gamma11

digital

GAMMA-11
Operator's Guide

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PREFACE

The GAMMA-11 system is an application system designed for acquisition and analysis of gamma camera data. GAMMA-11 has been developed for the user who processes a large number of patients.

GAMMA-11 does not require the user to know any computer language, but requires the user to have a working knowledge of nuclear medicine techniques and terminology, and the gamma camera and its related instruments.

The GAMMA-11 Operator's Guide describes the GAMMA-11 system and its operation, including loading and operating the system and acquiring data. The manual also explains the Foreground/Background (F/B) relationship to GAMMA-11. All applications are illustrated by examples and photographs that represent the different studies: dynamic, flood, list, multiple static, and static.

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

Throughout the manual, references are made to other documents that contain further information. They are:

RT-11 System Reference Manual (DEC-11-ORUGA-C-D)

PDP-11 Processor Handbook

PDP-11 Peripherals Handbook

RT-11 System Generation Manual (DEC-11-ORGMA-A-D)

NC11-A Camera Front-End (CSS-MO-F-14-3)

GAMMA-11 System Reference Manual (DEC-11-MGRMA-A-D)

This manual also supports the VT01 Storage scope. Please note that all references made to the VSV01 Color display also refer to the VT01 Storage scope. However, if a reference is made only to the VT01, the text is shaded. Chapter 6 is totally devoted to the VSV01 Color display.

CHAPTER 1

INTRODUCTION

The GAMMA-11 system extracts quantitative information from gamma camera data. The system yields information about radioactive tracer tests and studies of the distribution of radioactive quantities in patients.

A gamma camera records radionuclide distributions in patients. This information is collected following intraarterial, intravenous or intrathecal injection, inhalation or ingestion of a nuclide that localizes in a particular organ or pathological lesion. Such studies are divided into dynamic and static studies.

An example of a dynamic or flow study is the 131-I Hippuran renogram. Following intravenous injection, this radiopharmaceutical is extracted from the blood by the kidneys and excreted to the bladder. Abnormalities in kidney function cause abnormalities in the distribution and rate of movement of the radiopharmaceutical. A gamma camera shows the flow distribution of radioactivity in a region or regions of interest. The GAMMA-11 system allows this flow distribution to be quantitatively described.

An example of a static study is a liver scan using 99-mTc-Sulfur colloid. Following intravenous injection the radiopharmaceutical is selectively taken up by the liver and spleen. Malignant or other pathological processes distort the normal distribution of the nuclide causing abnormal uptake of the nuclide in these areas. Subsequent gamma-camera images show:

position of the organ

size of the organ

configuration of the organ

distribution of the radioactivity

pathological lesions

The GAMMA-11 system allows image manipulation for better visualization of such a study. When necessary, quantitative information may also be extracted from the raw or modified data.

1.1 DESIGN PHILOSOPHY AND GOALS

The basic goals in the design of the GAMMA-11 system are: to provide an easy-to-use system that gives quantitative data (from the gamma camera data) thereby enabling detailed and accurate diagnostic reports; to provide a high degree of file protection from loss or overlay; and to provide a system capable of future expansion to meet changing needs.

1.2 SYSTEM DESCRIPTION

The GAMMA-11 system is a series of programs that acquire and analyze 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 RT-11 single job operating system, and uses the RT-11 file structure for the patient (i.e., 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, analysis, and utility functions.

The background program can collect data only if there is no foreground program or if the user is running a single job RT-11 system (where there is no foreground job). Thus, while the user collects data in the foreground, he may also:

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

1.3 HARDWARE REQUIREMENTS

The minimum hardware requirements (excluding the scintillation camera and its related equipment) are as follows:

> PDP-11 CPU
>
> 28K of core 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 control and drive
>
> BM792-YB Bootstrap loader
>
> KW11-P Real-Time Clock (for data acquistion)
>
> KW11-L Line frequency clock (for RT-11 F/B)
>
> A second bulk storage media (RK05 disk, magtape, cassette)
>
> VSV01 Color display
>
> NC11A Gamma camera interface
>
> AR11 A/D Convertor for simultaneous joystick positioning and foreground acquisition

NOTE

> The VT01 storage scope is also supported on the GAMMA-11 system as part of the minimum hardware requirement only if the VSV01 Color display is not part of that requirement.

The following hardware is optional:

Additional disk drives for Data Acquisition and Data Analysis

Any bulk storage device that is supported by RT-11 (e.g., a TU10/TM11 9-track magtape)

For single users only 16K of core is required and the high-speed video alphanumeric terminal.

The video alphanumeric terminal, such as the VT52 or VT05, is used by the foreground data acquisition program, and the DECwriter keyboard and VSV01 Color display are used by the background. The LA36 DECwriter printer is not normally used. Output is directed to the DECwriter only when the user specifically asks for hardcopy output of reports, summaries, etc.

1.3.1 The Gamma Camera

The gamma camera interfaces to the GAMMA-11 system via the gamma camera interface (NC11A). 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 a CRT (Cathode Ray Tube) which may also be photographed. There are usually two CRT's:

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

Depending upon the organ being visualized, one time exposure photo, or several photos, of the CRT may be taken showing the distribution of radioactivity at different times. When one photo is taken, the procedure is called a Static study. When more than one photo, showing isotope movement as a function of time, is taken, the procedure is called a Dynamic study.

1.4 STUDY TYPES

The operations involved in the GAMMA-11 system are distinguished by the manner in which data are collected and structured. These operations include certain study types: Static, Dynamic, Flood, List, and Predefined.

1.4.1 Static Study

The Static study consists of one or more separate frames up to a maximum of eight, each representing a separate data collection run, combined into one study file, with camera and collection parameters that may be varied between frames. A multiple frame Static study may be used, for example, to show several different views of a single patient or particular organ.

1.4.2 Dynamic Study

The Dynamic study consists of a series of frames collected and structured by specified rates. A Dynamic study may be compared to a sequence of motion picture frames. For example, data are collected in sequential frames (i.e., the amount of radioactivity in an organ as a function of time can be obtained). A Dynamic study can consist of 1 to 512 frames. Different rates may be used during dynamic collection. This is implemented through groups. Up to 13 groups can be specified in one Dynamic study. At times, particular organs will have characteristic curves and deviations from the norm which may indicate malfunction. Thus, these curves may be presented to the user through the Dynamic study.

1.4.3 Flood Study

The Flood study is a single-frame Static study that is used to check and correct for a nonuniform camera response. In a Flood study, the camera is presented 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. The data are used to create a flood-correction matrix, which in turn is used to compensate for these irregularities while examining other studies. The Flood study is almost entirely predefined in that no patient data is required. Of the collection parameters, the user must supply only the duration of the run, in either elapsed time or in total number of counts and the orientation of the camera with respect to the flood source.

1.4.4 List Study

A List study contains unstructured data. Each pair of X- and Y-coordinates is stored in a list, with periodic time-reference marks. The "raw" information is structured at Data Analysis time. The procedure for a List Study (question and answer sequence) is similar to that for defining a Study Plan in a Static study.

1.4.5 Predefined Study

The Predefined study allows the user to save much time in setting up routines or often-used study plans. Collection parameters and other common data are defined in advance; only the specific run-time information needs to be added when the study plan is used to acquire data (i.e., patient name, ID, birthdate). The use of Predefined studies ensures that common (often-used) studies are always collected in the same manner. Thus, the user is assured of consistency.

CHAPTER 2

GAMMA-11 SOFTWARE ENVIRONMENT

2.1 INTRODUCTION TO RT-11

The RT-11 programming and 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. The user directs 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 which allow the user to develop programs using higher level languages, such as FORTRAN, FOCAL, and BASIC, or assembly language (MACRO).

The uses of a Foreground/Background 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 is designed to run critical jobs that do not rely upon a time factor. Some of these jobs are particularly related to analyzing data and the development of programs that run FORTRAN, BASIC, FOCAL, or MACRO as a single job in the background.

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. The most common event is the 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 and the central processor stops running the background job and resumes executing the foreground job. This allows a greater utilization of processor efficiency.

Consequently, an F/B system is designed to allow a time critical job (such as collecting, storing, and/or acquiring data) to run in the foreground.

2.2 GAMMA-11 AND RT-11

The GAMMA-11 programs run under RT-11 F/B. All GAMMA-11 programs (except for the data acquisition program) 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.

2.2.2 Data Analysis

The data analysis and review programs allow the user to view the data of a patient or flood study and perform analysis of the data; specifically:

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
5. Smooth the data (9-point)
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 which 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. Playback dynamic studies in a "movie-like" manner

2.2.3 Study Deletion

The study deletion routine allows the user to display and select those studies that are to be deleted; specifically:

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

2.2.4 Study Transfer

The study transfer routine allows the user to transfer patient studies between any bulk storage media (i.e., disks, magtape, DECtape, cassettes, etc.).

2.2.5 System Summary

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

2.2.6 Data Acquisition Used as Foreground or Background

The foreground program (FGAMMA) consists primarily of the data acquisition program. The user can set up and acquire data in the following formats:

1. Single or multiple static studies
2. Dynamic studies
3. Flood studies
4. List studies

All user interaction with FGAMMA is via the VT52 or VT05 terminal. The console terminal and VSV01 Color display are used by the background program. The foreground program is loaded via the console terminal by issuing the RT-11 command to load FGAMMA. The loading procedure for the foreground is discussed in Chapter 3.

The background data acquisition program is practically identical to the foreground data acquisition program, except that it uses the console DECwriter and VSV01 Color display. The background data acquisition program can be used only,

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

CHAPTER 3

GAMMA-11 STARTING PROCEDURES

3.1 LOADING GAMMA-11 FOR THE SINGLE AND BACKGROUND USERS

The operating procedures for loading and starting RT-11 and GAMMA-11 are outlined below. To load RT-11, see Steps 1-14; and to load GAMMA-11, see Steps 15-17. Only Steps 15-17 need be performed if RT-11 is already running.

CAUTION

> Whenever changing system disks, the user MUST start the system again. If the user does not start the system again, disk data destruction can result.

1. Turn computer console lock power switch clockwise to the ON position.
2. Turn the LINE/OFF/LOCAL switch on the console terminal to LINE.
3. Set the ENABLE/HALT switch on the PDP-11 console to HALT.
4. Pull the 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 disk drive door.
6. Set the LOAD/RUN switch on the 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 as indicated in the following diagram. ↓ (down-arrow) means push down on the switch and ↑ (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 as the starting address in the system.

10. Set the PDP-11 processor SWITCH REGISTER to 777406 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 and prints on the terminal the version number of RT-11.

13. The system responds with the version number of RT-11 and a dot on the console terminal. The user must type the DATE command into the system. The DATE command assigns a date to new patient studies until a new DATE command is issued.

    The form of the command is:

    ```
         DATE dd-mmm-yy
    or
         DAT dd-mmm-yy
    or
         DAT
    ```

    followed by the <CR> 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. If no arguments are typed in response to the command, the current date is printed.

    Examples:

    To enter the date, April 25, 1976 as the current date for the system, type:

    ```
    DAT 25-APR-76<CR>
    ```

    To have the current date printed by the system, type:

    ```
    DAT<CR>
    25-APR-76     (system response)
    ```

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

14. The system again responds with a dot. Type the TIME command into the system. The TIME command allows the user either to find out the current time of day kept by RT-11 or to enter a new time of day.

    The form of the command is:

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

followed by the <CR> key, where:

hh:mm:ss	represents the hour, minute, and second.

The time is in hours, minutes, and seconds past midnight. If no argument is indicated, the current time of day is output.

Examples:

```
TIME 14:48:32<CR>
```

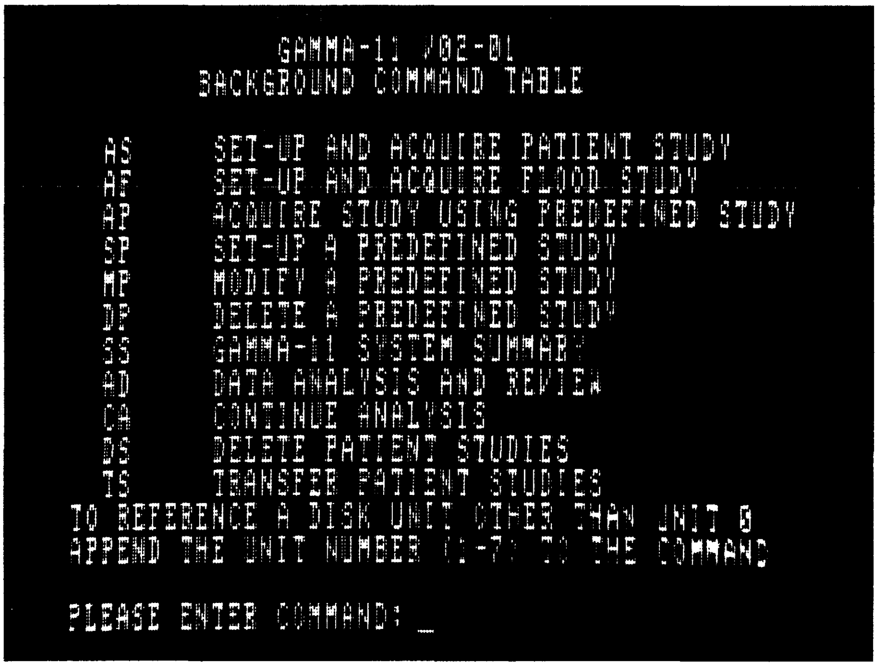
This sets the internal clock handler to 14 hours, 48 minutes, and 32 seconds.

```
TIME<CR>
14:58:36        (system response approximately ten
                 minutes later).
```

15. The system again responds with a dot. Next, type RUN BGAMMA<CR> on the terminal to call in GAMMA-11 from the system device.
16. The system responds with the background command table on the Color display (or VT01). (See Section 3.1.1.)
17. The background is now loaded and running.

3.1.1 Loading Commands

Once the GAMMA-11 software has been loaded into the system, it is the user's option to choose one of the GAMMA-11 programs. Figure 3-1 shows a VSV01 displaying the GAMMA-11 programs.



```
              GAMMA-11 V02-01
         BACKGROUND COMMAND TABLE

   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
   CA     CONTINUE ANALYSIS
   DS     DELETE PATIENT STUDIES
   TS     TRANSFER PATIENT STUDIES
  TO REFERENCE A DISK UNIT OTHER THAN UNIT 0
  APPEND THE UNIT NUMBER (1-7) TO THE COMMAND

  PLEASE ENTER COMMAND: _
```

Figure 3-1
Background Command Table

The user may make his selection by entering the two characters representing the function he wishes to perform followed by a carriage return. Each of the data acquisition commands is outlined in Chapter 4.

3.2 LOADING GAMMA-11 FOR THE FOREGROUND/BACKGROUND USERS

The procedure for loading GAMMA-11 is as follows:

1. Load RT-11.
2. Load the Foreground.
3. Load the Background.

CAUTION

> Whenever changing system disks, the user MUST start the system again, If the user does not start the system again, disk data destruction can result.

The operating procedures for loading and starting RT-11 and GAMMA-11 are outlined below. To load RT-11 F/B, see Steps 1-14; to load GAMMA-11 (foreground), see Step 15; and to load GAMMA-11 (background), see Steps 16-18.

GAMMA-11 STARTING PROCEDURES

1. Turn computer console lock power switch clockwise to the ON position.

2. Turn the LINE/OFF/LOCAL switch on both terminals to be used to LINE. Set to REMOTE for the LA36 and REM for the VT05. Also press the ON/OFF switch on the foreground terminal (VT52 or VT05) to ON (this can be done after loading).

3. Set the ENABLE/HALT switch on the PDP-11 console to HALT.

4. Pull the 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 disk drive door.

6. Set the LOAD/RUN switch on the 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 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 as the starting address in the system.

10. Set the PDP-11 processor SWITCH REGISTER to 777406 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 and prints on the terminal the version number of RT-11.

13. The system responds with the version number of RT-11 and a dot on the console terminal. The user must type the DATE command into the system. The DATE command assigns a date to new patient studies until a new DATE command is issued.

    The form of the command is:

    ```
        DATE dd-mmm-yy
    or
        DAT dd-mmm-yy
    or
        DAT
    ```

    followed by the <CR> 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. If no arguments are typed in response to the command, the current date is printed.

Examples:

To enter the date, April 25, 1976 as the current date for the system, type:

```
DAT 25-APR-76<CR>
```

To have the current date printed by the system, type:

```
DAT<CR>
25-APR-76        (System response)
```

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

14. The system again responds with a dot. Type the TIME command into the system. The TIME command allows the user either to find out the current time of day kept by RT-11 or to enter a new time of day.

    The form of the command is:

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

    followed by the <CR> key, where:

hh:mm:ss	Represents the hour, minute, and second.

    The time is in hours, minutes, and seconds past midnight. If no argument is indicated, the current time of day is output.

    Examples:

    ```
    TIME 16:48:32<CR>
    ```

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

    ```
    TIME<CR>
    16:58:36         (system response approximately ten
                      minutes later).
    ```

15. The system again responds with a dot. Next, type

    ```
    FRUN FGAMMA<CR>
    ```

    on the terminal to call in the foreground for GAMMA-11.

    There is a slight pause and the foreground command table is now present on the foreground terminal. (See Section 3.2.1.)

The following message is printed on the console:

~~FGAMMA LOADED AND RUNNING~~

Now, FGAMMA no longer references the DECwriter.

16. The system again responds with B> and a dot on the DECwriter. Type

```
RUN BGAMMA<CR>
```

    on the terminal to call in the background for GAMMA-11.

17. The system responds with the background command table on the Color display (or VT01). (See Section 3.1.1.) The commands that have a preceding asterisk are not operable when the foreground is running.

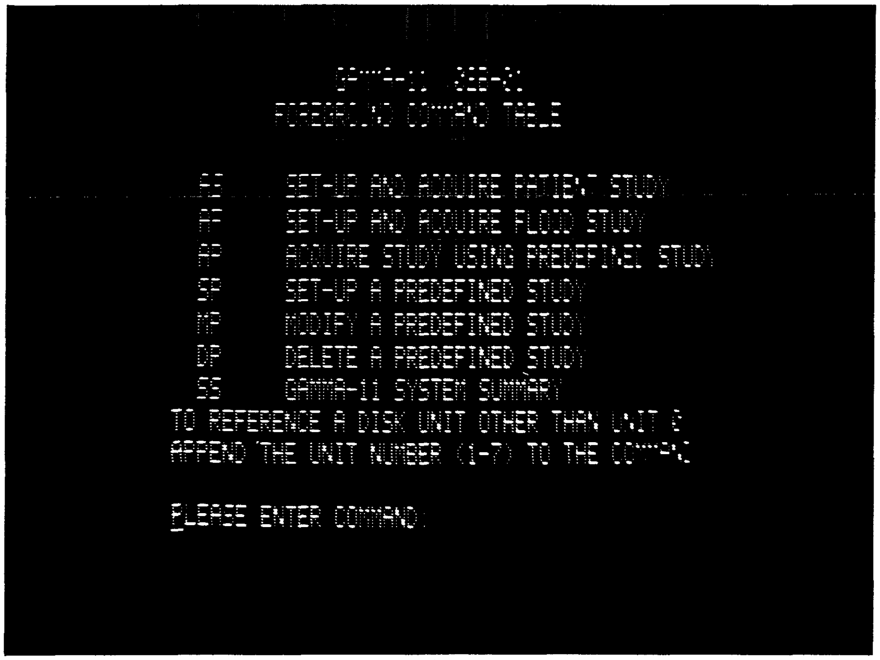
18. The background is now loaded and running.

3.2.1 Foreground Loading Commands

The Foreground Loading Commands are identical to those for the background, except that AD (Data Analysis and Review), CA (Continue Ayalysis), DS (Delete Patient Studies), and TS (Transfer Studies) are not used. With these exceptions, the foreground commands are displayed on the foreground terminal and are referenced through the foreground terminal. The following photograph (See Figure 3-2) is an example of the foreground command table.

NOTE

> If the VT05 has not been turned on yet, turn on the power switch and after the terminal has "warmed up", set the LOC/REM switch to REM and press <CR> and the foreground commands will be displayed.
>
> If the VT52 has not been turned on yet, push the ON/OFF switch on the right side of the terminal forward. When the blinking cursor appears, press the <CR> key.



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

    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
  TO REFERENCE A DISK UNIT OTHER THAN UNIT 0
  APPEND THE UNIT NUMBER (1-7) TO THE COMMAND

  PLEASE ENTER COMMAND:
```

Figure 3-2
Foreground Command Table

To select a function, type the two characters of the corresponding command followed by a carriage return. Each of the foreground commands is outlined in Chapter 4.

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

Keyboard commands provide communication with the RT-11 Monitor and allow the user to allocate system resources, manipulate core images, start programs, and exploit Foreground/Background services. These characters are discussed as follows:

1. Pressing the RETURN key (symbolized as <CR> in this manual) indicates that the user has completed typing a line of input and is now telling the computer to take control. Pressing <CR> also causes the console terminal to return to the left margin and space to the next line. The symbol <CR> is used in this manual to indicate pressing the <CR> key.

2. Pressing DELETE (RUBOUT) causes the preceding character (the very last one typed in) to be ignored by the computer. When the user types the DELETE key, the system terminal echoes a

backslash (\) plus the preceding character. The RUBOUT 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 RUBOUT is typed. The RUBOUT key has no effect after all characters up to the last <CR> have been deleted.

Example:

The patient name, GANEK was mistyped as GAKNE. Correct it by typing three RUBOUTs and then "NEK" as follows:

```
GAKNE\ENK\NEK
```

3. 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.

4. CTRL/C is typed by holding down the CTRL key while typing the C key. This echoes ^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/C's 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.

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 (see the RT-11 System Reference Manual).

7. CTRL/U deletes the current input line and echoes as ^U followed by a <CR> 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/Q does not echo. It causes the terminal to resume printing characters from the point at which printing previously stopped (via CTRL/S).

9. 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.

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 just 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. If an error is made while typing a response, before terminating it with a <CR>, press the RUBOUT key. The character # appears at the end of the erroneous line, and a colon (:) appears on the line below. The erroneous line is deleted, but remains on the screen until either ALTMODE or CTRL/E is typed (see below).

   Example:

```
ORGAN (12): THYRI#
:THYROID<CR>
```

2. The ESCAPE (ALTMODE) key (labeled ALT on the DECwriter) 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, type <CR>; the next question and answer appears. To change an answer, type RUBOUT and proceed as described above. After the new answer has been typed, all remaining completed questions and answers, up to the point at which the user typed ALTMODE, are redisplayed. The user may then finish the page, or, if errors remain, type ALTMODE again. For each use of ALTMODE, only one answer can be corrected.

3. 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 RUBOUT.

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, the user 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 a RT-11 command.

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

```
F>
```

The user must then type CTRL/C on the terminal. To exit the background program and return to the RT-11 Monitor, type another CTRL/C which outputs a ".". At this point, the user must type

```
UNLOAD FG<CR>
```

to free the core space used by the foreground program.

3.4 SYSTEM HIERARCHY

The principal program functions of GAMMA-11 are grouped in a hierarchy as shown in Figure 3-3. Typing the appropriate two characters from the foreground command table calls a principal function into operation.

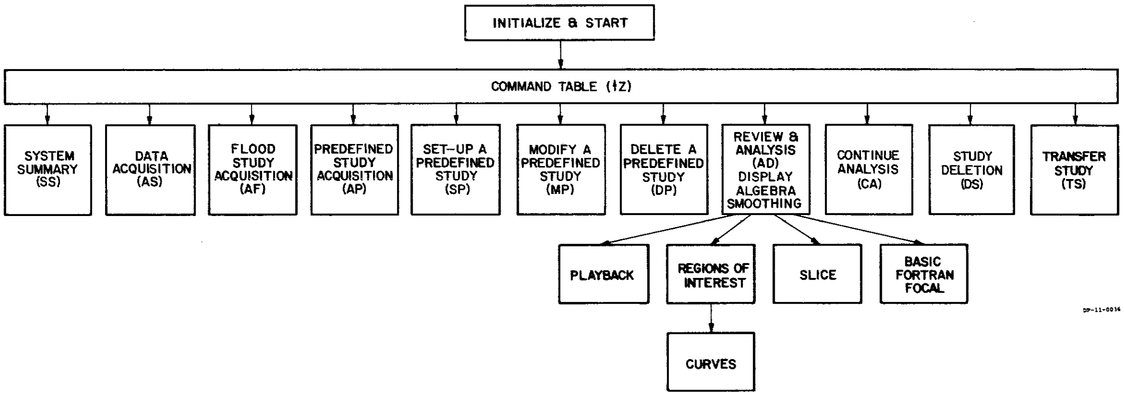


Figure 3-3
System Hierarchy

3.5 CONTROL CHARACTERS WITHIN GAMMA-11

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

1. CTRL/Z, which immediately bypasses any of the program hierarchy and displays either the background or foreground command table, depending upon the system being run.
2. CTRL/X, which immediately returns to the next level in the program hierarchy. For example, if the user is displaying Regions of Interest and types CTRL/X on the terminal, user 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.

CHAPTER 4

GAMMA-11 DATA ACQUISITION

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

The entire procedure is controlled from the keyboard (VT05 or VT52 for foreground, LA36 for background), in response to questions, instructions, or choices appearing on the display screen (VT05 or VT52 for foreground, VT01 or VSV01 for background).

SS

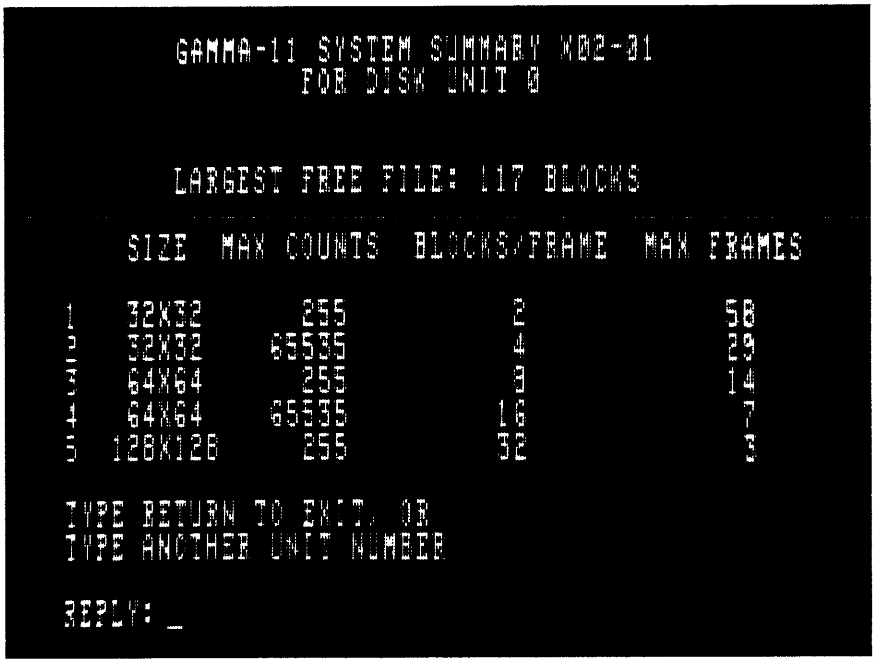
4.1 GAMMA-11 SYSTEM SUMMARY

The first command in the system hierarchy (Figure 3-3) is the System Summary (SS). Its purpose indicates the amount of disk space available for acquiring and storing patient data. When the background (or foreground) command table is present, type the SS command to obtain a GAMMA-11 System Summary:

```
SS n<CR>
```

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

The following display (Figure 4-1) is presented on the scope.



```
          GAMMA-11 SYSTEM SUMMARY X02-01
                FOR DISK UNIT 0


          LARGEST FREE FILE: 117 BLOCKS

     SIZE  MAX COUNTS  BLOCKS/FRAME  MAX FRAMES

1    32X32       255             2          58
2    32X32     65535             4          29
3    64X64       255             8          14
4    64X64     65535            16           7
5  128X128       255            32           3

TYPE RETURN TO EXIT, OR
TYPE ANOTHER UNIT NUMBER

REPLY: _
```

Figure 4-1
System Summary

The System Summary presents several different matrix configurations for the collection of data. The choice of matrix depends on several variables, among them the count rate, the image resolution desired, the amount of available disk storage space, and the kinds of analysis to be performed. 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	MAXIMUM CELL COUNT	MATRIX TYPE
1	32x32	255	Byte
2	32x32	65535	Word
3	64x64	255	Byte
4	64x64	65535	Word
5	128x128	255	Byte

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

For example, the disk is capable of holding approximately one million words of patient data. This space is described in terms of frames, for the five standard configurations (also see Section 4.9):

	SIZE	MAX COUNTS	BLOCKS/FRAME	MAX FRAMES OF DATA
1	32x32	255	2	~~2000~~
2	32x32	65535	4	1000
3	64x64	255	8	500
4	64x64	65535	16	250
5	128x128	255	32	125

If the user types <CR> in response to the SS reply (System Summary reply), the program returns to the Command Table. However, if the user types another unit number, the System Summary changes in accordance with the available disk space on that disk.

4.1.1 Maximum Cell Counts

It is convenient to distinguish matrices by cell count capacity, where a cell is one data point. (An image is made up of many cells. These cells can be either a byte or a word.) Configurations with a maximum cell count of 255 are called byte-matrices. Those with a maximum count of 65535 are called word-matrices. The difference is in the amount of PDP-11 memory storage space allotted to the cell. The 255-count cell requires one 8-bit byte (1/2-word) of memory, while the larger cell requires a full 16-bit word.

4.1.2 Insufficient Disk Space

If sufficient disk space is not available for the study that is to be acquired, squish the data already in the file (on the disk) or delete previous patient studies and then squish the disk. Details of these operations are given in Chapter 10.

AS

4.2 SET-UP AND ACQUIRE PATIENT STUDY

The second command in the system hierarchy is Data Acquisition (AS;Acquire Study), which sets up and acquires patient studies. This process is known as a Study Plan. The Study Plan consists of three display-pages of data as follows:

1. Page 1 contains administrative information about a patient. This information is used to create the Patient Study Index entry by which the study is accessed.
2. Page 2 contains gamma camera parameters and study-type specifications. Camera parameters refer to switch settings and other operational data about the scintillation camera.
3. Page 3 contains information about collection parameters. Collection parameters specify the type of study, the duration of the collection run, and the structure of the data.

To prepare a Study Plan, type,

```
AS n<CR>
```

where n is an optional disk unit number.

The first question of page 1 is now displayed on the scope.

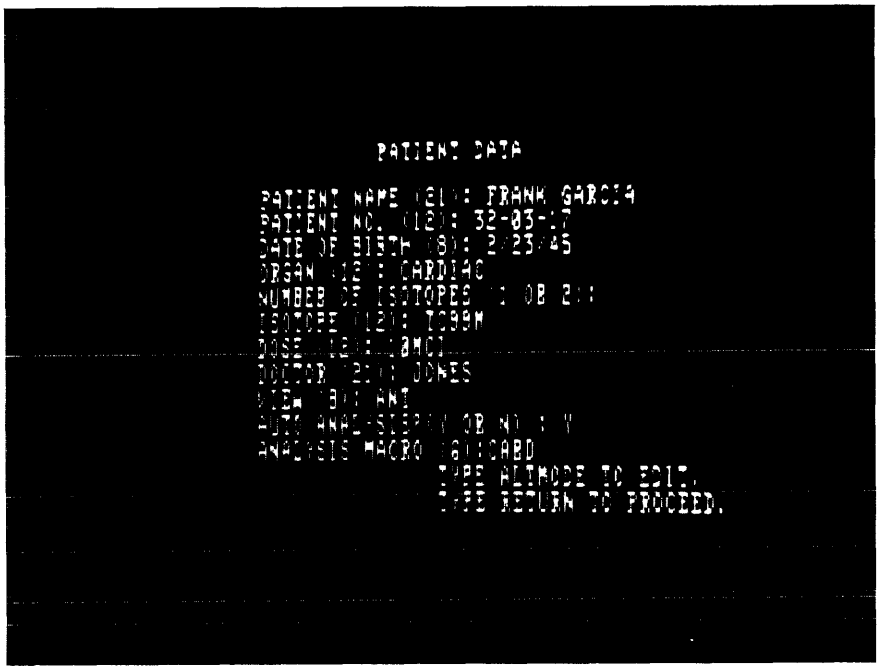
4.2.1 Study Plan Page 1: Patient Data

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 may contain any printing keyboard character, up to the maximum number indicated by the question. For example, the Study Plan question

```
PATIENT NAME (21):
```

expects a free-field answer of not more than 21 characters. If an answer is too long, it is automatically deleted, and a # sign and a colon are presented to the user waiting for a new response. (See Section 3.3.2.)

Answers to PATIENT NAME and PATIENT NUMBER are required; all other responses are optional and may be skipped by typing a <CR>. After each entry is made, the user must type a <CR> to proceed to the next question.



```
            PATIENT DATA

PATIENT NAME (21): FRANK GARCIA
PATIENT NO. (12): 32-03-17
DATE OF BIRTH (8): 2/23/45
ORGAN (12): CARDIAC
NUMBER OF ISOTOPES (1 OR 2):
ISOTOPE (12): TC99M
DOSE (12): 10MCI
DOCTOR (21): JONES
VIEW (8): ANT
AUTO ANALYSIS? (Y OR N) : Y
ANALYSIS MACRO (6):CARD
                    TYPE ALTMODE TO EDIT.
                    TYPE RETURN TO PROCEED.
```

Figure 4-2
Study Plan Page 1: Patient Data

The following entries are self-explanatory:

~~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 <CR>. If the user types in a <CR>, 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 Y is typed, the data acquisition program automatically calls the data analysis program after all the data has been acquired. The data analysis program automatically selects and displays the first frame of the study that has just been acquired for data analysis. If an analysis macro name is specified in the next question, this macro is automatically loaded and executed. See Sections 5.24 through 5.24.9. If auto analysis from FGAMMA (the foreground data acquisition program) is specified, 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.

If either of the conditions are not met, auto analysis does not take place. If auto analysis from the background data acquisition program is specified, the data analysis program will always be called. The last entry is:

ANALYSIS MACRO (6)

The data analysis macro filename is required if a macro is desired for auto analysis. A discussion of macros and macro commands appears in Sections 5.24 through 5.24.9.

The replies to all of the above items are optional except for PATIENT NAME and NUMBER.

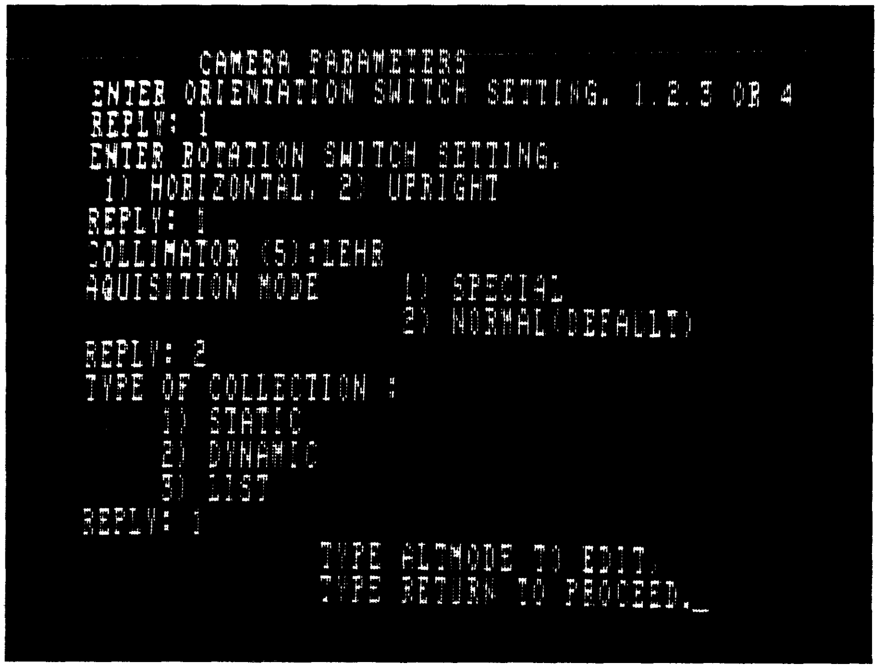
NOTE

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

When the page is complete, the user is given the opportunity to type ALTMODE, in order to verify and edit all of the answers, or to type <CR> and 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 scope when a <CR> is entered as a reply from Page 1. Figure 4-3 represents a complete example of the camera parameters from Page 2.



```
          CAMERA PARAMETERS
ENTER ORIENTATION SWITCH SETTING. 1.2.3 OR 4
REPLY: 1
ENTER ROTATION SWITCH SETTING.
 1) HORIZONTAL. 2) UPRIGHT
REPLY: 1
COLLIMATOR (5):LEHR
AQUISITION MODE        1) SPECIAL
                       2) NORMAL(DEFAULT)
REPLY: 2
TYPE OF COLLECTION :
     1) STATIC
     2) DYNAMIC
     3) LIST
REPLY: 1
                    TYPE ALTMODE TO EDIT.
                    TYPE RETURN TO PROCEED._
```

Figure 4-3
Study Plan Page 2: Camera Parameters

Notice the first and second questions asked:

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

ENTER ROTATION SWITCH SETTING
1) HORIZONTAL 2) UPRIGHT

The two questions are related, and the answers are required. The questions refer to switches on the scintillation 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 relations according to the following table (4-1), in which X and Y represent the camera's field coordinates, and X' and Y' represent the coordinates of the matrix displayed on the screen.

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

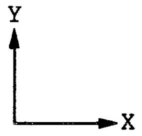
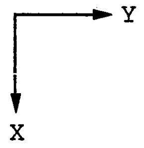
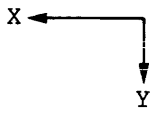
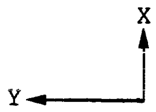
ORIENTATION SWITCH	ROTATION SWITCH	X-INVERT	Y-INVERT	X-Y EXCHANGE
		(1=ON, 0=OFF)		
1	1	0	1	1
2	1	1	1	1
3	1	1	0	1
4	1	0	0	1
1	2	0	1	0
2	2	0	0	0
3	2	1	0	0
4	2	1	1	0

Table 4-4
Toshiba Settings

ORIENTATION SWITCH	ROTATION SWITCH	TOSHIBA EQUIVALENT
3	2	G
4	1	
1	2	
2	1	
2	2	
1	1	
4	2	
1	1	

If the user has a camera type other than Searle or Ohio Nuclear, 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 only rotate the image 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 each answer followed by a <CR> has been entered, the user now has the option to enter the type of collimator used on the gamma camera as follows:

COLLIMATOR (5)

The answer is free-field and is not required. Only type <CR> to have the next question appear.

ACQUISITION MODE 1) SPECIAL
2) NORMAL (DEFAULT)

The Acquisition Mode refers to the use of the A/D Converters by the GAMMA-11 system. The A/D Converters have two program-selectable gains, which provide a choice of two different image sizes.

1. A "close-up" image, with a gain identifier of 1, gives an enlarged view of a portion of the field.
2. A normal image, with a gain identifier of 2, covers the entire field of view.

Actually, by adjusting the GAIN 1 and GAIN 2 controls on the A/D Converters, the user may set the gains to whatever he wishes. Refer to the Instruction Manual for the NC11-A Camera Front-End for a GAMMA-11 System. If the question is skipped, the default (Normal gain) is assumed.

The next question asked is

TYPE OF COLLECTION:
1) STATIC
2) DYNAMIC
3) LIST

This answer is required, because it determines, among other things, the questions to be asked on the third page of the Study Plan.

When the camera parameters and study type have been entered, edited if necessary, and verified, the program 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 the user answers Y (for YES) to the question, the screen is erased and prepared for the text to be entered. The user may type up to ten lines, each 49 characters maximum. Any printing character may be used. Errors are corrected by using the methods described in Section 3.3.2. The user may terminate the text by typing a "null" line, that is, two <CR>s in a row.

NOTE

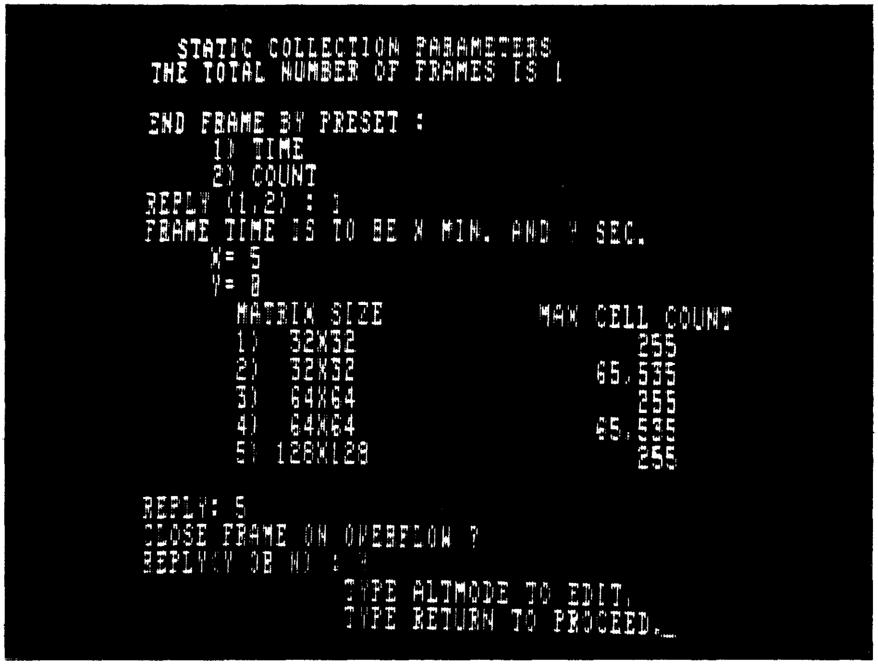
If the user answers NO to the request for comments at this time, he will be able to add comments during the review phase, but not immediately following collection.

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 4-4.



```
   STATIC COLLECTION PARAMETERS
THE TOTAL NUMBER OF FRAMES IS 1

END FRAME BY PRESET :
     1) TIME
     2) COUNT
REPLY (1,2) : 1
FRAME TIME IS TO BE X MIN. AND Y SEC.
     X= 5
     Y= 0
       MATRIX SIZE             MAX CELL COUNT
       1)  32X32                          255
       2)  32X32                       65,535
       3)  64X64                          255
       4)  64X64                       65,535
       5) 128X128                         255

REPLY: 5
CLOSE FRAME ON OVERFLOW ?
REPLY(Y OR N) : Y
                  TYPE ALTMODE TO EDIT.
                  TYPE RETURN TO PROCEED._
```

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

The first question asked is

THE TOTAL NUMBER OF FRAMES IS

A maximum of eight frames is allowed. If the user enters a 1, it is assumed that the Static Study is a single frame study. If the user enters a number in the range 2 to 8, it is assumed that the Static Study is multiple (i.e., more than one view will be acquired). Finally, if the user responded to the question by entering a <CR>, the default is 1 (Single Static Study). Also, if there is not enough space on the disk for the number of frames chosen, the program, after entering all the collection parameters, alerts the user who can either proceed or edit the page and enter a new number. If the user proceeds, the program does not collect more frames than the disk can hold.

The next question asked is

END FRAME BY PRESET:

1) TIME
2) COUNT

This question determines the period of time or the number of counts for collection. If the user chose "TIME", the following question appears:

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

The user must enter a value for X and Y, each followed by a <CR>. The maximum for X and Y is 999. If the user chose option 2, "COUNT", the following question appears on the scope:

```
PRESET COUNT IS
```

This allows the user to determine a preset count value to stop data collection. The maximum preset count that can be entered into the system is 999,999,999. (Note that the commas are not entered in response to this question; their presence here is for clarity.)

After the user has entered a <CR>, a table of possible matrix configurations is displayed. 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 the user replies with a "YES", the program stops collection of data as soon as any cell attempts to exceed its count capacity. This occurs only if overflow occurs before the preset time or count limit is reached. For example, if the user entered an X value of 5 and a Y value of 0 and chose matrix 5 as the size, it is possible that the maximum cell count of 255 might be reached before five minutes of collection are up. In this case, the system stops collecting data.

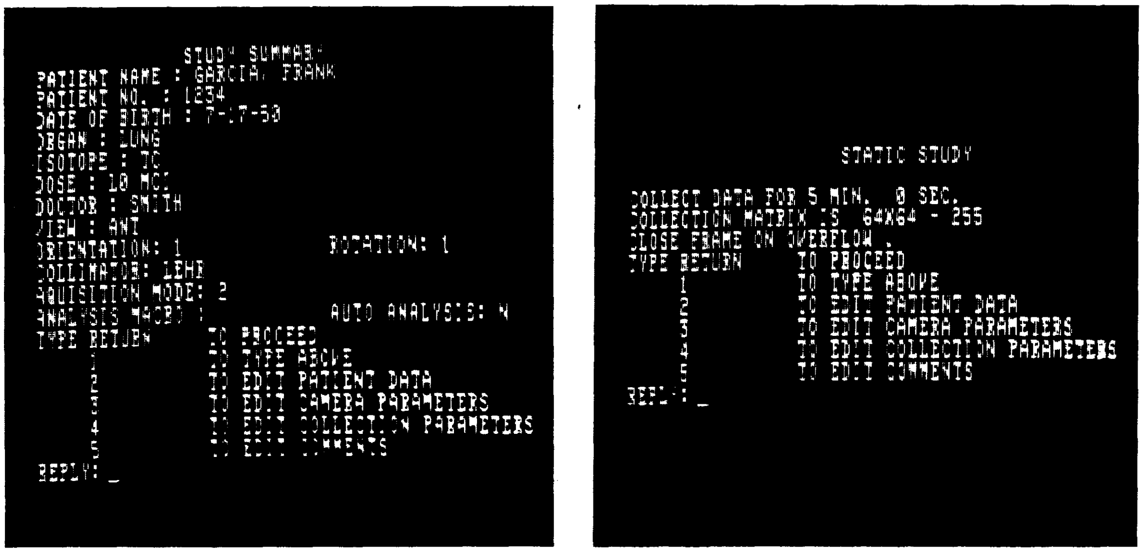
However, if the user replies with a "NO", the program allows cell overflow to occur during the run. When the count capacity for an element is exceeded, it remains at maximum count and collection continues.

This question does not need a reply. If <CR> is entered, the system automatically defaults to "NO".

An example of the use of the cell-overflow frame limit would be a lung or 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 all of the collection parameters have been entered, a summary of the entire Static Study Plan (except for comments) is displayed as shown in Figure 4-5. Changes to any of the entries are made 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 ALTMODE for the page indicated. Entries for the page appear one by one for examination. After editing, the entire summary is displayed once again for verification. To obtain a print-out of the summary, type "1". Print-out occurs only in the background version.



```
                 STUDY SUMMARY
PATIENT NAME : GARCIA, FRANK
PATIENT NO. : 1234
DATE OF BIRTH : 7-17-50
ORGAN : LUNG
ISOTOPE : TC
DOSE : 10 MCI
DOCTOR : SMITH
VIEW : ANT
ORIENTATION: 1                  ROTATION: 1
COLLIMATOR: LEHR
AQUISITION MODE: 2
ANALYSIS MACRO :                AUTO ANALYSIS: N
TYPE RETURN         TO PROCEED
      1             TO TYPE ABOVE
      2             TO EDIT PATIENT DATA
      3             TO EDIT CAMERA PARAMETERS
      4             TO EDIT COLLECTION PARAMETERS
      5             TO EDIT COMMENTS
REPLY: _
```

```
                 STATIC STUDY

COLLECT DATA FOR 5 MIN.  0 SEC.
COLLECTION MATRIX IS  64X64 - 255
CLOSE FRAME ON OVERFLOW .
TYPE RETURN         TO PROCEED
      1             TO TYPE ABOVE
      2             TO EDIT PATIENT DATA
      3             TO EDIT CAMERA PARAMETERS
      4             TO EDIT COLLECTION PARAMETERS
      5             TO EDIT COMMENTS
REPLY: _
```

Figure 4-5
Static Study Summary: Parts 1 and 2

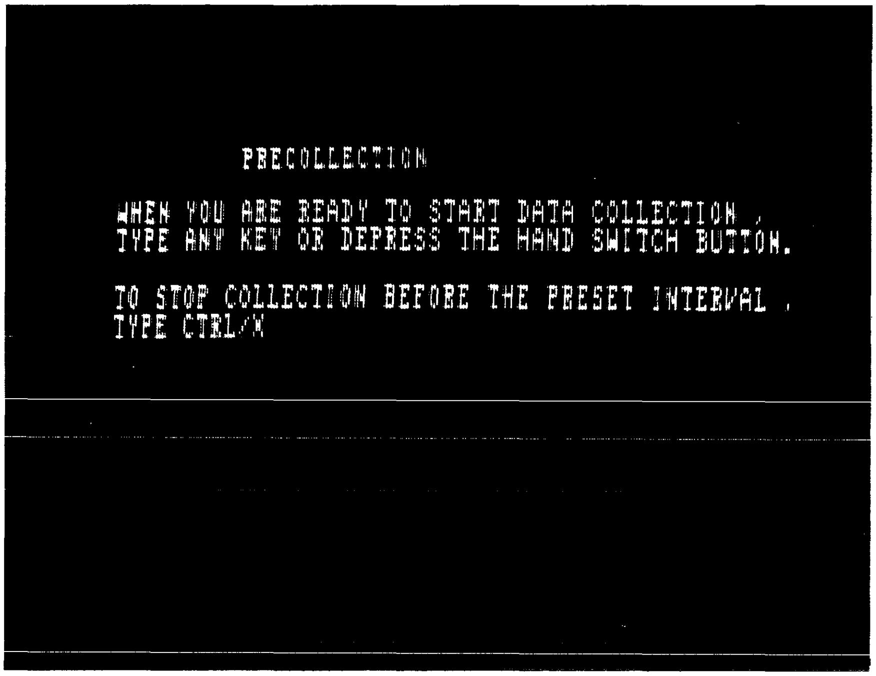
The example in Figure 4-5 is of a multiple-frame study. The message "FRAME 1 OF 4" identifies this summary as applying to the first frame of the study. Data collection is conducted as a separate run for each frame. The Static Study Plan may be changed between frames (see Section 4.2.7).

NOTE

> When performing a multiple Static Study, it is assumed that succeeding frames are the same matrix size as frame #1. If the user increases the matrix size of a frame after collecting frame #1, a "DISK FULL" message may appear on the terminal. The message does not imply that the disk is actually full, but that not enough disk space is allocated for an increased matrix size.

4.2.6 Precollection Frame

When the Static Study Summary has been verified, typing a <CR> brings the Precollection Frame to the screen (Figure 4-6). This is a programmed pause to allow final adjustments, wait for the patient, or reconsider the entire operation. If for any reason the user does not proceed with the collection, he must type CTRL/X or CTRL/Z. The entire study file is deleted. Otherwise, the user should proceed as directed.



```
          PRECOLLECTION

WHEN YOU ARE READY TO START DATA COLLECTION ,
TYPE ANY KEY OR DEPRESS THE HAND SWITCH BUTTON.

TO STOP COLLECTION BEFORE THE PRESET INTERVAL ,
TYPE CTRL/X
```

Figure 4-6
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, the frame is closed, transferred to the disk, and a "beep" or bell sounds. Subsequent events depend on the specifications of the Study Plan as follows:

1. If this is a single Static frame study with no comments, the study file closes and control returns to the Command Table (background or foreground).

2. If comments have been included, an opportunity to edit or add to the text is provided. When this has been done, the file closes and control returns to the Command Table. The only exception to this procedure is during auto analysis. The first image acquired will be displayed instead of the Command Table.

3. If this is a multi-frame study, (multiple Static Study), the request

> appears on the screen. VIEW is the most likely Study Plan entry to be changed between frames. Skipping the answer with a <CR> leaves a blank entry. If the VIEW is unchanged, the user must re-enter it. When the answer has been typed, the entire Study Summary, with the new VIEW, is displayed along with the list of editing options. Thus, any or all of the Study Plan entries may be changed between frames. Note, however, that if any of the items used in the Index entry (Patient Name, Patient Number, Organ) are changed, those for the first frame of the study are still used for the Index entry.

For each frame, the user has the option of repeating the procedures in Sections 4.2.5 - 4.2.7. After the last frame, the entire file is closed, and control returns to the Command Table.

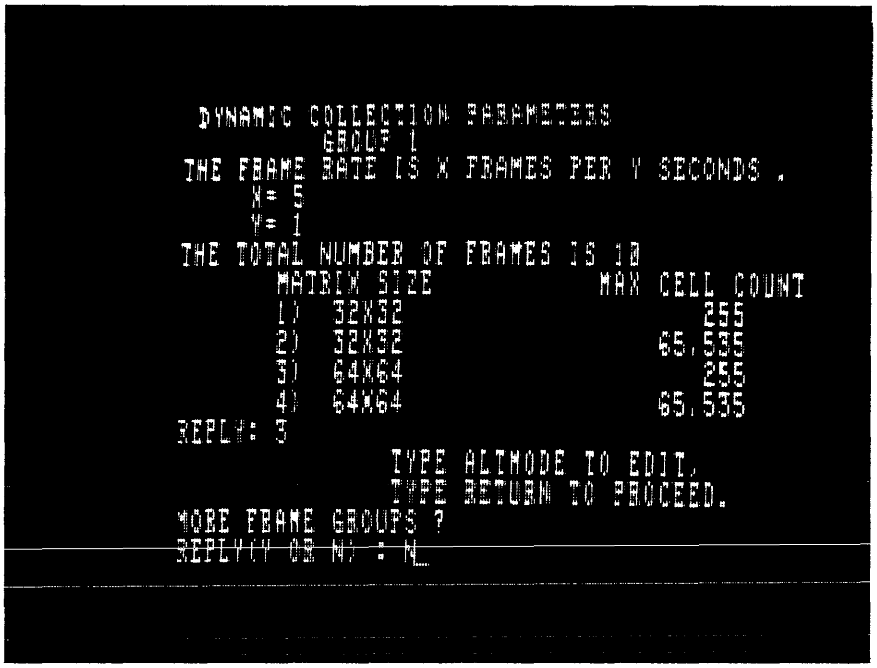
4.2.7.1 Special Comments on Dual-Isotope Studies

If two isotopes are being scanned, each collection run consists of two frames, one for each isotope. Once again, the largest matrix that can be used for static dual-isotope studies is, 64 x 64 x word. Some users may find the dual-isotope study useful for collection of "gated" studies.

4.2.8 Dynamic Collection Parameters

A complete example of Dynamic Collection parameters is shown in Figure 4-7. A separate page of collection parameters is required for each group of frames. All groups must be specified before collection begins. Each group of frames can have different frame rates, numbers of frames, and matrix configurations.

For example, the frame rate might be changed in a renal flow study. The rate of change of isotope distribution slows towards the end of study and the frame rate does not have to be as fast as during the initial phase of the study, to obtain the same resolution of flow change.



```
  DYNAMIC COLLECTION PARAMETERS
             GROUP 1
 THE FRAME RATE IS X FRAMES PER Y SECONDS .
      X= 5
      Y= 1
 THE TOTAL NUMBER OF FRAMES IS 10
       MATRIX SIZE               MAX CELL COUNT
       1)  32X32                           255
       2)  32X32                        65,535
       3)  64X64                           255
       4)  64X64                        65,535
 REPLY: 3
                TYPE ALTMODE TO EDIT,
                TYPE RETURN TO PROCEED.
 MORE FRAME GROUPS ?
 REPLY(Y OR N) : N_
```

Figure 4-7
Study Plan Page 3: Dynamic Collection Parameters

Page 3 for Dynamic Collection parameters appears if the user requested "DYNAMIC" under "TYPE OF COLLECTION" on Page 2.

The first question asked is

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

Each frame will be held open for Y/X seconds (frame rate). The maximum frame rate depends on the matrix configuration.

The next question asked is

```
THE TOTAL NUMBER OF FRAMES IS
```

The number of frames in a group also depends on the matrix configuration. The next question

```
MATRIX SIZE and CELL COUNT
```

are configurations identified by the number in the Study Summary.

The above collection parameters for a Dynamic Study are subject to the following limitations:

1. No more than 13 groups are allowed in one study.
2. No more than 512 frames are allowed in the entire study.

3. The 128 x 128 matrix cannot be used.

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	MULTIPLIER
1	32x32	255	50 frames/sec	8
2	32x32	65535	25 frames/sec	4
3	64x64	255	12 frames/sec	2
4	64x64	65535	6 frames/sec	1

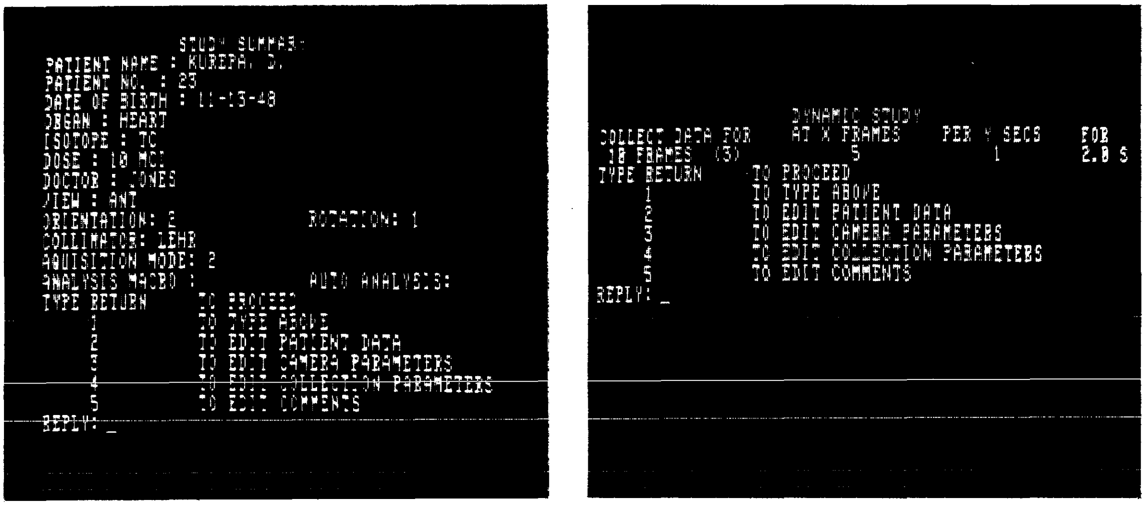
After the user has verified the collection parameters, another question appears on the scope.

MORE FRAME GROUPS?

If the user replies with a "Y", a new set of collection parameters is requested. If the user responds with an "N" or <CR>, the Study Summary is displayed.

4.2.9 Dynamic Study Summary

After all of the collection parameters have been entered, a summary of the entire Dynamic Study Plan (except for comments) is displayed, as shown in Figure 4-8. Note that each group of the Dynamic Study has the collection parameters listed in the summary. Changes to any of the entries is made 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 ALTMODE for the page indicated. After editing, the entire summary is displayed once again for verification. To obtain a printout of the summary, type "1". (Background only.)



```
                STUDY SUMMARY
PATIENT NAME : KUREPA, D.
PATIENT NO. : 23
DATE OF BIRTH : 11-13-48
ORGAN : HEART
ISOTOPE : TC
DOSE : 10 MCI
DOCTOR : JONES
VIEW : ANT
ORIENTATION: 2                 ROTATION: 1
COLLIMATOR: LEHR
AQUISITION MODE: 2
ANALYSIS MACRO :               AUTO ANALYSIS:
TYPE RETURN        TO PROCEED
     1             TO TYPE ABOVE
     2             TO EDIT PATIENT DATA
     3             TO EDIT CAMERA PARAMETERS
     4             TO EDIT COLLECTION PARAMETERS
     5             TO EDIT COMMENTS
REPLY: _
```

```
                  DYNAMIC STUDY
COLLECT DATA FOR     AT X FRAMES     PER Y SECS     FOR
 10 FRAMES  (3)            5              1         2.0 S
TYPE RETURN        TO PROCEED
     1             TO TYPE ABOVE
     2             TO EDIT PATIENT DATA
     3             TO EDIT CAMERA PARAMETERS
     4             TO EDIT COLLECTION PARAMETERS
     5             TO EDIT COMMENTS
REPLY: _
```

Figure 4-8
Dynamic Study Summary: Parts 1 and 2

4.2.10 Precollection Frame

When the Dynamic Study Summary has been verified, typing a <CR> brings the Precollection Frame to the screen (see Figure 4-6). This is a programmed pause to allow final adjustments, wait for the patient, or reconsider the entire operation. If for any reason the user does not proceed with the collection, he must type CTRL/X or CTRL/Z. The entire study file is deleted. Otherwise, the user should proceed as directed.

4.2.11 Data Collection

Once data collection has begun, the collection proceeds through every group of the study. As each group is started, a beep is sounded and "GROUP n" is displayed, where n is the group number. When all of the groups finish, the file is closed. Comments, if included, can be edited at this time and control returns to the Command Table (except during auto analysis; the first image acquired is displayed).

4.2.11.1 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. The frames are collected simultaneously and stored alternately in the study file.

That is, Frame 1 of Isotope 1, Frame 1 of Isotope 2, Frame 2 of Isotope 1, etc. The use of dual isotopes changes some of the limitations on the collection parameters:

1. No more than 256 frames per isotope are allowed 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. The 64 x 64 word-matrix (type 4) cannot be used for dual-isotope Dynamic studies.

4.2.12 Dynamic Collection Parameters

The absolute maximum frame rates for the GAMMA-11 system are described in Table 4-6.

Table 4-6
Maximum Frame Rates for GAMMA-11

MATRIX SIZE	DATA ACQUISITION
32 x 32 x 8	50 frames/sec.
32 x 32 x 16	25 frames/sec.
64 x 64 x 8	12 frames/sec.
64 x 64 x 16	6 frames/sec.

4.2.13 Dynamic Collection Parameters for F/B

When the user is collecting data via Foreground/Background, the maximum frame rates for Dynamic studies vary for foreground versus background. Table 4-7.

Table 4-7
Maximum Frame Rates

MATRIX SIZE	DATA ACQUISITION WITHOUT SUSPENDING BACKGROUND	DATA ACQUISITION IN BACKGROUND
32 x 32 x 8	12 frames/sec.	50 frames/sec.
32 x 32 x 16	6 frames/sec.	25 frames/sec.
64 x 64 x 8	3 frames/sec.	12 frames/sec.
64 x 64 x 16	1.5 frames/sec.	6 frames/sec.

If the user is collecting data in the foreground at a rate faster than those indicated in the second column of Table 4-7, the background is suspended.

The system determines the speed of the Dynamic Study through the questions answered on Page 3 of the Study Plan. If the system calculates those answers as a fast Dynamic Study (faster than those in Table 4-7, Data Acquisition in Foreground), the background is suspended when the Pre-collection Frame is displayed on the scope. No warning is given to a background job. Warning is given to the ~~foreground job at Study Summary time.~~

When data collection is finished or when the frame rate drops below those listed in Table 4-7, the background continues operation where it was suspended.

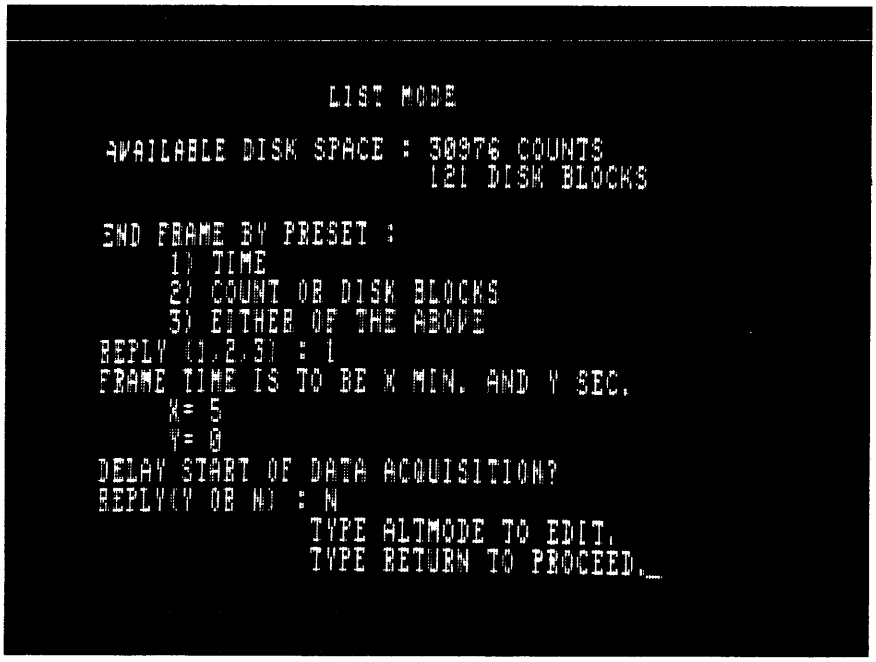
If the system determines the speed of the Dynamic Study to be slower than the values in Table 4-7, background execution proceeds as normal.

4.3 LIST STUDY

In the List Study collection mode, the data are not structured into matrices. Instead, each pair of X- and Y-coordinates is stored 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.

4.3.1 Collection Parameters

A complete page of collection parameters for a List study is shown in Figure 4-9. This page (3) only appears if LIST has been requested under TYPE OF COLLECTION on Page 2.



```
                  LIST MODE

 AVAILABLE DISK SPACE : 30976 COUNTS
                        121 DISK BLOCKS

 END FRAME BY PRESET :
     1) TIME
     2) COUNT OR DISK BLOCKS
     3) EITHER OF THE ABOVE
 REPLY (1,2,3) : 1
 FRAME TIME IS TO BE X MIN. AND Y SEC.
     X= 5
     Y= 0
 DELAY START OF DATA ACQUISITION?
 REPLY(Y OR N) : N
                 TYPE ALTMODE TO EDIT.
                 TYPE RETURN TO PROCEED._
```

Figure 4-9
List Study Collection Parameters

The first line

AVAILABLE DISK SPACE

represents the total number of counts and the number of disk blocks available to store these counts. The user may choose the most suitable terminating limit. Each disk block has a capacity of 256 counts.

The next line,

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

allows the user to choose the collection parameter that terminates collection. If option 3 is chosen, both time and counts or disk blocks must be specified. The collection stops at whichever limit is reached first.

If TIME is chosen, the question,

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

is displayed and collection stops after the specified time has elapsed.

If COUNT OR DISK BLOCKS is chosen

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

is displayed and the user must choose one or the other. Also, the total number (counts or blocks) may not exceed the limits given at the top of the displayed page (Figure 4-9).

The next line

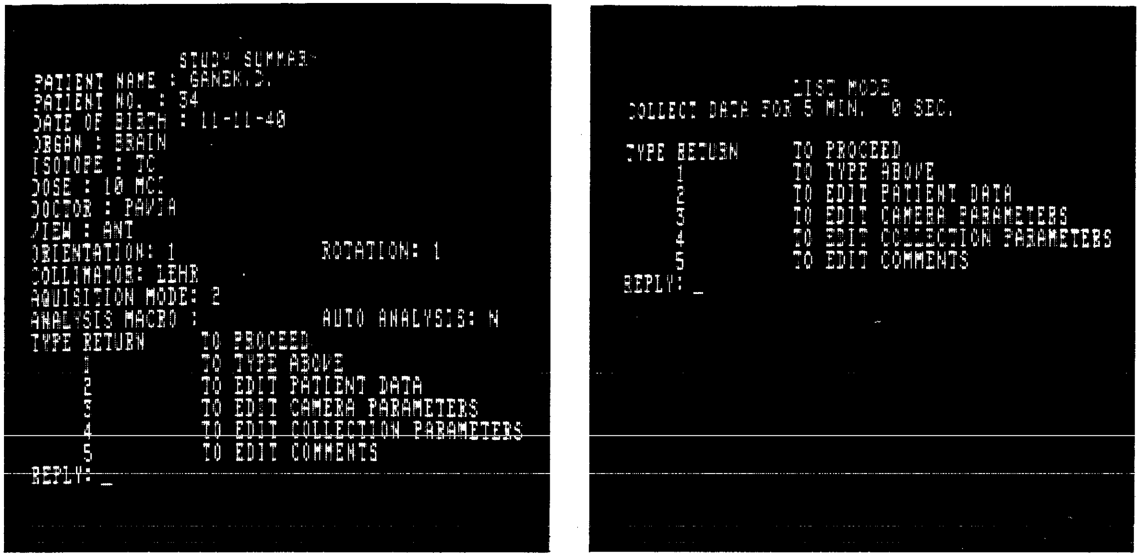
```
DELAY START OF DATA ACQUISITION?
```

requires a YES or NO answer. If YES is chosen, the start of the collection run is delayed until a specified count rate is reached. The time and/or count limit parameters are measured from the delayed starting point. The delay option is another aid in conserving storage space. The user may wait until the count rate rises to a meaningful level above the background before storing the data. If NO is chosen, no delay takes place.

The next line

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

is displayed only if a delayed start has been specified. Collection begins as soon as the rate reaches the given number of counts per second. After the user enters a carriage return to proceed, the List study summary is displayed on the screen (Figure 4-10).



```
              STUDY SUMMARY
PATIENT NAME : GANEK,D.
PATIENT NO. : 34
DATE OF BIRTH : 11-11-40
ORGAN : BRAIN
ISOTOPE : TC
DOSE : 10 MCI
DOCTOR : PAVIA
VIEW : ANT
ORIENTATION: 1              ROTATION: 1
COLLIMATOR: LEHR
AQUISITION MODE: 2
ANALYSIS MACRO :            AUTO ANALYSIS: N
TYPE RETURN       TO PROCEED
     1            TO TYPE ABOVE
     2            TO EDIT PATIENT DATA
     3            TO EDIT CAMERA PARAMETERS
     4            TO EDIT COLLECTION PARAMETERS
     5            TO EDIT COMMENTS
REPLY: _
```

```
                    LIST MODE
COLLECT DATA FOR 5 MIN.  0 SEC.

TYPE RETURN       TO PROCEED
     1            TO TYPE ABOVE
     2            TO EDIT PATIENT DATA
     3            TO EDIT CAMERA PARAMETERS
     4            TO EDIT COLLECTION PARAMETERS
     5            TO EDIT COMMENTS
REPLY: _
```

Figure 4-10
List Study Summary: Parts 1 and 2

4.3.2 Data Collection

The user should follow the precollection procedure as described in Section 4.2.6. At the end of the collection run, one of the following termination messages is displayed, 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 <CR> TO RETURN TO COMMAND TABLE
```

The maximum collectable data count rate is about 30,000 counts per second. If the rate exceeds this limit, collection continues, but data are lost. If a delayed start has been specified, the time-wasting line is drawn across the bottom of the screen until the actual collection begins. At this point, the line jumps up half an inch.

NOTE

The use of dual isotopes is not possible in a List study.

4.3.3 List Mode Collection Using F/B

Background program execution is always suspended during data acquisition when collecting list data using the foreground data acquisition programs.

4.4 FLOOD STUDY ACQUISITION

The third command in the system hierarchy is the Flood Study Acquisition (AF). The Flood Study is a single-frame static study and the study plan is almost entirely predefined. The only collection parameter information that is not predefined is the time and number of counts.

In a Flood Study, the camera is presented 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 those heretofore discussed. No patient data is required, and most of the collection parameters are automatically defined.

AF

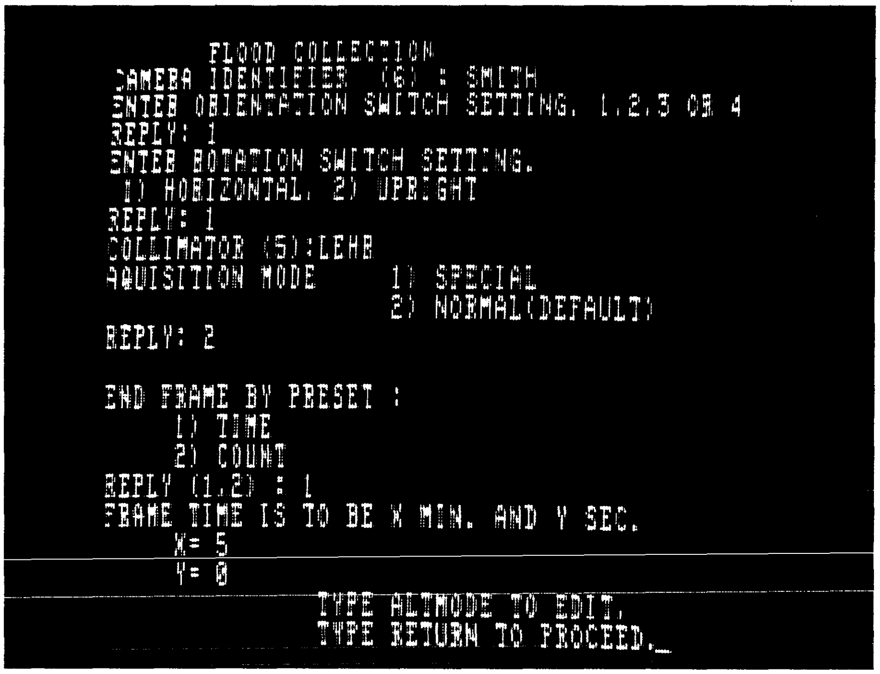
4.4.1 Flood Study Plan

To prepare a Flood Study, type,

```
AF n<CR>
```

where n is an optional disk unit number other than zero.

The following display is presented on the scope:



```
         FLOOD COLLECTION
CAMERA IDENTIFIER  (6) : SMITH
ENTER ORIENTATION SWITCH SETTING. 1,2,3 OR 4
REPLY: 1
ENTER ROTATION SWITCH SETTING.
 1) HORIZONTAL, 2) UPRIGHT
REPLY: 1
COLLIMATOR (5):LEHR
AQUISITION MODE      1) SPECIAL
                     2) NORMAL(DEFAULT)
REPLY: 2

END FRAME BY PRESET :
     1) TIME
     2) COUNT
REPLY (1,2) : 1
FRAME TIME IS TO BE X MIN. AND Y SEC.
     X= 5
     Y= 0
                TYPE ALTMODE TO EDIT.
                TYPE RETURN TO PROCEED._
```

Figure 4-11
Flood Collection

Instead of the usual patient data, the user is asked only for one item of administrative data.

CAMERA IDENTIFIER (6)

This is a free-field answer and corresponds to the Patient Name.

NOTE

> All three pages of the study plan discussed under the Static Study are incorporated into one page of the Flood Study.

Thus, the following questions asked in sequence 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, the user must supply only the duration of the run, either in elapsed time or in total counts. All other collection parameters are automatically defined, as follows:

Number of frames: 1
Matrix size: 64 x 64
Maximum cell count: 65535
Close frame on overflow? Yes

At this time, the user may now verify his parameters or proceed by typing <CR> and add comments.

Precollection and collection procedures are as described in Sections 4.2.6 and 4.2.7. At the conclusion of the run, the study is tagged 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 fourth, fifth, sixth, and seventh commands in the system hierarchy are the Predefined Study Acquisition commands. These commands are used for the following functions:

1. Setting up a Predefined Study
2. Acquiring a Patient Study
3. Modifying a Predefined Study
4. Deleting a Predefined Study

Much time can be saved in setting up routine or often-used study plans by creating this Predefined Study Plan. Collection parameters and other common data are defined in advance and only the specific run-time information need be added when the study plan is used to acquire data.

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

SP

4.6 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. These are:

1. Instead of the Patient Name, Birthdate, and Patient Number, the user is asked for a STUDY NAME. This identifies the entry in the Predefined Study Index. Also, the maximum number of characters allowed in the study name is 30.
2. Comments cannot be entered.
3. The following items must be defined 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,

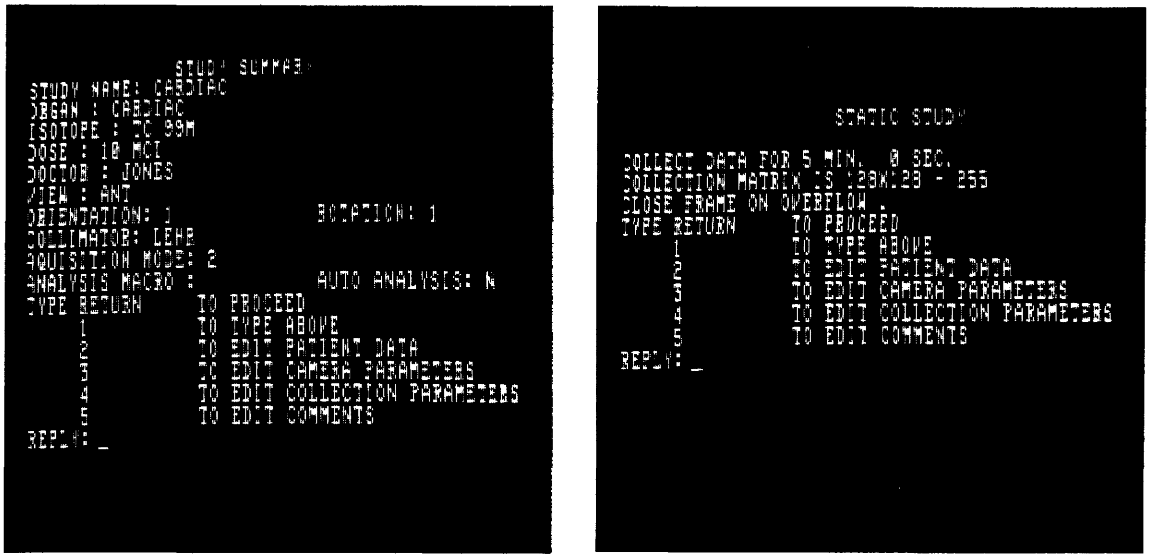
```
SP<CR>
```

A complete Predefined Study Summary is shown in Figure 4-12. When the study has been edited and verified, it is stored in the Predefined Study file on the disk. This yields an entry in the Predefined Study Index, which can then be displayed (see Figure 4-13).

NOTE

> Any question that is answered with just a carriage return causes that question to be asked when Predefined study is selected. In order to bypass a question (such as DOCTOR) type a space followed by a carriage return for the response to the question during the set-up of the Predefined study. Thus, the question is not asked when the Predefined study is selected.

Static, Dynamic, or List studies may be predefined. A Flood Study is itself a sort of predefined study, and cannot be set up in the manner described here.



```
              STUDY SUMMARY
STUDY NAME: CARDIAC
ORGAN : CARDIAC
ISOTOPE : TC 99M
DOSE : 10 MCI
DOCTOR : JONES
VIEW : ANT
ORIENTATION: 1                ROTATION: 1
COLLIMATOR: LEHR
AQUISITION MODE: 2
ANALYSIS MACRO :              AUTO ANALYSIS: N
TYPE RETURN      TO PROCEED
     1           TO TYPE ABOVE
     2           TO EDIT PATIENT DATA
     3           TO EDIT CAMERA PARAMETERS
     4           TO EDIT COLLECTION PARAMETERS
     5           TO EDIT COMMENTS
REPLY: _
```

```
                    STATIC STUDY

COLLECT DATA FOR 5 MIN.  0 SEC.
COLLECTION MATRIX IS 128X128 - 255
CLOSE FRAME ON OVERFLOW .
TYPE RETURN      TO PROCEED
     1           TO TYPE ABOVE
     2           TO EDIT PATIENT DATA
     3           TO EDIT CAMERA PARAMETERS
     4           TO EDIT COLLECTION PARAMETERS
     5           TO EDIT COMMENTS
REPLY: _
```

Figure 4-12
Predefined Study Summary: Parts 1 and 2

AP

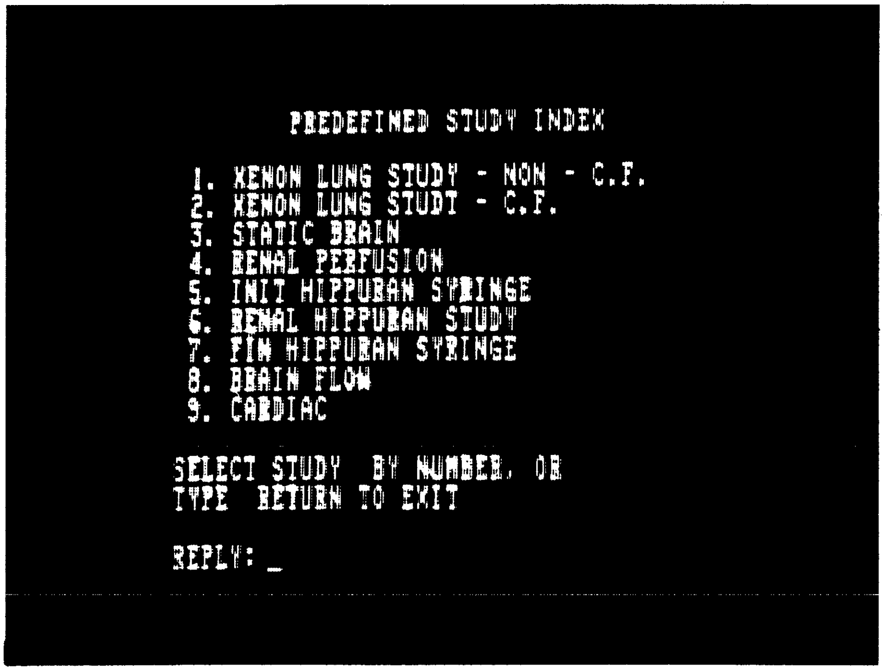
4.6.1 Acquiring Data with a Predefined Study

To display the index of Predefined studies, type,

```
AP n<CR>
```

where n is an optional disk unit number other than zero.

The current index of Predefined studies is displayed (see Figure 4-13).



```
          PREDEFINED STUDY INDEX

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

SELECT STUDY  BY NUMBER, OR
TYPE  RETURN TO EXIT

REPLY: _
```

Figure 4-13
Predefined Study Index

The user may have a maximum of twenty Predefined Studies in the index.

To print the index on the terminal, type,

```
P<CR>
```

If the user types a <CR> the system returns to the Command Table.

~~Next, the user should select the desired study by typing the index~~ entry number, followed by a <CR>. Once this is accomplished, the Predefined Study Index is erased. The user is asked 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 rest of the Patient Data and Camera Parameters are then displayed, stopping at each entry which has been left blank in the Predefined Study. At this point the user may enter the information needed or may enter a <CR> to continue and leave the question blank. Comments may be added at this time. As soon as the user finishes entering comments or types a <CR> if he wishes not to have comments, the Predefined Study Summary (Figure 4-12) is displayed. The collection run proceeds as a normal study (see Section 4.2.7). At the end of the run, the completed study is stored in the Patient Study file, and the Patient Study Index is updated.

NOTE

> If the user wishes to leave a field blank and does not want the program to stop and wait for user input, he should enter a space and a <CR> when setting up the Predefined Study.

Consequently, the Predefined Study is essential for minimizing the chance of error, standardizing collection procedures, and yielding fast setup time.

NOTE

> When performing a Predefined Study the user should not edit collection parameters to increase the number of frames or matrix size. Space on the disk has been allocated only for initial collection parameters. If there is an increase, a "DISK FULL" message appears on the terminal.

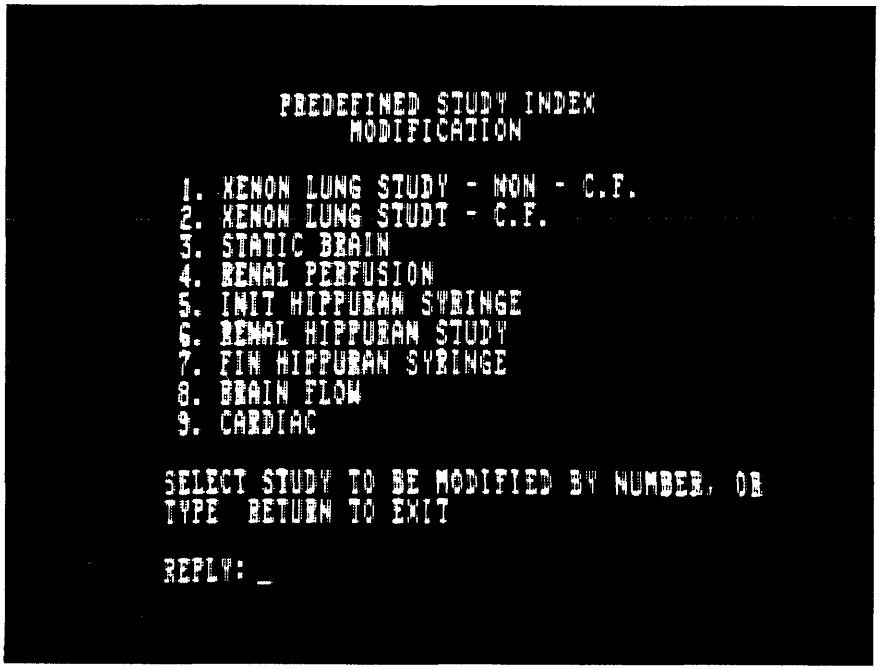
MP

4.7 MODIFY A PREDEFINED STUDY

The sixth command in the system hierarchy is the modification of a Predefined Study Index entry. Essentially, the user is able to modify a selected study in the Predefined Study Index. To modify the study, type,

```
MP<CR>
```

and the display shown in Figure 4-14 is presented on the scope.



```
            PREDEFINED STUDY INDEX
                 MODIFICATION

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

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

  REPLY: _
```

Figure 4-14
Predefined Study Index Modification

The Predefined Study Index is displayed and the user either types the number of the study to be modified, followed by a <CR>, or types P<CR> to print the index on the terminal. After the user enters the index number, the Predefined Study Summary is displayed, with the usual editing options. When complete, the edited study replaces the original one in the file.

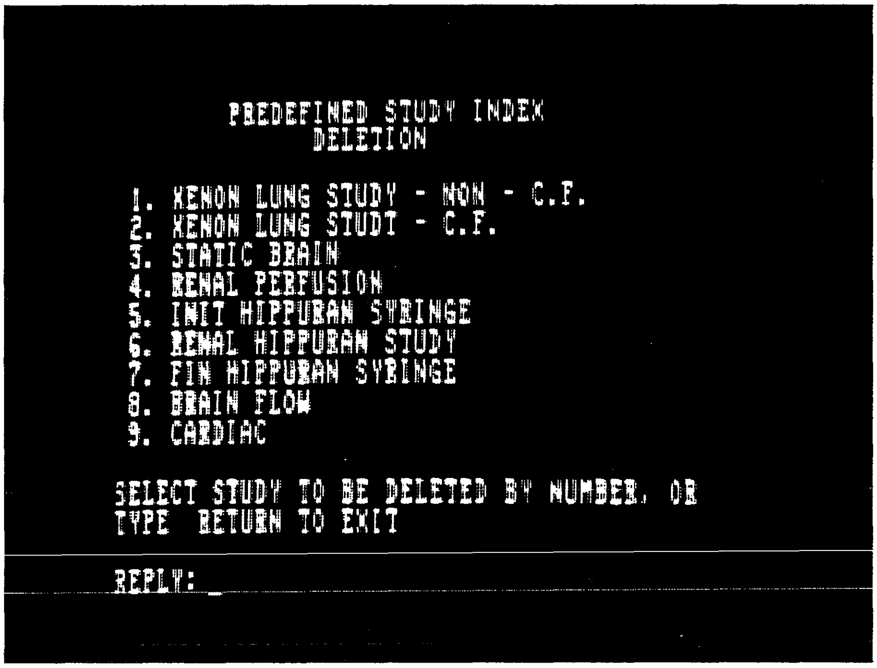
DP

4.8 DELETE A PREDEFINED STUDY

The seventh command in the system hierarchy is the deletion of a Predefined Study Index entry. To delete a study in the index, type,

```
DP<CR>
```

and the display shown in Figure 4-15 is presented on the scope.



```
        PREDEFINED STUDY INDEX
               DELETION

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

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

  REPLY: _
```

Figure 4-15
Predefined Study Index Deletion

The Predefined Study Index is displayed and the user either types the number of the study to be deleted, followed by a <CR>, or types P<CR> to print the index on the terminal. After the user enters the appropriate index number, the study is removed from the file, and the updated index is displayed. Only one index study at a time may be deleted from the Predefined Study file.

4.9 COMMENTS ABOUT ABORTING DATA ACQUISITION

At any time during the preparation of a study plan, up to and including the precollection frame display, the user may terminate the entire operation by typing CTRL/X or CTRL/Z. The study plan is not entered in the Patient file. Control returns to the Command Table.

4.10 COMMENTS ABOUT MATRICES

It should be noted that the flexibility provided by five different types of matrices allows the user to make efficient use of storage space. Careful selection of matrix size means that more patient data can be stored on the disk. The smaller the matrix used, the more frames the system can hold (see Section 4.1).

Notice the matrix size, 32x32x8, below. The number 32 represents the number of cells in a row or column. The number 8 represents the number of bits.

A second benefit results from the use of smaller matrices -- the maximum frame rate increases. Once again, the maximum frame rate for each type of matrix is the following:

MATRIX SIZE	MAX CELL COUNT	FRAME RATE
32 x 32 x 8	255	50 frames/sec.
32 x 32 x 16	65535	25 frames/sec.
64 x 64 x 8	255	12 frames/sec.
64 x 64 x 16	65535	6 frames/sec.

The user is not limited to a single matrix for dynamic collection. For fast studies a smaller matrix allows a faster frame rate.

A good example is: A renal study is started with a rapid frame rate and ends with a slow frame rate so that washout can be observed without wasting disk space. The collection parameters may be as follows:

1. Collect 30 frames of data in a 64 x 64 (MAX. CELL CT. = 255) matrix at 1 frame per 10 seconds.
2. Collect 10 frames of data in a 64 x 64 (MAX. CELL CT. = 65535) matrix at 1 frame per minute.

The above example yields a high frame rate and if the user carefully selects the type of collection matrix, the useful capacity of the disk is effectively increased.

CHAPTER 5

ANALYSIS AND REVIEW

The Analysis and Review procedures include display options, mathematical operations, and analytical tools for working with the collected data of a study. These functions, summarized below, are described in this chapter.

Display Control commands select frames, determine the size of the displayed matrix, and select isotopes in a dual-isotope study.

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.

Threshold Adjustment enhances contrast in particular areas of the matrix or eliminates unwanted background noise.

Frame Algebra includes operations to add, subtract, or multiply by a constant; complement a matrix to obtain a "negative" image; combine frames arithmetically; and generate images having a nonlinear intensity-to-count relationship.

Smoothing allows the user to extract significant information from images having a large amount of random variation.

In addition to these functions, the following subsets of operations, described in succeeding chapters, are also included in the Analysis and Review facility:

The Comment Editor allows the user to edit or add to existing text, or provide commentary not previously included.

Regions of Interest allows the user to define areas of rectangular or irregular shape and to examine the data within these areas. In Dynamic studies, time function curves can be derived from the data using these regions.

AD

5.1 DATA ANALYSIS AND REVIEW

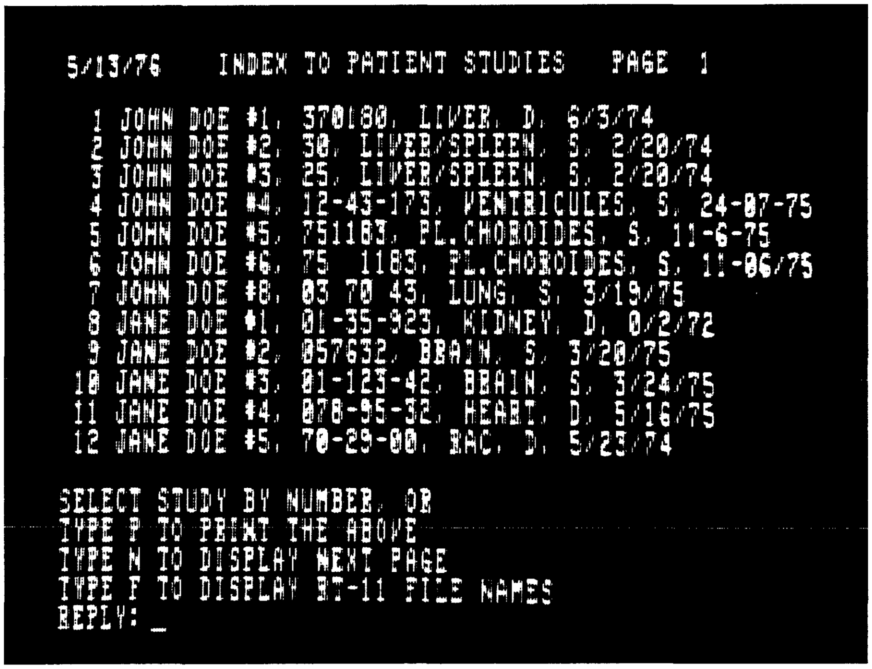
The Analysis and Review procedures run only as a single job under RT-11 or in the background for RT-11 F/B. These procedures do not run in the foreground.

To select a study for analysis and review, type

```
AD n<CR>
```

where n is a disk unit number other than zero.

The first page of the Patient Study Index is displayed on the scope as shown in Figure 5-1.



```
5/13/76    INDEX TO PATIENT STUDIES   PAGE  1

  1 JOHN DOE #1, 370180, LIVER, D, 6/3/74
  2 JOHN DOE #2, 30, LIVER/SPLEEN, S, 2/20/74
  3 JOHN DOE #3, 25, LIVER/SPLEEN, S, 2/20/74
  4 JOHN DOE #4, 12-43-173, VENTRICULES, S, 24-07-75
  5 JOHN DOE #5, 751183, PL.CHOROIDES, S, 11-6-75
  6 JOHN DOE #6, 75  1183, PL.CHOROIDES, S, 11-06/75
  7 JOHN DOE #8, 03 70 43, LUNG, S, 3/19/75
  8 JANE DOE #1, 01-35-923, KIDNEY, D, 0/2/72
  9 JANE DOE #2, 057632, BRAIN, S, 3/20/75
 10 JANE DOE #3, 01-123-42, BRAIN, S, 3/24/75
 11 JANE DOE #4, 078-95-32, HEART, D, 5/16/75
 12 JANE DOE #5, 70-29-00, RAC, D, 5/23/74

SELECT STUDY BY NUMBER, OR
TYPE P TO PRINT THE ABOVE
TYPE N TO DISPLAY NEXT PAGE
TYPE F TO DISPLAY RT-11 FILE NAMES
REPLY: _
```

Figure 5-1
Index To Patient Studies

Each page of the index is numbered sequentially, with the entries on the first page numbered from 1-15; second page, 16-30; third page, 31-45, 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.

Four procedure choices are displayed:

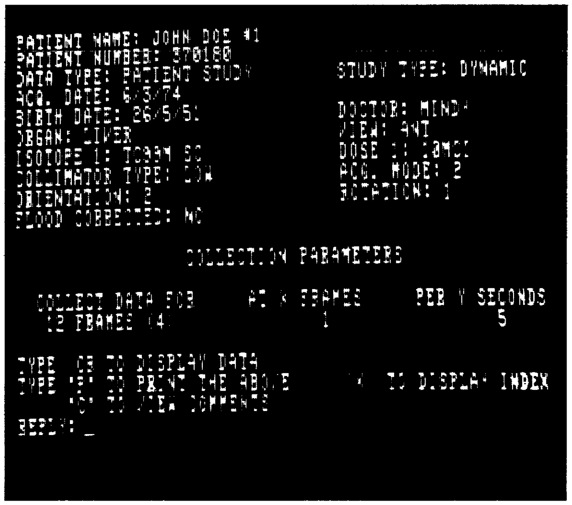
STUDY	Enter the number of the study to be reviewed.
N	The next page of the index is displayed. This choice is not offered on the last page of the index. To return to the first page, the user must type CTRL/Z to obtain the Background Command Table and again type AD<CR> to select analysis and review.
P	The displayed page is printed on the terminal.
F	Instead of the acquisition date appearing on the scope, 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 Richer, the first Richer to have a study performed would be RICHER.X00 and the second Richer to have a study performed would be RICHER.X01.

5.1.1 Study Summary

To obtain the Study Summary, type the appropriate study number (followed by a <CR>) from the Patient Study Index. The index is erased and the chosen Study Summary appears on the scope. 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), are displayed on the scope. In the latter, the matrix configuration is identified by its type number in parentheses. Five procedure choices are listed:

<CR>	displays the first frame of a study and starts the analysis and review procedure.
P	followed by a <CR>, prints the summary on the terminal.
C	followed by a <CR>, displays comments, if any exist. The text cannot be edited at this time, only examined or printed.
X	followed by a <CR>, 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.

```
PATIENT NAME: RICHARD DOW
PATIENT NUMBER: 3
DATA TYPE: PATIENT STUDY            STUDY TYPE: STATIC
ACQ. DATE: 6/11/75                  ACQ. TIME: 16:21.01
BIRTH DATE:                         DOCTOR: REDKAR
ORGAN: HEART                        VIEW: R4030
ISOTOPE 1: END SYSTOLE              DOSE 1: QRS COMPLEX
ISOTOPE 2: END DIASTOLE             DOSE 2: T DOWN SLOPE
COLLIMATOR TYPE: LOW                ACQ. MODE: 2
ORIENTATION: 3                      ROTATION: 1
FLOOD CORRECTED: NO

                 COLLECTION PARAMETERS

COLLECT DATA FOR 500000 COUNTS
COLLECTION MATRIX IS 64X64 - 65535

TYPE  CR TO DISPLAY DATA
TYPE 'P' TO PRINT THE ABOVE        'X' TO DISPLAY INDEX
     'C' TO VIEW COMMENTS
REPLY: _
```



```
PATIENT NAME: JOHN DOE #1
PATIENT NUMBER: 370180
DATA TYPE: PATIENT STUDY            STUDY TYPE: DYNAMIC
ACQ. DATE: 6/3/74
BIRTH DATE: 26/5/51                 DOCTOR: MIND
ORGAN: LIVER                        VIEW: ANT
ISOTOPE 1: TC99M SC                 DOSE 1: 10MCI
COLLIMATOR TYPE: LOW                ACQ. MODE: 2
ORIENTATION: 2                      ROTATION: 1
FLOOD CORRECTED: NO

                 COLLECTION PARAMETERS

  COLLECT DATA FOR        AT X FRAMES       PER Y SECONDS
   12 FRAMES (4)               1                  5

TYPE  CR TO DISPLAY DATA
TYPE 'P' TO PRINT THE ABOVE        'X' TO DISPLAY INDEX
     'C' TO VIEW COMMENTS
REPLY: _
```

Patient Study Summary

Figure 5-2
Static

Figure 5-3
Dynamic

CA

5.1.2 Continue Analysis

The Continue Analysis routine is obtainable only through the background command table. The Continue Analysis routine is an alternate entry point to the Data Analysis program. To select a study for continuing analysis, type

```
CA<CR>
```

When the CA command is issued, 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 informs the data analysis program to bypass the Index To Patients Studies display (see Figure 5-1) and the administrative data display. Thus, a direct route is chosen 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 the Data Analysis program is called via the CA command, the last study that the user 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, the user proceeds as usual.

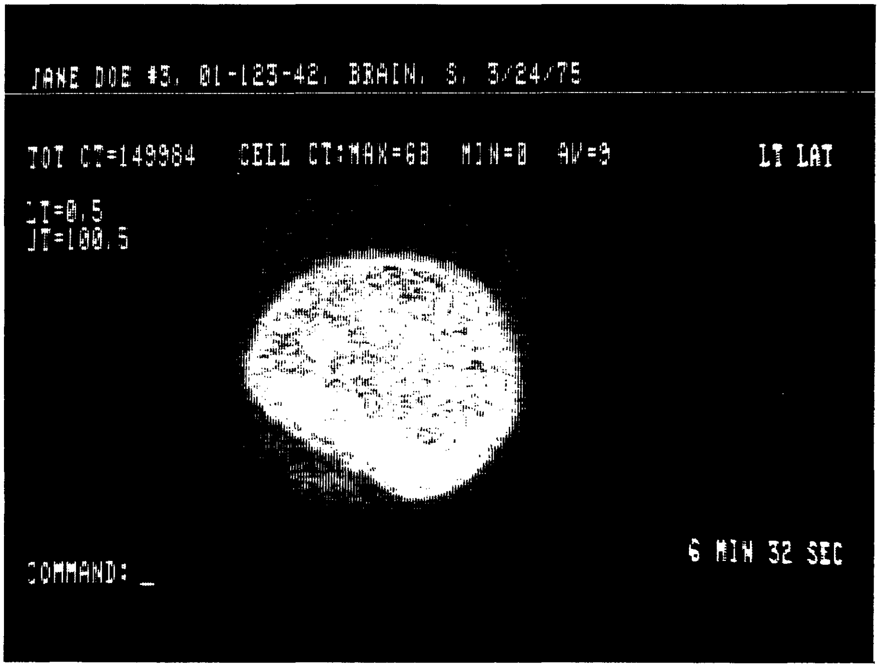
If the patient file cannot be found on the disk, the following error message is displayed on the screen.

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

"dev:filename" is the RT-11 device mnemonic and filename of the patient file. The background command table is displayed when the user presses <CR>.

5.2 THE DISPLAY FRAME

The basic display frame is shown in Figure 5-4.



```
JANE DOE #3, 01-123-42, BRAIN, S, 3/24/75

TOT CT=149984   CELL CT:MAX=68  MIN=0  AV=9          LT LAT

LT=0.5
UT=100.5




                                               6 MIN 32 SEC
COMMAND: _
```

Figure 5-4
Display Frame

Note these elements of the display:

1. Identification -- At the top left 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 plot of 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 (i.e., the number of intensified display points) depends on the number of counts in the cell, in proportion to the range of cell counts in the matrix. 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 VTV01 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 (see Figure 5-4) 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 - 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 the user that the data analysis program is waiting for the user 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 of which sets the condition, while the other removes it. This procedure is useful for Display Sizes. That is to say, matrices are displayed either full-sized or in miniature (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. The user has the choice of entering these commands with or without spaces. For example, the following commands are functionally identical:

```
SM 3

SM3
```

All spaces within the commands are ignored. However, please note in some procedures, the space itself is a command.

5.3.1 Error Processing

The Data Analysis command processor has the capability to detect 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 core resident data is displayed.
2. The command line is displayed only up to the point (character) at which the error is detected followed by a question mark (?).
3. The message, "COMMAND:" is redisplayed.

NOTE

When an error is detected, execution of the remainder of the command line and/or macro buffer is terminated.

5.3.2 Multiple Command Lines

The multiple command line feature allows the user to enter more than one command to the "COMMAND:" response on the screen. The individual commands are separated by a semicolon (;). Multiple command lines also increase the speed at which complex algorithms are performed. This 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 the user and the core-resident data differs from the last data displayed.

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,

```
DI
```

to display a full sized display on the screen. Keep in mind that there are 16 levels of color or 16 levels of gray scales for all of the matrices. 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 Miniature Display

There are two forms of the Miniature 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 miniature image, the 128 x 128 matrix is reduced in dimension 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 number of intensity levels is not changed in the miniature image, regardless of matrix dimension. Type,

```
DM
```

to display all four sequential miniature frames. An example of the display is shown in Figure 5-5.

```
JANE DOE #2, 057632, BRAIN, S, 3/20/75

TOT CT=249970   CELL CT:MAX=184  MIN=0  AV=15          ANT.
TOT CT=249991   CELL CT:MAX=148  MIN=0  AV=15          LT. LAT.
TOT CT=249986   CELL CT:MAX=174  MIN=0  AV=15          RT LAT
TOT CT=249974   CELL CT:MAX=188  MIN=0  AV=15           FRAME004

LT=0.5
UT=100.5

                                                  4 MIN 44 SEC
COMMAND: _
```

Figure 5-5
Miniature 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 and/or performs different processing to data and displays these four images simultaneously.

Command Format:

```
DM n
```

n represents that position of the display where the current contents of core are displayed. Hence, n can only be 1, 2, 3, or 4. If n=1, the screen is erased. With this command, the user can manipulate the core-resident data and display four images simultaneously. Furthermore, DM 1 does not set a prevailing mode. If the user types 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:

```
S5;DM1;SK;S5;DM2;SK;S5;DM3;SK;S5;DM4<CR>
```

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

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

which displays four Save Area images.

DX

5.3.5 Display Index

The Display Index command presents the same information as if the user first enters the Analysis and Review routine. Type,

```
DX
```

on the terminal to display a list of the Patient Index. See Figure 5-1. The DX command allows the user 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 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,

```
DP
```

on the terminal to display a Study Summary of the patient file that is currently being reviewed.

ND

5.3.7 No Display

The No Display command is applicable only if multiple command lines are in use. Type,

```
ND
```

at the end of the command line to avoid displaying any data. The command is essential if the user types 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 user types the following command line which is longer than 49 characters:

```
COMMAND:LT 20,5;S5;RO1;ID;DM1;RO2;ID;DM2;ND<CR>
COMMAND:RO3;ID;DM3;RO4;ID;DM4<CR>
```

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

5.4 FRAME SELECTION COMMANDS

Certain commands are used primarily for frame selection. They allow the user to operate displays such as requesting the next frame, skipping forward or backward on 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.

Space bar

5.4.1 Next Frame

The Next Frame command displays the next frame in sequence of a particular study. Type,

Space bar

to advance to the next frame. In miniature display mode, the display shifts ahead one frame.

Example:

If frames 3 through 6 are displayed on the screen, and the user requests 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 function 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 on displayed frames.

Command Format:

```
SK n
```

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

```
SK 4
```

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

```
SK
```

displays the next frame that is, frame 6 (or frames 6 through 9 in miniature). An attempt to skip beyond the end of the study is rejected.

BK

5.4.3 Skip Backward

The Skip Backward command (BK) skips backward on displayed frames.

Command Format:

```
BK n
```

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

```
BK 4
```

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

```
BK
```

displays the previous frame that is, frame 9 (or frames 9 through 12 in miniature). An attempt to back up beyond the first frame of the study is rejected.

⟨CR⟩

5.4.4 Restore Current Frame

The Restore Current Frame command restores to the screen the currently-selected frame, as indicated by the displayed frame number (or view). Type,

```
<CR> or ;
```

with no command preceding it to display the currently-selected frame. This command is useful, because it allows the user to start with an original frame after that core-resident frame has undergone modification such as Frame Algebra operations.

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

```
COMMAND: command line;<CR>
```

and

```
COMMAND: command line;;command line<CR>
```

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 <CR>. If there is no semicolon before the <CR> the command line is executed as normal.

The second command line has two semicolons in the middle. The command line decoder notices the first semicolon and realizes that a command follows it. In this case another semicolon is typed, which means no command exists, hence, restore the current frame of the data, and continue executing the remainder of the command line. Example:

```
COMMAND: S9;CM0.5;SM5;;S9;CM0.25;SM6;<CR>
```

This example stores a smoothed matrix (multiplied by 0.5) in Save Area 5 and another smoothed matrix (multiplied by 0.25) in Save Area 6.

BE

5.4.5 Beginning

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

```
BE
```

on the terminal. For example, if the user wants to skip forward or backward, or advance on 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 (i.e., 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. The isotope is selected by the commands in the following sections (5.5.1-5.5.4).

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,

```
IA
```

on the terminal to set the isotope to mode A. 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 force until another Isotope Selection Command is given.

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,

```
IB
```

on the terminal to set the isotope to mode B. 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 force until another Isotope Selection Command is given.

IX

5.5.3 Isotope Exchange

The Isotope Exchange command (IX) exchanges (or switches) one pair of isotopes. Type,

```
IX
```

on the terminal to exchange isotopes. That is, if Isotope A is displayed and the IX command is issued, the current frame number remains unchanged and Isotope B is moved into core in place of Isotope A.

Hence, if the message FRAME012A was displayed on the screen, frame 12 of Isotope A is currently being displayed. However, when the user issues the IX command, frame 12 of Isotope B moves into core and displays the message FRAME012B on the screen. Also, Isotope B data replaces Isotope A data.

NOTE

> Frame numbers are very important to the GAMMA-11 user. Frame numbers tell the user 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 miniature. Type,

```
DD
```

on the terminal. 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 miniature form). This operation is useful in a dual isotope static study, for example, to compare the distribution of each isotope in an organ.

Isotope A, displayed in the left miniature 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 another command is typed and 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 (8 or 32, depending upon the configuration) are distributed linearly over the range of cell counts in the matrix. Thus, if the lowest cell count (MIN) is zero, the highest (MAX) is 800, and there are 32 levels, each represents a change of 25 counts. There are 8 levels of the intensity only for 128x128 matrices. The count increment per level is represented by the following formula:

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

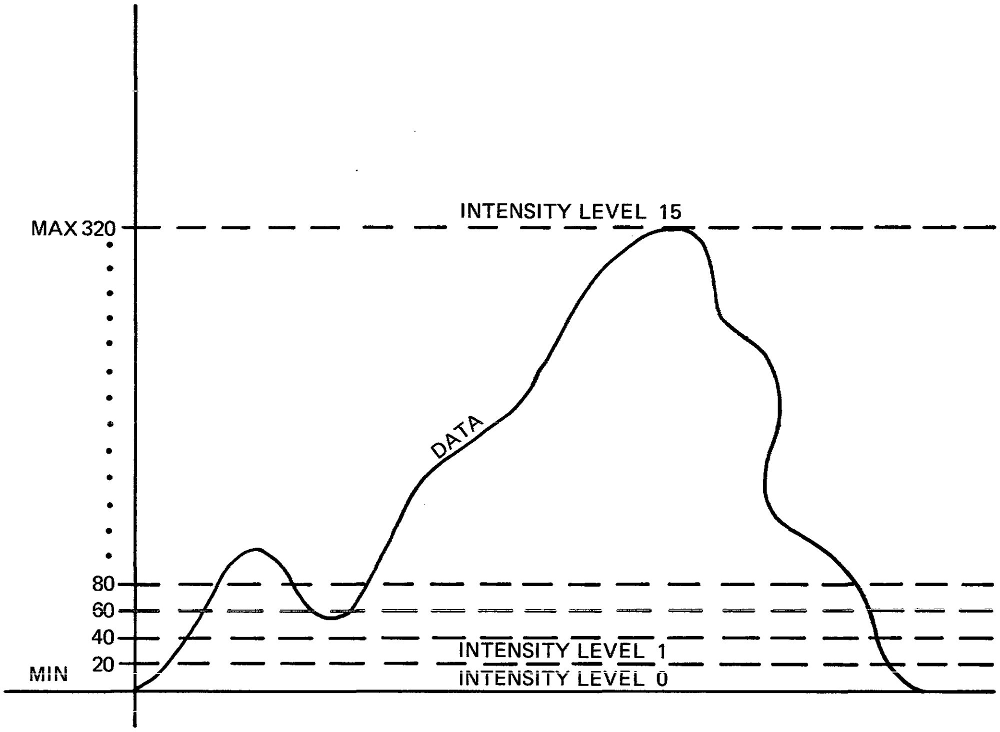
(800-0)/32 = 25 Counts/Level

In a normal full-size display, the 16 color levels or gray scale intensity levels are distributed linerarly over the range of cell counts in the matrix. Thus, if the lowest cell count (MIN) is zero, the highest (MAX) is 320, and there are 16 levels, each represents a change of 20 counts. The count increment per level is represented by the following formula:

MAX-MIN/16 Levels of intensity = Count Increment/Level

(320-0)/16 = 20 Counts/Level

This example may be described by the following diagram:



The data acquired under count change 20 is at intensity level 1. Data between 20-40 is at intensity level 2, 40-60 is at 3, etc. The data at level 300-320 has the highest intensity level, 15. Please note that data acquired at count change 0 is at intensity level 0. Therefore, the 16 levels of intensity range from 0 to 15.

At least one cell is at maximum intensity in every frame, and an empty cell always has zero intensity. In this way, the maximum possible contrast is provided for every frame, regardless of the absolute count. However, the exception to this is when the cell count range is smaller than the number of levels, in which case not all intensities are displayed, but the distribution still is linear.

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, and furthermore, that 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. The thresholds can be set and moved 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, the threshold specifications can be stored, 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. The amount by which each threshold can be changed is the step size, also expressed as a percentage of the maximum count. 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 percent of the maximum cell count. The commands also set the step size to a specified percent. 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 Lower Threshold and Step command (LT) sets the lower display threshold to a certain percent of the maximum cell count and also sets the step size to a particular percent.

Command Format:

```
LT m,n
```

The n is optional in this command.

Where:

m	is the lower threshold expressed as a percent of the maximum cell count.
n	is the percent step size.

Examples:

```
LT 15,5
```

sets the lower threshold to 15% and the step size to 5%.

```
LT 10
```

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

Thresholding is nothing more than specifying a percentage which eliminates cells above or below the indicated threshold. Those cells that lie outside the threshold percentage are not displayed.

UT

5.7.2 Set Upper Threshold and Step

The Set 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 m,n
```

The n is optional in this command.

Where:

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

Examples:

```
UT 10,5
```

sets the upper threshold to 10% and the step size to 5%.

```
UT 20
```

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

W

5.7.3 Raise the Lower Threshold by Step Size

Raise the Lower Threshold by Step Size command (W) raises the presently displayed lower threshold by the current step size. Type,

```
W
```

on the terminal to raise the lower threshold.

Example:

```
LT 10,5
```

displays the lower threshold at 10% of the maximum cell count and sets the step size to 5%. Each time

```
W
```

is typed on the terminal, the maximum cell count increases by 5%. Hence, in this case, the lower threshold is now displayed at 15% of the maximum cell count.

NOTE

> An attempt to step beyond the boundaries (0% and 100%) in either direction is rejected.

X

5.7.4 Lower the Lower Threshold by Step Size

Lower the Lower Threshold by Step Size command (X) lowers the presently displayed lower threshold by the current step size. Type,

```
X
```

on the terminal to lower the lower threshold.

Example:

```
LT 30,7
```

displays the lower threshold at 30% of the maximum cell count and sets the step size to 7%. Each time

```
X
```

is typed on the terminal, the maximum cell count decreases by 7%. Hence, in this case, the lower threshold is now displayed at 23% of the maximum cell count.

NOTE

> An attempt to step beyond the boundaries (0% to 100%) in either direction is rejected.

Y

5.7.5 Lower the Upper Threshold by Step Size

Lower the Upper Threshold by Step Size command (Y) lowers the presently displayed upper threshold by the current step size. Type,

```
Y
```

on the terminal to lower the upper threshold.

Example:

```
UT 13,8
```

displays the upper threshold at 13% of the maximum cell count and sets the step size to 8%. Each time

```
Y
```

is typed on the terminal, the maximum cell count decreases by 8%. Hence, in this case, the upper threshold is now displayed at 5% of the maximum cell count.

NOTE

> An attempt to step beyond the boundaries (0% and 100%) in either direction is rejected.

Z

5.7.6 Raise the Upper Threshold by Step Size

Raise the Upper Threshold by Step Size command (Z) raises the presently displayed upper threshold by the current step size. Type,

```
Z
```

on the terminal to raise the upper threshold.

Example:

```
UT 22,9
```

displays the upper threshold at 22% of the maximum cell count and set the step size to 9%. Each time

```
Z
```

is typed on the terminal, the maximum cell count increases by 9%. Hence, in this case, the upper threshold is now displayed at 31% of the maximum cell count.

NOTE

> An attempt to step beyond the boundaries (0% and 100%) in either direction is rejected.

UM

5.7.7 Set the Upper Threshold Display Switch

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

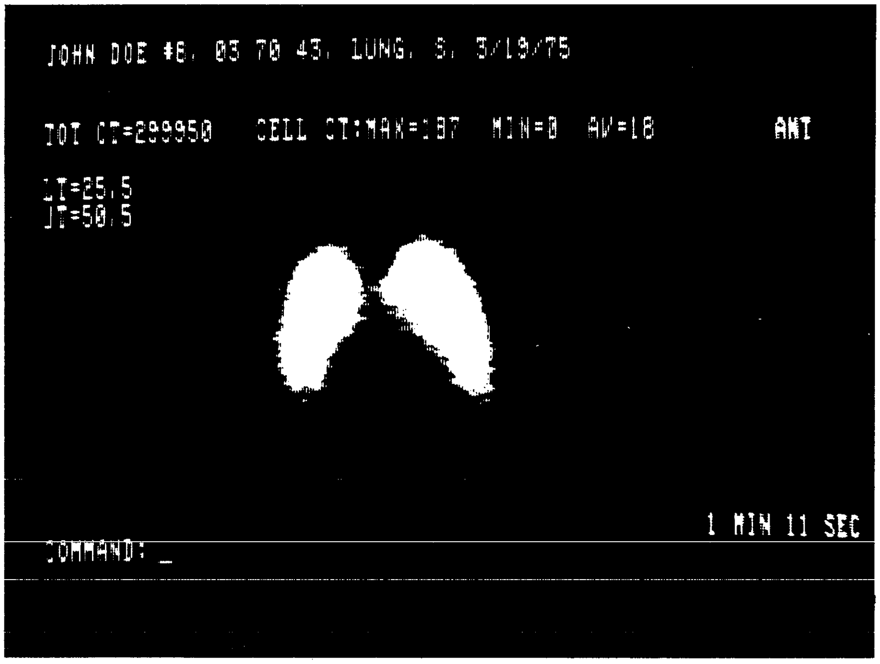
```
UM
```

to display the maximum intensity. For example, if the commands,

```
LT 25,5
UT 50,5
UM
```

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. Figure 5-6 uses the following command string:

```
LT 25,5;UT 50,5;UM<CR>
```



```
JOHN DOE #8, 03 70 43, LUNG, S, 3/19/75

TOT CT=299950   CELL CT:MAX=187  MIN=0  AV=18         ANT

LT=25.5
UT=50.5

                                                  1 MIN 11 SEC
COMMAND: _
```

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 primarily a clear switch for the UM command. Typing

```
UO
```

causes the counts above the upper threshold to be displayed with zero intensity (i.e., not displayed).

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 w,y
```

Where:

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

Example:

```
IS 15,20
```

sets the lower threshold at 15% of the maximum cell count and sets the upper threshold at 20% of the maximum cell count. Keep in mind that the lower threshold cannot be greater than or equal to the upper threshold or the command is rejected.

NOTE

> An attempt to move the band beyond the boundaries (0% and 100%) in either direction is rejected.

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, to raise the isocount band.

```
N
```

Example:

```
IS 10,20
```

sets the lower threshold at 10% of the maximum cell count and sets the upper threshold at 20% of the maximum cell count. When

```
N
```

is typed on the terminal, the upper and lower thresholds are raised by a step size equal to the difference between them.

20% - 10% = 10% (step size)

Hence,

New Lower Threshold = 10% + 10% = 20%

New Upper Threshold = 20% + 10% = 30%

NOTE

> An attempt to move the band beyond the boundaries (0% and 100%) in either direction is rejected.

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,

```
O
```

on the terminal to lower the isocount band.

Example:

```
IS 30,40
```

sets the lower threshold at 30% of the maximum cell count and sets the upper threshold at 40% of the maximum cell count. When

```
O
```

is typed on the terminal, the upper and lower thresholds are lowered by a step size equal to the difference between them.

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

Hence,

New Lower Threshold = 30% - 10% = 20%

New Upper Threshold = 40% - 10% = 30%

NOTE

> An attempt to move the band beyond the boundaries (0% and 100%) in either direction is rejected.

5.9 NO-ENHANCEMENT MODE COMMANDS

Thresholds may also be changed 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, background and hot spots are eliminated leaving intensities and contrast relationships unchanged in the areas of interest. No-enhancement commands are obtained by adding 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 m,n
```

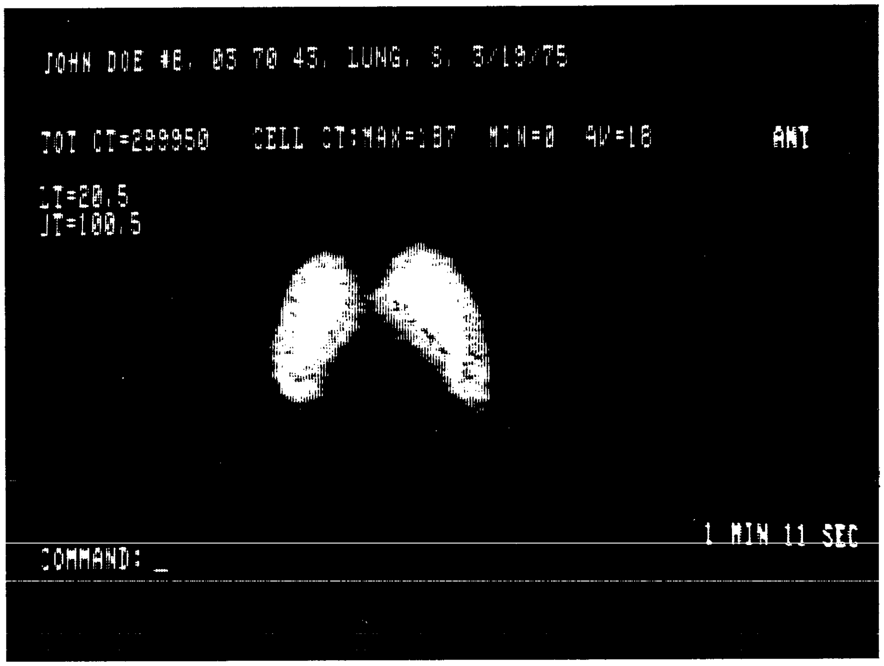
Where:

m	is the percent of the maximum cell count.
n	is the percent of the step size.

Example:

```
LT 20,5
```

sets the lower threshold to 20% and the step size to 5%. This is represented by the photograph in Figure 5-7.



```
JOHN DOE #8, 03 70 43, LUNG, 5, 3/19/75

TOT CT=299950   CELL CT:MAX=187  MIN=0  AV=18          ANT

LT=20,5
UT=100,5

                                                  1 MIN 11 SEC
COMMAND: _
```

Figure 5-7
Lower Thresholding and Step Size

Notice that the cells lying below 20% are not displayed and intensity levels 0-32 are displayed between 20% and 100%. If the user now types

```
LTN 20,5
```

on the terminal, the lower threshold still remains at 20%, however, the intensity levels are distributed over the entire count range starting with intensity level 3 (20% x 16 = 3). This is represented in Figure 5-8.

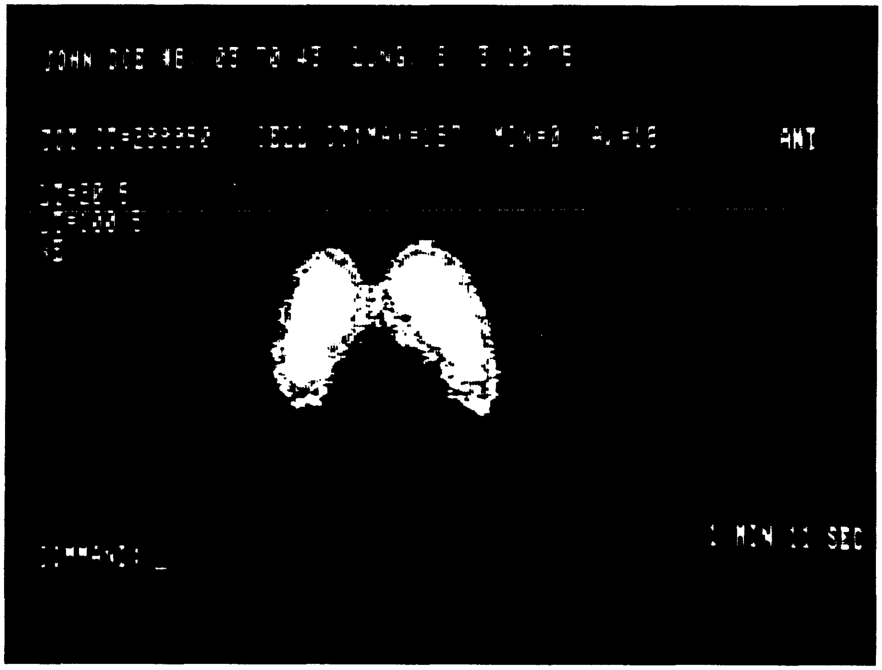


Figure 5-8
No-Enhancement Lower Threshold

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 m,n
```

Where:

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

n is the percent step size.

Example:

```
UT 70,5
```

sets the upper threshold to 70% and the step size to 5%. This is represented by the photograph in Figure 5-9.

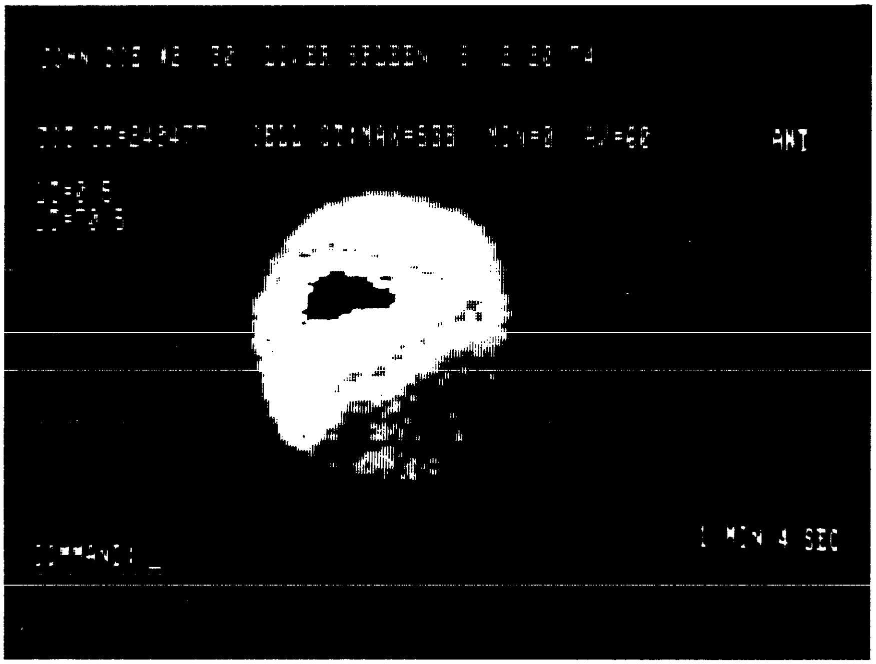


Figure 5-9
Upper Thresholding and Step Size

Notice that the cells lying above 70% are not displayed and intensity levels 0-15 are displayed between 0% and 70%. If the user now types

```
UTN 70,5
```

on the terminal, the threshold still remains at 70% however, the intensity levels are distributed over the entire count range, starting with intensity level 3 and ending with intensity level 11 (i.e., 70% x 16 = 11.) This is represented in Figure 5-10.

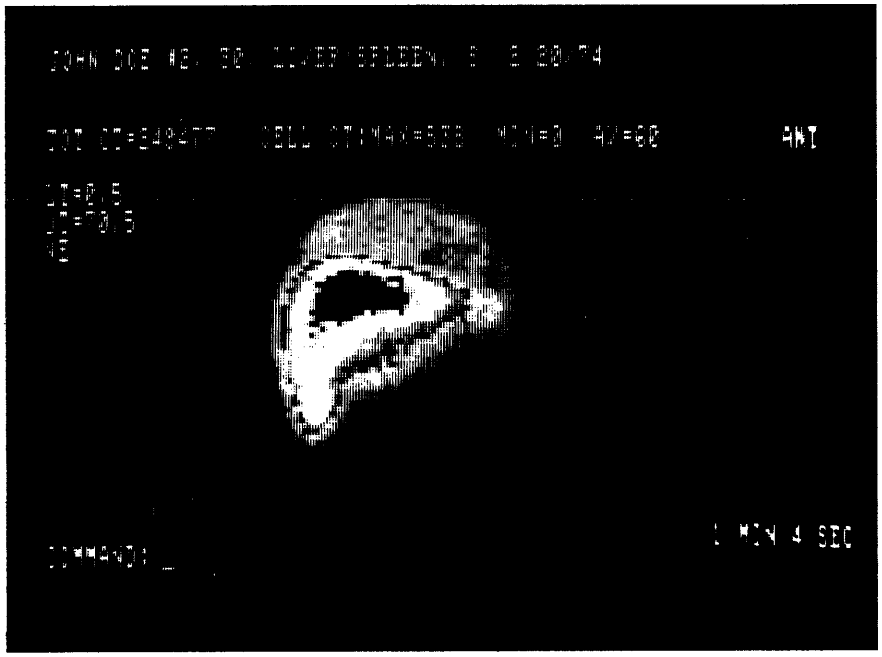


Figure 5-10
No-Enhancement Upper Threshold

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 w,y
```

Where:

w	is the percent of the maximum cell count in the lower threshold.

y is the percent of the maximum cell count in the upper threshold.

Example:

```
IS 10,20
```

sets the lower threshold to 10% and the upper threshold to 20% of the maximum cell count. This is represented by the photograph in Figure 5-11.

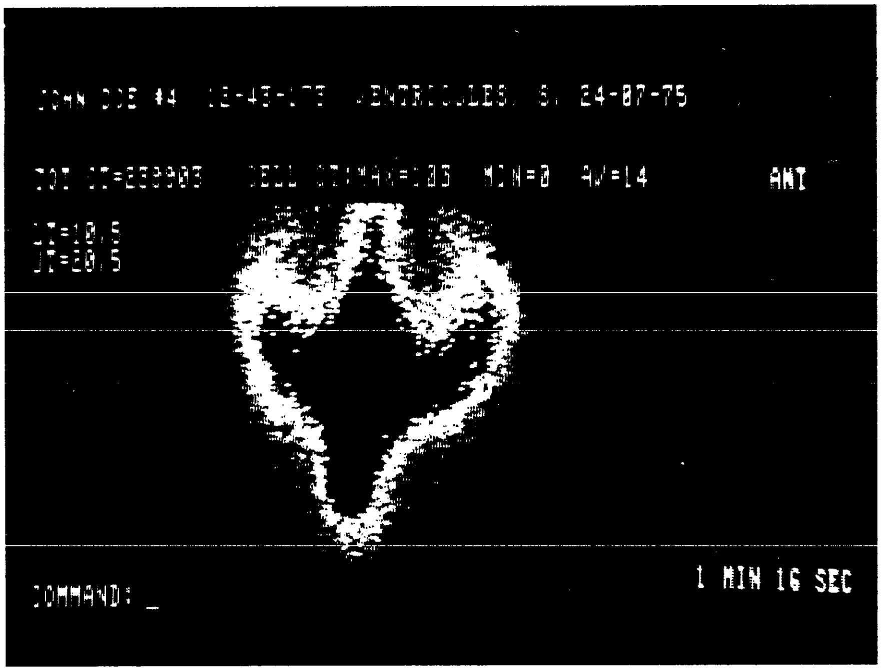


Figure 5-11
Isocount Thresholding

Notice that the cells lying above 20% and below 10% are not displayed, and intensity levels 0-15 are displayed between 10% and 20%. If the user now types

```
ISN 10,20
```

on the terminal, the intensity levels are distributed over the entire count range, starting with intensity level 1 and ending with intensity level 3. i.e.,

20% x 16=3 for the highest intensity level

10% x 16=1 for the lowest intensity level.

This is represented in Figure 5-12.

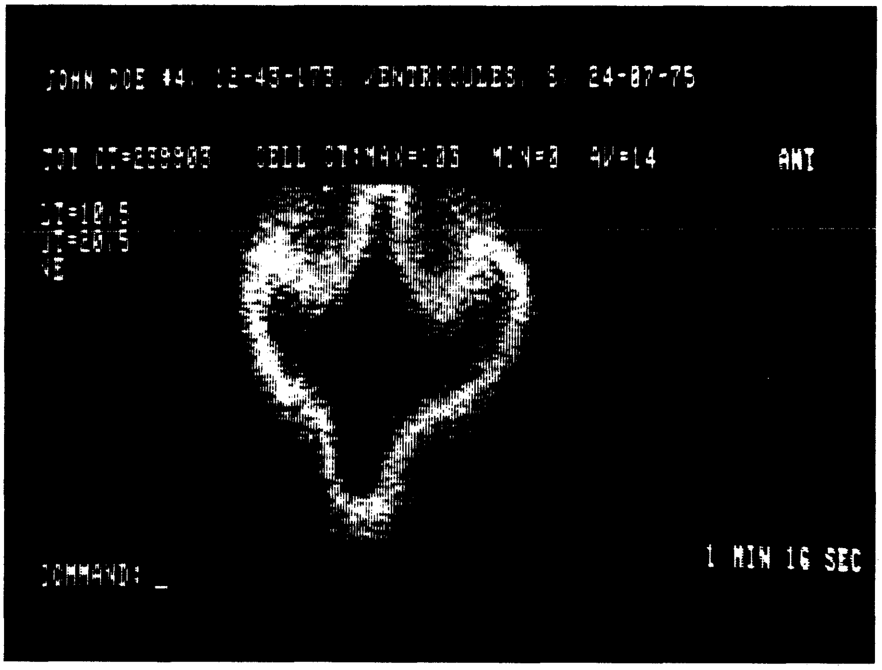


Figure 5-12
No-Enhancement Isocount Thresholds

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 message

FRAME ARITH: (exp)

appears on the scope, where (exp) is the typed command expression. This is displayed directly above the thresholds (LT and UT). The message remains on the screen until:

1. a new Frame Algebra command is executed, in which case the new command expression replaces the old.

2. or a new frame is selected by means of a BK, SK, BE or <CR> command, in which case the FRAME ALGEBRA message is erased. A Space bar command erases any FRAME ALGEBRA 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 the user to perform the indicated mathematical function with each cell of the core-resident matrix.

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
```

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 is left empty.

Example:

If there are cells (byte-matrix) that have a count of 175 and the user types

```
CA 100
```

on the terminal, the cell count results in an overflow, and the maximum count, 255, is the assumed count value 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
```

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 is left empty.

Example:

If there are cells (byte-matrix) that have a count of 100 and the user types

```
CA -150
```

on the terminal, the cell count results in an underflow, that is, the sum is less than zero, thus the cells are left empty.

CM

5.11.3 Constant Multiply

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

Command Format:

```
CM nn.nn
```

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

Example:

The following forms are all acceptable:

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

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. or a constant is added to a previously empty cell.

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

5.12 NEGATIVE (COMPLEMENTED) IMAGES COMMAND

Negative images are obtained by complementing the matrix data. The contents of each cell are complemented by subtracting them from the appropriate maximum cell count: 255 for a byte-matrix, 65535 for a word matrix, and a count of zero remains zero.

NI

5.12.1 Negate Image

The Negate Image command (NI) complements the data in a matrix, yielding a negative image. Type,

```
NI
```

on the terminal to subtract each cell from the appropriate maximum cell count.

Example:

To obtain a good negative image when there are many empty cells, the following sequence of commands is suggested:

```
CA1;NI
```

Adding 1 to an empty cell ensures a maximum display level in its complemented image. To restore the original uncomplemented image, the user must type <CR>.

A negative image is shown in Figure 5-13.

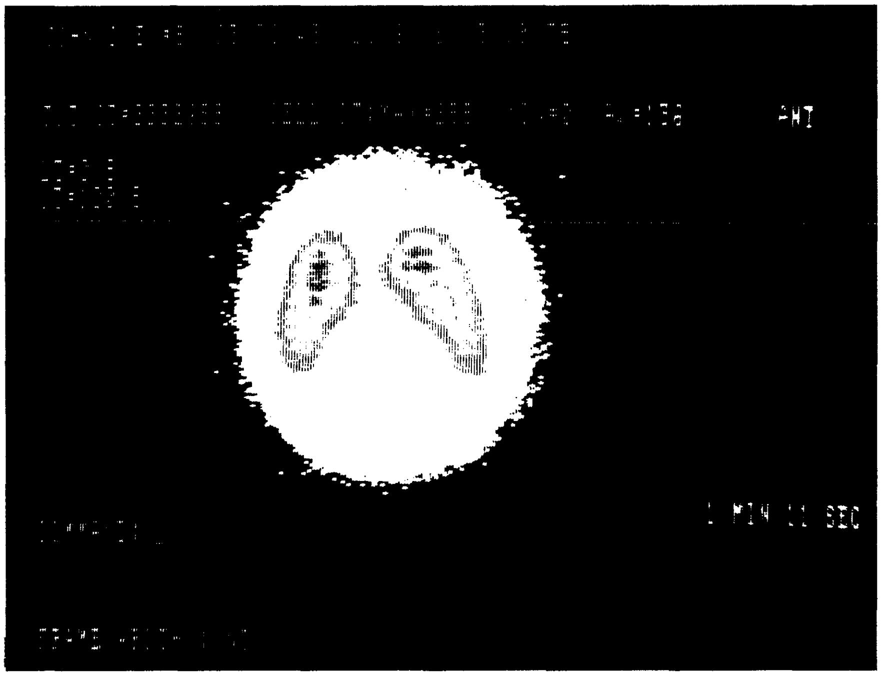


Figure 5-13
Negative (Complemented) Image

5.13 BYTE-WORD EXPANSION COMMANDS

To facilitate frame arithmetic, byte-matrix data can be stored 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, all byte-matrix data is automatically converted to word-matrix form when the data is transferred to core. Type,

```
EX
```

on the terminal to effect the Expand mode. This mode remains in effect during use of Regions of Interest. 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 if a byte-matrix has been expanded.

NX

5.13.2 No Expansion

The No Expansion command (NX) turns off the Expand capability at any time. Type,

```
NX
```

on the terminal to prohibit byte-matrix data from expanding on transfer to core.

5.14 FRAME ARITHMETIC COMMANDS

Addition, subtraction, multiplication, and division 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 and division do not. For convenience, all these operations are termed frame arithmetic. Addition, subtraction, 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, (i.e., frames with different dimensions or maximum cell counts cannot be combined).
2. The Frame Arithmetic (FA) command may be used only with Dynamic studies (see Section 5.14.2).
3. 128 x 128 matrices can be combined 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.

Command Format:

```
AD n
```

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

Example:

If frame 7 is core-resident and the user types

```
AD 2
```

on the terminal, the result is the sum of frames 7, 8, and 9 (i.e., the data in frames 7, 8, and 9 are added together, and frame 7 still remains as the core-resident frame).

The AD n command sets a prevailing mode that remains in effect for any subsequent Skip Forward, Backward, Space bar, or Display Miniature command. In addition, these commands result in an n+1 skip or backspace.

Example:

If the current core-resident frame is 6, and the displayed FRAME ALGEBRA command is AD3, striking the Space bar and then the <CR>, causes the routine to

1. step ahead to frame 10.
2. add frames 11, 12, and 13 to frame 10 and display them.

In miniature display mode, if the current core-resident frame is 1, and the displayed FRAME ALGEBRA command is AD4, striking the Space bar and then the <CR>, causes the routine to

1. display the sum of frames 1-5 in position 1.
2. display the sum of frames 6-10 in position 2.
3. display the sum of frames 11-15 in position 3.
4. display the sum of frames 16-20 in position 4.

The FRAME ALGEBRA message is unchanged by this operation.

5.14.2 Frame Arithmetic

The Frame Arithmetic command (FA) provides the capabilities of two distinct functions.

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

Command Format:

```
FA (exp)
```

where (exp) is either the operations for addition, subtraction, and multiplication, or a frame number.

Example:

If the user types

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

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. For example, if FA +5-12 is typed, frame 5 is added to the current core-resident data and then frame 12 is subtracted from this data.

Consequently, if the user types

```
FA 13
```

on the terminal, frame 13 is displayed.

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

The Save Area Arithmetic command (SA) is similar to the FA command in execution processes as follows:

1. Sequential adding, subtracting, and multiplying on Save Areas.
2. Selecting and displaying a particular Save Area.

Command Format:

```
SA (exp)
```

where (exp) is either an operation for addition, subtraction, and multiplication of Save Areas, or a designated Save Area by itself.

Example:

```
SA 3+2-7
```

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 and Save Area operations are strictly sequential and no arithmetic hierarchy is observed. If an operator (i.e., +, -, or *) precedes first Save Area number (e.g., -2, +3), the current core-resident data is used. For example, if SA -7+2 is typed, Save Area 7 is subtracted from the current core-resident data and then Save Area 2 is added to this data.

Furthermore, if the user types

```
SA 5
```

on the terminal, Save Area 5 is displayed.

After performing Save Area Arithmetic, use the command

```
RS 0
```

to return to the original frame.

5.15 FRAME DIVISION COMMANDS

The fixed-point division used in these operations imposes limitations on the magnitude of the ratios that can be calculated. The binary point is placed in the middle of the matrix cell, so that a ratio of 1/1 between corresponding cells of the dividend and the divisor results in a quotient-cell-count of 16 for a byte-matrix and 256 for a word-matrix. Thus, the range of meaningful ratios that can be accommodated in byte-matrix division is 1/16 through 15/1. In word-matrix division, the range is 1/256 through 255/1. Ratios outside these limits are treated as cases of underflow or overflow. Such cases are minimized by adjusting or normalizing the two matrices before division.

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
```

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 empty (which would cause an attempted division by zero) the quotient cell is assigned a maximum ratio 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).

The argument n may also be omitted from the command yielding,

```
FDH /m
```

which divides the core-resident frame by frame m.

Examples:

```
FDH 7/32

FDH /14
```

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
```

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 yielding,

```
FDL /m
```

which represents the division of the core-resident frame by frame m.

Examples:

```
FDL 5/4

FDL /9
```

SDH

5.15.3 Save Area Divide/High

The Save Area Divide/High command (SDH) divides one Save Area by another specified Save Area, and division by zero on the contents of the Save Area is treated as overflow.

Command Format:

```
SDH n/m
```

Where:

n	represents the dividend Save Area
m	represents the divisor Save Area.

Save Area n is divided by Save Area m. n and m specify only Save Areas 1 through 9. Save Area 0 cannot be used. The argument n may also be omitted from the command yielding,

```
FDL /m
```

which represents the division of the core-resident data by Save Area m.

SDL

5.15.4 Save Area Divide/Low

The Save Area Divide/Low command (SDL) divides one Save Area by another specified Save Area, and 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
```

Where:

n	represents the dividend Save Area.
m	represents the divisor Save Area.

Save Area n is divided by Save Area m. n and m specify only Save Areas 1 through 9. Save Area 0 cannot be used.

More meaningful images will result if the matrix (m; divisor Save Area) 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.

5.16 NONLINEAR IMAGES

Using Frame Algebra, nonlinear images may be obtained 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

Hyperbolic nonlinear images can be obtained 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 x and y 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, followed by the corresponding word-matrix count in parentheses.

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

$$C' = 16C/(256-C) \quad \text{[byte-matrix]}$$
$$C' = 256C/(65536-C) \quad \text{[word-matrix]}$$

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 (256) and above 240 (65280) will underflow and overflow, respectively. If there are cells of interest with counts above 240 (65280), subtract 16 (256) 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 (256) or above 240 (65280) will overflow and underflow, respectively. In this case adding 16 (256) or multiplying by 0.94 will bring out cells below 16 (256). The equations are:

$$C' = 16(256-C)/C \quad \text{[byte-matrix]}$$
$$C' = 256(65536-C)/C \quad \text{[word-matrix]}$$

5.16.2 A Multiplicative Nonlinear Image

Another commonly used means of obtaining a nonlinear image is by 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 54 (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. It can only be read by the user.

Save Areas are essential because there is only one core-resident frame at a time and the results of an analysis could be lost every time a new frame is selected. To prevent this, core-resident data modified by analysis is saved for future use by storing the frame in 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
```

n represents a Save Area. Only Save Areas 1 through 64 may be specified. The core-resident matrix with all identifying information is stored in Save Area n. Information cannot be explicitly stored in Save Area 0. When using 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
```

n represents a specified Save Area. Only Save Areas 1 through 9 may be specified and used. 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 (Register)

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

Command Format:

```
RS n
```

n represents a specified Save Area. The previous display frame is stored 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, it and the associated identification, thresholding data, and other information are displayed. Thresholding and constant arithmetic may be performed on the matrix. To restore the original display, type,

   ```
   RS 0
   ```

   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 6). To restore the original display, type CTRL/X, then RS 0<CR>.

3. If the contents is a set of dynamic curves calculated from Regions of Interest, these are plotted in Overlay Mode. Only the calculation and output commands (PN, PA, PO, PU, PR, PP) are executable at this point (See Chapter 6). Any other input has the effect of typing RS 0<CR>.

NOTE

> If the user wants to read a Save Area that contains ROI information, but does not want to automatically enter the Region of Interest program, use the Save Area Arithmetic command (i.e., SA n).

The user cannot write into Save Area 0 since it is system protected. However, the user 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 the user is analyzing. Anytime 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 reading from it. 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,

```
RS 0
```

to resume analysis of the original study.

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
```

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 the user 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
```

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.

5.18 SMOOTHING COMMAND

If statistical noise (i.e., low counts) results in an erratic image, meaningful information can still be extracted from the data. The noise is reduced by the 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.

S9

5.18.1 Nine-Point Smooth

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,

```
S9
```

on the terminal to perform a nine-point smooth. Essentially, 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. Thus,

$$\begin{matrix} 1 & 2 & 1 \\ 2 & 4 & 2 \\ 1 & 2 & 1 \end{matrix}$$

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.

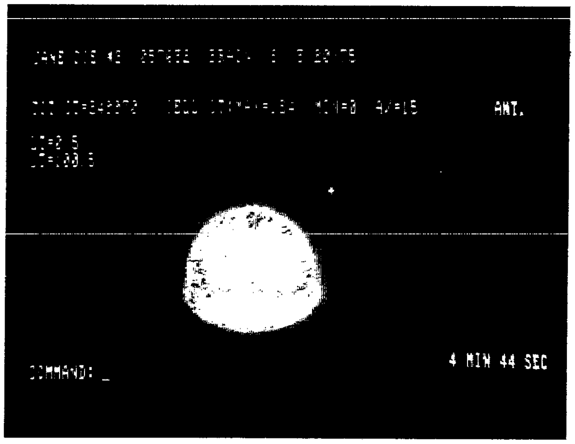


Figure 5-14
Smoothing-Original Matrix

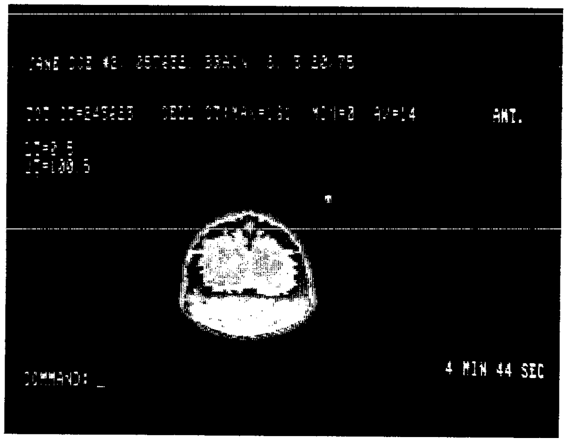


Figure 5-15
Nine-Point Smooth

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 converts a data matrix into an isocontour matrix using 1 to 15 isocontour lines. The command format is:

```
IC f,s,n
```

where,

f = is the first isocontour level, expressed as a percentage of the threshold level.

s = is a postive or negative threshold step size.

n = is the number of levels that are generated from the image.

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.

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 show a normal image of the lungs and an isocontour image, respectivley.

ICF

5.19.2 Isocontour Fill

The Isocontour Fill command is similar to the Isocontour Map command except that it fills the interior of the isocontours. The command format is:

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

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.

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<CR>
   ```

2. Blow-up the image for enhancement by typing,

   ```
   BU<CR>
   ```

3. Define the isocontour map and save it in Save Area 1. Type,

   ```
   IC 20,20<CR>
   SM1<CR>
   ```

4. Fill the isocontours and save it in Save Area 2 by typing,

   ```
   ICF 20,20<CR>
   SM2<CR>
   ```

5. Add the two Save Areas by typing,

   ```
   SA1+2<CR>
   ```

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

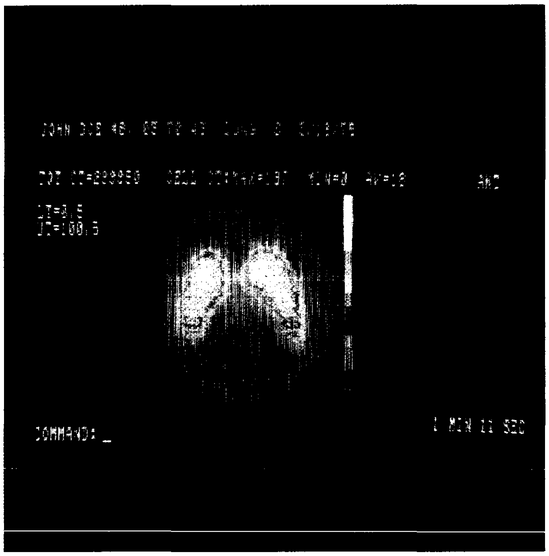


Figure 5-16
Lung-Normal Image

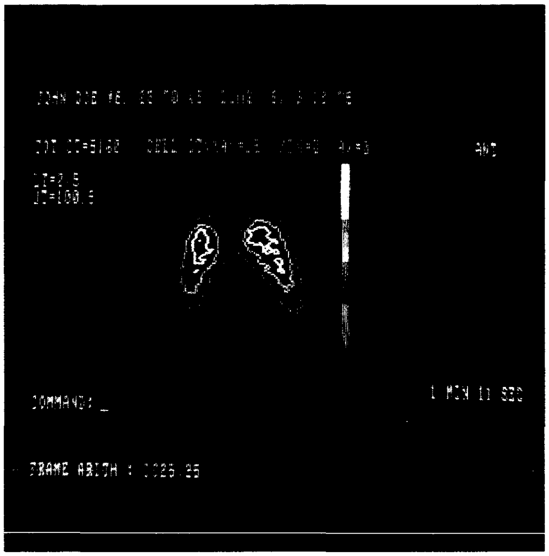


Figure 5-17
Isocontour Map

Figure 5-18
Isocontour Fill

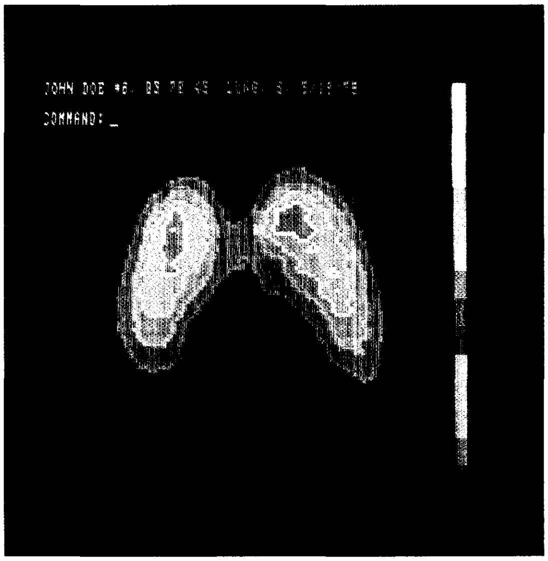


Figure 5-19
Isocontour Map and Fill

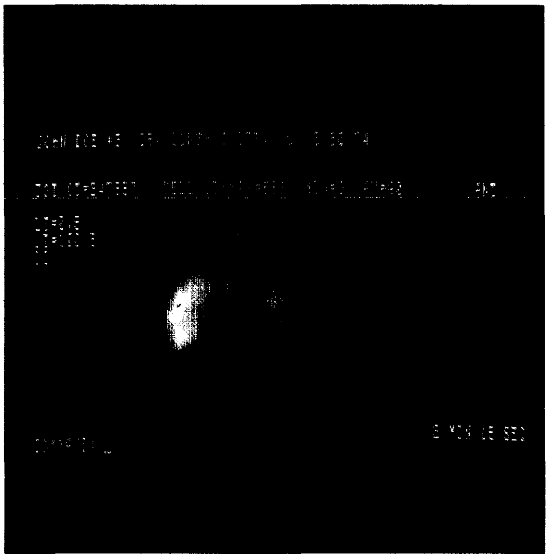


Figure 5-20
Normal Liver/Spleen Display

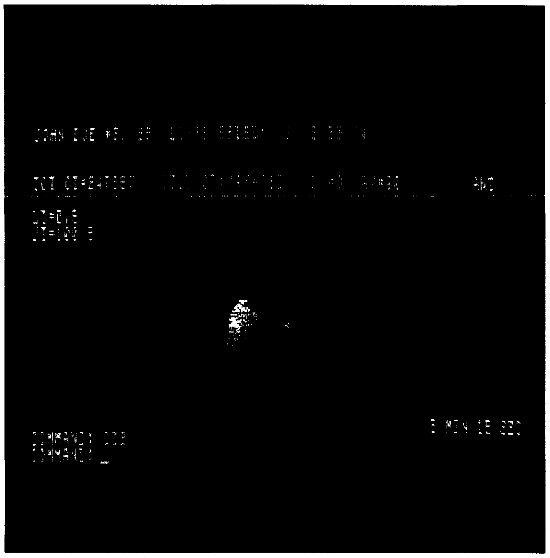


Figure 5-21
Isometrics Display

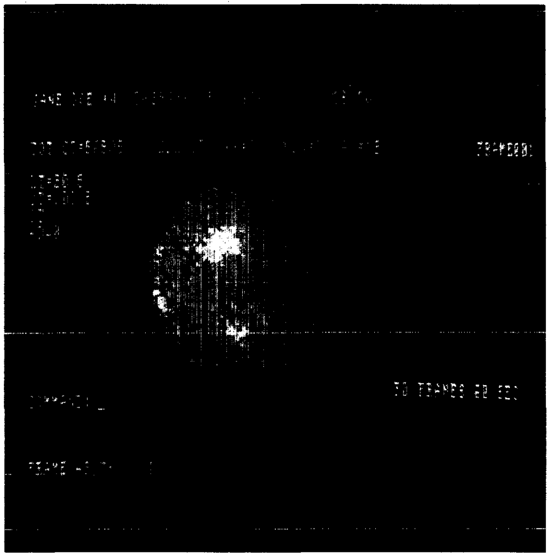


Figure 5-23
Data Rotated 90 Degrees

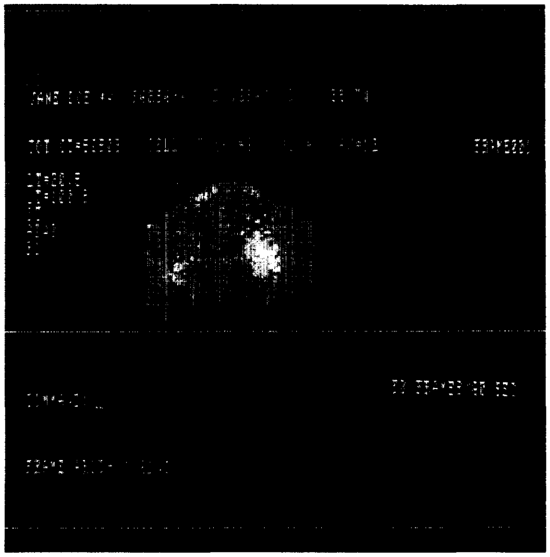


Figure 5-24
Data Rotated 180 Degrees

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, however, 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 displays data in an isometric pattern or a 3-dimensional mode. Type,

```
ID
```

This command causes all subsequent images to be presented in a 3-dimensional mode. Figures 5-20 and 5-21 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.

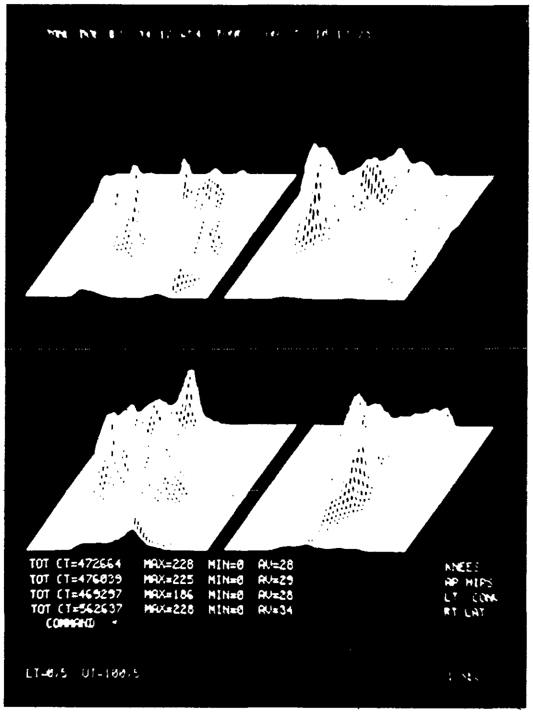
The Isometrics Display command is also useful for displaying four isometric displays in miniature.

```
ID;DM<CR>
```

Figure 5-22 shows the miniature 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 miniature form.



```
TOT CT=472664   MAX=228  MIN=0  AV=28                KNEES
TOT CT=476039   MAX=225  MIN=0  AV=29                AP HIPS
TOT CT=469297   MAX=186  MIN=0  AV=28                LT CON
TOT CT=562637   MAX=228  MIN=0  AV=34                RT LAT
  COMMAND *

LT-0.5  UT-100.5
```

Figure 5-22
Miniature Isometrics

DN

5.20.2 Display Normal

The Display Normal command converts an image from an isometrics display to the normal display mode and intensity. Type,

```
DN
```

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

5.21 IMAGE ROTATION COMMAND

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. This allows the user to manipulate or rotate any data that is read from a patient file. This process is performed via the Rotate Data command procedure.

5.21.1 Rotate Data

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

```
RO n
```

where n = 1, 2, or 3.

n is the number of 90 degrees clockwise rotations desired. Thus, if the user types,

```
RO 2
```

all data is rotated 180 degrees. When core resident data is rotated, data that is read after the RO command has been issued is automatically rotated when displayed. The rotation (R n) 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 additional rotate commands are issued, the rotation parameter (n) is added to the current parameter. That is, when RO2 and RO2 are typed, the display is in the upright position (0 degrees). If RO2 and RO3 are typed, the display is in the 90 degree position.

Example:

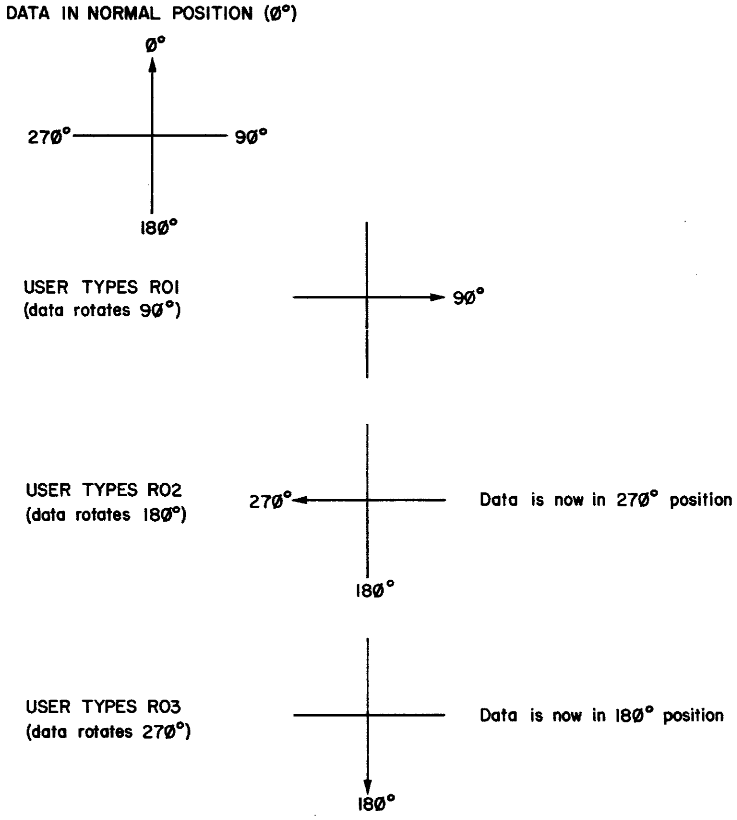


Figure 5-23 displays data that has been rotated 90 degrees and Figure 5-24 displays data that has been rotated 180 degrees.

The Rotate Data command is especially useful for isometric displays or if the patient study is not acquired in the correct orientation. For example, the user could use the Miniature Display command to show each rotation as a miniature.

5.22 COMMENT EDITOR COMMANDS

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

CO

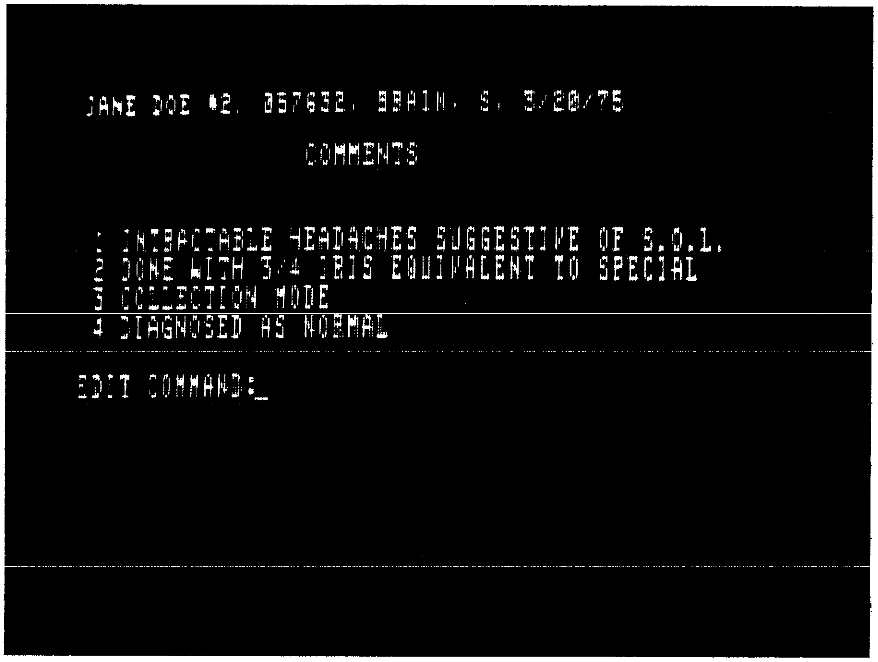
5.22.1 Call Comment Editor

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

on the terminal. The request,

EDIT COMMAND

appears beneath the text. 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 5-25.



```
JANE DOE #2, 057632, BRAIN, S, 3/20/75

                COMMENTS

 1 INTRACTABLE HEADACHES SUGGESTIVE OF S.O.L.
 2 DONE WITH 3/4 IRIS EQUIVALENT TO SPECIAL
 3 COLLECTION MODE
 4 DIAGNOSED AS NORMAL

EDIT COMMAND:_
```

Figure 5-25
Comment Text

When the EDIT COMMAND message appears, the user may use any of the following editing functions.

A<CR>	Append	Comments are added to the end of the displayed text. An asterisk is displayed to identify the beginning of the new text. The user 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 <CR>s in a row.
R n<CR>	Replace line n	An asterisk is displayed and the user must enter one line of text (maximum 49 characters), terminated by a <CR>. The new line will replace line n.
D<CR>	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.

<CR>	Edit and Return	When a <CR> is typed 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<CR>	Print	The contents of the data that are being edited is 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
```

on the terminal. The echo mode remains in effect until the NC command is given. Region of Interest commands (Chapter 7) are not echoed.

NC

5.23.2 No Echo

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

```
NC
```

on the terminal to use the No Echo mode.

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<CR>
```

All characters up to the carriage return are displayed on the screen in the command line. The text is automatically stored with the matrix and, if the matrix is recalled, 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 then be executed (at a later time) with a simple macro run command. For example, the user may find that whenever Regions of Interest is used, certain data manipulations prior to calling Regions of Interest may occur. That is, adding frames, smoothing, thresholding, etc. The user 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 the user 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. The macro buffer can be saved on the system device and loaded 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:

```
Mx filename
```

where x is a mnemonic for the specified command (e.g., S for Macro Save or R for Macro Run). The filename is the name of the file on the system device that contains the macro. A filename must consist of 1-6 alphanumeric characters (i.e., A-Z, 0-9).

MC

5.24.1 Macro Create

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

```
MC filename<CR>
```

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. The user should enter a macro file name during Macro Create, but it is not necessary. If the user decides to save this nameless macro, he will be told that he must provide a macro file name at that time. See Section 5.24.5, Macro Save.

ME

5.24.2 Macro Edit

The command used to call the Macro Editor is:

```
ME filename<CR>
```

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. See Section 5.22.1 for an explanation of the Comment Editor. During macro buffer editing

```
MACRO filename
```

appears at the top of the screen. 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.

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 loads the macro buffer with the contents of a macro file on the system device. The command format is:

```
ML filename<CR>
```

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 executes a macro. The following command format is:

```
MR filename,n<CR>
```

where filename is the name of the macro file on the system device. n is the line number (1-10) at which execution is to begin. 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. Processing the Macro Exit (MX) command.
2. Reaching the end of a macro buffer by using the command processor.
3. Typing a RUBOUT on the console terminal.
4. Detecting an error by using the command processor.

If the user types a RUBOUT 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.

Execution of a macro is suspended if a command requiring operator response is processed (i.e., RI, IR, SH, or SV). When the operator has made the required responses and then types CTRL/X, the execution of the macro is resumed from the point at which it was suspended.

MS

5.24.5 Macro Save

The Macro Save command saves the current contents of the macro buffer as a file on the system device. The following command format is:

```
MS filename<CR>
```

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, an error message is returned to the user and he must change the filename. If filename is not specified, the current macro name is used, and this macro filename need not be unique.

MD

5.24.6 Macro Delete

The Macro Delete command deletes a macro file from the system device. The following command format is:

```
MD filename<CR>
```

The filename MUST be specified. When the Macro Delete command is issued, neither the contents of the current macro file nor the current macro filename is affected.

MX

5.24.7 Macro Exit

The Macro Exit command stops execution of the macro. The following command format is:

```
MX<CR>
```

Execution of the Macro Exit command immediately returns control to the console terminal.

//

5.24.8 The Comment Line

The user 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<CR>
```

When the command is executed all text following the slashes (//) up to and including the <CR> is printed on the console terminal.

Example:

```
LT10;UT80;S5<CR>
//DEFINE ROI'S OVER LEFT AND RIGHT HEMISPHERES<CR>
IR<CR>
SD5<CR>
```

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, the macro resumes operation and the curves are stored in Save Area 5.

EL

5.24.9 Execute Line

The Execute Line command executes one line of the macro buffer. The command format is:

```
EL n<CR>
```

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 is:

```
filename.GMC
```

Thus, by using the PIP program (i.e., the PIP command string, *.GMC/L) the user can obtain a directory listing of all GAMMA-11 macro files. Since the macro is an ASCII file, the contents of a macro can be listed by PIP. For example, the PIP command:

```
TT:=NAME.GMC
```

lists the contents of the macro file, NAME, on the console terminal.

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
```

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 Data Analysis program. The command format is:

```
BA device:filename.ext
```

If the BASIC program is on the system disk, only the name of the program has to be specified. For example, to run a BASIC program called QPQS.BAS, type,

```
BA QPQS<CR>
```

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<CR>
```

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-writter FORTRAN program from the Data Analysis program. The command format is:

```
RU device:filename.ext
```

If the FORTRAN program is on the system disk, only the name of the program has to be specified. For example, to run a FORTRAN program called PAVIA.FOR, type,

```
RU PAVIA<CR>
```

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.FOR program resides on disk unit 2, type,

```
          RU RK2:PAVIA<CR>
```

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 Data Analysis program. The command format is:

```
          FO device:filename.ext
```

If the FOCAL program is on the system disk, only the name of the program has to be specified. For example, to run a FOCAL program called CAREY.FCL, type,

```
          FO CAREY<CR>
```

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 3, type,

```
          FO RK3:CAREY<CR>
```

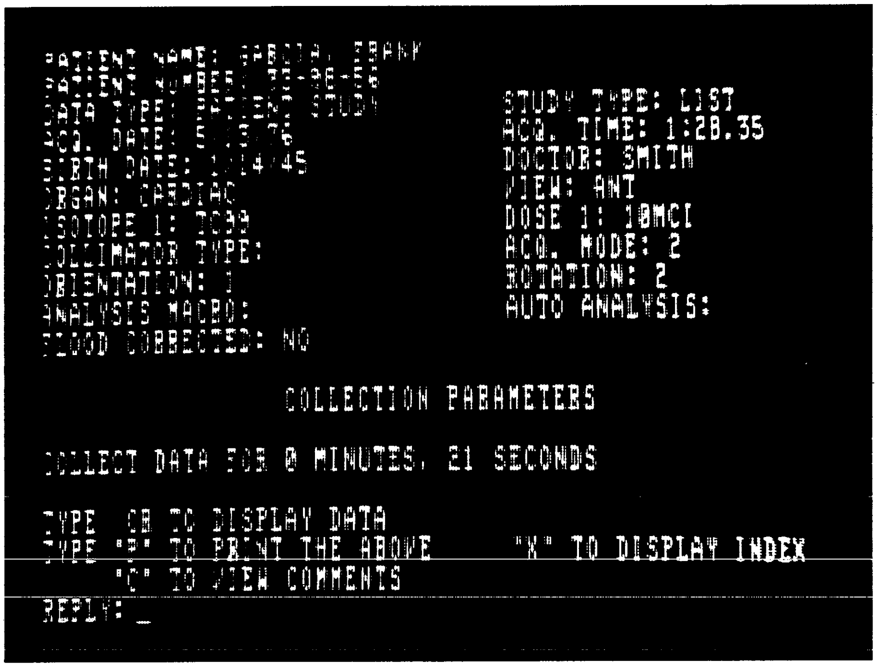
If the program name is not specified, the FOCAL interpreter remains in the immediate mode. For more information pertaining to the FOCAL language, please refer to the FOCAL-11 User's Manual.

5.26 LIST MODE PROCESSING

Data that is collected in a List Study are structured, or framed, in one of the five matrix configurations described previously (see Section 4.10). The data may be organized into a Static or Dynamic study of one or more frames. Frame rates other than those listed in Sections 4.2.12 and 4.2.13 may be used in a Dynamic Study. Framing is restricted to data collected during specific periods of time, within the study. The data may be reframed at any time. Finally, the framed data can be stored as a normal Static or Dynamic study in the disk Patient File.

5.26.1 List Study Framing

When a List study is selected from the Patient Study Index, the Study Summary appears on the screen as in Figure 5-26.

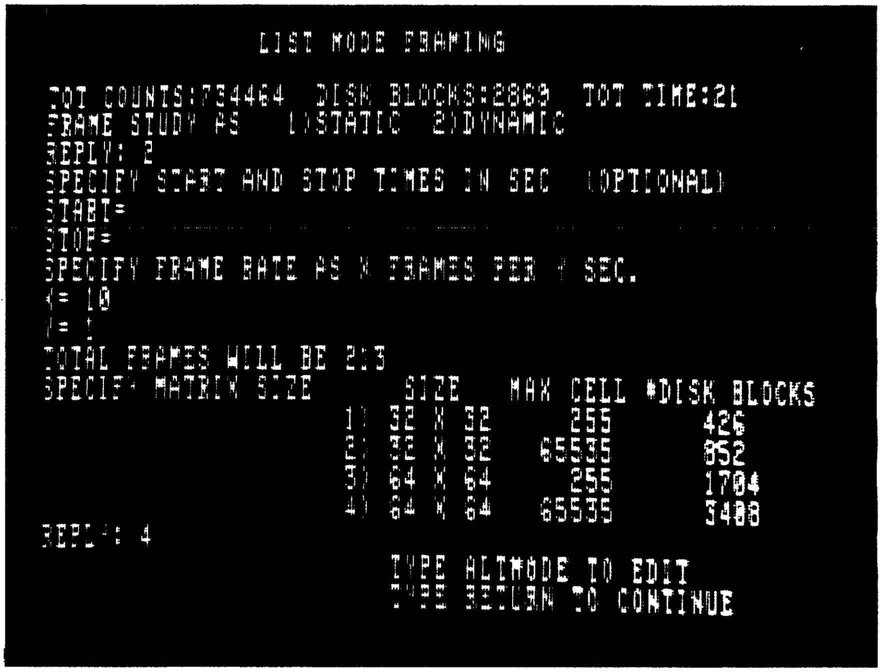


```
PATIENT NAME: GARCIA, FRANK
PATIENT NUMBER: 33-98-56
DATA TYPE: PATIENT STUDY                    STUDY TYPE: LIST
ACQ. DATE: 5/13/76                          ACQ. TIME: 1:28.35
BIRTH DATE: 1/14/45                         DOCTOR: SMITH
ORGAN: CARDIAC                              VIEW: ANT
ISOTOPE 1: TC99                             DOSE 1: 10MCI
COLLIMATOR TYPE:                            ACQ. MODE: 2
ORIENTATION: 1                              ROTATION: 2
ANALYSIS MACRO:                             AUTO ANALYSIS:
FLOOD CORRECTED: NO

                  COLLECTION PARAMETERS

COLLECT DATA FOR 0 MINUTES, 21 SECONDS

TYPE  CR TO DISPLAY DATA
TYPE "P" TO PRINT THE ABOVE       "X" TO DISPLAY INDEX
     "C" TO VIEW COMMENTS
REPLY: _
```

Figure 5-26
List Study Summary

The collection parameters disclose 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 <CR>. 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 5-27.



```
                LIST MODE FRAMING

TOT COUNTS:734464  DISK BLOCKS:2869  TOT TIME:21
FRAME STUDY AS   1)STATIC  2)DYNAMIC
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 ALTMODE TO EDIT
                           TYPE RETURN TO CONTINUE
```

Figure 5-27
List Framing Sequence

The first four lines of a List framing sequence are displayed immediately after the user presses <CR>.

TOTAL COUNTS
DISK BLOCKS
TOTAL TIME

These 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,

```
FRAME STUDY AS      1)STATIC
                    2)DYNAMIC
```

requests a reply to the type of study that is applicable. The next line appears as:

```
SPECIFY START AND STOP TIMES IN SEC
START=
STOP=
```

The starting and stopping times are optional and the user does not have to frame the entire study. For example, if the duration of the study is 42 seconds, the user can frame the data collected between 10 and 35 seconds of the run. Either limit may be skipped by pressing <CR> for each limit. If the user presses <CR> only for START and enters a number for STOP, zero is assumed for the STARTING time. If <CR> is pressed only for STOP, the maximum time in the study (TOTAL TIME) is assumed for STOPPING time. The next request is:

```
SPECIFY FRAME RATE AS X FRAMES PER Y SEC
X=
Y=
```

This question is asked only if a Dynamic study has been selected. 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, this being 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 an inadmissible rate is selected, the program offers the nearest permitted alternative. For example, if the user specifies 3 frames/sec, the program offers 100 frames every 33 seconds as an alternative. The user may accept this by pressing <CR>, or pressing ALTmode to enter a new rate.
3. No more than 511 frames may be made from any one study.

The next line to be 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,

```
SPECIFY MATRIX SIZE
```

is displayed and the possible matrix configurations are listed. The user should select the matrix type number of the desired configuration. The 128 x 128 matrix is available only for a Static study.

The user presses ALTmode to edit the framing parameters and presses <CR> to proceed to the next step.

5.26.2 Storage Options

When the framing parameters have been accepted, the list mode data are scanned. If a Dynamic study has been chosen, a table of framing pointers is set up and disk storage options are displayed on the screen as the following:

```
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
```

means that if the user wishes to save framed data by overlaying, he should type "1". This procedure, like all others which 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 is 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:

```
2) BY CREATING A NEW STUDY
```

If this option is selected, the message,

```
DISK UNIT:
```

is displayed. 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 study with its Administrative data and comments, is added to the Patient file, and a new entry is added to the Patient Study Index. The first frame of the study is then redisplayed. 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 messge appears:

```
NOT ENOUGH ROOM FOR FRAMED DATA ON UNIT N
```

At this point, the user may press ALTMODE to edit, press carriage return to display data, or enter a new disk number.

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. 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	Recall Framing Routine The Framing sequence (see Section 5.25.1) is recalled, so that framing parameters may be changed or so that the framed data can be saved as a study. Typing FR<CR> has the same effect as typing an ALTmode after completing the framing sequence.

5.26.4 Framing Method

A Static study is framed and stored temporarily on the system disk. A Dynamic study is scanned, and a table of timing pointers is set up. 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 the framing parameters are changed several times. The framing program saves time when parameters are changed 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.

Example:

> In changing from 4 frames/sec to 2 frames/sec, a new table is built from every other entry of the old one, thus obviating the need for a complete rescan of the list.

5.27 ERRORS

In general, an erroneous keyboard input is rejected. The command line is displayed to the point of error and a new COMMAND request is displayed beneath the preceding one. If there is no more room on the screen, the message:

```
TYPE ^N FOR NEXT PAGE
```

is displayed. When CTRL/N is typed, the screen is erased, and the COMMAND message appears. As soon as an acceptable input is received, the matrix display is restored. The DI command is useful at this point to restore the display without modifying the data.

If an error is detected, before typing a <CR>, it can be erased by using RUBOUT or CTRL/U.

5.28 AUTOMATING DATA ACQUISITION AND ANALYSIS

The GAMMA-11 system offers the user 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 allow the user to standardize and simplify the data acquisition set up, while the data analysis macro feature allows the user to perform the same for data analysis functions. These two features can then be combined through the autoanalysis feature which allows the acquisition program to call the analysis program. The combination of these three features allow the user to semi-automate acquisition and analysis.

CHAPTER 6

COLOR DISPLAY COMMANDS

This chapter describes the Color display 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

6.1 BLACK AND WHITE COMMANDS

The black and white commands allow the user 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
```

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
```

If the CHAN B button has been pressed, press it 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 the user to identify the high and low count areas.

DL

6.2.1 Intensity Scale Bar

The Intensity 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
```

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.

NL

6.2.2 Removing the Intensity Scale Bar

To remove the color scale bar from the display, type,

```
NL
```

When this command is issued, it 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 the 16 color levels of the Color display. Each level is made up of four intensities, one for each of the three colors. These colors are:

1. Red
2. Green
3. Blue

Each color can have one of four intensity levels (0-3), where 0 is off, and 1-3 are on (1 is lowest intensity, 3 is highest). Therefore, there are 64 possible color combinations.

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. Digital has supplied the user with two color tables:

1. A 16-color "rainbow" spectrum
2. An 8-color "hot body" spectrum

The user 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 contents of the current color table.

The color table currently in use is called the "current color". When the data analysis program is called, it defaults to color table zero, i.e., the last color table used.

Five commands are available to the user at the data analysis COMMAND level. These commands:

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 command to retrieve a previously defined color table from the system disk is:

```
CT n
```

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 n is not specified, the last color table used is retrieved.

ST

6.3.2 Saving a Color Table

The command to save the current color table on the system disk is:

```
ST n
```

where n must be specified and is the color table number (1-31). Once saved, a table can be retrieved at any time with the CT n command.

The ST command must be used when changing a color table on a displayed image; otherwise, the colors are not saved.

CL

6.3.3 Changing a Color Level

To change a color level at the COMMAND level, type:

```
CL n,rgb
```

where n represents the color level (0-15) to be changed. rgb is a 3-digit number representing the intensity levels 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:

```
DL
```

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 fifth color up on the color bar is red and the user wishes to change it to blue, the command

```
CL 5,003
```

will replace 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
```

A good example of this command appears in Figure 6-2. Figure 6-1 is a normal color image. The combination of these three colors and their intensity levels produces gray.

6.4 COLOR EDITING TABLE COMMANDS

The color table editor allows easy modification of the current color by:

1. zeroing the color table (i.e., setting all levels to off)
2. changing a color table element
3. inserting a new element into the color table

4. deleting an element from the color table
5. saving a newly created color table on the disk

ET

6.4.1 Color Table Editor

The command to call the color table editor is:

```
ET n
```

where n is the number of the color table that is to be modified. Color table n is retrieved from the disk and it becomes the current color table. If n is not specified, the color table that is currently displayed is used.

To the right of the displayed image is a 16-level color bar. To allow easier identification of the color level numbers, colors 3, 7, 11, and 15 are two times wider in the bar than the remaining colors.

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 lists the level numbers and their corresponding intensities.

	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). This message accepts any of the following 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
CTRL/X or <CR>	Exit

Z

6.4.2 Zeroing the Color Table

The command to set all color table elements to zero is:

```
Z
```

Therefore, it is strongly suggested that before attempting to zero a color table, the user 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 will 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
```

where n represents the color level (0-15), and rgb is a 3-digit number representing the intensity levels of 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
```

where n represents the color level (-15 to +15), and rgb is a 3-digit number representing the intensity levels of 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), etc.. 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), etc.. 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
```

where n represents one of the color levels (-15 to +15). The levels above n move up or the levels below n move down, 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), etc. Level 15 assumes a color value of zero.

If n is -7, the levels below level 7 move up on position. That is, old level 6 (n-1) becomes 7 (n), old level 5 (n-2) becomes level 6 ~~(n-1), etc. 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
```

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
```

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.

6.4.8 Exiting From the Color Table Editor

To exit from the color table editor, type either a <CR> 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 contains a 128 x 128 display matrix for displaying the images. To display a 64 x 64 image, each of the data cells are mapped into four cells of the display matrix (i.e., each cell is quadrupled). For a display of 32 x 32 images, each data cell is mapped 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. A more pleasing display can be obtained by interpolating the data.

IT

6.5.1 Interpolation Command

The command to interpolate the displayed data is:

```
IT
```

This command interpolates all 64 x 64 and 32 x 32 display 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 for an interpolated display and compare it to Figure 6-1, a normal color image.

6.5.2 Interpolation Algorithm

The following steps represent the algorithm that is used to obtain the interpolated image.

1. The number of display points is doubled horizontally by averaging adjacent horizontal points.
2. The real and interpolated (horizontal) display points are then doubled vertically by averaging adjacent vertical points.
3. The top row of points and the rightmost column of points are obtained by duplicating the preceding row or column.

The following diagram shows the interpolation algorithm.

```
R I R I R I . . . . . R I R R

R I R I R I . . . . . R I R R

I D I D I D . . . . . I D I I

R I R I R I . . . . . R I R R

I D I D I D . . . . . I D I I

.

.

.

.

R I R I R I . . . . . R I R R

I D I D I D . . . . . I D I I

R I R I R I . . . . . R I R R

I D I D I D . . . . . I D I I

R I R I R I . . . . . R I R R
```

In the preceding diagram, R, I, and D represent intensity levels:

R	Real data points.
I	Interpolated points obtained by averaging horizontal and vertical adjacent data points.
D	Interpolated points obtained by averaging vertical adjacent interpolated points.

For 64 x 64 data matrices, the resultant interpolated image is 128 x 128 and is mapped directly into the 128 x 128 display matrix. For 32 x 32 data matrices, the resultant image is 64 x 64 and is mapped into the display matrix by quadruplicating each point. The interpolation process takes place while the intensity levels are being calculated for the display. Remember that the actual core resident data is not modified. Interpolation will slightly increase the time required to generate an image but not enough to make the time unduly long.

NT

6.5.3 No Interpolation

The command to turn off the interpolation command is:

```
NT
```

When this command is issued, it omits interpolation from all subsequent images.

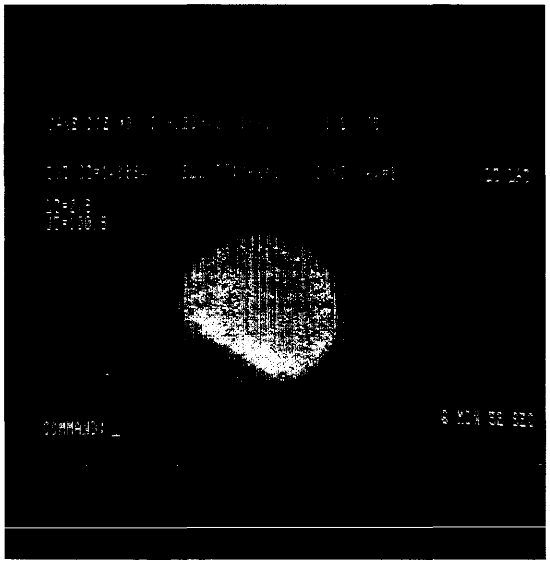


Figure 6-1
Normal Color Image

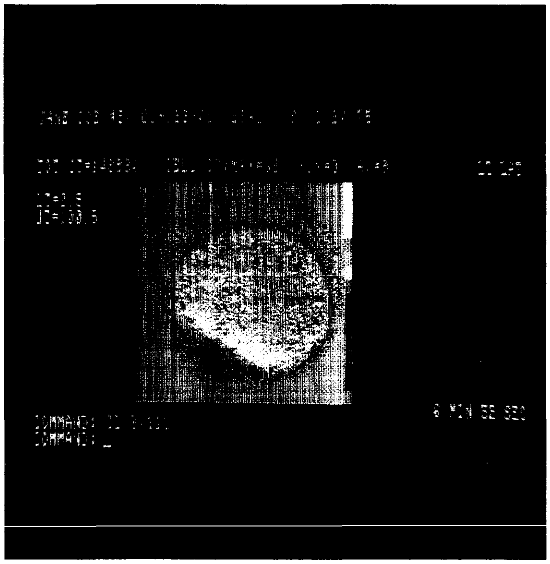


Figure 6-2
Changing a Color Level

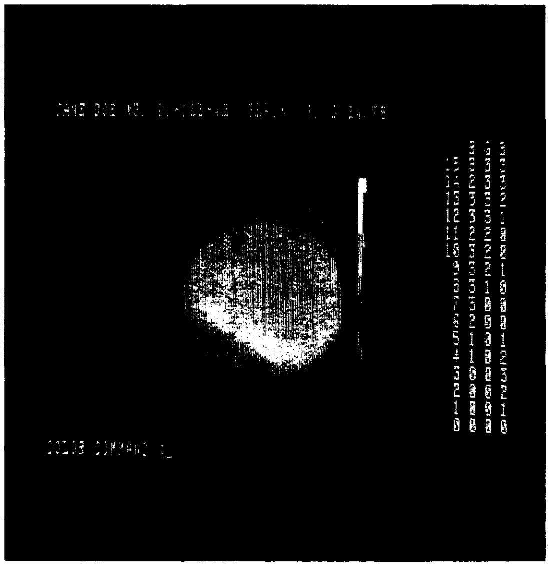


Figure 6-3
Color Table Editor

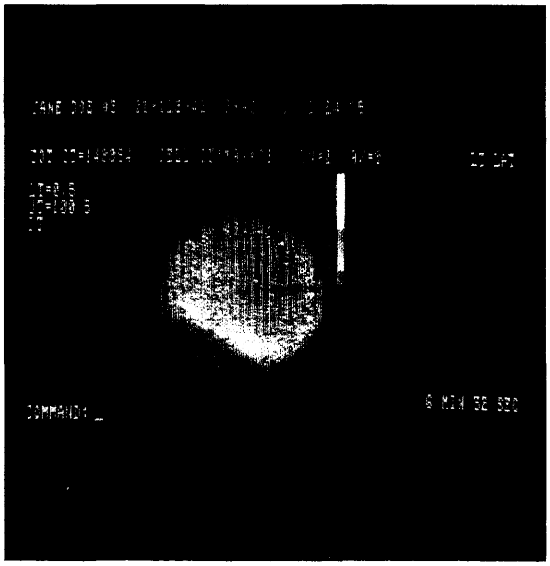


Figure 6-4
Interpolated Display

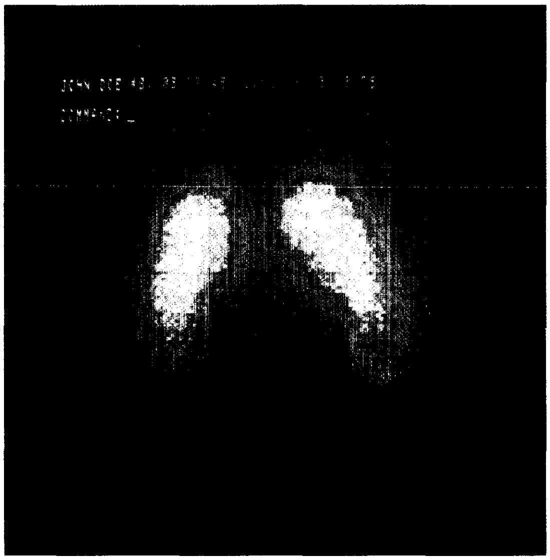


Figure 6-5
Blow-Up

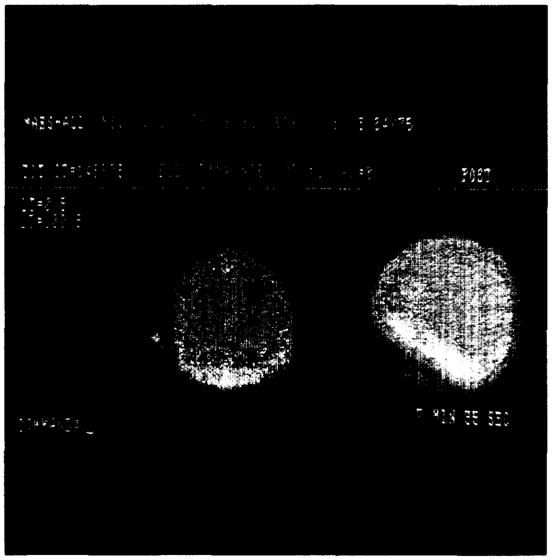


Figure 6-6
Dual Display

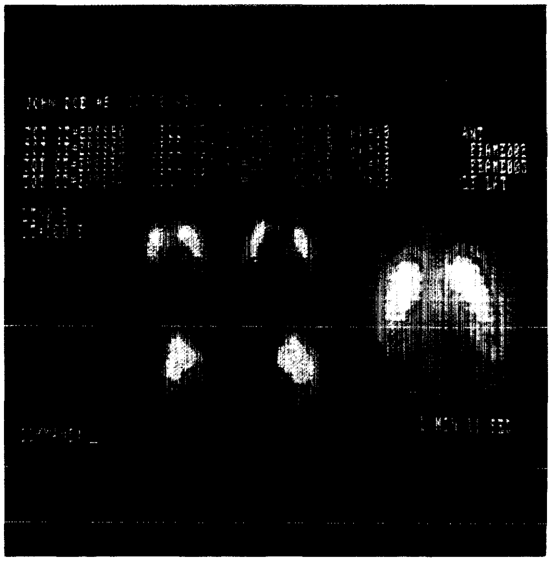


Figure 6-7
Miniature and Normal Dual Display

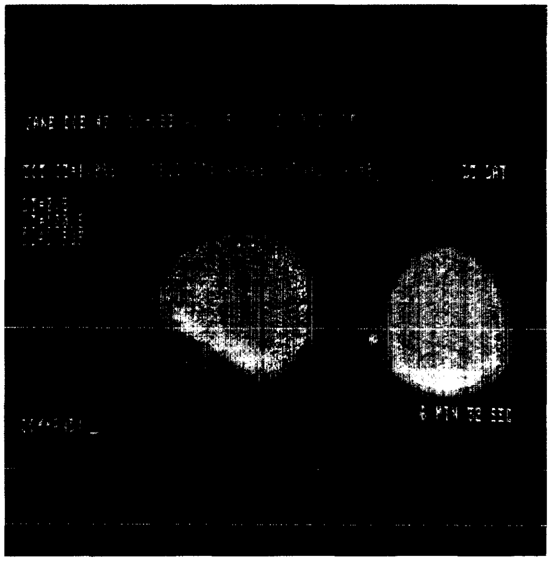


Figure 6-8
Swap

6.6 COLOR DISPLAY COMMANDS

Two color display commands enhance the visibility of the display by increasing the image to twice the normal size. These are the Blow-Up and No Blow-Up commands.

BU

6.6.1 Blow-Up

The command to increase the normal displayed image by a factor of two in each of the X and Y positions is:

```
BU
```

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, only the index line is displayed. COMMAND appears directly below the index line. Figure 6-5 is an example of the Blow-Up command.

NB

6.6.2 No Blow-Up

The command to switch from a blown-up image to a normal display image is:

```
NB
```

Typing this command causes all subsequent images to be normally displayed.

6.7 DUAL DISPLAY COMMANDS

Basically, the standard GAMMA-11 hardware system contains two bit maps. A bit map is defined as:

128 x 128 points = 1 normal full size display = 1 bit map

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 images are stored in a disk resident area called the "dual display buffer". The general procedure for generating a dual display is as follows:

1. The current core resident data is stored in the "dual display buffer" by using the Load (LD) command. This will be the right-hand image.
2. The core resident data is modified or changed to suit the user and then the dual display command is issued. This command is DU. 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 the No Dual Display command is issued. Once this command is issued, the left-hand image can be changed or modified by using the data analysis commands in the normal way.

To change the right-hand image, a Swap command (SW) can be issued. This command swaps the left and right images, (i.e., the core resident data goes to the "dual display buffer" and the contents of the "dual display buffer" becomes core resident.

LD

6.7.1 Loading Dual Displays

The command to load a dual display buffer is:

```
LD
```

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
```

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 (i.e., does not include Dynamic curves).

DU

6.7.2 Dual Display

The command to display the contents of the dual display buffer is:

```
DU
```

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. The user can change or modify the left-hand image with all the available commands in data analysis at the COMMAND level. The right-hand image cannot be modified unless the contents of the dual display buffer are mode core resident (see Section 6.7.4). Dual displays are only available at the COMMAND level. If the user leaves this level (e.g., to enter regions of interest or to slice), 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 mutally 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
```

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
```

This command displays the contents of the dual display over 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 the user wishes 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
```

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 represents the swapping of the two images in Figure 6-6.

6.8 DYNAMIC PLAYBACK

Dynamic Playback allows the user to playback patient studies in a "movie-like" manner. The speed and direction of the playback can be,

1. controlled by a joystick, or
2. preset to a specific rate, or

3. controlled manually (i.e., stepped) by using the terminal keyboard.

The playback feature can also be used to display a "closed loop" display of a small number of frames. For example, a two-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 allow the data to be played back at very fast rates. It is possible to playback images at a rate of up to 15 images per second. The prescaled images can be stored in one of three matrix sizes: 64 x 64, or 64 x 128, or 128 x 128. Chosing 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 (i.e., maximum) playback rate. The procedure for using the playback option is:

1. creating a playback buffer by specifying a buffer name, a disk unit number, the number of images, the image matrix, and the scaling factor.

2. storing data in the playback buffer.

3. displaying 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	10 images/sec	16 images/sec	8-10 images/sec

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 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. 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 the user wishes to determine from the playback. If an interest is in the overall flow and activity, both spatially and temporally, use the absolute scaling algorithm.

However, if an 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, the maximum and minimum scaling factors must be determined.

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 and/or macro allows the user 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 the user 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 storing any images in a playback buffer, a buffer must either be created or an existing buffer must be re-initialized. The command to create or initialize a playback buffer is:

```
PBI name,unit,n,r,max,min
```

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 this command is executed, a playback buffer is created on the specified disk unit. If a playback buffer already exists on the unit with this specified name, it is re-initialized. Any images previously stored on it 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 the Text command (TE) can be used prior to the PBI command to insert any comment. An alternate form of this command is:

```
PBI
```

The creation routine enters an interactive mode. The user is asked for the required parameters one at a time. The editing functions in the Data Acquisition program (i.e., ESCAPE to edit and DELETE to erase a line) can be used. In the interactive mode, the user is asked to enter a comment line.

If there is not enough disk space available for the playback buffer, the error message,

```
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, an ESCAPE can be typed to change some of the parameters (i.e., reduce the number of images, change the image matrix size, or select another disk unit). A carriage return can by typed 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 message:

```
BUFFER name ALREADY EXISTS ON UNIT n
```

is printed on the terminal. The user 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 the user to manually fill the buffer by typing PBS repeatedly.

The PBS command is intended to be used in a multiple command line and/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
```

S9 smooths the current data, PBS stores the smoothed data in a buffer, space bar skips to the next 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. The user can then issue the PB command (see Section 6.8.6) to display the buffer. Command execution can also be stopped 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

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
```

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
S9;PBS;  ;EL
```

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
S9;PBS;SK 1;EL
```

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 the user has 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
```

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 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 the joystick is moved further backward, the direction of the playback is reversed. The current image number, rate, and direction are displayed to the right of the image. The playback rate can be fixed at a constant rate or stepped manually by using the T, M, and S commands. See Section 6.8.7.

6.8.7 Playback Commands

The following commands can be used to control the mode of display and playback. All 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 (i.e., color table 0).
B	Display in black-or-white (i.e., monchrome).
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 a playback buffer is created it remains on the disk until it is deleted. The command to delete a playback buffer is:

```
PBD name,unit
```

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, else an error message is printed.

CHAPTER 7

REGIONS OF INTEREST

A Region of Interest (ROI) is a selected area of a displayed matrix from which count data can be extracted. ROIs are usually rectangular but may be irregularly shaped and are within the boundaries of the matrix. As many as twelve ROIs can be specified at any one time. The Regions may overlap, intersect, or be wholly contained within other Regions. In Dynamic studies, curves based on the count rate within each ROI can be calculated, and displayed, printed or punched. Dynamic study curves and matrices with ROIs can both be stored in Save Areas.

RI

7.1 REGION OF INTEREST COMMAND

The ROI commands constitute a subset of the Data Analysis routine. Thus, to enter the Region of Interest subset mode, type,

```
RI<CR>
```

on the terminal in response to the data analysis display, COMMAND:.

The matrix is redisplayed and a cursor is displayed approximately in the middle of the matrix. The cursor is used to outline or otherwise determine the matrix cells that are to be included in a Region of Interest. Figure 7-1 shows a matrix display with the cursor (cross hairs for the Color display). A regular ROI is rectangular and the motion of the cursor is controlled from the keyboard. The cursor can move only vertically or horizontally.

If the 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.

7.2 CONTROL COMMANDS

Each defined Region of Interest is identified 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 the following Sections, 7.2.1-7.2.6. Most of the Region of Interest commands are single character, immediate-effect commands (i.e., no carriage return is required). The command is executed as soon as the character is typed. None of the Region of Interest commands are echoed on the scope.

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 when typed, but the letter of the alphabet corresponding to number of the Region of Interest defined (i.e., A=1, B=2, C=3...), appears instead. In this case, since this is the first ROI to be defined, the letter A appears. This marks one corner of the Region. Next, the cursor has to be moved to a diagonally-opposite corner of the desired Region of Interest. This is accomplished by typing a series of other Control commands which cause the cursor to move up, down, left, or right. (See Sections, 7.2.1-7.2.5). When the diagonal corner is found, the user must type a second Mark. As soon as the second M has been pressed on the keyboard, the Region thus defined will have the letter A inside of it. See Figure 7-2. When using the VT01, the identifying letters designate the border of the Region.

The count data is tabulated to the right (beneath for a VT01) the matrix display.

NOTE

> To issue a Mark, make sure that the cursor has been moved to the desired cells for an ROI, by using the previous Control commands.

7.2.6.1 Region of Interest Count Data

As soon as an ROI has been defined by designating a second Mark, the following data are extracted from the Region and displayed to the right (beneath for a VT01) the matrix. See Figure 7-2.

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 another Region of Interest is requested, the procedure remains the same, except that this second Region contains the letter B. ROI count data is once again displayed to the right of the matrix along with the count data and outline of the first ROI. Figure 7-2 shows two Regions of Interest, with the count data for each Region displayed.

NOTE

> Although regular ROIs are limited in shape, the exact position of the cursor is always known, so that Regions as small as a single cell can be precisely located and marked.

S

7.2.7 Same Shape

The Same Shape command (S) defines a new Region of Interest with the same size and shape as the previous defined (last) Region. Type,

```
S a<CR>
```

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. The cursor should be moved 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. The Kill command cannot be used to erase a completely defined ROI. The E command is used 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<CR>
```

n represents the number of seconds a frame is displayed. n can only be a value from 0-9 seconds. Also, n is optional and if it is omitted, a rate of 0 seconds is used. To stop the automatic step, the user must type any printing character on the terminal.

As each frame comes to the screen, the currently defined ROIs are superimposed on the matrix in the prevailing display mode, and the count data for the frame are calculated and displayed.

E

7.2.10 Erase

The Erase command (E) erases specified ROIs.

Command Format:

```
E abc...<CR>
```

The ROIs are specified by the letters appearing in the argument of the command. These ROI's are deleted from the display. If no argument is given, all ROIs are deleted. The current matrix is displayed and new ROIs may be defined. If a ROI is deleted, the newly defined ROI will replace the ROI which has been deleted.

Example:

If 5 ROIs are defined, A, B, C, D, and E, and the user types,

```
E CE<CR>
```

on the terminal, the ROIs, C and E are erased. Now, if the user wishes to define two new Regions of Interest, the new ROIs are outlined with the letters C and E, respectively.

Note that commas are not required, and the ROIs need not be specified in alphabetical order.

If the user types

```
E ABGJ<CR>
```

on the terminal and realizes that he has made an error in an ROI he wants deleted, he may type CTRL/U on the terminal to erase the command line before pressing a <CR> on the terminal. The ROI procedure does not recognize RUBOUTs. For example.

```
E ABFJ^U
command line is erased and
new command line typed

E ABGJ<CR>
```

7.3 IRREGULAR REGIONS OF INTEREST

An Irregular Region of Interest is a selected area of a displayed matrix from which count data can be extracted. These irregular regions may be any shape or size within the boundaries of the matrix. As many as twelve irregular regions may be specified 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, the shape of an ROI is controlled by a joystick which in turn moves the cursor in any direction. An Interrupt Bar on the joystick control unit is used to record the path of the cursor.

The definition of an Irregular ROI is completed by marking its postion, using the Mark (M) command.

IR

7.3.2 Irregular Regions of Interest Command

The Irregular ROI commands constitute a subset of the Data Analysis routine. Thus, to enter the Irregular ROI subset mode, type,

```
IR<CR>
```

on the terminal in response to the data analysis display, COMMAND:. The screen is erased, then redisplayed 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. The user should pull the joystick toward his body to move the cursor to the bottom of the matrix. Moving the joystick away from the body moves 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. An identifying letter (A) immediately appears at the cursor location (VT01 only).
3. Keeping the Interrupt Bar depressed, move the joystick so that the cursor draws the outline of the ROI. The track of the cursor is illuminated by the identifying letter (A) only for the VT01.
4. Release the Interrupt Bar, and mark the ROI by typing the immediate-effect command, M. The letter A will appear inside the region. VSV01 only.

The count data are calculated and displayed.

To delete an ROI path before the Mark, press <CR>.

NOTE

Irregular Regions cannot be defined on 128 x 128 matrices. Use Regular ROIs for this configuration. For 128 x 128 matrices the IR command defaults to RI.

7.4 DEFINTION MODE COMMANDS

Irregular ROIs may be defined in one of two ways, by means of immediate-effect mode-setting commands. These are:

1. Circumference Mode
2. Fill Mode

C

7.4.1 Circumference Mode

Once again, a region is defined by outlining it with the cursor. 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 in the initial condition when the IR command is first issued. To advance into Circumference Mode, type,

C

with no carriage return. In Circumference mode, the path of the cursor may be simply- or multiply-connected, or not connected at all. If the path of the cursor is disconnected, each piece of the ROI will define a sub-ROI. The total ROI consists of all sub ROIs. The illustration in Figure 7-4 displays such an outline. Figure 7-3 is a simply-connected ROI.

Furthermore, an outline does not have to be closed, but the resulting ROI consists only of the path traced by the cursor. In other words, the total cell count is only those cells in which the indentifying letter is lying upon.

Also, the ends of the outline need not meet exactly, but if they do cross, the "loose" ends are included in the defined ROI (see Figure 7-5).

Notice that the total cell count includes the outlined area, plus the extra cells that the "loose ends" are lying upon.

F

7.4.2 Fill Mode

In Fill Mode, the defined ROI consists only of those cells through which the cursor actually passes when the Interrupt Bar is down. To advance to the Fill Mode, type,

F

with no carriage return. In Fill Mode, the path of the cursor may be simply- or multiply- connected, or not connected at all. An Irregular ROI may consist of a single curve, or of several non-contiguous areas obtained by filling in a patch, raising the Interrupt Bar, and moving the cursor to a new spot. Several such areas can be defined in one Irregular ROI, as the Region is not defined until the Mark command (M) is typed. Figure 7-6 shows a non-contiguous ROI. Unlike the Circumference Mode, the Fill Mode requires the user to define every point in the region.

7.5 DISPLAY MODE COMMANDS

Two modes of displaying Irregular ROIs are available. They are established by the following immediate-effect commands:

1. Boundary Display
2. Interior Display

B

7.5.1 Boundary Display

An outline of each Irregular ROI may be displayed by issuing the Boundary Display command. Type,

```
B
```

with no carriage return. When this command is typed, the screen is erased, and the frame is redisplayed with the outlines of the defined ROIs in their respective positions, but without the matrix. An example is shown in Figure 7-7. To restore the matrix display, press <CR>. The Irregular ROI outlines are superimposed on the matrix thenceforth.

I

7.5.2 Interior Display

The area (or interior) of an Irregular ROI may be displayed by issuing the Interior Display command. Type,

```
I
```

with no carriage return. Then this command is typed, the screen is erased, and the frame is redisplayed with the Irregular ROIs in their respective positions, but without the matrix. The interior of each Irregular ROI is filled with white (or letter if using the VT01) of the Region (see Figure 7-8). To restore the matrix display, press <CR>. The filled-in Irregular ROIs are superimposed on the matrix thenceforth.

The Boundary Display and Interior Display commands set a prevailing mode which holds until an alternate command is typed, but first they provide an Irregular ROI "only" display which is useful for verifying sizes, shapes, and positions without interference from matrix data in the background, which could make the display confusing in bright areas.

7.6 OTHER COMMANDS

There are some commands which have already been discussed. The following commands are also common to ROI subsets. All of these commands are immediate-effect commands.

W, X, Y, Z, N, O

These commands are the threshold-adjusting commands described in Sections 5.7.3-5.7.6, 5.8.2-5.8.3. The first four 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.

7.6.1 Carriage Return

The Carriage Return command <CR> restores the current frame, as indicated by the Frame Number, with ROIs in the prevailing mode. Type,

```
<CR>
```

on the terminal.

7.6.2 Space Bar

The Space Bar command displays the next frame of the study with current ROIs. Count data for the new frame are calculated and displayed. If the message,

```
FRAME ALGEBRA:  ADn
```

is on the screen when the space bar is typed, the indicated Sliding Add is performed.

7.6.3 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 sections to follow, the count rate for each Region of Interest can be calculated and plotted for the entire study, and the curve data may be stored in a Save Register. Curves derived from the average count-rate per cell in each Region may also be calculated and plotted. Tabular lists of counts per frame for each ROI may be printed or punched.

7.7.1 Curve Plot

A typical Dynamic curve is shown in Figure 7-9. Count rate is plotted on the Y-axis, time on the X-axis. The figure at the top of the Y-axis is a maximum count rate.

The X-axis is marked off in frames. This scale is linear in time. The frame marks of slower groups are further apart, as can be seen in Figure 7-9. The numbers on the X-axis are frame numbers.

7.8 CURVE CALCULATION COMMANDS

Curves can be calculated for each defined ROI and for the entire matrix. Individual curves are specified 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...<CR>
```

The curves are displayed two at a time each on its own axes in alphabetical order (Figure 7-10). If the command line is typed without an argument:

```
PN<CR>
```

the first two curves are brought to the screen. The top curve represents the TOTAL COUNT RATE VS TIME curve for all matrices. This is known as the T curve. The bottom curve is the first defined ROI. The next pair are brought to the screen by typing any printing keyboard character except the letter P. After the last curve is displayed, typing anything other than the letter P erases the plot and restores the matrix display, with ROIs.

At any time during the command, if the user wishes to issue another "P" command, he may do so by typing the appropriate command line.

Example:

If the user types,

```
PN ACFGI<CR>
```

on the terminal, the A curve and C curve are displayed. When a keyboard character is pressed (other than P, because P alerts the system that another command is going to be typed), curves F and G are displayed on the scope.

If the user types,

```
PN<CR>
```

on the terminal, all defined ROIs are displayed on the scope in alphabetical order. That is, if the user originally defined ROIs A, B, C, D, and E, those curves are presented on the scope in pairs (i.e., first the T curve 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 plots these curves on the same set of axes.

Command Format:

```
PO abc...<CR>
```

Each ROI is represented by a color. These colors are the intensity levels (6,9,12, and 15) of the current color table.

Level 6 = A,E,I
Level 9 = B,F,J
Level 12 = C,G,K
Level 15 = D,H,L

To display the total matrix curve, the color representation shifts to:

Level 6 = T,D,H,L
Level 9 = A,E,I
Level 12 = B,F,J
Level 15 = C,G,K

This configuration is displayed beneath the set of axes. Each curve is thus plotted in its respective color. Figure 7-11 is a typical example of the overlaid curve display.

Each curve is plotted with its ROI identification letter. The total matrix curve is plotted with the letter T. Each curve is still identified with its ROI identification letter.

If the argument is omitted from the command line by typing,

```
PO<CR>
```

all of the ROI curves are overlaid on one set of axes. Each curve is still identified with its ROI identification letter.

To restore the matrix ROI display, type any keyboard character except the letter P.

Example:

If the user types,

```
PO ABGJL
```

on the terminal, curves A, B, G, J, and L are overlaid with the identifying colors (letters for a VT01) of the ROIs. When a keyboard character is pressed (other than P, because P alerts the system that another command is going to be typed), the original ROI matrix is displayed.

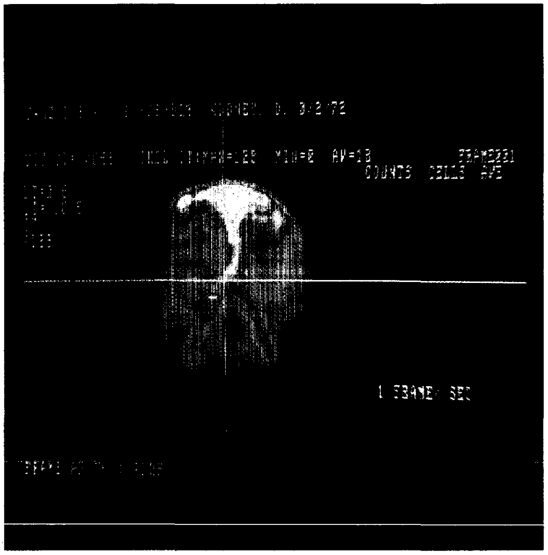


Figure 7-1
Matrix with Cursor

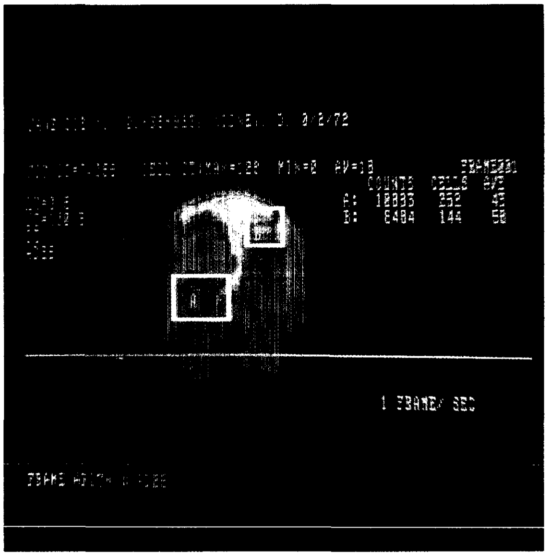


Figure 7-2
Two ROI's: A and B

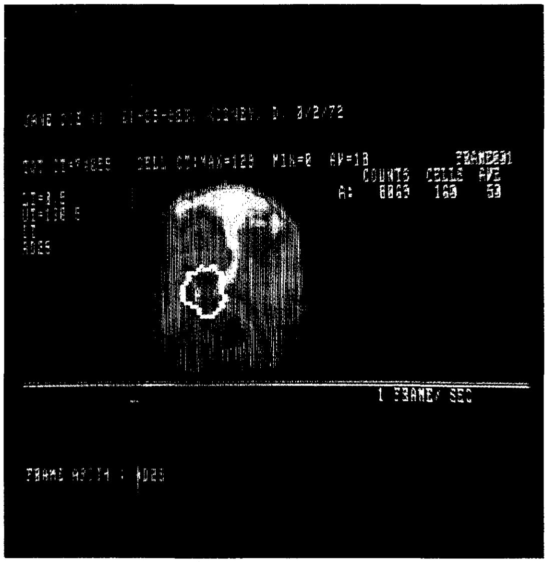


Figure 7-3
Simply-connected ROI

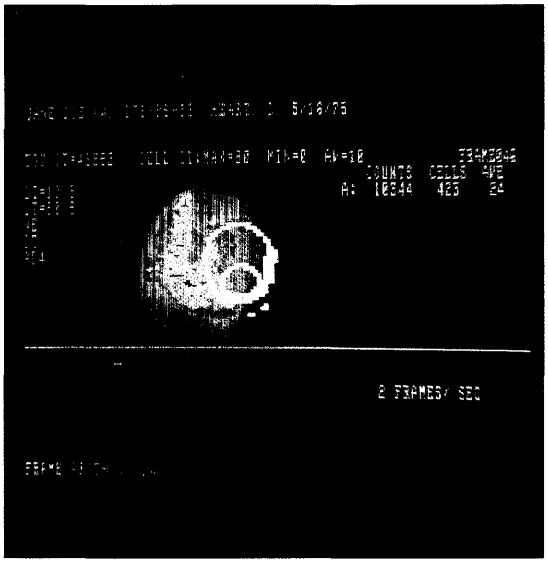


Figure 7-4
Multiply-connected ROI

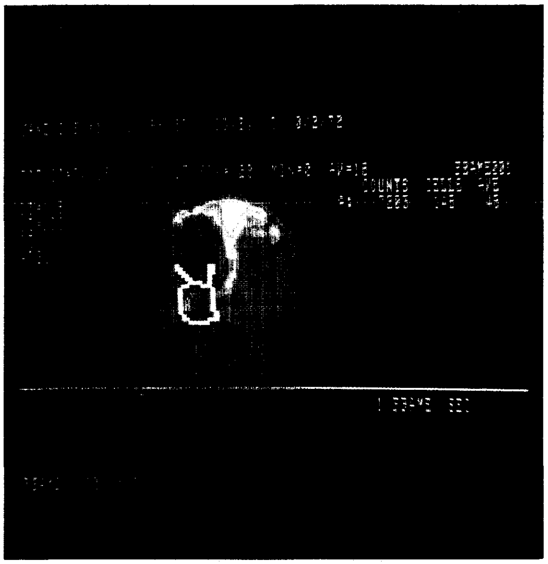


Figure 7-5
ROI with "loose ends"

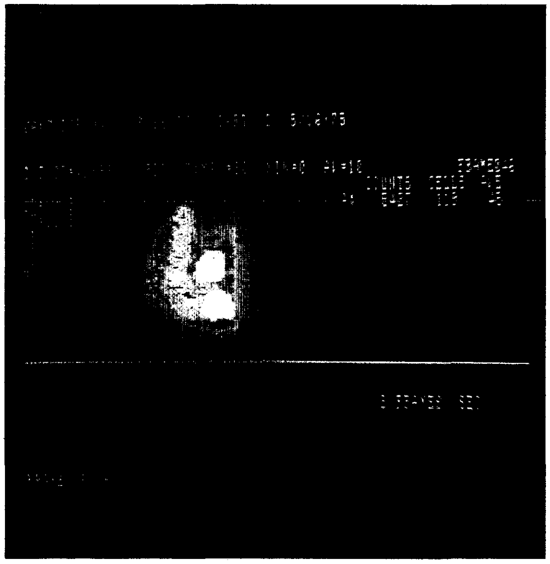


Figure 7-6
Non-Contiguous Irregular
Region (Fill Mode)

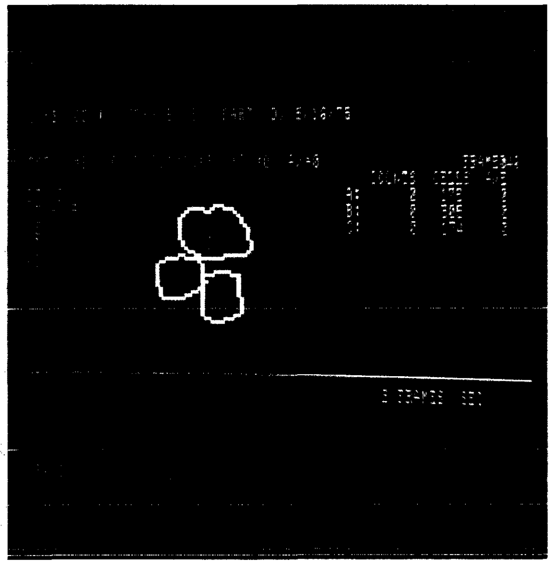


Figure 7-7
Boundary Display:
Three Regions

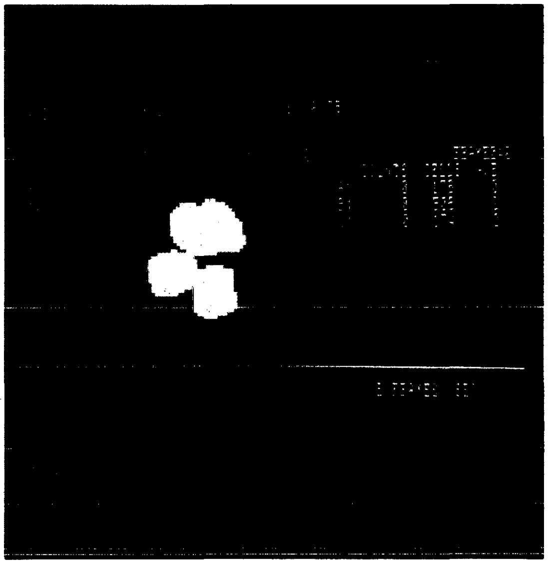


Figure 7-8
Interior Display:
Three Regions

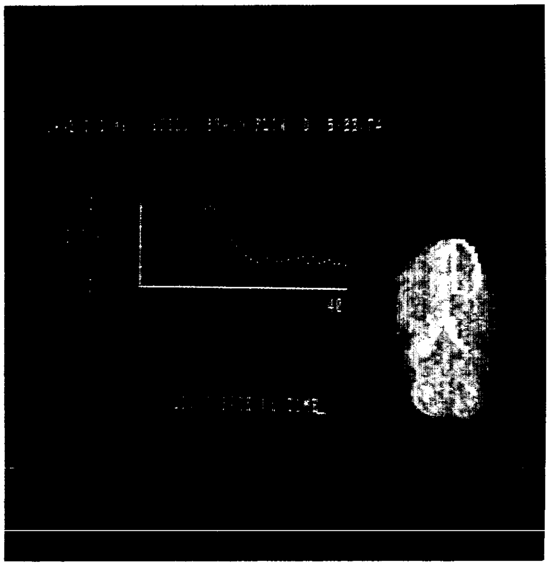


Figure 7-9
ROI Count Rate Curve

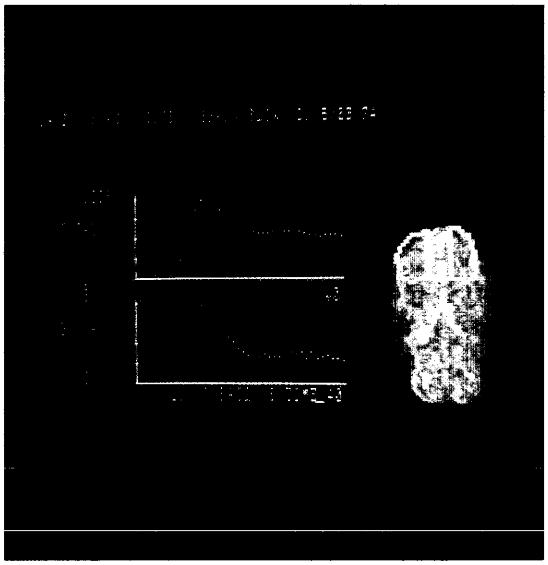


Figure 7-10
Individual Curve Display (PN)

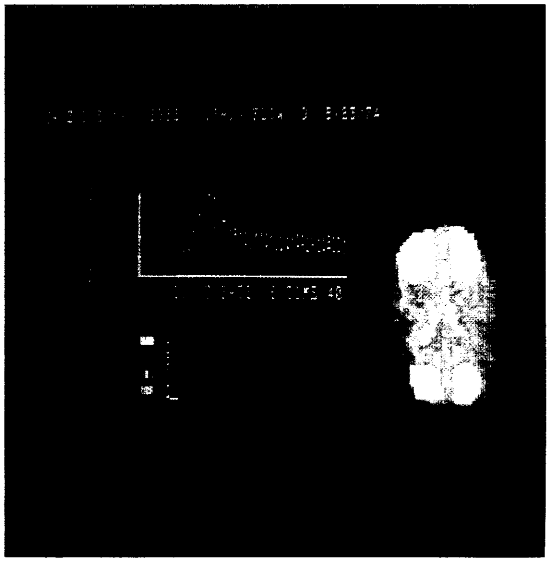


Figure 7-11
Overlaid Curve Display (PO)

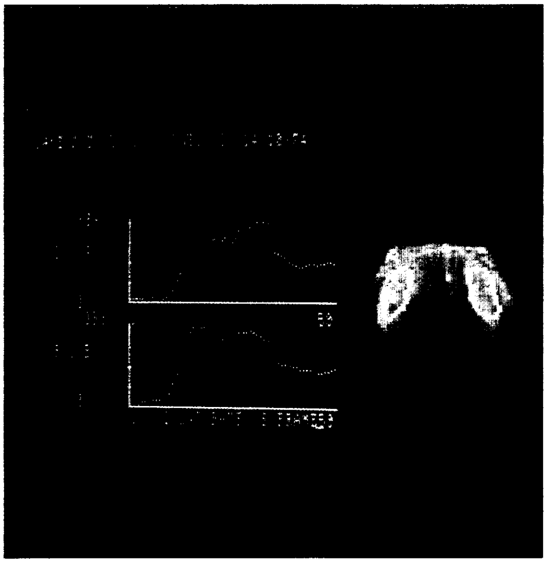


Figure 7-12
Frame-Linear
Curve Display (PNM)

PA

7.8.3 Plot Overlaid Average Rate Curves

The Plot Overlaid Average Rate Curve 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...<CR>
```

Each curve of average count rates per cell is plotted with its ROI identification color (letter for a VT01). The total matrix curve is plotted in yellow (or T for a VT01). If the command line is typed without an argument:

```
PA<CR>
```

All of the average count rate ROIs are overlaid 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 command is going to be issued.

7.9 FRAME-LINEAR SCALE COMMANDS

At times, the user may wish to provide the capability of making the X-axis linear in frame numbers than by time-intervals. He may do so by issuing the commands outlined in Sections 7.9.1-7.9.3.

PNM

7.9.1 Plot Normal Frame-Linear Curve

The Plot Normal Frame-Linear Curve command (PNM) allows the user to calculate the count-rate curves for the total matrix and for each specified ROI by frame number instead of time interval on the X-axis.

Command Format:

```
PNM abc...<CR>
```

The curves are displayed two at a time each on its own axes in alphabetical order (Figure 7-12). When the graph is drawn, the X-axis frame ticks are equally spaced and the graph rubric 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 7-10 to Figure 7-12. Notice, that in Figure 7-10 there are some tick marks close together at the beginning of the study and in Figure 7-12, the tick marks are equidistant to provide a linear curve.

The bottom curve is the first defined ROI. The next pair of curves are brought to the screen by typing any character on the keyboard except the letter P. Each time a character is typed, 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. The user may also omit the argument from the command line by typing,

```
PNM<CR>
```

on the terminal. This process brings all ROIs to the screen at the user's command.

At any time during the command, the user may type another "P" command by typing the appropriate command line.

POM

7.9.2 Plot Overlaid Frame-Linear Curve

The Plot Overlaid Frame-Linear Curve command (POM) allows the user to calculate the count-rate curves for the total matrix and for each specified ROI, by frame number instead of time-interval, on the same set of axes.

Command Format:

```
POM abc...<CR>
```

Each curve is plotted 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 X-axis frame ticks are equally spaced and the graph rubric changes to:

```
COUNT RATE VS FRAME NUMBER
```

to indicate that this is a Frame-linear curve. If the command line is typed without the argument:

```
POM<CR>
```

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 command is going to be entered.

PAM

7.9.3 Plot Average Frame-Linear Curve

The Plot Average Frame-Linear Curve command (PAM) allows the user to plot the average cell count rates for each specified ROI by frame number instead of time-interval on the same set of axes.

Command Format:

```
PAM abc...<CR>
```

Each curve of average count rates per cell is plotted with its ROI identification letter. The total matrix curve is yellow (or plotted with the letter T for a VT01). The X-axis frame ticks are equally spaced and the graph rubric 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<CR>
```

all of the average cell count rates for each ROI 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 command is going to be entered.

7.10 WINDOW COMMANDS (Partial Curve Plotting)

Window commands allow the user to partially plot a section of an entire curve. The commands are outlined in Sections 7.10.1-7.10.3.

PW

7.10.1 Plot Window

The Plot Window command (PW) allows the user to plot a particular number of frames (part of an entire curve), starting with a specified frame number.

Command Format:

```
PW f,n<CR>

PW f<CR>

PW ,n<CR>

PW<CR>
```

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 either parameter is omitted from the command, the previous value is used. If both parameters are omitted, all points are plotted.

One of the Plot commands (PO, PA, PN) must be issued first before this command works effectively.

For example, if the user types,

```
PN B
```

on the terminal, a plotted curve may look like the full plot shown in Figure 7-13.

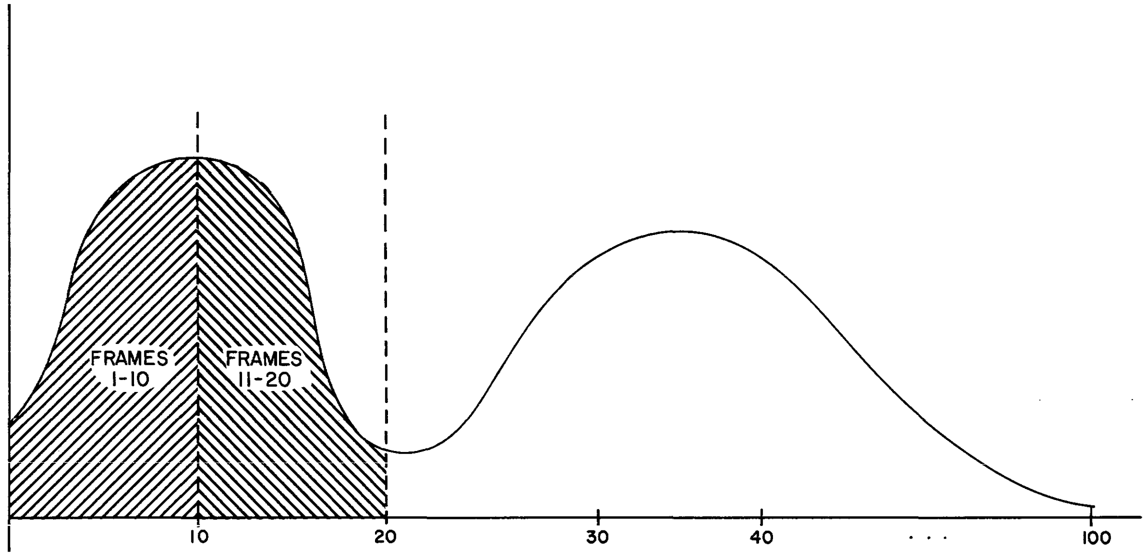


Figure 7-13
Full Plot

Next, if the user types,

```
PW 1,10
```

on the terminal. Where 1 represents the starting frame and 10 represents the number of frames to plot, the first ten frames of data for an ROI are brought to the screen. Hence, the diagram changes to look like the partial plot shown in Figure 7-14.

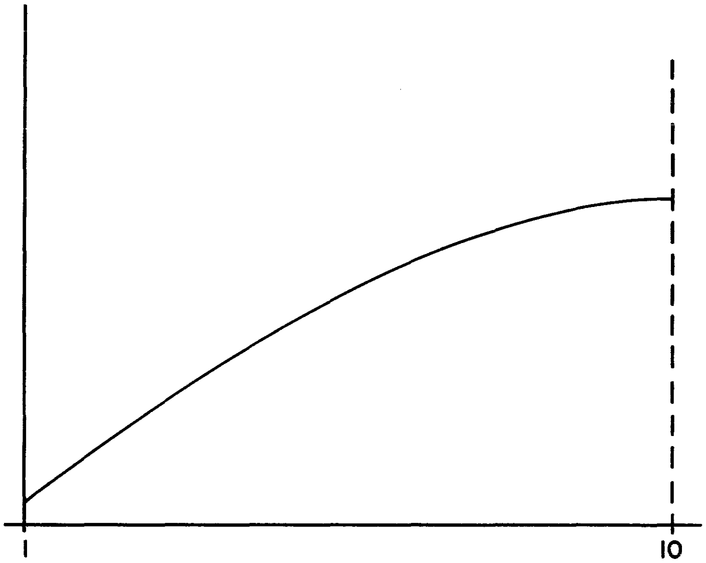


Figure 7-14
Partial Plot (Window Frames 1-10)

Notice that only the data from the ROI in frame #1 through frame #10 is displayed. This area represents the first shaded area in Figure 7-13.

This procedure is known as windowing.

To restore a full plot, type,

```
PW<CR>
```

on the terminal.

To restore the matrix ROI, type any keyboard character except the letter P. Typing P alerts the system that a new 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<CR>
```

on the terminal to briing the next group of frames specified via the PW command. For example, in Figure 7-13, the data of the first 10 frames is brought to the screen when,

```
PN<CR>
PW 1,10<CR>
```

is issued. If the PF command is issued, the next 10 frames of data (for an ROI plot) are brought to the screen. Thus, the diagram changes as shown in Figure 7-15.

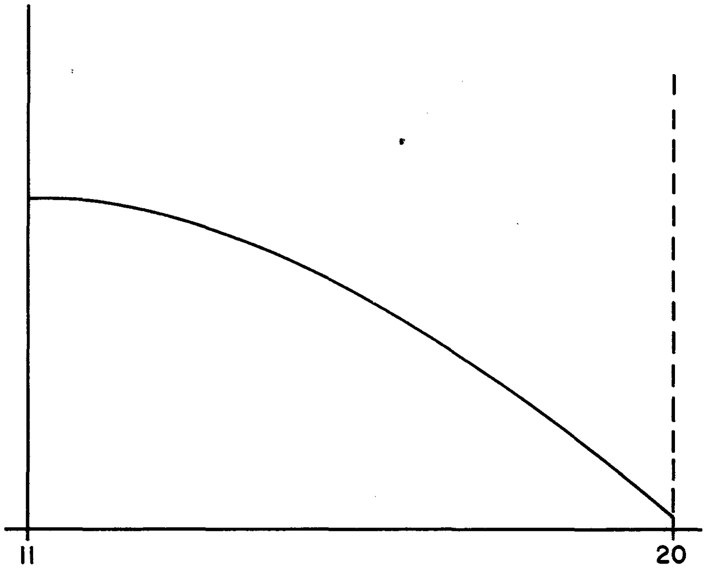


Figure 7-15
Partial Plot (Window Frames 11-20)

The diagram (Figure 7-15) represents the second shaded area from Figure 7-13.

Each time the PF command is issued, the next 10 frames are windowed (or shown on a full scale of the graph). Example:

```
PF<CR>
frames 21-30 are brought to the screen
PF<CR>
frames 31-40 are brought to the screen
etc.
```

To restore the matrix ROI, type any keyboard character except the letter P. Typing P alerts the system that a new command is going to be entered.

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<CR>
```

on the terminal to bring the previous group of frames specified via the PW command. For example, by typing,

```
PN<CR>
PW 1,100<CR>
```

the starting frame (1) through frame 100 is plotted. Next, if typing,

```
PF<CR>
```

on the terminal, frames 101 through 200 are plotted. Now, when typing,

```
PB<CR>
```

on the terminal, frames 1 through 100 are restored.

Example:

```
PW 1,10<CR>     (frames 1-10 are displayed)
PF<CR>          (frames 11-20 are displayed)
PF<CR>          (frames 21-30 are displayed)
PB<CR>          (frames 11-20 are displayed)
PF<CR>          (frames 21-30 are displayed)
PF<CR>          (frames 31-40 are displayed)
PB<CR>          (frames 21-30 are displayed)
```

To restore the matrix ROI type any keyboard character except the letter P. Typing P alerts the system that a new command is going to be entered.

7.10.4 Plotted Averages

When a study contains a large number of frames, the plotted points of a curve may be crowded together, making the curve difficult to read especially in overlaid graphs. If this should happen, points can be selectively averaged by including 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 frame 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 argument, n=1, is the default for the commands. In other words, if n is omitted, every point is plotted.

The digit may appear anywhere in the argument:

PA 3<CR>	Every three points of all curves are averaged and plotted.
PO BF2<CR>	Every two points of curves B and F are averaged and plotted.
PN 4AE<CR>	Every four points of curves A and E are averaged and plotted.

7.11 TABULAR DATA

For each ROI in a Dynamic Study, a table of counts per frame may be printed or punched. The data consists of the total number of counts in the Region in each frame of the study. Used without an argument, the commands produce output for every defined ROI. As with the curve plot commands, particular ROIs may be specified in an argument, using the ROI letters. The total-matrix table, consisting of the total number of counts in the entire matrix for each frame, must be specified by the letter "T". The total-matrix is not printed or punched when no argument is given.

PR

7.11.1 Print Count Data

The Print Count Data command (PR) provides the user with a tabular list of counts per frame for each (specified) ROI that is printed on the terminal.

Command Format:

```
PR abc...<CR>
```

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 7-16.

REGIONS OF INTEREST

```
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 7-16
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...<CR>
```

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 returns/line feeds between lines. Extra blank lines which appear on the terminal for legibility are deleted 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 is represented by their respective formats.

Command Format:

```
PP abc...<CR>
```

7.12 SAVE AREA USE

The Save Areas can be used to store matrix-plus-ROI information, and also the dynamic curve data. To save a displayed matrix with its ROIs, type the following command sequence:

```
CTRL/X
SM n
```

When CTRL/X is typed, the ROI display remains, and the request "COMMAND:" reappears. "SM n" is typed in response to "COMMAND:". The previous matrix-ROI display is stored in Save Area n.

When the contents of the Save Area are subsequently read, the matrix and ROIs are displayed, and the program automatically calls the ROI subset into operation.

To save a set of Dynamic study curve calculations, use the following sequence:

1. If the curves are on the screen, the user must type anything except "P" to restore the matrix-ROI display.

2. Type CTRL/X.

3. Type SD n.

"SD n" is typed in response to the displayed "COMMAND:" request, as described above. The curve data are stored in Save Area n. When the contents of the Save Area are subsequently read, the curves are displayed in an overlaid plot. At this point, only the commands PN, PA, PO, PU, PR, PW, PF, PB, and PP are executable. Any other input has the effect of an "RS 0" command, restoring the previous matrix display.

7.13 EXIT

The user can cancel a typing error in a <CR>-terminated command (E, PN, PO, PA, PR, PU, PP, PW, PF, PB), before reaching the <CR> terminator by typing,

```
CTRL/U
```

Note that RUBOUT is not honored by the the ROI procedure.

To leave an ROI procedure, type,

```
CTRL/X
```

CTRL/X returns to the data analysis mode and the word, COMMAND:, reappears.

CHAPTER 8

SLICING

The operations described in this chapter allow the user to examine the data patterns of slices through the matrix (i.e., horizontal or vertical strips of varying width). 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. New curves are automatically plotted when the new frame is displayed.

The Slice commands are a subset of the Region of Interest group. Six of them, U, D, L, R, M, and J, are all immediate-effect commands. They require no <CR> 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 may be horizontal or vertical, and may vary in width from 1 to 9 rows or columns. Up to 26 slices on the VT01 may be selected for any one display. On the VSV01, up to three slices may be displayed, as well as, the current position.

SH

8.1.1 Horizontal Slice

To prepare a horizontal slice procedure, type,

```
SH n<CR>
```

on the terminal. n is optional and represents the number of rows of the width of the matrix. If n is omitted, the slice is one row.

The program is now conditioned to accept horizontal slices. Figure 8-1 represents a preparatory display of a horizontal slice.

Notice, 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.

A cursor, shown as a long line, appears through the center of the matrix. Immediate-effect commands may now be issued (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 graph, plots 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, the scale factor is 1. The scale factor can be adjusted to a value desired by the user (see Section 8.5.1).

SV

8.1.2 Vertical Slice

To prepare a vertical slice procedure, type,

```
SV n<CR>
```

on the terminal. n is optional and represents the number of columns of the width of the matrix. If n is omitted, the slice is one column.

The program is now conditioned to accept vertical slices. Figure 8-2 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 cursor (white) is plotted vertically to the right of the matrix.

Notice that the cursor for a vertical slice appears at the bottom of the miniature matrix. For a slice of length n, n adjacent cursors are displayed.

Immediate-effect commands may now be issued (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. The scale factor can be adjusted to a value desired by the user (see Section 8.5.1).

8.2 IMMEDIATE-EFFECT SELECTION COMMANDS

The immediate-effect commands move the cursor or group of cursors and marks the position of the slice. For greater detail, see Section 7.2.1 through 7.2.5. These commands are:

U	Move the cursor(s) up one row.
D	Move the cursor(s) down one row.
L	Move the cursor(s) left one column.
R	Move the cursor(s) right one column.
J	Jump the cursor(s) 10 cells in the direction of the last typed U, D, L, or R command.

The cursor or cursor group 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 will 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. From each cursor, a line is drawn through the indicated row or column of the matrix, and a curve of cell counts along the line(s) of the slice is plotted. (See Figures 8-3 and 8-4.)

8.3 FRAME SELECTION (DYNAMIC STUDIES ONLY)

Each frame of a Dynamic study may be examined, using the currently marked slices. The user 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, the orientation (horizontal or vertical) and/or the width of the slice may be changed by using the commands,

```
SH n
SV n
```

as previously described. The existing display is erased, deleting all curves and slices. A new display, with new axes and cursor, appears on the screen.

Curves may be deleted without changing the other conditions, as follows:

E	Erase The screen is erased and all curves and marked slices are deleted. The preparatory display reappears. Orientation, slice width, and scale factor are not changed.

8.5 SLICE CURVE PLOTS

As soon as the user issues the Mark command (M) a line is drawn through the indicated row or column of the matrix, and a curve of cell counts along the line(s) of the slice is plotted. Figure 8-3 displays the plots of three-row horizontal (left) slices. Figure 8-4 displays the plots of three-column vertical (right) slices.

For each point on the cell-position axis, the sum of the counts in the three cells at the corresponding X-axis or Y-axis, respectively, on the slice is plotted. The plot points are identified by a color designating the slice. The current color table determines the colors. The most current slice is level 4, the second most current is level 8, and the third is level 12.

The plot points are identified by a letter designating the slice. The first slice is A, the second is B, and so on.

For horizontal slices, notice that the curve on the axes changes each time an immediate-effect command is issued. The first marked slice is level 4 and the plotted curve is represented in the level 4 color. The color in level 15 always represents the plot of the cursor. The second marked slice is marked by the color in level 4, while the first marked slice obtains a color at level 8. The third marked slice is represented by level 4, the second is represented by level 8, and now the most current slice is represented by level 12.

NOTE

> The Color display can only use three colors for marking a slice. When a fourth slice is marked, the first slice issued is "turned off" and each slice moves into its respective color.

Likewise, the vertical slice has the same slicing procedure as the horizontal slice.

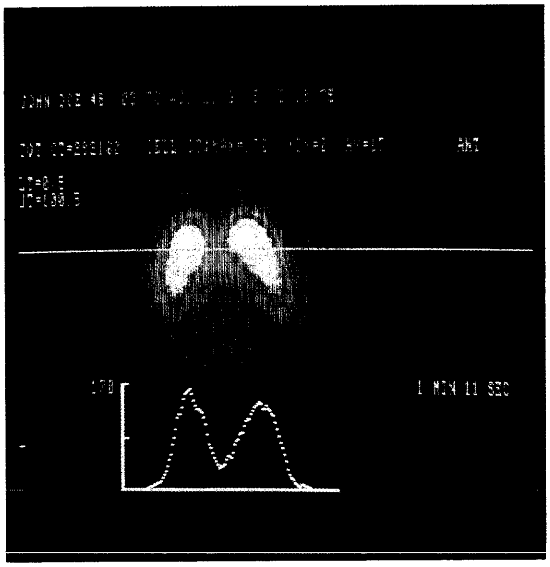


Figure 8-1
Preparatory Display:
Horizontal Slice

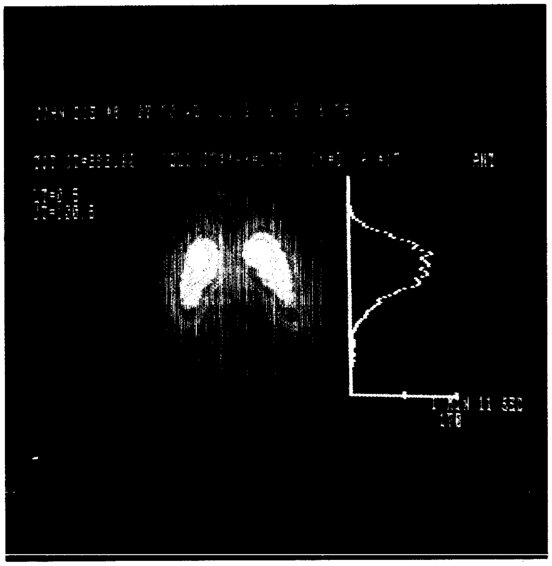


Figure 8-2
Preparatory Display:
Vertical Slice

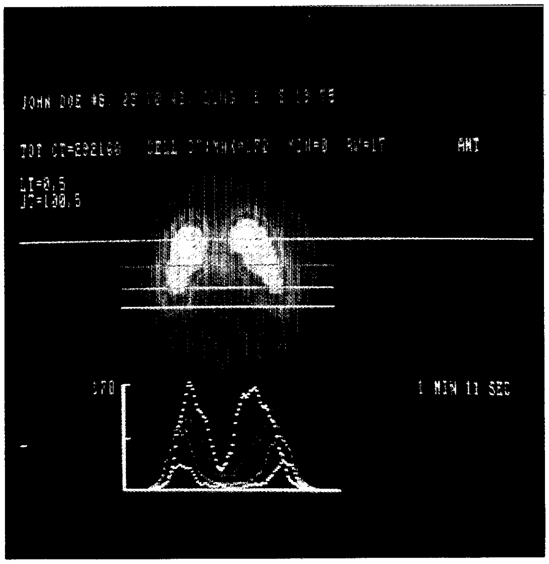


Figure 8-3
Horizontal:
Three-row slice and curve

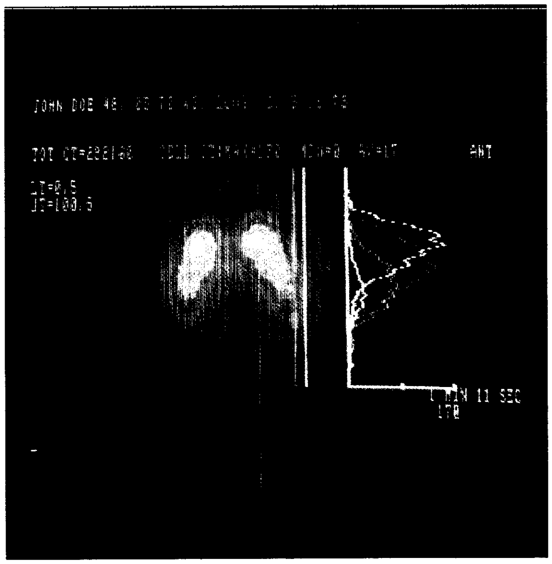


Figure 8-4
Vertical:
Three-column slice and curve

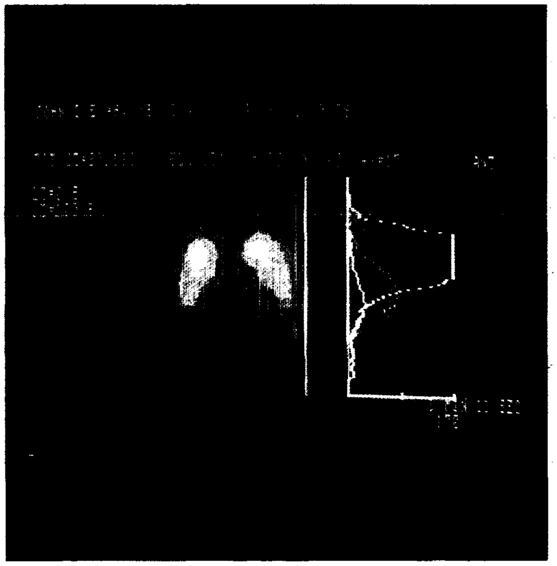


Figure 8-5
Scale Factor 1:
Truncated Curve

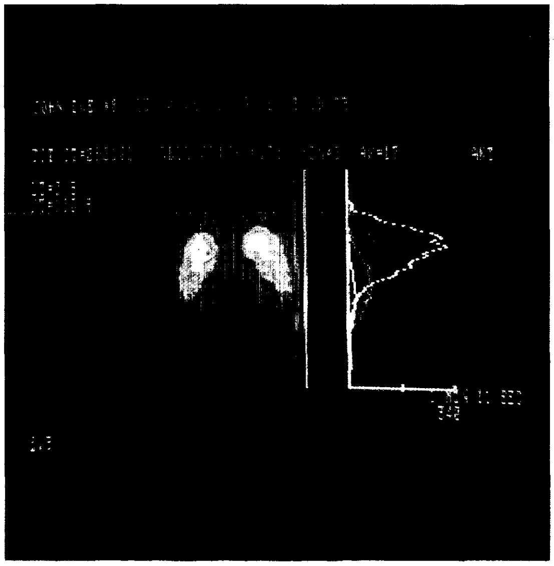


Figure 8-6
Scale Factor .5:
Truncation Eliminated

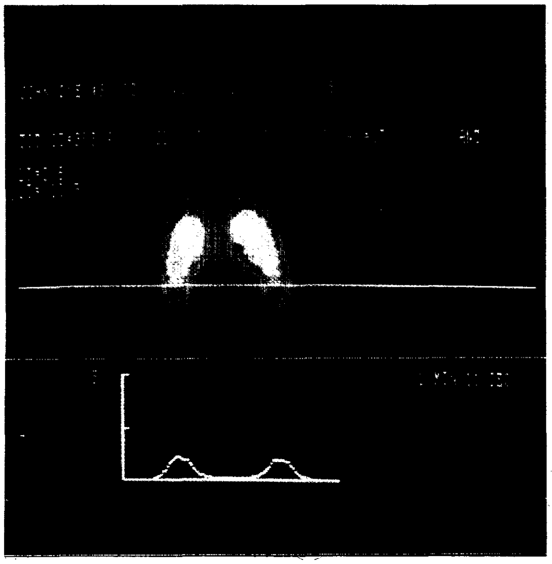


Figure 8-7
Scale Factor 1:
Low Contour Curve

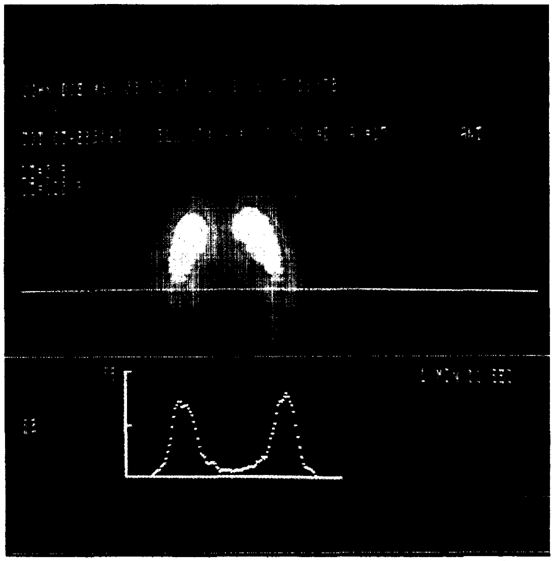


Figure 8-8
Scale Factor 2:
Contour Enhanced

8.5.1 Scale Factors

When the axes are first drawn, the count-axis is labeled at four points (the highest point being n times the maximum cell count). This point is also the upper (or rightmost) boundary of the graph. Points beyond the largest cell count may result when adjacent cells of an n-row (or n-column) slice are added together. These are plotted along the boundary. Likewise, at the base of the curve, cell counts below a minimum plottable level will 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 is 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.

S n.nn

8.5.2 Scale Factor Command

The Scale Factor command eliminates truncation and low contour curves by adjusting the count-axis scale. This can be obtained by typing,

```
S n.nn<CR>
```

on the terminal. 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.

To enhance 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.

Spaces, nonsignificant zeros, and decimal points may be omitted 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

Tabular data may be obtained on punched tape, printed copy, or screen display. The tabular data is provided for the last defined slice

(VT01). The cursor plot on the VSV01 is represented by the tabular data. If a complete record is desired, the data must be printed or punched after each slice is marked.

PR

8.6.1 Print Slice Data

The Print Slice Data command provides the user 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,

```
PR<CR>
```

on the terminal. The orientation (H MODE), slice width (ROW(5)), and position (10 to 12), 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

A table listing the total counts for each cell position of the slice is punched on paper tape. To obtain a punched table of slice data, type,

```
PU<CR>
```

on the terminal. 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 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,

```
PS<CR>
```

on the terminal. 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 scintillation camera may affect the accuracy of the data transmitted to the A/D Converter. These irregularities can be compensated for by developing a flood correction matrix to use in correcting the displayed or stored patient study data. A flood correction has three parts:

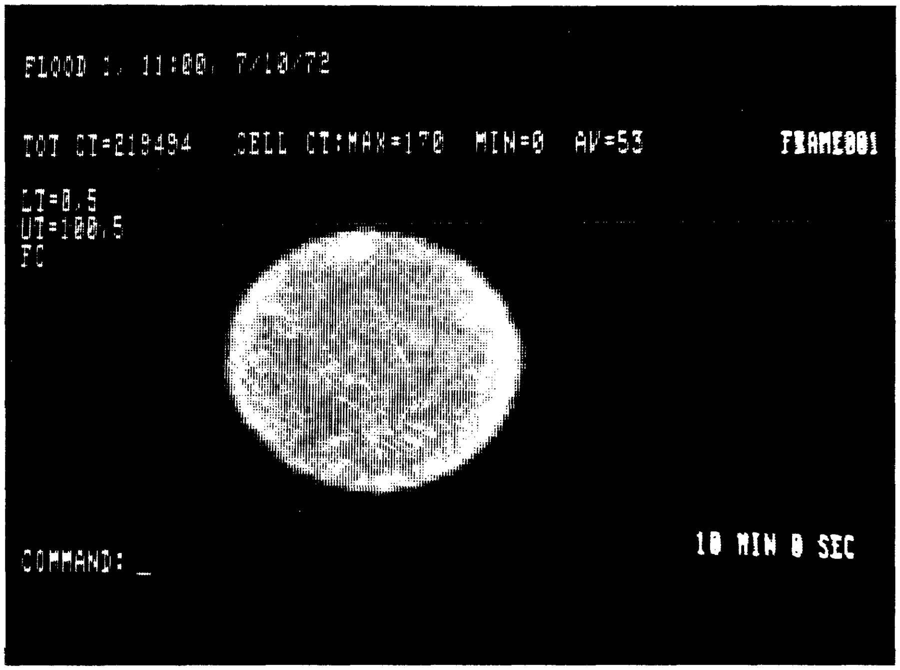
1. Acquiring a Flood study. This process is described in Section 4.4.
2. Converting the Flood study data into a flood correction matrix.
3. Correcting displayed or stored data, using the flood correction matrix.

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 requisite 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.



```
FLOOD 1, 11:00, 7/10/72

TOT CT=219494   CELL CT:MAX=170  MIN=0  AV=53          FRAME001

LT=0.5
UT=100.5
FC



                                               10 MIN 0 SEC
COMMAND: _
```

Figure 9-1
Flood Study Matrix

To create a flood correction matrix:

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

9.2 FLOOD CORRECTION COMMAND

The Flood Correction command converts data from a Flood study frame into a flood correction matrix.

Command Format:

```
FC n,m<CR>
```

where n is a Save Area, 1-64, and m is the percentage of cutoff from 0-100%. The cutoff, m, is a percentage of the calculated average count. Either argument, n or m, may 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, the space ~~between the command and the first argument must always be typed.~~ The form FCn,m is not permitted. The following forms are acceptable:

```
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%)
```

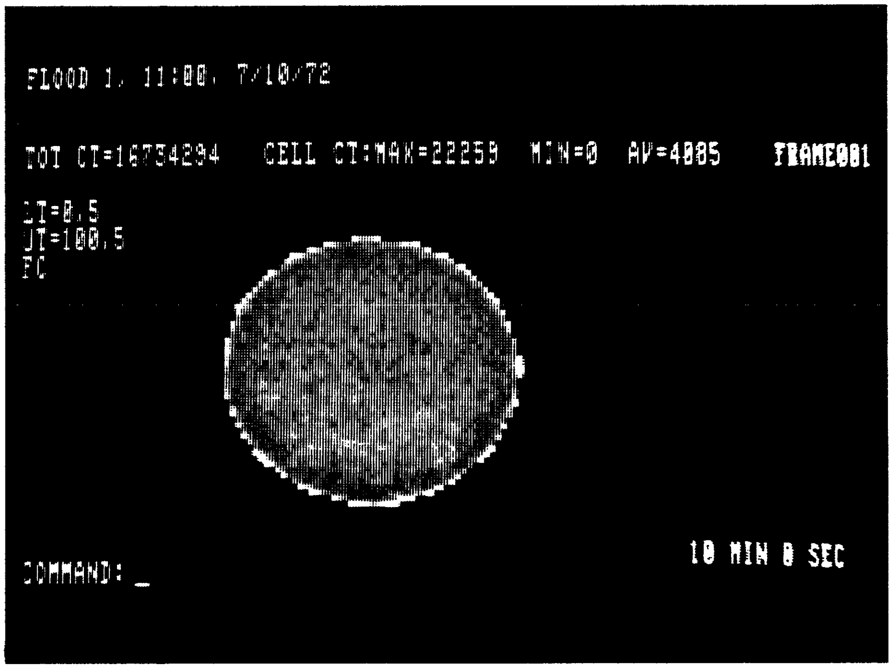
9.3 CONVERTING A FLOOD STUDY FRAME

The Flood study frame is converted 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.



```
FLOOD 1, 11:00, 7/10/72

TOT CT=16734294   CELL CT:MAX=22259  MIN=0  AV=4085    FRAME001
LT=0.5
UT=100.5
FC

                                                   10 MIN 0 SEC
COMMAND: _
```

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 signalled by messages displayed below the word "COMMAND:". In each case, the input is rejected, and the request "COMMAND:" is redisplayed below the error message.

INVALID CHARACTER	In the arguments n and m, the program detected a character other than a digit, space, comma, or <CR>.
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 which is neither

	internally identified as a Flood study, nor of 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. The user should type YES to convert it.
UNDEFINED "FC" COMMAND	A character other than a space or a <CR> 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. 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.

To prepare a flood correction, 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

The correction matrix stored in Save Area n is used to flood-correct the core-resident frame. The disk-resident data are not affected. The command format used to flood-correct the displayed frame (core-resident frame) is

```
FCD n<CR>
```

where n is a Save Area from 1-64. If the orientation and rotation switch settings of the two matrices do not match, the program returns with the message,

```
ROTATION AND ORIENTATION SWITCHES DIFFER
```

displayed on the screen.

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

The correction matrix in Save Area n is used to correct each frame of the current study. The resulting data replaces the original data in the disk file. Because of this, a confirmation process is required. The command format used to flood-correct a study is:

```
FCS n<CR>
```

where n is a Save Area from 1-64. After the FCS command is typed, 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 NO is typed, the procedure is terminated. If YES is typed, 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 is issued. If the rotation and orientation switches match, the message,

```
FINAL CONFIRMATION
REPLY (YES OR NO):
```

is displayed. To begin the flood correction, type YES.

Once the flood correction begins, it requires about one second per frame. When it is complete, the original core-resident frame is displayed. Note, however, that it 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 (if an FCD command) or study (if FCS) 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 <CR>.
INVALID FC COMMAND	A character other than a D or an S appeared as the third character of the command. (Note, 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 <CR>.)
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 matrixed 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, as this does not destroy the original data.
THIS IS A SAVE AREA, PLEASE "RSO"	FCS command only. An attempt was made to flood-correct a disk-resident study by referencing it through a frame read from a Save Area. This is not possible. 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 "RSO".

9.7 NOTES ON FLOOD CORRECTION

9.7.1 Orientation Matching

The orientation and rotation switches on the scintillation 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 factors, the difference between the averages AV1 and AV2 (see Section 9.3) are 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. This limits the maximum correction factor to 7.77774 (octal), or slightly more than 7.999 (decimal). This in turn implies a minimum cutoff of 13%. A smaller cutoff would result in a factor larger than the limit. Factors equal to or greater than 8 are set to zero.

9.7.3 Cell Overflow

Another potential 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.

Cells that overflow during acquisition cannot be recognized as such by the flood correction routine. They are treated simply as cases of maximum count. If such a cell count is reduced by a correction factor smaller than 1, the result will be too low, as 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 may 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 scintillation camera to reduce irregularities as much as possible, so that flood correction factors are all close to unity.
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 statistical accuracy of the Flood study data and on the uniformity of the radiation source used in the Flood study acquisition. Commercially available sheet sources are generally uniform within + or - 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:

$$PV = 100(N/N)$$
$$= 100/ N$$

and

$$N = 100 /(PV)(PV)$$
$$= 10{,}000/(PV)(PV)$$

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,

$$NTOT = (4096/2)(N) \quad \text{where } N = 10{,}000/(PV)(PV)$$
$$= 2x10 /(PV)(PV)$$

so that the number NTOT required for a given PV is shown in Table 9-1 which follows.

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.

CHAPTER 10

FILE DELETION

DS

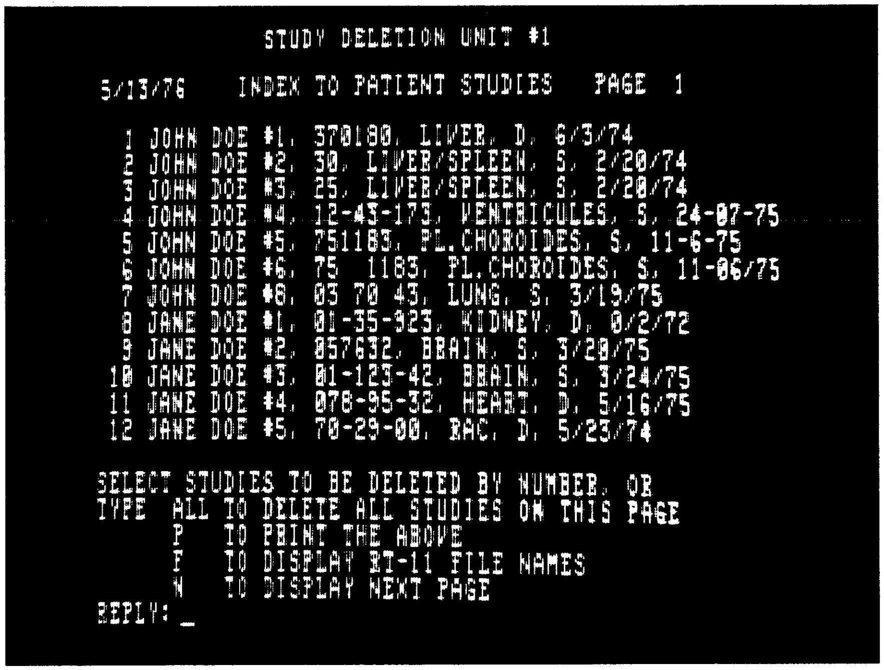
10.1 FILE DELETION

When studies are no longer needed, they can be removed from the Patient File to release space for new studies. To delete studies, type,

```
DS n<CR>
```

where n is an optional disk unit number other than 0.

Immediately, the first page of the Patient Study Index is displayed, with the procedure options at the bottom (Figure 10-1). The user may delete any or all of the studies on the page. Type "ALL" to delete all the studies on the page.



```
                STUDY DELETION UNIT #1

5/13/76    INDEX TO PATIENT STUDIES   PAGE  1

  1 JOHN DOE #1, 370180, LIVER, D, 6/3/74
  2 JOHN DOE #2, 30, LIVER/SPLEEN, S, 2/20/74
  3 JOHN DOE #3, 25, LIVER/SPLEEN, S, 2/20/74
  4 JOHN DOE #4, 12-43-173, VENTRICULES, S, 24-07-75
  5 JOHN DOE #5, 751183, PL.CHOROIDES, S, 11-6-75
  6 JOHN DOE #6, 75  1183, PL.CHOROIDES, S, 11-06/75
  7 JOHN DOE #8, 03 70 43, LUNG, S, 3/19/75
  8 JANE DOE #1, 01-35-923, KIDNEY, D, 0/2/72
  9 JANE DOE #2, 057632, BRAIN, S, 3/20/75
 10 JANE DOE #3, 01-123-42, BRAIN, S, 3/24/75
 11 JANE DOE #4, 078-95-32, HEART, D, 5/16/75
 12 JANE DOE #5, 70-29-00, RAC, D, 5/23/74

SELECT STUDIES TO BE DELETED BY NUMBER, OR
TYPE  ALL TO DELETE ALL STUDIES ON THIS PAGE
      P   TO PRINT THE ABOVE
      F   TO DISPLAY RT-11 FILE NAMES
      N   TO DISPLAY NEXT PAGE
REPLY: _
```

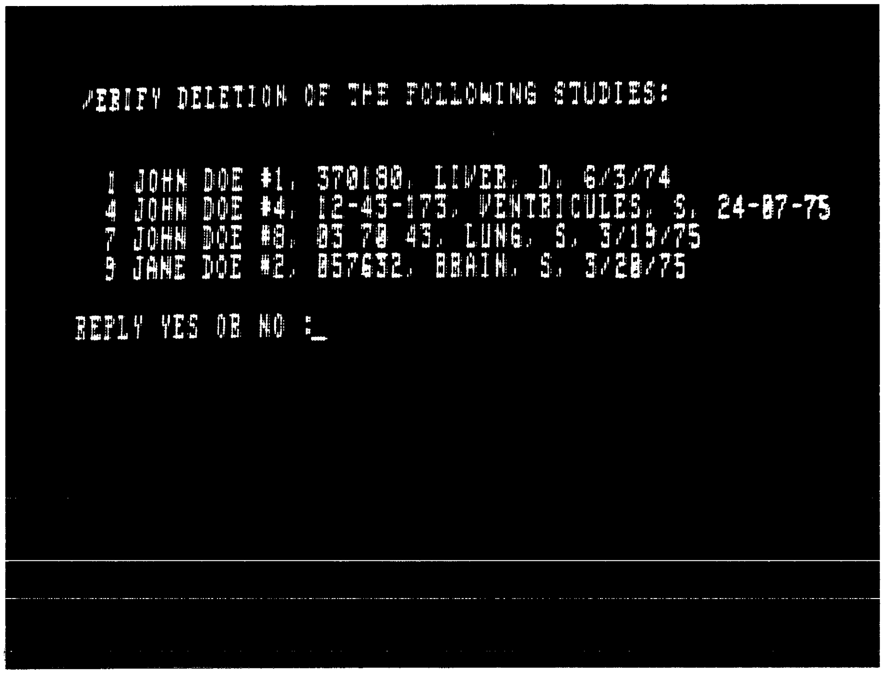
Figure 10-1
Patient Study Index for File Deletion

To delete selected studies, type the index numbers, separated by commas and terminated by an <CR>.

Examples:

5<CR>	Study 5 is to be deleted.
12,3,7<CR>	Studies 12,3,7 are to be deleted.
ALL<CR>	All studies on the displayed page are to be deleted.

After the user has made his selection, the index is erased, and the selected entries are redisplayed for verification (Figure 10-2).



```
VERIFY DELETION OF THE FOLLOWING STUDIES:

  1 JOHN DOE #1, 370180, LIVER, D, 6/3/74
  4 JOHN DOE #4, 12-43-173, VENTRICULES, S, 24-07-75
  7 JOHN DOE #8, 03 70 43, LUNG, S, 3/19/75
  9 JANE DOE #2, 057632, BRAIN, S, 3/20/75

REPLY YES OR NO :_
```

Figure 10-2
Verification Frame

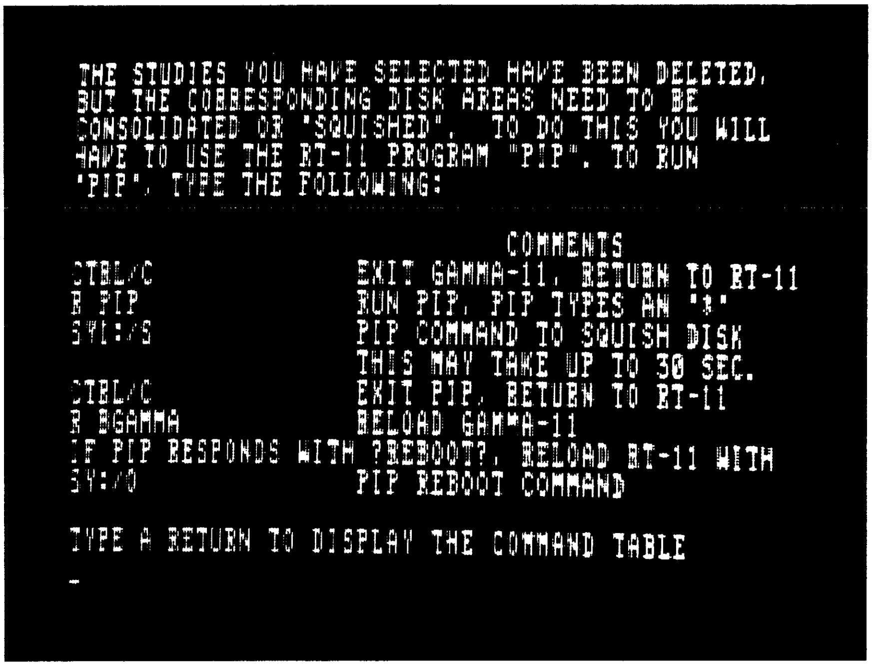
If the user answers "NO", the selection is ignored, and the page of the index is redisplayed. No deletions take place. If the user answers "YES", the message:

DELETIONS UNDER WAY

appears while the file is being deleted. After the selected studies have been deleted, the next page of the index is displayed, by answering the following message,

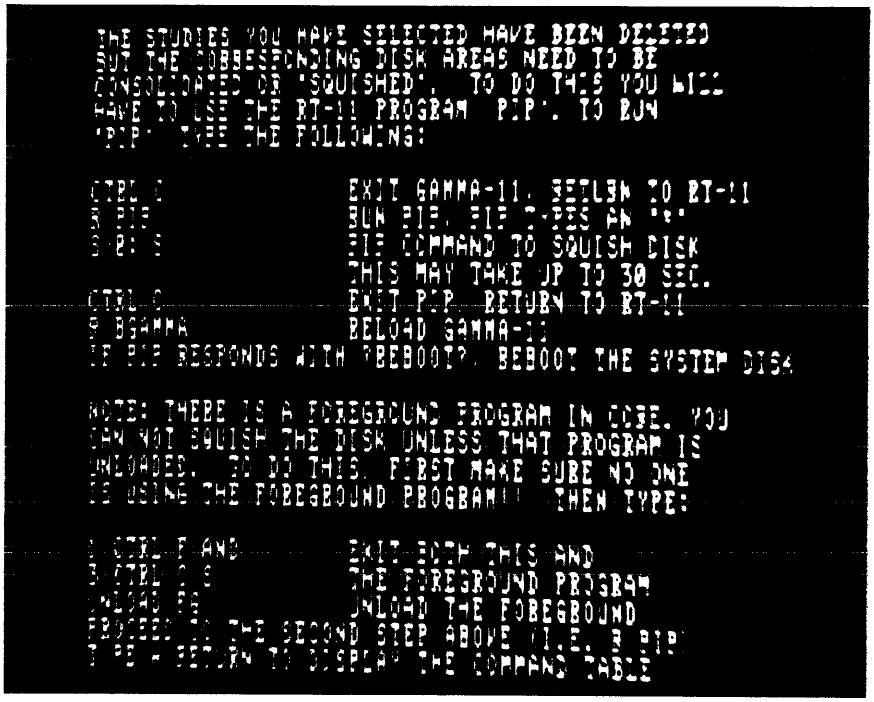
TYPE N FOR THE NEXT PAGE

If the user does not wish to delete any more files or if the last page has been verified and deleted, the user types <CR>. At this point Figure 10-3 appears on the screen only if the foreground is not in use. If the foreground is running, Figure 10-4 is displayed instead of Figure 10-3.



```
THE STUDIES YOU HAVE SELECTED HAVE BEEN DELETED,
BUT THE CORRESPONDING DISK AREAS NEED TO BE
CONSOLIDATED OR "SQUISHED".  TO DO THIS YOU WILL
HAVE TO USE THE RT-11 PROGRAM "PIP". TO RUN
"PIP", TYPE THE FOLLOWING:

                              COMMENTS
CTRL/C               EXIT GAMMA-11, RETURN TO RT-11
R PIP                RUN PIP, PIP TYPES AN "*"
SY:/S                PIP COMMAND TO SQUISH DISK
                     THIS MAY TAKE UP TO 30 SEC.
CTRL/C               EXIT PIP, RETURN TO RT-11
R BGAMMA             RELOAD GAMMA-11
IF PIP RESPONDS WITH ?REBOOT?, RELOAD RT-11 WITH
SY:/O                PIP REBOOT COMMAND

TYPE A RETURN TO DISPLAY THE COMMAND TABLE
_
```

Figure 10-3
Consolidating Disk Without Foreground Present



```
THE STUDIES YOU HAVE SELECTED HAVE BEEN DELETED
BUT THE CORRESPONDING DISK AREAS NEED TO BE
CONSOLIDATED OR "SQUISHED".  TO DO THIS YOU WILL
HAVE TO USE THE RT-11 PROGRAM "PIP". TO RUN
"PIP", TYPE THE FOLLOWING:

CTRL/C               EXIT GAMMA-11, RETURN TO RT-11
R PIP                RUN PIP, PIP TYPES AN "*"
SY:/S                PIP COMMAND TO SQUISH DISK
                     THIS MAY TAKE UP TO 30 SEC.
CTRL/C               EXIT PIP, RETURN TO RT-11
R BGAMMA             RELOAD GAMMA-11
IF PIP RESPONDS WITH ?REBOOT?, REBOOT THE SYSTEM DISK

NOTE: THERE IS A FOREGROUND PROGRAM IN CORE. YOU
CAN NOT SQUISH THE DISK UNLESS THAT PROGRAM IS
UNLOADED.  TO DO THIS, FIRST MAKE SURE NO ONE
IS USING THE FOREGROUND PROGRAM!!  THEN TYPE:

CTRL/F AND           EXIT BOTH THIS AND
2 CTRL/C'S           THE FOREGROUND PROGRAM
UNLOAD FG            UNLOAD THE FOREGROUND
PROCEED TO THE SECOND STEP ABOVE (I.E. R PIP)
TYPE A RETURN TO DISPLAY THE COMMAND TABLE
```

Figure 10-4
Consolidating Disk With Foreground Present

FILE DELETION

When the GAMMA-11 Delete program deletes studies from the disk, it does not consolidate available disk areas into one free area. The ~~RT-11 system program PIP should be used to consolidate (or squish) the~~ disk areas (files). If consolidating is not done, the GAMMA-11 data acquisition program cannot use all of the available disk space for a patient study. Figures 10-3 and 10-4 provide the user with instruction on how to load PIP and squish the disk. The following is an expanded description of this procedure.

Step 1. Under the F/B system there must be no foreground program running when PIP consolidates the disk. Therefore, the user must unload any foreground job before proceeding. To do this,

FIRST MAKE SURE THAT NO ONE IS USING THE FOREGROUND PROGRAM.

Then type CTRL/F and two CTRL/C's to kill the foreground program. Type another CTRL/C to exit from GAMMA-11 and return to the RT-11 Monitor. Next, type,

```
UNLOAD FG<CR>
```

to unload the foregroung program and proceed to STEP 3.

Step 2. If there is no foreground program, type CTRL/C to exit from GAMMA-11 and return to the RT-11 Monitor which outputs a "." (dot).

Step 3. To load PIP, type,

```
R PIP<CR>
```

PIP responds with an "*".

Step 4. To consolidate disk unit n, type,

```
SYn:/S<CR>
```

PIP consolidates (squishes) all the free disk areas into one large free area. This process may take up to 30 seconds.

Step 5. If PIP responds with ?REBOOT?, reboot RT-11 as described in Chapter 3. If PIP does not print ?REBOOT?, type a CTRL/C to return to the RT-11 monitor.

Step 6. Reload the GAMMA-11 programs, FGAMMA and BGAMMA, if desired. That is, type,

```
FRUN FGAMMA
and/or
R BGAMMA
```

CHAPTER 11

STUDY TRANSFERS

The GAMMA-11 Transfer Study program transfers GAMMA-11 patient studies between any RT-11 directoried device. Because magtapes and cassettes 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 the user requests the Transfer Study program, he must enter the source (from) and destination (to) devices. After the user has entered the devices, he selects the transfer of studies analogous to the GAMMA-11 Study Deletion program (see Chapter 10).

11.1 REQUIRED HARDWARE AND SOFTWARE

The Study Transfer program is part of the GAMMA-11 system and therefore requires the same minimum hardware and software as GAMMA-11 and (optionally) one or more additional RT-11 directoried or undirectoried (magtape or cassette) devices.

TS

11.2 STUDY TRANSFER COMMAND

The Study Transfer program is called from the background command table. Type,

```
TS<CR>
```

on the terminal. The optional disk unit number (n), honored by the background command table, is ignored by the Study Transfer program. Once the Study Transfer command has been issued, a list of commonly used RT-11 device mnemonics appear on the screen.

A description of each device and their associated mnemonic name is as follows:

SY	System device
RK	RK05 disk pack
MT	Magtape

DT	DECtape
RF	RF11 fixed head disk
CT	Cassette

The next line:

```
PLEASE ENTER THE SOURCE DEVICE
```

asks the user to enter a source device mnemonic and unit number followed by a carriage return. The mnemonic device name and unit number are optional. If the device mnemonic and the unit number are not specified, the source device, DK (which is normally the device in which the system is booted from), is assumed as the source device. If only a device mnemonic is specified and no unit number, a null is assumed as the unit number. If only a unit number is specified and no device mnemonic, device SY (system device) is assumed as the source device. Examples are,

<CR>	(DK; System device from which RT-11 is booted)
RK<CR>	(RK; disk pack on unit 0)
1<CR>	(SY1; System device on unit 1)
DT0<CR>	(DT; DECtape on unit 0)

If an unacceptable device mnemonic or unit number is entered, the following error message appears on the screen.

```
ILLEGAL RESPONSE, PLEASE TRY AGAIN
```

If the user types a non-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:

```
PLEASE ENTER THE DESTINATION DEVICE
```

asks the user to enter a destination device mnemonic and unit number followed by a carrage return. Both name and number are optional and the same method for defining a destination device applies as it is described for a source device.

If an unacceptable device mnemonic or unit number is entered for a destination device, the same error message appears, however, both source device and destination device must be re-entered.

Also, if two undirectoried devices (i.e., magtape and/or cassette) have been specified, the following error message appears immediately after inputting the second magtape or cassette, and a directoried device as either a source or destination device must be entered.

```
MAGTAPE-CASSETTE BOTH SOURCE AND DESTINATION DEVICE!
```

Once the system has accepted legal source and destination devices, the message,

```
READY THE DEVICES TO START THE TRANSFER
TYPE <CR> TO BEGIN
```

appears on the screen.

Also, 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 message:

```
DEVICE NOT READY!
THE DEVICE IS---, READY IT FOR TRANSFER
TYPE <CR> TO BEGIN
```

appears on the screen. When the devices are ready, Page 1 of the Patient Study Index from the source device is displayed.

NOTE

> Magtapes and cassettes do not display the Index because they are not RT-11 directoried devices. See Section 11.3.

The same options are available for study transfers as displayed during the Study Deletion and Data Analysis programs. These are,

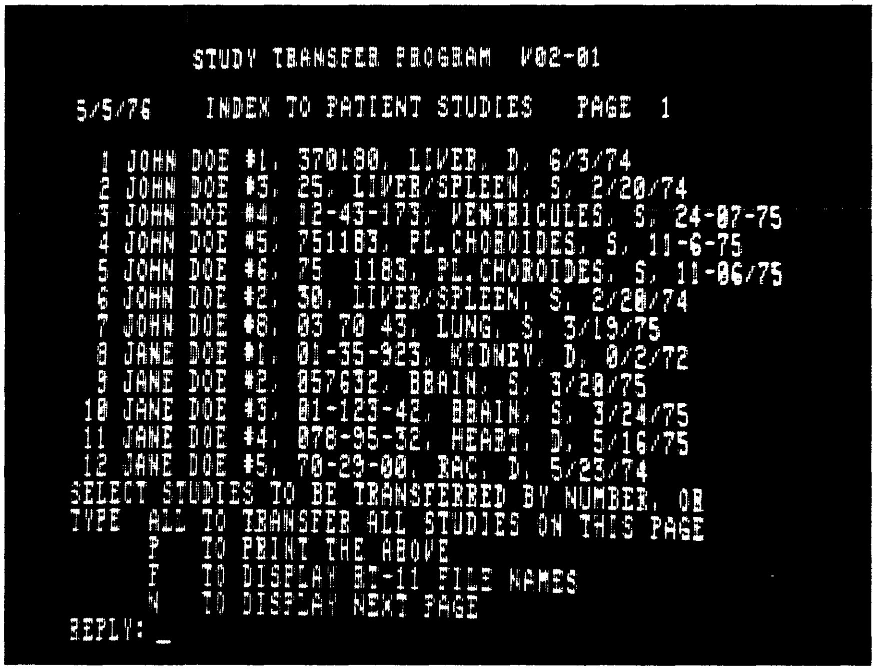
```
SELECT STUDIES TO BE TRANSFERRED BY ENTERING THE INDEX
NUMBERS

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 duplicate entries are entered, they are ignored by the system. If an illegal number is entered (i.e., one that does not exist) the following error message appears:

```
ILLEGAL STUDY NUMBER
```

on the screen. Typing "P" provides the user with a hard copy output of the Patient Index.

Typing "F" displays the Patient Index files with their associated RT-11 filenames. An example of this is shown in Figure 11-1.



```
           STUDY TRANSFER PROGRAM  V02-01

5/5/76    INDEX TO PATIENT STUDIES   PAGE  1

  1 JOHN DOE #1, 370180, LIVER, D, 6/3/74
  2 JOHN DOE #3, 25, LIVER/SPLEEN, S, 2/20/74
  3 JOHN DOE #4, 12-43-173, VENTRICULES, S, 24-07-75
  4 JOHN DOE #5, 751183, PL.CHOROIDES, S, 11-6-75
  5 JOHN DOE #6, 75  1183, PL.CHOROIDES, S, 11-06/75
  6 JOHN DOE #2, 30, LIVER/SPLEEN, S, 2/20/74
  7 JOHN DOE #8, 03 70 43, LUNG, S, 3/19/75
  8 JANE DOE #1, 01-35-923, KIDNEY, D, 0/2/72
  9 JANE DOE #2, 057632, BRAIN, S, 3/20/75
 10 JANE DOE #3, 01-123-42, BRAIN, S, 3/24/75
 11 JANE DOE #4, 078-95-32, HEART, D, 5/16/75
 12 JANE DOE #5, 70-29-00, RAC, D, 5/23/74
SELECT STUDIES TO BE TRANSFERRED BY NUMBER, OR
TYPE  ALL TO TRANSFER ALL STUDIES ON THIS PAGE
       P   TO PRINT THE ABOVE
       F   TO DISPLAY RT-11 FILE NAMES
       N   TO DISPLAY NEXT PAGE
REPLY: _
```

Figure 11-1
Patient Index Files

Typing "N" displays the next page of the Index. That is, patient studies 21-40.

Examples for transferring patient studies are

```
1,2,7,9,14<CR>
2,10,5<CR>
4<CR>
```

After the studies have been selected, the Index line of those studies to be transferred are displayed. At this point, the user is asked to verify the transfer of studies by typing YES<CR>. Any response other than YES causes the Index to be redisplayed, with no transfer taking place.

If the response is YES to the verification question, the destination device is readied for the transfer. The studies are transferred individually in the order specified by the user. If there is no room on the destination device for one of the source files, that particular patient study index line is displayed and the user is 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 free the file 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 will fit on the destination device. If the study does fit 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 PIP and squishing 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.

11.3 MAGTAPE OR CASSETTE AS A SOURCE DEVICE

Magtapes and cassettes as source devices are treated as special cases because they do not have RT-11 directories. If a magtape or cassette is specified as a source device, no index is displayed. Instead, the user is 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 "1" is typed, the Magtape or cassette is scanned and a hard copy of the Patient Index is listed on the terminal and the first 20 patient studies are displayed on the screen. (If more than 20 patients exist on a magtape, the screen erases and displays patients 21-40 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
Magtape 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
      <CR>  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 the user types "NO" or presses <CR>, the next patient index line is displayed and the same questions are asked. This procedure allows the user to step through the tape, a single study at a time, and transfers only those files that the user wishes to transfer.

If the user types a number, the program skips to that study on the tape and displays the index line with options. Thus, if the user knows that a study is further down the tape, he can have the program skip ahead quickly. If a patient index number is entered at a value less than the number displayed an

```
ILLEGAL RESPONSE
REPLY:
```

message appears on the screen. REPLY would be answered with an R (to rewind) or entering the new digit.

Typing "3" (Selectively Choose Index Number) displays:

```
SELECTIVE STEP MODE
CHOOSE THE INDEX NUMBERS YOU WISH TO DISPLAY
(MAXIMUM OF 20)
```

on the screen. The user 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, typing,

```
5,10,3,7,15<CR>
```

on the terminal, 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 with transfer options. Thus, patient index 3 is displayed on the screen with the same options as in the sequential mode.

NOTE

> To leave selective mode, the user must enter R or complete the list of studies chosen for transfer.

11.3.1 Non-GAMMA-11 Files on Cassette or Magtape

If a magtape-cassette contains files other than GAMMA-11 files, these files are identified by an index line of:

```
XXX NOT A GAMMA FILE
```

The user should not attempt transfer of such files since the program ignores such attempts.

11.3.2 Magtape or Cassette as a Destination Device

When a magtape or cassette is used 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 the user does not want this printed out, type a CTRL/O when the printing begins.

When a magtape or cassette is used as a destination device, device full conditions are not detected until the actual transfers take place. Thus, if the magtape 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 <CR>)
```

Transfer of the next study is then attempted.

11.4 ERROR PROCESSING

11.4.1 Input Errors

If an error occurs while reading the administration block of a file, that file is immediately skipped, the user is told of the error, and control is passed to the next file to be transferred.

If any other input error (source device) occurs, the index line of the current study is displayed and the user is asked if he wishes to ignore the errors. If the answer is "YES", the error is ignored. If the user answers anything else, the output file is purged and transfer of the next study commences. If an input error occurs and the user chooses to ignore the error and continue the transfer, the integrity of the transferred data cannot be guaranteed.

11.4.2 Magtape-Cassette Input Errors

Any magtape or cassette input error causes the transfer of data to fail. The RT-11 magtape handler upon receiving a hard error (an error which the system cannot continue with processing) automatically rewinds the tape. Thus, the study transfer program cannot ignore the error and proceed with the transfer. The program repositions the tape at the start of the file and gives the user 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 magtape are not physically removed and they cause input errors if their position on the tape is referenced by the study transfer program.

11.4.3 Output Errors

If an error occurs on the output device (destination), the index line of the current study is displayed, and an attempt is made to purge the current output file. No more transfers are attempted.

11.4.4 Other I/O Errors

Any other types of error (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

The operating procedures for loading and starting RT-11 and GAMMA are outlined below. To load RT-11, see Steps 1-14; and to load GAMMA-11, see Steps 15-17. Only Steps 15-17 need be performed if RT-11 is running.

CAUTION

> Whenever changing system disks, the user MUST start the system again. If the user does 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 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 disk drive door.

6. Set the LOAD/RUN switch on the 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 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 as the starting address in the system.

10. Set the PDP-11 processor SWITCH REGISTER to 777406 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 and prints on the terminal the version number of RT-11.

13. The system responds with the version number of RT-11 and a dot on the console terminal. The user must type the DATE command into the system. The DATE command assigns a date to new patient studies until a new DATE command is issued.

    The form of the command is:

    ```
         DATE dd-mmm-yy
    or
         DAT  dd-mmm-yy
    or
         DAT
    ```

    followed by the <CR> 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. If no arguments are typed in response to the command, the current date is printed.

    Examples:

    If the user wishes to enter the date, April 25, 1976 as the current date for the system, type:

    ```
    DAT 25-APR-76<CR>
    ```

    To have the current date printed by the system, type:

    ```
    DAT<CR>
    25-APR-76      (system response)
    ```

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

14. The system again responds with a dot. Type the TIME command into the system. The TIME command allows the user either to find out the current time of day kept by RT-11 or to enter a new time of day.

    The form of the command is:

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

    followed by the <CR> key, where:

    hh:mm:ss   Represents the hour, minute, and second.

The time is in hours, minutes, and seconds past midnight. If no argument is indicated, the current time of day is output.

Examples:

```
TIME 14:48:32<CR>
```

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

```
TIME<CR>
14:58:36     (system response approximately ten
             minutes later).
```

15. The system again responds with a dot. Next, type RUN BGAMMA<CR> on the terminal to call in GAMMA-11 from the system device.
16. The system responds with the background command table on the Color display (or VT01). (See Section 3.1.1.)
17. The background GAMMA-11 program is now loaded and running.

APPENDIX B

LOADING GAMMA-11 FOR THE FOREGROUND/BACKGROUND USERS

The operating procedures for loading and starting RT-11 and GAMMA are outlined below. To load RT-11 F/B, see Steps 1-14; to load GAMMA-11 (foreground), see Step 15; and to load GAMMA-11 (background), see Steps 16-18.

CAUTION

> Whenever changing system disks, the user MUST start the system again. If the user does 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 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 disk drive door.

6. Set the LOAD/RUN switch on the 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 as indicated in the following diagram. A ↓ (down-arrow) means push up 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 as the starting address in the system.

10. Set the PDP-11 processor SWITCH REGISTER to 777406 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 and prints on the terminal the version number of RT-11.

13. The system responds with the version number of RT-11 and a dot on the console terminal. The user must type the DATE command into the system. The DATE command assigns a date to new patient studies until a new DATE command is issued.

    The form of the command is:

    ```
         DATE  dd-mmm-yy
    or
         DAT   dd-mmm-yy
    or
         DAT
    ```

    followed by the <CR> 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. If no arguments are typed in response to the command, the current date is printed.

    Examples:

    If the user wishes to enter the date, April 25, 1976 as the current date for the system, type:

    ```
    DAT 25-APR-76<CR>
    ```

    To have the current date printed by the system, type:

    ```
    DAT<CR>
    25-APR-76      (System response)
    ```

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

14. The system again responds with a dot. Type the TIME command into the system. The TIME command allows the user either to find out the current time of day kept by RT-11 or to enter a new time of day.

    The form of the command is:

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

    followed by the <CR> key, where:

    hh:mm:ss   Represents the hour, minute, and second.

The time is in hours, minutes, and seconds past midnight. If no argument is indicated, the current time of day is output.

Examples:

```
TIME 16:48:32<CR>
```

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

```
TIME<CR>
16:58:36      (system response approximately ten
              minutes later).
```

15. The system again responds with a dot. Next, type

    ```
    FRUN FGAMMA<CR>
    ```

    on the terminal to call in the foreground for GAMMA-11.

    There is a slight pause and the foreground command table is now present on the VT05. (See Section 3.2.1) The following message is printed on the console:

    ```
    FGAMMA LOADED AND RUNNING
    ```

    Now, FGAMMA no longer references the DECwriter.

16. The system again responds with B> and a dot on the DECwriter. Type,

    ```
    RUN BGAMMA<CR>
    ```

    on the terminal to call in the background for GAMMA-11.

17. The system responds with the background command table on the Color display (or VT01). (See Section 3.1.1.) The commands that have a preceding asterisk are not operable when the foreground is running.

18. The background GAMMA-11 program is now loaded and running.

APPENDIX C

SUMMARY OF COMMANDS

C.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 reviews - (Background only)
CA	Continue analysis - (Background only)
DS	Delete patient studies - (Background only)
TS	Transfer Study - (Background only)

C.2 COMMAND SETS AND SUBSETS

C.2.1 Data Acquisition Commands

The entire procedure is controlled from the keyboard, in response to questions, instructions, or choices appearing on the display screen.

DELETE	Delete line
ESCAPE	Edit page
CTRL/E	Edit and redisplay page

C.2.2 Display and 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/U	Delete current line
RUBOUT	Delete last typed character
CTRL/N	No room for COMMAND; clear screen
<CR>	Restore current frame (after study summary)
Space Bar	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, miniature
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
R0 n	Rotate data

C.2.3 Thresholding Commands

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	Sets upper threshold display switch
U0	Clear upper threshold display switch

W, X, Y, Z, N, O threshold-adjusting commands are effective for both subsets.

C.2.4 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

C.2.5 Frame Algebra Commands

Includes operations to add, subtract, or multiply by a constant; complement a matrix to obtain a "negative" image; combine frames arithmetically; and generate nonlinear images.

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

C.2.6 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.
RS n	Read data from Save Area n.
SD n	Save Dynamic Curve data in Save Area n
SM n	Save matrix data in Save Area n
DS n	Delete Save Area

C.2.7 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

C.2.8 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

C.2.9 Comment Editor Commands

The Comment Editor commands allow the user 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

<CR>	Edit and store text, exit
CTRL/X	Exit immediately
P	Print edits on console

C.2.10 Region of Interest Commands

Areas of varying shape are defined, and the data within them examined. In Dynamic studies, curves can be derived from the data in these regions, in each frame of the study (see Chapter 6).

RI	Enter Region of Interest procedure

The following Region of Interest and Irregular 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
<CR>	Restore original frame
Space	Display next frame
-	Display previous frame

The following Region of Interest and Irregular ROI commands require a terminating carriage return and can be cancelled with CTRL/U.

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

C.2.11 Irregular Region of Interest Commands

Areas of any shape or size, within the boundaries of a matrix, are defined as Irregular Regions of Interest.

IR	Enter Irregular Region of Interest procedure

Irregular ROIs may be defined by means of immediate-effect mode-setting commands. These are

C	Circumference mode
F	Fill mode
B	Boundary display
I	Interior display

C.2.12 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
SV n	Vertical slice
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 C.2.10).

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

C.2.13 Macro Commands

The Data Analysis program has a resident macro buffer for the current macro that the user is using. Macro facilities of the Data Analysis program allows the user to create, edit, execute, save, and retrieve macro files. Commands used to perform these functions are all carriage return terminated.

MC filename	Creates a macro
ME	Edits the contents of a macro buffer
ML filename	Loads a macro buffer
MR filename,n	Executes or runs a macro
MS filename	Saves the current contents of a macro buffer
MD filename	Deletes a macro file from the system device
MX	Stops execution
EL n	Executes one line of a macro buffer
// text	Prints text as a comment

C.2.14 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	BASIC
FO	device:filename.ext	FOCAL
RU	device:filename.ext	FORTRAN

C.2.15 Color Display Commands

The commands described in this section apply only to the Color Display. These commands describe the color tables and their function, 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	Displays an intensity scale bar
NL	Removes the intensity scale bar
CT n	Retrieves a color table
ST n	Saves a color table
CL n,rgb	Changes a color level
ET n	Edits a color table
Z	Zeros a color table
C n,rgb	Changes a color element
I n,rgb	Inserts a color element
D n	Deletes a color level
S n	Saves an edited color table
G n	Gets a color table
IT	Interpolates a display
NT	Turns off an interpolated display
BU	Blows-up (increases) the size of the display
NB	Returns display to normal size
LD	Loads a dual display buffer
LD n	Loads and displays a dual image
DU	Displays the contents of a dual display
DO	Overlays the contents of two display buffers
NU	Display a single image
SW	Swaps the dual displays

C.2.16 Dynamic Playback Commands

The commands described in this section apply only to the Color Display. These commands allow the user to playback patient studies in a "movie-like" manner. The speed and direction of the playback can be controlled by a joystick, or preset to a specified rate, or controlled manually by using the terminal keyboard. These commands are:

PBI name,unit,n,r,max,min	Initializes a playback buffer
PBD name,unit	Deletes a playback buffer
PBS	Stores an image in a playback buffer
PB name,unit	Displays 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

APPENDIX D

LOADING GAMMA-11 ON THE 11/34

The operating procedures for loading and starting RT-11 and GAMMA-11 for the PDP-11/34 are outlined below.

CAUTION

> Whenever changing system disks, the user MUST start the system again. If the user does 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 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 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 BOOT/INIT switch.
8. Four numbers are printed on the terminal followed by a $.
9. Type DK followed by a carriage return.
10. The version number of RT-11 is printed on the terminal.

See steps 13 through 17 of Appendix A to load a single job.

See steps 13 through 18 of Appendix B to load the foreground/background version of GAMMA-11.

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 which 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 which 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 integration over a finite time period of the counts originating in a specific area of the gamma camera crystal.
Collimator	A device /aor producing a beam o/a parallel rays o/a light or other radiation or /aor /aorming an infinitely distant virtual image that can be viewed without parallax.
Command	A user order to a computer system, usually given through a terminal keyboard.

Cursor	Visible pointer to a grid point on a scope.
Dynamic	A condition which does change with respect to time.
Gamma Ray	High energy electro-magnetic radiation.
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 which 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, or 128. 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.
Scintillation	A flash of light produced in a phosphor by an ionization event.
Static	A condition which does not change with respect to time.
Thresholding	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 which 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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