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DIRECTORY AND FILE MANAGEMENT

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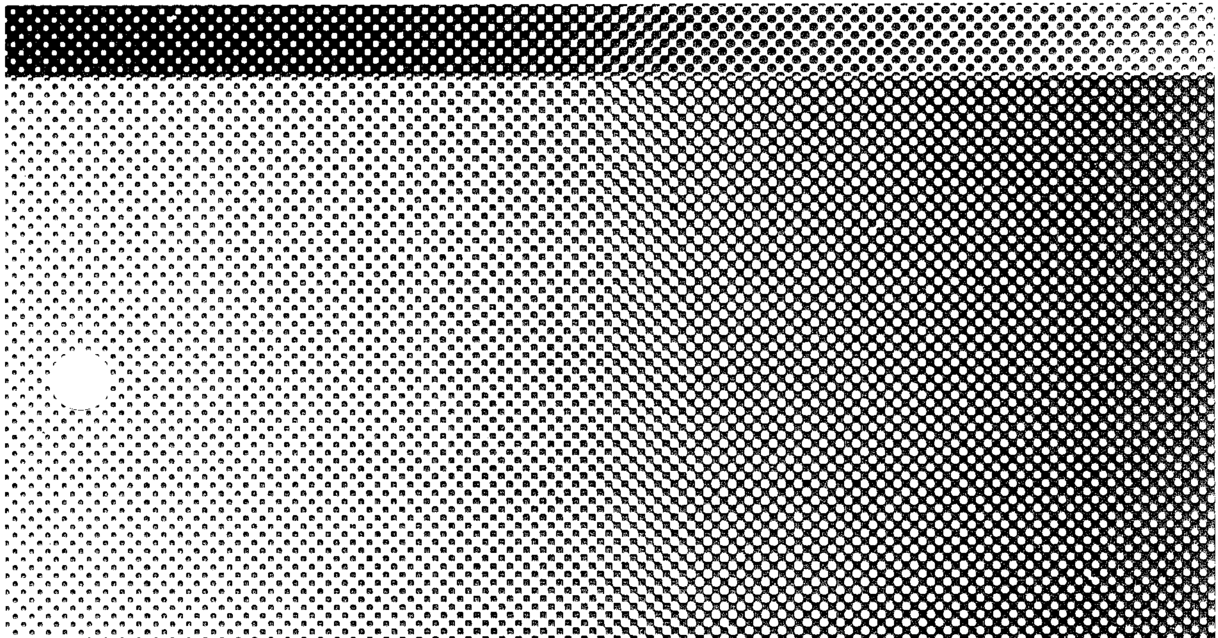
AT&T 3B2 Computer

UNIX™ System V Release 2.0
Directory and File Management
Utilities Guide



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INTRODUCTION

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Chapter 1

INTRODUCTION

GENERAL

This guide describes command formats (syntax) and use of the Directory and File Management Utilities provided with your AT&T 3B2 Computer. The commands and procedures described in this guide can be used by anyone who has a need for enhanced file and directory manipulation on the 3B2 Computer.

Directory and File Management Utilities are software tools to aid in managing your directories and files. With one-step commands, you can skillfully do any of the following:

- Search directories and files
- Compare their contents
- Manipulate file data.

GUIDE ORGANIZATION

The remainder of this guide, Chapter 2 -- "COMMAND DESCRIPTIONS," describes the command formats (syntax) for each command in the Directory and File Management Utilities. The descriptions include the purpose of the command, a discussion of the command syntax and options, and examples of using each command.

Chapter 2

COMMAND DESCRIPTIONS

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Chapter 2

COMMAND DESCRIPTIONS

COMMAND SUMMARY

The Directory and File Management Utilities Package provided with the 3B2 Computer includes twenty-seven **UNIX*** System commands. These commands with a brief description are listed in Figure 2-1.

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Commands	Description
ar	Maintains groups of files that are part of a single archive file.
awk	Searches input lines for a matching pattern and performs specific actions.
bdiff	Finds what lines should be changed for two files to agree.
bfs	A read-only editor, similar to the **ed** editor, that is used to scan big files.
comm	Selects or rejects lines common to two sorted files.
csplit	Splits a file into parts as specified.
cut	Cuts out selected fields of data on each line of a file.
diff3	Compares three versions of a file.
dircmp	Compares two directories.
egrep	Searches a file for an *egrep* pattern, that is, a full regular expression.
fgrep	Searches a file for an *fgrep* pattern, that is, a fixed string.

Figure 2-1. Directory and File Management Commands (Sheet 1 of 3)

Commands	Description
file	Determines information about a file.
join	Joins two sorted files.
newform	Reads lines from a file or the standard input and reproduces those lines in a reformatted form on the standard output.
nl	Numbers lines in a file.
od	Outputs data in octal, decimal, ASCII, or hexadecimal formats.
pack	Stores file data in a compressed form.
paste	Merges the lines of two or more files in a side-by-side fashion.
pcat	Unpacks a compressed file for viewing only.
pg	Allows you to view a file, one page at a time on a video display terminal.
sdiff	Compares two files to produce a side-by-side listing of different lines.
split	Splits a file into parts of equal length.

Figure 2-1. Directory and File Management Commands (Sheet 2 of 3)

Commands	Description
sum	Calculates the checksum and blocks of a file.
tail	Copies a file or portion of a file to standard output.
tr	Filters a file by translating specified characters to other characters.
uniq	Reports file lines that are repeated.
unpack	Stores a compressed file in uncompressed form.

Figure 2-1. Directory and File Management Commands (Sheet 3 of 3)

HOW COMMANDS ARE DESCRIBED

A common format is used to describe each of the commands. This format is as follows:

- **General:** The purpose of the command is defined. Any special or uncommon information about the command is also provided.
- **Command Format:** The basic command line format (syntax) is defined and the various arguments and options discussed.
- **Sample Command Use:** Example command line entries and system responses are provided to show you how to use the command.

In the command format discussions, the following symbology and conventions are used to define the command syntax.

- The basic command is shown in bold type. For example, **command** is in bold type.
- Arguments that you must supply to the command are shown in a special type. For example: **command** *argument*.
- Command options and fields that do not have to be supplied are enclosed in brackets ([]). For example: **command** [*optional arguments*].
- The pipe symbol (|) is used to separate arguments when one of several forms of an argument can be used for a given argument field. The pipe symbol can be thought of as an exclusive OR function in this context. For example: **command** [*argument1* | *argument2*]

In the sample command discussions, user inputs and 3B2 Computer response examples are shown as follows:

```
This style of type is used to show system generated
responses displayed on your screen.
```

This style of bold type is used to show inputs entered from your keyboard that are displayed on your screen.

These bracket symbols, < > identify inputs from the keyboard that are not displayed on your screen, such as: *<CR>* carriage return, *<CTRL d>* control d, *<ESC g>* escape g, passwords, and tabs.

This style of italic type is used for notes that provide you with additional information.

Refer to the *AT&T 3B2 Computer User Reference Manual* for UNIX System V manual pages supporting the commands described in this guide.

COMMANDS

"ar" — Archive and Library Maintainer for Portable Archives

General

The **ar** command is used to maintain groups of files that are part of a single archive file. The **ar** command is mainly used to create and update library files that are used by the link editor (**ld** command), but it can be used for any similar purpose. Refer to the *AT&T 3B2 Computer User Reference Manual* for information on the **ld** command. When the **ar** command creates an archive, the archive file is put into a format with headers that are portable across all computers that are compatible with your AT&T 3B2 Computer. These headers are placed at the beginning of each archive and have the following format:

```
#define ARMAG   "<ar>"
#define SARMAG  4


struct ar_hdr {/* archive header */
char  ar_magic[SARMAG]; /* magic number */
char  ar_name[16];/* archive name */
char  ar_date[4];/* date of last archive modification */
char  ar_syms[4];/* number of ar_sym entries */
};
```

The header is followed by an archive symbol table which is included in each archive that has common object files. This symbol table is automatically created by the **ar** command. The archive symbol table is used by the link editor to determine what archive members must be loaded during the link edit process.

There may be more than one archive symbol table. The number of symbol table entries is shown in the header under the *ar_syms* variable. Each archive symbol table has the following format:

```
struct  ar_sym {/* archive symbol table entry */
char sym_name[8];/* symbol name, recognized by ld */
char sym_ptr[4];/* archive position of symbol */
};
```

The archive symbol table is rebuilt each time the **ar** command is used to create or update the contents of an archive.

The archive symbol table is followed by the archive file members. A file member header precedes each file member. The file member header has the following format:

```
struct  arf_hdr {/* archive file member header */
char arf_name[16];/* file member name */
char arf_date[4];/* file member date */
char arf_uid[4];/* file member user identification */
char arf_gid[4];/* file member group identification */
char arf_mode[4];/* file member mode */
char arf_size[4];/* file member size */
};
```

All the information in the archive header, the archive symbol table, and the archive file member headers is stored in a machine (computer) independent fashion. Because of this, an archive file may be used on a computer that is compatible with the 3B2 Computer.

Command Format

The general format of the **ar** command is as follows:

ar *key* [*posname*] *afile name(s)*

The *key* argument uses the following options:

> ***Note:*** Options **v**, **u**, **a**, **i**, **b**, **c**, **l**, or **s** must be used in combination with at least one of options **d**, **r**, **q**, **t**, **p**, **m**, or **x**.

d Delete *name(s)* from the archive file.

r Replace *name(s)* in the archive file using the following options:

- **u** Replace only those files that have modified dates later than the archive files.
- **a** Place new files after *posname*.
- **b** or **i** Place new files before *posname*.

  The *posname* argument must be specified. If you do not specify where to place new files, they will be placed at the end.

q Quickly append the named files to the end of the archive file. The positioning options under the **r** option will not work if used with this option. The **ar** command does not check to see if the added members are already in the archive.

t Print a table of contents of the archive file. If *name(s)* is specified, only that file(s) will be placed in the table of contents. If *name(s)* is not specified, all files in the archive will be placed in the table of contents.

p Print the contents of *name(s)* in the archive file.

m Move *name(s)* to the end of the archive. The positioning options under the **r** option can be used to place the file in a specific place.

x Extract *name(s). If name(s) is not specified, extract all files in the archive. This option will not alter the archive file.*

v Verbose. When making a new archive from an old archive and the constituent files, a file–by–file description of the process is given. When this option is used with the **t** option, a long listing of all information about the files is given. When this option is used with the **x** option, each file is preceded by its name.

c Create *afile*. Normally, the **ar** command will create *afile* when it needs to. The normal message that is produced when *afile* is created will not appear when this option is specified.

l Place temporary files in the local directory. If this option is not specified, temporary files will be placed in **/tmp**.

s Regenerate the archive symbol table even if the **ar** command is invoked with an option that will not change the archive contents. This option is useful to restore the archive symbol table after the **strip** command has been used on the archive.

The *posname* argument is used to determine the position of a file that is being moved: either before or after *posname*. *posname* is the name of a file in the archive. The *posname* argument must be used when using the positioning options listed under the **r** option of the *key* argument.

The *afile* argument is the name of the archive file.

The *name(s)* argument is the name of the constituent files in the archive file. Take caution not to list *name(s)* twice. If *name(s)* is mentioned twice, it may be put in the archive twice.

Sample Commands

The following command line entries and system responses show you how to create an archive. The **ls** command is used to show you the files that will be placed in the archive. The **ar** command used with the **q** option shows you how to create an archive named **archive1**.

```
$ ls<CR>
cars
cities
people
states
streets
$ ar q archive1 cars cities people states streets<CR>
ar: creating archive1
$
```

The following command line entry and system response show you how to print a table of contents of the archive that was created in the previous example:

```
$ ar t archive1<CR>
cars
cities
people
states
streets
$
```

The following command line entry and system response show you how to print the contents of a file in an archive:

```
$ ar p archive1 cars<CR>
Camero
Ferrari
Jaguar
Mustang
Porsche
$
```

The following command line entry and system response show you how to print a long listing of the table contents in an archive:

```
$ ar tv archive1<CR>
rw------- 5516/ 5500   38 July 19 13:29 1985 cars
rw------- 5516/ 5500   51 July 19 13:33 1985 cities
rw------- 5516/ 5500   29 July 19 13:27 1985 people
rw------- 5516/ 5500   51 July 19 13:48 1985 states
rw------- 5516/ 5500   60 July 19 14:16 1985 streets
$
```

"awk" — Pattern Scanning and Processing Language

General

The **awk** command is used to search lines of input data for defined patterns and to do specified actions on the lines or fields when a match is found. Lines that do not contain a matching pattern are ignored. Conversely, a line that contains more than one matching pattern can be operated on and output several times. One primary use of **awk** is for the generation of reports. Input data is processed to extract counts, sums, and other pertinent information. The processed information is then output in a specified format.

The **awk** command has its own programming language for defining patterns and their corresponding actions. The language is designed to simplify the task of information retrieval and text manipulation. Initially, the novice user will find **awk** difficult to use and understand. Your understanding of **awk** will increase as you spend more time using (and experimenting with) the capabilities provided by the command. Remember that the use of this command is task oriented; you must establish a purpose for using the command. For example, the **awk** command can be used to output tabular material in a different sequence of columns. Certain basic arithmetic functions can also be performed on designated fields.

Input Data Characteristics

Input data is normally taken from files of data. The variable called **FILENAME** contains the name of the current input data file. Input data is divided into records with each record ended by a record separator. The record separator is stored in a variable named **RS**. The default record separator is a new-line character. This means that by default, **awk** reads and processes data on a line–by–line basis. The record separator can be redefined by setting the variable **RS** equal to the desired character. When the **RS** is empty (undefined), a blank line is used as the record separator. In addition, the field separators are defined as blanks, tabs, and new-lines. The novice user should not arbitrarily redefine the **RS** variable. The number of the current record (current line) is stored in a variable named **NR**.

Each input record (line) is divided into fields. Each field, except the last field, is ended by a field separator. The field separator is stored in a variable named **FS**. The default field separator is white space: blanks or tabs. The field separator can be redefined by setting the variable **FS** equal to the desired character. The novice user should not arbitrarily redefine the **FS** variable. Each field is identified by an uncommon variable. The variables are **$1**, **$2**, **$3**, and etc. The first field is named **$1**. The entire record (line) is named **$0**. The number of fields in the current record is maintained in a variable named **NF**.

Command Language Format

The instructions that tell the **awk** command what to do to the input data can be specified directly as an argument to the command, or the instructions can be read from a file. In either case, these instructions constitute an **awk** program. An **awk** program is a sequence of statements that are in the following form for each statement. Note that an action must be enclosed in braces to distinguish it from a pattern. Additional command format information is provided later in this description. The general form of each statement is as follows:

pattern { action }

The **awk** command operates on one record (line) of input data at a time. Each line of input data is tested against each of the command lines defined in an **awk** program. When a pattern match is found, the associated action is executed. When a command line defines a pattern without an associated action, then the input data record is output when a match is found. When a command line defines an action without an associated pattern, then the action is performed for all input lines (records). After all program command lines have been tested against the current record (line), the next record (line) is read and the process repeated until all records are read.

Patterns

A pattern is an expression that determines whether the associated action is to be performed. When a command line defines a pattern without an associated action, then the input data record is output when a match is found. A variety of expressions can be used as patterns. Patterns can be regular expressions as used with **ed** or **grep**, relational expressions, or special expressions. Combinations of these types of expressions can be used to define a pattern by using Boolean operators to connect each expression. The Boolean operators are OR (**||**), AND (**&&**), and NOT (**!**). Conventional arithmetic operators are also provided. The arithmetic operators are add (+), subtract (-), multiply (*****), divide (/), and modulus (**%**). Also, included are the increment (++) and decrement (--) operators.

Regular Expressions: Regular expressions, in their simplest form, are context search patterns in the form used by the **ed** or **grep** commands. The **awk** language adds operators to the regular expression to specify whether the corresponding action is to be executed if the pattern matches (~) or does not match (!~). For example, the following pattern outputs all records in which the first field does not contain the word "operates".

```
$1 !~ /operates/
```

Relational Expressions: Relationships are statements that express conditions such as greater than (>), less than (<), greater than or equal to (>=), less than or equal to (<=), equal to (==), and not equal to (!=). For example, the following relational expression selects lines that begin with any letter that is equal to or greater than the letter **s**: All lines beginning with the letters **s** through **z** are matched by this pattern.

```
$1 >= "s"
```

Special Expressions: Two special expressions named **BEGIN** and **END** are provided. The **BEGIN** expression defines a special pattern that matches the beginning of the input data before the first record is read. The **END** expression defines a special pattern that matches the end of the input data after the last record has been processed. These special expressions

provide the means to establish initial and post-processing conditions. When **BEGIN** is used, it must be the first pattern in the **awk** sequence of commands (program). The **END** must be the last pattern in the program. The following example shows a typical structure. In this example, the field separator (**FS**) is set to a colon at the beginning of the program; the number of each record (**NR**) is output at the end of the program.

```
BEGIN { FS = ":" }

...body of program...

END { print NR }
```

Two patterns, separated by a comma, can be used to control the execution of an action over a range of records. The action is executed for each record, starting with the match of the first pattern and continuing until the match of the second pattern, inclusive of the record containing the second pattern. The following example shows the general construction for a pattern range that controls an action:

```
/pattern1/, /pattern2/ { action }
```

Actions

An action specifies a function that is to be executed. When an action is associated with a pattern, then the action is executed only when the current record (line) matches the associated pattern. An action that does not have a corresponding pattern is executed for each input record (line).

The various action terms recognized by the **awk** command are as follows:

exp
index(s1,s2)
int
length
log
print
printf(" f" ,e1,e2,...)
split(s,array," sep")
sprintf(" f" ,e1,e2,...)
sqrt
substr(s,m,n)

Each of these action terms are described in the following paragraphs.

exp: The **exp** function computes *e* (2.7182818) raised to the *x* power, where *x* is a field argument. For example, when combined with the **print** function, the following statement outputs the value of e^X for each record, where *x* is the value of third field:

{ **print exp($3)** }

index(s1,s2): The index function is used to obtain the starting position of a string (**s2**) within another string (**s1**). A zero is returned when **s2** does not exist within **s1**. When combined with the print function, the following statement outputs the starting character position of a string **Smith** within the first field of each record:

{ **print index($1," Smith")** }

int: The integer function converts irrational numbers to rational numbers for a specified field; numbers expressed to some fractional quantity are converted to whole numbers. The function DOES NOT round off numbers. Fractional quantities are deleted. For example, the number 3.984 would be converted to the number 3. When combined with the **print** function, the following statement outputs the fifth field of each record expressed as whole numbers (integers):

{ **print int($5)** }

length: The **length** function computes the length of a string of characters. When combined with the **print** function, the following statement outputs the length of each record (line):

{ **print length($0)** }

The following statement outputs the length of each record, followed by the record:

{ **print length($0), $0** }

The **length** function can also be used to output records (lines) that are within a specified length range. For example, the following statement outputs all records that are less than 20 and greater than 10 characters in length. The || is the Boolean OR function.

{ **length > 10 || length < 20** }

The following statement outputs all records that are outside the 10 to 20 character range:

{ **length < 10 || length > 20** }

log: The **log** function computes logarithms to the base *e*. When combined with the **print** function, the following statement outputs the logarithm of fifth field for each record:

{ **print log($5)** }

print: The simplest action provided is the **print** function. For example, the following statement outputs the first two fields of each record in reverse order (field 2 followed by field 1):

{ **print $2, $1** }

The output of a **print** statement can be directed to a file. For example, the following statement outputs the first field to **file1** and the second field to **file3** for each record:

{ **print $1 >> " file1" ; print $2 >> " file3"** }

The output of a **print** statement can be directed to another program. For example, the following statement outputs the fifth field of each record to the **sort** command: The output of the **sort** command is directed to a file named **file5**.

{ **print $5 | " sort -o file5"** }

printf(" f" ,e1,e2,...): The **printf** converts, formats, and prints its arguments on the standard output. This function is exactly like the C Language **printf** function. The **f** argument specifies the format. The expressions to be formatted are specified by the **e** arguments. For example, the following statement prints the third field of each record as a floating point number that is ten digits wide with two decimal places. The fifth field is printed as a ten-digit long decimal number, followed by a new-line (\n).

```
{ printf(" %8.2f %10ld\n" , $3, $5) }
```

Remember that with this print function, you must specify the output field separators; no field separators are automatically output.

split(s,array," sep"): The split function is used to automatically divide a string into fields. The **sep** argument, if provided, defines the field separator. The **FS** variable is used as the field separator if the **sep** argument is omitted from the statement. The string **s** is divided into fields defined by the **array** argument. For example, the following statement divides the second field of a record into elements of an array named **z** based on the dash as the field separator. Each element of the array (field) is individually identified. The first element is named **z[1]**; the fifth element is **z[5]**. In the following example, the **print** function is used to output the fifth field of the array **z**:

```
{split($2,z," -" );print z[5]}
```

sprintf(" f" ,e1,e2,...): The string print function is used to place formatted output in a character array pointed to by a single character name. The **sprintf** converts, formats, and outputs its arguments to a string name. For example, the following statement sets **x** equal to the formatted result of the third and fifth field. The third field of each record is formatted as a floating point number that is ten digits wide with two decimal places.

The fifth field is formatted as a ten-digit long decimal number followed by a new-line (\n). Thus, the variable **x** is set to the string produced by formatting the values of fields $3 and $5. The variable **x** can be used in other statements to express these values as a formatted expression.

```
{ x = sprintf(" %8.2f %10ld\n" , $3, $5) }
```

sqrt: The square root function computes the second root of a specified item. When combined with the **print** function, the following statement outputs the square root of the first field for all records:

```
{print sqrt($1)}
```

substr(s,m,n): The substring function is used to obtain a specified part of a string. The **m** argument defines the starting character position of the substring. The beginning of the string is character position number 1. The **n** argument defines the number of characters to be included in the substring. If the **n** argument is omitted, the substring is defined from the beginning position **m** to the end of the string **s**. When combined with the **print** function, the following statement outputs part of the third field for all records. The portion of the field that is selected is the fifth character position to the end of the field.

```
{ print substr($3,5) }
```

Assigning Variables

Variables are assigned as either floating point numbers or as string values. Unlike C Language, variables DO NOT have to be declared at the beginning of a program. For example, the following sets **x** equal to the string **word**:

```
x = " word"
```

The following sets **x** equal to the number **100**:

```
x = " 100"
```

Arrays

Arrays are used to hold fields of data that are called elements. Each element or field in the array is identified by its sequential position. Array elements can also be named by nonnumeric values, which provides an associative type of memory. For example, the following **awk** program counts the number of times the patterns **apple** and **orange** occur. The results are stored in an array named **z**. The accumulated counts for each of these patterns is output at the end of the program. Note that the ++ operator increments the count by one each time it is called.

```
/apple/ {z[" apple" ]++}
/orange/ {z[" orange" ]++}
END {print z[" apple" ], z[" orange" ]}
```

The following example does the same function as the previous program. The only differences are that numeric designators are used for the elements of the array as opposed to associative names, and that the names are output to identify the counts.

```
/apple/ {z[1]++}
/orange/ {z[2]++}
END {print " apple = "  z[1] "   orange = "  z[2]}
```

Control Flow Statements

The **awk** programming language provides the following basic control flow statements: **if-else**, **while**, and **for**. Also provided are the following control statements: **break**, **continue**, and **next**. The **break** statement causes an immediate exit from an enclosing **while** or **for** construction. The **continue** statement causes the next cycle of a loop to begin. The **next** statement causes **awk** to immediately skip to the next record and begin processing.

Control flow constructions are exactly like that of the C Programming Language. For example, the following construction outputs all fields on a separate line using a **while** statement:

```
i=1
while (i<=NF) {
    print $i
    ++i
}
```

The following example construction outputs all fields on a separate line using a **for** control statement:

```
for (i=1;i<=NF;++i)
print $i
```

Commenting Programs

In general, the **awk** programs that you write are done so in files. Only the simplest of **awk** functions are done by specifying patterns and actions directly to **awk** as arguments. When writing a program, the importance of adequately providing comments that show what you are doing at various stages in the program cannot be over emphasized.

Comments are entered by preceding the comment with a pound symbol (#). The comment ends with the end of the line. When more than one line is used for a comment, each comment line must begin with the pound symbol. Remember that if your erase character is the pound symbol, you must precede the pound with a backslash (\) to enter the symbol. This is referred to as escaping the special meaning of the character. The following shows how you enter comments into a program:

```
print x, y # Print results
# This is a continued or new comment line.
```

Command Format

The general format of the **awk** command is as follows:

awk [**-f** *source* | '*cmds*'] [*parameters*] [*file*]

The instructions that tell the **awk** command what to do can be directly expressed to the command as arguments or they can be entered into a file that is then read by the command. When instructions are expressed as arguments, they are in the form *'cmds'*. Note that instructions that are expressed as arguments must be enclosed in single quotes. When instructions are placed in a file, the file is specified to the **awk** command in the form **-f** *file*. Note that the file name can be expressed as a full path name.

The *parameters* argument is used to identify the value of variables. The argument is: **x=... y=...**, and so on. Note that a space is used to separate each variable statement.

The *files* argument identifies the input data file. The file name can be expressed as a complete path name.

Sample Command Use

The following examples are based on a file named **list**. This file contains a list of names, addresses, and phone numbers as follows. Note that the format of each line of this file is name(tab)address(tab)phone.

```
$ cat list<CR>
Nancy  1080 Route 3, Farmington, NC  27015     919-736-2437
John   4589 Breckenridge, Clemmons, NC  27012  919-828-7512
Sam    2700 Route 67, Winston-Salem, NC  27106 919-234-1940
doctor 4100 First St, Winston-Salem, NC  27102 919-727-1111
$
```

The first example uses the **awk** command to output selected names and addresses from the **list** file in a format suitable for mailing labels. The program is in a file called **labelsprgm** and follows:

```
$ cat labelsprgm<CR>
BEGIN{FS="\t"}
$1~/Nancy/||$1~/Sam/{split($2,x,",")
printf("%s\n%s\n%s\n%s\n\n",$1,x[1],x[2],x[3])}
$
```

The second example uses the **awk** command to output selected names and phone numbers from the **list** file. The program is in a file called **numbers** and follows:

```
$ cat numbers<CR>
BEGIN{FS="\t"}
$1~/Nancy/||$1~/Sam/{printf("%s\t%s\n",$1,$3)}
$
```

The following command line entry and system responses show the use of the **labelsprgm**:

```
$ awk -f labelsprgm list<CR>
Nancy
1080 Route 3
Farmington
NC  27015

Sam
2700 Route 67
Winston-Salem
NC  27106

$
```

The following command line entry and system responses show the use of the **numbers** program:

```
$ awk -f numbers list<CR>
Nancy   919-736-2437
Sam     919-234-1940
$
```

The following example is based on a file named **gaintbl**. This file is a table containing columns of measured data, input and output voltage (**Vi** and **Vo**), and blank columns for new data.

```
$ cat gaintbl<CR>
Vi Vo Vo/Vi Log+Av Av(dB)
-- -- ----- ------ ------
 2  5
 8 15
10 18
$
```

In this example, the **awk** command performs several arithmetic operations on the data in **gaintbl**. The measured data and the resulting new data are output in a table format. Since the field separators of **gaintbl** are spaces, a **BEGIN** statement is not required. The program is in a file called **calcprgm** and follows:

```
$  cat calcprgm<CR>
#
#     PRINT TABLE HEADING
$1~/Vi/||$1~/--/{
printf " %s\t%s\t%s\t%s\t%s\n" ,$1,$2,$3,$4,$5}
#
#    CALCULATE & PRINT DATA
$1!~/Vi/&&$1!~/--/{$3=($2/$1);$4=log($3);$5=20*$4;
printf " %2ld\t%2ld\t%3.3f\t%3.4f\t%3.3f\n" ,\
$1,$2,$3,$4,$5}
$
```

The following command line entry and system responses show the use of the **calcprgm**:

```
$  awk -f calcprgm gaintbl<CR>
Vi     Vo      Vo/Vi  Log+Av  Av(dB)
--     --      -----  ------  ------
 2      5      2.500  0.9163  18.326
 8     15      1.875  0.6286  12.572
10     18      1.800  0.5878  11.756
$
```

"bdiff" — Big Differential File Comparator

General

The **bdiff** command operates much like the **diff** command covered later in this chapter. It compares two files and outputs instructions that tell what must be changed to bring the two files into agreement. The purpose of **bdiff** is to compare files that are too large for **diff** to process. It splits the files being compared into segments and performs **diff** on each segment. The output is identical to that of **diff**, except the line numbers are adjusted to account for the previous segments.

Command Format

The general format for the **bdiff** command is as follows:

bdiff *file1 file2* [**n**] [**-s**]

If no options are specified, **bdiff** ignores the lines that are common to the beginning of both files and splits the remainder of each file into 3500-line segments. The **diff** command is then performed automatically on the segments. The output will be the lines of the first named file followed by the lines of the second named file that are different. The less-than symbol (<) precedes the lines of the first named file. The greater-than symbol (>) precedes the lines of the second named file.

The optional third argument, **n**, is used to specify the number of lines to be contained in the file segments. If **n** is given in numeric form, the files are split into **n**-line segments instead of the 3500-line default count. These **n**–line segments are useful where the 3500-line segments are still too large for **diff** to handle.

The **-s** option will suppress any diagnostics that would be displayed by **bdiff**. However, any diagnostics output by **diff** will still be displayed.

If both the **n** and **-s** options are specified, they must be specified in the order shown in the command format, that is, the numeric value for **n** is entered before the **-s** option.

If a dash (—) is entered instead of *file1* or *file2*, the file that is named will be compared to what is input from the terminal. The input is entered exactly as it is to be compared to the named file. A "control d" is used to show the end of the input.

Sample Command Use

The following command line and system response shows how to output the differences between **chapter1.1** and **chapter1.2**:

```
$ bdiff chapter1.1 chapter1.2<CR>
23c23
< designed for Release 1.1 of the software.
---
> designed for Release 1.2 of the software.
104c104
< with update considerations for Release 1.2 compatibility.
---
> with update considerations for Release 1.3 compatibility.
$
```

The following command line and response show how to split the files into 1000-line segments:

```
$ bdiff file1 file2 1000<CR>
2124c2124
< is a sample of the command.
---
> is an example of how to use the command.
$
```

Note: The difference between the two files was found in the second segment, but **bdiff** adjusts the line count to specify the correct line number for the original file.

The following example shows how to format **chap1** and compare the formatted file to **OLDchap1**. The format program for this example is called **form**.

```
$ form chap1 | bdiff OLDchap1—<CR>
72c72
< will not be displayed on the screen.
---
> will be displayed on the screen.
$
```

Note: In this example, **OLDchap1** lines will be displayed first. The order may be reversed if the filename and — are reversed.

"bfs" — Big File Scanner Editor

General

> ***Note:*** This command does not follow the same format as the other commands in this Utilities Guide.

This part of the chapter describes the **bfs** (big file scanner) editor used on the 3B2 Computer. The bfs editor is similar to the *ed* editor, except that it is read-only. Since bfs cannot be used to change a file, commands such as: insert, append, substitute, delete, and move will not execute.

Bfs works with the file instead of a copy placed in a buffer (temporary memory). It is normally used for processing files that are too large for conventional editing. Bfs can access files up to 1024 kilobytes (maximum size) and 32,000 lines--with up to 255 characters per line.

The bfs editor is useful for identifying sections of a large file where the commands *csplit* or *split* can be used to divide it into more manageable pieces for editing. The *csplit* and *split* commands are included in this Utilities Guide.

This editor description assumes that you know how to log in to the 3B2 Computer. If you do not, refer to the *AT&T 3B2 Computer Owner/Operator Manual.*

Refer to the *AT&T 3B2 Computer User Reference Manual* for UNIX System V manual pages supporting the commands described in this guide.

Current Line Definition

Throughout this chapter, the term "current line" is used to identify what line in the file you are currently on. To display the current line, enter:

p<*CR*>

Any commands you execute will use this line as a reference point.

Getting Started

The **bfs** editor can only be used on existing files. To create a new file by inputting data directly, you must use another editor. However, **bfs** can be used to create a new file if you need to copy part of an existing file into another file. Commands to do this are discussed later in this chapter.

To execute the **bfs** editor, you must first be logged in to the 3B2 Computer. Once you are logged in, the UNIX System prompt (**$** or #) should be displayed. You are now ready to begin working with the **bfs** editor.

Accessing a File

To scan a file using the **bfs** editor, you will need to type **bfs** followed by a space, and then the name of the file you wish to scan. Execute the command by entering a carriage return <*CR*>. For example:

$ **bfs filename**<*CR*>

will execute the **bfs** editor against the file "filename". If you entered the command correctly, the response will be a number that represents the number of characters in the edited file.

If you do not enter the command correctly, you will receive a usage message indicating an incorrect syntax was used. When this occurs, verify the name of the file; make sure you are in the right directory; and reenter the command correctly.

If you do not want the editor to display the size of the file, enter:

$ bfs - filename<*CR*>

where **filename** is the name of the file you want to access. The 3B2 Computer will not display a response.

Once you are in the **bfs** editor, you may begin scanning the file. To begin displaying lines in the file, you must enter a line number (for example: **1**) followed by a carriage return. The editor will use the line as a reference point. After you display a line, any of the commands described in this chapter can be used.

Displaying a Prompt

The **bfs** editor does not display a prompt unless you request one. At times, absence of a prompt can be confusing. Most users find it easier to use the editor with the prompt (*) displayed. To display the prompt, enter:

P<*CR*>

Receiving Error Messages

When the prompt is not requested, any editor error message displayed will simply be "**?**". To receive self-explanatory error messages, the prompt must be turned on. See the previous discussion on "Displaying a Prompt".

Getting File Information

There are two editor commands that can be used to obtain information about the file you are editing. To display how many lines are in the file, enter:

=<*CR*>

To display the name of the file, enter:

f<*CR*>

Quitting the Editor

Because the **bfs** editor is read-only, it will allow you to quit without warning you to write the file. To quit the editor, enter:

q<*CR*>

The 3B2 Computer will return you to the UNIX System.

Displaying Lines in the File

As previously discussed in "Current Line Definition", the current line is always displayed whenever you move through the file. However, you can display more than one line by using the print command (**p**). An example of the print command would be:

1,10p<*CR*>

that would display lines 1 through 10. This form of the print command can be used to display as much of the file as you wish. The end of file symbol (**$**) can also be used with the print command to display lines. For example:

250,$p<*CR*>

will display lines 250 through the end of the file. As you become familiar with the editor, you will find that the lines will be displayed even if you leave the **p** off the end of the command. For example:

250,$<*CR*>

will display from line 250 to the end of the file.

The print command can also be used with other commands, such as searches and marks. These uses of the print command are discussed in the explanation of the individual commands.

Basic Movement Commands

As previously discussed, one way to move through a file is to use the carriage return. You can also use the + and - commands with the carriage return to move you forward or backward through the file. With these commands, you can move to an adjacent line in the file.

To move in larger steps, you can use numbers with the + and - commands. For example:

+15<*CR*>

will move you forward in the file 15 lines, and display the current line. Likewise,

-15<*CR*>

will move you backward 15 lines and then display the current line.

Each line in the file has a line number associated with it, although it is not displayed. The **bfs** editor allows you to move across large areas of the file by just entering a line number followed by a carriage return. For example:

375<*CR*>

will make 375 the current line and display the line.

Another movement command that is useful on large files is the **$**. If you enter:

$<*CR*>

bfs will move you to the last line of the file and display the line.

Forward and Backward Searches

If you do not know a specific line number, but you do know an exact pattern of characters on a line in the file, the quickest way to locate that line is with a search. **The pattern must be on one line.** There are several types of searches. The type you should use depends on your specific application.

Searches With Wrap-Around

When entering a command, the **bfs** editor interprets the character "/" as meaning "search for this pattern". The search command "/" searches from the current line forward through the file for the first occurrence of the pattern. When the end of the file is reached, the search will wrap-around to the beginning of the file and continue searching until the pattern is found or it reaches the line where the search started. If the pattern is found, the line will be displayed and will become the current line. An example of a forward search command would be:

/learning the bfs editor/*<CR>*

that will search for the first occurrence of a line containing the pattern "learning the bfs editor", make it the current line, and display the line. If the pattern is not found, the message:

" learning the bfs editor not found"

will be displayed. This means the pattern you searched for is not on one line in the file, and the current line does not change. Check to see if you entered the command correctly, or if it included any characters with a special meaning (see "Special Search Characters").

The character "**?**" also executes a search when used in a command. It works the same as the "/" search character, except that it searches backward through the file from the current line. This search will wrap-around to the end of the file and continue searching until the pattern is found or it reaches the line where the search started. An example of a backward search command would be:

?learning the bfs editor?*<CR>*

Searches Without Wrap-Around

Another set of search commands can be used that do not wrap-around the end of the file. These commands are similar to the wrap-around searches, except that they stop at the beginning or end of the file. The forward search command ">" searches for the first occurrence of the specified pattern until it reaches the end of the file. An example of this type of forward search command would be:

>**learning the bfs editor**>*<CR>*

If the pattern is found, the line will be displayed and will become the current line. If the pattern is not found, the message:

" learning the bfs editor not found"

will be displayed and the current line will not change.

The character "<" also executes a search. It works the same as the ">" search, except that it searches from your current position backwards until it reaches the beginning of the file. An example of this type of backward search command would be:

<**learning the bfs editor**<*<CR>*

Repeating a Search

Often when searching for a pattern, the first occurrence is not the one you were actually looking for. You could repeat the entire search command, but there is a much easier way. The editor remembers the last search pattern entered. If you enter the command:

//<CR>

a forward search will look for the remembered pattern. The commands **??**, >>, and << will also repeat searches. The type of search repeated depends on the command used. The repeated search does not have to be the same type as the original search.

Global Searches

The **bfs** editor also allows you to do global searches on the file. A global search is used to find all the occurrences of a specified pattern in a file. This type of search is useful when scanning for a pattern that occurs in several places. The two types of global searches that can be executed use the **g** and **v** commands.

The global search that uses the **g** command locates all the lines that contain a specified pattern. An example would be:

g/sample pattern/p<*CR*>

that will search for and display all lines containing the words "sample pattern". The current line will be the last line displayed.

The global search that uses the **v** command locates all lines that **do not** contain a specified pattern. An example would be:

v/sample pattern/p<*CR*>

that will search for and display all lines that **do not** contain the words "sample pattern." The current line will be the last line displayed.

Special Search Characters

Several characters have special meaning when used in specifying searches. These characters will work with all types of searches. They can be used to: match repetitive strings of characters, turn off special meanings of characters, or denote the placement of characters in the line. These characters are: "**.**", "*****", "\\", "[]", "**$**", and "^".

. The period matches any single character except the newline (carriage return) character. For example:

/bfs edit.r/<*CR*>

will search for a pattern such as "bfs editor", "bfs editxr", or with any other character on a line between "bfs edit", and "r".

* The asterisk matches any string of characters except the first ., \, [, or ˜ in that group. For example:

/the x* editor/<*CR*>

will search for a pattern such as "the xxx editor", "the xxxxxx editor", or a pattern with any amount of "x" characters on a line between "the" and "editor".

\ The backslash is used to nullify the meaning of the special characters. It should be placed immediately before the character it is to nullify. For example:

/This is a **$/**<*CR*>

will search for the pattern "This is a $", instead of interpreting the "$" as meaning "at end of line".

[] Brackets are used to enclose a variable string. For example:

/Search for file[**23**]/<*CR*>

will search for the patterns "Search for file2"or "Search for file3" and stop at the first occurrence of either pattern.

$ The dollar sign is interpreted by the editor to mean "end of the line". It is used to identify patterns that occur at the end of a line. For example:

/last character$/<*CR*>

will search for the next occurrence of a line ending in "last character", and make it the current line.

^ The circumflex (caret) works like "**$**" except it looks for the pattern at the beginning of the line. For example:

/^**First character**/<*CR*>

will search for the next occurrence of the pattern "First character" at the beginning of a line and makes it the current line.

To search for the characters ., *, \, [,], **$**, or ^, you must precede the characters with a backslash. This will nullify the characters special meaning.

Marking Lines

The **bfs** editor gives you the ability to set marks in the file. Marks are useful when you are planning on moving around in the file and you want to set some reference points. They can save you from having to search for the same address several times.

Marks are set by moving to the line where you want the mark set and using the **k** command. The mark must be a single, lower case letter. For example, if you wanted to identify a line with the mark "a", you would move to that line and enter the command:

ka<*CR*>

To move to that marked line from anywhere in the file, enter the command:

'**a**<*CR*>

The marked line will become the current line. To set another mark, repeat the **k** command using a different letter.

To change an existing mark, move to the line where you want the mark and use the **k** command with the existing mark. The new position will replace the previous one.

The **n** command will display a list of the active marks. For example, if the active marks in a file were a, b, and c, you could display them by entering:

n<*CR*>

The system response would be:

a
b
c

Notice that only the marks are displayed and not the lines.

> ***Note:*** All marks are removed if you quit the editor using the **q** command. However, if you leave the editor by using the **e** command and then return to the file with the **e** command, all marks are saved. See " Changing Files While Using the " bfs " Editor."

Writing to Another File

The **bfs** editor allows you to copy all or part of the file you are editing to another file. To copy the whole file to another file, use the **w** command and the name of the file you want to create. For example:

w newfile<*CR*>

will create a copy of the file you are editing and name it "newfile". The number of characters in the new file will be displayed to show that the new file was created.

Caution: Be careful when naming the new file. If you use an existing filename, the text in that file will be overwritten by the new text.

If you only want to write part of the file, you must specify the beginning and ending lines you want to write. For example:

50,220w newfile<*CR*>

will create a file named "newfile" which will contain lines 50 through 220 of the file you are editing.

Changing Files While Using the "bfs" Editor

When using the **bfs** editor, only one file can be scanned at a time. However, the "**e**" command allows you to change files without quitting the editor. For example, if you are scanning *file1* with the **bfs** editor and want to change to *file2*, you would use the command:

e file2<*CR*>

This will cause the editor to leave *file1* and enter *file2*. To reenter *file1*, you would need to use the **e** command again. Using the quit (**q**) command will cause you to leave the file you are now in and return you to the UNIX System.

Issuing UNIX System Commands

The **bfs** editor allows you to execute a single UNIX System command by entering a command of the form:

!cmd<*CR*>

where "cmd" represents the command you want to execute. The system will then execute the command. When finished, **bfs** will display an **!** and then return you to the current line in the file. You can then continue editing or issue another **!** command.

If you need to execute more than one UNIX System command, enter the command:

!sh<*CR*>

When you are finished executing UNIX System commands, enter a **control-d** (depress and hold the CONTROL "CTRL" key and simultaneously depress the "d" key). The editor will display an **!** and return to the current line in the file.

High-Level "bfs" Commands

A "command file" is an executable file that contains editor commands. Command files may be set up and run against other files with the **bfs** editor. When executing command files, the output is directed to another file.

"comm" — Select or Reject Common Lines

General

The **comm** command compares two files and produces an output showing the differences and similarities between them. The contents of the two files should be in alphabetical order, that is, in order according to the ASCII collating sequence. The output is formatted into three columns. The first column lists those lines found only in the first named file, the second column lists those lines found only in the second named file, and the third column lists those lines that are common to both files.

Command Format

The general format for the **comm** command is as follows:

comm [— [**123**]] *file1 file2*

The — [**123**] option suppresses the column corresponding to the number specified. For example, if **—1** is specified, the first column of the output is not displayed. Thus, only those lines uncommon to the second named file and those lines common to both named files are displayed.

If a dash (—) is entered in place of a file name, the standard input from the terminal is read. The **comm** command compares the input with the file and produces the three-column output as before.

Sample Command Use

The examples provided are based on the contents of two files named **listA** and **listB**. The contents of these two files are as follows:

listA:		listB:	
	birds		**birds**
	cats		**cats**
	dogs		**horses**
	horses		**mice**
	mice		**mules**
	snakes		**pigs**

The following command line and system response shows how to compare the two lists and receive all columns of the output:

```
$ comm listA listB<CR>
                birds
                cats
dogs
                horses
                mice
        mules
        pigs
snakes
$
```

The following command line and system response shows how to compare the two lists and output only those lines that are common to both files:

```
$ comm -12 listA listB<CR>
birds
cats
horses
mice
$
```

The following example shows how to alphabetize a file named **list** and compare it to **listB** with the same command line. The file **list** is:

birds
mice
dogs
cats
pigs

The command line uses **sort** to alphabetize the file **list**.

```
$ sort list | comm - listB<CR>
		birds
		cats
dogs
	horses
		mice
	mules
		pigs
$
```

"csplit" — Context Split

General

The **csplit** command splits a file into sections using input arguments as the boundaries of the sections. The sections are suffixed with a number starting with 00 and may go up to 99. The first section (00) will contain from the beginning of the file up to, but not including, the line defined by the first argument. The second section (01) will contain the line defined by the first argument up to, but not including, the line defined by the second argument. The last section will contain the line defined by the last argument through the end of the original file. The original file is not affected.

Command Format

The general format for the **csplit** command is as follows:

csplit [-**s**] [-**k**] [-**f** *prefix*] **filename arg1** [**arg2 ... arg***n*]

The **csplit** command normally outputs the character count of each section as the section is created. The **-s** option will suppress the printing of these character counts. The process is complete when the system response is returned.

If an error occurs during the **csplit** operation, the sections that have been created are removed. The **-k** option overrides the removal of previously created files. However, the process will halt at the point the error occurred. The current section and the remainder of the original file will not be processed.

The created files are normally named **xx00** thru **xxnn**. If the **-f** *prefix* option is used, the files are named *prefix***00** through *prefix***nn**.

The **filename** is the name of the original file that is to be split. The command will start at the beginning of the file and search for the first

argument. That section is then written into a file, and the argument is used as the beginning for the next section. The arguments for the **csplit** command can be any combination of the following:

/string/ A file will be created from the current line up to, but not including, the line containing the character string *string*. This string may be followed by a +*n* or -*n* where *n* is a line number. For instance, if your file should contain **Page 5** and the three lines that follow it in the original file, the expression would be **/Page 5/+3**. If the character string has blanks or other significant characters to the command, the string must be enclosed in quotes.

%string% This argument acts exactly like */string/* except that no file will be created for the section from the current line to the line containing *%string%*.

zzz A file will be created from the current line up to, but not including, line number *zzz*. The line numbered *zzz* would then become the current line, that is, the first line in the next section.

{num} The argument that appears before *{num}* will be repeated *num* times. If the argument is a *string* type argument, that argument is searched for *num* more times. By using *{num}* after the *zzz* argument, you can split a file *num* times every *zzz* lines. It is a good idea to use the **-k** option with this argument because if the *{num}* number is too high, you will receive an error message and lose the files that have already been created.

Sample Command Use

The following example shows how to split the file **basic** into three pieces, **bas00, bas01**, and **bas02. The first line of bas01** will contain the string *test procedures*. The first line of **bas02** will contain the string *2.05*.

```
$ csplit -f bas basic " /test procedures/" /2.05/<CR>
2345
1068
297
$
```

The following example shows how to split the file **doc** into pieces of 100 lines each. To be sure that the entire file is split, an arbitrary number, 99 has been used for the number of times to split the file. Any lines over 10,000 will not be split. The **-s** option is used to suppress the character counts of each 100-line file.

```
$ csplit -s -k doc 100 {99}<CR>
$
```

The 100-line files would be named **xx00** through **xx***nn*.

The following example shows how to save the last piece of the file **mail**. The saved file, **xx00**, contains the text from the line **MISC** to the end of the file.

```
$ csplit mail %MISC%<CR>
$
```

"cut" — Output Selected Fields of a File

General

The **cut** command is used to output selected columns or fields from a line of data. The lines of data operated on by the **cut** command can be from one or more files, the output of another command, or from the terminal (standard input).

Command Format

The general format of the **cut** command is as follows:

cut -c*list* [*file(s)*]

cut -f*list* [**-d***char*] [**-s**] [*file(s)*]

The **-c***list* argument identifies the character positions in each line that are to be output. Individual character positions are identified by integers. A comma (,) is used to separate each position identifier. Ranges are specified by using a dash between the starting and ending number in the range. For example, character positions 1, 5, and 7 through 10 are identified as follows:

-c1,5,7-10

The **-f***list* argument identifies the field positions of each line that are to be output. A comma (,) is used to separate each field identifier. Ranges are specified by using a dash between the starting and ending number in the range. For example fields 1, 5, and 7 through 10 are input as follows:

-f1,5,7-10

The **-s** option is used with the **-f***list* argument to prevent lines that do not contain field delimiters from being output.

The **-d***char* argument identifies the field delimiter. The default field delimiter is the tab character. For example, the argument **-d:** defines a colon as the field delimiter. Delimiter characters that have a special meaning to the shell must be either placed in single quotes or escaped by preceding the character with a backslash (\). For example, the space can be defined as a field delimiter by the following:

-d' '

The *file(s)* argument identifies the name or names of the files that are to be operated on by the command.

Sample Command Use

The following sample command line entries and system responses show you how to output the character positions 5 through 10 and 15 from each line of a file named **list**. In this example, the **cat** command is first used to display the contents of the **list** file.

```
$ cat list<CR>
ABCDEFGHIJKLMNOPQRSTUVWXYZ
         11111111111222222
12345678901234567890123456
$ cut -c5-10,15 list<CR>
EFGHIJO
     11
5678905
$
```

The following sample command line entries and system responses show you how to output the second and fifth fields from a file named **table**. The field separator (delimiter) is a colon (:). Note what happens when the delimiter is defined as a space by the **-d' '** argument. Also, note that the sequence in which you define the fields (**-f5,2** verse **-f2,5**) does not change the sequence in which they are output. The selected fields are output in the order that they appear in the data, from left to right. In this example, the **cat** command is used to display the contents of the **table** file.

```
$ cat table<CR>
field 1:field 2:field 3:field 4:field 5:field 6
field 1:field 2:field 3:field 4:field 5:field 6
field 1:field 2:field 3:field 4:field 5:field 6
$ cut -f2,5 -d: table<CR>
field 2:field 5
field 2:field 5
field 2:field 5
$ cut -f5,2 -d':' table<CR>
field 2:field 5
field 2:field 5
field 2:field 5
$ cut -f2,5 -d' ' table<CR>
1:field 4:field
1:field 4:field
1:field 4:field
$
```

"diff3" — 3-Way Differential File Comparator

General

The **diff3** command compares three files and outputs information showing the range of lines that differ between the files. The information is separated by a string of equal signs (====) to signify that the files are different. If the string of equal signs is alone, this shows that all files differ. If the string of equal signs is followed by a number, the number signifies what file is different. For example, ====**2** would show that the second named file is different and the information following the ====**2** would show the differences.

The range of lines that are different are shown in the format "**f:ln ed**" where;

> **f** = the number of the file as it was entered in the command line.
>
> **ln** = the line number that is different. This could be a range of lines.
>
> **ed** = the editor command that needs to be performed to bring the files into agreement with each other. If the **c** (change) operation is shown, the original contents of the file will be shown immediately after the range of lines information.

Command Format

The general format for the **diff3** command is as follows:

diff3 [-ex3] *file1 file2 file3*

The **-e** or **-x** options publish a script file with the editor commands needed to make the first named file agree with the third named file. The script file contains all the commands necessary to make the proper changes and may be applied directly to the file.

Sample Command Use

The sample commands used in this section are based on the usage of three files named **a**, **b**, and **c**. The contents of the three files are shown below:

a:	**b:**	**c:**
A	**B**	**C**
B	**C**	**D**
C	**D**	**E**
D	**E**	**A**
E	**A**	**B**

The following command and system response show how to compare the three files and have the standard output displayed:

```
$ diff3 a b c<CR>
====
1:1,2c
  A
  B
2:1c
  B
3:0a
====
1:5a
2:5c
  A
3:4,5c
  A
  B
$
```

The following command line and system response show how to compare the three files and receive an editor script file that will make **a** agree with **c**:

```
$ diff3 -e a b c<CR>
5a
A
B
1,2c
w
q
$
```

The script file that is produced can be applied directly to the file being changed. This can be done on the same command line as the **diff3** command. The following command line shows how to compare the three files and apply the script file to **a**. There will be no output from this command, completion is shown with the system prompt.

```
$ diff3 -e a b c | ed - a<CR>
$
```

"dircmp" — Directory Comparison

General

The **dircmp** command compares two directories and outputs information about the names and contents of the files in each directory. The output is paginated to list those files that are uncommon to each directory and then those files that have common file names. The files common to both directories are compared, and the output includes whether the contents are the "same" or "different".

Command Format

The general format for the **dircmp** command is as follows:

dircmp [**-d**] [**-s**] *dir1 dir2*

The **-d** option makes a comparison of the files common to both directories and gives information on what must be done to bring the two files into agreement. The format for the output is identical to the format of the **diff** command covered previously in this chapter.

The **-s** option will suppress any messages about identical files. That is, the output will only contain information on the files that are different from each other.

Sample Command Use

The examples provided in this section are based on the contents of the two directories **dir1** and **dir2**. The contents of the two directories follow:

dir1:		dir2:	
	appendix		**appendixA**
	chap1		**appendixB**
	chap2		**chap1**
	chap3		**chap2**
	chap4		**chap3**
	index		**chap4**
	table		**index**
	toc		**toc**
	trademarks		**trademarks**

The following command line and system response show how to compare **dir1** and **dir2**:

```
$ dircmp dir1 dir2<CR>

July 19 09:02 1985  ../dir1 only and ../dir2 only Page 1

./appendix        ./appendixA
./table           ./appendixB





July 19 09:02 1985  Comparison of ../dir1 ../dir2 Page 1

directory     .
same          ./chap1
different     ./chap2
different     ./chap3
different     ./chap4
same          ./index
different     ./toc
same          ./trademarks


$
```

Note: The output used in this example contains only the text of the output. The output is paginated with "white space" separating the uncommon files in each directory from the section displaying the common file names.

The following command line shows how to compare the files in **dir1** and **dir2** and output information that tells what must be done to bring the files into agreement:

```
$ dircmp -d dir1 dir2<CR>

Note: The first part of the output would appear
  the same as in the previous example. The
  last part of the output would be in the
  format identical to that of the diff
  command.

$
```

"egrep," "fgrep" — Search a File for a Pattern

General

The **egrep** and **fgrep** commands search files or input lines for matching character patterns. These commands are similar to the **grep** command explained in the *AT&T 3B2 Computer User Reference Manual.*

The input data to be searched can be the output of another command, one or more specified files, or the input from the terminal. When more than one file is searched, the file name is printed along with the matching input lines. The character patterns are regular expressions or fixed strings of characters in the style of the text editor (**ed**). Be careful when using the characters that have special meaning to the editor shell. In general, the pattern should be enclosed in single quotes ('pattern') to remove any special character meaning.

The *expression* **grep** (**egrep**) searches for full regular expressions. The **egrep** command accepts the following conventions for defining expressions:

- A pattern followed by a plus sign (+) matches one or more occurrences of the pattern.

- A pattern followed by a question mark (?) matches 0 or 1 occurrences of the pattern.

- Multiple patterns can be defined by separating each pattern by a pipe symbol (|) or by a new-line (carriage return). When a new-line is used, the secondary system prompt (>) is displayed. Each pattern is entered on a separate line following the prompt. The last pattern is entered on the same line as the remainder of the command. The command outputs matches for any or all patterns.

- Patterns can be grouped by enclosing the pattern in parentheses.

The *fast* **grep** (**fgrep**) command searches for fixed patterns. This command is fast and compact.

Command Format

The general format for each of these commands is as follows:

egrep [*options*] [*expression*] [*file(s)*]

fgrep [*options*] [*string(s)*] [*file(s)*]

The *options* recognized by these commands are explained as follows:

-b	Outputs the block number of the matching line. Each line is preceded by the number of the data block containing the line.
-c	Outputs only the number of lines that match the pattern.
-e *expression*	Same as a simple *expression* argument, but is useful when the *expression* contains a —.
-f *file*	The *pattern* (expressions or strings) is read (taken) from the specified *file*.
-l	Outputs only the names of the files that contain matching lines.
-n	Each line is preceded by its relative line number in the file.
-v	Outputs the lines that DO NOT contain the defined pattern.

-x Outputs the lines that match the pattern exactly and entirely. This option is used with the **fgrep** command only.

The *expression* and *string* arguments define the search pattern or patterns. The *file(s)* argument is used to identify the file or files that are to be searched. Note that the file names are separated by a space.

Sample Command Use

The following command line and system response show how you can search two files (**list1** and **list2**) for lines containing one of several patterns. The patterns to be searched for are *eggs* and *bacon*. The **-n** option is used to display the line number of the matching line.

```
$ egrep -n 'eggs¦bacon' list1 list2<CR>
list1:2:eggs
list2:1:bacon
list2:3:eggs
$
```

Note: The semicolon (:) is used to separate each field of the output of the **egrep** command. The first field is the file name. The second field is the line number of the matched pattern in the named file. The last field is the line containing the matching pattern.

The following command line and system response show you how to enter the previous example using a new-line (carriage return) to separate the patterns instead of a pipe symbol (¦):

```
$ egrep -n 'eggs<CR>
> bacon' list1 list2<CR>
list1:2:eggs
list2:1:bacon
list2:3:eggs
$
```

The following command line and system response show how you can search multiple files for lines that DO NOT contain a specified pattern. The **-v** option causes all lines that DO NOT match the specified patterns to be output. The **-n** option is used again to output the line number of the matching line.

```
$ egrep -nv 'eggs¦bacon' list1 list2<CR>
list1:1:milk
list1:3:toast
list1:4:ham
list2:2:milk
list2:4:juice
list2:5:bread
$
```

The following example shows how you can use a file containing a list of patterns to search a group of files. The file to search from is named **words** and contains the following patterns: **570ab[3-7], 448hj2, 747bg32**. The first line of the **words** file defines a pattern beginning with 570ab and ending with 3, 4, 5, 6, or 7. The **egrep** command will search all files in the current directory that begin with the characters **serials**.

```
$ egrep -f words serials*<CR>
serialsnet:570ab4
serialsnet:570ab5
serialsold:747bg32
serialsnew:570ab3
serialsnew:570ab7
serialsnew:448hj2
$
```

"file" — Determine File Type

General

The **file** command is used to determine the contents of one or more specified files. The command examines the contents of the first block of data (1024 bytes) of each file and attempts to classify the data. A file called **/etc/magic** is used by the **file** command to classify files containing certain special numeric or string constants. If you enter **cat /etc/magic**, an explanation of the **magic** file format is displayed.

Some of the file-types that can be classified are:

3b2/3b5 executable
3b2/3b5 executable not stripped
ASCII text
c program text
commands text
data
directory
empty
English text
[nt]roff, tbl, or eqn input text

Note: The file must have read permission before a classification can be made.

Command Format

The general format of the **file** command is as follows:

file [**-c**] [**-f** *ffile*] [**-m** *mfile*] *name(s)*

The **-c** argument causes the command to check the magic file for format errors. No file classification is done with this function.

The **-f** *ffile* option is used to specify the name of a file that contains a list of file names that are to be examined. The *ffile* argument identifies the name of the file containing the list of file names to be examined.

The **-m** *mfile* option is used to specify an alternate magic file. The *mfile* argument identifies the name of an alternate magic file.

Sample Command Use

The following command line entry and system responses show how you can determine the classification of a given file:

```
$ file /f1/house/bills/electric<CR>
/f1/house/bills/electric:      ascii text
$
```

The following command line entries and system responses show how you can determine the classification of several files. A file named **list** is first created that contains a listing of the files to be examined. The **file** command is then executed with the **-f** option to classify the files identified in the **list** file.

```
$ ed list<CR>
?list
a<CR>
/f1/house/bills/electric<CR>
/f1/house/bills/water<CR>
/f1/house/bills/gas<CR>
/f1/house/bills/telephone<CR>
.<CR>
w<CR>
94
q<CR>
$ file -f list<CR>
/f1/house/bills/electric:  ascii text
/f1/house/bills/water:  ascii text
/f1/house/bills/gas:  ascii text
/f1/house/bills/telephone:  ascii text
$
```

"join" — Relational Data Base Operator

General

The **join** command is used to join a common field of two files. The results are printed on your terminal screen. The fields that are to be joined must be sorted in an increasing ASCII collating sequence. Normally, the first field in each line is the field to be joined. A blank, tab, or new-line usually separates the fields. Multiple separators will be counted as one, and leading separators are discarded.

One line of output is generated for each pair of lines in the files that have identical join fields. The output line normally consists of the common field followed by the rest of the line from the first file, followed by the rest of the line from the second file.

Command Format

The general format of the **join** command is as follows:

join [*options*] *file1 file2*

The following options exist:

- **-a***n* — In addition to the normal output, a line is produced for each unpairable line in file *n* (where n is 1 or 2).
- **-e** *s* — Replace empty output fields by string *s*.
- **-j***n m* — Join on the *m*th field of file *n*. If *n* is missing, use the *m*th field in each file.
- **-o** *list* — Each output line includes the fields specified in *list* and each element of *list* has the form *n.m* (where *n* is a file number and *m* is a field number).

-t*c*   Use character *c* as a separator (tab character). Every appearance of *c* in a line is significant.

The *file1* and *file2* arguments are the names of the files that are to be joined.

Sample Command Use

The following command line entries and system responses show the basic operation of the **join** command. The **cat** command is used to display the contents of **file1** and **file2**. The **join** command is used to join an inventory of red and blue items.

```
$ cat file1<CR>
1. red balls (7)
2. red bicycles (3)
3. red cars (5)
4. red ink pens (10)
5. red shoes (2 pair)
$ cat file2<CR>
1. blue balls (4)
2. blue bicycles (2)
3. blue cars (3)
4. blue ink pens (5)
5. blue shoes (3 pair)
6. blue pants (2 pair)
$ join -a2 file1 file2<CR>
1. red balls (7) blue balls (4)
2. red bicycles (3) blue bicycles (2)
3. red cars (5) blue cars (3)
4. red ink pens (10) blue ink pens (5)
5. red shoes (2 pair) blue shoes (3 pair)
6. blue pants (2 pair)
$
```

"newform" — Change the Format of a Text File

General

The **newform** command is used to read lines from a file or the standard input, reformat those lines, and reproduce the lines on the standard output. The format is selected through the command line options listed under "Command Format".

Command Format

The general format of the **newform** command is as follows:

newform [**-s**] [**-i***tabspec*]
[**-o***tabspec*] [**-b***n*]
[**-e***n*] [**-p***n*]
[**-a***n*] [**-f**] [**-c***char*]
[**-l***n*] [*file(s)*]

where:

-i*tabspec* — This option expands tabs into spaces. The *tabspec* part of this option uses the same tab specifications used with the **tab** command. Tab specifications may be found on the first line of the standard input. Here, use a double minus sign (--)as the *tabspec*. If *tabspec* is not specified, **-8** is used. If **-0** is given as the *tabspec*, there should not be any tabs in the text. If tabs are found in the text, they are treated as **-1**.

-o*tabspec* — This option will replace spaces with tabs. The *tabspec* part of this option uses the same tab specifications as the *tabspec* part of the **-i***tabspec* option. If *tabspec* is not specified, **-8** is used. If a *tabspec* of **-0** is specified, spaces will not be converted to tabs.

-l*n* The effective line length is set to *n* characters. If this option is not specified, the effective line length is 80 characters. If **-l** is specified without *n*, the effective line length is set to **72**. Tabs and backspaces are considered to be one character. Remember, tabs may be expanded to spaces by the **i***tabspec* option.

-b*n* Shorten the beginning of the line by *n* characters when the line length is greater than the effective line length set by the **-l***n* option. If *n* is not specified, the line will be shortened by the amount of characters necessary to obtain the effective line length set by the **-l***n* option. It is a good idea to specify **-l***n* as **-l1** when using this option. That way, you will be sure that this option will be started, because the effective line length will be shorter than any line in the file.

-e*n* This option works the same as the **-b***n* option except that characters are removed from the end of the line.

-c*k* Change the prefix character (see **-p***n* option) and/or the append character (see **-a***n* option) to *k*.

-p*n* Prefix *n* characters to the beginning of a line when the line length is less than the effective line length set by the **-l***n* option. Spaces will be the prefix if the **-c***k* option is not specified. If *n* is not specified, the number of characters necessary to obtain the effective line length will be the prefix number.

-a*n* This option is the same as the **-p***n* option except that characters are appended to the end of a line.

-f Write the tab specification format line on the standard output before printing the output. The **-o***tabspec* option determines what tab specification format line is printed. If the *tabspec* part of the **-o***tabspec* option is not specified, the line printed will be the default specification of **-8**.

-s Shears the leading characters off each line up to the first tab. Up to eight of the sheared characters are placed at the end of the line. If more than eight characters are sheared, the eighth character is replaced by an * and the rest are discarded. The first tab is always discarded.

There must be a tab on each line of the file. If there is not a tab on each line, an error message and a program exit will occur. The characters sheared off are saved internally until all other options specified are applied to that line. These characters are then added at the end of the processed line.

files(s) The name of the file(s) that is to be read.

The command line options may appear in any order, may be repeated, and may be mingled with *file(s)*. However, if you use the **-s** option, it must be the first option specified.

Sample Command Use

The following command line entries and system responses show you a typical **newform** command output. The **cat** command is used to display the contents of **testfile**. The **newform** command is used to display the contents of **testfile** while removing the first three characters of each line and keeping the same column definition.

```
$ cat testfile<CR>
  RENTAL ITEM  DATE RENTED   DATE RETURNED

1. ladder      7/15/85       7/16/85
2. lawn mower  7/16/85       7/17/85
3. spray gun   7/17/85       7/18/85
4. tiller      7/18/85       7/19/85
5. weed eater  7/19/85       7/22/85
$ newform -i -l1 -b3 testfile<CR>
RENTAL ITEM    DATE RENTED   DATE RETURNED

ladder         7/15/85       7/16/85
lawn mower     7/16/85       7/17/85
spray gun      7/17/85       7/18/85
tiller         7/18/85       7/19/85
weed eater     7/19/85       7/22/85
$
```

The following command line entry and system response show how to display the contents of **testfile** without the last column:

```
$ newform -i -l1 -e13 testfile<CR>
  RENTAL ITEM  DATE RENTED

1. ladder      7/15/85
2. lawn mower  7/16/85
3. spray gun   7/17/85
4. tiller      7/18/85
5. weed eater  7/19/85
$
```

"nl" — Line Numbering Filter

General

The **nl** command is used to read lines from a file or the standard input. The lines that are read are numbered and printed on your terminal screen. The way the lines are numbered depends on the options you select.

The **nl** command views the text it reads in terms of logical pages. A logical page contains three sections: a header, a body, and a footer section. You can have empty sections. The options for numbering lines can be different for each of the three sections. In order for the three sections to be recognized, the following delimiter character(s) must be included in the input lines:

LINE CONTENTS	START OF
\:\:\:	header
\:\:	body
\:	footer

Note: There must not be any other input on the lines containing the delimiter character(s).

The **nl** command assumes the text being read is a single, logical page body unless you select other options.

Command Format

The general format of the **nl** command is as follows:

nl [-**h***type*] [-**b***type*] [-**f***type*] [-**v***start#*] [-**i***incr*] [-**p**] [-**l***num*] [-**s***sep*] [-**w***width*] [-**n***format*] [-**d***delim*] *file*

where:

-**h***type* — Used to specify what logical page header lines are to be numbered. The recognized types are:

- **a** — Number all lines
- **t** — Number lines with printable text only
- **n** — No line numbering
- **p***string* — Number only the lines that contain the regular expression specified in *string*.

The default *type* for the logical page header is **n**.

-**b***type* — Used to specify what logical page body lines are to be numbered. The recognized types are the same as -**h***type*. The default *type* for the logical page body is **t**.

-**f***type* — Used to specify what logical page footer lines are to be numbered. The recognized types are the same as -**h***type*. The default *type* for the logical page footer is **n**.

-**v***start#* — The initial value used to number the logical page lines. Default is **1**.

-**i***incr* — The increment value used to number the logical page lines Default is **1**.

-p Do not restart numbering at the logical page delimiters.

-l*num* The number of blank lines to be considered as one. The appropriate **-ha, -ba**, and **-fa** option must be set. A **-l2** results in only the second adjacent blank line being numbered. Default is **1**.

-s*sep* The character(s) used in separating the line number and the corresponding text line. Default is a tab.

-w*width* The number of characters to be used for the line number. Default is **6**.

-n*format* The line numbering format. The recognized values are:

- **ln** Left justified with no leading zeros
- **rn** Right justified with no leading zeros
- **rz** Right justified with leading zeros.

Default is **rn**.

-d*delim* Used to change the delimiter characters. If only one character is entered, the second character remains the default character (:). If you wish to use a backslash (\) as a delimiter character, you need to enter two backslashes (\\).

file The name of the file that is read by the **nl** command.

The options can be specified in any order and can be mingled with an optional file name. However, when intermingling options with a file, only one file can be moved.

Sample Command Use

The following command line entries and system responses show the basic operation of the **nl** command. The **cat** command is used to show the contents of file1. The **nl** command is used with several options to show how the command is input and the system response.

```
$ cat file1<CR>
\:\:\:
THIS IS THE HEADER SECTION
...
\:\:
This is the body section.
...
...
...
...
\:
THIS IS THE FOOTER SECTION
...
...
$ nl -ha -fa -v5 -i5 -nrz file1<CR>

000005  THIS IS THE HEADER SECTION
000010  ...

000015  This is the body section.
000020  ...
000025  ...
000030  ...
000035  ...

000040  THIS IS THE FOOTER SECTION
000045  ...
000050  ...
$
```

"od" — Octal Dump

General

The **od** command is used to output data in octal, decimal, ASCII, or hexadecimal formats. The name of the command, octal dump, is derived from the default output. Input can be from a named file, the output of another command, or from the standard input.

Command Format

The general format of the **od** command is as follows:

od [-**bcdoscx**] [*file*] [[+]*offset*[.][**b**]]

The meaning of the various format options are as follows:

-b Interpret bytes in octal (base 8).

-c Interpret bytes in ASCII.

-d Interpret words in unsigned decimal (absolute value).

-o Interpret words in octal. This is the default when no option argument is supplied.

-s Interpret 16-bit words in signed decimal.

-x Interpret words in hexadecimal (base 16).

The *file* argument identifies the name of the file to be output. If the *file* argument is omitted, input is taken from the standard input.

The *offset* argument identifies where the output is to start. This argument is normally expressed as the number of octal bytes to be skipped before data is output. If a period (.) is appended to the *offset*

argument, the argument is interpreted as a decimal number of bytes. If a letter **b** is appended to the argument, the argument is interpreted as the number of blocks to be skipped before data is output. If the *file* argument is omitted, the *offset* argument must be preceded by a plus sign (+) to identify what follows as being the *offset* argument.

Sample Command Use

The following command line entries and system responses show how you can output the contents of a file named **list1** using the default form of the **od** command. This form of the command outputs octal words. The **cat** command is first used to display the normal ASCII contents of the file.

```
$ cat list1<CR>
eggs
bread
milk
butter
meat
$ od list1<CR>
0000000 062547 063563 005142 071145 060544 005155 064554 065412
0000020 061165 072164 062562 005155 062541 072012
0000034
$
```

The following command line entries and system responses show how you can output the contents of a file named **list1** using the **-b** option of the command. This form of the command outputs the octal value for each character (byte). An *offset* of 27 bytes is used in this example. This *offset* causes the output to start at the last line of the file in this example. The **cat** command is first used to display the normal ASCII contents of the file. You need to refer to an octal map of the ASCII character set to make sense out of the output. For example, the letter "m" is octal 155; the letter "e" is octal 145; a new-line character is octal 012.

```
$ cat list1<CR>
eggs
bread
milk
butter
meat
$ od -b list1 27<CR>
0000027 155 145 141 164 012 000
0000034
$
```

"pack" — Compress Files

General

The **pack** command is used to compress and store files. Text files can be reduced between 60% and 75% of their original size. Load modules that use a larger character set and have a more uniform distribution of characters can be reduced to about 90% of their original size. The original file is removed and the compressed data is stored in a file with the same file name, except that a **.z** is added to the end of the file name. For example, if you compressed a file named **file1**, the compressed data will be stored in **file1.z**. The access modes, access and modified dates, and owner will remain the same as the original file. The compressed file can be restored to its original form using the **pcat** or **unpack** command.

How much a file is compressed depends on two things. They are:

1. The size of the input file
2. The character frequency distribution.

Usually, it is not worthwhile to compress files smaller than three blocks of data because a decoding tree is placed at the beginning of the compressed file. However, if the character frequency distribution is skewed, you may wish to compress the file even if the file is less than three blocks. Some reasons for the character frequency distribution being skewed are printer plots, pictures, or tables in the file.

The **pack** command will not work if:

1. The file appears to be already compressed.
2. The file name has more than 12 characters.

3. The file is linked to another file.
4. The file is a directory.
5. The file cannot be opened.
6. No disk storage blocks will be saved by compression.
7. A file called *name*.**z** already exists.
8. The **.z** file cannot be created.
9. An input/output error occurred during processing.

The **pack** command returns a value that is the number of files that it failed to compress.

Command Format

The general format of the **pack** command is as follows:

pack [-] *name ...*

where:

-	Used to set an internal flag that causes the number of times each byte is used, its relative frequency, and the code for the byte to be printed on the standard output. Additional occurrences of - in place of *name* will cause the internal flag to be set and reset.
name	The name of the file to be compressed.

Sample Command Use

The following command line entries and system responses show the basic operation of the **pack** command. The **ls -l** command is used to show what are the file sizes. The **pack** command is used to show how the command is inputted and the response you will receive. The **ls -l** command is used again to show the size of the files after they are compressed.

```
$ ls -l<CR>
total 109
-rw-------  1 cec  other   29727 July 19 13:14 file1
-rw-------  1 cec  other   24355 July 19 13:15 file2
$ pack - file1 file2<CR>
pack: file1: 36.2% Compression
        from 29727 to 18980 bytes
        Huffman tree has 15 levels below root
        90 distinct bytes in input
        dictionary overhead = 112 bytes
        effective  entropy  = 5.11 bits/byte
        asymptotic entropy  = 5.08 bits/byte
pack: file2: 36.2% Compression
        from 24355 to 15530 bytes
        Huffman tree has 15 levels below root
        85 distinct bytes in input
        dictionary overhead = 107 bytes
        effective  entropy  = 5.10 bits/byte
        asymptotic entropy  = 5.07 bits/byte
$ ls -l<CR>
total 73
-rw-------  1 cec  other   18980 July 19 13:14 file1.z
-rw-------  1 cec  other   15530 July 19 13:15 file2.z
$
```

"paste" — Side-by-Side File Merge

General

The **paste** command is used to combine two or more files of data in a side-by-side fashion. Each file of data is treated like a column of data in a table. The output of the paste command can be displayed on the terminal, redirected to a file, or redirected to another command.

Command Formats

Three general forms of the **paste** command are provided. These forms are as follows:

paste *file(s)*

paste -d *'list' file(s)*

paste -s [**-d** *'list'*] *file(s)*

The *file(s)* argument identifies the names of the files that are to be pasted together. The hyphen (-) can be used as a file name to read a line from the standard input. There is no prompting associated with the use of the hyphen.

The **-s** option is used to merge several lines from each input file as opposed to one line from each input file.

The **-d***list* argument option is used to define the delimiter(s) that is used between the merged lines. The tab character is the default delimiter. The *list* argument identifies what is to replace the tab delimiter. The items (characters) identified in the *list* argument are used in sequence until the end of the list. Then, the listed delimiters are reused in the same sequence. In general, the **list** argument should be in double quotes.

For example, to get one backslash, use **-d**'\\' as the argument; use **-d**' ' as the argument to define a space as the delimiter. Special characters are defined by escape sequences. These include the following:

- **n** for new-line character
- **t** for tab character
- \\\\ for the backslash character
- **0** for an empty string.

Sample Command Use

The following examples are based on the use of two files named **list1** and **list2**. The contents of these two files are as follows:

list1:	**list2:**
list1: item1	**list2: item1**
list1: item2	**list2: item2**
list1: item3	**list2: item3**
list1: item4	**list2: item4**
list1: item5	**list2: item5**
list1: item6	**list2: item6**
list1: item7	**list2: item7**

The following command line entries and system responses show how you can merge the contents of two files using the simplest form of the **paste** command. This form of the command requires no options. The named files are merged in a side-by-side fashion with a tab character as the delimiter between the lines of the files. The output of the **paste** command is redirected to a file named **save**. The **cat** command is used to display the contents of the resulting file.

```
$ paste list1 list2 > save<CR>
$ cat save<CR>
list1: item1    list2: item1
list1: item2    list2: item2
list1: item3    list2: item3
list1: item4    list2: item4
list1: item5    list2: item5
list1: item6    list2: item6
list1: item7    list2: item7
$
```

The following command line entries and system responses show how you can merge the contents of two files using the form of the **paste -d***list* command. The named files are merged in a side-by-side fashion with a slash (/) character as the delimiter between the lines of the file. The output of the **paste** command is redirected to a file named **save**. The **cat** command is used to display the contents of the resulting file.

```
$ paste -d'/' list1 list2 > save<CR>
$ cat save<CR>
list1: item1/list2: item1
list1: item2/list2: item2
list1: item3/list2: item3
list1: item4/list2: item4
list1: item5/list2: item5
list1: item6/list2: item6
list1: item7/list2: item7
$
```

"pcat" — Concatenate and Print Packed Files

General

The **pcat** command is used to concatenate and print files that have been compressed by the **pack** command. The compressed file is expanded and printed on your terminal screen in its original form.

The **pcat** command will not work if:

1. The file name (exclusive of **.z**) has more than 12 characters.
2. The file cannot be opened.
3. The file does not appear to be the output of the **pack** command.

The **pcat** command returns a value that is the number of files that it failed to expand.

Command Format

The general format of the **pcat** command is as follows:

pcat *name ...*

The *name* argument identifies the name of the file that needs to be expanded. The **.z** at the end of the file name does not need to be inputted when specifying *name*.

The standard output of the **pcat** command can be redirected to a file. You will have two files: one that contains the compressed data (*name*.**z**) and one that contains the original data.

The general format when redirecting the output of the **pcat** command follows:

pcat *name* > *new.file*

where:

name	Identifies the name of the file that needs to be expanded.
new.file	Identifies the name of the file that contains the expanded data.

Sample Command Use

The following command line entries and system responses show the basic operation of the **pcat** command. The **ls -l** command is used to display the compressed files before the **pcat** command is given. The **pcat** command is used to show you how the command is input using the redirection method. The **ls -l** command is used again to display the results of executing the **pcat** command.

```
$ ls -l<CR>
total 71
-rw-------  1 cec  other    18980 July 19 13:14 file1.z
-rw-------  1 cec  other    15530 July 19 13:15 file2.z
$ pcat file1 > new.file1<CR>
$ pcat file2 > new.file2<CR>
$ ls -l<CR>
total 181
-rw-------  1 cec  other    18980 July 18 13:14 file1.z
-rw-------  1 cec  other    15530 July 18 13:15 file2.z
-rw-------  1 cec  other    29727 July 19 07:47 new.file1
-rw-------  1 cec  other    24355 July 19 07:48 new.file2
$
```

"pg" — Command Description

General

The **pg** command is a filter that will allow you to view a file one page at a time on a soft-copy terminal screen. A prompt (:) is displayed after every page. If a carriage return is entered after the prompt, another page is displayed. Other options, listed in this section, may be chosen. What makes the **pg** command different from other similar commands is that the **pg** command allows you to back up and review something that has already passed. The **pg** command scans the **terminfo** data base for your terminal type to determine the terminal attributes. The variable **TERM** specifies your terminal type. If **TERM** is not specified, the terminal type **dumb** is assumed. Refer to the *AT&T 3B2 Computer Programmer Reference Manual* for information on the **terminfo** data base.

A pause will occur after each page is displayed and the prompt is given. There are three categories of responses that can be given when the prompt is displayed. The three categories are those that cause further perusal, those that search, and those that change the perusal environment.

Commands that cause further perusal normally take a preceding *address*. The *address* is an optionally signed number that indicates the point from which further text should be displayed. The *address* can be given in pages or lines. A signed *address* specifies a point relative to the current page or line. An unsigned *address* specifies an address relative to the beginning of the file.

The perusal commands are as follows:

<*newline*> or <*blank*>
: Display the next page. If a signed *address* is used, the **pg** command goes forward (+) or backward (-) the numbered amount of pages specified and displays that page on your terminal screen. If an unsigned *address* is used, the page

number specified will be displayed.

l Scroll one line forward. If a signed *address* is used, the **pg** command simulates scrolling the screen, forward (+) or backward (-), the number of lines specified. If an unsigned *address* is used, the **pg** command prints a screenful beginning at the line number specified.

d or **^D** Simulates scrolling half a screen forward (+**1** *address*) or half a screen backward (-**1** *address*).

The next two perusal commands do not use addresses.

. or **^L** Causes the current page to be redisplayed.

$ Displays the last window (page) in the file. If the input is a pipe, use with caution.

The following commands are available for searching for specific patterns of text. These commands must be ended by a <*newline*>, even if the -*n* option is specified. You may use the regular expressions of the **ed** command. Refer to the *AT&T 3B2 Computer User Reference Manual* for information about the **ed** command.

i/pattern/ Search forward for the *i*th (default is *i*=1) occurrence of *pattern*. Searching will begin after the current page and will continue until the end of the file is reached. If the entire *pattern* is not on the same line, *pattern* will not be found.

i?pattern? or *i^pattern^*

Search backward for the *i*th (default is *i*=1) occurrence of *pattern*. Searching will begin before the current page and will continue until the beginning of the file is reached. Use *i^pattern^* if using an Adds 100 terminal.

The line found at the top of the screen will be displayed after the search has ended. By appending **m** or **b** to the search command, you can display the line at the middle of the window or the bottom of the window. The suffix **t** can be used to restore the original file.

You can change the perusal environment with the following commands:

*i***n** — Begin perusing the *i*th next file in the command line. If *i* is not specified, 1 is used.

*i***p** — Begin perusing the *i*th previous file in the command line. If *i* is not specified, 1 is used.

*i***w** — Display another window of text. If *i* is present, set the window size to *i*.

s *filename* — Save the current file that is being perused in *filename*. This command must be ended by a <*newline*>, even if the *-n* option is specified.

h — Help command. An abbreviated summary of available commands is displayed.

q or **Q** — Quit the **pg** command.

!*command* — The *command* is executed by the shell. If the **SHELL** environment variable is set, that shell is used. If the **SHELL** environment variable is not set, the default shell is used. This command must be ended by a <*newline*>, even if the *-n* option is specified.

You can stop sending output to the terminal at any time by depressing the quit key (normally control-\) or the interrupt (break) key. The prompt will appear and you may then enter commands in the normal manner. Unfortunately, some output is lost when you stop the output. This happens because any characters waiting in the terminal output queue are flushed when the quit signal occurs.

The **pg** command acts like the **cat** command if the standard output is not a terminal screen. The only difference is that a header is printed before each file if there is more than one file. Refer to the *AT&T 3B2 Computer User Reference Manual* for information about the **cat** command.

Execution of the **pg** command is stopped if **BREAK**, **DEL**, or is depressed while the **pg** command is waiting for terminal input. If you are between prompts, these signals interrupt the current task and will place you in the prompt mode. Use the interrupt signals with caution when the input is coming from a pipe, since the interrupt is likely to stop the other commands in the pipeline.

There are a couple of bugs that you need to know about. The first one is that the terminal tabs should be set to every eight positions or you may get undesirable results. The second one is that when using the **pg** command as a filter with another command that changes the terminal input/output options, terminal settings may not be restored correctly.

Command Format

The general format of the **pg** command is as follows:

pg [*-number*] [**-p** *string*] [**-cefns**] [*+linenumber*] [*+/pattern/*] [*file(s)*]

where:

-number	The size (number of lines) of the window. If the size is not specified, the default value is one line less

than the total number of lines that can be displayed on your terminal screen.

-p *string* — Causes *string* to be used as the prompt. If **%d** appears in *string*, the first occurrence of **%d** in the prompt is replaced by the current page number when the prompt is issued.

-c — Take cursor to the home position and clear the screen before displaying a page. If **clear_screen** is not defined in the **terminfo** data base, this option will be ignored.

-e — Normally, a pause will occur at the end of each page and at the end of each file. This option eliminates the pause at the end of each file.

-f — Normally, if a line is longer than the terminal screen width, it is split into two lines. However, there are times when some sequences of characters in the text generate undesirable results; such as escape sequences for underlining. Here, you can use the option to inhibit the **pg** command from splitting lines.

-n — Normally, commands must be ended by a *<newline>* character. This option causes the command to end as soon as a command letter is entered.

-s — Causes all messages and prompts to be printed in the standout mode (usually inverse video).

+*linenumber* — Start up at *linenumber*.

+/*pattern*/ — Start up at the first line containing the pattern specified.

file(s) The name of the file to be examined. If *file(s)* is not specified or if a minus sign (-) is specified, the **pg** command reads the standard input.

Sample Command Use

The following command line entry and system response show the basic operation of the **pg** command. The **pg** command along with the **news** command is used in a pipeline to read the system news.

```
$ news | pg -p " (Page %d):" <CR>
Note: The first page of the news will appear next.
(Page 1): Note: This is the prompt. It will appear
          after each page with the number of the page
          you are on. You may now enter a
          command that manipulates the text or enter
          q to quit.
$
```

"sdiff" — Side-By-Side Difference Program

General

The **sdiff** command uses the output of the **diff** command (discussed earlier in this chapter) to produce a side-by-side listing of two files. If the lines are identical, each line of the two files are printed side-by-side with a blank gutter between the two files. If the line exists only in *file1*, a less than (<) symbol is in the gutter. If the line exists only in *file2*, a greater than (>) is in the gutter. If the line exists in both files and they are different, a pipe symbol (|) is in the gutter.

For example:

```
x  |  y
a     a
b  <
c  <
d     d
   >  c
```

Command Format

The general format of the **sdiff** command is as follows:

sdiff [*options ...*] *file1 file2*

The following options exist:

-w *n* — Use the next argument (*n*) as the width of the output line. If *n* is not specified, the line length will be 130 characters.

-l — Only print the left side of any lines that are identical.

-s Do not print identical lines.

-o *output* Use the next argument (*output*) to create a third file that will let you control the merging of *file1* and *file2*. All identical lines of *file1* and *file2* are copied to the *output* file. All different lines of *file1* and *file2* are printed on your terminal screen. After the different lines are printed, you will receive a prompt (**%**). After the prompt (**%**) is received, enter one of the following commands:

- **l** Append the left column to the output file.
- **r** Append the right column to the output file.
- **s** Turn the silent mode on; do not print identical lines.
- **v** Turn the silent mode off.
- **e l** Will let you edit the left column.
- **e r** Will let you edit the right column.
- **e b** Will let you edit the concatenation of the left and right columns.
- **e** Will let you edit a new file.
- **q** Exit from the program.

When you exit from the editor, the resulting file is concatenated on the end of the *output* file.

The arguments *file1* and *file2* are the files that are being compared.

Sample Command Use

The following command line entries and system responses show the basic operation of the **sdiff** command. The **cat** command is used to display the contents of file1 and file2. The **sdiff** command is then used to display a side-by-side comparison of file1 and file2.

```
$ cat file1<CR>
1000
2000
4000
8000
16000
32000
64000
128000
$ cat file2<CR>
500
1000
2000
3000
8000
16000
34000
64000
$ sdiff -w 30 file1 file2<CR>
          >     500
1000            1000
2000            2000
4000      |     3000
8000            8000
16000           16000
32000     |     34000
64000           64000
128000    <
$
```

"split" — Split a File Into Pieces

General

The **split** command is used to read a file and write it in *n* number of lines onto a set of output files. Default is 1000 lines per file. The name of the first output file is *name* with **aa** through **zz** appended. The output file will be appended with **aa**, then **ab**, then **ac**, and so forth until **zz** is reached. A maximum of 676 files can be created using the **split** command. There must not be more than 12 characters in *name*. If no output name is given, **x** is default.

Command Format

The general format of the **split** command is as follows:

split [*-n*] [*file* [*name*]]

where:

-n	The number of lines that are to be written onto each output file.
file	The name of the file to be split.
name	The name of the output file.

If no input file is given or if - is given, the standard input is used.

Sample Command Use

The following command line entries and system responses show the basic operation of the **split** command. The **cat** command is used to display the contents of **file1**. The **split** command is used to split **file1** into 3 lines per output file. The **ls -l** command is used to display the new files that are created. The **cat** command is used again to display the contents of each new file.

```
$ cat file1<CR>
This will be the first line of the first output file.
...
...
This will be the first line of the second output file.
...
...
This will be the first line of the third output file.
...
...
$ split -3 file1 new.file1<CR>
$ ls -l<CR>
total 5
-rw-------  1 cec  other   187 July 19 10:52 file1
-rw-------  1 cec  other    62 July 19 10:53 new.file1aa
-rw-------  1 cec  other    63 July 19 10:53 new.file1ab
-rw-------  1 cec  other    62 July 19 10:53 new.file1ac
$ cat new.file1aa<CR>
This will be the first line of the first output file.
...
...
$ cat new.file1ab<CR>
This will be the first line of the second output file.
...
...
$ cat new.file1ac<CR>
This will be the first line of the third output file.
...
...
$
```

"sum" — Print Check Sum and Block Count of a File

General

The **sum** command is used to calculate and output a 16-bit checksum for a specified file. Typically, the command is used to look for bad data or to validate a file transmitted over a communications interface. The number of blocks in the specified file is also output.

To use the **sum** command to validate transmitted data, the checksum is executed on the file before transmission and the results are sent to the destination. At the destination, the **sum** command is again executed on the received data. The before and after checksums are then compared. Matching checksums show a successful transfer of data and a mismatch shows a problem. Note that you must know whether to use the **-r** option when validating transferred data or not. You must use the same form of the command to calculate the checksum at the source and destination to be able to validate the transmitted data.

Command Format

The general format of the **sum** command is as follows:

sum [-r] *file*

The **-r** option causes the command to use a different rationale (algorithm) in computing the checksum. The *file* argument identifies the name of the file to be processed. Note that the file name can be expressed as a complete path name.

Sample Command Use

The following command line entries and system responses show you a typical **sum** command output. The first field output is the checksum, followed by the number of blocks (1), followed by the name of the file (**list1**).

```
$ sum list1<CR>
2496 1 list1
$ sum -r list1<CR>
55792    1 list1
$
```

"tail" — Output End of a File

General

The **tail** command is used to output the last portion of some data. The source data operated on by the command can be from a file, the output of another command, or from the terminal. Options are provided to tell the command at what point from the beginning or end of the input data to start passing data to the output. The start can be expressed in the number of lines, blocks, or characters from the beginning or end of the data.

Command Format

The general format of the **tail** command is as follows:

tail [±[*number*][**lbc**[**f**]]] [*file*]

The *number* argument identifies the number of units from the beginning or from the end of the input where the output is to begin. A plus sign preceding the number means from the beginning of the input data. A minus sign preceding the number means from the end of the input. The units used for the *number* argument are lines (**l**), blocks (**b**), or characters (**c**). The unit identifier immediately follows the *number* argument (no space).

The **-f** option is used to continuously read data from a file. The option provides the ability to monitor the growth of a file that is being written by some other process. The **-f** option is not applicable when data is being piped to the **tail** command.

The *file* argument identifies the name of the source file. Note that the file name can be expressed as a complete path name.

Sample Command Use

The following examples are based on the contents of a file named **sample**. The contents of this file are as follows:

line 1
line 2
line 3
line 4
line 5
line 6
line 7
line 8
line 9
line 10
line 11
line 12

The following command line entries and system responses show how you can output the end of a file of data using the simplest form of the **tail** command. This form of the command outputs the last ten lines of the contents of the **sample** file. The default of the *number* argument is **-10l**.

```
$ tail sample<CR>
line 3
line 4
line 5
line 6
line 7
line 8
line 9
line 10
line 11
line 12
$
```

The following sample command lines and system responses show you how to output the contents of the **sample** file starting 45 characters from the beginning of the file:

```
$ tail +45c sample<CR>
ne 7
line 8
line 9
line 10
line 11
line 12
$
```

"tr" — Translate Characters

General

The **tr** command is used as a filter to change data that is passed through it on a character basis. The command functions like a stream editor. Repeated occurrences of a character in succession can be reduced to a single occurrence of the character. Characters can be identified by ASCII letter or octal value. Octal values are preceded by a backslash (\). Ranges of characters are identified by enclosing the range in brackets. For example, [**a-c**] represents the letters a, b, and c. The entire lower case ASCII range is identified by [**a-z**]. Multiple occurrences of a character is represented by an expression [**x*n**], where the **x** is any character and the **n** is the number of repetitions of **x**. The number is treated as an octal number if the most significant digit is a zero. The number is treated as a decimal number if the most significant digit is other than a zero.

Command Format

The general format of the **tr** command is as follows:

tr [**-cds**] [*string1* [*string2*]]

The **-c** option reverses the meaning of *string1*. The *string1* argument identifies the characters that ARE NOT to be translated. The characters identified in the *string1* argument pass unchanged to the output. When the **-c** option is omitted, *string1* characters are translated to *string2* characters.

The **-d** option causes the characters identified by *string1* to be deleted from the output. The *string2* argument is not used with the **-d** option. If the *string2* argument is provided, it will be ignored.

The **-s** option causes multiple occurrences of the characters identified by *string2* to be replaced by a single occurrence of the characters. If only one string argument is given, then *string1* defines the character(s) to be operated on by the command.

The *string1* argument identifies input characters that are to be operated on by the command. When a *string2* argument is also provided, the characters found in *string1* are mapped to the corresponding character in *string2*.

Sample Command Use

The following command line entries and system responses show how you can change all lower case letters in a file named **list1** to upper case letters. The **cat** command is used to display the contents of **list1**. The output of the **tr** command is redirected to a file named **LIST**.

```
$ cat list1<CR>
eggs
bread
milk
butter
meat
$ tr "[a-z]" "[A-Z]" < list1 > LIST<CR>
$ cat LIST<CR>
EGGS
BREAD
MILK
BUTTER
MEAT
$
```

The following command line entries and system responses show how you can use the **tr** command to reduce multiple consecutive occurrences of a space character to a single occurrence throughout a file of data. The **cat** command is used to display the contents of the files.

```
$ cat list3<CR>
This   file  contains  lines
with multiple   spaces  between words.
$ tr -s " " < list3 > newlist<CR>
$ cat newlist<CR>
This file contains lines
with multiple spaces between words.
$
```

The following command line entries and system responses show how you can use the **tr** command to put each word in a file on a separate line. The **cat** command is used to display the contents of the sample file. The output of the **tr** command is displayed on the terminal in this example.

```
$ cat file<CR>
This file contains one line of text.
$ tr -cs "[A-z]" "[\012*]" < file<CR>
This
file
contains
one
line
of
text
$
```

"uniq" — Report Repeated Lines in a File

General

The **uniq** command is used to read an input file while comparing adjacent lines. The second and succeeding copies of repeated lines are removed in the normal output mode and the remaining lines are written on the output file. Repeated lines must be adjacent to be found. The input and output files must have different names.

Command Format

The general format of the **uniq** command is as follows:

uniq [*-udc* [+*n*] [*-n*]] [*input* [*output*]]

where:

-u The lines that are not repeated in the input file are written on the output file.

-d Only one copy of just the repeated lines is written on the output file.

-c The output file is generated in the normal output mode with a count of the number of times each line occurs. This option supersedes *-u* and *-d*.

+*n* *n* amount of characters are ignored. Fields are skipped before characters. A field is defined as a string of nonspace, nontab characters separated by tabs and spaces from its neighbors.

-n The first *n* amount of fields together with any blanks before each field are ignored.

input The name of the input file.

output The name of the output file.

The normal output mode is the union of the *-u* and *-d* options.

Sample Command Use

The following command line entries and system responses show the basic operation of the **uniq** command. The **cat** command is used to display a grocery list. The **sort** command is used to alphabetize the grocery list. To learn more about the **sort** command, refer to your *AT&T 3B2 Computer User Reference Manual*. The **cat** command is used again to display the alphabetized grocery list. The **uniq** command is used to remove the repeated lines and to count the number of times each item was listed. The **cat** command is used again to display the results. This is shown in the next example.

```
$ cat file1<CR>
bread
milk
butter
ice cream
meat
milk
vegetables
potato chips
drinks
orange juice
bread
vegetables
$ sort file1 > file2<CR>
$ cat file2<CR>
bread
bread
butter
drinks
ice cream
meat
milk
milk
orange juice
potato chips
vegetables
vegetables
$ uniq -c file2 file3<CR>
$ cat file3<CR>
  2 bread
  1 butter
  1 drinks
  1 ice cream
  1 meat
  2 milk
  1 orange juice
  1 potato chips
  2 vegetables
$
```

"unpack" — Expand Files

General

The **unpack** command is used to expand files created by the **pack** command. The compressed data is expanded to its original form. The compressed file is removed and the expanded data is placed in a file with the same file name, except that the **.z** is dropped. For example, if you expanded a file named **file1.z**, the expanded data will be placed in **file1**. The access modes, access and modified dates, and owner will remain the same as the compressed file.

The **unpack** command will not work if:

1. The file name (exclusive of **.z**) has more than 12 characters.
2. The file cannot be opened.
3. The file does not appear to be the output of the **pack** command.
4. A file with the "unpacked" name already exists.
5. The unpacked file cannot be created.

The **unpack** command returns a value that is the number of files that it failed to expand.

Command Format

The general format of the **unpack** command is as follows:

unpack *name ...*

The *name* argument identifies the name of the file that needs to be expanded. The **.z** at the end of the file name does not need to be input when specifying *name*.

Sample Command Use

The following command line entries and system responses show the basic operation of the **unpack** command. The **ls -l** command is used to display the character size of the compressed files before they are expanded. The **unpack** command is used to expand the compressed files. The **ls -l** command is used again to display the character size of the expanded files.

```
$ ls -l<CR>
total 71
-rw-------  1 cec  other    18980 July 19 13:14 file1.z
-rw-------  1 cec  other    15530 July 19 13:15 file2.z
$ unpack file1 file2<CR>
unpack: file1: unpacked
unpack: file2: unpacked
$ ls -l<CR>
total 110
-rw-------  1 cec  other    29727 July 19 13:14 file1
-rw-------  1 cec  other    24355 July 19 13:15 file2
$
```