

# W6

*Irlanda Ayon-Moreno*

*4/15/2018*

## Inspecting Data in the Terminal

Command	Description	R alternative
<code>wc nba2017-players.csv</code>	count lines, words, and bytes	<code>object.size()</code> , <code>nrow()</code>
<code>wc -l nba2017-players.csv</code>	count number of lines	<code>nrow()</code>
<code>head nba2017-players.csv</code>	inspect first 10 rows	<code>head()</code>
<code>tail nba2017-players.csv</code>	inspect last 10 rows	<code>tail()</code>
<code>less nba2017-players.csv</code>	see contents with a paginator	<code>View()</code>

## Manipulation of Data

Command	Description	R alternative
<code>head -n 11 nba2017-players.csv &gt; data10.csv</code>	redirection to new file	<code>sink()</code>
<code>cat data10.csv</code>	display contents on screen	
<code>cut -d "," -f 3 data10.csv</code>	select (third) column	
<code>sort positions10.txt</code>	sort the lines of a stream of data	
<code>cut -d "," -f 3 data10.csv   tail +2</code>	excludes the 1st value (of the col)	

`|` is a pipe operator. takes the output of a command and sends it as the input of another command

## Filters

### Extracting columns with `cut`

`cut` operates based either on character position within the column when using the `-c` flag, or on delimited fields when using the `-f` flag. By default, `cut` expects tabs as the delimiter. If a file separates fields with spaces or commas or any other delimiter, you need to use the option `-d` indicating the character used as field delimiter between quote marks.

Option	Description
<code>-f 1,5</code>	return columns 1 and 5, delimited by tabs.
<code>-f 1-5</code>	return columns 1 through 5, delimited by tabs.
<code>-d ","</code>	use commas as the delimiters.
<code>-c 2-7</code>	return characters 2 through 7 from the file.

## Sorting lines with **sort**

Option	Description
<b>-n</b>	sort in numerical order rather than alphabetically.
<b>-r</b>	sort in reverse order, z to a or decreasing numbers.
<b>-f</b>	fold uppercase into lowercase (i.e. ignore case).
<b>-u</b>	return a unique representative of repeated items.
<b>-k 3</b>	sort lines based on column 3 (tab or space delimiters)
<b>-t ", "</b>	use commas for delimiters.
<b>-b</b>	ignore leading blanks.
<b>-d</b>	sort in dictionary order.

## Isolating unique lines with **uniq**

This command removes consecutive identical lines from a file, leaving one unique representative. More precisely, what **uniq** does is compare each line it reads with the previous line. If the lines are the same, **uniq** does not list the second line.

Option	Description
<b>-c</b>	adds a count of how many times each line occurred.
<b>-u</b>	lists only lines that are not repeated.
<b>-d</b>	lists only lines that are duplicated.
<b>-i</b>	ignore case when determining uniqueness
<b>-f 4</b>	ignore the first 4 fields (space delimiter)

To get a single representative of each unique line from the entire file, in most cases you would need to first sort the lines with the **sort** command to group matching lines together. Interestingly, **uniq** can be used with the flag **-c** to count the number of occurrences of a line. This gives a quick way, for example, to assess the frequencies of values in a given column.

## Redirecting

Description	bash example
Send <i>standard output</i> to <i>file</i>	<code>cmd &gt; file</code>
Send <i>standard error</i> to <i>file</i>	<code>cmd 2&gt; file</code>
Take <i>standard input</i> from <i>file</i>	<code>cmd &lt; file</code>
Send <i>standard output</i> to end of <i>file</i>	<code>cmd &gt;&gt; file</code>