

XTRACT

THE DATA EXTRACTION TOOL
FOR NORLAND DXA DATA

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This guide describes two methods of using the XTRACT program, namely the 'commandline' interface, and the 'graphical' user interface. Detailed information on both interfaces, as well as all other *XTRACT* operations, may be found in the sections listed below:

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INTRODUCTION

Norland densitometry software is designed so that all patient personal and scan data is preserved in an efficient and proprietary format. Special index files provide rapid data retrieval for speedy scan and analysis tasks. The Data XTRACT program (referred to herein as XTRACT) takes advantage of these index files to retrieve patient and scan information without harm to original files. This extracted data is written into new file(s) (named PATIENTS.DBF, SCANS.DBF, and REGIONS.DBF) in a format that is readily accessed by popular database and spreadsheet programs. Data in these newly-created files may then be manipulated in any way desired for such tasks as caseload management, patient mailings, statistical analysis, or other purposes.

NOTE: This guide uses the term 'media' when referring to all types of magnetic storage devices, such as hard drives, floppy diskettes, etc.

Many popular database and spreadsheet programs, such as dBASE and Paradox from Borland, 1-2-3 from Lotus, Excel from Microsoft, Quattro Pro from Novell, popular share-ware programs like PC-FILE from ButtonWare, are able to use XTRACT-created files. Certain database or spreadsheet programs, however, may require that the extracted data files be 'converted'. Utility programs supplied with these programs make the conversion task easy.

PLEASE NOTE: Although XTRACT is a simple program that performs a simple task, XTRACT is not recommended for use by untrained users. XTRACT merely creates a set of data files that may safely be manipulated by third party programs. No other use is intended or recommended.

An understanding of database or spreadsheet principles is a prerequisite for use of XTRACT-created files. This guide is written for an experienced audience and will not attempt to explain how to use the database or spreadsheet program with the XTRACT-created files.

This guide describes two methods of using XTRACT, namely the '**command line**' interface, and the '**graphical user**' interface. The command line interface uses a command and a series of options typed on a single DOS command line. After the line has been typed and the <Enter> key pressed, XTRACT will perform the requested actions. The command line interface is able to be used with both XR and pDEXA® software and is described in detail later in this guide.

The graphical user interface (denoted herein as 'GUI', pronounced "gooey") is a special screen that looks identical to XR and pDEXA® screens and is available within the XR (Version 3.0 or later) and pDEXA® programs. The operator may use this screen to specify the exact patient and scan data that is to be extracted using the mouse and pointer tool. The operator then initiates the extraction process. The GUI interface is also described later in this guide.

INSTALLATION

Ordinarily, XTRACT is pre-installed on your host computer. However, XTRACT software may be easily installed or reinstalled as a DOS operation. The XTRACT Program diskette contains all files needed for installing Norland XTRACT software on your host computer. Please read and follow the instructions listed below to (re)install this software.

To install XTRACT files on your host computer,

- Exit normally from XR or pDEXA® software to the 'C:\>' prompt.
- Insert the XTRACT (388A636) diskette in the 'A' drive.
- From the 'C:\>' prompt, type "A:INSTALL", then press **<Enter>**.

Press **<Enter>** again to continue at the XTRACT Installation screen.

- Press **<Enter>** at the "...CONFIG.SYS..." message to acknowledge any changes made to the CONFIG.SYS file.

Press **<Enter>** at the "...installation complete..." message.

Remove the XTRACT diskette from the 'A' drive and store it in a safe place (perhaps with your pDEXA® or XR software diskettes). XTRACT software files are now loaded on the hard drive.

To activate changes made to the CONFIG.SYS file (if any), press and hold the **<Alt>** and **<Ctrl>** keys, then tap the **** key. The computer will re-boot.

XTRACT installation is now complete. Should you encounter any problems in this installation, please carefully re-read the instructions and perform the installation once again. If you are again unsuccessful, please contact your Norland representative for assistance.

COMMAND LINE INTERFACE

XTRACT commands are accessed by the operator using one of two methods. This section describes the 'command line interface' (used with early versions of XR software) and depends on accurate instructions being added to the DOS command used to invoke the program. The GUI interface is described in a later section. Data file(s) created by XTRACT are identical regardless of which operator interface is used when the same extraction criteria are specified.

Please remember that XTRACT is a simple program that performs a relatively simple task. It was developed after repeated customer requests for an expedient method of patient data manipulation. It is not recommended for use by naive or untrained users. Trained investigators, however, may easily define a data processing protocol, one that can be used by unsophisticated operators using DOS batch files, for example.

Later in this guide, a section entitled *Standard Database Form* describes one specific command line in detail that creates a set of extracted data files that will fulfill most needs we have heard of. Close examination of this section may result in a better understanding of how this command line interface works. When using the command line interface, the operator invokes the XTRACT program from the 'C:\>' prompt, not from within XR software. The program protects previously-extracted data by asking if existing data can be overwritten if such data exists.

Certain database or spreadsheet programs may require that the extracted data files be 'converted'. This conversion should be made using utilities supplied with the programs requiring the conversion and performed after XTRACT has completed its task.

To use XTRACT, simply type one of the XTRACT commands at the 'C:\>' prompt and press <Enter>. The patient records will be located and the requested information extracted and written to the specified files.

NOTE: The XTRACT commands described in this command line interface section require that a PATH be defined to the C:\XR26\BIN or C:\PDEXA\BIN directory. Please use the AUTOEXEC.BAT and CONFIG.SYS files modified by the XTRACT installation software to ensure proper PATH definition.

For ordinary operation, XTRACT expects to find the source patient records in the 'C:\XR26' or 'C:\PDEXA' sub-directory. And it expects to write its data files to the 'current' directory (the DOS directory from which the XTRACT command is invoked). As an operator convenience, though, the XTRACT program may be instructed where to find the patient records and/or where to write its data files.

To use XTRACT,

- Exit normally from the XR or pDEXA® program.
- When the 'C:\>' prompt appears, change to the directory in which the extracted files are to be created.

This directory could be where the spreadsheet or database program

resides. It could also be any existing drive and/or sub-directory. For example, type "**cd \dbase**" and press <Enter>. Subsequent DOS commands will assign the \DBASE directory as the 'current directory'.

- At the DOS 'C:\>' prompt, type the command line. An example of a modest XTRACT command line is seen below:

```
XTRACT -s@SF1 -P@PF1 a:  
d:\xr26
```

Observe that this example XTRACT command is seen in the form:

```
XTRACT [options] [dst] [src]
```

Observe also that the XTRACT command is followed by two [options] (shown as -s@SF1 and -P@PF1). Also shown is a [dst] destination parameter (a:), and a [src] source parameter (d:\xr26). Descriptions and usage instructions for [options], [dst] and [src] are found later in this section.

- Check that all keystrokes are correct, then press <Enter>. The XTRACT program automatically performs its sequence of operations.

XTRACT shows its progress by displaying the number of patient records it has processed based on the selection criteria defined by the command line. When complete, XTRACT will return the DOS prompt.

[options]

The term 'options' refers to letter commands preceded by a hyphen (minus sign). All parameters provided for XTRACT may be seen in a 'help' message, which can be invoked at any DOS prompt.

To obtain an on-screen help message similar to that seen in Figure 1,

- At the 'C:\>' prompt, type the command shown below:

```
xtract ?
```

and press the <Enter> key.

The letters within the '['] brackets on this help screen indicate parameters that may be entered as described later in this section, but are not required for command completion. Note that the brackets '['] themselves are not entered as part of the command, merely the information within the brackets. Please

also note that it is not necessary to use any of the command line parameters shown within [brackets] to create a workable XTRACT command.

NOTE: Rules for entering command lines:

Keystrokes used on the command line may be in either upper or lower case characters (either 'A' or 'a' and '-M' or '-m' is acceptable).

Each [options] command must be separated from adjacent [options] and [dst] or [src] commands by a space (one tap of the space bar).

Examples of command lines given herein are depicted in a way that correctly shows where spaces and commas are used (in a **monospace** font).

```
XTRACT - pDEXA Series Database Extract - v3.1.1 29 July 96
Usage:  XTRACT [options] [dst [src]]
Where:
  dst          = Destination drive and/or path for the .DBF Files
  src          = Source drive and/or path for the pDEXA or XR series files
Options are:
  ?            = This message
  -P[fields]   = Extract listed fields into PATIENTS.DBF (may be @file)
  -S[fields]   = Extract scans and regions into SCANS.DBF
  -R[fields]   = Extract scans into SCANS.DBF and regions into REGIONS.DBF
  -O           = Overwrite existing .DBF files without warning
  -D[yy]ymmdd[@hhmm[ss]] = Select scans taken on or after date/time.
  -M[yy]ymmdd[@hhmm[ss]] = Select data modified on or after date/time.
  -Iidlist     = Only select patients with ID matching "id". "id" may end
                  with "*" or include "?" (may be @file)
  -Nnamelist   = Only select patients with name matching "name". "name"
                  may end with "*" or include "?" (may be @file)
  -Ttypelist   = Only select scans of specified type(s). Valid types are:
    1/7        = AP/Lateral Spine           2/3        = Left/Right Hip
    8/9        = L/R Forearm (XR Comac)      12/13       = Left/Right Forearm (pDEXA)
    14/15      = L/R Forearm (XR HA)         4/10/11     = Pre-v240/DF/NDF Body
    5/6        = Research/Small Sub.(XR)    16/17       = Research/Small Sub.(pDEXA)
```

Figure 1 - On-screen HELP message

The option commands are described as follows:

If the command **XTRACT** is entered all by itself, the program will create one file named **PATIENTS.DBF**, containing patient information extracted for all default fields, in the 'current' directory. The default fields are identified in the **PATIENTS.DBF** listing provided in the *File Structures* section.

[-P]

If the **XTRACT** command line includes a **-P[fields]** option, as in:

XTRACT -Ppat_id,scan_date

for example, **XTRACT** will create one file named **PATIENTS.DBF**, which contains only that patient information extracted using the fields listed in the option. Each listed field must be spelled as shown in the **PATIENTS.DBF** listing provided in the *File Structures* section and must be separated only by a comma (no spaces), as seen above.

To simplify the task of listing all the desired fields, the fields parameter may be replaced with the name of an ASCII text file (please refer to the '@file' technique, described later.)

If **'-P'** alone is entered, the **PATIENTS.DBF** file will contain patient information for all default fields.

[-S]

If the **XTRACT** command line includes a **-S[fields]** option, as in:

XTRACT -Spat_name,scan_date

for example, the program will create the file named **PATIENTS.DBF** (which contains patient information extracted for default or requested fields) and one file named **SCANS.DBF**, which contains only that scan information

extracted using the fields listed in the option. Each listed field must be spelled as shown in the **SCANS.DBF** listing provided in the *File Structures* section and must be separated only by a comma (no spaces), as depicted above.

To simplify the task of listing all the needed fields, the fields parameter may be replaced with the name of an ASCII text file (please refer to the '@file' technique, described later.)

If **'-S'** alone is entered, the **SCANS.DBF** file will contain scan information for all default fields. The default scan fields are identified in the **SCANS.DBF** listing provided in the *File Structures* section.

Region data included in the **SCANS.DBF** file is sorted by region type number, then by region name. If any scans don't have the region type number filled in (which may happen with early XR version records), then the type number is determined from the type text string.

[-R]

If the command **XTRACT** includes a **-R[fields]** option, as in:

XTRACT -Rpat_name,reg_type

XTRACT will create the file named **PATIENTS.DBF** (which contains patient information extracted for default or requested fields), the file named **SCANS.DBF** (which contains scan information extracted for default or requested fields) and one file named **REGIONS.DBF**, which contains only that region information extracted using the fields listed in the option. Each listed field must be spelled as shown in the **REGIONS.DBF** listing provided in the *File Structures* section and must be separated only by a comma (no spaces), as seen above.

The regions are sorted in the REGIONS.DBF file by region type number, then by region name. If any scans don't have the region type number filled in (which may happen with early XR version records), then the type number is determined from the type text string.

To simplify the task of listing all the needed fields, the fields parameter may be replaced with the name of an ASCII text file (please refer to the '@file' technique, described later.)

If '-R' alone is entered, the REGIONS.DBF file will contain region information for all default fields. The default region fields are identified in the REGIONS.DBF listing provided in the *File Structures* section.

[-O]

If the XTRACT command line includes a -O option, as in:

XTRACT -O

XTRACT will overwrite any existing .DBF files without warning you. This option may prove useful in DOS batch files. If the '-o' option is not included, XTRACT will provide warning messages if it finds existing PATIENTS.DBF, SCANS.DBF, or REGIONS.DBF files in the 'current' directory.

[-D]

The -D[yy]yymmdd[@hhmm[ss]] option directs the XTRACT program to create the database file(s) only for scans taken on or after the specified date and/or time.

The first [yy] parameter is an optional century designator, such as '19' or '20'. The date may be entered as -d19910101, specifying 'January 1, 1991'. A two digit year designator may also be used, such as -d910101, again specifying 'January 1, 1991'.

An example of a valid XTRACT command using a '-d' option is:

```
XTRACT -Rpat_name,reg_type  
-d910101
```

For this example line, the REGIONS.DBF file would contain patient name and region type for all region data acquired after January 1, 1991.

The optional '@hhmm[ss]' parameter permits the entry of desired time inclusion criteria. The final [ss] parameter is an optional seconds designator, which permits the inclusion of seconds in the extraction process. These parameters are not mandatory.

An example of a valid date and time option is:

```
XTRACT -d910101@0830
```

which specifies that data is to be extracted only for scans obtained later than 8:30 AM on January 1, 1991.

NOTE: The time option is valid only for scans taken with host software version 3.0 or later. All other records will have zero for the scan time.

[-M]

The -M[yy]yymmdd[@hhmm[ss]] option directs the XTRACT program to create the database file(s) only for scans acquired or modified on or after the specified date and/or time.

NOTE: The '-m' option is valid only for scans taken with host software version 3.0 or later. All other records will have zero for the modification date/time and will not be selected. Use the '-d' option for scans taken with earlier releases of software.

Similar to the '-d' option described earlier, the first [yy] parameter is an optional century designator, the '@hhmm[ss]' is an optional time inclusion criteria, with the final [ss] an optional seconds designator. An example of an '-m' command is:

XTRACT -m950701@1400

which specifies that data is to be extracted only for scans whose analysis was modified after 2:00 PM on July 1, 1995 or for all new scans made after that date/time.

Typical usage of the '-m' option could involve performing an XTRACT without this option to extract all patients and scans. Then periodically perform an XTRACT with this option to extract all patient or scan records which have been added or modified since that original XTRACT.

[-I]

The -Iidlist option directs the XTRACT program to create the database file(s) only for specified patients whose ID matches the 'id' parameter. The @file technique may be used to list the specific ID's desired. For example,

XTRACT -I334567899

directs the XTRACT program to extract data only for the patient whose ID exactly matches "334567899".

XTRACT -I256T,278F

directs XTRACT to extract data only for patients whose ID exactly matches "256T" or "278F".

XTRACT -I334*

directs the XTRACT program to extract data for all patients whose ID begins with "334".

ID's or names may be entered using upper or lower case characters for a successful match. However, any

punctuation (commas, hyphens, etc.) used originally must be included.

The wild card characters "*" and "?" may be used to generalize a word or character search, so it is important that these two characters NOT be used for patient identification. As with customary usage, the "*" wild card character is effective only at the end of the character sequence in which it is used.

[-N]

The -Nnamelist option directs the XTRACT program to create the database file(s) only for specified patients whose name matches the "namelist" parameter. For example, a '-Nsmith' parameter directs the XTRACT program to extract data only for patients whose name matches "SMITH" or "smith", etc. The @file protocol may be used to list the specific names desired. See the NOTE above regarding character case.

[-T]

The -Ttypelist option directs the XTRACT program to create the database file(s) only for the specified scan types. The help message lists the current selection of scan types available. For example, a '-t7' option specifies lateral spine data, a '-t12,13' option specifies left and right pDEXA forearm data.

NOTE: The '-Ttypelist' option requires that all desired scan types be listed on the command line, separated only by commas (no spaces). This means that a request for more than one type will look something like this:

XTRACT -T1,4,13,6.

[dst]

The '[dst]' parameter signifies the destination media drive and/or path XTRACT is to use to store the *.DBF files it creates. For example, '**A:\XRP**' would instruct XTRACT to create the *.DBF files in the 'XRP' sub-directory on the media in the 'A:' drive. This parameter is not needed if the operator wants the files written into the 'current' directory. To speed the extraction process, it is recommended that a hard drive directory be used as the destination. The XTRACTed files may then be copied onto removable media. This technique is especially recommended if the source patient records are extensive.

[src]

The '[src]' parameter signifies the source media drive and/or path XTRACT is to use when locating the index files for pDEXA® or XR data extraction. This parameter is not needed if patient records are kept in the standard locations. The [src] parameter is not recognized unless a [dst] is also specified.

NOTE: XTRACT uses information stored when the host computer is initially powered-up, so be sure to use the AUTOEXEC.BAT and CONFIG.SYS files modified by the XTRACT installation software.

@file

The '@file' technique permits the operator to list all the desired fields, names, or ID's in a separate ASCII text file, created with any DOS text editor program or with a conventional word processing program able to save files as ASCII text. To create an @file list file, merely enter each desired field on a line by itself, then save the file.

For example, field lists can be created as shown below. The fields should be listed in the order you want them to appear in the database analysis report. It is not necessary to use all uppercase letters:

```
PAT_ID
PAT_NAME
ADDR1
ADDR2
HOME PHN
BIRTHDAY
SEX
RACE
NO_SCANS
```

Once created, the list is saved as an ASCII text file. The file name may be as brief as 'PF1' or 'S1.DAT', thus simplifying the command line.

For an example of how this file is used, a command line using the @file technique may look like this:

```
xtract -s@S1.DAT -p@PF1
```

This command would direct XTRACT to select patient data using only the fields listed in the file 'pf1' into a file named PATIENTS.DBF, and the scan data using only the fields listed in the file 's1.dat' into a file named SCANS.DBF.

Putting It All Together

Specific individual [options] for XTRACT were described in the previous section. The following information provides examples of how these options may be combined to perform useful data extractions.

Standard Database Form

This example shows how to create a simple row and column database with one record for each region (such as L2, L3, etc.). To create this database, proceed as follows:

- Create an ASCII text file containing a list of the fields to include in the database.

For example, use the @file technique to create a file with the following line entries:

```
PAT_SEQ_NO
PAT_NAME
PAT_ID
SEX
BIRTHDAY
SCN_SEQ_NO
SCAN_TYPE
SCAN_TYPNO
SCAN_DATE
REG_SEQ
REG_TYPE
REG_T_NO
REG_TBM
REG_TBA
```

This file defines a series of records, each of which contain the patient sequence number, the patient name, the patient ID, and so forth. The field names and types are listed later in this guide.

Save the field list as an ASCII text file with the name 'F1.DAT' in the 'current' directory.

- Perform the data extraction by entering the following command:

```
xtract -r@F1.DAT -sSCN_SEQ_NO -pPAT_SEQ_NO
```

- Carefully check that the command is correctly entered as shown, then press <Enter>.

The XTRACT program will create a REGIONS.DBF file which contains the fields listed in the file F1.DAT, a SCANS.DBF file containing only a scan sequence number, and a PATIENTS.DBF file containing only a patient sequence number.

In actual use, the SCANS.DBF and PATIENTS.DBF files would be deleted since they contain only a placeholder. The data in the REGIONS.DBF file is imported into your application program and manipulated as desired.

This technique yields only that data needed for analysis as data is extracted from all relevant patient, scan, and region records and combined into one file. This eliminates the need for the application program to merge data from two or three files into one.

More Examples

An assortment of sample XTRACT commands is given below. In each case, it may be helpful to compare the way the command appears below with the help message depicted in [Figure 1](#).

XTRACT

Create the file 'PATIENTS.DBF' in the current directory on drive C from the data in the 'C:\XR26\PATIENTS.FIL' or 'C:\PDEXA\PATIENTS.FIL' using the default list of fields for PATIENTS.DBF.

XTRACT ?

Display the on-screen help message (seen in [Figure 1](#)).

XTRACT -S C: A:\XR26

Create the files 'PATIENTS.DBF' and 'SCANS.DBF' in the current directory on drive C from the data in the \XR26 sub-directory on a disk in the 'A:' drive.

**XTRACT -r@R1 -s@S1 A: **

Create the files 'SCANS.DBF', and 'REGIONS.DBF' in the root directory on a disk in the 'A:' drive. Data is selected, based on the region field list found in the 'R1' ASCII file, the scan field list found in the 'S1' file; the R1 and S1 files were created in the 'current' directory using the @file technique.

XTRACT -r@R2 -d931015 -t2,3

Create the files 'PATIENTS.DBF', 'SCANS.DBF', and 'REGIONS.DBF' in the 'current' directory from the patient data in the 'current' patient directory that was acquired on or after October 15, 1993. Further, limit the extraction to those region fields listed in the 'R2' ASCII file and only to Left and Right Hips. This command may be used as an update operation, since data prior to October 15, 1993 may have been exported for a previous report.

XTRACT -s@S2 -n#L* D:\DB4

Create the files 'PATIENTS.DBF' and 'SCANS.DBF' in the D:\DB4 sub-directory from the data in the 'current' patient directory. Data is selected from those fields listed in the 'S2' file and extracted only for those patients whose name begins with the characters '#L'.

This example illustrates a method for defining subject names for a particular study by using the symbol '#' as the subject name first character and denoting handedness (L or R) with the subject name second character. Therefore, this search would select fields for all scans of subjects in the # group that are left-handed. This method may also be used with the '-lidlist' parameter, with similar characters or letters used to designate membership in a particular study group.

XTRACT -R -T13 D: A:

Create the files 'PATIENTS.DBF', 'SCANS.DBF', and 'REGIONS.DBF' on the 'D:' drive for all right forearm pDEXA scan data found on the 'A:' drive.

Error Messages

In most cases, the message “dBase files have been created successfully” will appear on the computer screen at the completion of XTRACT processing. This message means that the requested command was successfully completed, including creation of the desired *.DBF files. However, certain conditions may cause the appearance of an error message or the reappearance of the on-screen help message.

The following error messages include suggestions for resolving the problems. In most cases, the problem that caused the error is displayed. Carefully reenter the XTRACT command and verify that each keystroke is correct before pressing the <Enter> key.

Output file filename exists. Overwrite?

XTRACT has detected the presence of one of the *.DBF files it needs to create.

To preserve the existing files, press the 'N' key, then the <Enter> key. The 'Operation Terminated' message appears, as does the DOS prompt. Either rename the existing files or specify an alternate [dst] or drive.

To permit XTRACT to overwrite the existing files, press the 'Y' key, then the <Enter> key. The program will continue to completion. To automatically overwrite the *.DBF files if you use this command in a batch file, make sure you add the [-o] option to the command line.

Cannot open {filename}

Cannot write to *.DBF

Cannot read *.FIL

For these error messages, XTRACT could not locate a file it needs to complete its processing. Check to be sure the correct [src] was entered or that the installation-modified AUTOEXEC.BAT and CONFIG.SYS files were used to

'boot' the host computer. It is also possible that patient and scan records may be corrupted, so you may need to review the Operator's Guide chapters on XR or pDEXA® file system integrity.

Out of memory

Cannot update .DBF header in PATIENTS.FIL

Other possible errors could result if the destination disk is write protected or if the destination disk does not have enough space to store the XTRACT-generated files.

Invalid '-P' parameter

Invalid '-S' parameter

Invalid '-R' parameter

For these and similar option specification error messages, XTRACT could not complete the data processing because one of the option parameters was incorrect. Review the command line and correct the error specified by the error message.

IMPORTANT NOTE: In the event of any error, please carefully re-enter the command line and verify that each keystroke is correct before pressing the <Enter> key. If the error persists and you cannot resolve it yourself, make careful notes of the screen messages (do a 'print screen'), then contact your local Norland Customer Service provider.

'On-Line Documentation'

When XTRACT was installed on the host computer, an ASCII text file named XTRACT.DOC was copied into the c:\xr26\doc\orc\pdexa\doc\ subdirectory. This file provides much of the information seen in this Operator's Guide, and is updated with each software release. The file may be viewed and/or printed using your favorite text editor.

GUI INTERFACE

XTRACT commands are accessed by the operator using one of two methods. This section describes the Graphical User Interface (GUI) method, as supplied currently with Norland pDEXA® systems and with XR v3.0 and later software. The other (command line) interface was described previously. Data file(s) created by XTRACT are identical regardless of which operator interface is used when the same extraction criteria are specified.

For ordinary GUI operation, XTRACT expects to find the source patient files in the same sub-directory as the XR or pDEXA program. And it expects to write the extracted data files to the same directory. However, XTRACT may be instructed where to find the patient files and/or where to write the extracted data files. XTRACT may also be instructed to extract specific data, such as that data created or modified for specific patients or patient I.D.'s. Output files may also be

customized to contain only that data required by the user.

To use the GUI operator interface for XTRACT processes,

- Select **Disk** from the Main Menu.
Click on **Database Extract**.

A screen similar to that seen below in [Figure 2](#) appears.

Selecting Parameters

The upper box shown in [Figure 2](#) provides a means for the operator to instruct XTRACT where to find the patient data, the specific patient name or I.D. information, Scan Type(s), and date and time requirements.

The lower box permits the operator to instruct XTRACT which output files to create, where to store the newly-created data files, to choose the desired fields to be included in the output files, and to select an overwrite warning.

XTRACT - Database Extraction Utility

Source Directory: C:\PDEXA

Patient Names: Patient IDs:

1: 1:

2: 2:

3: 3:

4: 4:

Use data ☐ created ☒ modified after

date __/__/__ and time __:__

Scan Type(s):

L Forearm HA R Forearm HA

Output Directory: C:\PDEXA

Output: ☒ PATIENTS.DBF ☒ SCANS.DBF ☒ REGIONS.DBF

Overwrite Warning: ☒ Enabled ☐ Disabled

Choose Fields: ☐ PATIENTS.DBF ☐ SCANS.DBF ☐ REGIONS.DBF

Figure 2- XTRACT input screen showing default pDEXA® values.

Source Directory

In the upper box, the *Source Directory* parameter designates the media drive and path XTRACT is to use to find the index files needed for data extraction. This parameter defaults to the same directory used by the main program. For example, enter "A:\PDEXA", and XTRACT will use the A:\PDEXA directory as the source drive and directory.

Patient Name/ID

The desired *Patient Names*: and *Patient IDs*: parameters may be used to specify specific patients or study subjects for data extraction. Use the pointer to select a field, then enter the desired patient name and/or ID information.

Wild cards may also be used. For example, entering '**gre***' in the #1: *Patient Names* field forces XTRACT to select all patients whose first three characters match 'gre', in either upper or lowercase letters. Similarly, entering '**?33**' in the #1 *Patient IDs* field forces XTRACT to select all patients whose ID begins with any letter or character and '33'. All four sets of Names and IDs may be used. If no names or IDs are entered, data for all patients will be extracted.

A note for Boolean Algebra fans: selecting more than one name field uses the logical 'OR' of the lists - selecting more than one option field (name and ID fields, for example) uses the logical 'AND' of the lists.

Create/Modify

This parameter permits the operator to instruct XTRACT to use only data that was **created** after the specified date or

time or to use data newly acquired or **modified** after the specified date or time. This choice may be used, for example, to create a list of all patients who have been reanalyzed after a certain date or time.

Date/Time

In conjunction with the created and modified parameters, **date** and **time** parameters direct the XTRACT program to originate database file(s) only for scans taken on or after the specified date or time. For example, entering '**01/01/96**' for date directs XTRACT to ignore all patient scan data created or modified before January 1, 1996 when producing its *.DBF files.

Scan Type

Selection of specific scan type parameters causes the XTRACT program to create the database file(s) only for the selected scan type(s). For example, clicking on [**L F Arm H**] forces XTRACT to create *.DBF files only for left forearm scans, clicking on [**Right Hip**] forces XTRACT to create *.DBF files only for right hip scans.

Output Directory

In the lower box, the *Output Directory* parameter designates the media drive and path XTRACT is to use to store the files it creates. For example, enter "C:\DBASE", and XTRACT will use the C:\DBASE directory as the target or destination directory. Similarly, 'A:\STUDY1' would instruct XTRACT to create the *.DBF files in the 'STUDY1' sub-directory on the media in the 'A:' drive.

Output File Creation

Up to three ***.DBF** files are created by XTRACT. Each file contains the requested data in a form directly compatible with many database and spreadsheet programs. The operator may select the fields to be included in the file(s), as described later in *Choose Fields*. The exact composition of each of these files is described later in *File Structures*.

- If **[PATIENTS.DBF]** is selected, the program will create one file named PATIENTS.DBF, which contains the extracted patient information.
- If **[SCANS.DBF]** is selected, the program will create the same PATIENTS.DBF file, and another separate file named SCANS.DBF, which contains scan and summary region information. Note that the **[PATIENTS.DBF]** button will also be highlighted.
- If **[REGIONS.DBF]** is selected, the program creates the same PATIENTS.DBF file, a smaller SCANS.DBF file, and a third file named REGIONS.DBF, which contains only region information. The SCANS.DBF file will not include any region information. Note that the **[PATIENTS.DBF]** and **[SCANS.DBF]** buttons will also be highlighted.

Overwrite Warning

The *.DBF files created in the Output Directory each time XTRACT is invoked may or may not need to be protected. The program can be directed to ignore the presence of previously-generated *.DBF files, thus overwriting them when new files are created.

To 'turn-off' the generation of overwrite warning messages,

- Click on **[Disabled]**.

The program will overwrite existing *.DBF files without generating any warnings.

The program can also be directed to present warning messages if previously-generated *.DBF files exist when the new files are created.

To force XTRACT to generate overwrite warning messages,

- Click on **[Enabled]**.

During subsequent XTRACT operation, if the message "Output file filename exists. Overwrite?" appears, one or more of the *.DBF files it needs to create already exists in the Output Directory.

To permit XTRACT to overwrite the existing file(s) respond to the screen message by pressing the 'Y' key, then the **<Enter>** key. The program will continue to completion.

To preserve the existing file(s), press the 'N' key, then the **<Enter>** key. The 'Operation Terminated' message appears, and pDEXA® restarts. The solution is to rename the existing files, move them to another sub-directory, or specify an alternate output directory.

Choose Fields

The operator may direct XTRACT to create its data files containing the default fields, or may select only those files required for further analysis or use.

To choose the desired Scan data fields, for example,

- Click on [SCANS.DBF].

The screen seen in Figure 3 appears. The highlighted fields are the default fields that would be included if the XTRACT operation were to proceed at this point.

Figure 4 depicts the upper portion of the screen that appears if [PATIENTS.DBF] is selected. The same five control buttons appear at the bottom of the screen as seen in Figure 3.

Similarly, Figure 5 on the next page depicts a typical screen which appears if [REGIONS.DBF] (and [SCANS.DBF]) is selected. The same five control buttons appear at the bottom of the screen as seen in Figure 3.

- If only the default fields are required for the intended purpose, simply click on [Default].
- If most of the fields are required for the intended purpose, click on [Select All]. Then click once on each field you do not need, which de-selects that field.
- If only a few fields are required for the intended purpose, click on [Select None]. The highlight is removed from all field names. Then click once on each desired field to select it.

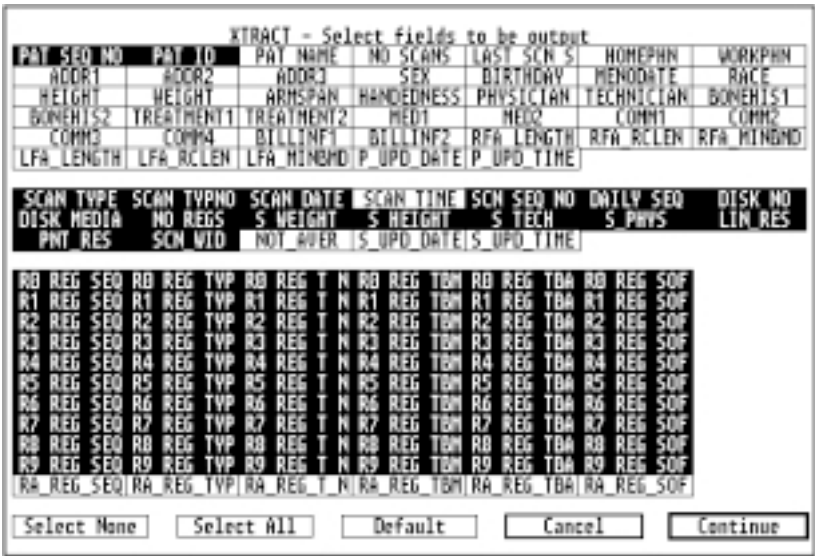


Figure 3 - SCANS.DBF XTRACT - Select fields to be output screen showing the default extraction fields.



Figure 4 - PATIENTS.DBF XTRACT - Select fields to be output screen showing the default extraction fields.

After all desired fields are highlighted,

- Click on **[Continue]** to complete the field selection process.

Or click on **[Cancel]** to abandon the selection process.

The XTRACT screen seen earlier in [Figure 2](#) reappears.

Setup Files

XTRACT permits the operator to save all the XTRACT setup information selected in the GUI interface in a file that can be recalled on demand. This operation will save time if a similar data extraction is to be performed at a later date. Except for the file extension (.XTR), each setup file may be saved with a unique name, perhaps corresponding to its intended use. For example, the name 'JONES.XTR' could be used to save setup parameters for extracting all data needed by Dr. Jones. Or 'R334A.XTR', for example, could be used to save XTRACT parameters relevant to research protocol 334, first iteration.

To save all of the presently-defined XTRACT parameters,

- Click on **[Save Setup]**.

An information box similar to [Figure 6](#) appears asking for a name for the XTRACT parameters file. Enter up to eight keyboard characters as the file name. Make sure the file extension (.XTR) is present in the name.

Click on **[Continue]** to store the parameters.

Click on **[Cancel]** to abandon the process.

To recall and use a previously-saved XTRACT parameter file,

- Click on **Load Setup**.

Verify the correct name is shown, similar to that seen in [Figure 6](#), and that the file extension (.XTR) is present.

Click on **[Continue]** to recall the parameters.

Click on **[Cancel]** to abandon the process.

XTRACT - Select fields to be output

PAT SEQ NO	PAT ID	PAT NAME	NO SCANS	LAST SCN S	HOMEPHN	WORKPHN
ADDR1	ADDR2	ADDR3	SEX	BIRTHDAY	MEMO DATE	RACE
HEIGHT	WEIGHT	ARMSPAN	HANDEDNESS	PHYSICIAN	TECHNICIAN	BONERIST
BONERIS2	TREATMENT1	TREATMENT2	MED1	MED2	COMM1	COMM2
COMM3	COMM4	BILLINF1	BILLINF2	RFA LENGTH	RFA RCLEN	RFA MINOMD
LFA LENGTH	LFA RCLEN	LFA MINOMD	P UPD DATE	P UPD TIME		

SCAN TYPE	SCAN TYPNO	SCAN DATE	SCAN TIME	SCN SEQ NO	DAILY SEQ	DISK NO
DISK MEDIA	NO REGS	S WEIGHT	S HEIGHT	S TECH	S PHVS	LIN RES
PNT RES	SCN WID	NOT AVER	S_UPD DATE	S_UPD TIME		

REG SEQ	REG TYPE	REG T NO	REG SHAP	REG PTO	REG LNO
REG PT1	REG LN1	REG PT2	REG LN2	REG PT3	REG LN3
REG TBM	REG TBN	REG SOFT			

[Figure 5](#) - REGIONS.DBF XTRACT - Select fields to be output screen showing the default extraction fields.

Please enter the name of the XTRACT parameters file.

C:\PDEXA\PARAMS.XTR

Continue **Cancel**

[Figure 6](#) - Setup File name screen.

XTRACT Execution

To initiate the XTRACT operation from the GUI interface screen,

- Check that all keystroke entries and field selections are as desired.

Press **<Enter>** or click on **[Continue]**.

XTRACT automatically performs its sequence of operations.

Or click on **[Cancel]** to abandon the process.

The message “dBase files have been created successfully” will briefly appear on the computer screen as the XTRACT program ends. This message means that all the requested XTRACT commands were successfully completed and the *.DBF files were created.

If a different message appeared, a problem may have been encountered during XTRACT operation. Such problems may be discovered when using the generated data with the application program. Resolve such problems by selecting a different set of extraction parameters and re-generate the *.DBF files. It may be helpful to **Enable** the *Overwrite Warning* messages. Should repeated problems occur, please make careful notes of any screen messages, then contact your local Norland Representative.

FILE STRUCTURES

Regardless of the operator interface used, XTRACT will create one, two, or all three *.DBF files each time it is invoked. A description of the records and fields in each of these files is presented in this section, as well as examples of the file contents.

NOTE: Because the XTRACT program has evolved over the product life of XR software, certain fields and parameters may not exist in early sets of patient records. Extraction of data from these early files is permitted, but certain fields in the *.DBF files (namely date fields) may be filled with zeros after the XTRACT operation. If it is required that valid data exist in all fields you wish to use, it is necessary to re-analyze the patient records with Version 3.0 or later software. When stored after re-analysis, all currently-used fields will be filled with appropriate data.

Patients File

The file created by XTRACT named "PATIENTS.DBF" typically contains patient information. The field types, widths, and contents available for use in all XTRACT-created files are listed in the following table (where N=numeric data, C=character data, D=date as YYYYMMDD). When a decimal value appears in the *Width* column, the field includes the specified number of decimal places. For example, a *Width* value of '6.2' means there is space reserved for three integer digits, a decimal point, and two decimal digits, for a total of 6 characters in the field. A ❖ symbol in the *Def?* column indicates the field is one of the default PATIENTS.DBF fields:

FieldName	Type	Width	Def?	Description
PAT_SEQ_NO	N	5	❖	Patient's unique sequence number
PAT_ID	C	12	❖	Patient's unique ID number
PAT_NAME	C	22	❖	Patient's name
NO_SCANS	N	5	❖	Number of patient scans
LAST_SCN_S	N	5		Seq. # of patient's last scan
HOMEPHN	C	12	❖	Patient's home phone number
WORKPHN	C	12	❖	Patient's work phone number
ADDR1	C	35	❖	Line 1 of the patient's address
ADDR2	C	35	❖	Line 2 of the patient's address
ADDR3	C	35	❖	Line 3 of the patient's address
SEX	C	1	❖	Patient's gender
BIRTHDAY	D	8	❖	Date of birth
MENODATE	D	8	❖	Menopause onset year
RACE	C	9	❖	Patient's ethnicity
HEIGHT	C	5	❖	Patient's height
WEIGHT	C	5	❖	Patient's weight
ARMSPAN	C	7	❖	Patient's arm span
HANDEDNESS	C	1	❖	Dominant hand (not used)
PHYSICIAN	C	20	❖	Physician name or ID
TECHNICIAN	C	20	❖	Technician name or ID
BONEHIS1	C	22	❖	Bone history comment line 1
BONEHIS2	C	35	❖	Bone history comment line 2
TREATMENT1	C	25	❖	Treatment comment line 1
TREATMENT2	C	35	❖	Treatment comment line 2
MED1	C	17	❖	Medication comment line 1
MED2	C	35	❖	Medication comment line 2
COMM1	C	26	❖	General comment line 1
COMM2	C	35	❖	General comment line 2
COMM3	C	35	❖	General comment line 3
COMM4	C	35	❖	General comment line 4
BILLINF1	C	15	❖	Billing info. line 1
BILLINF2	C	35	❖	Billing info. line 2
RFA_LENGTH	N	5		Right forearm length
RFA_RCLN	N	5		Recomputed right forearm length
RFA_MINBMD	N	6.2		Right forearm min. BMD
LFA_LENGTH	N	5		Left forearm length
LFA_RCLN	N	5		Recomputed left forearm length
LFA_MINBMD	N	6.2		Left forearm min. BMD
P_UPD_DATE	D	8		Date patient record was updated last
P_UPD_TIME	N	6		Time patient record was updated last

PATIENTS.DBF Example Listing

An extract from an example PATIENTS.DBF data listing is seen below in Figure 7. Note that the data appears in a columnar array, with column widths arbitrarily set here for readability (the author used Microsoft Excel to create these example listings). This file was created with the XTRACT command “**XTRACT -o**”.

PAT_SEQ_NO	PAT_ID	PAT_NAME	NO_SCANS	HOMER IN	WORK IN	ADDR1	ADDR2	ADDR3	SEX
23	433-24-9118	Arthur, Bea	4	123-333-3214		W5238 Randolph Drive	Jamestown, PA 20456		F
17	Lateral A	Betty Smith	1						F
16	Forearm	Betty Smith	1						F
19	Hip Scan A	Bonnie Smith	1						F
18	AP Spine A	Bonnie Smith	1	414-563-8456	414-563-8456	5835 Sunset Lane	Lake Wabegone, MN 66616		F
20	5236	Nelson, Mary	2						F
21	523	Payne, Rhoda	1						F
24	201-44-3950	SMITH, MATILDA	4	312-456-3211		541 Mountain Jack	Apache, Washington		F
22	443-04-3333	Todd, Michael	1	444-333-1122	444-333-3344	1234 Center Street	Centerville, OH 44566		M
25	303-04-0277	Wendell, Betty	1						F

BIRTHDAY	MENODATE	RACE	HEIGHT	WEIGHT	ARMSPAN	HANDEDNESS	PHYSICIAN	TECHNICIAN	BONEHS1	BONEHS2
2/22/28	1/1/00	Caucasian	5'2"	125						
10/23/44	1/1/00	Caucasian	5'6"	125						
10/23/45	1/1/00	Caucasian	5'6"	125						
10/23/44	1/1/00	Caucasian	5'6"	125						
10/23/44	1/1/47	Caucasian	5'6"	130			T. Sanchez	K. Nelson	No bone disease.	
10/23/40	1/1/00	Caucasian	6'	180			KN	HN		
10/23/45	1/1/00	Caucasian	6'	180						
11/10/35	1/1/84	Caucasian	168cm	***	167cm		NV Sanchez	TV Sanchez	As noted in clinic	files.
10/15/60	1/1/00	Caucasian	6'0"	152						
3/3/30	1/1/00	Caucasian	6'5"	115#			Smith	Wilson		

TREATMENT1	TREATMENT2	MED1	MED2	COMM1	COMM2	COMM3	COMM4	BILLINF1	BILLINF2
Estrogen replacement	therapy.	None.		Standard ERT, re-scan	In six months.			General Plan	
		As noted in	clinic central files.					CFTI Program.	

Figure 7- Example listing, PATIENTS.DBF

Scans File

The file created by XTRACT containing scan data is called the 'SCANS.DBF' file. The field types, widths, and contents available for use in the XTRACT-created SCANS.DBF and/or REGIONS.DBF files are listed in the following tables (N= numeric data, C=character data, D=date as YYYYMMDD). When a decimal value appears in the *Width* column, the field includes the specified number of decimal places. For example, a *Width* value of '6.1' means there is space reserved for four integer digits, a decimal point, and one decimal digit, for a total of 6 characters in the field. A ♦ symbol in the *Def?* column indicates the field is one of the so-called default SCANS.DBF fields:

FieldName	Type	Width	Def?	Description
PAT_SEQ_NO	N	5	♦	Same field described in Patients File
PAT_ID	C	12	♦	Same field described in Patients File
SCAN_TYPE	C	10	♦	ASCII text string defining type of scan, where: "Spine" = AP spine scan "LatSpine" = Lateral spine scan "Left Hip" = Left hip scan "Right Hip" = Right hip scan "Body" = Original body scan "DF Body" = Body scan with dynamic filtration "NDF Body" = Body scan without dyn. filt. "LF Forearm" = Left forearm XR (COMAC) scan "RF Forearm" = Right forearm XR (COMAC) scan "LF Arm H" = Left forearm XR (HA) scan "RF Arm H" = Right forearm XR (HA) scan "LF ForearmP" = Left forearm pDEXA scan "RF ForearmP" = Right forearm pDEXA scan Certain scan names are user entered. 'COMAC' denotes COMAC calibration, 'HA' denotes hydroxyapatite calibration
SCAN_TYPNO	N	3	♦	Unique number defining scan type, where "0" = All Rev. 1 scans "1" = Spine scan "2" = Left hip scan "3" = Right hip scan "4" = Body scan "5" = Research scan "6" = Small subject scan "7" = Lateral spine scan "8" = Left forearm XR (COMAC) scan "9" = Right forearm XR (COMAC) scan "10" = Dynamic filter body scan "11" = Non-dynamic filter body scan "12" = Left forearm pDEXA scan "13" = Right forearm pDEXA scan "14" = Left forearm XR (HA) scan "15" = Right forearm XR (HA) scan "16" = pDEXA Research scan "17" = pDEXA Small Subject scan
SCAN_DATE	D	8	♦	Date of the scan: YYYYMMDD
SCAN_TIME	N	6	♦	Time of the scan: HHMMSS
SCN_SEQ_NO	N	5	♦	Unique scan sequence number
DAILY_SEQ	N	3	♦	Daily sequence number (returns to 1 after 255 scans)
DISK_NO	N	5	♦	Volume number or hard disk partition number if DISK_MEDIA is type '10'; Copy disk if DISK_NO is '65535'.

DISK_MEDIA	N	3	❖	Storage media type, where: "10" = Fixed disk "20" = 3 1/2" (1.44MByte) "30" = 5 1/4" (360KByte) "40" = 5 1/4" (1.2MByte) "50" = 3 1/2" (720KByte) "60" = Other removable media
NO_REGS	N	5	❖	Number of regions for the scan. Each octagonal region uses three file system regions for storage.
S_WEIGHT	C	5	❖	Patient's weight, entered at scan time
S_HEIGHT	C	5	❖	Patient's height, entered at scan time
S_TECH	C	20	❖	Scan technician name or ID
S_PHYS	C	20	❖	Scan physician name or ID
LIN_RES	N	6.1	❖	Line resolution in mm/10
PNT_RES	N	6.1	❖	Point resolution in mm/10
SCN_WID	N	6.1	❖	Scan width in mm
NOT_AVER	N	1		1 - Raw data, 0 - Processed data
S_UPD_DATE	D	8		Date scan record last updated: YYYYMMDD
S_UPD_TIME	N	6		Time scan record last updated: HHMMSS
S_HOST-REV	N	1		Host software revision (stored in non-interpreted form)
S_SCNR_ID	C	10		Scan's originating scanner serial number

When the default SCANS.DBF fields are requested (and the '-r' option is not used), additional fields containing the first ten region's information are added to SCANS.DBF. For the sake of brevity, the 'y' in the Field Name listed below will be replaced with the hexadecimal digits '0' to '9' when viewing actual Field Names generated in a SCANS.DBF file. For example, region 1's field names will appear as 'R1_REG_SEQ', 'R1_REG_TYP', region 2's field names will appear as 'R2_REG_SEQ', 'R2_REG_TYP', and so forth.

The NO_REGS value (listed above) specifies the number of groups of these fields that will have real data extracted for each scan. Fields in this group are filled with blanks or zero's when there are less than 10 (hex 'a') regions. Note that none of these fields are added to the SCANS.DBF file when REGIONS.DBF is requested. The three file system regions for an octagonal region will be summarized and fill only one of the groups. See *Regions File* for more elaborate descriptions of these fields.

FieldName	Type	Width	Def?	Description
Ry_REG_SEQ	N	3	❖	Same data described later as REG_SEQ
Ry_REG_TYP	C	10	❖	Same data described later as REG_TYP
Ry_REG_T_N	N	3	❖	Same data described later as REG_T_N
Ry_REG_TBM	N	10.3	❖	Same data described later as REG_TBM
Ry_REG_TBA	N	10.3	❖	Same data described later as REG_TBA
Ry_REG_SOF	N	10.3	❖	Same data described later as REG_SOF
Ry_REG_LEA	N	10.3	❖	Same data described later as REG_LEA

SCANS.DBF Example Listing

An extract from an example SCANS.DBF file is seen below in Figure 8, with column widths arbitrarily set for readability. Although only a portion of the region field data is depicted here, XTRACT will produce eleven sets of data in similar format. This file was created with the XTRACT command "**XTRACT -s**".

PAT_SEQ_NO	PAT_ID	SCAN_TYPE	SCAN_TYPNO	SCAN_DATE	SCN_SEQ_NO	DAILY_SEQ	DISK_NO	DISK_MEDIA	NO_REGS	S_WEIGHT
23	433-24-9118	DF Body	10	12/8/92	1	1	0	10	9	125
23	433-24-9118	DF Body	10	11/19/91	4	1	0	10	9	125
23	433-24-9118	DF Body	10	12/21/90	3	1	0	10	9	125
23	433-24-9118	DF Body	10	10/12/89	2	1	0	10	9	125
17	Lateral A	Lat Spine	7	3/15/92	1	1	0	10	2	
16	Forearm	L Forearm	8	10/10/91	1	1	0	10	4	
19	Hip Scan A	Left Hip	2	3/31/92	1	1	0	10	3	
18	AP Spine A	Spine	1	10/8/91	1	1	0	10	3	
20	5236	DF Body	10	8/2/92	1	1	0	10	9	

S_HEIGHT	S_TECH	S_PHYS	LIN_RES	PNT_RES	SCN_WID	RO_REG_SEQ	RO_REG_TYP	RO_REG_T_N	RO_REG_TBM	RO_REG_TBA
5'2"	Tom V. Sanchez		7.8	2.7	627.2	1	total	13	1950.105	2119.563
5'2"	Tom V. Sanchez		7.8	2.7	627.2	1	total	13	1966.639	2168.226
5'2"	Tom V. Sanchez		7.8	2.7	627.2	9	total	13	1982.807	2129.903
5'2"	Tom V. Sanchez		7.8	2.7	627.2	9	total	13	1989.541	2139.711
			0.5	0.5	80.0	1	lspn L3	17	6.738	9.476
			1.0	1.0	60.0	1	distal	20	1.051	2.228
			0.5	0.5	90.0	1	lorn neck	4	2.850	3.955
			0.5	0.5	80.0	3	vert L2	1	10.179	11.627

RO_REG_SOF	R1_REG_SEQ	R1_REG_TYP	R1_REG_T_N	R1_REG_TBM	R1_REG_TBA	R1_REG_SOF	R2_REG_SEQ	R2_REG_TYP	R2_REG_T_N	
158cm	65272.367	9	head N	24	373.653	229.278	3622.668	8	chest N	25
...	65375.758	9	head N	24	370.519	236.808	3725.189	8	chest N	25
...	65400.414	1	head N	24	375.838	234.139	3734.862	2	chest N	25
...	65316.031	1	head N	24	369.454	232.061	3646.003	2	chest N	25
6'0"	69.955	2	lspn L2	19	6.258	9.556	61.075	0	*NOT USED*	0
6'5"	10.751	3	proximal	21	1.255	1.281	15.041	2	d radius	22
	22.954	2	troch	5	5.777	9.731	109.834	3	wards tri	6
	112.931	2	vert L3	2	10.379	12.411	115.080	1	vert L4	3
	77106.148	9	head N	24	578.935	267.560	6163.760	8	chest N	25
	11.433	3	proximal	21	1.477	1.377	14.369	2	d radius	22
	73571.992	9	head N	24	616.672	285.491	4869.050	8	chest N	25
	600.194	2	vert L3	2	9.233	10.659	593.716	1	vert L4	3
	767.588	2	vert L3	2	8.916	10.747	736.039	1	vert L4	3
	816.235	2	vert L3	2	8.897	10.481	759.383	1	vert L4	3
	880.952	2	vert L3	2	10.785	10.660	829.664	1	vert L4	3
	66602.063	9	head N	24	519.054	266.946	4839.607	8	chest N	25
	62956.836	9	head N	24	425.472	246.077	3359.417	8	chest N	25

R9_REG_TYP	R9_REG_T_N	R9_REG_TBM	R9_REG_TBA	R9_REG_SOF
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000
NOT USED	0	0.000	0.000	0.000

Figure 8 - Example listing, SCANS.DBF

Regions File

The file created by XTRACT containing region data is called the 'REGIONS.DBF' file. The field types, widths, and contents available for use in the XTRACT-created REGIONS.DBF file are listed in the following table (N=numeric data, C=character data). When a decimal value appears in the *Width* column, the field includes the specified number of decimal places. For example, a *Width* value of '5.3' means there is space reserved for one integer digit, a decimal point, and three decimal digits, for a total of 5 characters in the field. A ❖ symbol in the *Def?* column indicates the field is one of the REGIONS.DBF fields made default when both SCANS.DBF and REGIONS.DBF files are requested:

FieldName	Type	Width	Def?	Description
PAT_SEQ_NO	N	5	❖	Same field described in Patients File
PAT_ID	C	12	❖	Same field described in Patients File
SCN_SEQ_NO	N	5	❖	Same field described in Scans File
REG_SEQ	N	3	❖	Unique region sequence number
REG_TYPE	C	10	❖	ASCII text string describing the type of region: "vert L2"=AP spine L2 vertebra "vert L3"=AP spine L3 vertebra "vert L4"=AP spine L4 vertebra "fem neck"=Hip Femoral neck "troch"=Hip Trochanter "wards tri"=Hip Wards triangle "lspn L2"=Lateral spine L2 vertebrae "lspn L3"=Lateral spine L3 vertebrae "lspn L4"=Lateral spine L4 vertebrae "distal"=Distal R+U forearm site "proximal"=Proximal R+U forearm site "d radius"=Distal Radius forearm site "p radius"=Proximal Radius forearm site "findex"=Forearm index "1/20 Len"=IKI region Original Body scan (see Figure 9): "head"=Head "trunk"=Trunk. REV 1 only "pelvis"=Pelvis "legs"=Legs "right arm"=Right arm "left arm"=Left arm "total"=Total "chest"=Chest "abdomen"=Abdomen - Rev. 2.0+later Revision 2.4 and later Body (see Figure 9): "head N"=Head "chest N"=Chest "midriff N"=Midsection "pelvis N"=Pelvis "l leg N"=Left leg "r leg N"=Right leg "l arm N"=Left arm "r arm N"=Right arm Special regions for all scan types are user entered.
REG_T_NO	N	3	❖	Number describing region type: 01=AP Spine, L2 Vertebra 02=AP Spine, L3 Vertebra 03=AP Spine L4 Vertebra 04=Hip, Femoral neck 05=Hip, Trochanter 06=Hip, Wards Triangle

				32=Hip, Femoral shaft
				07=Original Body, Head
				08=Original Body, Trunk (REV 1)
				09=Original Body, Pelvis
				10=Original Body, Legs
				11=Original Body, Right Arm
				12=Original Body, Left Arm
				13=Original Body, Total
				14=Original Body, Non-bone
				15=Original Body, Chest
				16=Revision 2+ Body, Abdomen
				24=Rev. 2.4 Body, Head
				25=Rev. 2.4 Body, Chest
				26=Rev. 2.4 Body, Midriff
				27=Rev. 2.4 Body, Pelvis
				28=Rev. 2.4 Body, Left leg
				29=Rev. 2.4 Body, Right leg
				30=Rev. 2.4 Body, Left arm
				31=Rev. 2.4 Body, Right arm
				17=Lateral Spine L3 vertebrae
				18=Lateral Spine L4 vertebrae
				19=Lateral Spine L2 vertebrae
				20=Forearm Distal R+U site
				21=Forearm Proximal R+U site
				22=Forearm Distal Radius site
				23=Forearm Proximal Radius site
				33=Forearm 1/20 Length site
				255=Special Region
REG_SHAP	N	3	❖	Shape of the region, where: 1=Non-rotated rectangle 2=Rotated rectangle 3=Non-rectangular quadrilateral 4=Triangle 5=Circle 6=Other
Note: Scans taken at Rev. 1 and 2.0 are all shape 1; hips prior to 2.3 are shape 1; hips 2.3 and later are shape 3; body 2.4 and later are shape 6				
REG_PT0	N	3		Integer value for region upper left corner position (used only to re-draw region on bone image.)
REG_LN0	N	3		"
REG_PT1	N	3		" for lower left corner
REG_LN1	N	3		"
REG_PT2	N	3		" for lower right corner
REG_LN2	N	3		"
REG_PT3	N	3		" for upper right corner
REG_LN3	N	3		"
REG_FP0	N	5.3		Fractional position value of upper left corner
REG_FL0	N	5.3		"
REG_FP1	N	5.3		" for lower left corner
REG_FL1	N	5.3		"
REG_FP2	N	5.3		" for lower right corner
REG_FL2	N	5.3		"
REG_FP3	N	5.3		" for upper right corner
REG_FL3	N	5.3		" - Note, fractional positions are only used for shapes 1 and 6. Add the integer and fractional parts to get actual position
REG_TBM	N	10.3	❖	Total bone mineral (g)
REG_TBA	N	10.3	❖	Bone area in cm ²
REG_SOFT	N	10.3	❖	Soft tissue (g)
REG_LEAN	N	10.3	❖	Other tissue (g) after Rev. 2.3

REG_CSEQ	N	1	Octagonal region sequence number
REG_QNUM	N	1	Octagonal region quadrilateral number - if non-zero, shows the order in which the regions must be used to obtain eight vertices in the original order. Each such region will have three records with the same sequence number. The first region is number one, the second is number two, and so forth.

NOTE: Norland recommends that when extracting hip data, such data be considered as two groups, namely pre-revision 2.3 and post-revision 2.3. The reason for this is that improved patient positioning and analysis algorithms in revision 2.3 software make previously-acquired data less compatible. To help differentiate between these two types of hip scans, hip data acquired prior to revision 2.3 is stored as (REG_SHAP) shape 1 and hip data acquired beginning with revision 2.3 is stored as shape 3.

All definitions of body region types are depicted in Figure 9. This illustration is provided to help the user understand the actual body regions scanned and to label the body regions from all revisions of XR and pDEXA® software.

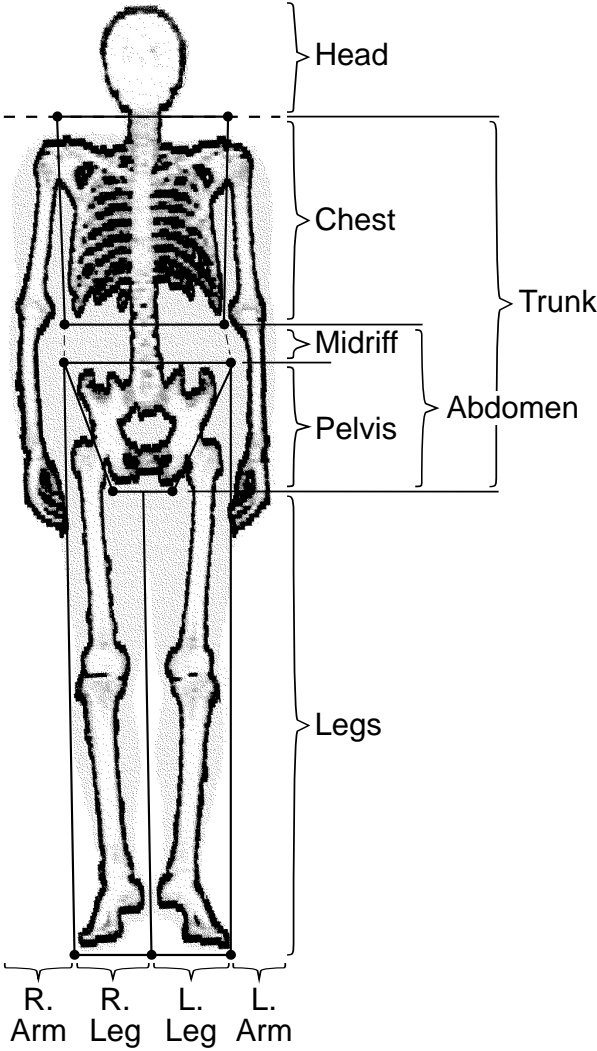


Figure 9 - Body regions, as defined in XR and pDEXA® software

REGIONS.DBF Example Listing

An extract of an example REGIONS.DBF data listing is seen below in Figure 10. This file was created with the XTRACT command "XTRACT -r".

PAT_SEQ_NO	PAT_ID	SCN_SEQ_NO	REG_SEQ	REG_TYPE	REG_I_NO	REG_SHAP	REG_PTD	REG_LNO
23	433-24-9118	1	1	total	13	6	0	0
23	433-24-9118	1	9	head N	24	6	0	0
23	433-24-9118	1	8	chest N	25	6	65	74
23	433-24-9118	1	6	midriff N	26	6	0	0
23	433-24-9118	1	7	pelvis N	27	6	99	112
23	433-24-9118	1	5	leg N	28	6	0	0
23	433-24-9118							
23	433-24-9118							
23	433-24-9118							
17	Lateral A							
17	Lateral A	71	30	161	30	174	74	351.057
16	Forearm	0	0	0	0	0	0	31.981
16	Forearm	60	82	176	82	139	112	250.826
16	Forearm	0	0	0	0	158	211	326.523
16	Forearm	0	0	0	0	107	211	343.884
19	Hip Scan A	0	0	0	0	0	0	140.626
19	Hip Scan A	0	0	0	0	0	0	131.553
19	Hip Scan A	6	61	98	67	100	124	6.738
18	AP Spine A	8	0	95	4	98	67	6.258
18	AP Spine A	1	16	60	16	60	20	1.051
18	AP Spine A	1	93	60	93	60	97	1.255
20	5236	30	16	60	16	60	20	0.661
20	5236	30	93	60	93	60	97	0.666
20	5236	31	83	81	35	102	56	2.850
20	5236	161	0	180	0	180	187	6.777
20	5236	64	82	79	68	93	83	0.659
20	5236	1	23	160	23	160	84	10.179
20	5236	1	85	160	85	160	146	10.379
20	5236	1	147	160	147	160	206	10.461
20	5236	0	0	0	0	0	0	3234.054
20	5236	0	0	0	0	0	0	678.935
20	5236	55	37	171	37	173	89	694.389
20	5236	0	0	0	0	0	0	35.555
20	5236	45	95	177	95	130	129	376.922
21	523	0	0	0	0	154	245	680.939
21	523	0	0	0	0	94	245	686.748
21	523	0	0	0	0	0	0	237.730
21	523	0	0	0	0	0	0	242.837
21	523	1	22	60	22	60	26	0.894
21	523	1	123	60	123	60	127	1.477
21	523	30	22	60	22	60	26	0.618
21	523	33	123	60	123	60	127	0.810
21	523	0	0	0	0	0	0	3121.151
24	201-44-3950	0	0	0	0	0	0	516.672
24	201-44-3950	66	33	174	33	178	89	612.824
24	201-44-3950	0	0	0	0	0	0	30.432
25	303-04-0277	62	95	178	95	138	134	355.724
25	303-04-0277	0	0	0	0	178	249	644.951
25	303-04-0277	0	0	0	0	113	249	666.684
25	303-04-0277	0	0	0	0	0	0	237.938
25	303-04-0277	0	0	0	0	0	0	256.025
25	303-04-0277	1	27	93	27	93	46	11.268
25	303-04-0277	1	47	93	47	93	66	10.785
25	303-04-0277	1	67	93	67	93	87	12.899
25	303-04-0277	0	0	0	0	0	0	2364.781
0	0	0	0	0	0	0	0	425.472
69	29	155	29	171	79	491.641	651.791	12994.524
0	0	0	0	0	0	34.114	27.772	2034.781
39	84	178	84	123	117	348.059	332.701	9763.147
0	0	0	0	0	141	223	399.723	407.902
0	0	0	0	0	107	223	398.633	411.738
0	0	0	0	0	0	0	0	127.895
0	0	0	0	0	0	0	0	139.244

REG_PT1	REG_LN1	REG_PT2	REG_LN2	REG_PT3	REG_LN3	REG_TBM	REG_TBA	REG_SOFT
0	0	0	0	0	0	1950.105	2119.563	55272.367
0	0	0	0	0	0	373.653	229.278	3622.668
71	30	161	30	174	74	351.057	480.442	14478.146
0	0	0	0	0	0	31.981	32.391	3492.277
60	82	176	82	139	112	250.826	256.150	9129.938
0	0	0	0	158	211	326.523	385.182	8639.294
0	0	0	0	107	211	343.884	387.776	9231.958
0	0	0	0	0	0	140.626	176.591	3480.040
0	0	0	0	0	0	131.553	171.754	3198.045
6	61	98	67	100	124	6.738	9.476	69.955
8	0	95	4	98	67	6.258	9.556	61.075
1	16	60	16	60	20	1.051	2.228	10.751
1	93	60	93	60	97	1.255	1.281	15.041
30	16	60	16	60	20	0.661	1.282	6.104
30	93	60	93	60	97	0.666	0.672	7.950
31	83	81	35	102	56	2.850	3.955	22.954
161	0	180	0	180	187	6.777	9.731	109.834
64	82	79	68	93	83	0.659	0.995	4.333
1	23	160	23	160	84	10.179	11.627	112.931
1	85	160	85	160	146	10.379	12.411	115.080
1	147	160	147	160	206	10.461	13.053	112.172
0	0	0	0	0	0	3234.054	2602.809	77106.148
0	0	0	0	0	0	678.935	267.660	5163.750
55	37	171	37	173	89	694.389	600.592	23763.061
0	0	0	0	0	0	35.555	25.403	3328.226
45	95	177	95	130	129	376.922	277.654	11333.523
0	0	0	0	154	245	680.939	461.961	12315.461
0	0	0	0	94	245	686.748	467.652	12423.768
0	0	0	0	0	0	237.730	250.479	4306.702
0	0	0	0	0	0	242.837	251.608	4471.655
1	22	60	22	60	26	0.894	2.224	11.433
1	123	60	123	60	127	1.477	1.377	14.369
30	22	60	22	60	26	0.618	1.370	6.345
33	123	60	123	60	127	0.810	0.751	7.859
0	0	0	0	0	0	3121.151	2969.784	73571.992
0	0	0	0	0	0	516.672	285.491	4869.050
66	33	174	33	178	89	612.824	705.527	21141.734
0	0	0	0	0	0	30.432	24.888	2253.039
62	95	178	95	138	134	355.724	336.898	11786.068
0	0	0	0	178	249	644.951	464.771	12103.689
0	0	0	0	113	249	666.684	476.854	12458.867
0	0	0	0	0	0	237.938	337.947	4330.062
0	0	0	0	0	0	256.025	337.407	4629.484
1	27	93	27	93	46	11.268	10.428	880.952
1	47	93	47	93	66	10.785	10.660	829.664
1	67	93	67	93	87	12.899	12.088	805.353
0	0	0	0	0	0	2364.781	2423.665	52956.836
0	0	0	0	0	0	425.472	246.077	3359.417
69	29	155	29	171	79	491.641	651.791	12994.524
0	0	0	0	0	0	34.114	27.772	2034.781
39	84	178	84	123	117	348.059	332.701	9763.147
0	0	0	0	141	223	399.723	407.902	9563.917
0	0	0	0	107	223	398.633	411.738	9730.547
0	0	0	0	0	0	127.895	170.383	2687.339
0	0	0	0	0	0	139.244	175.301	2823.162

Figure 10- Example listing, REGIONS.DBF

SAMPLE APPLICATION PROGRAMS

Two application programs are supplied with XTRACT and written for use with dBASE III (and later) programs. They serve as examples of how extracted patient data may be examined or manipulated. They may provide a basis for much more sophisticated uses of the files created by XTRACT. They may also be translated for use with other database or spreadsheet programs. However, the specific command sequence given here applies only to dBASE.

NOTE: Before attempting to use these programs, copy them from the XR26 or PDEXA sub-directory into the same sub-directory as the dBASE program files.

The purpose of this section is to describe these application programs and provide a listing of the program. We will not support their use beyond the text given here, nor will we attempt to teach the use of dBASE or other application programs. A working knowledge of such application programs is needed in order to use these sample programs.

NOTE: These programs have been thoroughly tested and will operate as described. And, even though all processes related to XTRACT are harmless (with respect to Norland software and data files), no guarantee is made that the use of these programs won't interfere with or affect other database or spreadsheet files in use. Please take adequate backup precautions before using XTRACT.

XRDUMPP.PRG

XRDUMPP.PRG provides a way to use dBASE to browse through the Patients, Scans, and Regions files created by XTRACT. Make sure the XTRACT-created *.DBF files are copied into the same sub-directory used by the dBASE program.

Invoke XRDUMPP in dBASE by entering 'do xrdumpp' at the dBASE 'dot prompt'. Soon a message appears, asking for the desired patient ID number. Enter the number and press <Enter>. The program will find the requested patient or the one closest to the number specified, and will display the data it found on the screen.

Press the <Esc> key when done examining the displayed material, and the following message appears:

```
PRESS Q TO QUIT
PRESS 1 TO BROWSE THROUGH
PATIENTS
PRESS 2 TO BROWSE THROUGH
SCANS
PRESS 3 TO BROWSE THROUGH
REGIONS
OR ANY OTHER KEY TO
CONTINUE
```

Respond by pressing the desired key, and proceed with the record review. Pressing the keyboard's 'Q' key causes the program to exit to the dBASE 'dot prompt'.

The following is the program listing of XRDUMPP.PRG, supplied with the XTRACT program, and installed in the PDEXA or XR26 sub-directory. This program was written using the dBASE program editor. This listing is provided so that users may view the actions performed as the program executes.

XTRACT

```
**PROGRAM LISTING - XRDUMPP.PRG **
*dBase files created by 'XTRACT -R'.
*Reset dBase and limit output.
SET TALK OFF
CLEAR ALL

*Load all three dBase files.
SELECT 1
USE patients
SELECT 2
USE scans
SELECT 3
USE regions

*Continue until the user quits.
done = .F.
DO WHILE .NOT. done

    *Prompt the user to type in a patient ID number.
    CLEAR
    ACCEPT "ENTER PATIENT ID NUMBER " TO id
    CLEAR

    *Using the patients file locate the record with the given ID.
    SELECT 1
    LOCATE FOR TRIM(UPPER(PAT_ID)) = TRIM(UPPER(id))

    *Check if we found the given ID.
    IF EOF()
        ? ' NO SUCH ID NUMBER :',id
    ELSE

        *We found the patient record so display the name and ID.
        ? patients->PAT_ID,patients->PAT_NAME

        *Try to locate the first scan for the patient.
        SELECT 2
        LOCATE FOR PAT_ID = patients->PAT_ID

        *Loop through all the scans for the patient.
        DO WHILE .NOT. EOF()

            *We must store the record number of the current scan we are
            *displaying because when we switch files the locate
            *information used to get the next scan is destroyed.
            STORE RECNO() TO scanrec

            *Display the scan type and date.
            ? ' ',scans->SCAN_TYPE,DTOC(scans->SCAN_DATE)

            *Create a 'regions' key and find the first one
            r_key = TRIM(UPPER(scans->PAT_ID+STR(scans->SCN_SEQ_NO)))
            SELECT 3
            LOCATE FOR TRIM(UPPER(PAT_ID+STR(SCN_SEQ_NO))) = r_key

            *Display region type and TBM and TBA for all the regions.
            *The continue command will get the next region (if any).
            DO WHILE .NOT. EOF()
                ? ' ',regions->REG_TYPE,regions->REG_TBM,regions->REG_TBA
                CONTINUE
            ENDDO

            *Now we must get the next scan for the patient. Starting on
            *the record after the current one we will locate the next
            *matching patient ID number.
```

```

        SELECT 2
        GO scanrec
        IF .NOT. EOF()
            SKIP
            LOCATE NEXT 65535 FOR PAT_ID = patients->PAT_ID
        ENDIF

    ENDDO

ENDIF

*Prompt the user to see what they want to do.
rsp = ' '
? ""
? "PRESS Q TO QUIT"
? "PRESS 1 TO BROWSE THROUGH PATIENTS"
? "PRESS 2 TO BROWSE THROUGH SCANS"
? "PRESS 3 TO BROWSE THROUGH REGIONS"
WAIT "OR ANY OTHER KEY TO CONTINUE " to rsp

*If the user wants to quit then set the done flag to TRUE. If
*they wish to browse a file then select the correct file and
*browse.
DO CASE
    CASE UPPER(rsp) = 'Q'
        done = .T.
    CASE rsp = '1'
        SELECT 1
        BROWSE
    CASE rsp = '2'
        SELECT 2
        BROWSE
    CASE rsp = '3'
        SELECT 3
        BROWSE
ENDCASE

CLEAR

ENDDO
****END OF PROGRAM LISTING - XRDUMPP.PRG****

```

XRLIST.PRG

The program XRLIST.PRG provides a way for dBASE to organize the XTRACT files into a listing that brings together the scan and region information for each patient. XRLIST.PRG uses all three *.DBF files, opening them simultaneously to present the requested information. The output of this program may be sent to a disk file or onto hard copy using dBASE commands. Make sure all three XTRACT-created *.DBF files are located in the same sub-directory as the dBASE program.

Invoke XRLIST in dBASE by entering 'do xrlist' at the dBASE 'dot prompt'. The first patient name in the patient file appears, followed by the first scan for

that patient. The regions found for the first scan are listed next. The second scan is displayed along with its regions, followed by the third scan, and so forth.

When all scans for the patient have been found, the next patient in the list is displayed, along with sequential scan and region listings. This process continues until all records for all extracted data have been displayed. The program then exits to the dBASE dot prompt. To exit the program at any time, press the <Esc> key.

The following is the XRLIST.PRG program listing, written using the dBASE program editor.

XTRACT

****PROGRAM LISTING -

XRLIST.PRG****

*dBase files created by 'XTRACT -
R'.

*LIST ALL PATIENTS/SCANS/REGIONS

*Reset dBase and limit output.

SET TALK OFF

CLEAR ALL

*Load all three dBase files.

SELECT 1

USE patients

SELECT 2

USE scans

SELECT 3

USE regions

CLEAR

*Start at the top of the patients
file

SELECT 1

GO TOP

*Continue until we hit the end of
the file

DO WHILE .NOT. EOF()

*Display the name and ID.

? patients->PAT_ID,patients-
>PAT_NAME

*Try to locate the first scan
for the patient.

SELECT 2
LOCATE FOR TRIM(UPPER(PAT_ID)) =
TRIM(UPPER(patients->PAT_ID))

*Loop through all the scans for
the patient.

DO WHILE .NOT. EOF()

*We must store the record
number of the current scan we are

*displaying because when we switch files the locate information

*used to get the next scan is destroyed.

STORE RECNO() TO scanrec

*Display the scan type and date.

? ' ',scans->SCAN_TYPE,DTOC(scans->SCAN_DATE)

*Create a key for the regions of the scan and find the first

*one

SELECT 3

LOCATE FOR PAT_ID+STR(SCN_SEQ_NO) = scans->PAT_ID+STR(scans->SCN_SEQ_NO)

*Display region type and TBM and TBA for all the regions. The

*continue command will get the next region (if any).

DO WHILE .NOT. EOF()

? ' ',regions->REG_TYPE,regions->REG_TBM,regions->REG_TBA
CONTINUE

ENDDO

*Now we must get the next scan for the patient. Starting on

*the record after the current one we will locate the next

*matching patient ID number.

SELECT 2

GO scanrec

IF .NOT. EOF()

SKIP

LOCATE NEXT 65535 FOR PAT_ID = patients->PAT_ID

ENDIF

ENDDO

*Go on to the next patient

SELECT 1

SKIP

ENDDO

****END OF PROGRAM LISTING - XRLIST.PRG****

This completes the descriptions of Data XTRACT and its sample application programs. Because any use of XTRACT is unique and noteworthy, please contact the factory to find out about Norland's incentive program established to obtain case-history information.

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