRAN, or BASIC) will find this feature quite useful when switching between their own programs and GAMMA-11.

Once you call the data analysis program via the CA command, the last study that you analyzed is reselected and displayed on the screen (i.e., the data file referenced by save area 0 is opened, and the contents of the save area are displayed). At this point, you proceed as usual.

If the patient file cannot be found on the disk, the following error message is displayed on the screen.

```
PATIENT STUDY: dev:filename
index line of study
CANNOT BE FOUND
TYPE RETURN TO EXIT
```

The "dev:filename" is the RT-11 device mnemonic and filename of the patient file. The background command table is displayed when you press RETURN.

5.2 THE DISPLAY FRAME

A display frame is shown in Figure 5-4. The display frame shows the organ as well as pertinent administrative and analytical data.

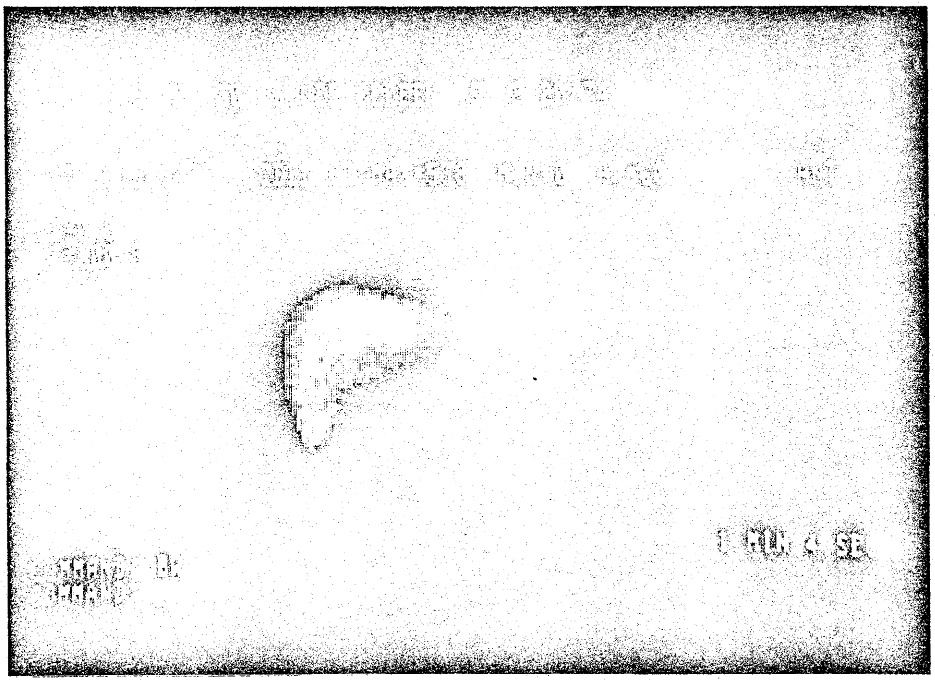


Figure 5-4
Display Frame

Note these elements of the display shown in Figure 5-4:

1. Identification -- At the top left of the display an index entry identifies the study. Identification consists of PATIENT NAME, PATIENT NUMBER, ORGAN, STUDY TYPE, and DATE OF ACQUISITION. Identification appears in every display frame.

2. Matrix -- The matrix occupies most of the screen in the normal full-size display mode as shown. Each cell is represented by a small square whose size depends on the dimensions of the matrix, and whose intensity depends on the number of counts in the cell. The result is a visual image of the count distribution.

3. Counts and Frame Number -- The total number of counts in the frame (TOT CT=) appears directly beneath the matrix (for the VT01) or appears directly above the matrix (for the VSV01 color display), followed by the largest (MAX), smallest (MIN), and average (AV) number of counts per cell. At the extreme right is the frame number. In a dual-isotope study, the selected isotope is indicated by the letter A or B after the frame number:

    ```
    FRAME001A
    ```

    designates the first frame of isotope A.

    In a static study, the VIEW, entered at data acquisition setup time, is displayed instead of the frame number.

4. Threshold and Step Size -- Near the upper left corner of the matrix are the lower (LT) and upper (UT) display threshold data. The threshold and step size are displayed in the lower left corner of the screen on the VT01. Each is specified by a pair of numbers. The first of these numbers is the threshold level. The second is the step size by which the threshold may be changed. Both are expressed as percentages of the maximum cell count (MAX). (See Sections 5.6 through 5.7.6)

5. Frame Rate or Duration -- In a dynamic study, the frame rate of the current group is shown in the lower right corner. In a static study, the duration of the frame is displayed here.

Immediately below the matrix, the word COMMAND: appears. This is a prompt to you that the data analysis program is waiting for you to enter a command. The rest of this chapter describes, in detail, the available commands that can be entered.

5.3 DISPLAY MODE COMMANDS

Certain operating conditions and display modes are established by pairs of commands: one sets the condition, while the other removes it. This procedure is useful for display sizes. That is, matrices are displayed either full-sized or minified (groups of four). There are certain commands which determine the size of these matrix displays. They set the prevailing mode until changed. These commands are described in the following sections.

The action of any of the commands is clear from the context. You have the choice of entering these commands with or without spaces. For example, the following commands are functionally identical:

```
SM 3

SM3
```

All spaces between the commands and their parameters are ignored. However, please note in some procedures, the space itself is a command.

Should you type a character string that is not a recognized command, the system will try to find a macro by that name and execute that macro. (See Section 5.24 for macros.) If no macro by that name exists the system will issue an illegal command error message and will prompt you to type in a new command.

5.3.1 Error Processing

The data analysis command processor detects errors in a command line. Three basic procedures are used during error processing. These are:

1. If the core-resident data differs from the data last displayed, the system displays the core-resident data.

2. The system displays the command line only up to the point (character) at which the error is detected followed by a question mark (?).

3. The message, COMMAND: is redisplayed.

An error occurs in two cases: either you have typed a command that GAMMA-11 does not recognize (i.e., a typographical error) or GAMMA-11 cannot do the command (as in trying to place more frames into a playback file than exist in the patient file).

If the command is unrecognizable, GAMMA-11 will try to find a macro by that name and execute it. If there is no macro by that name, an error occurs.

If a valid command cannot be executed but is preceded by an exclamation point (!), an error does not occur and control passes to the next command line.

NOTE

> When the system detects an error, it terminates execution of the remainder of the command line and/or macro buffer.

5.3.2 Multiple Command Lines

The multiple command line feature allows you to enter more than one command to the COMMAND: response on the screen. Multiple command lines increase the speed at which the system performs complex algorithms. This speed results from eliminating redisplay functions which usually take anywhere from 1 to 10 seconds to accomplish on the VT01 and up to 2 seconds on the color display.

No redisplay of data takes place between commands unless

1. A display command (DI, DM, DN, or ID) is issued.
2. The command processor is ready to accept a new command from you and the core-resident data differs from the last data displayed.

Separate the individual commands in a multiple command line by a semicolon (;). For example,

```
RS1;DM1;RS2;DM2;RS3;DM3;RS4;DM4<RET>
```

This example displays four save areas at one time.

DI

5.3.3 Full Size Display

The Full Size display command (DI) displays the core-resident frame at full size (Figure 5-4). Type the following command to display a full sized image on the screen.

DI (RET)

Keep in mind that there are 16 levels of color or 16 levels of gray for the matrices. In the VT01, there are 32 levels of intensity for the 32 x 32 and 64 x 64 matrices. For the 128 x 128 matrix there are 8 levels. The display levels are distributed linearly over the range of cell counts (MIN to MAX) in the displayed matrix. If the thresholds have been changed to enhance contrast, the levels are distributed over the range of counts between the thresholds. (See Sections 5.6 through 5.7.6 for a discussion of thresholds and intensity levels.)

DM

5.3.4 Minified Display

There are two forms of the minified display commands, DM and DM n. Each has its own unique set of functions. The DM command reduces the size of the displayed image and displays four sequential frames. These frames are displayed simultaneously along with the count data for each frame.

To produce a minified image, the system reduces the 128 x 128 matrix to 64 x 64. The four adjacent cells of the matrix are averaged to produce one cell of the smaller image. The 64 x 64 and 32 x 32 matrices are unchanged. The system does not change the number of intensity levels in the minified image, regardless of matrix dimension. Type the following command to display all four sequential minified frames.

DM (RET)

An example of the display is shown in Figure 5-5.

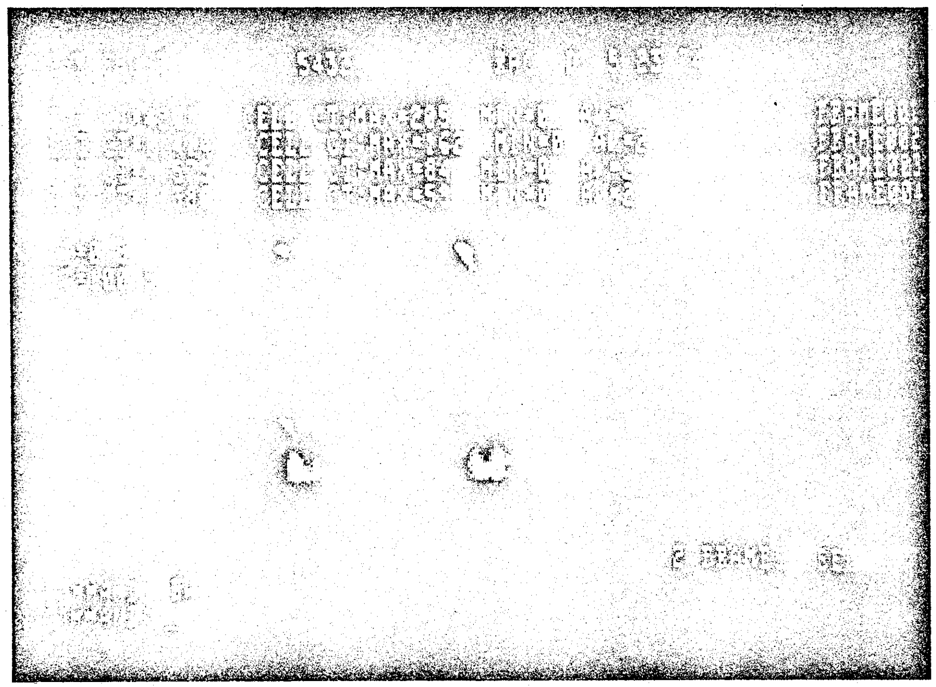


Figure 5-5
Minified Display

Notice that the core-resident frame is at the upper left, the succeeding frames in the upper right, lower left, and lower right.

The DM n command displays up to four non-sequential frames of data simultaneously. Type the following command where n represents that position of the display in which the current contents of core are displayed.

```
DM n (RET)
```

The value of n can be only 1, 2, 3, or 4. If n=1, the screen is erased. With this command, you can manipulate the core-resident data and display four images simultaneously. Furthermore, DM 1 does not set a prevailing mode. If you type a command other than DM n in response to "COMMAND:" (such as SK, skip), the display is presented in full size.

An example using the DM n command is:

```
S9;DM1;SK;S9;DM2;SK;S9;DM3;SK;S9;DM4 (RET)
```

This command line displays four smoothed images of a multiple static study. Another example is:

```
RS1;DM1;RS2;DM2;RS3;DM3;RS4;DM4 (RET)
```

which displays four save area images.

DX

5.3.5 Display Index

The Display Index command (DX) presents the patient index. Type the following command to display a list of the patient index.

```
DX(RET)
```

See Figure 5-1. The DX command allows you to select another patient study easily without returning to the command table.

DP

5.3.6 Display Patient Data Summary

The Display Patient Data Summary command (DP) is useful because it avoids typing CTRL/X which returns to the command table, and then AD to enter the analysis and review routine. See Section 5.1.1 for a discussion about the study summary. Type the following command to display a study summary of the patient file that is currently being reviewed.

```
DP(RET)
```

ND

5.3.7 No Display

The No Display command (ND) is applicable only if you are using multiple command lines. Type the following command at the end of the command line to avoid displaying any data.

```
ND(RET)
```

The command is essential if you want to type more than 49 characters in a command line. The system only responds to 49 characters on a line and then displays the data of that command line. The ND command eliminates a display and continues with the "COMMAND:" message on the next line. For example, the following command line is longer than 49 characters:

```
COMMAND:LT 20;AD4;S9;DN1;SK5;S9;DM2;SK5;ND(RET)
COMMAND:S9;DM3;SK5;S9;DM4(RET)
```

Notice that ND (no display) appears at the end of the first command line. You may finish the command line on the next line.

5.4 FRAME SELECTION COMMANDS

Certain commands are used primarily for frame selection. They allow you to manipulate displays such as requesting the next frame, skipping forward or backward through the frames, restoring current frames, and returning to the beginning of the study. The only command in this group that applies to a single-frame static study is the BE or beginning command, discussed in Section 5.4.5.

SP

5.4.1 Next Frame

The Next Frame command (space bar) displays the next frame in sequence of a particular study. Press the space bar to advance to the next frame.

SP RET

In minified display mode, the display shifts ahead one frame.

For example, if frames 3 through 6 are displayed on the screen, and you request the Next Frame command, the display shifts to frames 4 through 7. The matrix at the upper left is core-resident.

NOTE

The space bar has an additional effect when the Consecutive Add (AD) message is displayed. See Section 5.14.1.

SK

5.4.2 Skip Forward

The Skip Forward command (SK) skips ahead through the study. To skip ahead n number of frames, type:

SK n RET

The n is optional in this command. For example, if frame 5 is displayed (or frames 5 through 8 in a minified display), the command,

SK 4 RET

brings frame 9 (or frames 9 through 12 in a minified display) to the screen. If the n is omitted the command,

SK RET

displays the next frame, that is, frame 6 (or frames 6 through 9 in a minified display). An attempt to skip beyond the end of the study causes an error.

BK

5.4.3 Skip Backward

The Skip Backward command (BK) skips backward through the study. To skip backward n number of frames, type:

BK n RET

The n is optional in this command. For example, if frame 10 is displayed (or frames 10 through 13 in a minified display), the command,

BK 4 RET

brings frame 6 (or frames 6 through 9 in a minified display) to the screen. If the n is omitted the command,

BK RET

displays the previous frame; that is, frame 9 (or frames 9 through 12 in a minified display). An attempt to back up beyond the first frame of the study causes an error.

RET

5.4.4 Restore Current Frame

The Restore Current Frame command (RETURN) restores to the screen the currently-selected frame, as indicated by the displayed frame number (or view). Type a RETURN with no command preceding it to display the currently-selected frame.

RET or ;

This command is useful, because it allows you to start with an original frame after the core-resident frame has undergone modification (such as frame algebra operations).

When using the RETURN command in multiple command lines, two new forms of the command take place. These are:

```
COMMAND:  command line;(RET)
```

and

```
COMMAND:  command line;;command line(RET)
```

The first command line executes all of the functions in the command line and restores the current frame because the semicolon is present before the RETURN. If there is no semicolon before the RETURN the command line is executed as normal.

The second command line has two semicolons in the middle. The system notices the first semicolon and expects that a command follows it. In this case another semicolon is typed, which means no command exists; hence, the system restores the current frame of the data and continues executing the remainder of the command line.

The following example stores a smoothed matrix (multiplied by 0.5) in save area 5; the original frame is restored, smoothed, multiplied by 0.25, and stored in save area 6; and finally the original frame is redisplayed.

```
COMMAND:  S9;CM0.5;SM5;;S9;CM0.25;SM6;(RET)
```

BE

5.4.5 Beginning

The Beginning command (BE) returns the display to the first frame of the study. Type:

```
BE(RET)
```

on the terminal. For example, if you want to skip forward or backward, or advance frames, the BE command returns the display to the first frame of that particular study. Upon doing this, all initial operating conditions are also restored (thresholding, step sizing, etc.).

5.5 DUAL ISOTOPE SELECTION COMMANDS

A dual-isotope study is identified by the letter A or B that appears after the displayed frame number. For most analysis procedures, only one isotope at a time is examined. The study is treated as if it were a single-isotope study. You select the isotope by the commands in the following sections (5.5.1 through 5.5.4).

IA

5.5.1 Select Isotope A

The Select Isotope A command (IA) transfers the frames of isotope A to core for display and analysis. Type the following command on the terminal to set the isotope to mode A.

```
IA RET
```

Because only isotope A is displayed and analyzed (including during regions of interest), the study, for all practical purposes, is a single isotope study. Mode A remains in effect until you give another isotope selection command.

IB

5.5.2 Select Isotope B

The Select Isotope B command (IB) transfers the frames of isotope B to core for display and analysis. Type the following command on the terminal to set the isotope to mode B.

```
IB RET
```

Because only isotope B is displayed and analyzed (including regions of interest), the study, for all practical purposes, is a single isotope study. Mode B remains in effect until you give another isotope selection command.

IX

5.5.3 Isotope Exchange

The Isotope Exchange command (IX) exchanges (or switches) one pair of isotopes. Type the following command on the terminal to exchange isotopes.

```
IX RET
```

That is, if isotope A is displayed and you type the IX command, the current frame number remains unchanged, and the system moves the frame for isotope B into core in place of the frame for isotope A.

For example, if the message FRAME012A is displayed on the screen, frame 12 of isotope A is currently being displayed. However, when you issue the IX command, frame 12 of isotope B moves into core and the system displays the message FRAME012B on the screen. The isotope B data replaces isotope A data.

NOTE

> Frame numbers are very important to the GAMMA-11 user. Frame numbers tell you what part of a study is being used. Remember that the current frame is always the frame number that is displayed.

DD

5.5.4 Dual Isotope Display

The Dual Isotope Display command (DD) displays two matrices of a current frame in minified mode. Type the following command on the terminal.

```
DD RET
```

A dual isotope consists of two sets of data, one for isotope A and one for isotope B. The dual display command displays both isotopes simultaneously (in minified form). For example, this operation is useful in a dual isotope static study to compare the distribution of each isotope in an organ.

Isotope A, displayed in the left minified frame, automatically becomes the selected one, regardless of the prevailing selection mode when the DD command is typed. The display returns to normal size as soon as you type another command. Isotope A remains core-resident.

The data analysis routine can analyze only one set of isotopes (either A or B) at a time. Thus commands IA, IB and IX are used to select which isotope's data is to be displayed and analyzed.

5.6 THRESHOLD INTENSITY LEVELS AND CONTRAST ENHANCEMENT

In a normal full-size matrix display, the intensity levels are distributed linearly over the range of cell counts in the matrix. There are 16 intensity levels (0 to 15) for the color display and 33 intensity levels (0 to 32) for the VT01. With the VT01, there are only 8 levels of intensity for 128 x 128 matrices. The count increment per level is represented by the following formula:

(MAX-MIN)/(Levels of intensity in matrix) = (Count Increment)/Level

In a normal full-size display, 15 of the 16 color levels (32 of 33 for the VT01), or gray scale intensity levels, are visible and distributed linearly over the range of cell counts in the matrix. Level 0 represents only those cells with zero counts. Thus, if the lowest cell count (MIN) is zero, the highest (MAX) is 300, and there are 15 nonzero levels, each intensity level represents a range of 20 counts. The count increment per level is represented by the following formula:

MAX-MIN/15 levels of intensity = counts/level

(300-0)/15 = 20 counts/level

Those cells with count 0 are at intensity level 0. Those cells with counts between: 1-20 are at intensity level: 1

21-40	2
41-60	3
61-80	4
.	.
.	.
.	.
281-300	15

At least one cell is at maximum intensity in every frame, and each cell with 0 counts always has zero intensity. In this way, the system provides the maximum possible contrast for every frame, regardless of the absolute count. However, when the cell-count range is smaller than the number of levels, not all intensities are displayed, but the distribution still is linear.

You can distribute the range of the intensity levels over a smaller range of counts by specifying the lower and upper thresholds. A lower threshold is a percentage of the maximum counts below which no intensities are displayed. An upper threshold is a percentage of the maximum counts above which no intensities are displayed. For example, if the maximum count is 300,

1. A lower threshold of 10 means that cells whose counts are less than 30 (10% of 300) are not displayed.
2. An upper threshold of 80 means that cells whose counts are greater than 240 (80% of 300) are not displayed.

When detectable background radiation exists, contrast in the areas of interest is reduced because the display levels have to include cells with only a few counts. Similarly, unwanted hot spots (as in a brain scan) also reduce contrast by using up levels at the high end of the range. Both difficulties can be eliminated by setting the display thresholds so that cells with the counts lying above or below them are not displayed. The intensity levels are distributed only over the range of counts lying between the thresholds. In this way, contrast is enhanced in the areas of interest. You can set the thresholds and move them up or down at will, so that an optimum display can easily be obtained.

NOTE

> The threshold-setting commands affect only the display, not the core-resident data. However, you can store the threshold specifications, along with the matrix, in a save area.

5.6.1 Display Thresholds and Steps

Each display threshold is expressed as a percentage of the maximum cell count in the frame. You can alter the thresholds by setting them, or you can increment or decrement them in steps using the step size. Thresholds can be set and changed individually or together. Initially, the lower and upper thresholds are set to zero percent and 100 percent, respectively, each with a step size of 5 percent.

5.7 THRESHOLD ADJUSTMENT COMMANDS

The threshold adjustment commands are used to lower and raise threshold values to a percentage of the maximum cell count. The commands also set the step size to a specified percentage. These commands are described in the following Sections 5.7.1 through 5.7.8.

LT

5.7.1 Set Lower Threshold and Step

The Set the Lower Threshold and Step command (LT) sets the lower display threshold to a certain percentage of the maximum cell count and also sets the step size to a particular percentage.

Command format:

```
LT lower,step(RET)
```

where:

lower	is the lower threshold expressed as a percentage of the maximum cell count.
step	is the optional percent step size.

For example, the following command sets the lower threshold to 15% and the step size to 2%.

```
LT 15,2(RET)
```

The following command sets the lower threshold to 10% and the step size remains unchanged.

```
LT 10(RET)
```

Thresholding is nothing more than specifying percentages of the maximum cell count for the frame. Those cells that lie outside the threshold percentages are not displayed.

UT

5.7.2 Set Upper Threshold and Step

The Set the Upper Threshold and Step command (UT) sets the upper threshold to a certain percentage of the maximum cell count and also sets the step size to a particular percentage.

Command format:

```
UT upper,step(RET)
```

where:

upper	is the upper threshold expressed as a percentage of the maximum cell count.
step	is the optional percent step size.

For example, the following command sets the upper threshold to 10% and the step size to 8%.

```
UT 10,8(RET)
```

The following command sets the upper threshold to 20% and the step size remains unchanged.

```
UT 20(RET)
```

W

5.7.3 Raise the Lower Threshold by Step Size

The Raise the Lower Threshold by Step Size command (W) raises the presently displayed lower threshold by the current step size. Type the following command on the terminal to raise the lower threshold.

```
W(RET)
```

For example, the following command displays the lower threshold at 10% of the maximum cell count and sets the step size to 5%.

```
LT 10,5(RET)
```

Each time you type the following command on the terminal, the maximum cell count increases by 5%.

```
W(RET)
```

In this case, the lower threshold is now displayed at 15% of the maximum cell count.

NOTE

The system rejects any attempt to step beyond the boundaries (0% and 100%) in either direction.

X

5.7.4 Lower the Lower Threshold by Step Size

The Lower the Lower Threshold by Step Size command (X) lowers the presently displayed lower threshold by the current step size. Type the following command on the terminal to lower the lower threshold.

```
X RET
```

For example, the following command displays the lower threshold at 30% of the maximum cell count and sets the step size to 7%.

```
LT 30,7 RET
```

Each time you type the following command on the terminal, the maximum cell count decreases by 7%.

```
X RET
```

In this case, the lower threshold is now displayed at 23% of the maximum cell count.

NOTE

The system rejects any attempt to step beyond the boundaries (0% to 100%) in either direction.

Y

5.7.5 Lower the Upper Threshold by Step Size

The Lower the Upper Threshold by Step Size command (Y) lowers the presently displayed upper threshold by the current step size. Type the following command on the terminal to lower the upper threshold.

```
Y RET
```

For example, the following command displays the upper threshold at 50% of the maximum cell count and sets the step size to 8%.

```
UT 50,8(RET)
```

Each time you type the following command on the terminal, the maximum cell count decreases by 8%.

```
Y(RET)
```

In this case, the upper threshold is now displayed at 42% of the maximum cell count.

NOTE

> The system rejects any attempt to step beyond the boundaries (0% and 100%) in either direction.

Z

5.7.6 Raise the Upper Threshold by Step Size

The Raise the Upper Threshold by Step Size command (Z) raises the presently displayed upper threshold by the current step size. Type the following command on the terminal to raise the upper threshold.

```
Z(RET)
```

For example, the following command displays the upper threshold at 22% of the maximum cell count and set the step size to 9%.

```
UT 22, 9(RET)
```

Each time you type the following command on the terminal, the maximum cell count increases by 9%.

```
Z(RET)
```

In this case, the upper threshold is now displayed at 31% of the maximum cell count.

NOTE

> The system rejects any attempt to step beyond the boundaries (0% and 100%) in either direction.

UM

5.7.7 Set the Upper Threshold Display Switch

The Set Upper Threshold Display Switch command (UM) displays the counts above the upper threshold with the maximum intensity instead of using a zero intensity. Type the following command to display the maximum intensity.

```
UM RET
```

For example, if the following commands are typed, the counts above the upper threshold (50%) are at maximum intensity, and the counts below the lower threshold (25%) remain at level zero.

```
LT 25
UT 50
UM
```

In Figure 5-6, the image on the left was derived from the following command string:

```
LT25;UT50 RET
```

The image on the right is derived from:

```
LT25;UT50;UM RET
```

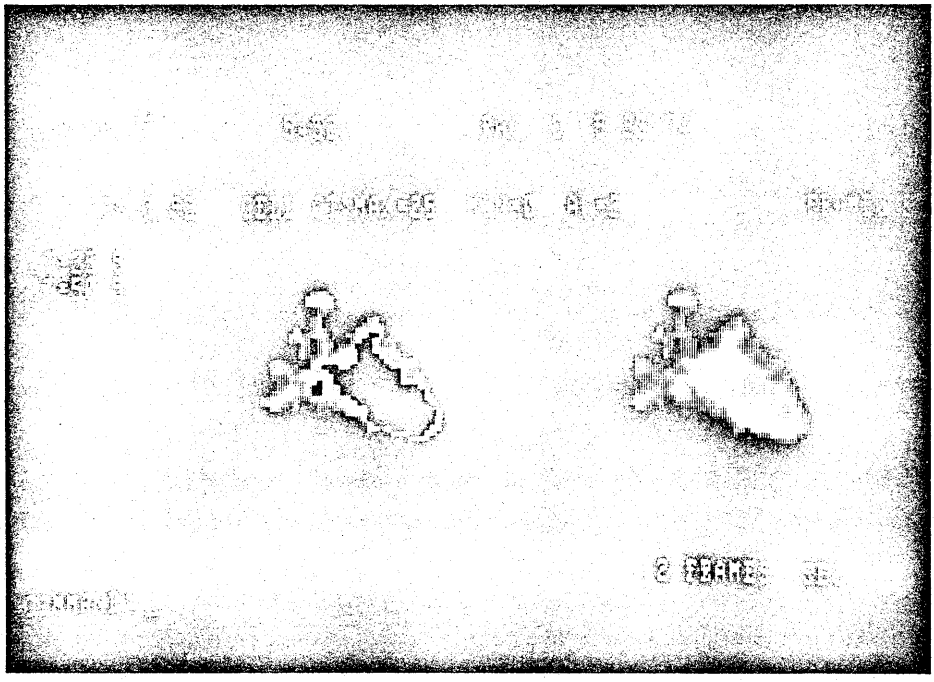


Figure 5-6
Upper Threshold Display Switch

UO

5.7.8 Clear the Upper Threshold Display Switch

The Clear the Upper Threshold Display Switch command (UO) is a clear switch for the UM command. Typing the following command causes the counts above the upper threshold to be displayed with zero intensity (i.e., not displayed).

```
UO RET
```

5.8 ISOCOUNT BAND COMMANDS

It is often useful to examine a narrow range, or band of counts in the matrix. This narrow range is known as an isocount. The thresholds of such an isocount band can be shifted up or down while maintaining the bandwidth. The commands are described in the following sections 5.8.1 through 5.8.3.

IS

5.8.1 Set Isocount Thresholds

The Set Isocount Thresholds command (IS) sets the lower and upper thresholds to individual maximum cell counts.

Command format:

```
IS lower,upper RET
```

where:

lower	is the lower threshold expressed as a percentage of the maximum cell count.
upper	is the upper threshold expressed as a percent of the maximum cell count.

For example, the following command sets the lower threshold at 15% of the maximum cell count and sets the upper threshold at 20% of the maximum cell count.

```
IS 15,20 RET
```

Keep in mind that the lower threshold cannot be greater than or equal to the upper threshold or the command is rejected.

NOTE

The system rejects any attempt to move the band beyond the boundaries (0% and 100%) in either direction.

N

5.8.2 Raise Band

The Raise Band command (N) raises the upper and lower thresholds by a step size equal to the difference between them. Type the following command to raise the isocount band.

```
N(RET)
```

For example, the following command sets the lower threshold at 10% of the maximum cell count and sets the upper threshold at 25% of the maximum cell count.

```
IS 10,25(RET)
```

When you type the following command on the terminal, the upper and lower thresholds are raised by a step size equal to the difference between them.

```
N(RET)
```

In this example, the upper and lower thresholds are raised 15%, as shown in the following formula.

25% - 10% = 15% (step size)

Thus,

new lower threshold = 10% + 15% = 25%

new upper threshold = 25% + 15% = 40%

NOTE

The system rejects any attempt to move the band beyond the boundaries (0% and 100%) in either direction.

O

5.8.3 Lower Band

The Lower Band command (O) lowers the upper and lower thresholds by a step size equal to the difference between them. Type on the terminal to lower the isocount band.

```
O(RET)
```

For example, the following command sets the lower threshold at 30% of the maximum cell count and sets the upper threshold at 40% of the maximum cell count.

```
IS 30,40(RET)
```

When you type the following command on the terminal, the upper and lower thresholds are lowered by a step size equal to the difference between them.

```
O(RET)
```

In this example, the upper and lower thresholds are raised 10%, as shown in the following formula.

40% - 30% = 10% (step size)

Thus,

new lower threshold = 30% - 10% = 20%

new upper threshold = 40% - 10% = 30%

NOTE

> The system rejects any attempt to move the band beyond the boundaries (0% and 100%) in either direction.

5.9 NO-ENHANCEMENT MODE COMMANDS

Thresholds may also be changed without contrast-enhancement. Without contrast enhancement, only those cells whose counts lie between the thresholds are displayed; however, the intensity levels are still distributed over the entire count range. Thus, you can eliminate background noise and hot spots, leaving intensities and contrast relationships unchanged in the areas of interest. The no-enhancement commands add the letter N to the UT, LT, and IS commands.

LTN

5.9.1 No-Enhancement Lower Threshold

The No-Enhancement Lower Threshold command (LTN) changes the lower threshold without contrast enchancement.

Command format:

```
LTN lower,step(RET)
```

where:

lower	is the percent of the maximum cell count.
step	is the optional percent of the step size.

Figure 5-7 shows an image with a lower threshold of 20 with contrast enhancement. The command to obtain this image is:

```
LT 20(RET)
```

In Figure 5-7, the cells lying below 20% are not displayed, and all 15 intensity levels are displayed between 20% and 100%.

Figure 5-8 shows an image with a lower threshold of 20 without contrast enhancement. The command to obtain this image is:

```
LTN 20(RET)
```

In this case, the intensity levels are distributed over the entire count range, starting with instensity level 3 (20% x 15 = 3).

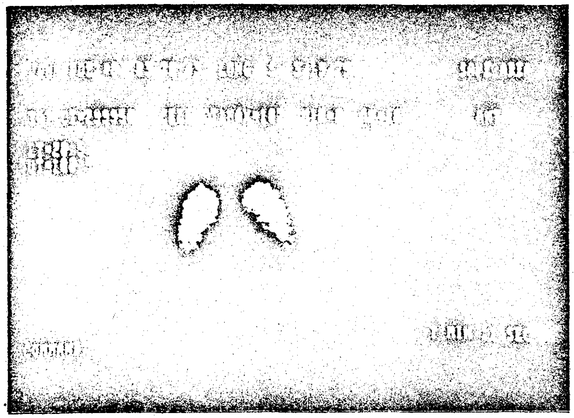


Figure 5-7
Lower Thresholding
with Enhancement

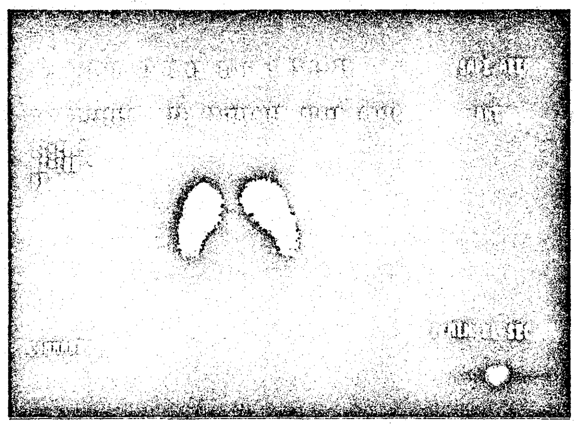


Figure 5-8
No-Enhancement
Lower Threshold

Notice the background has been eliminated while leaving the contrast relationship unchanged in areas of interest. Also, a reminder note, NE, is displayed underneath the threshold levels as long as the mode is in effect. To restore contrast enhancement, type the LT command once again.

UTN

5.9.2 No-Enhancement Upper Threshold

The No-Enhancement Upper Threshold command (UTN) changes the upper threshold without contrast enhancement.

Command format:

```
    UTN upper,step(RET)
```

where:

upper	is the upper threshold expressed as a percent of the maximum cell count.
step	is the percent step size.

Figure 5-9 shows an image with an upper threshold of 70 with contrast enhancement. The command to obtain this image is:

```
UT 70(RET)
```

In Figure 5-9, the cells lying above 70% are not displayed, and all 15 intensity levels are displayed between 0% and 70%.

Figure 5-10 shows an image with an upper threshold of 70 without contrast enhancement. The command to obtain this image is:

```
UTN 70(RET)
```

In this case, the intensity levels are distributed over the entire count range, starting with intensity level 0 and ending with intensity level 10 (70% x 15 = 10).

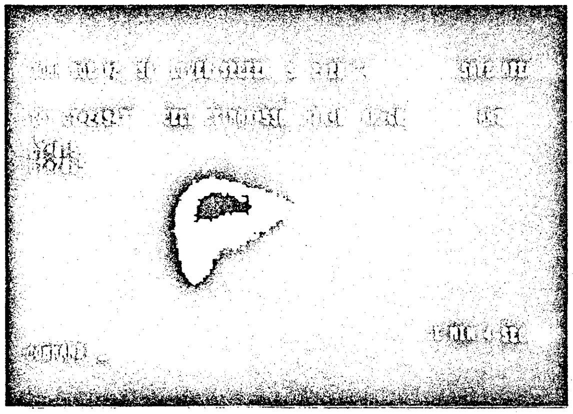


Figure 5-9
Upper Threshold
and Step Size

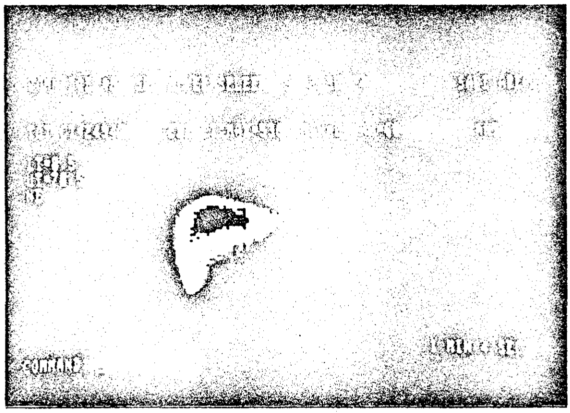


Figure 5-10
No-Enhancement
Upper Threshold

Notice the background has been eliminated while leaving the contrast relationship unchanged in areas of interest. Also a reminder note, NE, is displayed at the bottom of the screen as long as the mode is in effect. To restore contrast enhancement, type the UT command once again.

ISN

5.9.3 No-Enhancement Isocount Thresholds

The No-Enhancement Isocount Thresholds command (ISN) changes the lower and upper thresholds without contrast enhancement.

Command format:

```
ISN lower,upper(RET)
```

where:

lower	is the percent of the maximum cell count for the lower threshold
upper	is the percent of the maximum cell count for the upper threshold

Figure 5-11 shows an image with a lower threshold of 10% and an upper threshold of 20% with contrast enhancement. The command to obtain this image is:

```
IS 10,20(RET)
```

In Figure 5-11, the cells lying above 20% and below 10% are not displayed. All of the intensity levels 1 through 15 are displayed between 10% and 20%.

Figure 5-12 shows an image with an upper threshold of 20% and a lower threshold of 10% without contrast enhancement. The command to obtain this image is:

```
ISN 10,20(RET)
```

In this case the intensity levels are still distributed over the entire range of counts. The displayed levels start with intensity level 1 and end with intensity level 3. That is,

> 20% of 15 levels is level 3 for the highest displayed intensity level
> 10% of 15 levels is level 1 for the lowest displayed intensity level

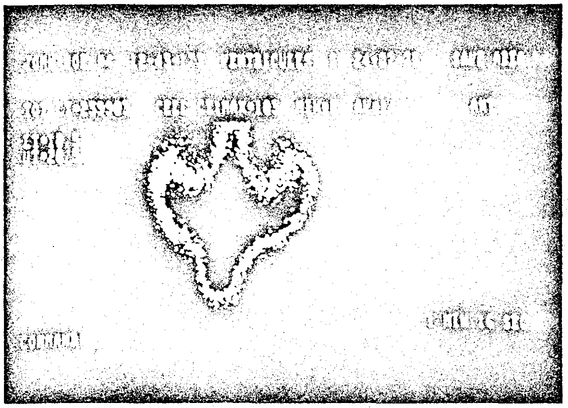


Figure 5-11
Isocount Thresholding

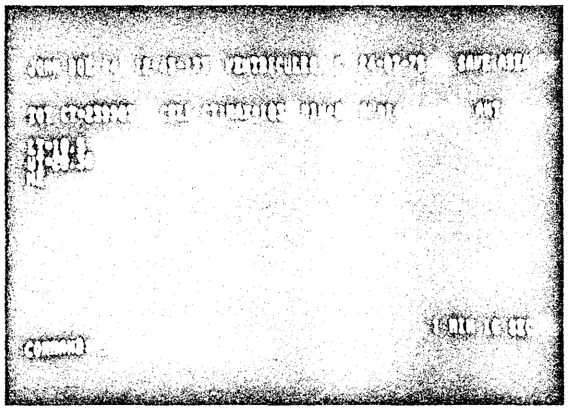


Figure 5-12
No-Enhancement
Isocount Thresholds

Notice the background has been eliminated while leaving the contrast relationship unchanged in areas of interest. Also, a reminder note, NE, is displayed underneath the threshold levels as long as the mode is in effect. To restore contrast enhancement, type the IS command once again.

5.10 FRAME ALGEBRA

Frame algebra operations represent any command that changes the core-resident data. When a frame algebra command is executed, the following message appears on the display, where (exp) is the typed command expression.

```
FRAME ARITH: (exp)
```

This message is displayed directly above the thresholds (LT and UT). The message remains on the display until one of the following occurs.

1. You execute a new frame algebra command, in which case the new command expression replaces the old.
2. You select a new frame by means of a BK, SK, BE or RETURN command, in which case the FRAME ARITH message is erased. A space bar command erases any FRAME ARITH message except the AD command. See Section 5.14.2.

5.11 CONSTANT ARITHMETIC COMMANDS

In each constant arithmetic operation, the Constant Add, Constant Subtract, and Constant Multiply allow you to perform the indicated mathematical function with each cell of the core-resident matrix.

Because the display levels are spread linearly over the cell count or threshold range, constant arithmetic does not change the display unless:

1. Underflow or overflow occurs
2. A constant is added to a previously empty cell

CA n

5.11.1 Constant Add

The Constant Add command (CA) adds a constant, n, to each cell of the core-resident matrix.

Command format:

```
CA n(RET)
```

where n is an integer that is added to each cell of the matrix. For a byte-matrix, the limits are -255 and +255. For the word-matrix, the limits are -65535 and +65535. If the arithmetic results in an overflow (more than the maximum cell count; 255 or 65535), the maximum count is stored in the cell. If the result is an underflow, that is, if the sum is less than zero, the cell remains zero.

For example, if there are cells (byte-matrix) that have a count of 175, and you type the following command, the cell count results in an overflow.

```
CA 100(RET)
```

The program assumes the maximum count, 255, in those cells.

CA -n

5.11.2 Constant Subtract

The Constant Subtract command (CA) subtracts a constant, n, from each cell of the core-resident matrix.

Command format:

```
CA -n RET
```

where -n is an integer that is subtracted from each cell of the matrix. For a byte-matrix the limits are -255 and +255. For the word matrix, the limits are -65535 and +65535. If the arithmetic results in an overflow (more than the maximum cell count), the maximum count is stored in the cell. If the result is an underflow, that is, if the sum is less than zero, the cell remains zero.

For example, if there are cells (byte-matrix) that have a count of 100, and you type the following command, the cell count results in an underflow.

```
CA -150 RET
```

The sum is less than zero, thus the cells remain at zero.

CM

5.11.3 Constant Multiply

The Constant Multiply command (CM) multiplies each cell of the core-resident matrix by a constant, nn.nn.

Command format:

```
CM nn.nn RET
```

where nn.nn is a decimal constant whose limits are 0.01 and 99.99. You can obtain larger or smaller factors by successive multiplications. Leading and trailing nonsignificant zeros may be omitted.

The following forms of the command are all acceptable:

```
CM 45
CM.31
CM 0.2
CM5.4
```

Constant multiplication is often used to normalize a matrix before combining its data with other frames.

NI

5.12 NEGATIVE (COMPLEMENTED) IMAGES COMMAND

The Negate Image command (NI) creates a negative (complemented) image. The program complements the contents of each cell by subtracting them from the appropriate maximum cell count: 255 for a byte-matrix, 65535 for a word matrix. A count of zero remains zero. Type the following command to obtain a negated image.

```
NI RET
```

For example, to obtain a good negative image when there are many empty cells, use the following suggested sequence of commands.

```
CA1;NI RET
```

Adding 1 to an empty cell ensures a maximum display level in its complemented image. To restore the original uncomplemented image, type RETURN.

A negative image is shown in Figure 5-13.

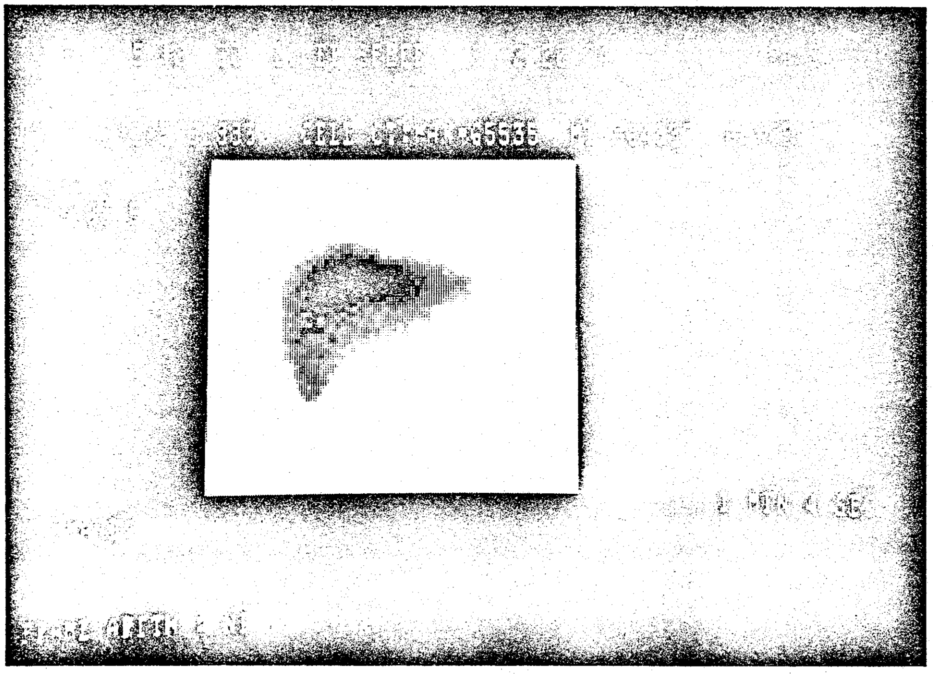


Figure 5-13
Negative (Complemented) Image

5.13 BYTE-WORD EXPANSION COMMANDS

To prevent overflow and underflow in frame arithmetic, you can store byte-matrix data in core in word-matrix form. The byte-to-word expansion occurs as the data is read from the disk. The disk contents are unaffected. The mode of transfer is set by the commands in Sections 5.13.1 and 5.13.2.

EX

5.13.1 Expand

The Expand command (EX) sets a prevailing operation mode. If the command is in effect, the program automatically converts all byte-matrix data to word-matrix form when the data is transferred to core. Type the following command on the terminal to expand the data.

```
EX RET
```

This mode also remains in effect during use of regions of interest and slice. The expand mode is another space saving feature of GAMMA-11, in that it allows the data to be stored on the disk in byte form but analyzed in word form. Without the expand mode, adding byte frames together could lead to cell overflow (maximum cell count of 255). However, with expand in effect, many byte-matrices can be added together since they will be converted to word format (maximum cell count 65535) when read into core. While the command is in effect, the condition note "EX" appears at the bottom of the screen.

NX

5.13.2 No Expansion

The No Expansion command (NX) turns off the Expand capability at any time. Type the following command to prohibit byte-matrix data from expanding on transfer to core.

```
NX RET
```

5.14 FRAME ARITHMETIC COMMANDS

Addition, subtraction, multiplication, division, and merging of frames are all performed on a cell-by-cell basis, that is, corresponding cells of two matrices are combined to produce the resulting cell. Thus, while addition and subtraction follow normal matrix arithmetic rules, multiplication, division, and merging do not. For convenience, all these operations are termed frame arithmetic. Addition, subtraction, merge, and multiplication may be combined in a single expression, but division requires a separate command.

The following restrictions apply to frame arithmetic operations:

1. Matrix configurations must match. You cannot combine frames with different dimensions or cell sizes (word or byte).
2. You can use the frame arithmetic (FA) command only with dynamic studies (see Section 5.14.2).
3. You can combine 128 x 128 matrices only by using the save areas (See Section 5.17).

AD n

5.14.1 Consecutive Add

The Consecutive Add command (AD) adds a selected number of frames to the core-resident frame. The AD commands work only for dynamic studies.

Command format:

```
AD n RET
```

where n is the number of frames that are added to the core-resident frame.

For example, if frame 7 is core-resident, and you type the following command, the sum of frames 7, 8, and 9 appears on the display.

```
AD 2 RET
```

The data in frames 7, 8, and 9 are added together, and frame 7 still remains as the current frame number.

The AD n command sets a prevailing mode that remains in effect for any subsequent skip forward, backward, space bar, or display minified command. In addition, these commands result in an n+1 skip or backspace.

For example, if the current frame number is 6, and the displayed FRAME ALGEBRA command is AD3, striking the space bar and then the RETURN, causes the routine to:

1. Step ahead to frame 10. That is, the core-resident frame is the sum of frames 6, 7, 8, and 9. The Space Bar command skips forward one frame to frame 10.
2. Add frames 11, 12, and 13 to frame 10 and display the sum.

In minified display mode, if the current frame number is 1, and the displayed FRAME ALGEBRA command is AD4, striking the space bar and then the RETURN, causes the routine to:

1. Display the sum of frames 6-10 in position 1.
2. Display the sum of frames 11-15 in position 2.
3. Display the sum of frames 16-20 in position 3.
4. Display the sum of frames 21-25 in position 4.

The FRAME ALGEBRA message is unchanged by this operation.

FA

5.14.2 Frame Arithmetic

The Frame Arithmetic command (FA) provides two distinct functions for dynamic studies:

1. Sequential adding, subtracting, multiplying, or merging.
2. Selecting and displaying of particular frames.

Command format:

```
FA (exp) RET
```

where (exp) represents the combination of arithmetic operators and their operands, which are the frame numbers of the frames to be manipulated. The operators are +, -, *, and ! (for merge which is described below).

For example, if you type

```
FA 7-4+32*5 RET
```

on the terminal, the following processes take place:

1. Frame 4 is subtracted from frame 7.
2. The result is added to frame 32.
3. The sum is then multiplied by frame 5.

NOTE

> The operations are strictly sequential and no arithmetic hierarchy is observed. If an operator (i.e., +, -, *, or !) precedes the first frame number (e.g., +7, -4), the current core-resident data is used as the first operand. For example, if you type FA +5-12, frame 5 is added to the current core-resident data and then frame 12 is subtracted from this data.

Consequently, if you type the following command on the terminal, frame 13 is displayed.

```
FA 13(RET)
```

In the merge operation, each cell of the resultant matrix is equal to the larger cell count of the two matrices being merged. The ! is the merge operator.

For example, the following command merges frame 1 and frame 2.

```
FA 1!2 (RET)
```

NOTE

> To combine frames in a static study or from different studies, or to combine 128 x 128 matrices, the save areas must be used (see Section 5.17).

SA

5.14.3 Save Area Arithmetic

Similar to the Frame Arithmetic command, the Save Area Arithmetic command (SA) does the following:

1. Sequential adding, subtracting, multiplying, and merging of save areas.
2. Selecting and displaying a particular save area.

Command format:

```
SA (exp)(RET)
```

where (exp) is an operation for addition, subtraction, multiplication or merging of save areas, or a designated save area by itself.

For example,

```
SA 3+2-7(RET)
```

causes the following processes to occur:

1. The contents of save area 3 and save area 2 are added.
2. The contents of save area 7 are subtracted from the sum.

NOTE

> Save area 0 cannot be used in this command. Save area operations are strictly sequential and no arithmetic hierarchy is observed. If an operator (+, -, !, or *) precedes first save area number (e.g., -2, +3), the current core-resident data is used. For example, if you type SA -7+2, save area 7 is subtracted from the current core-resident data and then save area 2 is added to this data.

Whenever you use the SA command, the mode of operation becomes the mode of the core-resident data.

For example, the following command adds the contents of save areas 3 and 2.

```
SA 3+2(RET)
```

The mode of operation is now save area mode. To exit save area mode, you have to type the following command to be able to perform other GAMMA-11 commands.

```
RS 0(RET)
```

The following command merges the contents of save area 2 to the core-resident image.

```
SA !2(RET)
```

This command does not leave you in save area mode unless you were in save area mode to begin with.

NOTE

> To get out of save area mode, type RS0.

If you type the following command, save area 5 is displayed.

```
SA 5(RET)
```

After performing save area arithmetic, use the following command to return to the original frame.

```
RS 0(RET)
```

5.15 FRAME DIVISION COMMANDS

The frame division is fixed point, which imposes limitations on the results. Unlike other frame algebra commands where the binary point is to the right of the matrix cell (integer number), the division commands move the point to the middle of the cell. For byte-matrices, each cell has four bits to the left and four bits to the right of the binary point; and the values of each cell range from 1/16 to 15 15/16. For word-matrices, each cell has eight bits to the left and eight bits to the right of the binary point; and the values of each cell range from 1/256 to 255 255/256.

FDH

5.15.1 Frame Divide High

The Frame Divide High command (FDH) divides one frame by another specified frame, and division by zero is treated as overflow.

Command format:

```
FDH n/m RET
```

where:

n   represents the dividend frame.

m   represents the divisor frame.

Frame n is divided by frame m. If any cell of frame m is zero (which would cause an attempted division by zero) the quotient cell is assigned a maximum value. That is, division by zero (except 0/0, which yields zero) is treated as a case of overflow (i.e., 15 for bytes or 255 for words divided by 0).

You can omit the argument n from the command, which divides the core-resident frame by frame m.

```
FDH /m RET
```

For example,

```
FDH 7/32 RET

FDH /14 RET
```

FDL

5.15.2 Frame Divide Low

The Frame Divide Low command (FDL) divides one frame by another specified frame, and division by zero is treated as underflow.

Command format:

```
FDL n/m(RET)
```

where:

n represents the dividend frame.

m represents the divisor frame.

Frame n is divided by frame m. Division by zero is treated as a case of underflow (i.e., 1 divided by any number greater than 16 for bytes, or 256 for words). If this occurs, the quotient cell count will be zero.

The argument n may also be omitted from the command, which represents the division of the core-resident frame by frame m.

```
FDL /m(RET)
```

For example,

```
FDL 5/4(RET)

FDL /9(RET)
```

SDH

5.15.3 Save Area Divide High

The Save Area Divide High command (SDH) divides one save area by another specified save area. Division by zero on the contents of the save area is treated as overflow.

Command format:

```
SDH n/m(RET)
```

where:

n represents the dividend save area

m represents the divisor save area.

Save area n is divided by save area m. Only save areas 1 through 9 can be specified by n and m. Save area 0 cannot be used. The argument n may also be omitted from the command, which represents the division of the core-resident data by save area m.

```
SDH /m(RET)
```

SDL

5.15.4 Save Area Divide Low

The Save Area Divide Low command (SDL) divides one save area by another specified save area. Division by zero on the contents of the save area is treated as underflow. If this occurs, the quotients are zero.

Command format:

```
SDL n/m(RET)
```

where:

n	represents the dividend save area.
m	represents the divisor save area.

Save area n is divided by save area m. Only save areas 1 through 9 can be specified by m and n. Save area 0 cannot be used.

More meaningful images will result if the matrix in save area m is first subjected to the commands, CA-b and CAb, where b is the number of counts that correspond to the background. This procedure ensures a more uniform background level and avoids division by zero.

5.16 NONLINEAR IMAGES

The default algorithm for computing the number of counts/intensity is the linear formula:

(Max counts - Min counts)/15 = #counts/intensity level

This formula does not have to be linear.

Using frame algebra, you can obtain nonlinear images for the purpose of increasing the density of display levels in certain areas, while reducing them in other parts of the display. A complete discussion of the process is found in the following sections.

5.16.1 Hyperbolic Images

You can obtain hyperbolic nonlinear images by using the frame division or save area division commands. The image is shown as a rectangular hyperbolic display; that is, the asymptotes are perpendicular, and parallel to the count and intensity axes. The aim of a non-linear display is to bring out areas of interest by increasing the density of display levels in those areas while reducing the density in other areas.

For hyperbolic images, the smaller the semi-axes of the curve, the greater the nonlinearity. Two images are discussed in these sections. Other images can be obtained with algebraic operations on the frame data. In the discussion, byte-matrix counts are given.

1. Frame divided by its complement:

   This is a positive image in which the density of display levels increases in high-count regions. The equation for this image is

   $$C' = 16C/(256-C) \quad \text{[byte-matrix]}$$

   where C' is a cell of the nonlinear matrix, and C is the corresponding cell of the original matrix. The image is obtained by

SM j	(Save the matrix in save area j)
NI	(Complement the image. Use "CA 1" if necessary)
SM k	(Save the negative image)
SDH j/k	(Divide frame by complement)

   Cells with counts below 16 and above 240 will underflow and overflow, respectively. If there are cells of interest with counts above 240, subtract 16 from the frame (or multiply by 0.94) before division.

2. Complement divided by frame:

   This is a negative image in which the density of display levels increases in low-count areas. Cells with counts below 16 or above 240 will overflow and underflow, respectively. In this case adding 16 or multiplying by 0.94 will bring out cells below 16. The equation is:

   $$C' = 16(256-C)/C \quad \text{[byte-matrix]}$$

5.16.2 A Multiplicative Nonlinear Image

Another commonly used means of obtaining a nonlinear image is multiplying a frame by itself. This yields a matrix of the squares of the cell counts, with the density of levels increasing in high-count regions.

5.17 SAVE AREA COMMANDS

The Save Matrix, Save Dynamic Curves, Read Save Area, Read Regions of Interest, and Delete Save Area commands are known as save area commands. These commands provide direct access to ten (0-9) permanent save areas and 55 (10-64) optional save areas. The commands are outlined in Sections 5.17.1 through 5.17.5. Save area 0 is a special area used by the data analysis program. You can only read from save area 0, not store data in it.

Save areas are essential because GAMMA-11 has only one core-resident frame at a time. Consequently, the results of an analysis could be lost every time you select a new frame. To prevent this loss, you can save core-resident data modified by analysis for future use by storing the frame in one of these save areas.

SM

5.17.1 Save Matrix

The Save Matrix command (SM) stores the core-resident matrix, with all identifying, thresholding, and other displayed information in a particular save area.

Command format:

```
SM n(RET)
```

where n represents a save area number. Save areas 1 through 64 can be specified for matrices. The core-resident matrix with all identifying information is stored in save area n. You cannot specifically store information in save area 0. When you use the save matrix command, all of the previous contents of save area n are lost, and the display remains unchanged.

SD

5.17.2 Save Dynamic Curves

The Save Dynamic Curves command (SD) stores the most recently calculated set of dynamic curves, derived from regions of interest, in a particular save area.

Command format:

```
SD n(RET)
```

where n represents a specified save area number. Only save areas 1 through 9 may be specified and used for dynamic curves. The previous contents of save area n are lost and the display is unchanged. The use of this command is described in greater detail in Chapter 6.

RS

5.17.3 Read Save Area

The Read Save Area command (RS) displays the contents of a specified save area.

Command format:

```
RS n(RET)
```

where n represents a specified save area number. The system stores the previous display frame in save area 0. The legend SAVE AREA n appears in the upper right corner of the screen. The execution of this command depends on the contents of the save area accessed:

1. If the contents are a simple matrix, the matrix and all associated information (identification, thresholding data, etc.) are displayed. You can perform thresholding and constant arithmetic on the matrix. To restore the original display, type:

   ```
   RS 0(RET)
   ```

   The previous frame is displayed, and the legend "SAVE AREA n" disappears.

2. If the contents of the save area are a matrix with regions of interest, the program automatically places itself in the region of interest mode, with the cursor displayed (see Chapter 7). To restore the original display, type CTRL/X, then RS 0.

3. If the contents are a set of dynamic curves calculated from regions of interest, these curves are plotted in plot average. Only the calculation and output commands (PN, PA, PO, PU, PR, PP) are executable at this point (see Chapter 7). Any other input brings the display matrix to the screen (save area 0).

NOTE

If you want to read a save area that contains region of interest information, but do not want to automatically enter the region of interest program, use the save area arithmetic command (i.e., SA n).

You cannot write into save area 0 since it is system protected. However, you may read from save area 0. Save area 0 is basically used by the data analysis program to keep track of which patient's data you are analyzing. Any time when the data matrix is going to be destroyed (i.e., through frame algebra), the data analysis program writes out patient information to save area 0 before destroying the image. Save area 0 is a temporary storage area used by the system.

Whenever the message SAVE AREA n appears in the upper right corner of the display, type the following command to resume analysis of the original study.

```
RS 0(RET)
```

RR

5.17.4 Read Regions of Interest

The Read Regions of Interest command (RR) reads regions of interest information from a specified save area and overlays this information on the currently displayed frame.

Command format:

```
RR n(RET)
```

where n represents a specified save area. Save area n must contain matrix data with region of interest information. The regions of interest program is automatically called. This operation allows you to define regions of interest in one study, save them, and then apply them to another study. See Chapter 7.

DS

5.17.5 Delete Save Area

The Delete Save Area command (DS) deletes any of the optional save areas (10-64).

Command format:

```
DS n(RET)
```

where n represents a specified save area. This command is useful for eliminating data from the disk if it starts to approach capacity. (Each save area is 33 blocks long.) Save areas 0-9 cannot be deleted.

NOTE

A quick overview of the save area commands follows:

The result of the SA n command is to display the matrix stored in save area n. If a save area is read with the RS n command, the matrix in save area n is displayed with regions of interest, and the system enters region of interest mode. If a save area is read with the RR n command, the regions of interest stored in save area n are superimposed on the core-resident matrix.

S9

5.18 SMOOTHING COMMAND

If statistical noise (i.e., low counts) results in an erratic image, you can still extract meaningful information from the data. GAMMA-11 reduces noise by a smoothing process, leaving a somewhat clearer image. Successive smoothing applications may increase clarity, but at the expense of data, as a certain amount of information is lost each time.

In the smoothing process, each cell is averaged with its neighbors, after weighting the cell counts. If a cell count is greatly different from those around it, the smoothing process brings it more nearly in line with its neighbors.

The Nine-Point Smooth command (S9) applies a weight of 4 to a cell and a weight of 1 to each neighboring corner cell and a weight of 2 to each cell directly next to or below the weighted 4 cell. Type the following command on the terminal to perform a nine-point smooth.

```
S9 RET
```

The value of the cell (which is represented by the diagram below) in the center is multiplied by 4 and each of the surrounding cells is multiplied by 1 or 2. The values of all the cells are added together and then divided by 16.

```
1 2 1
2 4 2
1 2 1
```

When the process is complete, the screen is erased, and the resulting frame is displayed. The effect of smoothing is shown in Figures 5-14 and 5-15.

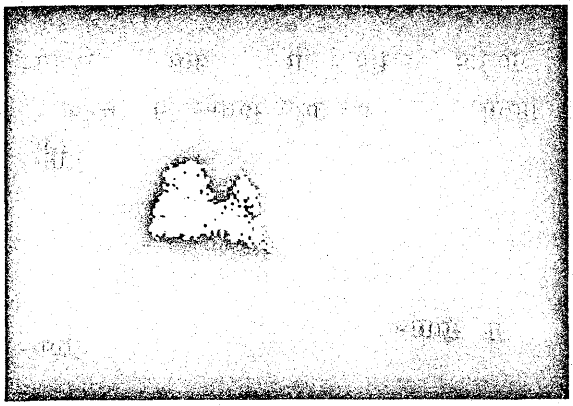


Figure 5-14
Original Matrix

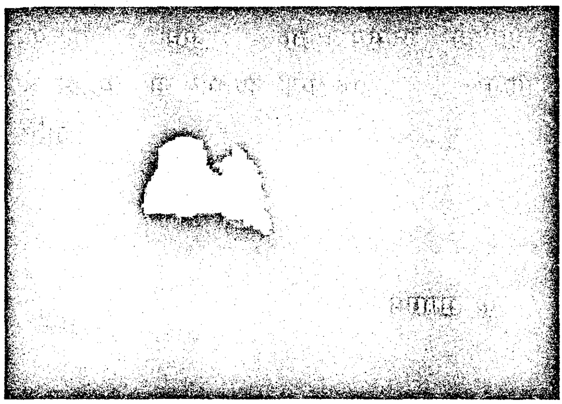


Figure 5-15
Nine-Point Smooth

5.19 ISOCONTOUR COMMANDS

An isocontour is a line which separates those cells above a given count level from those that are below the count level. Isocontours make the visualization of some image features easier. For example, an isocontour can be the outline of an organ or the outline of a ventricular wall. These commands are discussed in Sections 5.19.1 and 5.19.2.

IC

5.19.1 Isocontour Map

The Isocontour Map command (IC) converts a data matrix into an isocontour matrix using 1 to 15 isocontour lines. The command format is:

```
IC f,s,n(RET)
```

where:

f	is the first isocontour level, expressed as a percentage of total number of counts; i.e., a threshold level.
s	is a positive or negative threshold step size.
n	is the optional number of threshold levels that are generated from the image (from 1 to 15).

The isocontour map is generated at the following threshold levels:

```
f, f+s, f+2s,...,f+14s
```

The threshold level cannot be greater than 100 or less than 0. If s and n are absent, only one level is generated. If n is absent, as many levels as possible are generated up to a maximum of 15. The maximum number of levels that can be used in one image is 15.

The data matrix is converted into an isocontour matrix. A cell count of 15 is used for the highest isocontour level. The cell counts of the lower isocontours have evenly distributed lower cell counts. Thus, each isocontour is represented by a different cell count and intensity level.

Examples:

IC commands	Levels generated at
IC 50	50
IC 50, 10	50, 60, 70, 80, 90, 100
IC 60, -10	60, 50, 40, 30, 20, 10
IC 60, -20, 2	60, 40

Figures 5-16 and 5-17 (color insert) show a normal image of the lungs and an isocontour image, respectively.

NOTE

> Isocontours generally look better if you have smoothed the data first.

ICF

5.19.2 Isocontour Fill

The Isocontour Fill command (ICF) is similar to the isocontour map command except that it fills the interior of the isocontours. The command format is:

```
ICF f,s,n RET
```

where:

f	is the first isocontour level, expressed as a percentage of the threshold level.
s	is a positive or negative threshold step size.
n	is the number of levels that are generated from the image.

The threshold level cannot be greater than 100 or less than 0. If n is absent, as many levels as possible are generated up to a maximum of 15. The maximum number of levels that can be used in one image is 15. Compare Figure 5-16, a normal image to Figure 5-18 (color insert).

A good example (Figure 5-19) of using both of the isocontour commands (map and fill) is:

1. Smooth the data twice by typing

   ```
   S9;S9(RET)
   ```

2. Blow-up the image for enhancement by typing

   ```
   BU(RET)
   ```

3. Define the isocontour map and save it in save area 1. Type

   ```
   IC 20,20(RET)
   SM1(RET)
   ```

4. Fill the isocontour and save it in save area 2 by typing

   ```
   ICF 20,20(RET)
   SM2(RET)
   ```

5. Add the two save areas by typing

   ```
   SA1+2(RET)
   ```

   Notice that Figure 5-19 is a combination of mapping and filling isocontours.

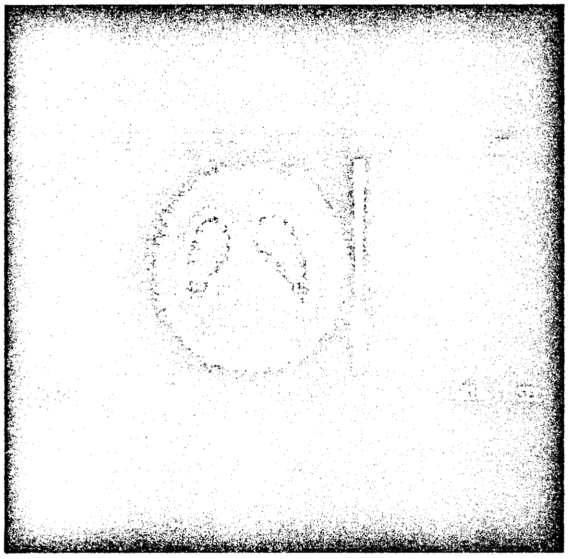


Figure 5-16
Lung-Normal Image

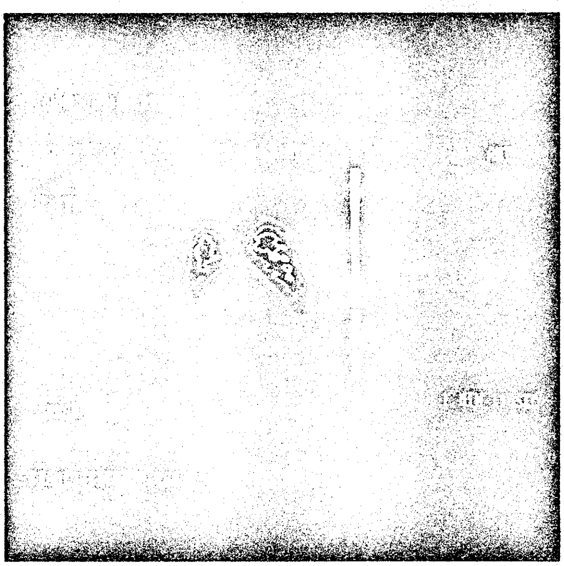


Figure 5-17
Isocontour Map

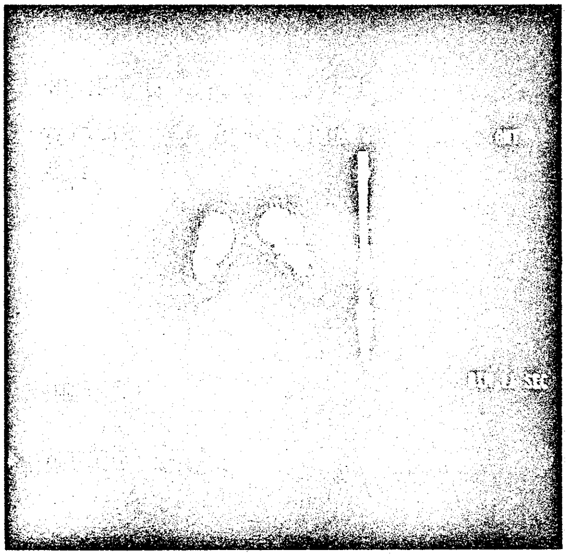


Figure 5-18
Isocontour Fill

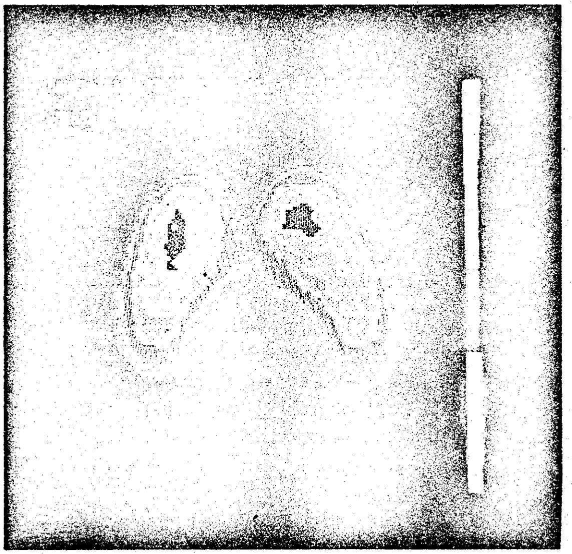


Figure 5-19
Isocontour Map and Fill

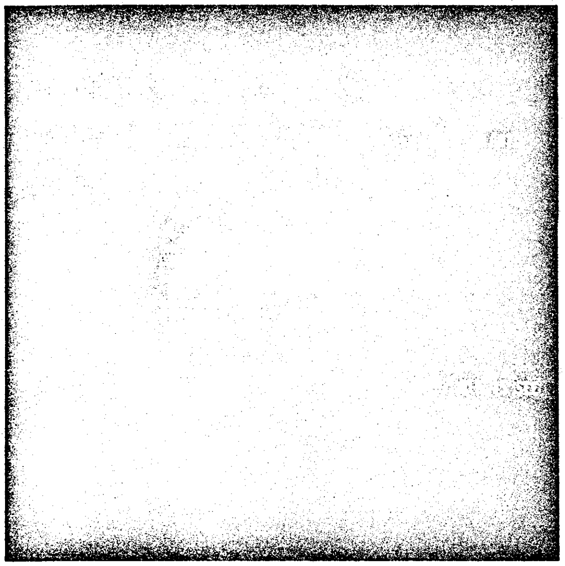


Figure 5-20
Normal Liver/Spleen Display

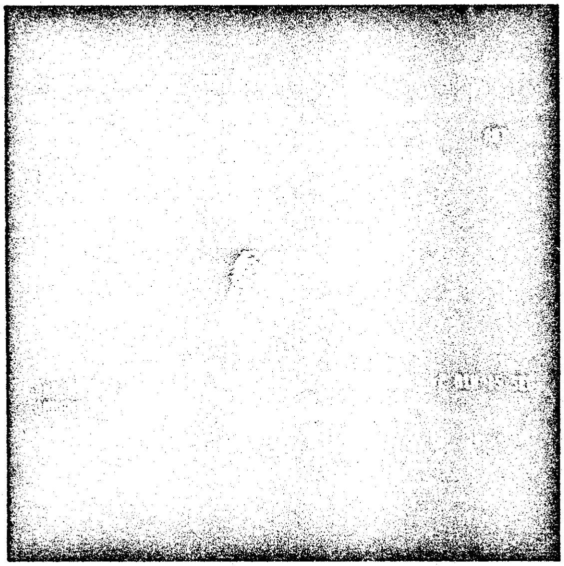


Figure 5-21
Isometrics Display

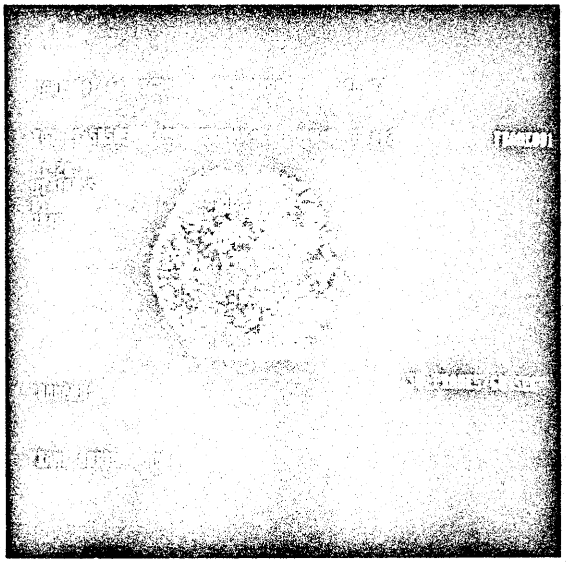


Figure 5-22A
Data Rotated 90 Degrees

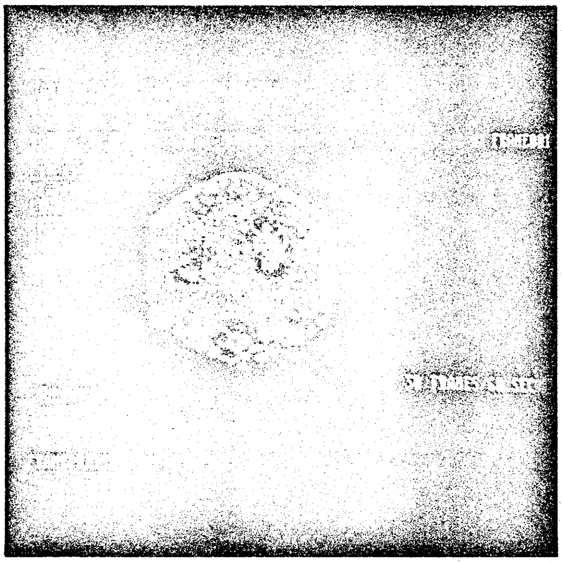


Figure 5-22B
Data Rotated 180 Degrees

5.20 ISOMETRIC COMMANDS

Isometrics are displayed in two different ways. The color display shows a modulated 3-dimensional to a 2-dimensional intensity image. This image is defined as being volumetric. That is the intensity levels reside in the Z-axis. The VT01 displays the 3-dimensional image using a line representation of the intensity. These commands are described in Sections 5.20.1 and 5.20.2.

ID

5.20.1 Isometrics Display

The Isometrics Display command (ID) displays data in an isometric pattern or a 3-dimensional mode. Type:

```
ID RET
```

This command causes all subsequent images to be presented in a 3-dimensional mode. Figures 5-20 and 5-21 (color insert) show a normal color image and its corresponding isometrics. Notice that the highest points on the Z-axis represent the cells with the highest count level. Refer to Chapter 6 for an explanation of color intensities.

On the VT01 only, the isometrics display command is also useful for displaying four minified isometric displays.

```
ID;DM RET
```

Figure 5-23 shows the minified isometrics display. Also notice that the figure is (from the VT01) in a line isometric mode instead of being volumetric as displayed on the color display.

NOTE

> The color display does not have the capability of displaying isometrics in minified form.

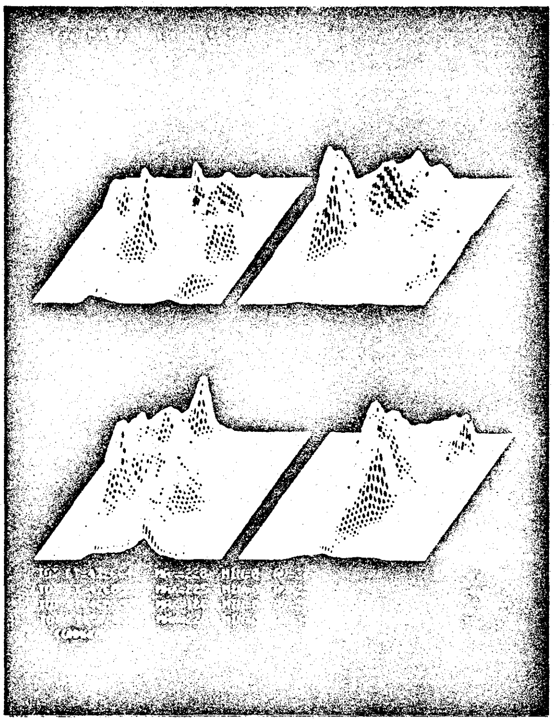


Figure 5-23
Minified Isometrics

DN

5.20.2 Display Normal

The Display Normal command (DN) converts an image from an isometrics display to the normal display mode and intensity. Type:

```
DN(RET)
```

The size of the display frame (i.e., full size or minified) is unaffected by the DN command.

5.21 IMAGE ROTATION AND TRANSLATION COMMANDS

Data that is core resident can be rotated, and a rotation mode can be set for subsequent data which is read from a patient file. Rotation enables you to manipulate any data that is read from a patient file. This process is performed via the Rotate Data command procedure.

A matrix can also be translated vertically or horizontally -- that is, moved up, down, left or right on the display. Translation is done using the Translate Vertical or Translate Horizontal command.

RO

5.21.1 Rotate Data

Any data read from a patient file automatically rotates clockwise 90, 180, or 270 degrees when the Rotate Data command (RO) is issued. The command format is:

```
RO n(RET)
```

where n = 1, 2, or 3.

The parameter n is the number of 90 degree clockwise rotations desired. Thus, if you type the following command, all data is rotated 180 degrees (two 90 degree rotations).

```
RO 2(RET)
```

Data that are read after you have issued the RO command are automatically rotated when displayed. The rotation (ROn) appears below the threshold information to indicate that the data has been rotated. On the VT01, the rotation (R n) appears to the right.

When you issue additional rotate commands, the rotation parameter (n) is added to the current parameter. That is, if you type RO2 followed by another RO2, the display is in the upright position (0 degrees). If you type RO2 followed by RO3, the display is in the 90 degree position.

Figure 5-22A (color insert) displays data that has been rotated 90 degrees and Figure 5-22B (color insert) displays data that has been rotated 180 degrees. The following drawings, Figures 5-24A and 5-24B also show rotated data.

The rotate data command is especially useful for isometric displays or for patient study data that is not acquired in the correct orientation. For example, you could use the minified display command to show each rotation as a minified image.

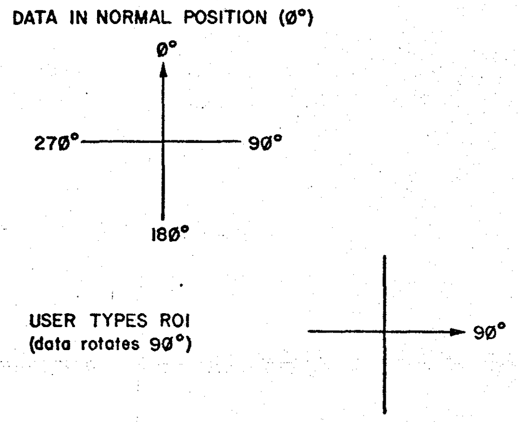


Figure 5-24A
90° Rotation

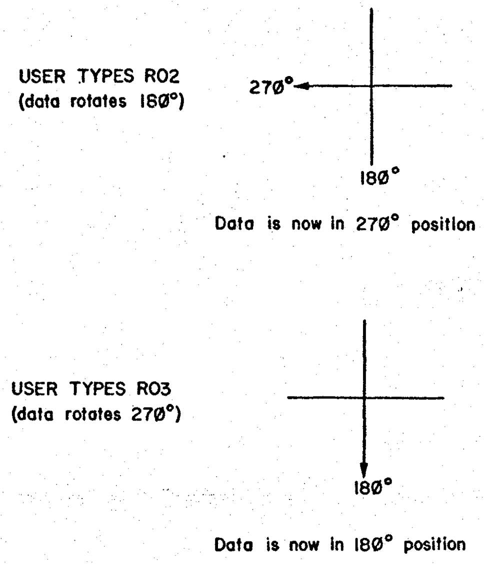


Figure 5-24B
180° Rotation

5.21.2 Translate Vertical

The Translate Vertical command (TV) has the two forms:

TVn RET
TV-n RET

If you use TVn, the matrix is moved up on the display n rows. The top n rows are lost. If you use TV-n, the matrix is moved down on the display n rows. The bottom n rows are lost.

The TV command sets a prevailing mode. Once you have typed the command, the system will display all subsequent frames similarly until you issue a BE command or analyze a new study.

Figure 5-25A shows a full matrix. Figure 5-25B shows the matrix after a TV20 command has been given.

5.21.3 Translate Horizontal

The Translate Horizontal command (TH) has the two forms:

```
THn(RET)
TH-n(RET)
```

If you use THn, the matrix is moved right on the display n rows. The rightmost n rows are lost. If you use TH-n, the matrix is moved left on the display n rows. The leftmost n rows are lost.

Like the TV command, the TH command sets a prevailing mode. Once you have typed the TH command, all subsequent frames are displayed similarly until you issue a BE command or analyze a new study.

Figure 5-25C shows a matrix after a TH-20 command has been given.

NOTE

Both the Rotate (RO) and Translate (TV,TH) commands set prevailing modes. If both are in effect, rotation is always done prior to translation.

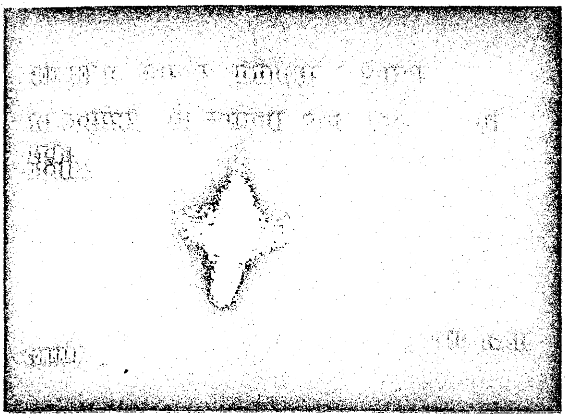


Figure 5-25A
Full Size Matrix

Figure 5-25B
TV20

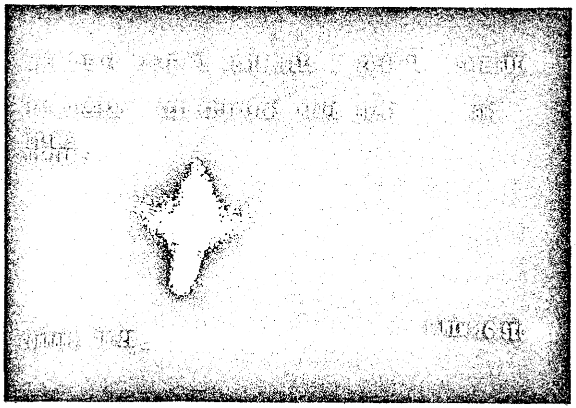


Figure 5-25C
TH-20

NOTE

The prevailing modes set by the Rotate (RO) and Translate (TV,TH) commands affect only the patient files and not the save areas.

5.22 COMMENT EDITOR COMMANDS

At any time during the examination of a study, you may edit or add to the comments associated with the study. The comment editor is a small set of operations obtained by issuing the Call Comment Editor command.

CO

5.22.1 Call Comment Editor

The Call Comment Editor command (CO) stores the current display in save area 0. The screen is erased and the comments associated with study are displayed. Type:

```
CO RET
```

The following request appears beneath the text.

```
EDIT COMMAND
```

If there are no comments, the request appears alone. Each displayed line is numbered for reference. The numbers are not part of the commentary. An example is shown in Figure 5-26.

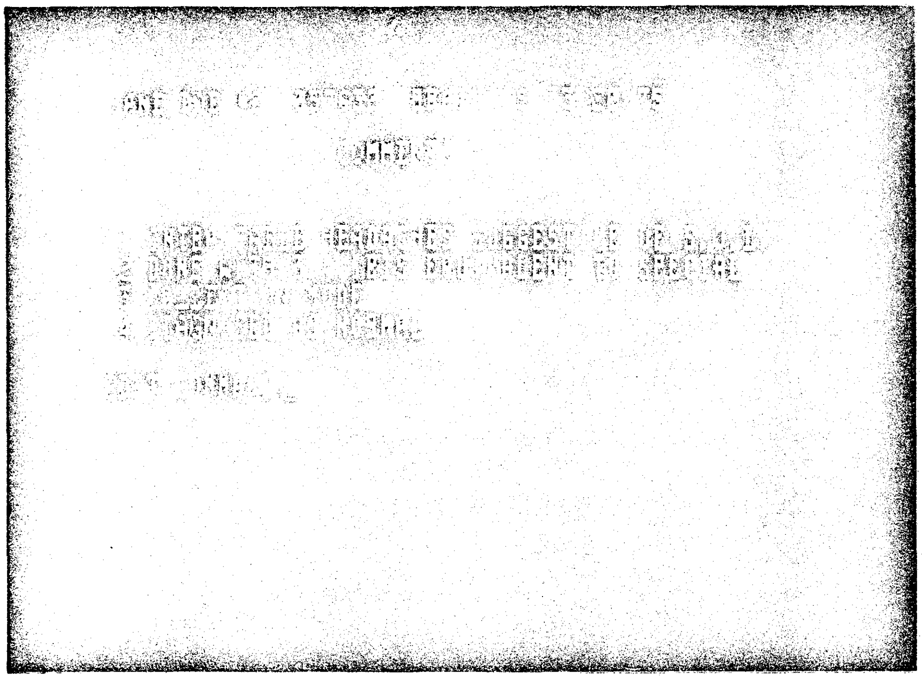


Figure 5-26
Comment Text

When the EDIT COMMAND message appears, you may use any of the following editing commands.

A RET	Append	Comments are added to the end of the displayed text. An asterisk is displayed to identify the beginning of the new text. You can enter the desired commentary. The entire block of text may not exceed ten lines of up to 49 characters each. Terminate the text by typing a null line, that is, two RETURNs in a row.
R n RET	Replace line n	An asterisk is displayed and you must enter one line of text (maximum 49 characters), terminated by a RETURN. The new line will replace line n.
D RET	Display Edited Text	The screen is erased, and the newly edited comments are displayed. Further editing is possible. This is generally used to clean up the display and verify the edited comments.
RET	Edit and Return	When you type a RETURN as an EDIT COMMAND response, the edited text is written into the comment block of the study on the disk. The previously saved frame reappears.

P(RET)	Print	The contents of the data that are being edited are redisplayed on the screen and printed on the console terminal.
CTRL/X	Direct Return	The edited comments are not written into the file. Control returns immediately to the last frame displayed. The original comments are unaffected.

5.23 KEYBOARD ECHO-PRINT COMMANDS

Normally, keyboard input does not appear on the terminal's printer when it is typed, though most entries are displayed on the screen. To obtain a printer echo of all typed input, use the commands in Sections 5.23.1 and 5.23.2.

EC

5.23.1 Echo Keyboard Input

The Echo Keyboard Characters command (EC) echoes all keyboard characters on the terminal printer. Type:

EC(RET)

The echo mode remains in effect until the NC command is given. Region of interest commands (Chapter 7) are never echoed.

NC

5.23.2 No Echo

The No Echo command (NC) does not print keyboard input on the terminal printer. Type:

NC(RET)

TE

5.23.3 Text

At any time, during data analysis, a line of text may be displayed on the screen to provide useful comments about the data. The command to display text is:

```
TE text RET
```

All characters up to the carriage return are displayed on the screen in the command line. The text is automatically stored with the matrix if you then store the matrix in a save area. If you recall the matrix by reading the save area, the text is displayed once again.

5.24 DATA ANALYSIS MACRO COMMANDS

A data analysis macro is a sequence of predefined data analysis commands. These sequences can be entered once into a macro file and can then be executed (at a later time) with a simple Macro Run command. For example, you may find that whenever regions of interest is used, certain data manipulations prior to calling regions of interest occur; that is, adding frames, smoothing, thresholding. You can predefine these set-up commands by using a macro, and from then on, simply call the macro and automatically execute the commands.

The macro facility of the data analysis program also allows you to create, edit, execute, save, or retrieve macro files. A macro consists of 1 to 10 command lines, each command line containing up to 49 characters.

The data analysis program has a resident macro buffer for the macro currently in use. You can save the macro buffer on the system device and load it from the system device by name. The same editor that is used to edit the patient comment block is used to edit the macro buffer.

The general format of a macro command is:

```
Mz filename RET
```

where z is a mnemonic for the specified command (e.g., MS for macro save or MR for macro run). The filename is the name of the file on the system device that contains the macro. A filename must consist of 1 to 6 alphanumeric characters (a combination of A-Z and 0-9).

Sections 5.24.1 through 5.24.12 explain how the macro commands work. Section 5.24.13 will give a complete example of how to create and run a macro.

MC

5.24.1 Macro Create

The Macro Create command (MC) clears the macro buffer and automatically calls and appends to the macro editor. The command format to create a new macro is:

MC filename(RET)

The commands to create a file in the macro editor are the same for the comment editor. At this point you are ready to type in your macro.

The filename replaces the current macro file name. If filename is absent, the current macro file name is cleared (replaced with nulls). That is, the current macro file name is undefined. You should enter a macro file name during macro create, but it is not necessary.

If you want to save your macro, a MS, macro save command should follow the macro create.

ME

5.24.2 Macro Edit

The command used to call the macro editor is:

ME filename(RET)

The filename is the name of the file to be edited. If the filename is absent, the current contents of the core-resident macro buffer are edited. The same editor is used to edit both the macro buffer and the patient study comment block. During macro buffer editing the following heading appears at the top of the screen.

MACRO filename

Take special note that this macro editor command edits only the contents of the macro buffer and not the macro file on the system device.

When the EDIT COMMAND message appears, you may use any of the following editing commands.

A(RET)	Append	Macro lines are added to the end of the displayed text. An asterisk is displayed to identify the beginning of the new text. You can enter the desired macro commands. The entire block of text may not exceed ten lines of up to 49 characters each. Terminate the text by typing a null line, that is, two RETURNs in a row.
R n(RET)	Replace line n	An asterisk is displayed and you must enter one line of text (maximum 49 characters), terminated by a RETURN. The new line will replace line n.
D(RET)	Display Edited Text	The screen is erased, and the newly edited macro is displayed. Further editing is possible. This is generally used to clean up the display and verify the edited macro.
(RET)	Edit and Return	When you type a RETURN as an EDIT COMMAND response, the edited text is written into the macro buffer of the study on the disk. The previously saved frame reappears.
P(RET)	Print	The contents of the data that are being edited are redisplayed on the screen and printed on the console terminal.
CTRL/X	Direct Return	The edited macro is not written into the file. Control returns immediately to the last frame displayed. The original macro is unaffected.

CAUTION

During the macro buffer editing, the macro file on the system device is not updated. Only the contents of the macro buffer are modified. To save the edited macro use the macro save command, MS (see Section 5.24.5).

ML

5.24.3 Macro Load

The Macro Load command (ML) loads the macro buffer with the contents of a macro file on the system device. The command format is:

```
ML filename RET
```

The filename MUST be specified. The previous contents of the macro buffer are lost and the specified filename becomes the current macro file name. This command does not execute the macro, but just loads the buffer. To execute the macro, use the macro run command.

MR

5.24.4 Macro Run

The Macro Run command (MR) executes a macro. The command format is:

```
MR filename,n RET
```

where n is the line number (1-10) at which execution is to begin. Filename is the name of the macro file on the system device. This command loads the macro buffer with the contents of the named macro file and begins execution at line n. If filename is omitted, the contents of the current macro buffer are executed. If n is omitted, execution begins at line 1. The specified filename becomes the current macro file name. Each command in the macro buffer is automatically executed.

Execution of a macro can be stopped in four ways:

1. The system executes the macro exit (MX) command within the macro.
2. The system reaches the end of a macro buffer (finishes the macro).
3. You type a DELETE on the console terminal.
4. The system detects an error during execution.

If you type a DELETE to stop execution, execution is not stopped until the command being executed is finished. Thus, execution may stop immediately, or in the case of some commands, it may take a few seconds.

The system suspends execution of a macro if it executes a command requiring operator response (i.e., RI, IR, SH, or SV). When the operator has made the required responses and then types CTRL/X, the system resumes execution of the macro from the point at which it was suspended.

The MR command is optional if the first two letters of the macro name are not a legal GAMMA-11 command. If you type a command that is not a GAMMA-11 command, GAMMA-11 assumes that it is a macro name and attempts to execute that macro.

For example, if you have a macro called HEART and you type in

```
HEART(RET)
```

it will be treated as if you had typed

```
MR HEART(RET)
```

However, if you type

```
SKIP(RET)
```

SKIP will be treated as the SK command, not as the macro SKIP. In this case, you must type

```
MR SKIP(RET)
```

to execute the macro.

If you have made a typographical error, and the letters you typed are neither a command nor a macro name, the system issues an error message.

MS

5.24.5 Macro Save

The Macro Save command (MS) saves the current contents of the macro buffer as a file on the system device. The command format is:

```
MS filename (RET)
```

The filename must be unique (i.e., a file of that name must not already exist on the system device). If the filename is not unique, the system returns an error message, and you must change the filename. If you do not specify the filename, the current macro name is used, and this macro filename need not be unique.

If the current macro in the buffer does not have a name, you must type:

```
MS filename(RET)
```

The program does not prompt you to type a filename.

If the macro in the buffer already has a name, and you want to save this version under the same name, type:

```
MS(RET)
```

You will get an error message if you try to type the same filename as the macro currently in the buffer. You can type a different filename to create a new macro.

MD

5.24.6 Macro Delete

The Macro Delete command (MD) deletes a macro file from the system device. The command format is:

```
MD filename(RET)
```

The filename MUST be specified. When you issue the Macro Delete command, neither the contents of the current macro buffer nor the current macro filename is affected.

MX

5.24.7 Macro Exit

The Macro Exit command (MX) stops execution of the macro. The command format is:

```
MX(RET)
```

Execution of the macro exit command immediately returns control to the console terminal.

//

5.24.8 The Comment Line

You can insert comment lines or operator instructions in a macro. These comments are printed on the console terminal when the macro is executed. The command format is:

```
//text(RET)
```

When the command is executed all text following the slashes (//) up to and including the RETURN is printed on the console terminal.

For example,

```
LT10;UT80;S9(RET)
//DEFINE ROI'S OVER LEFT AND RIGHT HEMISPHERES(RET)
//PLOT OVERLAID DYNAMIC CURVES(RET)
IR(RET)
SD5(RET)
```

The above example sets the lower and upper thresholds, smooths the image, prints the text on the console and calls the irregular regions of interest routine. It also suspends operation of the macro. Upon returning from the irregular regions of interest routine when the operator types CTRL/X, the macro resumes operation and the curves are stored in save area 5.

EL

5.24.9 Execute Line

The Execute Line command (EL) executes one line of the macro buffer. The command format is:

```
EL n(RET)
```

where n is a line number contained in the macro buffer. If n is omitted, the current command line is re-executed.

5.24.10 Listing Macro Files

The actual RT-11 file name of a macro is:

```
filename.GMC
```

Thus, by using the DIRECTORY monitor command (with the file specification *.GMC) you can obtain a directory listing of all GAMMA-11 macro files. To obtain this list of all the macro files, type the following monitor command:

```
DIR *.GMC(RET)
```

Remember that a monitor command is not a GAMMA-11 command.

Since the macro is an ASCII file, the contents of a macro can be listed by the monitor command TYPE. For example,

```
TYPE PLAY.GMC(RET)
```

lists the contents of the macro file, PLAY, on the console terminal.

5.24.11 The Repeat-line Command

To repeat a whole line of GAMMA-11 commands any number of times, type the number of times as the first command in the line followed by a colon. For example,

```
48:S9;PBS;SK(RET)
```

will execute the line

```
S9;PBS;SK
```

48 times. The general form of the repeat-line command is:

```
n: line of commands(RET)
```

As the command line is being repeated, the message

```
REPEAT  m
```

is displayed. The m is the number of times that the command line has been executed.

5.24.12 The Conditional Command

When the command line processor detects an error in a command line, command execution stops. Occasionally, you may expect an error condition and would rather that execution not stop. For example, upon reaching the end of a study with a skip command, you may wish to continue processing the command line rather than stopping execution.

To denote this expected error condition to GAMMA-11, type an exclamation point (!) before the command to be tested for an error. For example:

```
!SK 10(RET)
```

This command will skip 10 frames if it is possible. If it is not possible to skip 10 frames, no error message is generated. Instead, control passes to the next command line of a macro. The exclamation point immediately precedes the command to be checked.

For example, suppose you have the following macro:

```
(1)  PBI GSA,0,48,1 (Create a playback buffer with 48 frames)
(2)  48: PBS;!SK    (fill the playback buffer)
(3)  PB GSA         (playback the  buffer)
```

Line (1) initializes a playback buffer named GSA with a 48 frame capacity. If the study has 48 frames or more, then there is no problem in line (2) which fills the buffer. However, if there are less than 48 frames, an error will occur which will stop the macro without ever having executed line (3) unless you have the '!'.

The form of the conditional is:

```
!command RET
```

If the command can be executed, the system executes it. If the command cannot be executed, control will pass to the next command line of a macro. If the command is not in a macro, command processing will stop with no error indication given.

?

5.24.13 Inputting Commands While Running a Macro

To request input from the operator at the time a macro is run, put a question mark ('?') as the first character of a macro line. Explanatory text may follow the question mark. For example, the following macro command:

```
?SET THE THRESHOLD LEVELS RET
```

will display the text (SET THE THRESHOLD LEVELS), then will display:

```
COMMAND:
```

The macro processor then waits for the operator to type in one line of commands, executes that command line, and finally continues executing the macro. The text following the question mark is displayed but ignored by the system. A question mark appearing anywhere but the first position of a macro command line is considered an error.

5.24.14 A Macro Example

Suppose that you usually want to play back your in-core gate-synchronized studies in movie mode. If you know that you will normally acquire 48 frames, you can write a macro called GSA which will do all of the following:

1. Initialize the playback buffer.
2. Fill the buffer.
3. Play back the buffer in movie mode.

The steps involved in writing and saving this macro are listed below:

1. Type MC GSA(RET) to create this macro.

2. The GAMMA-11 will respond with an asterisk (*). Now you can type in your macro as follows:

```
*PBI GSA,0,48,1(RET)
*48:PBS;!SK(RET)
*PB GSA(RET)
*(RET)
```

3. A RETURN will get you out of typing a macro. The GAMMA-11 will respond with:

```
EDIT COMMAND
```

   Here you can use any of the editor commands listed in Section 5.24.2. A RETURN will get you out of the editor and back into the study.

4. Once you are back in the study, to save the macro type:

```
MS(RET)
```

5. Now, to run the macro at any time, in any of your gate-synchronized studies, type:

```
MR GSA(RET)
```

   The playback buffer will automatically be initialized, filled, and played back.

5.25 LANGUAGE EXECUTION COMMANDS

Three commands (BA, RU, and FO) run user-written BASIC, FORTRAN and FOCAL programs. These commands run directly from the GAMMA-11 data analysis program without the user having to exit from GAMMA-11. No typing of RT-11 commands is necessary.

The form of the command is:

```
XX device:filename.ext(RET)
```

where XX is:

BA	for BASIC
RU	for FORTRAN
FO	for FOCAL

and device:filename.ext is the standard RT-11 file description.

BA

5.25.1 BASIC

The BASIC command runs a user-written BASIC program from the GAMMA-11 data analysis program. The command format is:

```
BA device:filename.ext(RET)
```

If the BASIC program is on the system disk, you need to specify only the name of the program. For example, to run a BASIC program called QPQS.BAS, type:

```
BA QPQS(RET)
```

If the program is on a disk other than the system disk (or another device), the device descriptor must precede the program name. For example, if the QPQS.BAS program resides on disk unit 1, type:

```
BA RK1:QPQS(RET)
```

If the program name is not specified, the BASIC interpreter prints an error message and remains in the immediate mode. For more information pertaining to the BASIC language, please refer to the BASIC/RT-11 Language Reference Manual.

RU

5.25.2 FORTRAN

The FORTRAN command runs a user-written FORTRAN program or any RT-11 .SAV file from the GAMMA-11 data analysis program. The command format is:

```
RU device:filename.ext(RET)
```

If the FORTRAN program is on the system disk, you need specify only the name of the program. For example, to run a FORTRAN program called PAVIA.SAV, type:

```
RU PAVIA(RET)
```

If the program is on another device instead of the system disk, the device descriptor must precede the program name. For example, if the PAVIA.SAV program resides on disk unit 1, type:

```
RU RK1:PAVIA(RET)
```

For more information pertaining to the FORTRAN language, please refer to the PDP-11 FORTRAN Language Reference Manual.

FO

5.25.3 FOCAL

The FOCAL command runs a user-written FOCAL program from the GAMMA-11 data analysis program. The command format is:

```
FO device:filename.ext(RET)
```

If the FOCAL program is on the system disk, you need specify only the name of the program. For example, to run a FOCAL program called CAREY.FCL, type:

```
FO CAREY(RET)
```

If the program is on another device instead of the system disk, the device descriptor must precede the program name. For example, if the CAREY.FCL program resides on disk unit 1, type:

```
FO RK1:CAREY(RET)
```

If the program name is not specified, the FOCAL interpreter remains in the immediate mode. For more information pertaining to the FOCAL language, please refer to the FOCAL-11 User's Manual.

5.26 LIST MODE PROCESSING

To analyze list-mode data, you must structure (frame) the data collected in a list study in one of the five matrix configurations described previously (see Section 4.1). You can organize the data into a static or dynamic study. Frame rates other than those listed in Sections 4.2.12 and 4.2.13 can be used when you reformat the list study into a dynamic study. You can reframe the data at any time and more than once (in many different ways). Finally, the framed data can be stored as a normal static or dynamic patient study file.

5.26.1 List Study Framing

When you select a list study from the patient study index, the study summary appears on the screen as in Figure 5-27.

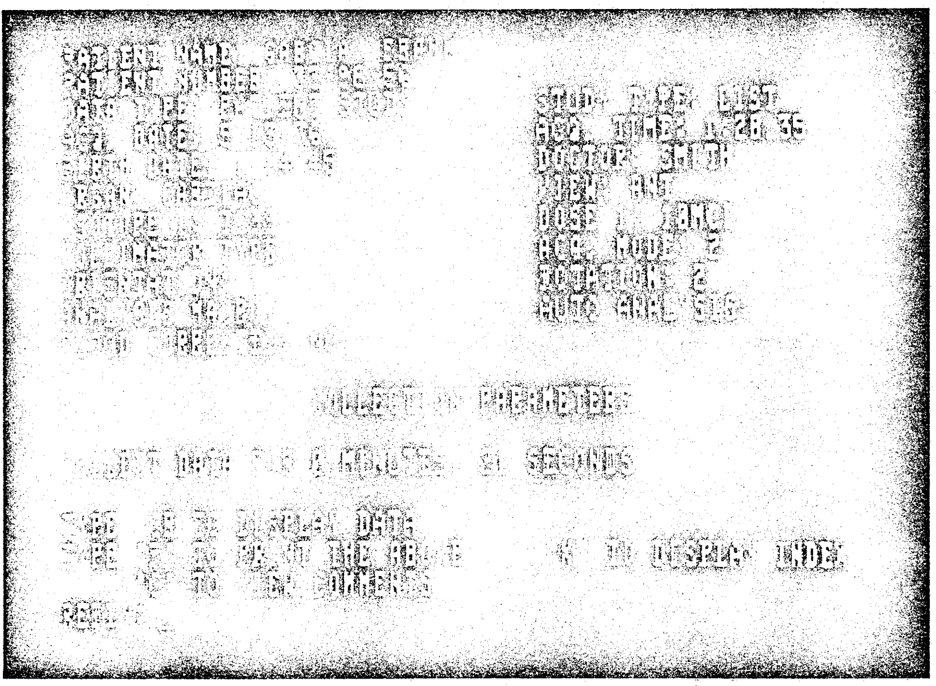
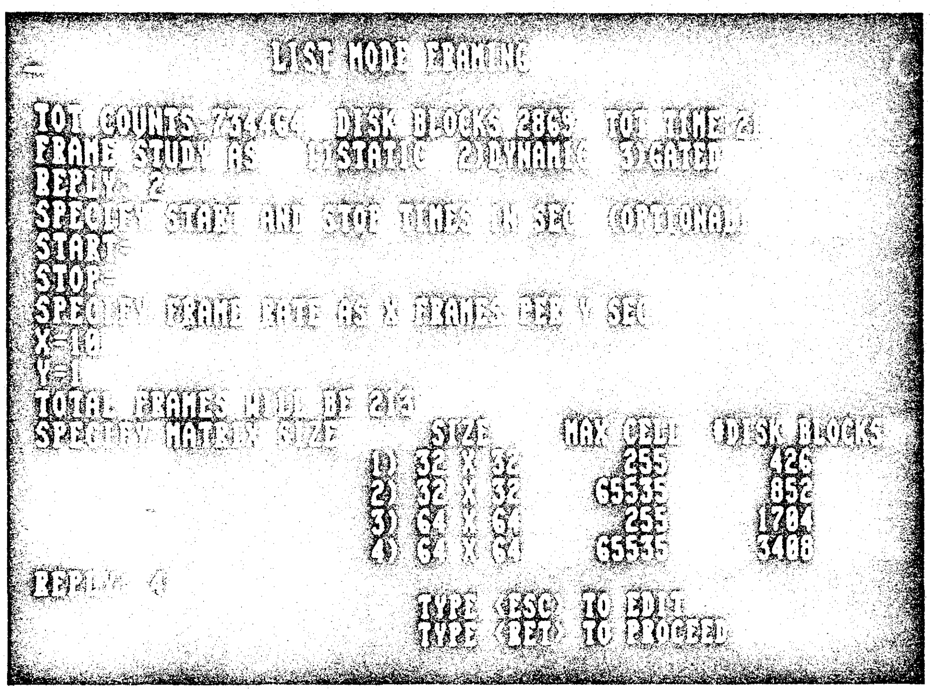


Figure 5-27
List Study Summary

The collection parameters show the starting point and duration of the collection run. The P and C options operate as described in Section 5.1.1.

To begin the list framing procedure, press RETURN. The procedure is a question and answer sequence similar to that for defining a study plan. That is, the error-correcting methods for a list study and those of a static or dynamic study, are the same (see Section 3.3.2). A complete framing sequence is shown in Figure 5-28.



```
              LIST MODE FRAMING

TOT COUNTS 734464  DISK BLOCKS 2869  TOT TIME 2
FRAME STUDY AS   1)STATIC  2)DYNAMIC  3)GATED
REPLY> 2
SPECIFY START AND STOP TIMES IN SEC (OPTIONAL)
START=
STOP=
SPECIFY FRAME RATE AS X FRAMES PER Y SEC
X=10
Y=1
TOTAL FRAMES WILL BE 213
SPECIFY MATRIX SIZE       SIZE     MAX CELL  (DISK BLOCKS)
                      1) 32 X 32     255       426
                      2) 32 X 32   65535       852
                      3) 64 X 64     255      1704
                      4) 64 X 64   65535      3408
REPLY> 4
                         TYPE <ESC> TO EDIT
                         TYPE <RET> TO PROCEED
```

Figure 5-28
List Framing Sequence

The first four lines of a list framing sequence are displayed immediately after you press RETURN.

TOT COUNTS: DISK BLOCKS: TOT TIME:

The items in the line above are, respectively, the total number of counts collected, the number of disk blocks occupied by the list, and the duration of the collection run. The next line requests a reply to the type of study that is applicable.

```
FRAME STUDY AS      1)STATIC
                    2)DYNAMIC
                    3)GATED
```

(Refer to Section 5.27 for gated list mode processing.) The next line appears as:

```
SPECIFY START AND STOP TIMES IN SEC (OPTIONAL)
START=
STOP=
```

The starting and stopping times are optional, and you do not have to frame the entire study. For example, if the duration of the study is 42 seconds, you can frame the data collected between 10 and 35 seconds of the run. Either limit may be skipped by pressing RETURN for each limit. If you press RETURN only for START and enter a number for STOP, the system assumes zero for the STARTING time. If you press RETURN only for STOP, the system assumes the maximum time in the study (TOTAL TIME) for STOPPING time. The next request is:

```
SPECIFY FRAME RATE AS X FRAMES PER Y SEC
X=
Y=
```

This question is asked only if you have selected a dynamic study. The frame rate is subject to the following restrictions:

1. The fastest permitted rate is 100 frames/second.
2. The rate must be an integral multiple of 10 milliseconds, the interval between timing marks in the list. Thus, 4 frames/sec (1 every 250 msec) is acceptable, but 3 frames/sec (1 every 333 1/3 msec) is not. If you select an inadmissible rate, the program offers the nearest permitted alternative. For example, if you specify 3 frames/sec, the program offers 100 frames every 33 seconds as an alternative. You may accept this by pressing RETURN, or pressing ESCape to enter a new rate.
3. No more than 511 frames can be made from any one study.

The next line displayed is:

```
TOTAL NUMBER OF FRAMES IS xxx
ONLY THE FIRST 511 WILL BE FRAMED
```

The first line gives the total number of frames (xxx) possible over the specified period at the given rate. If this total is greater than 511, the second line is also displayed. The next line is displayed and the possible matrix configurations are listed.

```
SPECIFY MATRIX SIZE
```

You should select the number of the desired matrix configuration. The 128 x 128 matrix is available only for a static study.

You press ESCape to edit the framing parameters or press RETURN to proceed to the next step.

5.26.2 Storage Options

When you have accepted the framing parameters, the system scans the list mode data. If you have chosen a dynamic study, the system sets up a table of framing pointers and displays disk storage options on the screen as follows:

```
IF YOU WISH DATA CAN OVERLAY LIST MODE DATA
FOR MATRIX TYPE 4 OR LESS
YOU HAVE SELECTED MATRIX TYPE 3

TYPE ALTMODE TO EDIT
     RETURN TO DISPLAY DATA

TO SAVE FRAMED DATA

     1) BY OVERLAYING LIST MODE DATA
     2) BY CREATING A NEW STUDY

REPLY:
```

The first statement of the storage option is:

```
     1) BY OVERLAYING LIST MODE DATA
```

If you wish to save framed data by overlaying the new study on top of the list mode data, you should type 1. This procedure, like all others that destroy data, requires verification. The following message is displayed:

```
OVERLAY CONFIRMATION
FRAMED DATA WILL REPLACE LIST MODE DATA
TYPE "YES" TO INITIATE OVERLAY PROCEDURE
REPLY:
```

Type YES to confirm the procedure. The original list study data are lost, and the framed information, along with the administrative data, comments, and index entry, replaces the original study.

CAUTION

Original data are lost entirely when overlaying occurs. To avoid this problem transfer the list mode study to another device (i.e., magtape or another disk) before framing. If sufficient disk space is not available, an error message appears on the screen.

NOTE

> If the overlay procedure would result in the destruction of data that has not yet been framed, the program will not offer the overlay option. This situation usually arises when the count rate is low at the beginning of the study, and it can be overcome by reframing with a later starting time. The problem can be anticipated and avoided by specifying a delayed start during the acquisition run.

The second statement of the storage option is:

2) BY CREATING A NEW STUDY

If this option is selected, the following message is displayed.

```
DISK UNIT:
```

Enter the disk unit number (0-7) where the new study is going to be saved. Typing only a carriage return saves the study on disk unit 0. The system adds the study with its administrative data and comments to the patient file, and adds a new entry to the patient study index. Then the system displays the first frame of the study. The program is still in list mode, as indicated by the "LM" note on the screen. To access the saved study as a normal study, type CTRL/X and select the study from the index. However, if there is not enough room on the disk to save the framed study, the following error message appears:

```
NOT ENOUGH ROOM FOR FRAMED DATA ON UNIT N
```

At this point, you may press ESCape to edit, press carriage return to display data, or enter a new disk number.

FR

5.26.3 Display Frame Command

Each frame of the structured study is identified by the note "LM" that appears at the bottom of the screen. Otherwise, the display is as usual, and the formatted study is now a static or dynamic study. All display and analysis commands are permitted in list mode. In addition, the following command is available whenever a list study is being displayed:

FR(RET)	Recall framing routine The system recalls the framing sequence (see Section 5.26.1) so that you can change the framing parameters or save the framed data as a study. Typing FR RETURN has the same effect as typing an ESCape after completing the framing sequence.

5.26.4 Framing Method

The system frames a static study and temporarily stores it on the system disk. The system scans a dynamic study and sets up a table of timing pointers. The list data is then framed continuously (on the fly) as it is transferred to core for display. The framing is done at a rate of approximately 30,000 counts per second, so that for most studies there should be no noticeable delay in the production of a display frame. The original scan, however, does require a detectable amount of time, which could become tedious if you change the framing parameters several times. The framing program saves time when you change parameters by attempting to build a new pointer table from the old one. This can be done if the old frame rate is multiple of the new one.

For example, if you want to change the rate of a list study from 4 frames/sec to 2 frames/sec, the system builds a new table from every other entry of the old one, removing the need for a complete rescan of the list.

5.27 GATED-LIST-MODE PROCESSING

A gated-list-mode study differs from a regular list-mode study in two ways:

1. Gate marks (triggers) occur only in the gated-list-mode study.

2. Time marks occur every millisecond in the gated-list-mode study instead of every ten milliseconds in the regular list-mode study.

A gated-list-mode study generates a representative cycle study similar to the in-core gate-synchronized study. Advantages of the gated-list-mode study not found in the in-core gate-synchronized study are:

1. You can combine high temporal resolution with high spatial resolution.

2. You can perform complete arrhythmia rejection.

3. You can begin formatting prior to the trigger (pretriggering).

At the same time, the gated-list-mode study has the following disadvantages:

1. RK05 disks can hold up to 1.2 million counts and RK06 disks up to 7.2 million.

2. Formatting time extends from 2 to 15 minutes, and longer in extreme cases.

3. The initial study requires large amounts of disk space.

4. The maximum count rate for acquisition is 70,000 counts/sec.

5.27.1 Gated-List-Mode Study Framing

A gated-list-mode study and a regular list-mode study have identical starting routines. The gated framing procedure begins at choice 3) GATED (see Section 5.26.1). Figure 5-29 shows a complete framing sequence.

After you press RETURN, the program immediately displays the first few lines of the gated list framing sequence.

The following line is the first line of the framing sequence.

```
        TOT COUNTS:     DISK BLOCKS:     TOT TIME:
```

TOTAL COUNTS is the number of counts collected, DISK BLOCKS is the number of occupied disk blocks, and TOTAL TIME is the duration of the collection run.

The program then prints:

```
    FRAME STUDY AS 1)STATIC 2)DYNAMIC 3)GATED
```

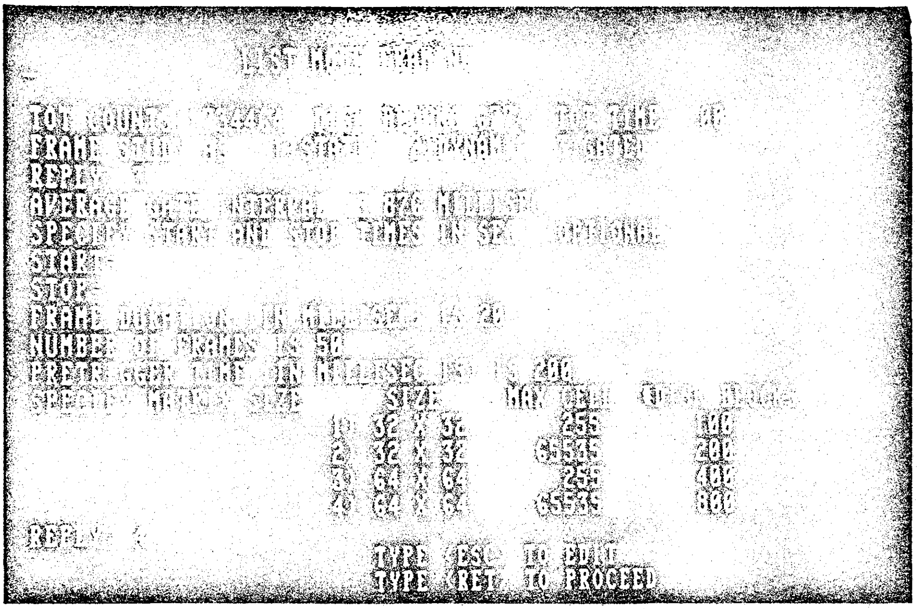
After you type 3, the following line appears:

```
    AVERAGE GATE INTERVAL IS xxx MILLISEC.
```

where xxx represents the number of milliseconds in the average gate interval. Next, the program prints:

```
    SPECIFY START AND STOP TIME IN SEC (OPTIONAL)
        START=
        STOP=
```

The starting and stopping times are optional, and you need not frame the entire study. For example, in a study of 300 second duration, you can frame the data collected between 10 and 200 seconds of the run. You have the option to press RETURN each time you wish to omit the starting limit or the stopping limit of the run. If you press RETURN for START and enter a number for STOP, the program will use zero as the starting time. Similarly, if you enter a number for START and press RETURN for STOP, the program will use the maximum time in the study for stopping time.



```
              [illegible]

TOT COUNTS [illegible]
FRAME [illegible]
REPLY [illegible]
AVERAGE [illegible] 1.87[illegible] MILLISEC
SPECIFY START AND STOP TIMES IN SEC [illegible]
START=
STOP=
FRAME DURATION (IN MILLISEC) IS 20
NUMBER OF FRAMES IS 50
PRETRIGGER TIME (IN MILLISEC) [illegible] IS 200
SPECIFY MATRIX SIZE        SIZE      MAX CELL   [illegible]
                       1) 32 X 32       255         [illegible]
                       2) 32 X 32     65535         200
                       3) 64 X 64       255         400
                       4) 64 X 64     65535         800
REPLY [illegible]
                         TYPE <ESC> TO EDIT
                         TYPE <RET> TO PROCEED
```

Figure 5-29
A Gated List Mode Framing Sequence

The next two questions asked are:

FRAME DURATION (IN MILLISEC) IS

and

NUMBER OF FRAMES IS

You may answer both of these questions and the program will use both of your answers; or you may answer one of the questions and default the response to the second. If you choose to answer only one of the questions, the program calculates the answer to the other using a complete cycle time.

Answering Only the Frame-Duration Question

Should you choose to answer only the frame-duration question, the following sequence would appear:

FRAME DURATION (IN MILLISEC) IS

You should respond to this question with the duration of a single frame in milliseconds. The program then calculates the number of frames required in order to generate an entire cycle by dividing the average cycle duration by the frame duration. This is displayed next as:

xxx FRAMES REQUIRED FOR A COMPLETE CYCLE

The next question is:

NUMBER OF FRAMES IS

which you default by typing a RETURN. If you default this question, the program uses the number of frames calculated for a complete cycle. The maximum number of frames is 511.

Answering Only the Number-of-Frames Question

When the following question appears:

FRAME DURATION (IN MILLISEC) IS

you respond by typing a RETURN to default the answer. If you default this question, the following question appears:

NUMBER OF FRAMES IS

You must answer this question if you defaulted the first. In this case, the frame duration is calculated by dividing the average cycle time (over the last 30 seconds) by your response to the number of frames.

No matter how you answered the FRAME DURATION and NUMBER OF FRAMES IS questions, in all cases you are then asked:

PRETRIGGER TIME (IN MILLISEC) IS

Here you enter the pretrigger time in milliseconds. This is the time PRIOR to the gate signal at which the first frame of the representative cycle will start. You can enter this value in three forms:

1. a postive number -- which is the number of milliseconds prior to the gate signal
2. a negative number -- which is the number of milliseconds after the gate signal
3. 0 or RETURN -- which means to start at the gate signal

The program then asks for the matrix type as follows:

```
SPECIFY MATRIX SIZE
                              SIZE  MAX CELL DISK BLOCKS
                         1) 32 x 32     255     nnn
                         2) 32 x 32   65535     nnn
                         3) 64 x 64     255     nnn
                         4) 64 x 64   65535     nnn

REPLY:
```

You must enter 1, 2, 3, or 4 in the normal manner. The program then asks that you verify your answers by typing a RETURN or that you edit your answers by typing an ESCape. When you complete this verification, the program erases the screen and asks for the unit number of the disks on which the framed data will be stored. The default is unit 0. If there is not enough room on this disk, the following message appears:

NOT ENOUGH ROOM FOR FRAMED DATA ON DISK UNIT n

At this point you must either enter another disk unit number or type an ESCape to edit the framing parameters (i.e., number of frames or matrix type.)

The program then asks:

SAVED FRAMED DATA AS PATIENT STUDY? (Y OR N)

If you respond with a Y, the framed data will be saved as a GAMMA-11 patient study; that is, it will always be available for analysis. Y is the default response.

If you respond with N, the framed data will not be saved as a patient study and will have to be reformatted from the list-mode data in subsequent analysis sessions. The program will normally delete the framed data when you exit the data analysis program. However, if you exit the data analysis program via a BA (BASIC), FO (FOCAL), or RU (RUN FORTRAN) command and re-enter the data analysis program via the CA command, the program will not delete the framed data. If you exit the data analysis program via a CTRL/X or enter data analysis by the AD command, the framed data will be deleted.

The last question asked is:

```
TOLERANCE CHECK? (Y OR N)
```

If you specify N or RETURN, the formatting procedure begins (see Section 5.27.2). If you answer with a Y, a histogram showing the distribution of the gate intervals (in milliseconds) is displayed. See Figure 5-30.

```
!
!
!                 *
!                * *
!               *   *
!              *     *
!             !       *
!            *         *
!           *           *
!          *             *
!        *                 *
!----------------------------------------
```

Figure 5-30 Histogram of Gate Intervals

A vertical cursor is displayed at the point equal to 1/2 the maximum of the gate intervals during acquisition. You can choose to make the system reject arrhythmic gate intervals in this study by moving the cursor with the commands R (right), L (left), and J (jump 10 spaces) in order to specify the lower and upper bound of the allowable gate intervals. Below the histogram is:

```
LOW BOUND nnn
```

where nnn is the current position (in milliseconds) of the cursor. This nnn changes as you move the cursor. When you have positioned the cursor for the lower bound, press RETURN. Then do the same for the upper bound. The cursor will move to an equivalent position to the right of the maximum as its initial position. The program will not allow the upper bound to be less than the lower bound.

If you move the cursor to the extreme left, the lower bound will be 0 milliseconds. If you move it to the extreme right, the upper bound will be 65,535 milliseconds.

5.27.2 Formatting the Data

After you have answered all the questions, the program begins formatting the data into a dynamic study. The formatting has two steps. First the program makes one complete pass through the data in order to find the gate signals and generates a table of pointers for the formatting passes. The table of pointers corresponds to the start of each cycle and is stored in an internal GAMMA-11 file. The following message is displayed during this pass.

```
STUDY BEING SCANNED FOR TIME MARKS, PLEASE WAIT
```

Then the program begins its actual formatting. During this time the following message is displayed.

```
mmm FRAMES OF nnn FORMATTED
xx MIN.  FOR THE REMAINDER
```

This message tells you how many frames have been generated and how much more time is required for generating the rest. The time given is approximate. This message is updated at each pass through the data, which is about every 30 to 60 seconds.

The actual time that is required to format the data depends on the following factors:

1. The total counts being framed. The formatting time is proportional to the number of counts. For example, 2 million counts will take twice as long as 1 million counts.
2. Disk type, RK05 or RK06. In general, the RK06 is about twice as fast as an RK05, but an RK06 holds up to six times the data of an RK05.
3. Matrix type. A 32 x 32 matrix is about four times faster than a 64 x 64 matrix. There is only a minimal time difference between byte and word mode.
4. Available free core space. The framing program makes multiple passes through the data, framing as many frames as will fit in core on each pass. Thus, the more free space available for buffers, the fewer passes are required. If possible, foreground/background users should remove the FGAMMA program from the foreground when formatting gated-list-mode studies.

The following table shows example framing times. In the two cases given, each study has 64 frames. The first case is a one million count study on a RK05 disk, and the second is a one million count study on an RK06 disk.

	1 M counts/RK05	1 M counts/RK06
32 x 32 NO FGAMMA	2 MIN.	1 MIN.
64 X 64 NO FGAMMA	5 MIN.	2 MIN.
32 X 32 WITH FGAMMA	5 MIN.	2 MIN.
64 X 64 WITH FGAMMA	17 MIN.	8 MIN.

The times given in this example are approximate and for a GAMMA-11 system with 28K of core. Users with 16K of core should use the times listed with FGAMMA.

Once framing of a gated-list-mode study is complete, the study takes the form of a gate-synchronized study, and all of the analysis and display commands are applicable.

5.28 ERRORS

In general, the system rejects erroneous keyboard input. It displays the command line to the point of error and then displays a new COMMAND request beneath the preceding one. If there is no more room on the screen, the following message is displayed.

```
TYPE ^N FOR NEXT PAGE
```

When you type CTRL/N, the screen is erased, and the COMMAND message appears. As soon as you type in an acceptable input, the matrix display is restored. The DI command is useful at this point to restore the display without modifying the data.

If you detect an error before typing a RETURN, you can erase it by using the DELETE key or pressing CTRL/U.

5.29 AUTOMATING DATA ACQUISITION AND ANALYSIS

The GAMMA-11 system offers you three powerful tools for minimizing the efforts of entering initial information into the system and for performing common analysis procedures. The tools are:

1. Predefined studies
2. Data analysis macros
3. Autoanalysis

Predefined studies enable you to standardize and simplify the data acquisition set up, while the data analysis macro feature enables you to simplify data analysis procedures. You can combine these two features through autoanalysis, enabling the acquisition program to call the analysis program. The combination of these three features enables you to semiautomate acquisition and analysis.

CHAPTER 6

ADDITIONAL ANALYSIS COMMANDS FOR THE COLOR DISPLAY

This chapter describes the color display and playback functions provided by the data analysis program. The features described in this chapter are for the color display only. None are available for the VT01 storage scope. This chapter describes:

1. the color tables and their functions
2. the color table editor
3. interpolated displays
4. dual full size displays
5. dynamic playback routines
6. 8 and 16 image displays

6.1 BLACK AND WHITE COMMANDS

The black and white commands allow you to switch from a color image to a monochrome (green) image to a true black and white image.

BW

6.1.1 From Color to Black and White

The command to switch from a color image to a monochrome display is:

BW (RET)

This command causes all subsequent displays to be presented in a 16-level monochrome (green) scale. To obtain a true black and white display, press the CHAN B button on the color display monitor. To return to the green display press the CHAN B button again.

CL

6.1.2 From Black and White to Color

The command to switch from a green image to a color display is:

CL RET

If the display does not change to color, press the CHAN B button again to obtain a color display.

6.2 INTENSITY COMMANDS

The intensity commands display a color scale bar next to the image. This bar enables you to identify the high and low count areas.

DL

6.2.1 Intensity Scale Bar

The Display Levels command (DL) causes all subsequent displays to be presented with a color scale bar to the right of the image. To use this command, type:

DL RET

This command displays a color bar that shows the current 16 colors used in the image. The scale runs from bottom to top, where the bottom color corresponds to the lowest number of cell counts, and the top color corresponds to the highest number of cell counts. That is, if dark red is at the top of the bar, then the greatest number of counts occur in the dark red portion of the image. If the display mode is monochrome, the 16 intensity levels are displayed in green or gray. In monochrome, the highest areas have the maximum counts and the dark areas have the minimum counts.

NL

6.2.2 Removing the Intensity Scale Bar

To remove the color scale bar from the display, type:

NL(RET)

When this command is issued, the system omits the scale bar from all subsequent images.

6.3 THE COLOR TABLE AND THE COLOR TABLE COMMANDS

The data analysis program supports up to 31 color tables. Each color table consists of 16 elements which correspond to 16 of the color levels of the color display. Each intensity level of the display is made up of a combination of the following three colors.

1. Red
2. Green
3. Blue

Each of the above colors has an intensity ranging from 0 to 3, where 0 is off (absence of color) and 3 is maximum intensity. For example, an intensity level of the display can be represented by the following three numbers:

1 0 2

where 1 is the intensity of the red, 0 is the intensity of the green and 2 is the intensity of the blue. Therefore, there are 64 possible colors available for the display.

Each color table has an identifying number (from 1 to 31). The number of the color table that is currently in use is called the current color table number. The color tables are stored on the system disk and are referenced by the color table number. GAMMA-11 has supplied you with two color tables:

1. A 16-color "rainbow" spectrum
2. An 8-color "hot body" spectrum

You may make up the other 29 color tables. Although a 32nd color table exists with a color table number of 0, it is reserved for system use only. This 32nd table contains the current color table. When the data analysis program is called, it defaults to color table zero, that is, the last color table used.

ADDITIONAL ANALYSIS COMMANDS FOR THE COLOR DISPLAY

Five commands are available to you at the data analysis COMMAND: level. These commands are:

1. Retrieve a color table from the system disk
2. Save the current color table on the system disk
3. Call the color table editor
4. Change a color level at the COMMAND level
5. Switch to and from monochrome (green) displays (discussed in Sections 6.1.1 and 6.1.2)

CT

6.3.1 Retrieving a Color Table

The Retrieve a Color Table command (CT) to retrieve a previously defined color table from the system disk is:

```
CT n RET
```

where n is the color table number (1-31). Color table n becomes the current color table, which is used until another color table is retrieved or until the current color table is modified. The display changes in respect to the newly retrieved color table. If you do not specify n, the system retrieves the last color table used.

ST

6.3.2 Saving a Color Table

The Save Color Table command (ST) to save the current color table on the system disk is:

```
ST n RET
```

where n is the color table number (1-31), which you must specify. Once saved, a table can be retrieved at any time with the CT n command.

You must use the ST command when you want to save a changed color table from a displayed image; otherwise, the colors are not saved.

CL

6.3.3 Changing a Color Level

The Change Color Level command (CL) to change a color level at the COMMAND level is:

```
CL n,rgb(RET)
```

where n represents the color level (0-15) to be changed, and rgb is a 3-digit number representing the color of level n (made up of a combination of the colors red, green, and blue). Individually, the digits r, g, and b can have only one of the four values (0-3).

The best way to change a color level is to first display the color intensity bar by typing the following command.

```
DL(RET)
```

Next, count from the bottom up on the color bar to the level that needs to be changed (the n parameter). For example, if the sixth color up on the color bar is red (color level 5) and you wish to change it to blue, type the command:

```
CL 5,003(RET)
```

This command replaces all of the red cells with the most intense (3) blue color. Notice that the 00 shows that the red and green colors have been turned off.

To change the first color level to gray, type:

```
CL 0,111(RET)
```

A good example of this command appears in Figure 6-2 (color insert). Figure 6-1 (color insert) is a normal color image. The combination of these three colors, each at level 1, produces gray.

6.4 COLOR-TABLE EDITING COMMANDS

The color-table editor enables you to modify the current color table with commands to do the following:

1. Zero the color table (i.e., setting all levels to off)
2. Change a color table element
3. Insert a new element into the color table

4. Delete an element from the color table
5. Save a newly created color table on the disk
6. Print the color table on the terminal
7. Display a ramp of the colors

ET

6.4.1 Color-Table Editor

The Edit Color Table command (ET) to call the color table editor is:

```
ET n RET
```

where n is the number of the color table that you want to modify. The program retrieves color table n from the disk, and it becomes the current color table. If you do not specify n, the color table that is currently displayed becomes the current color table.

To the right of the displayed image is a 16-level color bar. To allow easier identification of the color level numbers, color levels 3, 7, 11, and 15 are two times wider in the bar than the other color levels.

To the right of each level is a color level number (0-15) and an intensity number (0-3) for each of the red, green, and blue colors. The following example shows a sample color table and lists the level numbers with their corresponding intensities.

COLOR TABLE n

	R	G	B
15	3	3	3
14	2	3	3
13	3	3	2
12	3	3	1
11	2	2	0
10	3	2	0
9	3	2	1
8	3	1	0
7	3	0	0
6	2	0	0
5	1	0	1
4	1	0	3
3	0	0	3
2	0	0	2
1	0	0	1
0	0	0	0

Notice that below the image is the message COLOR COMMAND (see Figure 6-3 in the color insert). This message accepts any of the following color-table editor commands:

Z	Zero all of the color table elements
C	Change an element value
I	Insert an element value
D	Delete a color level
S	Save a color table
G	Get a color table from the disk
R	Display a ramp of the current color table
M	Display the matrix image
P	Print the color table on the terminal
CTRL/X or RET	Exit

Z

6.4.2 Zeroing the Color Table

The command to set all color table elements to zero is:

```
Z RET
```

It is strongly suggested that before attempting to zero a color table, you save the current color table (see Section 6.4.6). Since all elements will have a value of zero, the image and the color bar disappear.

C

6.4.3 Changing a Color Element

The command to change a single color element without affecting any of the other color elements is:

```
C n,rgb RET
```

where n represents the color level (0-15), and rgb is a 3-digit number representing the colors red, green, and blue. Individually, the digits, r, g, and b can have only four values (0-3). Both the color bar and the image will change to reflect the new value. The C command is equivalent to the CL command at the COMMAND level. See Section 6.3.3.

I

6.4.4 Inserting a Color Element

The command to insert a new color element into the color table is:

```
I n,rgb RET
```

where n represents the color level (-15 to +15), and rgb is a 3-digit number representing the colors red, green, and blue. Individually, the digits, r, g, and b can have only four values (0-3).

If n is a positive number, the elements above the inserted element move up one level.

For example, if n is 4, the old level 4 and all of the levels above 4 move up one level. That is, old level 4 now becomes 5 (n+1), old level 5 becomes 6 (n+2), and so forth. Level 15 is lost, and all levels below 4 are left unchanged.

If n is a negative number, the elements below the inserted element move down one level. For example, if n is -4, the old level 4 and all of the levels below 4 move down one level. That is, old level 4 now becomes 3 (n-1), old level 3 becomes 2 (n-2), and so forth. Level 0 is lost and all levels above 4 are left unchanged.

D

6.4.5 Deleting a Color Level

The command to delete a color level from the color table is:

```
D n RET
```

where n represents one of the color levels (-15 to +15). The levels above n move down or the levels below n move up, depending upon the sign of n.

For example, if n is 7, level 7 is deleted and the levels above 7 move down one position. That is, old level 8 (n+1) becomes 7 (n), old level 9 (n+2) becomes 8 (n+1), and so forth. Level 15 assumes a color value of zero.

If n is -7, the levels below level 7 move up one position. That is, old level 6 (n-1) becomes 7 (n), old level 5 (n-2) becomes level 6 (n-1), and so forth. Level 0 assumes a color value of zero.

S

6.4.6 Saving an Edited Color Table

The command to save an edited color table on the system disk is:

```
S n RET
```

where n is the color table number (1-31). The n must be specified because the current color table number is not affected by this command. Do not forget to use this command BEFORE zeroing a color table, because the zeroed color table can never be retrieved again unless it has been previously saved. See Section 6.4.2.

G

6.4.7 Getting a Color Table

The command to obtain a color table from the system disk is:

```
G n RET
```

where n is the color table number (1-31). The display changes in respect to the newly obtained color table. Thus, n now becomes the current color table number. If n is not specified, the last color table used will be the one obtained.

This command is equivalent to the CTn command at the command table level.

P

6.4.8 Printing a Color Table

The command to print the color table is:

```
P RET
```

The P command causes the color table number and the contents of the current color table to be printed on the terminal.

R

6.4.9 Displaying a Ramp

To display a ramp of the colors in the current color table type:

R(RET)

Should you choose to change a color while the ramp is displayed, the ramp will be updated and redisplayed.

NOTE

> If you were in dual display mode previous to displaying a ramp, the dual display will be lost. Upon exiting the ramp, you will have to retype:
>
> DU(RET)
>
> to redisplay the dual display.

M

6.4.10 Displaying the Matrix

To display the core-resident matrix in the color table editor, type:

M(RET)

This command can also be used to exit from a ramp.

6.4.11 Exiting from the Color Table Editor

To exit from the color table editor, type either a RETURN or a CTRL/X. Control returns to the COMMAND level and the edited color table becomes the current color table.

6.5 THE INTERPOLATED DISPLAY

The color display has a 128 x 128 display matrix for displaying the images. To display a 64 x 64 image, the system maps each of the data cells into four cells of this display matrix (i.e., each cell is quadrupled). To display a 32 x 32 image, the system maps each data cell into 16 display cells of the 128 x 128 display matrix. This duplication of data causes 64 x 64 and 32 x 32 images to have a boxed appearance. That is, each cell looks like a box instead of a point. You can obtain a more pleasing display by interpolating the data.

The commands to interpolate a display depend on the number of bit maps in the VSV01. One bit map contains 128 x 128 matrix points, which is one full-size display on the VSV01.

IT

6.5.1 Interpolation Command

The command to interpolate the displayed data is:

```
IT RET
```

This command interpolates all 32 x 32 matrices to 64 x 64 and all 64 x 64 matrices to 128 x 128. If the VSV01 has four bit maps, all 128 x 128 matrices are interpolated to 256 x 256. If the VSV01 does not have 4 bit maps, the system ignores the IT command for 128 x 128 matrices. It also causes all subsequent data to be interpolated. Note that the actual core-resident data is not modified and that the interpolation mode determines only the display format. See Figure 6-4 (color insert) for an interpolated display and compare it to Figure 6-1 (color insert), a normal color image.

The interpolation algorithm is a linear interpolation. For each real data point, the system generates three interpolated points.

NT

6.5.2 No Interpolation

The command to turn off interpolation is:

```
NT RET
```

When you type this command, none of the subsequent images are interpolated.

IT2

6.5.3 Double Interpolation

The command to doubly interpolate the displayed data is:

```
IT2 (RET)
```

This command interpolates all 32 x 32 matrices to 128 x 128. If the VSV01 has four bit maps, 64 x 64 matrices are interpolated to 256 x 256. If the VSV01 does not have 4 bit maps, the system interpolates as far as it can with the IT2 command. For example, 64 x 64 matrices are interpolated to 128 x 128.

The IT2 command also causes all subsequent data to be interpolated. The actual core-resident data is not modified, and interpolation mode affects only the color display. The NT command turns off the IT2 command also.

The interpolation algorithm is a linear interpolation. For each real data point, the system generates fifteen interpolated points.

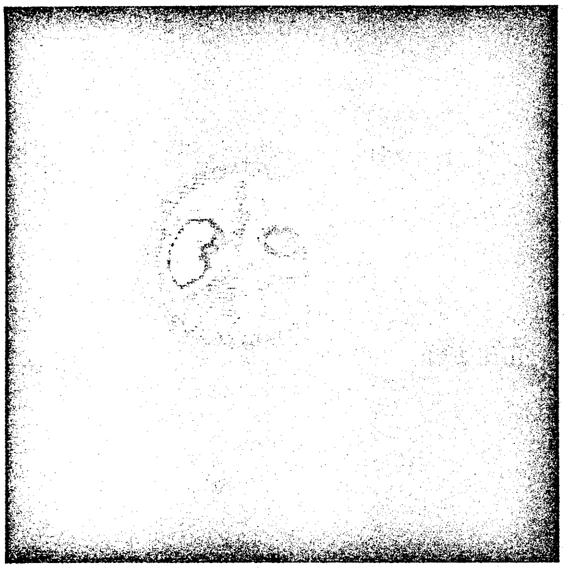


Figure 6-1
Normal Color Image

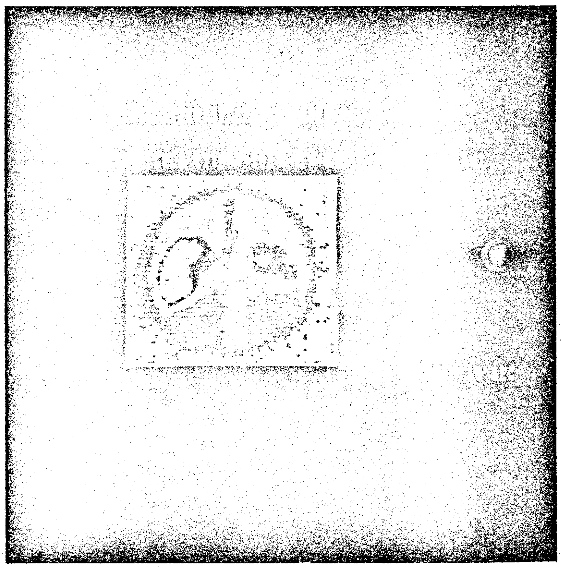


Figure 6-2
Changing a Color Level

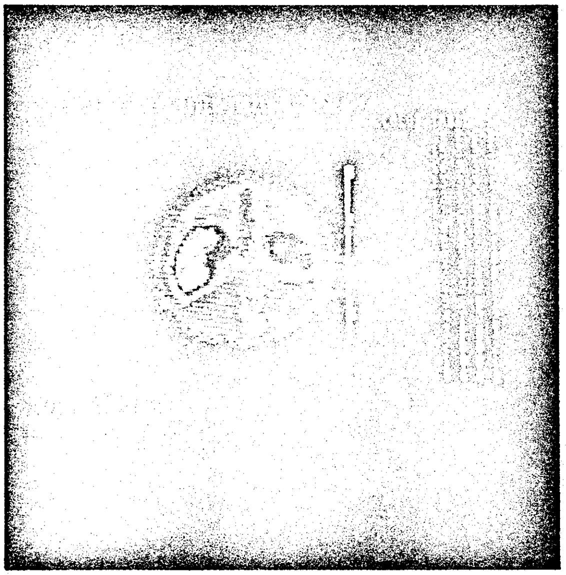


Figure 6-3
Color Table Editor

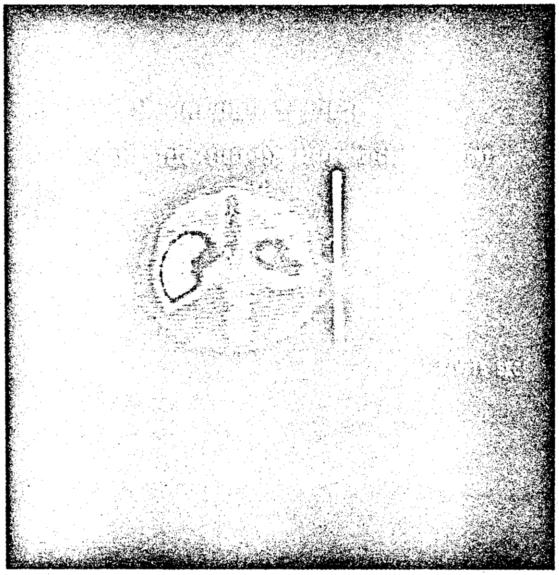


Figure 6-4
Interpolated Display

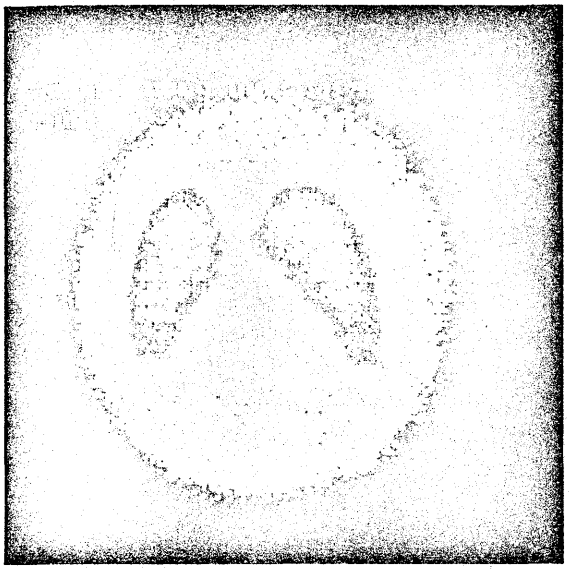


Figure 6-5
Blow-Up

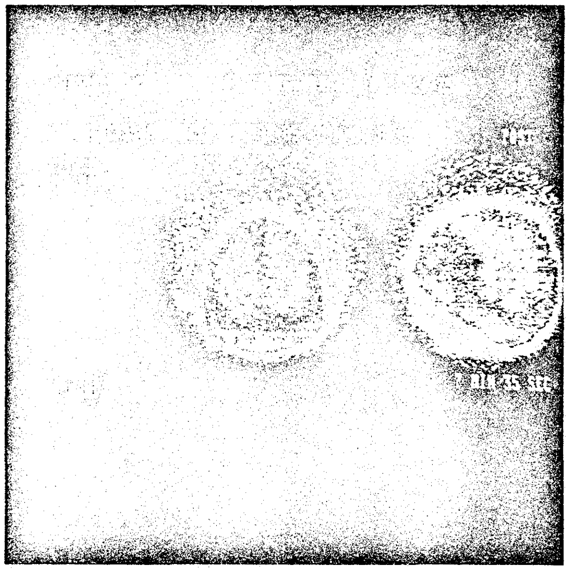


Figure 6-6
Dual Display

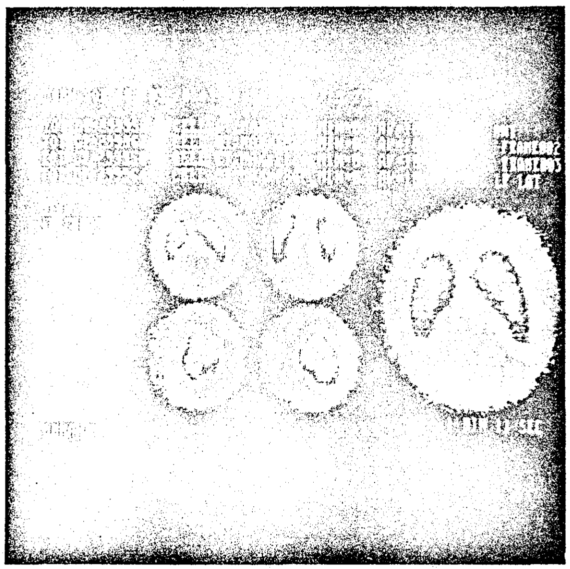


Figure 6-7
Miniature and Normal Dual Display

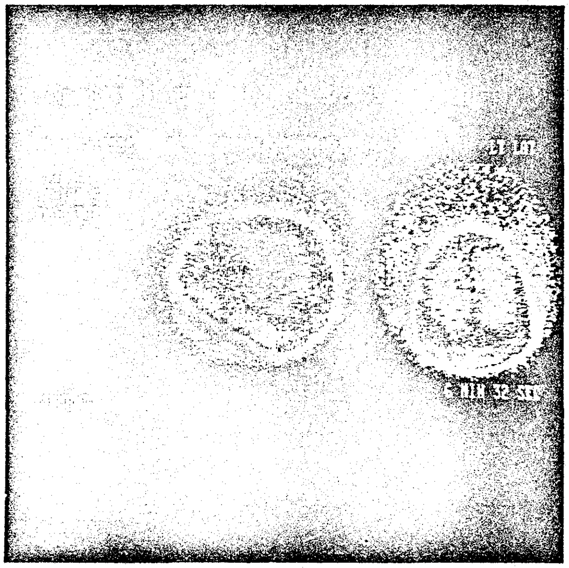


Figure 6-8
Swap

6.6 DISPLAY COMMANDS

Two color display commands enhance the visibility of the display. These are the blow-up and no blow-up commands.

BU

6.6.1 Blow-Up

The Blow-Up command (BU), which increases the normal displayed image by a factor of two in each of the X and Y positions, is:

BU (RET)

This command causes all subsequent image displays to be presented four times larger than the normal displayed image. This command is particularly useful in enhancing the visibility of the display. A blown-up image almost occupies the entire screen. To prevent the normal text information from overlaying and interfering with the display, the program displays only the index line. COMMAND: appears directly below the index line. Figure 6-5 shows an example of the blow-up command.

NB

6.6.2 No Blow-Up

The No Blow-Up command (NB), which switches from a blown-up image to a normal display image, is:

NB (RET)

This command causes all subsequent images to be displayed normally.

6.7 DUAL DISPLAY COMMANDS

The standard GAMMA-11 hardware system contains two bit maps. One bit map contains 128 x 128 matrix points, which is one full-size display.

Normally, only one bit map is used to display images. A special dual full size display mode is available for displaying two full size images simultaneously. The left-hand image is the current core-resident data and can be manipulated in the normal manner. The right-hand image remains fixed. The right-hand image is stored in a disk-resident area called the dual display buffer. The general procedure for generating a dual display is as follows:

1. Store the current core-resident data in the dual display buffer by using the Load (LD) command. This stored image will be the right-hand image.

2. Modify or change the core-resident data to suit you, and then issue the Dual Display (DU) command. The core-resident data will be displayed on the left and the contents of the dual display buffer will be displayed on the right.

The DU command causes the dual display to remain in effect until you issue the no dual display command. Once you have issued this command, you can change or modify the left-hand image by using the data analysis commands in the normal way.

To change the right-hand image, issue a swap command (SW). This command swaps the left and right images (the core-resident data go to the dual display buffer and the contents of the dual display buffer become core resident).

LD

6.7.1 Loading Dual Displays

The command to load a dual display buffer is:

LD RET

The LD command causes the current core-resident data to be transferred to the disk-resident dual display buffer. This command does not initiate a dual display, it merely loads the buffer.

The command to load and display an image is:

LD n RET

This command transfers the contents of save area n (where n is 1-64) to the dual display buffer and invokes the dual display mode. That is, this command causes the contents of the save area to be displayed on the right with the core-resident data on the left.

NOTE

Only matrix save areas can be displayed (not dynamic curves).

DU

6.7.2 Dual Display

The command to display the contents of the dual display buffer is:

DU RET

This command causes the contents of the dual display buffer to be displayed full size on the right side of the screen. The core-resident data is displayed on the left side. You can change or modify the left-hand image with all the available commands in data analysis at the COMMAND: level. You cannot modify the right-hand image unless you make the contents of the dual display buffer core resident (see Section 6.7.4). Dual displays are only available at the COMMAND: level. If you leave this level (e.g., to enter regions of interest or the slice procedure), the display reverts to the normal image. For an example of a dual display, see Figures 6-6 and 6-7.

NOTE

> The Dual Display and Blow-Up commands are mutually exclusive. If blow-up is in effect when the Dual Display command is issued, the display reverts to normal size.

NU

6.7.3 No Dual Display

The command to return to the normal single image display is:

NU RET

The right image is turned off and the left image (core-resident data) becomes the single image. This command causes all subsequent displays to be single images. The dual display mode can be initiated at any later time by entering the Dual Display command, DU.

DO

6.7.4 Dual Overlay

The command to overlay the contents of the two display buffers is:

DO RET

This command displays the contents of the dual display on top of the core-resident image. Different color scales may be used in this mode. However, if one of the two overlayed images is in black-and-white, the combined images will be entirely black-and-white while they are overlayed. The conditions used for reverting to a normal display mode are the same for dual displays.

SW

6.7.5 Swap

If you wish to modify the contents of the dual display buffer (right image), the buffer must be core-resident. Thus, the buffers must be swapped. To swap buffers, type:

```
SW(RET)
```

This command swaps the current core-resident data and the data in the dual display buffer; it also swaps the displayed images. The previous contents of the dual display buffer can now be modified, since they are core-resident. After performing the desired operations, issue SW again. The display returns to its original state, but the right-hand image is modified. Figure 6-8 (color insert) represents the swapping of the two images in Figure 6-6.

6.8 DYNAMIC PLAYBACK

Dynamic playback allows you to play back patient studies in a movie-like manner. You establish the speed and direction of the playback in one of the following three ways.

1. Control with a joystick
2. Presetting to a specific rate
3. Manual control (i.e., stepped) by using the terminal keyboard

The playback feature can also be used to show a closed-loop show of a small number of frames. For example, a twelve-frame gated cardiac study (end-diastole, end-systole) can be played back to view cardiac wall motion.

Dynamic playback uses a disk-resident playback buffer. This buffer contains formatted prescaled images that are ready to be displayed. The use of prescaled images allows the data to be played back at very fast rates. It is possible to playback images at a rate exceeding 15 images per second. The prescaled images can be stored in one of three matrix sizes: 64 x 64, 64 x 128, or 128 x 128. Choosing a matrix is determined by:

1. The desired image resolution
2. The desired playback rate
3. The available disk space

In general, larger matrices require more disk space and have a lower maximum playback rate. The procedure for using the playback option is:

1. Create a playback buffer by specifying a buffer name, a disk unit number, the number of images, the image matrix, and the scaling factor.
2. Store data in the playback buffer.
3. Display the playback buffer.

The images that are stored in the buffer can be preprocessed images (i.e., smoothed images). Any data analysis command available at the COMMAND: level can be used to enhance data prior to storing the image in the playback buffer. Once a playback buffer has been created, it can be displayed at any time.

The actual matrix size and playback image matrix size do not have to match. A scaling routine converts the data to the correct matrix size when the image is stored in the buffer. That is, it interpolates or condenses data to match matrix sizes. For example, 64 x 64 data is interpolated when it is stored in a 128 x 128 image buffer. Conversely, 128 x 128 data is condensed by averaging four points when it is stored in a 64 x 64 buffer.

6.8.1 Playback Buffer

A playback buffer is a disk-resident buffer. Buffers can exist on any disk unit and each buffer has a unique 1-6 alphanumeric character name. The actual buffers are individual RT-11 files and the file extension is GPB. For example, if a playback buffer is named HEART, it is really an RT-11 file called HEART.GPB.

The playback buffer consists of a series of prescaled images. The internal format of these images is such that they can be loaded directly into the color display without any time-consuming processes, thus maximizing the playback rate. Images stored in the playback buffer can be one of three matrix sizes: 64 x 64, 64 x 128, or 128 x 128. The matrix size (i.e., 32 x 32, 64 x 64, or 128 x 128) does not have to match the playback matrix size. If the data matrix size is less than the playback image size, the data is interpolated to the playback image size. If the matrix size is greater than the playback matrix size, the data will be averaged prior to storage in the playback buffer. The following table describes the process for all possible combinations.

Table 6-1
Matrix Sizes

Data Matrix		Playback Matrix	
	64 x 64	64 x 128	128 x 128
32 x 32	Interpolate x and y	Interpolate x and y Duplicate x	Interpolate x and y Duplicate x and y
64 x 64	No conversion required	Interpolate x	Interpolate x and y
128 x 128	Average 4 points	Average 2 points	No conversion required
Disk Blocks per Image	4	8	16
Maximum Playback Rate	14 images/sec	15 images/sec	8 images/sec 15 (for RK06)

NOTE

> The playback rates described in the table are for 11/40 processor or the equivalent. Playback rates for the 11/10 or the equivalent are less.

Note, from Table 6-1 that 32 x 32 data is always interpolated. Storing 32 x 32 matrices in a playback matrix of 128 x 128 is not necessary and is wasteful of disk space. The fourth row of the table indicates the number of disks blocks required to store one image. For example, consider a playback buffer with 100 images, where matrix size 1 requires 400 disk blocks, matrix size 2 requires 800 disk blocks, and matrix size 3 requires 1600 disk blocks. One RK05 disk has slightly more than 4800 blocks, thus, in this case, the 128 x 128 matrix size would require one third of the total disk capacity.

The fifth row of the table indicates the maximum playback rates for each image matrix size. The 64 x 128 playback has the fastest playback rate.

NOTE

> It might be assumed that the 64 x 64 matrix size has the fastest playback rate, however, this storage mode requires some unpacking when the images are displayed.

The 64 x 64 playback rate is determined by the processor speed, while the 128 x 128 playback rate is limited by the disk transfer rate. Thus, the 64 x 128 matrix size has the best match to processor speed, disk transfer rates, and disk storage.

6.8.2 Scaling Algorithms

The actual data stored in the playback buffer are intensity levels rather than counts. Storing intensity levels instead of counts not only saves disk space, but also saves time during playback (i.e., the playback routine does not have to scale each image). The data are scaled when the playback buffer is loaded.

There are two scaling algorithms available. The first algorithm is the same algorithm that is used to scale data for the normal display. This algorithm scales each image to its own maximum and minimum cell counts, using the upper and lower threshold settings. This method is referred to as the relative scaling algorithm.

The second scaling algorithm scales every image to the same user-specified maximum and minimum cell count. This scaling algorithm is referred to as the absolute scaling algorithm. The data is scaled to a specific cell count independent of the maximum and minimum cell count of the individual frames. Upper and lower thresholds are not used in this method.

For either algorithm, cells with contents above the upper threshold or maximum scaling factor are displayed with the maximum intensity level. Cells below the lower threshold or lower scaling cell count are displayed with zero intensity. Each algorithm generates images that differ somewhat when played back. The absolute scaling algorithm approximates what is seen on the gamma camera console when the data is acquired.

For example, if a cardiac flow study is played back, the bolus initially appears very bright. As the bolus disperses, the overall brightness of the display decreases. The actual brightness depends upon the scaling factors used to scale the data.

If the relative scaling algorithm is used to generate the playback buffer, the overall brightness of the image remains fairly constant. In this case, as the bolus disperses, the brightness and contrast are enhanced by the scaling algorithm. This algorithm compensates for any changes in the absolute count rate. The resultant images are independent from the actual count rate. Statistical fluctuations (noise) cause low count rate images that are somewhat grainy and random. Choosing an algorithm depends upon what you wish to determine from the playback. If your interest is in the overall flow and activity, both spatially and temporarily, use the absolute scaling algorithm.

However, if your interest is in the relative spatial activity, the relative scaling algorithm would provide a better overall display. The relative scaling algorithm is easier to use since the algorithm scales each image for perfect contrast. To use the absolute scaling algorithm, you must establish the maximum and minimum scaling factors before the playback buffer is created.

6.8.3 Storing Images in the Playback Buffer

A playback buffer is created or re-initialized by using the PBI command (see Section 6.8.4). Each image is stored in the playback buffer with the PBS command (see Section 6.8.5). Any GAMMA-11 data analysis command available at the COMMAND: level can be used to modify or process a data frame before storing it in the playback buffer. A multiple command line or macro allows you to set up a closed loop series of commands that can enhance each frame before storing it in the buffer.

After creating a playback buffer, the buffer can be played back with the PB command. The playback routine allows you to control the playback via the joystick, keyboard, or fix the playback at a specified rate. Images can be displayed in the forward or reverse direction.

The following sections describe the procedures for:

1. Creating or initializing a playback buffer
2. Storing images in the buffer
3. Playing back the buffer

PBI

6.8.4 Creating a Playback Buffer

Before any images can be stored in a playback buffer, you must create a buffer or re-initialize an existing buffer. The command to create or initialize a playback buffer is:

```
PBI name,unit,n,r,max,min RET
```

where:

name	is a 1-6 alphanumeric character name for the buffer.
unit	is the disk unit number (0-7) on which the buffer resides.
n	is the total number of images in the buffer.
r	is the playback buffer image matrix size (1-3) 1 is for 64 x 64 matrices 2 is for 64 x 128 matrices 3 is for 128 x 128 matrices
max	is the maximum number of cell counts that are used to scale the data for the absolute scaling algorithm. If max is zero or absent from the command line, the relative scaling algorithm is used.
min	is the minimum number of cell counts that are used to scale the data for the absolute scaling algorithm. Min is only present when max is greater than zero.

When the system executes this command, it creates a playback buffer on the specified disk unit. If a playback buffer with this specified name already exists on the unit, the buffer is re-initialized. Any images previously stored in the buffer are erased. This command stores the current index line in the buffer and uses the current frame algebra message for the comment line. Note that you can use the Text command (TE) prior to the PBI command to insert any comment to be displayed during playback. An alternate form of this command is:

```
PBI (RET)
```

With this alternate form, the creation routine enters an interactive mode. You are asked for the required parameters one at a time. You can use the editing functions in the data acquisition program (i.e., ESCape to edit and DELETE to erase a line). In the interactive mode, you are asked to enter a comment line.

If there is not enough disk space available for the playback buffer, the following error message appears.

```
NOT ENOUGH DISK SPACE ON UNIT n
THIS BUFFER REQUIRES xxx BLOCKS, ONLY
yyy BLOCKS ARE AVAILABLE
```

At this point, if the system is in the interactive mode, you can type an ESCape to change some of the parameters (i.e., reduce the number of images, change the image matrix size, or select another disk unit). You can type a carriage return to return to the COMMAND level. If the system is not in the interactive mode, a carriage return must be typed.

If the system is in the interactive mode and a buffer name is specified that already exists on the disk, the following message appears.

```
BUFFER name ALREADY EXISTS ON UNIT n
```

You can type an ESCape to change the buffer name or type a carriage return to re-initialize the existing playback buffer. If the system is not in the interactive mode, an existing playback buffer is automatically re-initialized and no message is printed.

Note that the first form of the PBI command is most useful within a data analysis macro. This command automatically sets up a buffer, while the second form of the command, PBI (the interactive mode), is easier to use when not running a macro.

PBS

6.8.5 Storing Images in a Playback Buffer

When a buffer has been created or initialized by using the PBI command, data images are converted or stored in the playback buffer by using the following command:

```
PBS
```

This command converts the current core-resident data into the playback buffer format and stores it in a buffer. The first time the PBS command is executed (following the PBI command), the image is stored as image number one. The next time PBS is executed, the data is stored as image number two. The data analysis program keeps track of the last image number stored. The PBS command stores the current data in the next sequential position of the playback buffer. Since the PBS command stores only one image at a time, it would be very time consuming for you to manually fill the buffer by typing PBS repeatedly.

The PBS command is intended to be used in a multiple command line or a data analysis macro along with the execute line (EL) command. The EL command allows the set-up of a closed loop command string. This process handles and stores frames sequentially in the buffer. For example, the following simple command line causes the data analysis program to store a series of smoothed images in the buffer.

```
S9;PBS;! ;EL RET
```

S9 smooths the current data, PBS stores the smoothed data in a buffer, the exclamation point and space bar skips to the next frame unless it is the last frame, and the EL command causes the entire command line to be re-executed. Thus, the playback buffer is filled with a series of smoothed images. The above command will not be repeated indefinitely because:

1. the playback buffer will be filled, or

2. the end of the study will be reached.

In either case, command execution stops. You can then issue the PB command (see Section 6.8.6) to display the buffer. You can also stop command execution by pressing the DELETE key.

The following data analysis commands are helpful for handling data prior to storing it in a buffer.

S9	Smooth data to eliminate noise
AD n	Add sequential frames
SK n or Space bar	Skip frames
IC n or ICF n	Isocontour (useful for wall motion)
SA +n	Save area add

See Sections 5.3.1 and 5.24.12 for an explanation of the exclamation point. The save area add command, SA +n, is useful for generating composite images. For example, an outline (such as a ventricular wall) can be stored in a save area and then added to every image as it is stored in the playback buffer. One possible form of a command string could be:

```
S9;SA +3;PBS; ;EL RET
```

The AD n command is useful for storing a sum of frames in each image of the playback buffer. Consider the following sequence:

```
AD 4 RET
S9;PBS;! ;EL RET
```

AD 4 adds four frames to the current frame (i.e., sums five frames). The next line stores the smoothed sum, skips five frames, sums the next five frames, and then re-executes the line. Note that the space bar command skips n+1 frames (five, in this case). Thus, the playback buffer will contain a sequence of images, each having a smoothed sum of five. A modification to this command sequence is:

```
AD 4(RET)
S9;PBS;!SK 1;EL(RET)
```

In this case, five frames are summed but only one is skipped. This process may be called a temporal smoothing algorithm. This procedure is useful when images are stored from a very fast dynamic study. The summing of images improves the statistics of the data, while skipping only one frame preserves the dynamics of the study.

PB

6.8.6 Playing Back the Playback Buffer

After you have initialized and stored at least one image in a playback buffer, the buffer can be played back by using the following command:

```
PB name,unit(RET)
```

where:

name	is the name of the playback buffer.
unit	is the disk unit on which the buffer resides.

If unit is not specified, unit zero is assumed. If both name and unit are absent from the command line, the most recently initialized playback buffer is used.

When a playback buffer is displayed, the images appear in the center of the screen. To the right of the image is the current image number, the current playback rate in images per second, and the playback direction, FORWARD or REVERSE. The index line and comment line, which was optionally entered at creation of the playback buffer, appear at the top of the screen. When playback begins, the joystick controls the speed and direction of the playback. Moving the joystick forward causes the playback rate to increase. Moving the joystick backward causes the playback rate to decrease. If you move the joystick further backward, the direction of the playback reverses. The current image number, rate, and direction are displayed to the right of the image. You can fix the playback rate at a constant rate, or you can step through the study manually by using the T, M, and S commands. See Section 6.8.7.

All playback files are stored on the disks with the extension .GPB. To get a list of all the playback files stored on the system disk, type the following monitor command:

```
DIR *.GPB(RET)
```

To get a list of all the playback files stored on disk unit 1, type:

```
DIR DK1:*.GPB(RET)
```

Remember that monitor commands are not the same as GAMMA-11 commands.

6.8.7 Playback Commands

You can use the following commands to control the mode of display and playback. All of these commands are immediate effect commands (i.e., no carriage return is needed).

The following four commands control the display mode:

C	Display in color, the current color table is used.
B	Display in black-and-white (i.e., monochrome).
U	Display in blow-up mode.
N	Display in normal size mode.

The next four commands control the speed and direction of the playback:

T	Timed mode; locks the playback rate at the current rate.
M	Manual mode; playback stops; type a carriage return to display the next frame.
J	Joystick mode; speed and direction are controlled by the joystick (i.e., initial mode).
S	Switch direction; T or M mode only.

To exit the playback mode and return to the COMMAND: level, type a CTRL/X.

PBD

6.8.8 Deleting a Playback Buffer

When you create a playback buffer, it remains on the disk until you delete it. The command to delete a playback buffer is:

```
PBD name,unit(RET)
```

where:

name is the name of the buffer.

unit is the disk unit number.

If unit is absent, disk unit zero is assumed. Name must always be specified, otherwise an error message is printed.

PBM

6.8.9 Playback Merge

The Playback Merge command can merge up to four playback buffers into one buffer that displays up to four images simultaneously. The command to create a merged playback buffer is:

```
PBM name,unit,buf1,unit1,buf2,unit2,buf3,unit3,buf4,unit4 RET
```

where:

name	is the name of the new buffer which will hold the merged buffers
unit	is the unit number where the new buffer will be stored
buf1	is the name of the first buffer to be merged
unit1	is the unit number where buf1 is stored
buf2	is the name of the second buffer to be merged
unit2	is the unit number where buf2 is stored
buf3	is the name of the third buffer to be merged
unit3	is the unit number where buf3 is stored
buf4	is the name of the fourth buffer to be merged
unit4	is the unit number where buf4 is stored

For example,

```
PBM MERGED,1,GANEK,1,PAVIA,2,GOODMN,2,SHIELS,1 RET
```

or

```
PBM MERGED,1,GANEK,1,,,GOODMN,2,PAVIA,2 RET
```

The total number of frames in the new merged buffer is the minimum number of frames of the four existing buffers. You may leave any of the four buffer names and units blank which will leave a blank area in the merged buffer. The merged display is filled in the order shown in Figure 6-9.

The alternate form of the PBM command is:

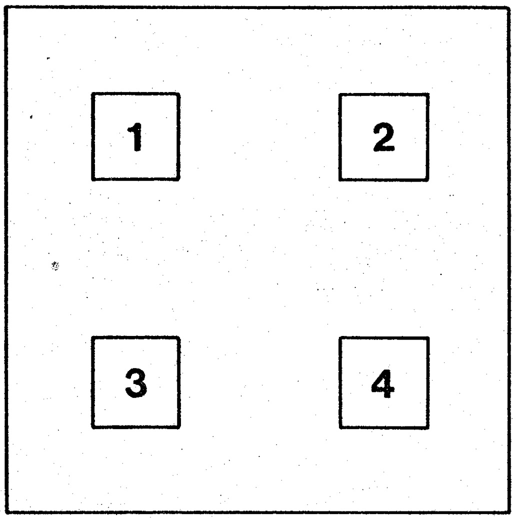
```
PBM RET
```

If you type only PBM, GAMMA-11 enters an interactive mode which prompts you to type in each buffer name and unit number individually. The rules for editing your responses and adding comments are the same as for PBI. The error messages and messages dealing with available disk space are the same as PBI also.

Should you type an incorrect buffer name or unit number for buffer 1 through buffer 4, the following message appears on the display.

```
NONEXISTENT BUFFER
```

Then you will be prompted to retype that buffer name and unit number.



The area marked 1 is the area filled by buffer 1. If buffer 1 is left blank, area 1 is left blank.

The area marked 2 is the area filled by buffer 2. If buffer 2 is left blank, area 2 is left blank.

The area marked 3 is the area filled by buffer 3. If buffer 3 is left blank, area 3 is left blank.

The area marked 4 is the area filled by buffer 4. If buffer 4 is left blank, area 4 is left blank.

Figure 6-9
Filling the Playback Merge Buffer

6.9 EIGHT AND SIXTEEN IMAGE DISPLAYS

The following two commands are variations of the minified-display mode that work only on the color display.

D8

6.9.1 Display Eight Images

The command to display eight images is:

D8 RET

This command produces up to eight minified images on the display. These eight images are sequential frames of a dynamic study beginning with the core-resident image. The core-resident image is in the upper left corner of the display.

D16

6.9.2 Display Sixteen Images

The command to display sixteen images is:

D16 RET

This command produces up to sixteen minified images on the display only if the VSV01 has four bit maps. If the VSV01 has only two bit maps, the D16 command stops at only eight images.

The sixteen images are sequential frames of a dynamic study beginning with the core-resident image. The core-resident image is in the upper left corner of the display.

CHAPTER 7

REGIONS OF INTEREST

You can select regions of interest (ROIs) within an image. GAMMA-11 uses these ROIs to plot curves and display count data. ROIs are sometimes rectangular but can be irregularly shaped, and they are within the boundaries of the matrix. You can specify as many as 12 ROIs at one time. The ROIs may overlap, intersect, or be wholly contained within other ROIs. In dynamic studies, GAMMA-11 can calculate curves based on the count rate within each ROI, and can display, print, or punch them. GAMMA-11 can store both dynamic-study curves and matrices with ROIs in save areas.

The ROI commands are a subset of the data-analysis routine (command AD at the command-table level). The ROI commands set a prevailing mode that must be exited before returning to the study.

Two types of ROIs exist: regular, and irregular. Regular ROIs are rectangular, and irregular ROIs can take any shape.

NOTE

> Type CTRL/X to exit from ROI mode back to the study. Reentering ROI mode restores all of the previously defined ROIs.

The DELETE key does not work for correcting typing errors in ROI mode. You can cancel a typing error in a RETURN-terminated command (before typing the RETURN) by typing:

```
CTRL/U
```

The CTRL/U cancels the whole line, and you must retype the command.

The ROI commands do not appear on the display or on the console.

RI

7.1 REGULAR REGION OF INTEREST (ROI) COMMAND

To enter the regular ROI mode, type the following command on the terminal in response to the COMMAND: request.

RI (RET)

GAMMA-11 redisplays the matrix with a cursor approximately in the middle of the matrix. You use the cursor to outline or otherwise determine the matrix cells that are to be included in an ROI. Figure 7-10 (color insert) shows a matrix display with the cursor (cross hairs for the color display). You control the motion of the cursor from the keyboard. The cursor can move only vertically or horizontally.

If the VT01 display is bright at the center, the cursor may not be readily visible. Use the control commands to move the cursor into a sparse area of the matrix. Often the motion itself makes the cursor apparent.

To define a regular ROI, you must mark the diagonally opposed corners of the region by moving the cursor and typing the Mark command, once for each corner. When you have marked the two corners using the control commands, the rectangle defining the ROI appears on the display, superimposed on the matrix.

When you have defined the ROI, the program identifies it with a letter of the alphabet, rather than a number. That is, the first ROI defined is labeled A, the second B, up to the twelfth, L. The letter is placed in the interior of the ROI for the color display. For the VT01, the identifying letter designates the border of the region. You always know the exact position of the cursor, so that regions as small as a single cell can be precisely located and marked.

7.2 CONTROL COMMANDS

The ROI program identifies each defined ROI by a letter of the alphabet, from A through L. A region, its associated count data, and its derived dynamic curve are all identified by the same letter. This procedure is described in greater detail in Sections 7.2.1 through 7.2.6. Most of the ROI commands are single character, immediate-effect commands (i.e., no carriage return is required). The system executes the command as soon as you type the character. The system does not echo any of the ROI commands on the display.

U

7.2.1 Up

The Up command (U) moves the displayed cursor up one cell. Type

    U

with no carriage return since the command is an immediate-effect command. The letter U does not appear on the screen.

D

7.2.2 Down

The Down command (D) moves the displayed cursor down one cell. Type

    D

with no carriage return since the command is an immediate-effect command. The letter D does not appear on the screen.

L

7.2.3 Left

The Left command (L) moves the displayed cursor left one cell. Type

    L

with no carriage return since the command is an immediate-effect command. The letter L does not appear on the screen.

R

7.2.4 Right

The Right command (R) moves the displayed cursor right one cell. Type

R

with no carriage return since the command is an immediate-effect command. The letter R does not appear on the screen.

J

7.2.5 Jump

The Jump command (J) moves the cursor ten cells in the direction of the last typed U, D, L, or R command. Type

J

with no carriage return since the command is an immediate-effect command. The letter J does not appear on the screen.

M

7.2.6 Mark

The Mark command (M) marks the present location of the cursor. Type

M

with no carriage return since all of the control commands are immediate-effect commands. The letter M does not appear on the screen.

Region of Interest Count Data - As soon as you have defined an ROI by designating two marks, the program extracts the following data from the region and displays it to the right of (beneath for a VT01) the matrix. See Figure 7-11 (color insert).

ROI COUNT	is the sum of the counts of all the cells in the region.
# OF CELLS	is the total number of cells in the region.
AV CELL COUNT	is the average cell count in the region (i.e., (ROI COUNT)/(# OF CELLS)).

When you mark another ROI, the procedure remains the same, except that this second region is labeled with the letter B. The system once again displays ROI count data to the right of the matrix along with the count data and outline of the first ROI. Figure 7-2 shows two ROIs, with the count data for each region displayed.

S

7.2.7 Same Shape

The Same Shape command (S) defines a new ROI with the same size and shape as a previously defined region. Type

S a (RET)

where "a" is an identifying letter of a defined ROI. If "a" is absent, the last ROI definition is used. The letter S does not appear on the screen. You should move the cursor by using the control commands. The position of the cursor marks the lower right corner of the new ROI.

K

7.2.8 Kill

The Kill command (K) erases the first mark of a pair of marks.

NOTE

The Kill command must be typed before the second Mark is issued.

Type

```
    K
```

on the terminal with no carriage return. This is an immediate-effect command and the letter K is not displayed on the screen. You cannot use the Kill command to erase a completely defined ROI. Use the E command for this purpose (see Section 7.2.10).

T

7.2.9 Step Through the Study

The Step Through the Study command (T) displays the current frame of a dynamic study and then displays each succeeding frame in turn at a specified rate.

Command format:

```
    T n RET
```

where n represents the delay in seconds between frames. The argument n can range from 0-9 seconds. The argument n is optional. If you omit n, the program uses a delay of 0 seconds. If n is 0, the program displays the frames as quickly as possible. To stop the automatic step, you must type any printing character on the terminal.

As each frame comes to the screen, the program superimposes the currently defined ROIs on the matrix in the prevailing display mode, and calculates and displays the count data for the frame.

E

7.2.10 Erase

The Erase command (E) erases specified ROIs.

Command format:

```
    E abc... RET
```

You specify the ROIs by typing their letters as the arguments of the command. The system deletes these ROIs from the display. If you give no argument, all ROIs are deleted. The system displays the current matrix, and you can define new ROIs. If you delete an ROI, the newly defined ROI replaces the ROI that you deleted.

For example, if you have previously defined five ROIs, A, B, C, D, and E, and you type

```
E BD(RET)
```

on the terminal, the ROIs B and D are erased. Now, if you define two new ROIs, GAMMA-11 labels the new ROIs with the letters B and D respectively.

Note that commas are not required, and the ROIs need not be specified in alphabetical order.

You can correct errors that you type. For example, suppose you type the following command, and then you realize that you listed an ROI that you really do not want to delete.

```
E ABGJ
```

If you have not already typed RETURN, you can type CTRL/U on the terminal to erase the command line. The ROI procedure does not recognize DELETEs. For example, if you type the following line,

```
E ABFJ^U
```

the CTRL/U causes the incorrect line to be ignored. You can now enter the correct command line.

```
E ABGJ(RET)
```

7.3 IRREGULAR REGIONS OF INTEREST (ROIs)

Irregular ROIs can be any shape or size within the boundaries of the matrix. You can specify as many as 12 irregular regions at any one time. The regions may overlap, intersect, or be wholly contained in other regions.

7.3.1 Joystick Positioning

Since the irregular ROI may be any shape, you control the shape of an ROI using a joystick that moves the cursor in any direction. When you press the INTERRUPT bar on the joystick, the program records the path of the cursor.

You complete the definition of an irregular ROI by marking its postion using one Mark (M) command.

IR

7.3.2 Irregular ROI Command

To enter the irregular ROI mode, type the following command on the terminal in response to the COMMAND: request.

```
IR(RET)
```

The system erases the screen and then redisplays it with the cursor somewhere in the matrix, depending upon the position of the joystick. The COMMAND: request does not appear. If the cursor is not readily apparent when using the VT01, wiggle the joystick a bit to find it. Orient the control unit so that the tip of the joystick reflects the position of the cursor. You should pull the joystick toward your body to move the cursor to the bottom of the matrix. Move the joystick away from your body to move the cursor toward the top. Move the joystick left or right for corresponding motions.

In general, the method for defining an irregular ROI is as follows:

1. Move the cursor to the desired point.
2. Press the INTERRUPT bar on the joystick control.
3. Keeping the INTERRUPT bar depressed, move the joystick so that the cursor draws the outline of the ROI.
4. Release the INTERRUPT bar, and mark the ROI by typing the immediate-effect command, M. The letter A appears inside the region on the VSV01 only.

The system calculates and displays the count data for each region.

To delete an ROI path before the mark, press RETURN.

You cannot define irregular regions on 128 x 128 matrices. Use regular ROIs for this configuration. For 128 x 128 matrices the IR command defaults to RI.

Irregular ROIs appear regular within the regular ROI procedure. If you reenter irregular ROI mode, the irregular ROIs again appear irregular.

NOTE

Sections 7.3.3 and 7.3.4 apply only to the VSV01 Color Display.

K A

7.3.3 Erase Cells

The Erase Cells command enables you to erase part of an irregular ROI while you are outlining it. The following immediate-effect command switches the mode from marking to unmarking.

K

As in marking, you control the unmarking with the joystick. As you move the crosshairs along the partial ROI, the system erases the previously defined cells.

To switch back from unmarking, type the following immediate-effect command.

A

You can use the K and A commands to erase only a partial ROI and not a region that has already been marked with an M command. To erase a marked ROI, use the E command (see Section 7.2.10).

Q

7.3.4 Enlarging an Area of the Display

You can enlarge an area of an image to define an ROI more easily. To enlarge the area, move the crosshairs to the middle of the area to be enlarged (see Figure 7-1). Then type the following immediate-effect command, which enlarges the area by a factor of 4 (see Figure 7-2).

Q

Once the area is enlarged, you can define the ROI in the normal manner. The image automatically returns to the normal size with any command but K or A.

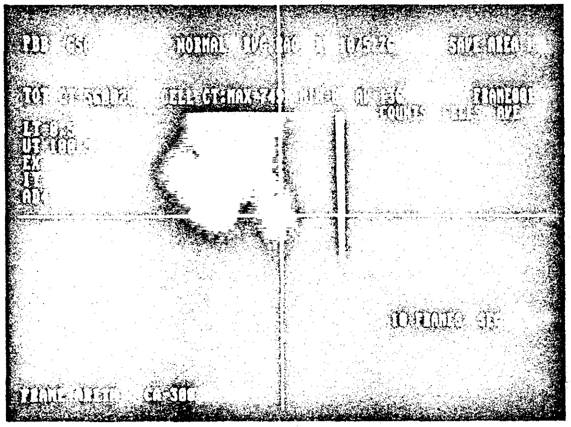


Figure 7-1
Positioning the Crosshairs

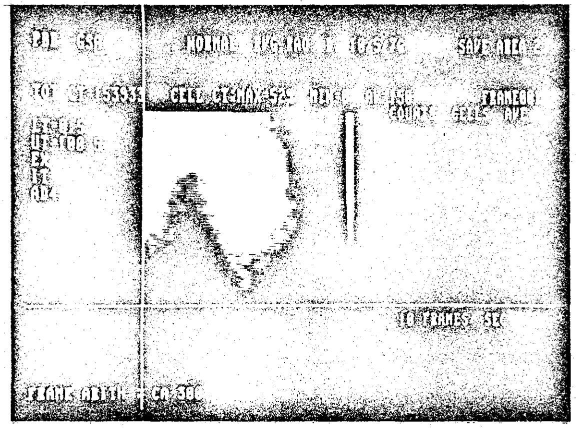


Figure 7-2
Enlarged Area of the Image

7.4 DEFINITION MODE COMMANDS

You can define irregular ROIs by means of two immediate-effect mode-setting commands.

1. Circumference mode
2. Fill mode

Circumference mode is the default.

C

7.4.1 Circumference Mode

Once again, you define a region by outlining it with the cursor. In circumference mode, an irregular ROI consists of cells along a circumference path and all of the cells in the interior of the outlined area. This mode is the default condition when you first issue the IR command.

To switch to circumference mode from fill mode, type the following command with no carriage return.

```
C
```

In circumference mode, the path of the cursor can be simply or multiply connected, or not connected at all. If the path of the cursor is disconnected, each piece of the ROI defines a sub-ROI. The total ROI consists of all sub-ROIs. The illustration in Figure 7-13 (color insert) displays such an outline. Figure 7-12 (color insert) displays a simply connected ROI.

The ends of the outline need not meet exactly, but if they cross, the loose ends are included in the defined ROI (see Figure 7-14 in the color insert). Notice that the total cell count includes the outlined area, plus the extra cells that the loose ends cover.

You do not have to close an outline. However, if you do not close the outline, the resulting ROI consists of only the path traced by the cursor. The total cell count is the sum of only those cells in the border of the ROI (i.e., those cells specifically marked by the joystick).

F

7.4.2 Fill Mode

In fill mode, the defined ROI consists of only those cells through which the cursor actually passes when the INTERRUPT bar is down. That is, you must fill in every cell in the ROI. To switch to the fill mode, type the following command with no carriage return.

```
     F
```

In fill mode, the path of the cursor can be simply or multiply connected, or not connected at all. An irregular ROI can consist of a single curve or of several noncontiguous areas obtained by filling in a patch, raising the INTERRUPT bar, and moving the cursor to a new spot. You can define several such areas in one irregular ROI, since the region is not defined until you type the mark command (M). Figure 7-15 (color insert) shows a noncontiguous ROI. Unlike the circumference mode, the fill mode requires you to define every point in the region.

NOTE

Section 7.4.3 applies only to the VSV01 color display.

V

7.4.3 Defining an ROI Using Threshold Levels

You can use a threshold level or an isocontour to create an ROI. To use a threshold level as an ROI, you must first obtain an image with lower and upper threshold levels that define the ROI (see Figure 7-3). You can obtain this image using the LT, LTN, UT, UTN, W, X, Y, and Z commands. Alternately, to use an isocontour as an ROI, obtain the appropriate isocontour image using the IC or ICF command.

Then, enter ROI mode and define an ROI using the joystick in the normal manner (see Figure 7-4). You can use either fill mode or circumference mode (see Section 7.4). Instead of typing M for mark, type

V

to mark the ROI. You do not need to type RETURN because V is an immediate effect command. The new ROI is defined by those cells that are in both the area circled by the joystick and the displayed cells of the isocontour (see Figure 7-5). The new ROI is defined in the prevailing mode, circumference mode or fill mode. Figures 7-6, 7-7, 7-8, and 7-9 show defining an ROI using an isocontour.

NOTE

> If you enter ROI mode and type V without having used the joystick to circle the threshold or isocontour, the entire threshold or isocontour defines the ROI.

This method of defining an ROI is very useful when you desire to see the exact shape of an organ; for example, defining the left ventricle.

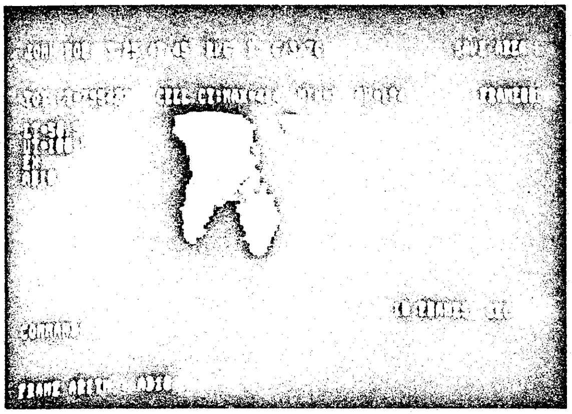


Figure 7-3
Defining Threshold Level

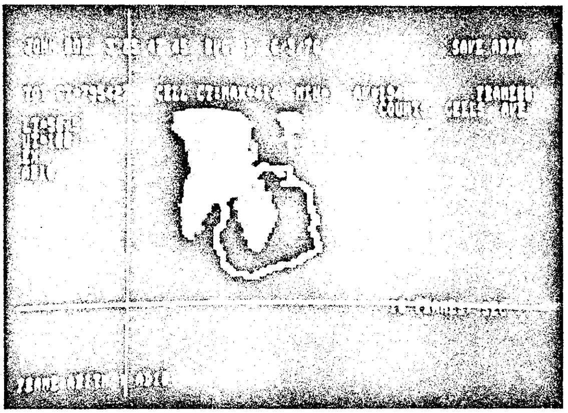


Figure 7-4
Defining the ROI

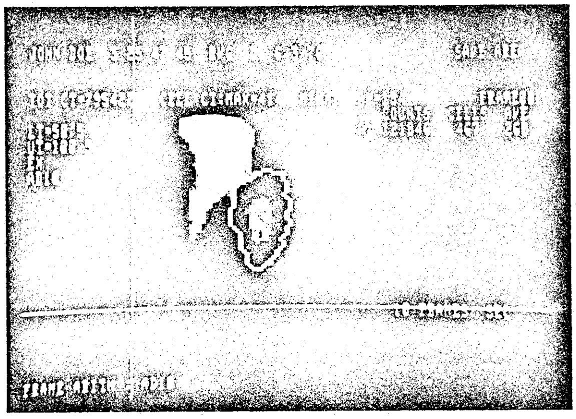


Figure 7-5
The New ROI

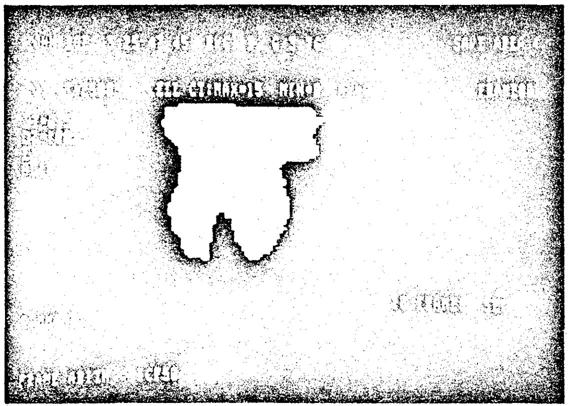


Figure 7-6
Defining an Isocontour

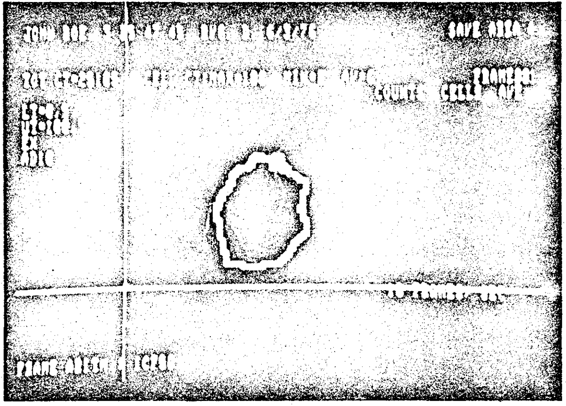


Figure 7-7
Defining the ROI

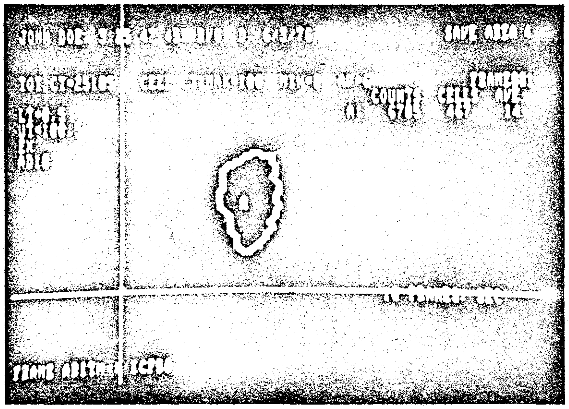


Figure 7-8
The New ROI

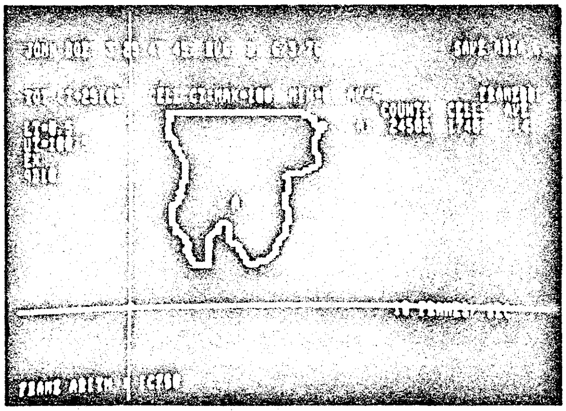


Figure 7-9
The ROI if the
Iscontour Is Not
Circled by the Joystick

7.5 DISPLAY MODE COMMANDS

GAMMA-11 provides two modes of displaying irregular ROIs. You establish these modes with the following immediate-effect commands:

1. Boundary display

2. Interior display

B

7.5.1 Boundary Display

You can display an outline of each ROI (regular or irregular) by issuing the Boundary Display command. Type:

```
B
```

with no carriage return. When you type this command, the system erases the screen, and redisplays the frame with the outlines of the defined ROIs displayed in their respective positions without the matrix. An example is shown in Figure 7-16 (color insert). To restore the matrix display, press RETURN. The irregular ROI outlines remain superimposed on the matrix.

I

7.5.2 Interior Display

You can display the area (or interior) of an irregular ROI by issuing the Interior Display command. Type the following command with no carriage return.

```
I
```

When you type this command, the system erases the screen and redisplays the frame with the irregular ROIs in their respective positions without the matrix. The interior of each irregular ROI is filled with white (or its letter if using the VT01) (see Figure 7-17 in the color insert). To restore the matrix display, press RETURN. The filled-in irregular ROIs remain superimposed on the matrix.

The Boundary Display and Interior Display commands set a prevailing mode that remains in effect until you type an alternate command. These commands display only the irregular ROIs, which is useful for verifying sizes, shapes, and positions without interference from matrix data in the background.

7.6 OTHER COMMANDS

The following sections (7.6.1 through 7.6.4) describe the other commands applicable during ROI mode.

7.6.1 Threshold Adjustment

The following immediate-effect commands are threshold-adjusting commands. These commands are also effective within ROI mode.

W, X, Y, Z, N, O

These commands are described in Sections 5.7.3 through 5.7.6, and 5.8.2 through 5.8.3. The first four commands adjust the thresholds individually according to step sizes currently displayed. The last two adjust the threshold band up or down according to the thresholds currently displayed.

RET

7.6.2 Carriage Return

The Carriage Return command (a RETURN by itself) restores the current frame, as indicated by the frame number, with ROIs in the prevailing mode. Type:

RET

on the terminal.

SP

7.6.3 Space Bar

The Space Bar command displays the next frame of the study with current ROIs. Type:

SP

on the terminal. No carriage return is required because this is an immediate-effect command. The program calculates and displays count data for the new frame. If the message

FRAME ARITH: ADn

is on the screen when you type the space bar, or if ADn appears under the threshold settings, the program performs the indicated sliding add.

-

7.6.4 Hyphen

The Hyphen command displays the previous frame of the study with all current ROIs and new count data. Type:

```
- (hyphen)
```

on the terminal. No carriage return is required, because this is an immediate-effect command.

7.7 DYNAMIC-STUDY CURVES

In a normal dynamic study, the count-collection rate varies from frame to frame. With the commands described in the following sections, the system can calculate the count rate for each ROI and can plot curves for each region over the entire study. You can store the curve data in a save area. The system can also calculate and plot curves derived from the average count-rate per cell in each region. You can print or punch tabular lists of counts per frame for each ROI.

A typical dynamic curve is shown in Figure 7-18 (color insert). The system plots count rate on the Y-axis and time on the X-axis. The figure at the top of the Y-axis is a maximum count rate.

The system marks off the X-axis in frames. This scale is linear in time. The frame marks of slower groups are further apart, as you can see in Figure 7-18. The numbers on the X-axis are frame numbers.

7.8 CURVE-CALCULATION COMMANDS

The ROI program can calculate curves for each defined ROI and for the entire matrix. You can specify individual curves by an argument consisting of the letters of the ROIs whose curves are to be calculated. The letters need not appear in order, and commas are not required.

PN

7.8.1 Plot Normal Dynamic Curves

The Plot Normal Dynamic Curves command (PN) calculates the count-rate curves for the total matrix and for each (specified) ROI.

Command format:

```
PN abc... RET
```

The program displays the curves up to two at a time, each on its own axes, in alphabetical order (see Figure 7-19 in the color insert). If you type the command line without an argument:

```
PN RET
```

the program displays the first two curves. The top curve represents the total-count-rate-versus-time curve for all frames. The "versus time" means that the abscissa scaling reflects any frame-rate changes. However, the units of the abscissa are the frame numbers (not the time). This curve is called the T curve. The bottom curve is the first defined ROI. The system displays the next pair of curves when you type any printing keyboard character except the letter P. After the system displays the last curve, typing anything othdr than the letter P erases the plot and restores the matrix display with ROIs.

At any time during the plot display, if you wish to issue another plot command, you can do so by typing the appropriate command line. For example, if you type the following command on the terminal, the program displays curves A and C.

```
PN ACFGI RET
```

When you press any keyboard character (other than P, because P alerts the system that another plot command is going to be typed), the program displays curves F and G.

If you type:

```
PN RET
```

on the terminal, the program displays all defined ROIs in alphabetical order. That is, if you originally defined ROIs A, B, C, D, and E, those curves are presented on the display in pairs (that is, first curves T and A, then B and C, then D and E, etc.).

PO

7.8.2 Plot Overlaid Dynamic Curves

The Plot Overlaid Dynamic Curves command (PO) calculates the count-rate curves for the total matrix and for each specified ROI, and then plots these curves on the same set of axes.

Command format:

```
PO abc... RET
```

Each ROI is represented by a color. These colors are yellow, red, blue, and green.

yellow = the first, fifth, ninth, and thirteenth curves
red = the second, sixth, and tenth curves
blue = the third, seventh, and eleventh curves
green = the fourth, eighth, and twelfth curves

This configuration is displayed beneath the set of axes. The system plots each curve in its respective color. Figure 7-20 (color insert) is a typical example of the overlaid curve display.

On the VT01, the system plots each curve with its ROI identification letter. The total matrix curve is plotted with the letter T. Each curve on the VT01 is still identified with its ROI identification letter.

If the argument is omitted from the command line by your typing:

```
PO RET
```

the program overlays all of the ROI curves on one set of axes. Each curve on the VT01 is still identified with its ROI identification letter.

To restore the matrix ROI display, type any keyboard character except the letter P.

For example, if you type:

```
PO ABGJL RET
```

on the terminal, the program overlays curves A, B, G, J, and L with the following identifying colors (letters for a VT01):

curve A = yellow
B = red
G = blue
J = green
L = yellow

When you press a keyboard character (other than P, because P alerts the system that another plot command is going to be typed), the program displays the original ROI matrix.

PA

7.8.3 Plot Overlaid Average Rate Curves

The Plot Overlaid Average Rate Curves command (PA) calculates the average count rate per cell for each specified ROI and plots the curves on the same set of axes.

Command format:

```
PA abc... RET
```

The program plots each curve of average count rates per cell with its ROI identification color (letter for a VT01). The total matrix curve is plotted in yellow (or T for a VT01). If you type the following command line without an argument:

```
PA RET
```

the program overlays all of the average-count-rate ROIs on one set of axes. Each curve is still identified with the ROI identification color.

To restore the matrix ROI display, type any keyboard character except the letter P. P alerts the system that a new plot command is going to be issued.

7.9 FRAME-LINEAR SCALE COMMANDS

At times, you may wish to make the X-axis linear with respect to frame numbers rather than to time intervals. You can do so by issuing the commands outlined in Sections 7.9.1 through 7.9.3.

PNM

7.9.1 Plot Normal Frame-Linear Curves

The Plot Normal Frame-Linear Curves command (PNM) displays the count-rate curves as counts versus frame numbers rather than counts versus time intervals. That is, the X-axis units are frame numbers rather than time intervals.

Command format:

```
PNM abc... RET
```

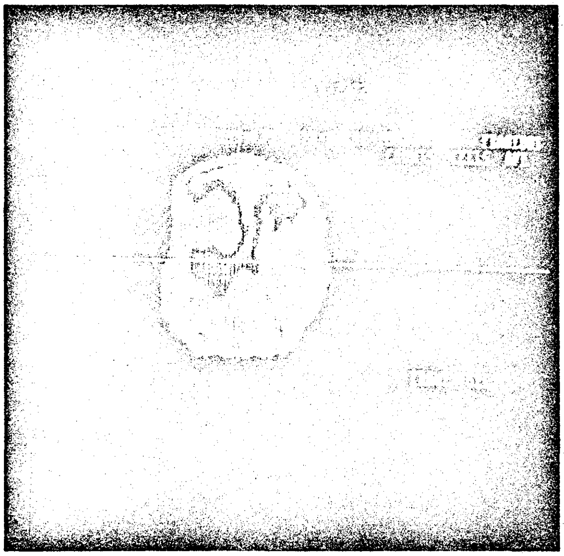


Figure 7-10
Matrix with Cursor

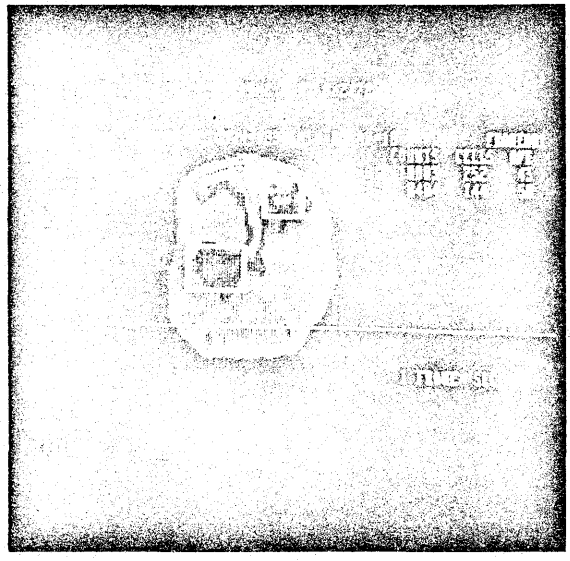


Figure 7-11
Two ROIs: A and B

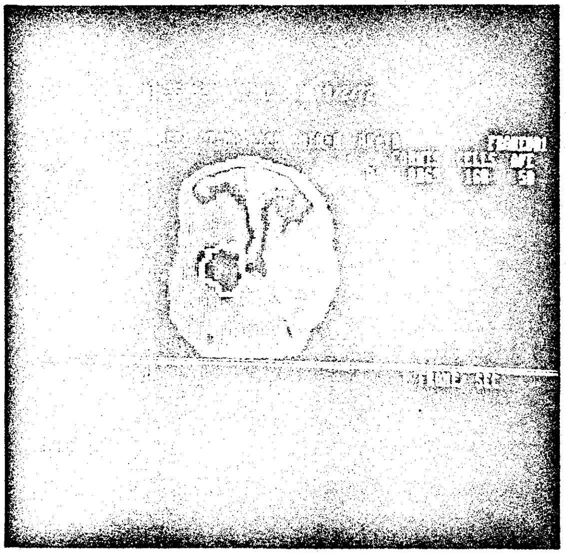


Figure 7-12
Simply Connected ROI

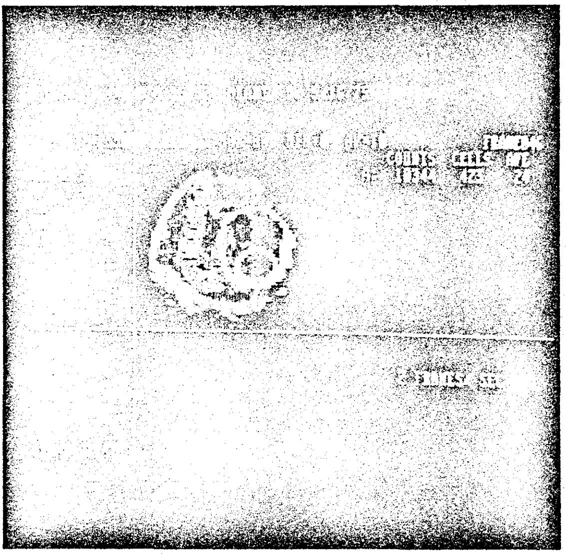


Figure 7-13
Multiply Connected ROI

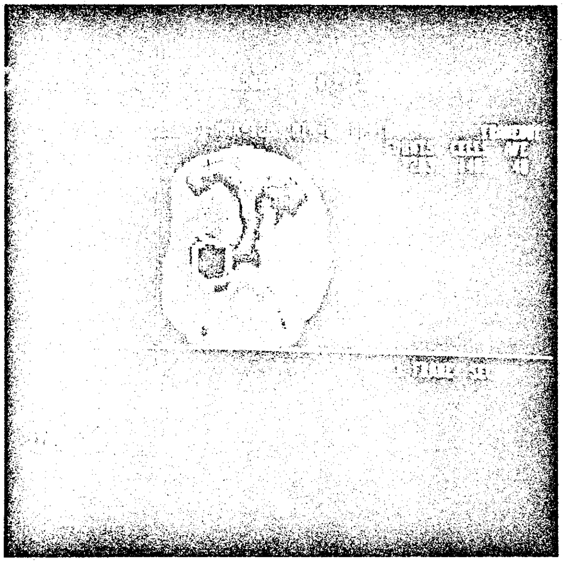


Figure 7-14
ROI with "Loose Ends"

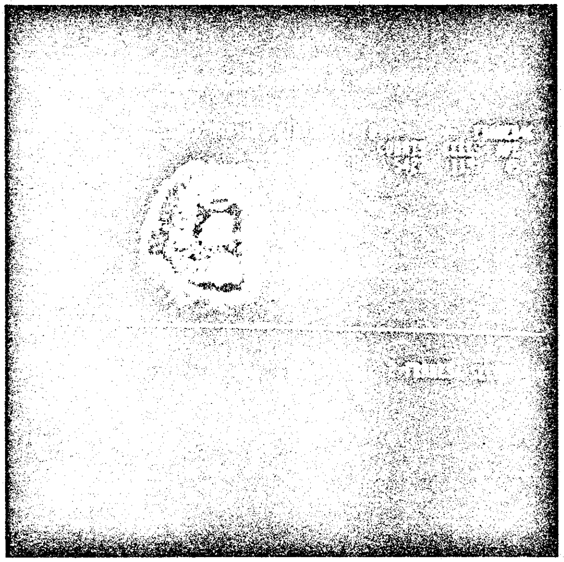


Figure 7-15
Noncontiguous Irregular
Region (Fill Mode)

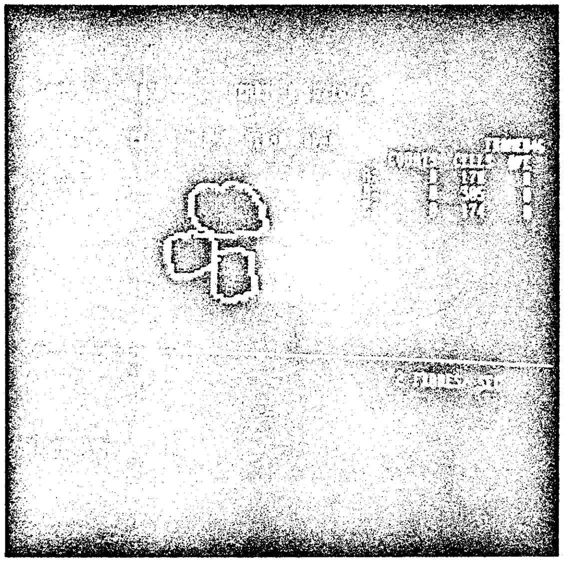


Figure 7-16
Boundary Display:
Three Regions

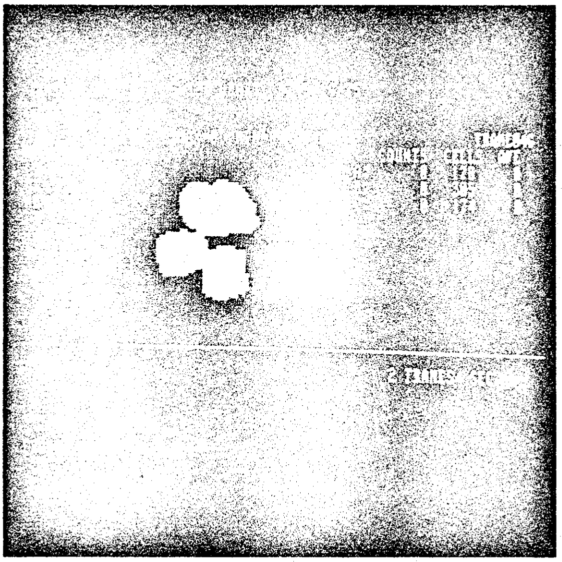


Figure 7-17
Interior Display:
Three Regions

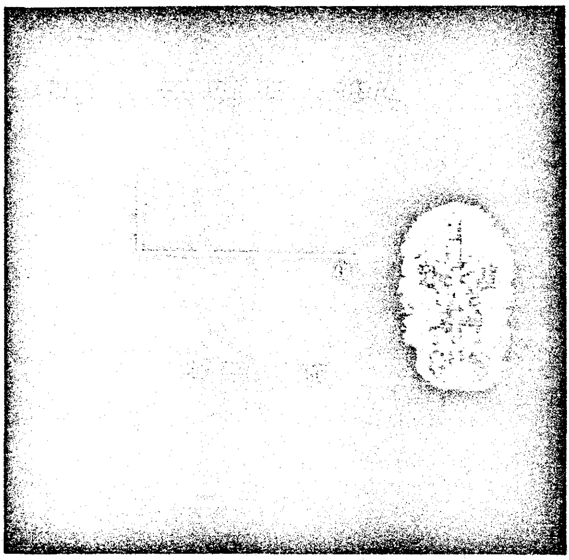


Figure 7-18
ROI Count Rate Curve

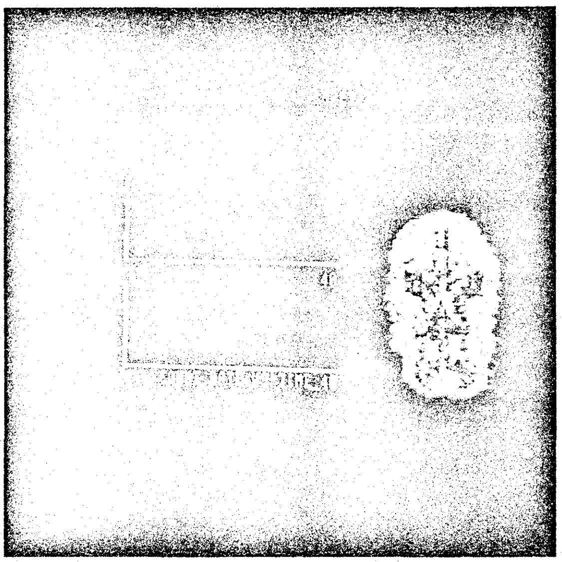


Figure 7-19
Individual Curve Display (PN)

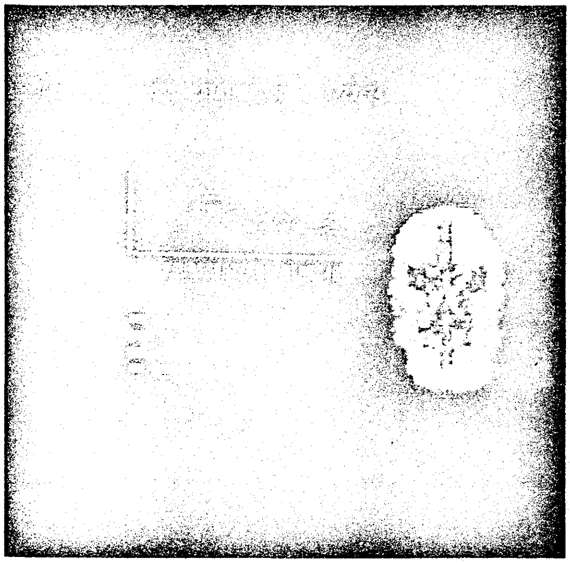


Figure 7-20
Overlaid Curve Display (PO)

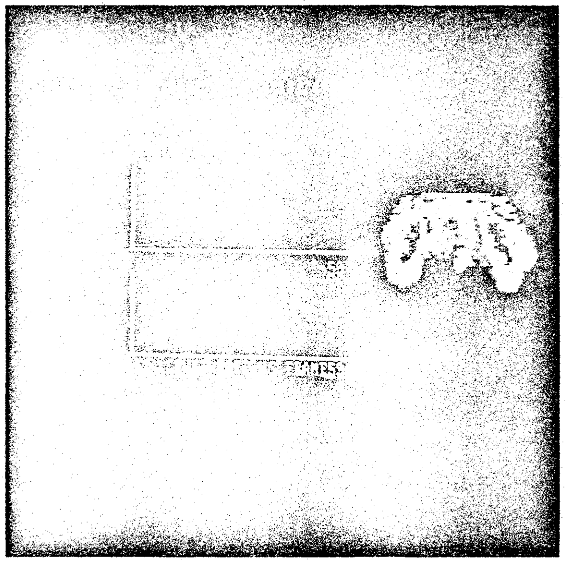


Figure 7-21
Frame-Linear
Curve Display (PNM)

The program displays the curves two at a time in alphabetical order (Figure 7-21 in the color insert), each on its own axes. When the graph is drawn, the X-axis frame ticks are equally spaced and the graph title changes to:

ROI x COUNT RATE VS FRAME NUMBER

to indicate that this is a frame-linear curve. The top frame represents the TOTAL COUNT RATE VS FRAME number (where number is the total frame number) for all ROIs. The program automatically expands that part of the X-axis so that the distance between ticks produces a legible curve plot. Compare Figure 7-19 to Figure 7-21 (color insert). Notice, that in Figure 7-19 there are some tick marks close together at the beginning of the study, and in Figure 7-22 the tick marks are equidistant to provide a linear curve.

The bottom curve is the first defined ROI. The program brings the next pair of curves to the screen when you type any character on the keyboard except the letter P. Each time you type a character, the next pair of ROI curves appear on the screen. After the last curve is displayed, typing any keyboard character restores the matrix display with ROIs. You can omit the argument from the command line by typing:

```
PNM RET
```

This process brings all ROIs to the screen at your command.

At any time during the plot display, you can initiate another plot by typing the appropriate command line.

POM

7.9.2 Plot Overlaid Frame-Linear Curves

The Plot Overlaid Frame-Linear Curves command (POM) displays the frame-linear curves overlaid on the same set of axes.

Command format:

```
POM abc... RET
```

The program plots each curve with its ROI identification color (letter for a VT01). The total matrix curve is yellow (or plotted with the letter T for a VT01). The program spaces the X-axis frame ticks equally, and the graph title changes to:

COUNT RATE VS FRAME NUMBER

to indicate that this is a frame-linear curve. If you type the command line without the argument:

```
POM RET
```

all of the ROI curves are overlaid on one set of axes and the tick marks are equally spaced to indicate frame-linear curves.

To restore the matrix ROI, type any keyboard character except the letter P. Typing P alerts the system that a new plot command is going to be entered.

PAM

7.9.3 Plot Average Frame-Linear Curves

The Plot Average Frame-Linear Curves command (PAM) displays the count-rate curves as average cell count versus frame number. The program overlays the curves on the same set of axes.

Command format:

```
     PAM abc... (RET)
```

The program plots each curve of average count rates per cell with its ROI identification color. The total matrix curve is yellow (or plotted with the letter T for a VT01). The program spaces the X-axis frame ticks equally, and the graph title changes to:

```
     COUNT RATE VS FRAME NUMBER
```

to indicate that this is a frame-linear curve. If the command is typed without an argument:

```
     PAM (RET)
```

the program overlays all of the average cell count rates for each ROI on one set of axes, and spaces the tick marks equally to indicate frame-linear curves.

To restore the matrix ROI, type any keyboard character except the letter P. Typing P alerts the system that a new plot command is going to be entered.

7.10 WINDOW COMMANDS (PARTIAL CURVE PLOTTING)

Window commands plot a portion of a curve. The window commands are outlined in Sections 7.10.1 through 7.10.3.

PW

7.10.1 Plot Window

The Plot Window command (PW) plots a particular number of frames (part of an entire curve), starting with a specified frame number.

Command format:

```
PW f,n RET

PW f RET

PW ,n RET

PW RET
```

where,

f is an integer indicating the first frame to plot.

n is an integer indicating the number of frames to plot.

Both f and n are optional. If you omit either parameter from the command, the program uses the previous value. If you omit both parameters, all points are plotted.

You must issue one of the plot commands (PO, PA, PN) before the window commands can work.

For example, if you type:

```
PN B RET
```

on the terminal, the plotted curve looks like the full plot shown in Figure 7-22.

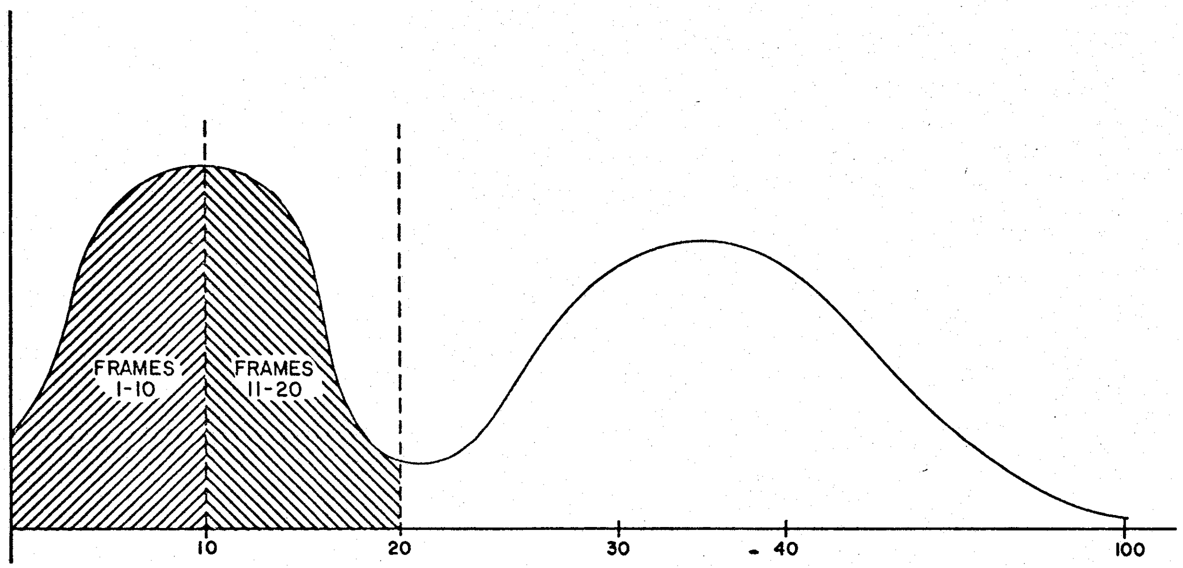


Figure 7-22
Full Plot

If you then type:

```
PW 1,10(RET)
```

on the terminal, the program plots the first 10 frames of data. The 1 represents the starting frame and the 10 represents the number of frames to plot. The plot changes to look like the partial plot shown in Figure 7-23.

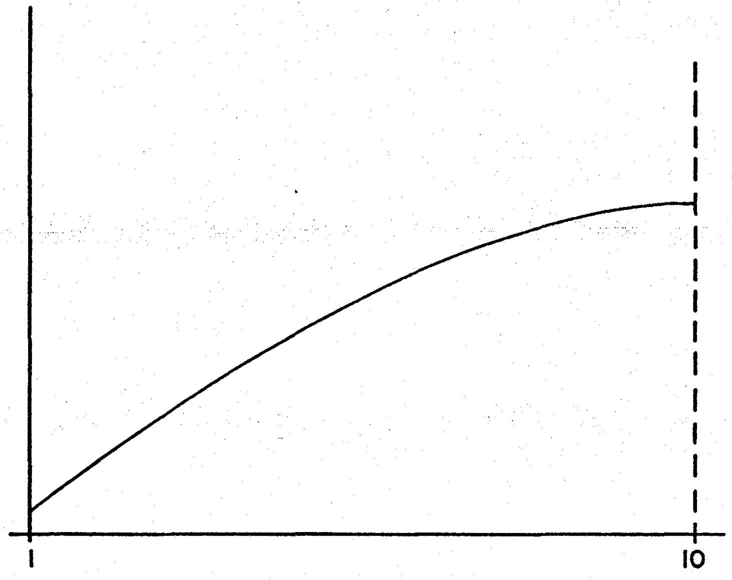


Figure 7-23
Partial Plot (Window Frames 1-10)

Notice that the program displays only the data from the ROI in frame #1 through frame #10. This area represents the first shaded area in Figure 7-22. This procedure is known as windowing.

To restore a full plot, type:

```
PW(RET)
```

To restore the matrix ROI, type any keyboard character except the letter P. Typing P alerts the system that a new plot command is going to be entered.

PF

7.10.2 Plot Forward Window

The Plot Forward Window command (PF) brings the next group of frames from the specified number of frames to plot and displays this partial curve on the screen. Internally, the program computes a new f value by adding the window size n to the previous f value. Type:

```
PF (RET)
```

on the terminal to bring the next group of frames specified via the PW command. For example, in Figure 7-22 the data of the first 10 frames is brought to the screen when you type the following commands.

```
PN (RET)
PW 1,10 (RET)
```

If you then type the PF command, the program brings the next 10 frames of data (for an ROI plot) to the screen. Thus, the diagram changes as shown in Figure 7-24.

The display in Figure 7-24 represents the second shaded area from Figure 7-22.

Each time you type the PF command, the next 10 frames are windowed (or shown on a full scale of the graph). Example:

Command	Effect
PF (RET)	Frames 21-30 are brought to the screen.
PF (RET)	Frames 31-40 are brought to the screen, and so forth.

To restore the matrix ROI, type any keyboard character except the letter P. Typing P alerts the system that a new plot command is going to be entered.

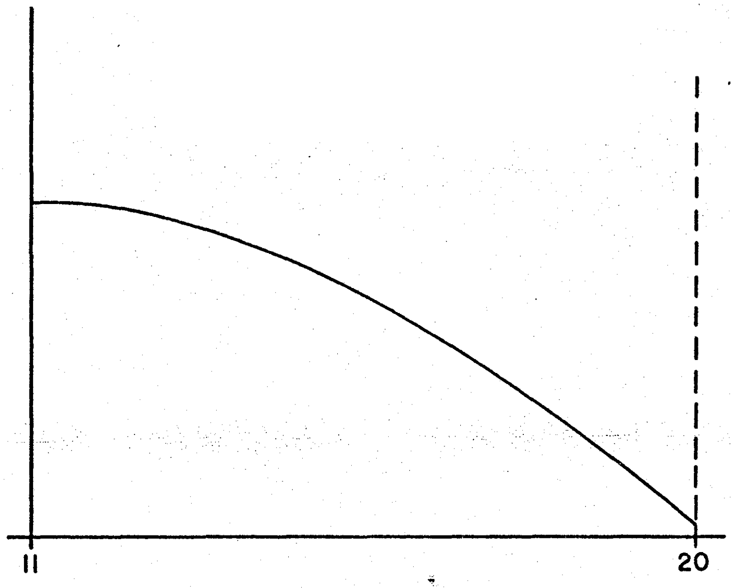


Figure 7-24
Partial Plot (Window Frames 11-20)

PB

7.10.3 Plot Backward Window

The Plot Backward Window command (PB) brings the previous group of frames from the specified number of frames to plot and displays this partial curve on the screen. Type:

```
PB RET
```

on the terminal to bring the previous group of frames specified with the PW command. For example, when you type:

```
PN RET
PW 1,100 RET
```

frames 1 through 100 are plotted. Next, typing:

```
PF RET
```

on the terminal causes frames 101 through 200 to be plotted. Now, typing:

```
PB RET
```

on the terminal causes frames 1 through 100 to be restored.

Example:

Command	Effect
PW 1,10 RET	frames 1-10 are displayed
PF RET	frames 11-20 are displayed
PF RET	frames 21-30 are displayed
PB RET	frames 11-20 are displayed
PF RET	frames 21-30 are displayed
PF RET	frames 31-40 are displayed
PB RET	frames 21-30 are displayed

To restore the matrix and ROI, type any keyboard character except the letter P. Typing P alerts the system that a new plot command is going to be entered.

7.10.4 Plotted Averages

When a study contains a large number of frames, the points of a curve may be crowded together, making the curve difficult to read. This is especially true in overlaid graphs. If this should happen, GAMMA-11 can selectively average points when you include a digit n as part of the argument of any curve-plot command (PN, PO, PA). The permitted values of n are 1 through 9,

where n=1, every point is plotted
n=2, every two points are averaged and plotted
n=3, every three points are averaged and plotted
n=4, every four points are averaged and plotted
.
.
.
n=9, every nine points are averaged and plotted

The value n=1 is the default for all of the commands. In other words, if you omit n, the program plots every point.

The digit may appear anywhere in the argument. For example:

Command	Effect
PA 3 RET	Every three points of each curve are averaged. All of the averaged curves are overlaid.
PO BF2 RET	Every two points of each curve, B and F, are averaged. Then B and F are plotted on the same axes.
PN 4AE RET	Every four points of each curve, A and E, are averaged and plotted.

7.11 TABULAR DATA

You can print a table of counts within an ROI for each frame in each ROI in a dynamic study. If you give the tabular data commands without arguments, the commands produce output for every defined ROI. By specifying ROI identification letters as arguments to the commands, you command only the tables for those ROIs to be printed.

You must specify the total-matrix table, consisting of the total number of counts in the entire matrix for each frame, by the letter T. The total-matrix is not printed or punched when you give no argument.

PR

7.11.1 Print Count Data

The Print Count Data command (PR) provides you with a tabular list of counts per frame for each ROI that is listed as an argument. If no argument is given, all ROIs are printed.

Command format:

PR abc... RET

The tables are prefaced with an identifying header consisting of the study's index entry, the number of curves to be printed, and the number of frames in the study. An example of an ROI tabular list is represented in Figure 7-25.

```
CAYER, 49-06-81, CARDIAC, D, 11/15/73

  1 CURVES

 50 FRAMES IN STUDY

ROI A CELL COUNTS PER FRAME

         0
        12
       164
      1564
      2608
      1950
      1590
      1154
       793
       675
       613
       730
       850
       803
       974
       751
       696
       715
       574
       515
       498
       486
       444
       472
       438
       458
       381
       423
       401
       369
       355
       384
       375
       400
       386
       374
       402
       359
       363
       410
       370
       371
       361
       343
       347
       343
       366
       339
       325
       363
```

Figure 7-25
ROI Tabular Data (Command: PR A)

PU

7.11.2 Punch Count Data

The Punch Count Data command (PU) punches the count-data tables on paper tape.

Command format:

```
PU abc... RET
```

The format of the count-data tables on paper tape is the ASCII equivalent of the printed information, except that there is only one pair of carriage return/line feeds between lines. For legibility, the program deletes extra blank lines that appear on the terminal from the punch output.

PP

7.11.3 Print and Punch Count Data

The Print and Punch Count Data command (PP) outputs count data simultaneously on the terminal and onto paper tape. The data are represented by their respective formats.

Command format:

```
PP abc... RET
```

7.12 SAVE AREA USE

You can use the save areas to store matrix-plus-ROI information and dynamic curves. To save a displayed matrix with its ROIs, type the following command sequence (from either ROI mode):

```
CTRL/X
SM n RET
```

When you type CTRL/X, the ROI display disappears and the request COMMAND: reappears. If you type SM n in response to COMMAND:, the previous matrix-ROI display is stored in save area n. You can store matrices in save areas 1 through 64.

When the system reads the contents of the save area, it displays the matrix and ROIs and automatically calls the ROI subset into operation.

To save a set of dynamic-study curves, use the following sequence:

1. If the curves are on the screen, type anything except P to restore the matrix-ROI display.
2. Type CTRL/X
3. Type SD n RET

When you type SD n in response to the displayed COMMAND: request, as described above, the program stores the curve data in save area n. You may store dynamic curves only in save areas 1 through 9. When the system reads contents of the save area, it displays the curves as plot average. At this point, only the commands PN, PA, PO, PU, PR, PW, PF, PB, and PP are executable. Any other input has tne effect of an RS0 command, restoring the previous matrix display.

7.13 EXIT

To leave an ROI procedure, type:

```
CTRL/X
```

CTRL/X returns to the data-analysis mode, and the COMMAND: request reappears.

CHAPTER 8

SLICING

The operations described in this chapter allow you to examine the data patterns of slices through the matrix (i.e., horizontal or vertical strips of varying width). For each slice, the program plots a curve of the cell-count distribution. You can copy the curve data in tabular form on printed copy, punched tape, or screen display. In a dynamic study, once you have selected the slices, you may examine each frame in sequence. New curves are automatically plotted when the new frame is displayed.

Six of the slice commands, U, D, L, R, M, and J, are all immediate-effect commands. They require no RETURN terminator and do not appear on the screen when typed. The remaining commands are all carriage-return terminated.

8.1 SLICE SELECTION COMMANDS

A slice can be horizontal or vertical and can vary in width from 1 to 9 rows or columns. On the VT01, 26 slices can be selected for one display. On the VSV01, three slices can be displayed, as well as the current position.

SH

8.1.1 Horizontal Slice

To initiate the horizontal slice procedure, type the following command on the terminal.

```
SH n(RET)
```

The argument n is optional and represents the number of rows of the width of the slice. If you omit n, the slice is one row.

The program is now prepared to accept horizontal slices. Figure 8-1 (color insert) represents a preparatory display of a horizontal slice.

At the top of the screen is a display of the core-resident matrix. Directly beneath it are the axes on which the curves are plotted.

On the VSV01, a cursor appears as a long line through the center of the matrix. You can now issue immediate-effect commands (U, D, M, and J). (See Sections 8.2 and 8.2.1.) On the VT01, the cursor is shown as a small open circle, and it appears to the right of the matrix.

Additional study data (i.e., thresholds, counts, frame number, etc.) remain on the screen. The unlabeled axis (X-axis) of the plot represents cell position along the slice. The other axis (Y-axis), labeled at two points (four points for the VT01), plots the number of counts per cell or group of cells. The scale of this axis is determined by the maximum number of counts per cell (CELL CT: MAX) in the matrix. Initially, as shown in Figure 8-1 (color insert), the scale factor is 1. You can adjust the scale factor to any desired value (see Section 8.5.1).

SV

8.1.2 Vertical Slice

To initiate the vertical slice procedure, type the following command on the terminal.

```
SV n RET
```

The argument n is optional and represents the number of columns of the width of the slice. If n is omitted, the slice is one column.

The program is now prepared to accept vertical slices. Figure 8-2 (color insert) represents a preparatory display of a vertical slice.

Notice that the cursor for a vertical slice appears vertically through the center of the matrix. The curve of the slice is plotted in white vertically to the right of the matrix.

On the VT01, the cursor for a vertical slice appears at the bottom of the minified matrix.

You can now issue immediate-effect commands (L, R, M, and J). (See Sections 8.2 and 8.2.1.)

The unlabeled axis (Y-axis) of the graph plots cell position along the slice. The other axis (X-axis), labeled at two points (four points for the VT01), plots the number of counts per cell or group of cells. The scale of this axis is determined by the maximum number of counts per cell (CELL CT: MAX) in the matrix. Initially, as shown in Figure 8-2, the scale factor is 1. You can adjust the scale factor to any desired value (see Section 8.5.1).

8.2 IMMEDIATE-EFFECT SELECTION COMMANDS

The immediate-effect commands move the cursor and mark the position of the slice. For greater detail, see Sections 7.2.1 through 7.2.5. These commands are:

U	Move the cursor up one row.
D	Move the cursor down one row.
L	Move the cursor left one column.
R	Move the cursor right one column.
J	Jump the cursor 10 cells in the direction of the last typed U, D, L, or R command.

The cursor moves as indicated. Commands U and D are valid only for horizontal slices, L and R are valid only for vertical slices. In no case does the cursor move past the boundaries of the matrix in any direction.

8.2.1 Mark

To mark a slice, type M with no carriage return. The program draws a line through the indicated row or column of the matrix and plots a curve of cell counts along the line of the slice. (See Figures 8-3 and 8-4 in the color insert.)

8.3 FRAME SELECTION (DYNAMIC STUDIES ONLY)

You may examine each frame of a dynamic study using the currently marked slices. You must press the space bar on the terminal to advance to the next frame. The next frame in the study is displayed, and curves are plotted for each slice using the new data.

8.4 STARTING THE SLICE OVER

At any time during the slice procedure, you can change the orientation (horizontal or vertical) or the width of the slice by using the commands

```
SH n RET
SV n RET
```

as previously described. The system erases the existing display, deleting all curves and slices. A new display, with new axes and cursor, appears on the screen.

You can delete curves without changing the other conditions using the following command.

E RET	Erase The screen is erased and all curves and marked slices are deleted. The preparatory display reappears. The orientation, slice width, and scale factor are not changed.

8.5 SLICE CURVE PLOTS

As soon as you issue the Mark command (M), the program draws a line through the indicated row or column of the matrix and plots a curve of cell counts along the line of the slice. Figure 8-3 (color insert) displays the plots of one three-row horizontal slice. Figure 8-4 (color insert) displays the plots of three one-column vertical slices.

Each point on the horizontal slice curve in Figure 8-3 represents the sum of the three points in that position of the slice. That is, the first point of the curve represents the sum of the three points in the first column of the horizontal slice. Since the slices in Figure 8-4 are one column wide, each point on a slice curve represents the number of counts in that position of the slice.

On the VT01, the curves are identified by a letter designating the slice. The first slice is A, the second is B, and so on.

Each marked slice and its associated curve is identified by a different color. The current color table determines the color of the slices. The most currently marked slice is at level 4 of the color table, the second most currently marked slice is at level 8, and the third is at level 12. The color at level 15 always represents the curve of the cursor.

Since "the most currently marked slice" is at level 4 of the color table, the colors of the slices can change. As you mark each new slice, the associated colors change. You can mark only three slices on the VSV01 (26 on the VT01). If you mark a fourth slice, the first one is lost. As you mark each new slice, the least recently marked slice is lost. The vertical slice has the same color-coding procedure as the horizontal slice.

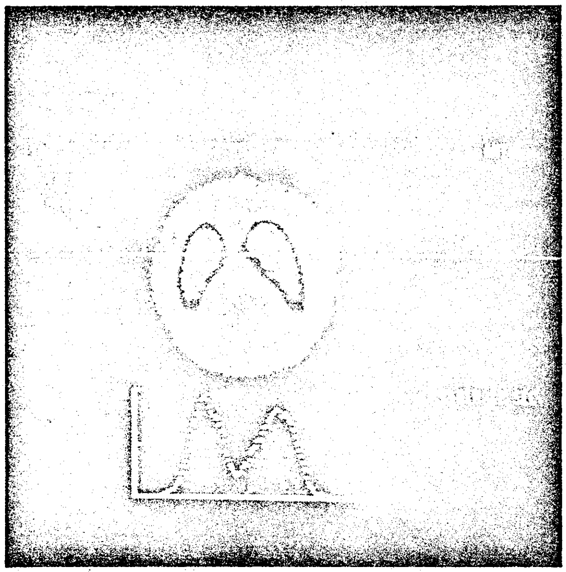


Figure 8-1
Preparatory Display:
Horizontal Slice

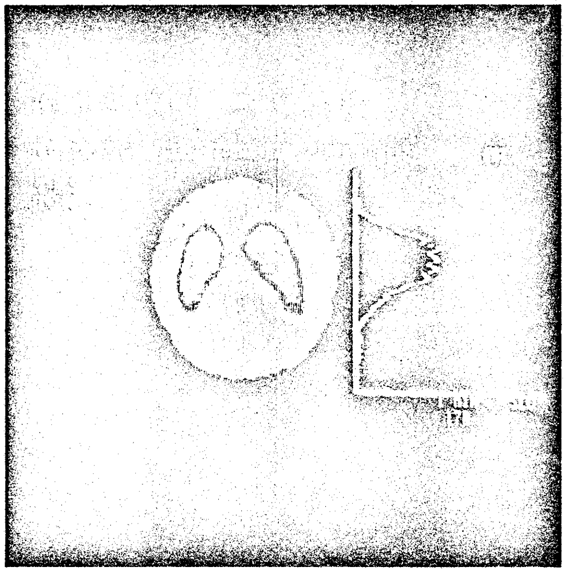


Figure 8-2
Preparatory Display:
Vertical Slice

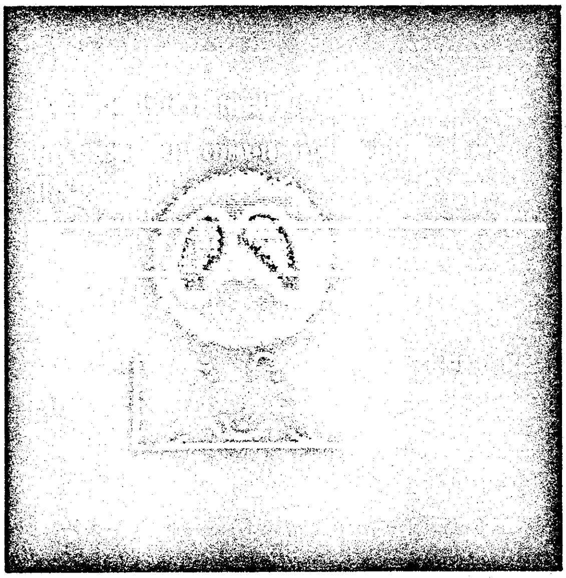


Figure 8-3
Horizontal: Three-Row
Slice and Curve

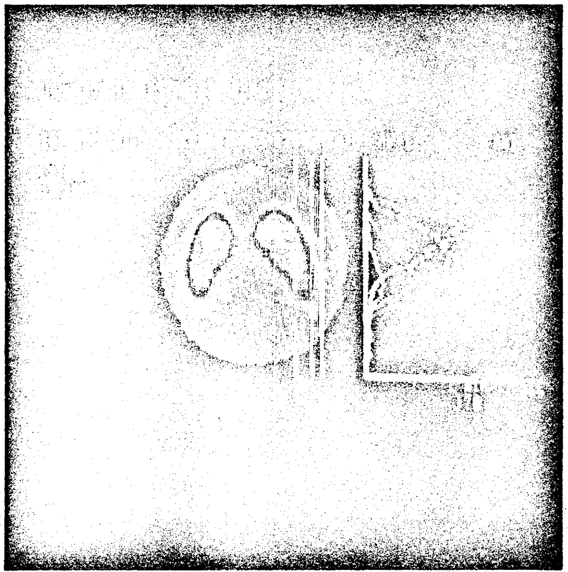


Figure 8-4
Vertical: Three
One-Column Slices
and Curves

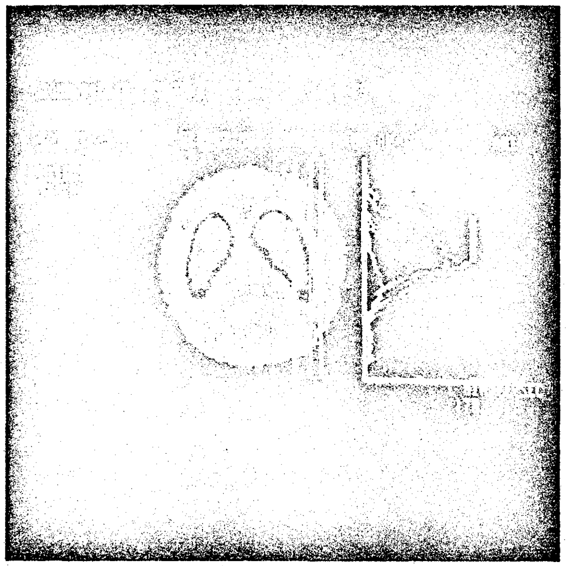


Figure 8-5
Scale Factor 1:
Truncated Curve

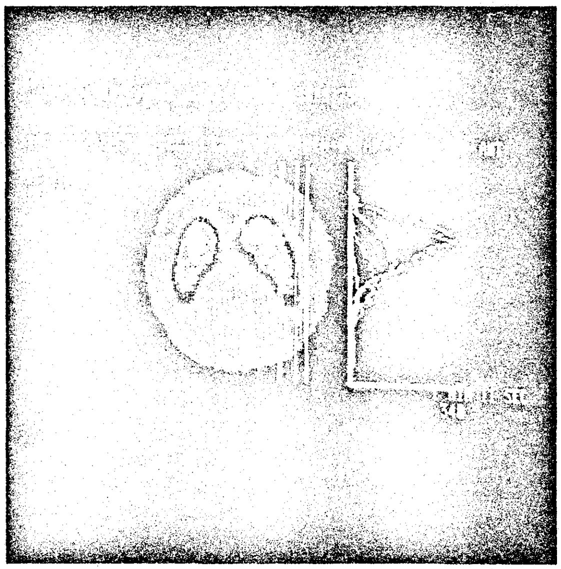


Figure 8-6
Scale Factor .5:
Truncation Eliminated

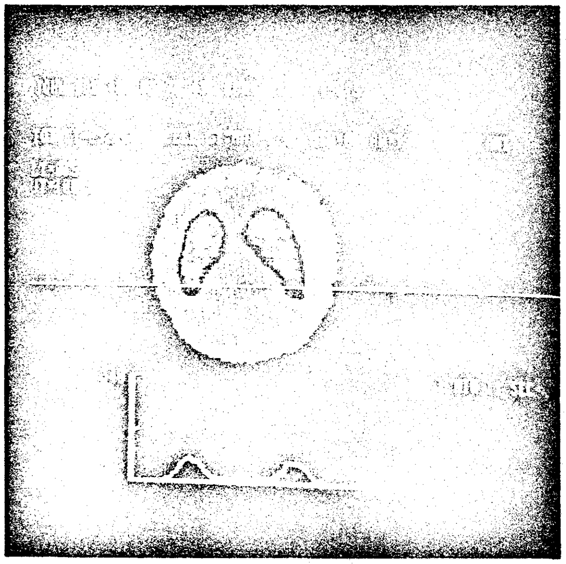


Figure 8-7
Scale Factor 1:
Low Contour Curve

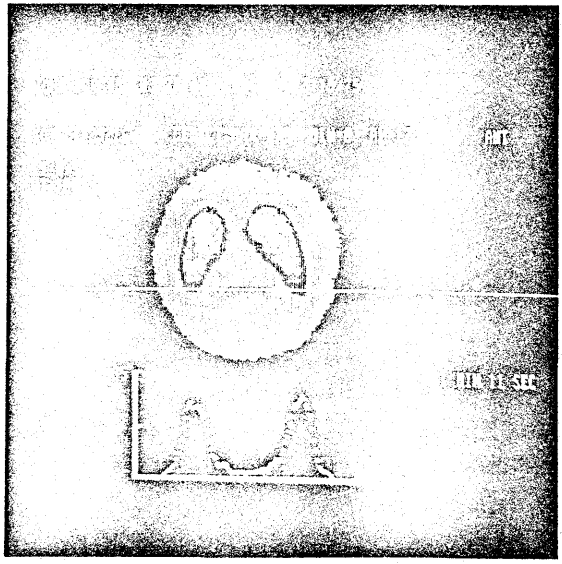


Figure 8-8
Scale Factor 2:
Contour Enhanced

8.5.1 Curve Scales

When the program first draws the axes for a slice curve, the count axis is labeled at two points, the highest point being n times the maximum cell count. This point is also the upper (or rightmost) boundary of the graph. Thus, the scale of the graph is determined (by default) by the maximum cell count along the slice. Sometimes, however, this default scale is not appropriate.

One effect of an inappropriate count-axis scale occurs when points on the curve are beyond the maximum cell count (255 or 65,535), which may result when adjacent cells of an n-row (or n-column) slice are added together. These points are plotted along the boundary of the curve. Likewise, at the base of the curve, cell counts below the minimum plottable level appear on the axis, which is the lower boundary of the graph. As a result, parts of the curve may have no real meaning. These curves are said to be truncated.

Another effect of an inappropriate count-axis scale occurs when a slice through a relatively sparse region of the matrix results in a curve with very little contour. These curves are known as low-contour curves.

When the scale of the curve is inappropriate, it can be altered with the Scale Factor command.

S n.nn

8.5.2 Scale Factor

The Scale Factor command eliminates truncation and low-contour curves by adjusting the count-axis scale. Type the following command on the terminal to alter the scale by a factor of n.nn.

```
S n.nn RET
```

The current count-axis scale is divided by the scale factor.

The scale factor may range from 0.01 to 9.99. To eliminate truncation, expand the scale by using factors less than 1.0. An example of truncation is shown in Figure 8-5, and a correction of truncation is shown in Figure 8-6 (color insert).

To enhance low-contour curves, contract the scale by using factors greater than 1.0. Figure 8-7 displays a curve with low contour. Figure 8-8 enhances contour.

You can omit spaces, nonsignificant zeros, and decimal points from the Scale Factor command. The following forms are all acceptable:

```
S5.3
S9
S0.05
S.8
S 2
```

8.6 SLICE TABULAR DATA

You can obtain tabular data on punched tape, printed copy, or screen display. The system provides the tabular data for the last defined slice (VT01). The cursor plot on the VSV01 is represented by the tabular data. If you desire a complete record, the data must be printed or punched after each slice is marked.

PR

8.6.1 Print Slice Data

The Print Slice Data command (PR) provides you with a table listing (from the terminal) of the total number of counts for each cell position in a slice. A typical output is shown in Figure 8-9. To obtain a listing of slice data, type the following command on the terminal.

```
PR RET
```

The orientation (HORIZONTAL SLICE), slice width (ROW(S)), and positions are given.

```
HORIZONTAL SLICE        ROW(S) 16

COL   CNTS              COL   CNTS
  1      0               17     54
  2      0               18     45
  3      0               19     46
  4      0               20     60
  5      1               21     65
  6      3               22     90
  7     13               23     83
  8     17               24     88
  9     24               25     69
 10     42               26     38
 11     89               27     17
 12     86               28      9
 13     87               29      2
 14     95               30      0
 15     89               31      0
 16     76               32      0
```

Figure 8-9
Tabular Data

PU

8.6.2 Punch Slice Data

The Punch Slice Data command (PU) provides you with a table listing the total counts for each cell position of the slice punched on paper tape. To obtain a punched table of slice data, type the following command on the terminal.

```
PU (RET)
```

The data lines are separated by carriage return/line feed pairs. No identifying information or column headers are punched.

PS

8.6.3 Place Data on Screen

The Place Data on Screen command (PS) provides the same information as the Print Slice Data (PR) command, but displays it on the screen instead of printing it. To obtain slice data on the screen, type the following command on the terminal.

```
PS (RET)
```

To restore the original slice display, type any character on the terminal.

8.7 EXIT

To leave the slice procedure at any time, type:

```
CTRL/X
```

CHAPTER 9

FLOOD CORRECTION

Irregularities in the view-field response of a gamma camera can affect the accuracy of the data transmitted to an image. GAMMA-11 can compensate for these irregularities by creating a correction matrix that can correct the displayed or stored patient-study data.

You can acquire a flood study by taking an image of a uniformly radioactive field. GAMMA-11 can then create a correction matrix that increases the low-response areas and decreases the high-response areas. Then, by multiplying each patient image by the correction matrix, you can compensate for the irregularities in the image due to poor camera response.

A flood correction has three parts:

1. Acquiring a flood study (described in Section 4.4)
2. Converting the flood-study data into a flood-correction matrix
3. Correcting displayed or stored data, using the flood-correction matrix

Items 2 and 3 are described in this chapter. All the flood-correction commands are carriage-return terminated.

9.1 CREATING A FLOOD-CORRECTION MATRIX

A flood-correction matrix is created only from a flood-study frame or from a static-study frame with a 64 x 64 word-matrix configuration. In either case, the settings of the orientation and rotation switches for the flood study should match those of the study or studies to be corrected (see Section 9.7.1).

A flood-study frame is shown in Figure 9-1.

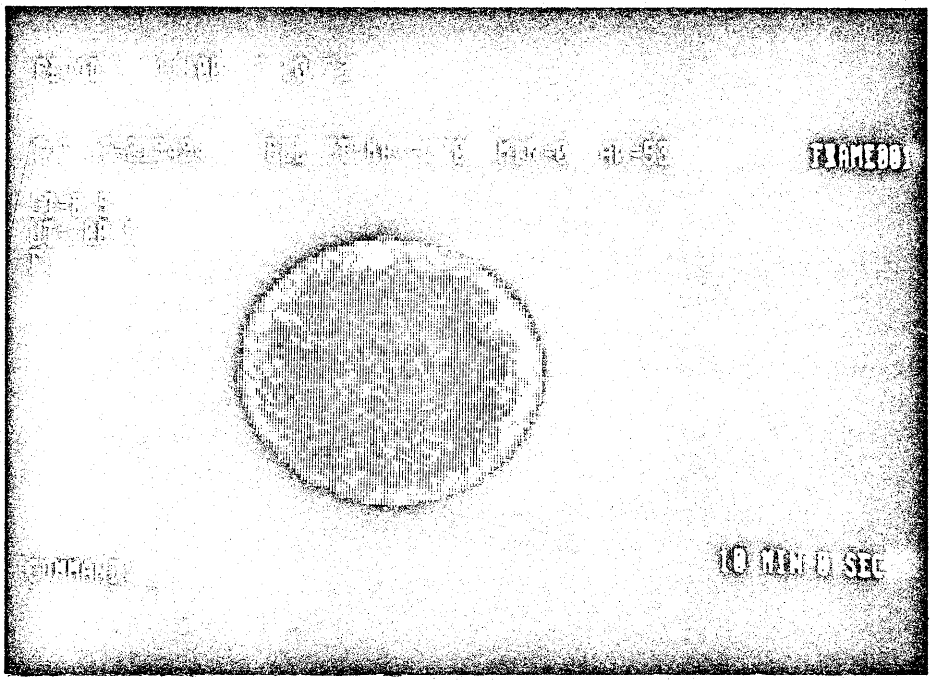


Figure 9-1
Flood-Study Matrix

To create a flood-correction matrix, you must perform the following steps.

1. Select a flood study from the patient study index.
2. If necessary, adjust the display thresholds of the frame.
3. Type the Flood Correction command (FC).

FC

9.2 FLOOD CORRECTION COMMAND

The Flood Correction (FC) command converts data from a flood-study frame into a flood-correction matrix.

An average cell count is calculated for the whole matrix. A cutoff is a percentage of this calculated average cell count. Those cells whose counts are below the cutoff are zeroed, and a new average is calculated using the remaining cells. The higher the cutoff, the more an image will be altered by the flood-correction matrix.

Command format:

```
FC n,m(RET)
```

where n is a save area (1-64) and m is the percentage of cutoff from 0-100%. Either argument, n or m, can be omitted. If n is absent, the resulting matrix is not stored in a save area, but remains in core. If m is omitted, a cutoff of 50% is used. In any case, you must always type the space between the command and the first argument. The form FCn,m is not permitted. The following forms are acceptable:

Command	Effect
FC 2,20	save area 2, cutoff 20%
FC ,35	matrix in core, cutoff 35% (PLEASE NOTICE COMMA!)
FC 4	save area 4, cutoff 50% by default
FC	matrix in core, cutoff 50%

9.3 CONVERTING A FLOOD-STUDY FRAME

The flood-correction program converts the flood-study frame into a flood-correction matrix in the following manner.

1. All cells whose counts lie outside the display thresholds are zeroed.
2. The average cell count (which in this case is called AV1, for clarification purposes only) of the remaining nonzero cells is computed.
3. All cells below the cutoff, that is, with counts smaller than m% of AV1, are zeroed. A new average cell count (AV2) of the nonzero cells now remaining is calculated.
4. Each of these remaining nonzero cells is converted into a flood-correction factor by replacing its contents with the value AV2/CT, where CT is the original number of counts in the cell.

When the conversion is complete, the correction matrix is displayed (see Figure 9-2), and if specified by the command, is stored in a save area.

For further notes on the calculation method, see Section 9.7.

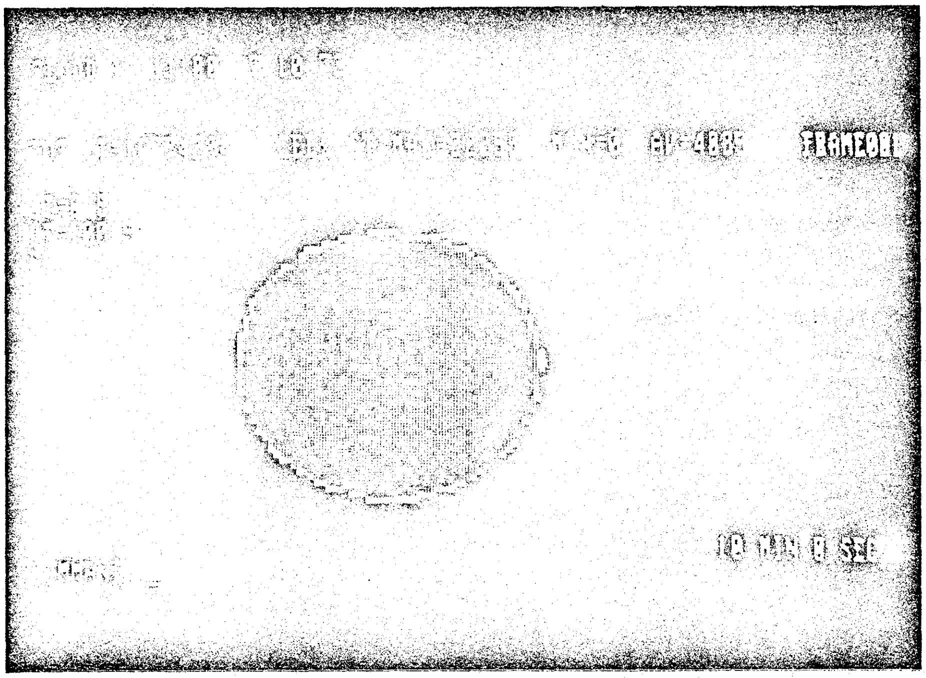


Figure 9-2
Resulting Flood-Correction Matrix (m=50%)

9.4 ERROR MESSAGES FOR FC COMMAND

Errors resulting from the use of the FC command are signaled by messages displayed below the word COMMAND:. In each case, the input is rejected, and the request COMMAND: is redisplayed below the error message. The error messages and their explanations follow.

INVALID CHARACTER	In the arguments n and m, the program detected a character other than a digit, space, comma, or RETURN.
INVALID SAVE AREA	The argument n was not in the range 1-64.
INVALID %	The argument m was not in the range 1-100.
NO NON-ZERO CELLS	The frame is empty and cannot be converted. This error may occur during the process of creating the correction matrix, if the cutoff and averaging computation result in an empty matrix.
THIS IS A FLOOD CORRECTION MATRIX	An attempt was made to convert what is already a correction matrix into such a matrix.
THIS IS NOT A FLOOD STUDY	An attempt was made to convert a study frame that is neither a flood

	study nor the proper matrix configuration.
THIS IS NOT A FLOOD STUDY, DO YOU WISH TO USE IT AS SUCH? REPLY (YES OR NO):	Although the selected frame is not internally identified as a flood study, it has the proper configuration (64x64 word-matrix), and can be used as such. You should type YES to convert it.
UNDEFINED "FC" COMMAND	A character other than a space bar or a RETURN was typed after the letters FC. A space must always separate FC and its arguments.

9.5 FLOOD-CORRECTING COMMANDS

The correction matrix must be stored in a save area if it is to be used. A flood correction can be performed either on a core-resident frame or on all the frames of a study. In the latter case, the original data in the disk study file are replaced by the flood-corrected data.

NOTE

> If a whole study is flood-corrected, the original data on the disk is altered.

To prepare to flood-correct a study, select the study to be corrected from the patient study index. The flood-correcting commands are discussed in Sections 9.5.1 and 9.5.2.

FCD

9.5.1 Flood-Correct the Displayed Frame

When correcting the displayed frame only, use the correction matrix stored in save area n. In this case, the disk-resident data are not affected. The command format used to flood-correct the displayed frame (core-resident frame) is

```
FCD n RET
```

where n is the save area holding the correction matrix. If the orientation and rotation switch settings of the two matrices do not match, the program returns with the following message, which is displayed on the screen.

```
ROTATION AND ORIENTATION SWITCHES DIFFER
```

When the correction is complete, the corrected matrix is displayed, and the note FC appears at the bottom of the screen.

FCS

9.5.2 Flood-Correct a Study

When you are flood-correcting an entire study, the correction matrix in save area n corrects each frame of the current study. The resulting data replace the original data in the disk file. Because the disk is being altered, you must also confirm the process.

The command format used to flood-correct a study is

```
FCS n RET
```

where n is the save area holding the flood-correction matrix. After you type the FCS command, the selected correction matrix is displayed with the following question:

```
IS THIS THE FLOOD CORRECTION MATRIX YOU WISH TO USE?
REPLY (YES OR NO):
```

If you type anything but YES, the procedure is terminated. If you type YES, the orientation and rotation switch settings of the two matrices are compared. If they match, the process goes to the final confirmation (see below). If the two matrices do not match, the following message appears:

```
ORIENTATION AND ROTATION SWITCHES DO NOT MATCH
```

The system returns to the last procedure in use before the FCS command was issued.

If the rotation and orientation switches match, the following message is displayed.

```
FINAL CONFIRMATION
REPLY (YES OR NO):
```

To begin the flood correction, type YES.

Once the flood correction begins, it takes about one second per frame. When the correction is complete, the original core-resident frame is redisplayed. Note, however, that the frame is now flood-corrected, as are all the frames in the study. The note FC appears at the bottom of the screen as a reminder.

9.6 ERROR MESSAGES FOR FCS AND FCD COMMANDS

The following error messages may appear when an FCS or FCD command is typed.

ALREADY FLOOD CORRECTED	The current frame (for FCD command) or study (for FCS command) has already been flood-corrected.
CAN'T FLOOD CORRECT A LIST MODE STUDY	FCS command only. The unstructured data of a list study cannot be flood-corrected.
INVALID CHARACTER	In the argument n, the program detected a character other than a digit, space, comma, or RETURN.
INVALID FC COMMAND	A character other than a D or an S appeared as the third character of the command. (This is the same error message described in Section 9.4. It does not appear if the third character is D, S, space, or a RETURN.)
INVALID SAVE AREA	The number n was not in the range 1-64.
NO FLOOD CORR. MATRIX IN SAVE AREA	The matrix in the specified save area is not a flood-correction matrix.
NO MATRIX IN SAVE AREA	The specified save area does not contain matrix data.
THIS IS A FLOOD STUDY	FCS command only. An attempt was made to correct a disk-resident flood study, which is not permitted. A flood study can be flood-corrected only by using the FCD command, since this command does not destroy the original data.
THIS IS A SAVE AREA, PLEASE "RS0"	FCS command only. An attempt was made to flood-correct a disk-resident study by referencing the study through a frame read from a save area. In other words, an FCS command is invalid whenever the message SAVE AREA n appears at the upper right corner of the display. To remove the message and restore the previous core-resident frame, type RS0.

9.7 NOTES ON FLOOD CORRECTION

The following sections provide more detail for flood correction. They explain camera orientation, correction-matrix calculation, cell overflow, and the statistical accuracy of flood correction.

9.7.1 Orientation Matching

The orientation and rotation switches on the gamma camera determine the relation between the camera's X- and Y-axes and those of the GAMMA-11 display. Because flood correction is dependent on the camera's orientation, the settings of these switches at the time a flood study is acquired must match those of the studies to be corrected.

9.7.2 Correction-Matrix Calculation

In the calculation of the correction factors, the difference between the averages AV1 and AV2 (see Section 9.3) is not significant unless the cutoff, m, is very large.

The correction factors are stored as 16-bit fixed-point fractions with the binary point between bits 12 and 13. The size of the factor limits the maximum correction factor to 7.77774 (octal), or slightly more than 7.999 (decimal). Therefore, the minimum cutoff must be 13% because a smaller cutoff results in a maximum factor larger than the limit (maximum factor x minimum cutoff = 100%). Factors equal to or greater than 8 are set to zero.

9.7.3 Cell Overflow

A source of image distortion in the flood-corrected study is cell-count overflow. Overflow can occur at two points:

1. During the acquisition of the patient study data
2. When a cell at or near the maximum count is flood-corrected

The flood-correction routine cannot recognize cells that have overflowed. These cells are treated simply as cases of maximum count. If such a cell count is multiplied by a correction factor smaller than 1, the resulting count will be too low since the correction process has no way of knowing by how much the cell overflowed.

Similarly, if a cell count is almost at a maximum, a correction factor greater than 1 can result in a corrected count larger than the maximum, thus causing an overflow. The effect is to distort the data in areas of the patient study matrix where cell counts are close to maximum.

Overflow of either sort is not usually a problem with word matrices. Byte-matrix cells, on the other hand, have a cell capacity of only 255 counts, making overflow quite likely.

Here are a few ways to reduce or eliminate the possibility of overflow.

1. Adjust the gamma camera to reduce irregularities as much as possible, so that flood-correction factors are all close to 1.

2. If space is available on the disk, use word matrices for studies to be flood-corrected, rather than byte matrices.

3. In dynamic studies, collect data at frame rates high enough to lessen the possibility of overflow in any one frame.

A check for overflow should be made by flood-correcting a few individual frames of a study (with FCD) before correcting the entire disk-resident study (with FCS).

9.7.4 Statistical Accuracy

The accuracy of the flood correction depends on the uniformity of the radiation source used in the flood-study acquisition. Commercially available sheet sources are generally uniform within plus or minus 5%. The statistical accuracy of the flood-study data should be equal to, or preferably greater than, 5%.

The standard deviation of the cell count is equal to the square root of cell count. If the cell count is N, the percentage variance, PV, is defined as:

$$\begin{aligned} PV &= 100(\sqrt{N}/N) \\ &= 100/\sqrt{N} \end{aligned}$$

and

$$\begin{aligned} N &= 100^2/(PV)(PV) \\ &= 10{,}000/(PV)(PV) \end{aligned}$$

The total number of counts required in a flood study is equal to the number of cells in the matrix times N. In a flood study, the 64 x 64 matrix contains 4096 cells, but only about half of these are actually used, so that the total number of counts, NTOT, can be given by:

$$\begin{aligned} NTOT &= (4096/2)(N) \qquad \text{where } N = 10{,}000/(PV)(PV) \\ &= 2\text{x}10^7/(PV)(PV) \end{aligned}$$

so that the number NTOT required for a given PV as shown in Table 9-1.

Table 9-1
Total Number of Counts Table

PV	NTOT
10%	200,000
5%	800,000
2%	5,000,000
1%	20,000,000

Thus, the minimum desirable number of counts in a flood study is 800,000.

PART 4

GAMMA-11 UTILITIES

CHAPTER 10

FILE DELETION

The file deletion program is called from the background command table. it allows you to delete studies from a disk and to squeeze the disk.

DS

10.1 FILE DELETION

When studies are no longer needed, you can remove them from the patient file to release space for new studies. To delete studies, type the Delete Study (DS) command as follows, where n is an optional disk unit number.

```
DS n RET
```

Immediately, the program displays the first page of the patient study index, with the procedure options at the bottom (see Figure 10-1). You may delete any or all of the studies on the page. Type ALL to delete all the studies on the page.

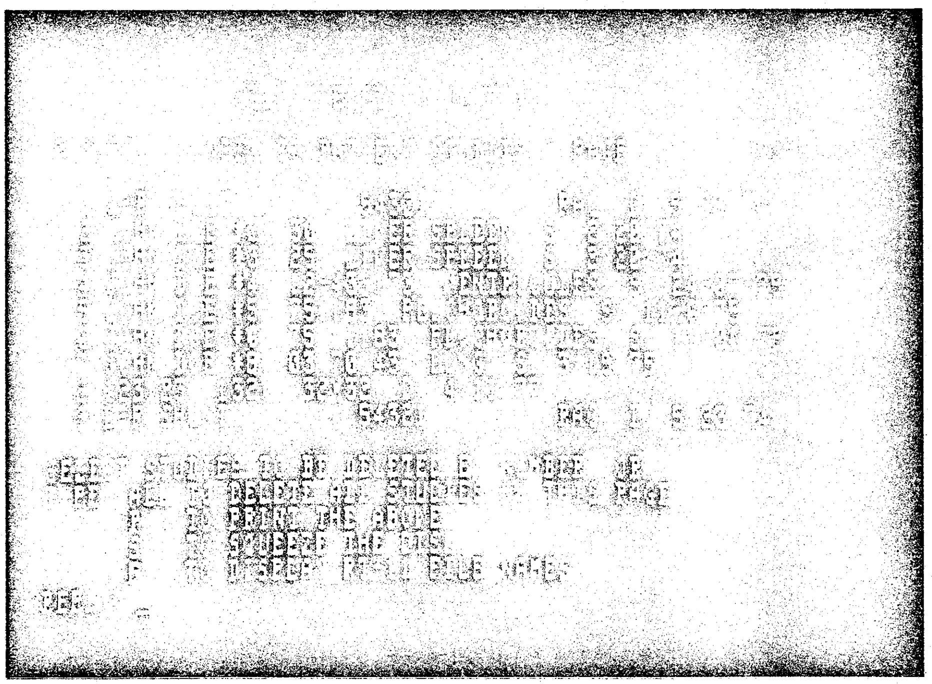


Figure 10-1
Patient Study Index for File Deletion

To delete selected studies, type the index numbers, separated by commas and terminated by a RETURN.

Examples:

5 RET	Study 5 is to be deleted.
12,3,7 RET	Studies 12,3,7 are to be deleted.
ALL RET	All studies on the displayed page are to be deleted.

After you have made your selection, the index is erased, and the selected entries are redisplayed for your verification (see Figure 10-2).

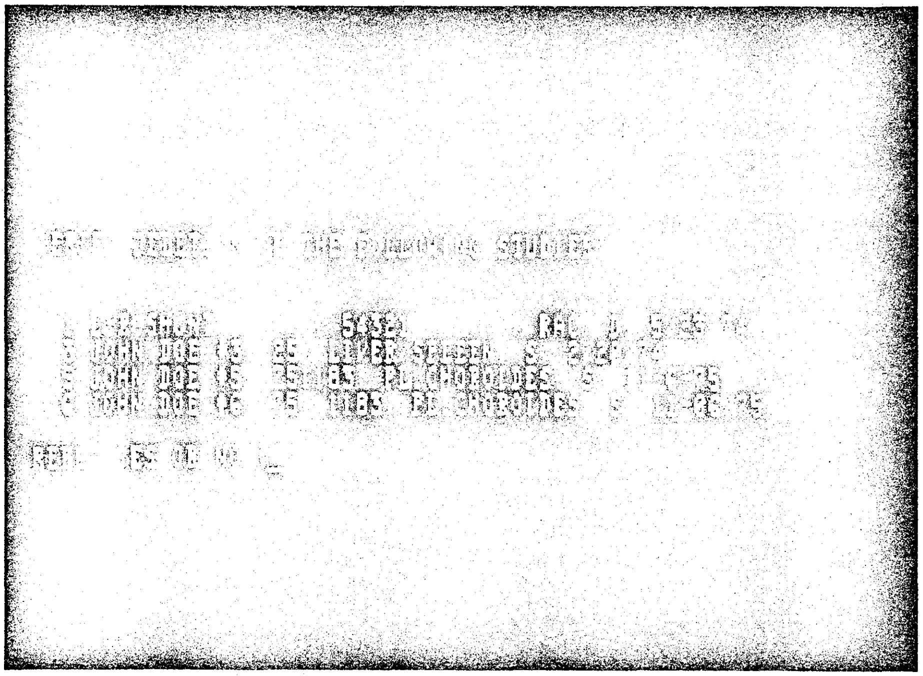


Figure 10-2
Verification Frame

If you type anything but YES, the selection is ignored, and the page of the index is redisplayed. No deletions take place. If you answer YES, the following message appears while the file is being deleted.

```
DELETIONS UNDER WAY
```

After you have deleted the selected studies, the program displays the next page of the index when you type N for the next page in response to:

```
TYPE N FOR THE NEXT PAGE
```

If you do not wish to delete any more files or if you have verified and deleted the last page, type RETURN. At this point the following message appears:

```
DO YOU WISH TO SQUEEZE THE DISK?
REPLY YES OR NO:
```

If you type anything but YES, GAMMA-11 returns to the background command table.

If you reply YES and the foreground is at the foreground command table (or is absent), the following appears on the display and on the console terminal:

```
DISK SQUEEZE UNDERWAY, PLEASE WAIT....
```

If the program squeezes the disk while the foreground is present, the foreground program is automatically stopped while the disk is being squeezed. After the disk is squeezed, both the GAMMA-11 foreground and background are automatically rebooted.

If the foreground is not at the foreground command table when you request the disk to be squeezed, the following message appears:

```
FGAMMA IS BUSY
DISK CAN'T BE SQUEEZED

TYPE A CARRIAGE RETURN TO EXIT
```

In this case, you must exit to the background command table. You can squeeze the disk later, when the foreground is idle, by using the DS command and choosing S to squeeze the disk (see Section 10.2).

10.2 SQUEEZING A DISK

The Study Deletion program can also be used to squeeze a disk without deleting any studies. Choose the S option to squeeze the disk.

If the foreground is not at the foreground command table when you request the disk to be squeezed, the following message appears:

```
FGAMMA IS BUSY
DISK CAN'T BE SQUEEZED

TYPE A CARRIAGE RETURN TO EXIT
```

If the disk squeeze can be done (i.e., the foreground is at the foreground command table or is absent) the following message appears on the display and on the console terminal:

```
DISK SQUEEZE UNDERWAY, PLEASE WAIT....
```

If the disk is squeezed while the foreground is present, the foreground program is automatically stopped while the disk is being squeezed. After the disk is squeezed, both the foreground and background are automatically rebooted.

CHAPTER 11

STUDY TRANSFERS

The GAMMA-11 Transfer Study program transfers GAMMA-11 patient studies between any RT-11 devices that have directories. Because magnetic tapes do not have RT-11 directories, they are treated as special cases.

The Transfer Study program runs only as a background GAMMA-11 program. It is called from the background command table via the TS (Transfer Study) command. When you request the Transfer Study program, you must enter the source (from) and destination (to) devices. After you have entered the devices, you select the transfer of studies analogous to the GAMMA-11 Study Deletion program (see Chapter 10).

TS

11.1 TRANSFER STUDY COMMAND

The Transfer Study program is called from the background command table. Type the following command on the terminal.

```
TS RET
```

The optional disk unit number (n), which appears in many of the commands, is ignored by the Transfer Study program. Once the Transfer Study command has been issued, a list of commonly used RT-11 device mnemonics appear on the screen.

Following is a description of each device and its associated mnemonic name:

SY	System device
RK	RK05 disk pack
MT	Magnetic tape
DM	RK06
DX	Floppy disk

> NOTE
>
> The Transfer Study program does not support cassettes. Use the RT-11 COPY command or the PIP utility program to transfer a study to cassettes.

The next line asks you to enter a source-device mnemonic and unit number followed by a carriage return.

```
PLEASE ENTER THE SOURCE DEVICE
```

The mnemonic device name and unit number are optional.

- If the device mnemonic and the unit number are not specified, DK (the device from which the system is normally booted) is the default source device.
- If only a device mnemonic is specified but no unit number, a null is the default unit number.
- If only a unit number is specified but no device mnemonic, SY (system device) is the default source device.

Examples:

RET	(DK: System device from which RT-11 is booted)
RK RET	(RK: disk pack on unit 0)
1 RET	(SY1: System device on unit 1)
DX0 RET	(dx: Floppy disk on unit 0)

If you enter an unacceptable device mnemonic or unit number, the following error message appears on the screen:

```
ILLEGAL RESPONSE, PLEASE TRY AGAIN
```

If the device is not a file-structured device (e.g., line printer, high-speed reader), the following message appears on the screen:

```
THE SOURCE (DESTINATION) DEVICE IS ILLEGAL
NOT A FILE STRUCTURED DEVICE, PLEASE TRY AGAIN
```

The next line asks you to enter a destination-device mnemonic and unit number followed by a carriage return.

```
PLEASE ENTER THE DESTINATION DEVICE
```

Both name and number are optional. The same method for defining a source device can be used to define a destination device.

If you enter an unacceptable device mnemonic or unit number for a destination device, the same error message appears; however, both source device and destination device must be re-entered.

Also, if two devices without directories (for example, two magnetic tapes) have been specified, the following error message appears immediately after you have specified the second magnetic tape:

```
MAGTAPE BOTH SOURCE AND DESTINATION DEVICE!
```

A device with a directory must be entered as either the source or destination device. Once the system has accepted legal source and destination devices, the following message appears on the screen.

```
READY THE DEVICES TO START THE TRANSFER
TYPE RETURN TO BEGIN
```

For example, if a device has been specified as a source or destination device and there is no device on the system, or the device unit is not ready, the following message appears on the screen.

```
DEVICE NOT READY!
THE DEVICE IS---, READY IT FOR TRANSFER
TYPE RETURN TO BEGIN
```

When the devices are ready, page 1 of the patient study index from the source device is displayed.

NOTE

> Magnetic tapes do not display the index because they are not RT-11 devices that have directories. See Section 11.3.

The same options that are available with study deletion and data analysis are available with study transfers. These are:

```
SELECT STUDIES TO BE TRANSFERRED BY ENTERING THE INDEX
NUMBERS

TYPE P TO PRINT THE INDEX
TYPE F TO DISPLAY THE RT-11 FILENAMES
TYPE N FOR THE NEXT PAGE OF THE INDEX
TYPE ALL TO TRANSFER ALL STUDIES ON THE PAGE
```

The studies selected for transfer must be on the displayed page. If you enter duplicate entries, the first entry is transferred and the second is ignored. If you enter an illegal number (i.e., one that does not exist), the following error message appears on the screen.

```
ILLEGAL STUDY NUMBER
```

Typing P provides you with a hard-copy output of the patient index.

Typing F displays the patient index files with their associated RT-11 file names. An example of this display is shown in Figure 11-1.

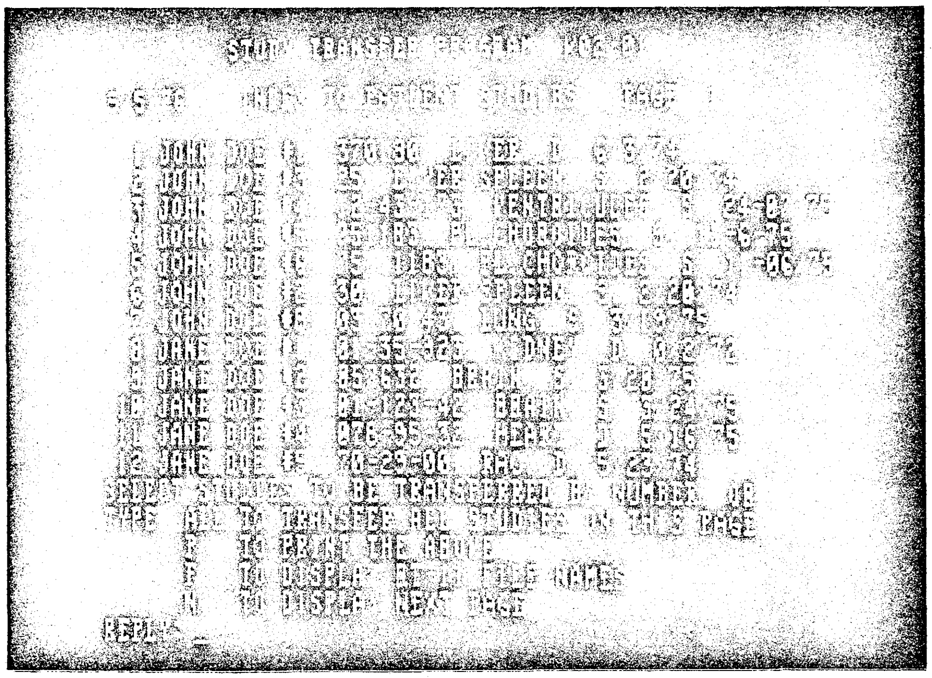


Figure 11-1
Patient Index File

Typing N displays the next page of the index (that is, patient studies 13-24).

Examples for transferring patient studies are:

1,2,7,9 (RET)
2,10,5 (RET)
4 (RET)

After the studies have been selected, the index line of each study to be transferred is displayed. At this point, you are asked to verify the transfer of studies by typing YES RETURN. Any response other than YES causes the index to be redisplayed, with no transfer taking place.

If your response is YES to the verification question, the destination device is readied for the transfer. The studies are transferred individually in the order you specified. If there is no room on the destination device for one of the source files, that particular patient study index line is displayed and you are given the following option:

```
THERE IS NOT ENOUGH ROOM FOR THE FILE
ON THE DESTINATION DEVICE
THE FILE IS xxxx BLOCKS LONG
THE DESTINATION DEVICE ONLY HAS xxx BLOCKS LEFT
DO YOU WANT TO TRY TO TRANSFER THE NEXT FILE?
TYPE YES TO CONTINUE
```

This message gives the size of the file to be transferred and the amount of free space available in the destination device.

At this point, the next study for transfer is scanned to see if it can fit on the destination device. If the study fits on the remaining space on the destination device, it is transferred. If not, the option line appears once more on the screen.

NOTE

> By using the monitor SQUEEZE command to squeeze the destination device, it may be possible to complete the transfer of the patient files on the source device.

If anything but YES is typed on the terminal in response to the option, the system returns to the background command table.

11.2 MAGNETIC TAPE AS A SOURCE DEVICE

Magnetic tapes as source devices are treated as special cases because they do not have RT-11 directories. If a magnetic tape is specified as a source device, no index is displayed. Instead, you are given three alternatives to transfer studies. These are:

```
     TYPE  1  TO RECEIVE A HARD COPY OF PATIENT INDEX
           2  SEQUENTIALLY CHOOSE FILES TO BE TRANSFERRED
           3  SELECTIVELY CHOOSE INDEX NUMBER
```

If you type 1, the program scans the magnetic tape, lists a hard copy of the patient index on the terminal, and displays the first 12 patient studies on the screen. (If more than 12 patient studies exist on a magnetic tape, the screen erases and displays patients 13-24 as the next display.) An example of the hard copy is represented in Figure 11-2.

```
5/23/76     INDEX TO PATIENT STUDIES
  1 JOHN DOE #3, 25, LIVER/SPLEEN, S, 2/20/74
  2 JOHN DOE #4, 12-43-173, VENTRICULES, S, 24-07-75
  3 JOHN DOE #5, 751183, PL.CHOROIDES, S, 11-6-75
  4 JOHN DOE #6, 75  1183, PL.CHOROIDES, S, 11-06/75
```

Figure 11-2
Magnetic Tape Study Index

Typing 2 displays the index line of the first file on the tape, and the system asks the following questions:

```
DO YOU WISH TO TRANSFER THIS FILE?

TYPE  YES     TO TRANSFER THIS FILE
      NO      TO CONTINUE TO NEXT FILE
      RETURN  TO CONTINUE TO NEXT FILE
      R       TO REWIND TAPE AND START AGAIN
      DIGIT   TO SKIP TO THAT FILE INDEX NUMBER
                 (ONLY IN SINGLE STEP MODE)
```

If you type NO or press RETURN, the next patient index line is displayed and the same questions are asked. This procedure allows you to step through the tape, a single study at a time, and transfers only those files that you wish to transfer.

If you type a number, the program skips to that study on the tape and displays the index line with options. Thus, if you know that a study is further down the tape, you can have the program skip ahead quickly. If you enter a patient index number with a value less than the number displayed, the following message appears on the screen.

```
ILLEGAL RESPONSE
REPLY:
```

Answer the REPLY with an R (to rewind) or with the new index number.

Typing 3 (selectively choose index number) displays the following message on the screen.

```
SELECTIVE STEP MODE
CHOOSE THE INDEX NUMBERS YOU WISH TO DISPLAY
(MAXIMUM OF 20)
```

You may enter the patient index number in any order with a maximum of 20 numbers. The program automatically sorts these numbers in ascending order. For example, when you type:

```
5,10,3,7,15 RET
```

the system sorts the numbers (3,5,7,10,15) and ignores any duplicate entries. The program then scans the tape and displays the index line of each study along with its transfer options. Thus, patient index 3 is displayed on the screen with the same options as provided in the sequential mode.

NOTE

> To leave selective mode, enter R or complete the list of studies chosen for transfer.

11.2.1 Non-GAMMA-11 Files on Magnetic Tape

If a magnetic tape contains files other than GAMMA-11 patient files, these files are identified by the following index line.

```
XXX NOT A GAMMA FILE
```

You cannot transfer such files.

11.2.2 Magnetic Tape as a Destination Device

When you use a magnetic tape as a destination device, a hard-copy index of patient studies is automatically printed on the terminal as the program moves to the end of the tape. As each file is output to the tape, the patient index line is also printed. Thus, whenever studies are added to the tape, a new hard copy of the index is printed. If you do not want this copy printed out, type a CTRL/O when the printing begins.

When you use a magnetic tape as a destination device, device-full conditions are not detected until the actual transfers take place. Thus, if the magnetic tape fills up, the index line of the offending study is displayed, the output file is deleted and the following message appears:

```
OUTPUT ERROR !!!

MAGTAPE HIT END OF TAPE MARK
FILE DELETED!

PROGRAM NOW CONTINUED: (TYPE RETURN)
```

The background command table is now displayed.

11.3 ERROR PROCESSING

The following sections describe errors that can occur during study transfers.

11.3.1 Input Errors

If an error occurs in reading the administrative block of a file, that file is immediately skipped, you are told of the error, and control is passed to the next file to be transferred.

If any other input error for the source device occurs, the index line of the current study is displayed and you are asked if you wish to ignore the errors. If the answer is YES, the error is ignored. If you answer anything else, the output file is purged and transfer of the next study begins. If an input error occurs and you choose to ignore the error and continue the transfer, the integrity of the transferred data cannot be guaranteed.

11.3.2 Magnetic Tape Input Errors

Any magnetic tape input error causes the transfer of data to fail. The RT-11 magnetic tape handler, upon receiving a hard error (an error that prevents the system from continuing operation) automatically rewinds the tape. Thus, the Transfer Study program cannot ignore the error and proceed with the transfer. The program repositions the tape at the start of the file and gives you the following options:

```
TYPE  1  SKIP TO THE NEXT FILE
      2  REWIND THE TAPE AND RESTART
      3  SKIP TO A NUMBERED FILE
              (SINGLE MODE ONLY)
```

NOTE

Deleted files on magnetic tape are not physically removed, and they cause input errors if their position on the tape is referenced by the Transfer Study program.

11.3.3 Output Errors

If an error occurs on the output (destination) device, the program displays the index line of the current study, and attempts to purge the current output file. No more transfers are attempted.

11.3.4 Other I/O Errors

Any other types of errors (e.g., fetching handlers, opening or closing files, etc.) are reported as fatal errors. Control returns to the background command table after such errors.

APPENDIX A

LOADING GAMMA-11 FOR THE SINGLE AND BACKGROUND USERS ON AN 11/40

The operating procedures for loading and starting RT-11 and GAMMA-11 with RK05 disks are outlined below. The disk loading procedure (steps 4 through 7) is for an RK05 disk. To load RK06 disks, see Appendix C.

CAUTION

> Whenever changing system disks, you MUST start the system again. If you do not start the system again, disk destruction results.

1. Turn computer console lock power switch clockwise to the ON position.
2. Turn the LINE/OFF/LOCAL switch on the terminal to be used to LINE.
3. Set the ENABLE/HALT switch on the PDP-11 console to HALT.
4. Pull the RK05 disk drive (unit #0) door down and place the removable disk cartridge in the disk drive with the metal ring on the bottom of the cartridge facing down.
5. Close the RK05 disk drive door.
6. Set the LOAD/RUN switch on the RK05 disk drive controller to RUN.
7. Make sure that the disk controller WRITE PROTECT light is off. If the light is not off, press the WRITE PROTECT switch once. This places the system in the WRITE ENABLE position.
8. When the disk READY light comes on, set the PDP-11 processor SWITCH REGISTER to 773100 (octal) as indicated in the following diagram. A ↓ (down-arrow) means push down on the switch and an ↑ (up-arrow) means push up on the switch.

17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	0
↑	↑	↑	↑	↑	↑	↓	↑	↑	↓	↓	↑	↓	↓	↓	↓	↓	↓

9. Press the processor LOAD ADDR switch down. This places 773100 (octal) as the starting address in the system.

10. Set the PDP-11 processor SWITCH REGISTER to 777406 (octal) as follows:

17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	0
↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↓	↓	↓	↓	↓	↑	↑	↓

11. Raise the PDP-11 ENABLE/HALT switch to ENABLE.

12. Press the PDP-11 processor START switch down. This calls in RT-11 from the disk.

13. Four numbers are printed on the terminal followed by a $.

14. Type DK followed by a carriage return for RK05 disks. Type DM followed by a carriage return for RK06 disks.

15. The system responds with the version number of RT-11.

    The system then types:

    ```
    PLEASE ENTER
    TODAY'S DATE:
    ```

    and waits for you to enter the current date in the form

    ```
    dd-mmm-yy
    ```

    followed by the RETURN key, where dd-mmm-yy is the day, month, and year to be entered. dd is a decimal number in the range 1-31; mmm is the first three characters of the name of the month, and yy is a decimal number in the range 73-99.

    Example:

    To enter May 25, 1977 as the current date for the system, type

    ```
    25-MAY-77(RET)
    ```

    If the date is entered in an incorrect format, the message is repeated.

16. The system then responds with the prompt

    ```
    CURRENT TIME:
    ```

    and waits for you to respond in the form

    ```
    hh:mm:ss
    ```

    or

    ```
    hh:mm
    ```

    or

    ```
    hh
    ```

    followed by a RETURN, where hh:mm:ss represents the hour, minute, and second. The time is in hours, minutes, and seconds past midnight.

Example:

```
CURRENT TIME:  14:48:32(RET)
```

sets the internal clock to 14 hours, 48 minutes, and 32 seconds.

17. The system responds with the background command table on the color display (or VT01).

18. The background is now loaded and running.

APPENDIX B

LOADING GAMMA-11 FOR THE FOREGROUND/BACKGROUND USERS ON AN 11/40

The operating procedures for loading and starting RT-11 and GAMMA-11 are outlined below. The disk loading procedure (steps 4 through 7) is for an RK05 disk. To load RK06 disks, see Appendix C.

CAUTION

> Whenever changing system disks, you MUST start the system again. If you do not start the system again, disk destruction can result.

1. Turn the computer console lock power switch clockwise to the ON position.
2. Turn the LINE/OFF/LOCAL switch on the terminal to be used to LINE. (Set to REMOTE if an LA30.) Also press the ON/OFF switch on the VT05 or VT52 to ON.
3. Set the ENABLE/HALT switch on the PDP-11 console to halt.
4. Pull the RK05 disk drive (unit #0) door down and place the removable disk cartridge in the disk drive with the metal ring on the bottom of the cartridge facing down.
5. Close the RK05 disk drive door.
6. Set the LOAD/RUN switch on the RK05 disk drive controller to RUN.
7. Make sure that the disk controller WRITE PROTECT light is off. If the light is not off, press the WRITE PROTECT switch once. This places the system in the WRITE ENABLE position.
8. When the disk READY light comes on, set the PDP-11 processor SWITCH REGISTER to 773100 (octal) as indicated in the following diagram. A ↓ (down-arrow) means push down on the switch and an ↑ (up-arrow) means push up on the switch.

17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	0
↑	↑	↑	↑	↑	↑	↓	↑	↑	↓	↓	↑	↓	↓	↓	↓	↓	↓

9. Press the processor LOAD ADDR switch down. This will place 773100 (octal) as the starting address in the system.

10. Set the PDP-11 processor SWITCH REGISTER to 777406 (octal) as follows:

17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2	1	0
↑	↑	↑	↑	↑	↑	↑	↑	↑	↑	↓	↓	↓	↓	↓	↑	↑	↓

11. Raise the PDP-11 ENABLE/HALT switch to ENABLE.

12. Press the PDP-11 processor START switch down. This calls in RT-11 from the disk.

13. Four numbers are printed on the terminal followed by a $.

14. Type DK followed by a carriage return for RK05 disks. Type DM followed by a carriage return for RK06 disks.

15. The system responds with the version number of RT-11.

    The system then types

    ```
    PLEASE ENTER
    TODAY'S DATE:
    ```

    and waits for you to enter the current date in the form

    ```
    dd-mmm-yy
    ```

    followed by the RETURN key, where dd-mmm-yy is the day, month, and year to be entered. dd is a decimal number in the range 1-31; mmm is the first three characters of the name of the month, and yy is a decimal number in the range 73-99.

    Example:

    If you wish to enter May 25, 1977 as the current date for the system, type

    ```
    25-MAY-77(RET)
    ```

    If the date is entered in an incorrect format, the message is repeated.

16. The system then responds with the prompt

    ```
    CURRENT TIME:
    ```

    and waits for you to respond in the form

    ```
    hh:mmm:ss
    ```

    or

    ```
    hh:mm
    ```

    or

    ```
    hh
    ```

    followed by a RETURN, where hh:mm:ss represents the hour, minute, and second. The time is in hours, minutes, and seconds past midnight.

Example:

```
CURRENT TIME:  16:48:32(RET)
```

sets the internal clock to 16 hours, 48 minutes, and 32 seconds.

17. There is a slight pause, and the system responds by presenting the foreground command table on the VT52 (see Section 3.2.1). The following message is printed on the console:

    ```
    FGAMMA LOADED AND RUNNING
    ```

18. The system now responds with the background command table on the color display (or VT01). (See Section 3.1.1.)

19. Both the background and foreground GAMMA-11 programs are now loaded and running.

APPENDIX C

LOADING AN RK06K CARTRIDGE

1. Prepare an RK06K cartridge for loading as follows:
    a. Lift the cartridge by grasping the handle with the right hand.
    b. Support the cartridge from underneath with the left hand (Figure 1).
    c. Lower the handle and push the handle slide to the left with the thumb of the right hand (Figure 1).
    d. Raise the handle to its full upright position to separate the cartridge from the protection cover (Figure 2).
2. Place the cartridge in the drive shroud with the handle recess facing the rear of the machine (Figure 3).
3. Rotate the cartridge a few degrees clockwise and counter-clockwise to ensure that it is properly seated within the shroud.
4. Gently lower the handle to a horizontal position to engage the drive spindle (Figure 4).
5. Place the protection cover on top of the cartridge.
6. Carefully close the drive lid.

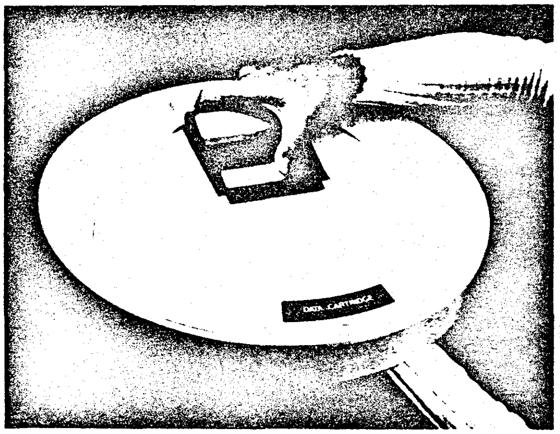


Figure 1

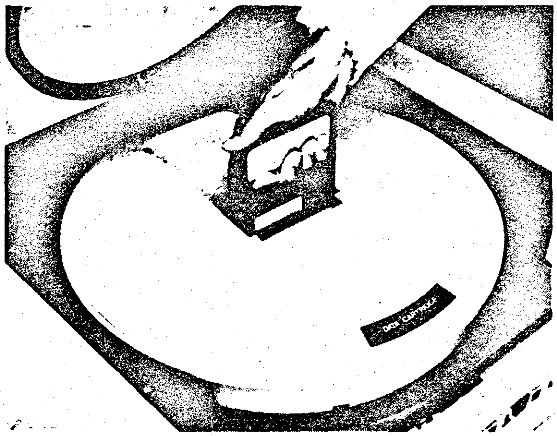


Figure 3

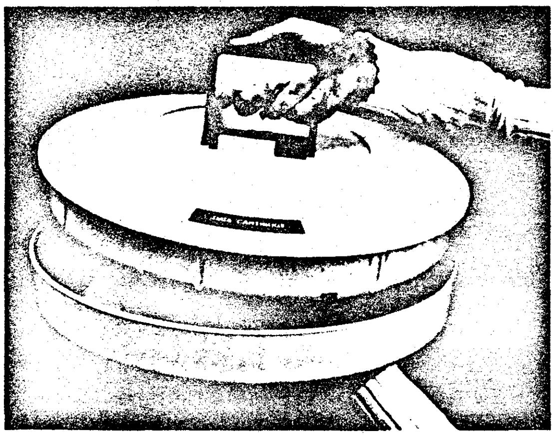


Figure 2

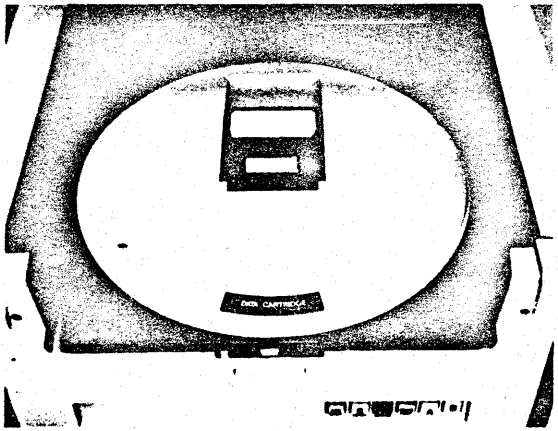


Figure 4

APPENDIX D

SUMMARY OF COMMANDS

D.1 CONTROL COMMANDS

All GAMMA-11 functions are carried out or initiated in response to commands typed on the keyboard. The principal functions are called into operation by the Control Commands, which are of the form:

AS	Set up and acquire patient study
AF	Set up and acquire flood study
AP	Acquire study using predefined study
SP	Set up a predefined study
MP	Modify a predefined study
DP	Delete a predefined study
SS	GAMMA-11 system summary
AD	Data analysis and review (background only)
CA	Continue analysis (background only)
DS	Delete patient studies (background only)
TS	Transfer study (background only)
PM	Patient monitor (background only)

D.1.1 General-Purpose GAMMA-11 Control Commands

CTRL/X	Return GAMMA-11 to previous functional level
CTRL/Z	Return GAMMA-11 to background command table

D.1.2 GAMMA-11 Editing Commands

DELETE	Delete character (same as RUBOUT)
CTRL/U	Delete line
ESC	Edit page (same as ALT)
CTRL/E	Edit and redisplay page

D.1.3 RT-11 Monitor Commands

CTRL/C	Return control from GAMMA-11 to monitor
CTRL/F	Direct terminal input to foreground job
CTRL/B	Reverse CTRL/F
CTRL/O	Inhibit output from printing or displaying
CTRL/S, CTRL/Q	Suspend, reinstate output to terminal

D.2 DATA ACQUISITION COMMANDS

The entire procedure is controlled from the keyboard, in response to questions, instructions, or choices appearing on the display screen.

CTRL/R	Restart a static frame
CTRL/Z	Terminate the study early
CTRL/X	Terminate the study early

D.3 DATA ANALYSIS COMMANDS

Procedures include display options, mathematical operations, and analytical tools for working with the collected data of study. These functions are summarized below.

CTRL/N	No room for COMMAND; clear screen
RET	Restore current frame (after study summary)
SP	Display next frame
BE	Restore first frame and initial conditions
BK n	Backspace n frames
SK n	Skip forward n frames
DI	Display matrix, normal size
DM n	Display matrix, minified
ID	Display isometrics
DN	Display normal
IC f,s,n	Isocontour map
ICF f,s,n	Iscontour fill
DX	Display index
DP	Display patient data
ND	No display; multiple command lines
EC	Echo keyboard on printer
NC	No echo
TE	Display text
S9	Nine-point smooth
RO n	Rotate data
TV n	Translate matrix vertically
TH n	Translate matrix horizontally

D.3.1 Color Display Commands

The commands described in this section apply only to the color display. These commands describe the color tables and their functions, the color table editor, interpolated displays, and dual full size displays. These commands are all carriage return terminated.

BW	From color to black and white
CL	From black and white to color
DL	Display an intensity scale bar
NL	Remove the intensity scale bar
CT n	Retrieve a color table
ST n	Save a color table
CL n,rgb	Change a color level
ET n	Edit a color table
Z	Zero a color table
C n,rgb	Change a color element
I n,rgb	Insert a color element
D n	Delete a color level
S n	Save an edited color table
G n	Get a color table

P	Print color table
R	Display Ramp
M	Display matrix using current color table
RET ,CTRL/X	Exit color table editor
IT	Interpolate a display
NT	Turn off an interpolated display
BU	Blow up (increase) the size of the display
NB	Return display to normal size
LD	Load a dual display buffer
LD n	Load and display a dual image
DU	Display the contents of a dual display
DO	Overlay the contents of two display buffers
NU	Display a single image
SW	Swap the dual displays
D8	Display 8 minified images
D16	Display 16 minified images
IT2	Interpolate display twice

D.3.2 Frame Algebra Commands

The Frame Algebra commands include operations to add, subtract, or multiply by a constant; complement a matrix to obtain a "negative" image; combine frames arithmetically.

AD n	Consecutive add
CA n	Constant add
CA -n	Constant subtract
CM nn.nn	Constant multiply
EX	Expand data, byte-to-word
NX	No data expansion
FA (exp)	Frame arithmetic
FDH n/m	Frame divide, high
FDL n/m	Frame divide, low
NI	Negate image
SA (exp)	Save area arithmetic
SDH n/m	Save area divide, high
SDL n/m	Save area divide, low

D.3.3 Thresholding Commands

Threshold adjustment is used to enhance contrast in particular areas of the matrix or to eliminate unwanted background noise. The commands are:

LT m,n	Set lower threshold and step size
UT m,n	Set upper threshold and step size
IS w,y	Set isocount band
W	Raise LT one step
X	Lower LT one step
Y	Lower UT one step
Z	Raise UT one step
N	Raise isocount band (step=UT-LT)
O	Lower isocount band (step=UT-LT)
LTN,UTN,ISN	Set threshold, no enhancement
UM	Set upper threshold display switch
UO	Clear upper threshold display switch

The W, X, Y, Z, N, and O threshold-adjusting commands are effective for both enhancement and no enhancement.

D.3.4 Dynamic Playback Commands

The commands described in this section apply only to the color display. These commands allow you to play back patient studies in a movie-like manner. The speed and direction of the playback can be controlled by a joystick, preset to a specified rate, or controlled manually by using the terminal keyboard. These commands are:

PBI name,unit,n,r,max,min	Initialize a playback buffer
PBD name,unit	Delete a playback buffer
PBS	Store an image in a playback buffer
PB name,unit	Display a playback buffer
C	Color display
B	Black-and-white display
U	Blow-up display
N	Normal size display
T	Timed mode
M	Manual mode
J	Joystick mode
S	Switch direction
CTRL/X	Exit playback
PBM	Playback merge

D.3.5 Regular Region of Interest Commands

The Region of Interest (ROI) commands define areas of varying shape and allow you to examine the data within them. In Dynamic studies, curves can be derived from the data in these regions, in each frame of the study (see Chapter 6).

RI	Enter regular ROI procedure

The following regular ROI commands are immediate mode commands (i.e., no carriage return is required).

U	Move cursor up one cell
D	Move cursor down one cell
L	Move cursor left one cell
R	Move cursor right one cell
J	Move cursor 10 cells in last direction
M	Mark cursor location
S a	Define ROI with same shape and size as last one
K	Kill last marked point
RET	Restore original frame
SP	Display next frame
-	Display previous frame
CTRL/X	Exit regions-of-interest mode

D.3.6 Irregular Region of Interest Commands

Areas of any shape or size, within the boundaries of a matrix, are defined as irregular ROIs.

IR	Enter irregular ROI procedure

Irregular ROIs may be defined by means of immediate-effect mode-setting commands. These are:

M	Mark ROI
RET	Restore original frame
SP	Display next frame
-	Display previous frame
CTRL/X	Exit ROI
C	Circumference mode
F	Fill mode
B	Boundary display
I	Interior display
K	Switch mode from marking to unmarking ROI (VSV01 only)
A	Switch mode from unmarking to marking ROI (VSV01 only)
Q	Blow up a quadrant (VSV01 only)
V	Use threshold levels to mark ROI

D.3.7 Dynamic Curve Commands

The following dynamic curve commands work from within the ROI mode. They work for both regular and irregular ROIs. They are carriage return terminated.

T n	Step through study
E abc	Erase ROIs
PN abc	Plot dynamic curves, normal
PO abc	Plot dynamic curves, overlaid
PA abc	Plot averaged curves, overlaid
PR abc	Print tabular data
PU abc	Punch tabular data
PP abc	Print and punch simultaneously
PNM abc	Plot normal frame linear curve
PAM abc	Plot average frame linear curve
POM abc	Plot overlay frame linear curve
PW f,n	Plot window
PF	Plot window forward
PB	Plot window backward
CTRL/X	Exit Plot

D.3.8 Save Area Commands

Save areas are disk storage areas used to save data. They facilitate arithmetic operations between frames, including frames from different studies, and can be used to store curves derived from regions of interest in dynamic studies. The save areas are also used to transmit data between GAMMA-11 and any BASIC programs you may be using.

RR n	Read ROIs from save area n (regions only)
RS n	Read data from save area n (matrix and regions)
SD n	Save dynamic curve data in save area n
SM n	Save matrix data in save area n
DS n	Delete save area
SA (exp)	Save area arithmetic (access save area excluding ROIs)

D.3.9 Macro Commands

The data analysis program has a resident macro buffer for the current macro that you are using. Macro facilities of the data analysis program allow you to create, edit, execute, save, and retrieve macro files. The macro commands are all carriage return terminated.

MC filename	Create a macro
ME	Edit the contents of a macro buffer
ML filename	Load a macro buffer
MR filename,n	Execute or run a macro
MS filename	Save the current contents of a macro buffer
MD filename	Delete a macro file from the system device
MX	Stop execution
EL n	Execute one line of a macro buffer
// text	Print text as a comment
?	Immediate mode input

The macro editor commands are:

A	Append
D	Display edited macro
R n	Replace line n
(RET)	Edit, store macro, exit
CTRL/X	Exit immediately
P	Print edits on console

D.3.10 Slice Commands

For each slice, a curve of the cell count distribution is plotted. The curve data may be recovered in tabular form on printed copy, punched tape, or screen display. In a dynamic study, once the slices have been selected each frame may be examined in sequence. The slice commands are all carriage return terminated.

SH n	Horizontal slice of width n
SV n	Vertical slice of width n
S n.nn	Scale factor
E	Erase definition

Six of the Slice commands, U, D, L, R, M, and J are all immediate-effect commands (see Region of Interest Commands, Section D.3.5).

Tabular data is provided for the last defined slice. These commands are all carriage return terminated.

PR	Print slice data
PU	Punch slice data
PS	Place data on screen

D.3.11 Flood Correction Commands

Irregularities in the view-field response of a scintillation camera may affect the accuracy of the data transmitted to the A/D Converter. These irregularities can be compensated for by using the following flood-correction commands:

FC n,m	Create a flood correction matrix
FCD n	Flood-correct the displayed frame
FCS n	Flood-correct a study

D.3.12 Dual Isotopes Commands

A dual-isotope study is identified by the letter A or B, which appears after the displayed frame number. For most analysis procedures, only one isotope at a time is examined; the study is treated as if it were a single-isotope study. The isotope is selected by the following commands:

IA	Display isotope A
IB	Display isotope B
IX	Exchange isotopes
DD	Display dual, miniature

D.3.13 List Mode Command

Data that are collected in a list study are structured, or framed, in one of five matrix configurations. The command to display list study frames is carriage return terminated.

FR	Recall framing routine

D.3.14 Comment Editor Commands

The Comment Editor commands allow you to edit or add to existing text, or insert commentary not previously included.

CO	Call comment editor

The comment editor commands are:

A	Append comments
D	Display edited text
R n	Replace line n
RET	Edit and store text, exit
CTRL/X	Exit immediately
P	Print edits on console

D.3.15 Language Execution Commands

There are some commands that run high-level language programs directly from the GAMMA-11 Data Analysis program without having to exit from GAMMA-11 and type RT-11 commands. These commands are all carriage return terminated.

BA	device:filename.ext	Run a BASIC program
FO	device:filename.ext	Run a FOCAL program
RU	device:filename.ext	Run a FORTRAN program (or any .SAV file)

APPENDIX E

GAMMA-11 COMMANDS IN ALPHABETICAL ORDER

Below are the GAMMA-11 commands in aphabetical order. Each explanation of a command is followed by a description in parentheses. This description tells from which function in GAMMA-11 this command can be called. For example,

AD Analyze data (command table)

means that this form of the AD command can be called only from the GAMMA-11 command table. The other form of the AD command,

AD n Add n frames to core-resident frame (frame algebra)

can only be used in frame algebra that can be called during data analysis.

A	Append (comment editor)
A	Switch mode from marking to unmarking (irregular ROI)
AD	Analyze Data (command table)
AD n	Add n frames to the core resident frame (frame alegbra)
AF	Set up and acquire a flood study (command table)
ALT	See <ESC>
AP	Acquire a predefined study (command table)
AS	Set up and acquire a study (command table)
B	Switch from color to black and white (playback)
B	Boundary display (ROI)
BA dev:filename	Run BASIC (data analysis)
BE	Return to beginning of study (data analysis)
BK n	Skip backwards n frames (data analysis)
BU	Blow up an image (data analysis)
BW	Switch from color to black and white (data anaysis)
C	Switch from black and white to color (playback)
C	Circumference mode (ROI)
C n,rgb	Change a color level (color table editor)
CA	Continue analysis (command table)
CA n	Constant add (frame algebra)
CA -n	Constant subtract (frame algebra)
CL	Switch from black and white to color (data analysis)
CL n,rgb	Change a color level (data analysis)
CM nn.nn	Constant multiply (frame algebra)
CO	Call comment editor (data analysis)
CT n	Retrieve color table n from disk (data analysis)
CTRL/B	Reverses CTRL/F (monitor)
CTRL/C	Returns GAMMA-11 to monitor (from any mode)
CTRL/F	Catches the attention of the foreground terminal (monitor)
CTRL/N	No room for COMMAND; clear screen (data analysis)

GAMMA-11 COMMANDS IN ALPHABETICAL ORDER

CTRL/O	Kills output from printing (monitor)
CTRL/R	Restart a static frame (data acquisition)
CTRL/S	Suspend output to the terminal (monitor)
CTRL/Q	Reinstate output to the terminal (monitor)
CTRL/U	Deletes current input line (any mode)
CTRL/X	Return GAMMA-11 to previous level (any mode)
CTRL/X	Exit comment editor
CTRL/X	Exit color table editor
CTRL/X	Exit playback mode
CTRL/X	Exit ROI mode
CTRL/X	Exit slice
CTRL/X	Exit dynamic curves
CTRL/Z	Return GAMMA-11 to background command table
D	Display edited text (comment editor)
D	Move cursor down one cell (regular ROI)
D	Move cursor down one row (slice)
D n	Delete a color level (color table editor)
D8	Display 8 minified images (data analysis)
D16	Display 16 minified images (data analysis)
DD	Dual isotope display (data analysis)
DELETE	Erase a character (any mode) (same as RUBOUT)
DI	Display full size matrix (data analysis)
DL	Display color bar (data analysis)
DM n	Display minified images (data analysis)
DN	Display normal image (data analysis)
DO	Dual overlay (data analysis)
DP	Delete predefined study (command table)
DP	Display patient summary (data analysis)
DS	Delete study (command table)
DS	Delete save area (data analysis)
DU	Dual display (data analysis)
DX	Display index (data analysis)
E	Erase (slice)
E abc...	Erase ROI (ROI)
EC	Echo keyboard characters on the terminal printer (data analysis)
EL	Execute line (data analysis, macros)
ESC	Edit a page (data acquisition) (same as ALTmode)
ET n	Edit color table n (color table editor)
EX	Expand byte mode to word mode (frame algebra)
F	Fill mode (irregular ROI)
FA (exp)	Frame arithmetic (frame algebra)
FC n,m	Flood correction (Data analysis)
FCD n	Flood correct the displayed frame (data analysis)
FCS n	Flood correct a study (data analysis)
FDH n/m	Frame divide high (frame algebra)
FDL n/m	Frame divide low (frame algebra)
FO dev:filename	Run FOCAL
FR	Recall framing sequence (list mode data analysis)
G n	Get color table (color table editor)
I	Interior display (irregular ROI)
I n,rgb	Insert new color element (color table editor)
IA	Select isotope A (data analysis)
IB	Select isotope B (data analysis)
IC f,s,n	Isocontour map (data analysis)
ICF f,s,n	Isocontour fill (data analysis)
ID	Isometric display (data analysis)
IR	Enter irregular ROI mode (data analysis)
IS w,y	Set isocount thresholds (data analysis)

GAMMA-11 COMMANDS IN ALPHABETICAL ORDER

ISN w,y	Set isocount thresholds/no enhancement (data analysis)
IT	Interpolate display once (data analysis)
IT2	Interpolate display twice (data analysis)
IX	Isotope exchange (data analysis)
J	Enter joystick mode (playback)
J	Move cursor 10 cells in last direction (regular ROI)
J	Move cursor 10 cells in last direction (slice)
K	Kill the first mark of a pair of marks (regular ROI)
K	Switch from marking to unmarking (irregular ROI)
L	Move cursor left one cell (regular ROI)
L	Move cursor left one row (slice)
LD	Load core-resident image into dual display (data analysis)
LD n	Load save area n in dual display (data analysis)
LT m,n	Set lower thresold/contrast enhancement (data analysis)
LTN m,n	Set lower threshold/no enhancement (data analysis)
M	Display matrix with current color table (color table editor)
M	Manual mode (playback)
M	Mark a slice (slice)
M	Mark the present cursor location (regular ROI)
M	Mark ROI (irregular ROI)
MC filename	Macro create (macros)
MD filename	Macro delete (macros)
ME filename	Macro edit (macros)
ML filename	Macro load (macros)
MP	Modify predefined study (command table)
MR filename,n	Run macro starting at line n (macros)
MS filename	Macro save (macros)
MX	Macro exit (macro)
N	Raise isocount band (data analysis)
N	No blowup of image (playback)
NB	No blowup of image (data analysis)
NC	No printing of commands on terminal (data analysis)
ND	No display (data analysis)
NI	Negate image (data analysis)
NL	Remove color bar (data analysis)
NT	No interpolation (data analysis)
NU	No dual display (data analysis)
NX	No expansion of byte mode to word mode (data analysis)
O	Lower isocount band (data analysis)
P	Print file on console (comment editor)
P	Print color table (color table editor)
PA abc...	Plot overlaid average rate curves (ROI)
PAM abc...	Plot average frame-linear curve (ROI)
PB	Plot backward window (ROI)
PB name,unit	Play back the playback buffer (playback)
PBD name,unit	Delete playback (playback)
PBI	Create playback buffer (playback)
PBM	Playback merge (playback)
PBS	Store the core-resident data in playback buffer (playback)
PF	Plot forward window (ROI)
PM	Patient monitor (data acquisition)
PN abc...	Plot normal dynamic curve (ROI)
PNM abc...	Plot normal frame-linear curve (ROI)
PO abc...	Plot overlaid dynamic curves (ROI)
POM abc...	Plot overlaid frame-linear curve (ROI)

GAMMA-11 COMMANDS IN ALPHABETICAL ORDER

PP abc...	Print and punch count data (ROI)
PR	Print slice data (slice)
PR abc...	Print count data (ROI)
PS	Place data on screen (slice)
PU	Punch slice data (slice)
PU Bc...	Punch count data (ROI)
PW f,n	Plot window (ROI)
Q	Blow up a quadrant (irregular ROI)
R	Display ramp (color table editor)
R	Move cursor right one cell (regular ROI)
R	Move cursor right one row (slice)
R n	Replace line n (comment editor)
RET	Accept line as input (at end of any typed line)
RET	Display current frame in core (data analysis)
RET	Edit and return (comment editor)
RET	Exit color table editor (color table editor)
RET	Redisplay current frame with ROIs (ROI)
RI	Enter regular ROI mode (data analysis)
RO	Rotate matrix (data analysis)
RR	Read ROIs (data analysis)
RS	Read save area (save area)
RU dev:filename	Run FORTRAN or any RT-11.SAV file (data analysis)
S	Switch direction (playback)
S a	Same shape as ROI a (regular ROI)
S n	Save color table n on disk (color table editor)
S n.nn	Scale factor (slice)
S9	Nine-point smooth of matrix (data anaysis)
SA (exp)	Save area arithmetic (save area)
SD n	Save dynamic curves in save area n (data analysis)
SDH n/m	Save area divide high (save area)
SDL n/m	Save area divide low (save area)
SH	Slice horizontal (slice)
SK n	Skip forward n frames (data analysis)
SM m	Save matrix in save area m (data analysis)
SP	Set up predefined study (command table)
SP	Display next frame (data analysis)
SP	Display next frame with regions of interest (ROI)
SS	System summary (command table)
SW	Swap the dual displays (data analysis)
ST n	Save color table n on disk (data analysis)
SV	Slice vertical (data analysis)
T	Timed mode (playback)
T n	Step through the study (ROI)
TE <text>	Text inserted with matrix (data analysis)
TH n	Translate matrix horizontally + right, - left (data analysis)
TS	Transfer study (command table)
TV n	Translate matrix vertically + up, - down (data analysis)
U	Blow up image (playback)
U	Move cursor up one cell (ROI)
U	Move cursor up one row (slice)
UM	Set upper threshold display switch (data analysis)
UO	Clear upper threshold display switch (data analysis)
UT n,m	Set upper threshold/contrast enhancement (data analysis)
UTN n,m	Set upper threshold/no enhancement (data analysis)

GAMMA-11 COMMANDS IN ALPHABETICAL ORDER

V	Use threshold level to mark ROI (irregular ROI)
W	Raise the lower threshold by step size (data analysis)
X	Lower the lower threshold by step size (data analysis)
Y	Lower the upper threshold by step size (data analysis)
Z	Raise the upper threshold by step size (data analysis)
Z	Zero the color table (color table editor)
//text	Put comment in a macro (comment editor)
- (hyphen)	Display previous frame with ROIs and count data (ROI)

APPENDIX F

EXITING AND REENTERING GAMMA-11

Occasionally it is necessary to exit GAMMA-11. For example, program development cannot be done from GAMMA-11, and in-core gate synchronized data analysis is best done with only the single job monitor (and thus the foreground programs must be removed).

To exit the foreground program (FGAMMA) type:

```
CTRL/F
CTRL/C
CTRL/C
```

Now only the background GAMMA-11 program is running. However, FGAMMA is still in the memory taking up space.

To exit the background program type:

```
CTRL/C
```

The monitor will respond with a dot.

To free the memory from FGAMMA type:

```
UNLOAD FGAMMA(RET)
```

at the dot.

To restart only the background GAMMA-11, type:

```
RUN BGAMMA(RET)
```

at the monitor dot.

To restart the foreground and background GAMMA-11, type:

```
FRUN FGAMMA(RET)
```

at the monitor dot. There is a slight pause, and then the foreground command table is present on the foreground terminal. The following message is printed on the console:

```
FGAMMA LOADED AND RUNNING
```

Now, FGAMMA no longer references the DECwriter. The system then responds with a B> and a dot on the DECwriter. Type:

```
RUN BGAMMA(RET)
```

on the terminal to call in the background program. The system responds with the background command table on the color display (or

VT01). The commands that have a preceding asterisk are not operable when the foreground is running.

NOTE

If you are a single-job user, type CTRL/C to exit GAMMA-11 and R BGAMMA to reenter.

APPENDIX G

GLOSSARY

Term	Definition
Algorithm	A prescribed set of well-defined rules or processes for the solution of a problem in a finite number of steps.
Analog	Numbers represented by directly measurable quantities (as voltages, resistances, or rotations).
Array	A list or table of elements, usually variables or data.
Asymptote	A line that is the limiting position of a tangent to a curve as its point of contact recedes indefinitely along an infinite branch of the curve.
Bit	A binary digit that can only have two values, 0 and 1. This corresponds to an electrical switch, where 0 represents the OFF position and 1 represents the ON position.
Block of Data	A set of consecutive machine words, characters, or digits handled as a unit, particularly with reference to Input/Output (256 words per block).
Byte	A computer memory cell that represents a group of binary digits usually operated upon as a unit. In the PDP-11, one byte consists of eight bits of data. There are two bytes per word.
Cell	An element of the matrix representation of the gamma camera field of view. The analog to digital converters of GAMMA-11 transform the analog signals of the gamma camera into a digital matrix representation of this data. Each cell of the matrix represents the sum of the counts originating in a specific area of the gamma-camera crystal.
Collimator	A device for confining the elements of a beam within an assigned solid angle.
Command	An instruction to a computer system, usually given through a terminal keyboard.
Cursor	Visible pointer to a grid point on a terminal display.

Dynamic	A condition that changes with respect to time.
Frame	A GAMMA-11 image representing the organ over a finite amount of time. Like a frame of a movie, or one photograph.
Gamma Ray	High energy electromagnetic radiation.
Image	The GAMMA-11 representation of the data from a gamma camera.
Input	Information put into a peripheral device which is transferred to the internal storage of a computer.
Mass Storage	Pertaining to a device, such as a disk or DECtape, that stores large amounts of data readily accessible to the central processing unit.
Matrix	In GAMMA-11 a matrix is a 2-dimensional array of cells, n rows by n columns, where n is 32, 64, 128, or 256. The matrix represents the surface area of the gamma camera.
Output	Information transferred from the internal storage of a computer to output devices or external storage.
Overflow	A condition that occurs when a mathematical operation yields a result whose magnitude is larger than the space allocated for storing the result.
Parameter	A variable or an arbitrary constant appearing in a mathematical expression, each value of which restricts or determines the specific form of the expression.
Prevailing Mode	A data-analysis mode that remains in effect until GAMMA-11 is commanded to change the mode. For example, ROI, rotation.
Scintillation	A flash of light produced in a phosphor by an ionization event.
Static	A condition that does not change with respect to time.
Threshold	A setting of a level above which or below which data is not displayed, analyzed, etc.
Truncation	The reduction of precision by dropping one or more of the least significant digits; e.g., 3.141597 truncated to four decimal digits 3.141.
Underflow	A condition that occurs when a mathematical operation yields a result whose magnitude is smaller than the space allocated for storing the result. For unsigned arithmetic, a result that is negative.
Weight	A numerical representation of importance.
Word	A computer memory cell. In the PDP-11, one word consists of 16-bits of data.

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READER'S COMMENTS

NOTE: This form is for document comments only. DIGITAL will use comments submitted on this form at the company's discretion. Problems with software should be reported on a Software Performance Report (SPR) form. If you require a written reply and are eligible to receive one under SPR service, submit your comments on an SPR form.

Did you find errors in this manual? If so, specify by page.

Did you find this manual understandable, usable, and well-organized? Please make suggestions for improvement.

Is there sufficient documentation on associated system programs required for use of the software described in this manual? If not, what material is missing and where should it be placed?

Please indicate the type of user/reader that you most nearly represent.

☐ Assembly language programmer
☐ Higher-level language programmer
☐ Occasional programmer (experienced)
☐ User with little programming experience
☐ Student programmer
☐ Non-programmer interested in computer concepts and capabilities

Name ______________________ Date ______________

Organization ______________________

Street ______________________

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Please cut along this line