

# Text manipulations

Mikhail Dozmorov

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# Text format

- The most cross-platform format to share data
- Typically, data is stored as field-delimited columns (think Excel). Delimiter may be tab character (“.tsv” or “.txt” file extension), or comma (comma-separated values, “.csv”)
- Disadvantage - can be large. Solution - compression (**gzipping**), with tools to manipulate compressed files without uncompressing

# Windows file compatability

- Saving files in Windows and then trying to process them on Unix may cause issues
- A common type of error comes from control characters, commonly seen as end of line characters in Windows.
- To run script successfully, we need to remove these characters either by hand using `vim` or `emacs` to edit the file, or by running `dos2unix myfile.sh`.

# String manipulation

- **RegEx** - is a language for describing patterns in strings
- **grep** - finds lines containing a pattern, and outputs them
- **sed** - (stream editor) applies transformation rules to each line of text based on a pattern
- **awk** - powerful text processing language

# Regular expressions - everywhere

Metacharacter	Description
<code>^</code>	Matches the starting position within the string. In line-based tools, it matches the starting position of any line.
<code>.</code>	Matches any single character (many applications exclude <a href="#">newlines</a> , and exactly which characters are considered newlines is flavor-, character-encoding-, and platform-specific, but it is safe to assume that the line feed character is included). Within POSIX bracket expressions, the dot character matches a literal dot. For example, <code>a.c</code> matches "abc", etc., but <code>[a.c]</code> matches only "a", ".", or "c".
<code>[ ]</code>	A bracket expression. Matches a single character that is contained within the brackets. For example, <code>[abc]</code> matches "a", "b", or "c". <code>[a-z]</code> specifies a range which matches any lowercase letter from "a" to "z". These forms can be mixed: <code>[abcx-z]</code> matches "a", "b", "c", "x", "y", or "z", as does <code>[a-cx-z]</code> .  The <code>-</code> character is treated as a literal character if it is the last or the first (after the <code>^</code> , if present) character within the brackets: <code>[abc-]</code> , <code>[-abc]</code> . Note that backslash escapes are not allowed. The <code>]</code> character can be included in a bracket expression if it is the first (after the <code>^</code> ) character: <code>[ ]abc</code> .
<code>[^ ]</code>	Matches a single character that is not contained within the brackets. For example, <code>[^abc]</code> matches any character other than "a", "b", or "c". <code>[^a-z]</code> matches any single character that is not a lowercase letter from "a" to "z". Likewise, literal characters and ranges can be mixed.
<code>\$</code>	Matches the ending position of the string or the position just before a string-ending newline. In line-based tools, it matches the ending position of any line.
<code>( )</code>	Defines a marked subexpression. The string matched within the parentheses can be recalled later (see the next entry, <code>\n</code> ). A marked subexpression is also called a block or capturing group. <b>BRE mode requires</b> <code>\( \)</code> .
<code>\n</code>	Matches what the <i>n</i> th marked subexpression matched, where <i>n</i> is a digit from 1 to 9. This construct is vaguely defined in the POSIX.2 standard. Some tools allow referencing more than nine capturing groups.
<code>*</code>	Matches the preceding element zero or more times. For example, <code>ab*c</code> matches "ac", "abc", "abbcc", etc. <code>[xyz]*</code> matches "", "x", "y", "z", "zx", "zyx", "xyzy", and so on. <code>(ab)*</code> matches "", "ab", "abab", "ababab", and so on.
<code>{m,n}</code>	Matches the preceding element at least <i>m</i> and not more than <i>n</i> times. For example, <code>a{3,5}</code> matches only "aaa", "aaaa", and "aaaaa". This is not found in a few older instances of regexes. <b>BRE mode requires</b> <code>\{m,n\}</code> .

# Regular expressions

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Expression	Description
[]	Matches a set. [abc] matches a, b, or c. [a-zA-Z] matches any letter. [0-9] matches any number. “^” negates a set, [^abc] matches d, e, f, etc.
^	Starting position anchor. ^abc finds lines starting with abc
\$	Ending position anchor. xyz\$ finds lines ending with xyz
\	Escape symbol, to find special characters. \* will find *. \n matches new line character, \t – tab character
*	Match the preceding element zero or more times. a*b matches ab, aab, aaab, etc.

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## Extended regular expressions

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Expression	Description
?	Matches the preceding element zero or one time. $a^*b$ matches $b$ , $ab$ , but not $aab$
+	Matches the preceding element one or more times. $a^+b$ matches $ab$ , $aab$ , etc.

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# The grep command

- Find lines in an input file or stream that match a specific pattern you are looking for

```
grep "chrX" regions.bed | head
chrX    41190000    41195000
chrX    154020000   154025000
chrX    81355000    81360000
chrX    80805000    80810000
chrX    88340000    88345000
chrX    58420000    58425000
chrX    98615000    98620000
chrX    62330000    62335000
chrX    153335000   153340000
chrX    30660000    30665000
```

- Result: Only lines that contain the text “chrX” (case-sensitive)



## grep usage

Basic syntax: `grep "pattern" <filename>`, e.g., `cat README.md | grep "use"`

`ls | grep "^[w|b]"` - lists files/directories starting with "w" or "b"

Use `--color` argument to highlight matched patterns

## Fine-tuning your grep

- v - inverts the match (lines that *do not* contain pattern)
  - i - matches case insensitively
  - H - prints the matched filename
  - n - prints the line number
  - f - gets patterns from a file, each pattern on a new line
  - w - forces the pattern to match an *entire word* (e.g., "chr1" but not "chr11")
  - x - forces patterns to match the whole line
- Escape special characters, e.g., `grep \"gene\\\"`

## sed - stream editor

Most common usage – substitute a pattern with replacement. Basic syntax:

```
sed 's/pattern/replacement/'
```

`echo "The Internet is made of dogs" | sed 's/dogs/cats/'` - replaces “dogs” with “cats”, so the final output is “The Internet is made of cats”

`echo "dogs, dogs, dogs" | sed 's/dogs/cats/g'` - global substitution with “g” modifier. The final output is “cats, cats, cats”

## sed - stream editor

Special characters – escape with “\”

```
echo "1*2*3" | sed 's/\*/-/g' - outputs "1-2-3"
```

Regular expressions – use as in grep, with “-E” argument for extended regex

```
echo "tic-tac-toe" | sed 's/[ia]/o/g' | sed 's/e$/c/' -  
outputs "toc-toc-toc"
```

Delete line(s) – sed 'X[,Y]d' deletes line X through Y

```
cat <filename> | sed '1d' - deletes first line (e.g., header)  
cat <filename> | sed '10,37d' - deletes lines from 10 through 37
```

A more traditional programming language for text processing than sed. Awk stands for the names of its authors “Alfred **A**ho, Peter **W**einberger, and Brian **K**ernighan”

- Each column is referred to by number, e.g. \$1 for the first column
- \$0 is referred to the whole line
- Note “column” is defined as a non-contiguous text. So, space- and tab-separated words are equivalent for awk
- Use -F "\t" to override field separator, use OFS="\t" to override spaces to tabs as an output field separator
- awk process each row, and operates on column values
- Commands are wrapped in single quotes
- `man awk` for more

## Conditional output with awk

- Only report annotations in `cpg.bed` that are for chromosome 1

```
awk '$1 == "chr1"' cpg.bed
```

# Equivalently

```
cat cpg.bed | awk '$1 == "chr1"'
```

- Only report annotations in `cpg.bed` where the end coordinate is less than the start coordinate.

```
awk '$3 < $2' cpg.bed
```

# Special variables

- The **NR** (number of records) variable
- Example: Report the 100th line in the file

```
awk 'NR == 100' cpg.bed
```

- The **NF** (number of fields) variable
- Example: Report the number of tab-separated columns in the first 10 lines of cpg.bed

```
awk -F "\t" '{print NF}' cpg.bed | head
```

## Impose multiple filtering criteria with the AND (“&&”) operator

- Report the 100th through the 200th lines in the file

```
awk 'NR>=100 && NR <= 200' cpg.bed
```

- Report lines if they are the 100th through the 200th lines in the file OR (||) they are from chr22

```
awk '(NR>=100 && NR <= 200) || $1 == "chr22"' cpg.bed
```



# Computations in awk

- Print the BED record followed by the length (end - start) of the record
- \$0 refers to the entire input line
- If using a `print` statement, you must add curly brackets between the single quotes describing the program.
- Example: Prints first 3 columns, the 2nd numerical column is increased by 100, the 3rd is decreased by 100

```
awk '{print $1, $2+100, $3-100}' cpg.bed
```

## By default, output is separated by a space. Prefer tabs

- **BEGIN**: before anything else happens, execute what is in the BEGIN statement. Then start processing the input.
- Print the BED record followed by the length (end - start) of the record. Separated by a TAB, the OFS (output field separator)

```
awk 'BEGIN{OFS="\t"}{print $0, $3-$2}' cpg.bed
```

```
# or
```

```
awk '{len=($3-$2); print $0"\t"len}' cpg.bed
```

# bioawk - awk modified for biological data

- Bioawk is an extension to Brian Kernighan's awk, adding the support of several common biological data formats, including optionally gzip'ed BED, GFF, SAM, VCF, FASTA/Q and TAB-delimited formats with column names.
- It also adds a few built-in functions and an command line option to use TAB as the input/output delimiter.
- When the new functionality is not used, bioawk is intended to behave exactly the same as the original BWK awk.

<https://github.com/lh3/bioawk>

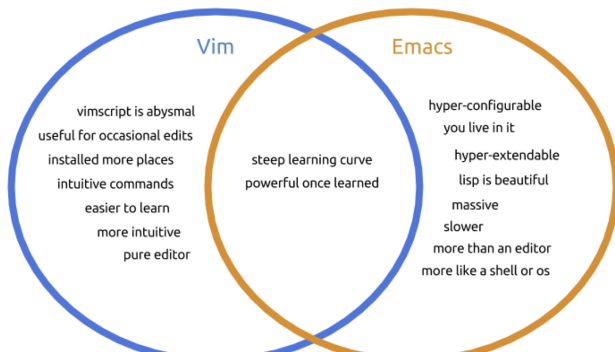
<https://github.com/vsbuffalo/bioawk-tutorial>

<https://github.com/ialbert/bioawk/blob/master/README.bio.rst>

<https://gif.biotech.iastate.edu/bioawk-basics>

# Command-line text editor

- nano - simple editor
- vim - Created by Bill Joy, 1976. Advantages: Supremely intuitive once basics are learned
- emacs - Created by Richard Stallman, 1976. Advantages: Unparalleled power and configuration



# vim basics

Start vim on a file: `vim <filename>`

Keyboard shortcuts for two modes:

- i - editor mode, to type - Esc - command mode. Press ":" and enter a command

Important keyboard shortcuts:

- :w - write changes - :wq - write changes and quit - :q! - force quit and ignore changes

## Basic vim commands

**k, j, l, h, or arrows** - navigation

**v** - (visually) select characters **V (shift-v)** - (visually) select whole lines **d** - cut (delete) into clipboard **dd** - cut the whole line **y** - copy (yank) into clipboard **P (shift-p)** - paste from clipboard **u** - undo

# Find and replace in vim

In command mode:

- `/pattern` - search for pattern, “n” – next instance -
- `:s/pattern/replacement/g` - search and replace
- `:help tutor` - learn more vim

# References

- Regular expression, Unix commands, Python quick reference, SQL reference card.  
[http://practicalcomputing.org/files/PCfB\\_Appendices.pdf](http://practicalcomputing.org/files/PCfB_Appendices.pdf)