

Training Day

Modify and extract information from large text files with

sed & awk



Objectives

At the end of the day, you will be able to use command line in order to:

- Edit big files (beyond excel files)
- Extract information from big files
- Build new files from existing ones



Planning of the day

Part I: 09h00 - 10h30

Regular expressions - TP1

Part II: 10h45 - 12h30

File editing with sed - TP2

Part III: 14h00 - 17h00

Extracting information with awk - Combining unix sed and awk within pipes - TP3



Part I Regular expressions

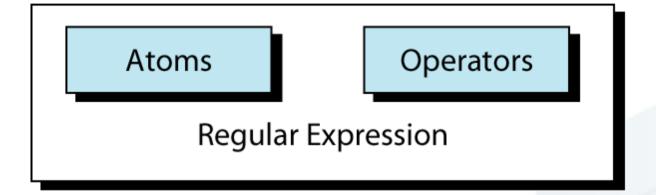


Regular expression?

- Commonly called regex
- A simple set of characters with special meanings (called metacharacters) to test for matches quickly and easily.
- Regular expressions are used thoughout UNIX:
 - grep
 - sed
 - awk
 - ...



Regular expression?

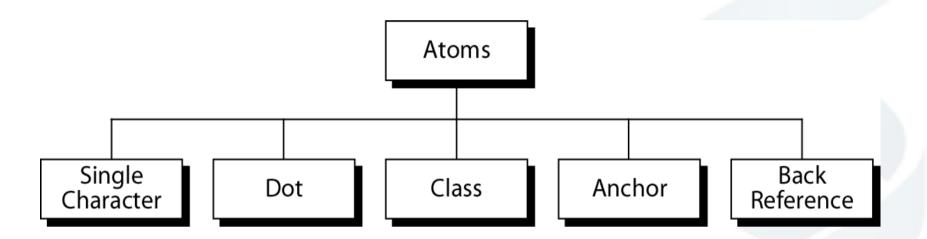


An atom specifies <u>what</u> text is to be matched and <u>where</u> it is to be found.

An operator combines regular expression atoms.



An atom specifies <u>what</u> text is to be matched and <u>where</u> it is to be found.



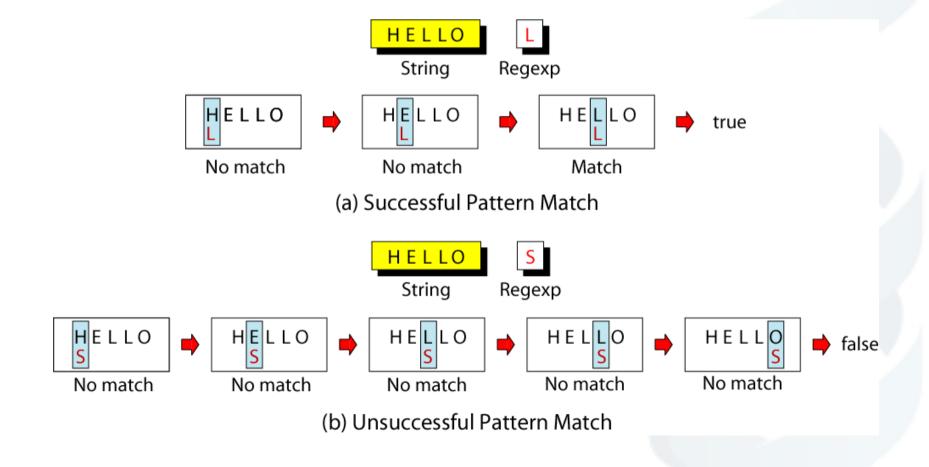


Regular expression

Atoms

Single-Character Atom

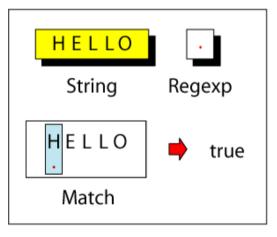
A single character matches itself



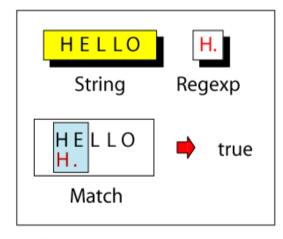


Dot Atom:.

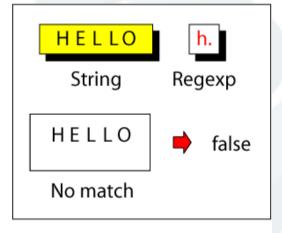
matches any single character except for a new line character (\n)



(a) Single-Character



(b) Combination-True



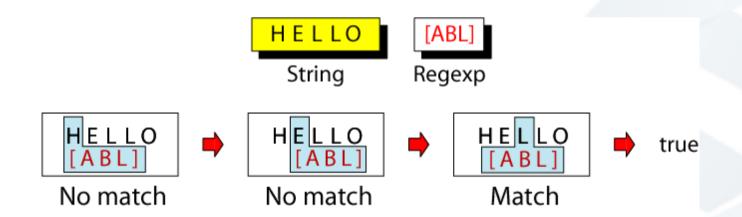
(c) Combination-False



Class Atom

matches only single character that can be any of the characters defined in a set:

Example: [ABC] matches either A, B, or C.

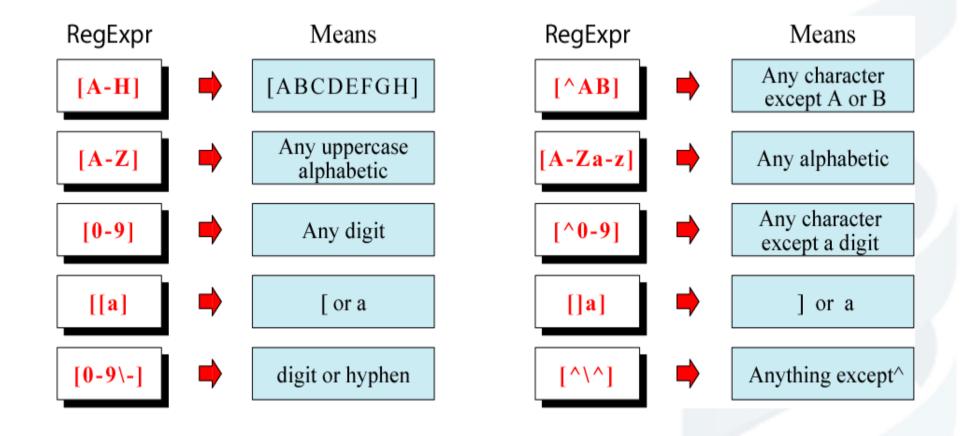


Notes:

- 1) A range of characters is indicated by a dash, e.g. [A-Q]
- 2) Can specify characters to be excluded from the set, e.g. [^0-9] matches any character other than a number.



Example: Classes



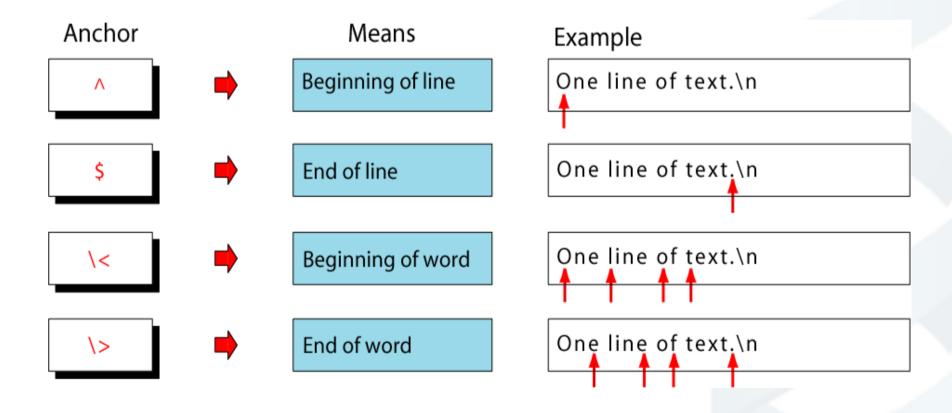


Regular expression

Atoms

Anchors

Anchors tell where the next character in the pattern must be located in the text data.





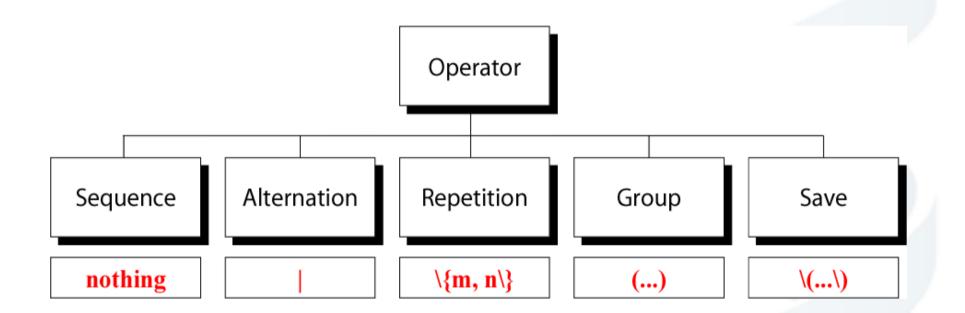
Back References: \N

- used to retrieve saved text in one of nine buffers
- can refer to the text in a saved buffer by using a back reference:

ex.: \1 \2 \3 ...\9

more details on this later

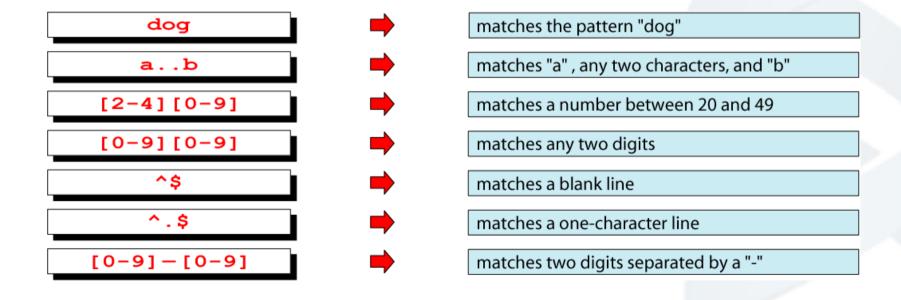






Sequence Operator

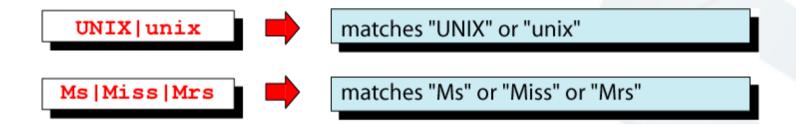
In a sequence operator, if a series of atoms are shown in a regular expression, there is no operator between them.





Alternation Operator: | or \|

operator (| or \|) is used to define one (depends on version of "grep")
or more alternatives





Repetition Operator: \{...\}

The repetition operator specifies that the atom or expression immediately before the repetition may be repeated.

matches previous character m to n times.

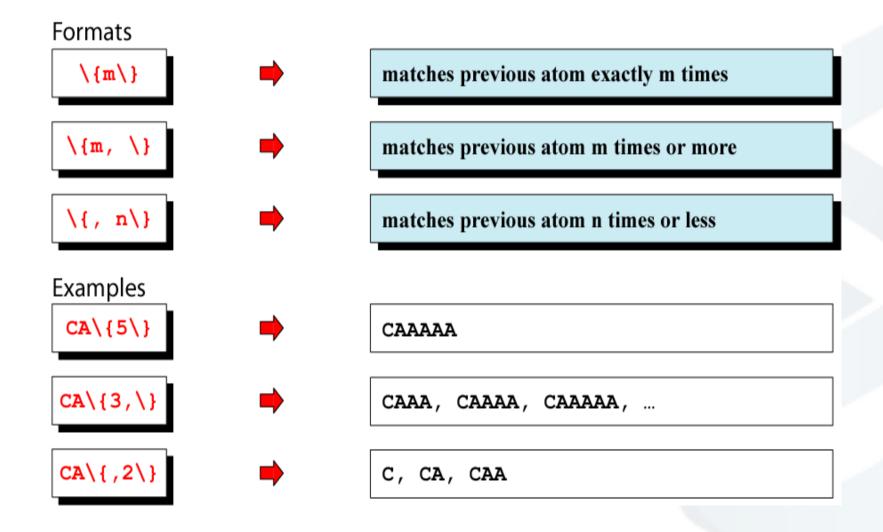
M\{3 , 5\}

matches "AAA" , "AAAAA"

matches "BAAA" , "BAAAAA"



Basic Repetition Forms





Short Form Repetition Operators:

Formats		
*	⇒	special case: matches previous atom zero or more times
+	⇒	special case: matches previous atom one or more times
?	⇒	special case: matches previous atom 0 or one time only
Examples		
BA*	→	B, BA, BAA, BAAA,
B.*	⇒	B, BA BZ, BAA BZZ, BAAA BZZZ,
.*	⇒	zero or more characters
.+	⇒	one or more characters
[0-9]?	⇒	zero or one digit



Group Operator

In the group operator, when a group of characters is enclosed in parentheses, the next operator applies to the whole group, not only the previous characters.



Note: depends on version of "grep" use \(and \) instead



Regular expression Examples

- Pipe the output of the « Is -I » command to grep and list/select only directory entries
 ls -l | grep '^d'
- Display the number of lines where the pattern was found ls -1 | grep -c '^d'
- Look at the file /home/cgaspin/TP/TP_REGEX/All_RFAM_bostaurus_ncRNA.gff.
 - Print all the line containing the word « SNORA5 ».
 cd /home/cgaspin/TP/TP_REGEX/
 grep '\<SNORA5\>' All_RFAM_bostaurus_ncRNA.gff
 - Print the lines that containing either the expression "SRP" or the expression « MRP »
 grep 'SRP\|MRP' All_RFAM_bostaurus_ncRNA.gff
 - Print all lines containing « _ » followed by either « MRP » or « SRP ».
 grep '_\((SRP\|MRP\))' All_RFAM_bostaurus_ncRNA.gff
 - Print all the lines corresponding to chromosome 1 (beginning by « 1 »)
 grep '^\<1\>' All_RFAM_bostaurus_ncRNA.gff



Regular expressions Metacharacters

- .: un caractère quelconque
- ^: début de ligne
- \$: fin de ligne
- < : début d'un mot
- \> : fin d'un mot
- \: considère littéralement le caractère suivant
- : spécifie un intervalle (A-Z)
- X*: zéro ou plus d'occurrences de X
- X+: une ou plus occurrences de X

- X?: zéro ou une occurrence unique du caractère X
- [...] : plage de caractères permis
- [^...]: plage de caractères interdits
- \{n\}: pour définir le nombre de répétitions n du caractère placé devant
- \{n,m\}: n to m of preceding item (plus others)
- \(...\): désigne une sous-chaîne
- \entier : désigne le numéro de sous-chaîne



Part I

TP1

Exercises



Part II File editing with sed



Introduction to sed

Sed: Stream-oriented, Non-Interactive, Text Editor

- Look for patterns one line at a time
- Change lines of the file
- Non-interactive text editor
 - Editing commands can come in as *script*
 - There is an interactive editor ed which accepts the same commands
- A Unix filter
 - Superset of previously mentioned tools



Syntax

```
sed [-n] [-e] ['command'] [file...] sed [-n] [-f scriptfile] [file...]
```

Options

- "-n": only print lines specified with the print command
- "-f" scriptfile: next argument is a filename containing editing commands
- "-e" command: the next argument is an editing command rather than a filename, useful if multiple commands are Specified

Brackets {} can be used to apply multiple commands to an address

```
[/pattern/[,/pattern/]] {
command1
command2
command3
}
```



sed command line

- A sed command line consists of up to two addresses and an action, where the address can be a regular expression or a line number.
- If the addresses are not given the action is performed on all the lines.

```
>echo day
day
>echo day | sed -e 's/day/night/'
night
```

```
>echo "day" > day.txt
>sed -e 's/day/night/' < day.txt
night
>sed -e 's/day/night/' day.txt
night
```



sed commands

- General form :
 - [address[, address]][!]command [arguments]
- sed copies each input line into a pattern space :
 - if the address of the command matches the line in the pattern space, the command is applied to that line,
 - if the command has no address, it is applied to each line as it enters *pattern space*,
 - if a command changes the line in *pattern space*, subsequent commands operate on the modified line.
- When all commands have been read, the line in pattern space is written to standard output and a new line is read into pattern space.



sed commands address

- An address can be either
 - a line number or
 - a pattern
- An address is enclosed in slashes (*|pattern|*).
 - A pattern is described using *regular expressions* (Basic Regular Expressions, as in **grep**)
 - If no pattern is specified, the command will be applied to **all** lines of the input file.
 - To refer to the last line: \$



sed commands address

- Most commands will accept two addresses :
 - if only one address is given, the command operates only on that line,
 - if two comma separated addresses are given, then the command operates on a range of lines between the first and second address, inclusively.
- The ! operator can be used to negate an address, ie; address!command causes command to be applied to all lines that do not match address.
- The I operator can be used after the address to ignore character case.



Bioinfo "S" substitution function

- Substitute the first or all occurrences of a string by another one
 - sed "s/toto/TOTO/" file
 - → substitute the first occurrence of « toto » by « TOTO »
 - sed "s/toto/TOTO/3" file
 - → substitute the 3rd occurrence of « toto » by « TOTO »
 - sed "s/toto/TOTO/q" fichier
 - → substitute all occurences of « toto » by « TOTO »
 - sed "s/toto/TOTO/p" fichier
 - → print the lines with subtitution done
 - sed "s/toto/TOTO/w resultat" fichier
 - → print the lines with subtitution done in a file named resultat
 - sed -e "s/[Ff]raise/FRAISE/g" fichier
 - → substitute all occurences of « Fraise » or « fraise » by « FRAISE »
 - sed "s/(.*)-(.*)/2-1/" fichier
 - → permute the two fields separated by a « »

/black/!s/cow/horse/ would substitute "horse" for "cow" on all lines except those that contained "black"



```
>cat inputfile.txt
one two three, one two three
four three two one
one hundred
>sed 's/one/ONE/' < inputfile.txt
ONE two three, one two three
four three two ONE
ONE hundred</pre>
```

What is remarkable in the example presented here above?

```
>sed 's/one/ONE/2' < inputfile.txt
one two three, ONE two three
four three two one
one hundred
>sed 's/one/ONE/g' < inputfile.txt
ONE two three, ONE two three
four three two ONE
ONE hundred</pre>
```



```
>cat inputfile2.txt
one two three, one two three, one two three
four three two one, four three two one
one hundred, one hundred
>sed -e '1s/one/ONE/g' < inputfile2.txt
>sed -e '/hundred/s/one/ONE/g' < inputfile2.txt
>sed -e '/^one/s/one/ONE/g' < inputfile2.txt</pre>
```

What are the results of the three command lines?

```
>sed -e '1s/one/ONE/g' < inputfile2.txt
ONE two three, ONE two three, ONE two three
four three two one, four three two one
one hundred, one hundred
>sed -e '/hundred/s/one/ONE/g' < inputfile2.txt
one two three, one two three, one two three, one two three
four three two one, four three two one
ONE hundred, ONE hundred
>sed -e '/^one/s/one/ONE/g' < inputfile2.txt
ONE two three, ONE two three, ONE two three
four three two one, four three two one
ONE hundred, ONE hundred</pre>
```



What is the result of the command line?

```
>cat inputfile3.txt
one two three, one two three, one two three
four three two one, four three two one
one hundred, one hundred
one two three, one two three, one two three
four three two one, four three two one
one hundred, one hundred
>sed -e '2,3s/one/ONE/g' < inputfile3.txt
```



Build a command line to put all

- 'two' word in uppercase for lines beginning with 'one' and
- 'three' word in uppercase for lines having numbers between 3 and
 5.

```
[cklopp@beraldi:/tmp] cat inputfile3.txt
one two three, one two three, one two three
four three two one, four three two one
one hundred, one hundred
one two three, one two three, one two three
four three two one, four three two one
one hundred, one hundred
[cklopp@beraldi:/tmp] sed -e '/^one/{s/two/TWO/g;s/three/THREE/g}' inputfile3.txt
one TWO THREE, one TWO THREE, one TWO THREE
four three two one, four three two one
one hundred, one hundred
one TWO THREE, one TWO THREE, one TWO THREE
four three two one, four three two one
one hundred, one hundred
one TWO THREE, one TWO THREE, one TWO THREE
four three two one, four three two one
one hundred, one hundred
```

or

```
>sed -e '/^one/s/two/TWO/g' < inputfile3.txt | sed -e '3,5s/three/THREE/g' one TWO three, one TWO three, one TWO three four three two one, four three two one one hundred, one hundred one TWO THREE, one TWO THREE, one TWO THREE four THREE two one, four THREE two one one hundred, one hundred
```



"d" deletion function

sed '[address1][,address2]d' file

- Delete the addressed line(s) from the pattern space; line(s) not passed to standard output.
- A new line of input is read and editing resumes with the first command of the script.



"d" deletion function

Address examples

- d : deletes the all lines

- **6d** : deletes line 6

- I^\$Id : deletes all blank lines

- 1,10d : deletes lines 1 through 10

- 1,/^\$/d : deletes from line 1 through the first blank line

- /^\$/,\$d : deletes from the first blank line through the last

line of the file

- I^\$I,10d : deletes from the first blank line through line 10

- /^ya*y/,/[0-9]\$/d : deletes from the first line that begins with yay, yaay,

yaaay, etc. through the first line that ends with a digit



Hands-on sed deletion

- sed "20,30d" fichier: supprime les lignes 20 à 30 du fichier
- sed "/toto/d" fichier: supprime les lignes contenant la chaîne toto
- sed "/toto/!d" fichier: supprime toutes
 les lignes ne contenant pas la chaîne toto
- sed "/^ *\$/d" fichier: supprime les lignes vides
 - 1,5!d would delete all lines except 1 through 5



Other useful functions "print" - "= »

- p : By default, sed prints every line. When using "sed -n," it will not, by default, print any new lines. Using the "p" flag will cause the modified line to be printed. Without "-n", the line is duplicated
 - 1,5p
 - → will display lines 1 through 5
 - /^\$/,\$p
 - → will display the lines from the first blank line through the last line of the file
- = : prints the current line number to standard output.
 - Examples
 - •
 - •
 - sed "/toto/=" fichier: affiche le numéro de la ligne contenant la chaîne toto.



append - insert - change

 Syntax for these functions is a little strange because they must be specified on multiple lines

append [address]a\

text

insert [address]i\

text

change [address(es)]c\

text

append/insert for single lines only, not range



Differences: append - insert

- Append places text after the current line in pattern space
- Insert places text before the current line in pattern space
 - Each of these commands requires a \ following it.
 text must begin on the next line.
 - If text begins with whitespace, sed will discard it unless you start the line with a \mathbb{\lambda}

```
>sed -e 'ajsdklfjslkjflskqjfdmlkj' < inputfile3.txt
one two three, one two three, one two three, one two three
isdklfislkiflskqifdmlki
four three two one, four three two one
jsdklfjslkjflskqjfdmlkj
one hundred, one hundred
jsdklfjslkjflskqjfdmlkj
one two three, one two three, one two three, one two three
jsdklfjslkjflskgjfdmlkj
four three two one, four three two one
jsdklfjslkjflskqjfdmlkj
one hundred, one hundred
jsdklfjslkjflskqjfdmlkj
>sed -e '1ajsdklfjslkjflskqjfdmlkj' < inputfile3.txt
one two three, one two three, one two three, one two three
jsdklfjslkjflskgjfdmlkj
four three two one, four three two one
one hundred, one hundred
one two three, one two three, one two three, one two three
four three two one, four three two one
one hundred, one hundred
```

```
>sed -e '1i
                          jsdklfjslkjflskqjfdmlkj' < inputfile3.txt</pre>
jsdklfjslkjflskqjfdmlkj
one two three, one two three, one two three, one two three
four three two one, four three two one
one hundred, one hundred
one two three, one two three, one two three, one two three
four three two one, four three two one
one hundred, one hundred
                         jsdklfjslkjflskqjfdmlkj' < inputfile3.txt
>sed -e 'i
jsdklfjslkjflskqjfdmlkj
one two three, one two three, one two three, one two three
jsdklfjslkjflskqjfdmlkj
four three two one, four three two one
jsdklfjslkjflskgjfdmlkj
one hundred, one hundred
<u>isdklfjslkjflskqjfdmlkj</u>
one two three, one two three, one two three, one two three
jsdklfjslkjflskajfdmlkj
four three two one, four three two one
jsdklfjslkjflskqjfdmlkj
one hundred, one hundred
```



append - insert - change

- Unlike Insert and Append, Change can be applied to either a single line address or a range of addresses
- When applied to a range, the entire range is replaced by text specified with change, not each line
- What is the result of the following command?

```
cgaspin@belloc:~/TP/TP_REGEX$ cat fich2
$USA
$USSS
$US
$UAD
UAD-DUA
$UAD
```



append - insert - change

- Unlike Insert and Append, Change can be applied to either a single line address or a range of addresses
- When applied to a range, the entire range is replaced by text specified with change, not each line
- What is the result of the following command?

```
→ sed '1,2c aaacccc \
   kkkk' fich2
```

```
cgaspin@belloc:~/TP/TP_REGEX$ cat fich2
$USA
$USSS
$US
$UAD
UAD-DUA
$UAD
```



```
cgaspin@belloc:~/TP/TP_REGEX$ sed '1,2c aaacccc \
> kkkk' fich2
aaacccc
kkkk
$US
$UAD
UAD-DUA
$UAD
```



Working with multiple lines

• The ${\mathbb N}$ command reads/appends the next line of input into the pattern space

What are the results of the commands?

```
→ sed -e 'N' file

→ sed -e '{N; s/\n//}' file

→ sed -e '{N;N; s/\n//g}' file
```



Part II

TP2

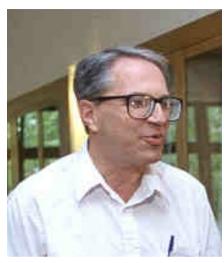
Exercises

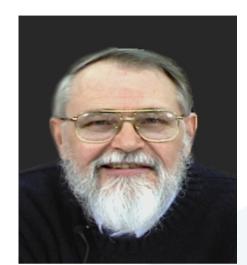


Part III Programmable filter with awk









Aho

Weinberger

Kernighan

- A general purpose programmable filter that handles text (strings) as easily as numbers
- Processes fields while sed only processes lines
- Gets input from
 - files
 - redirection and pipes
 - directly from standard input



- A pattern-action language, like sed
- Looks a little like C but automatically handles input, field splitting, initialization, and memory management :
- A great prototyping language
 - awk 'programme' file1 file2 ... :
 instructions between « ' »
 - awk 'programme' : with standard input
 - awk -f pfile file1 file2 ...: instructions are in « pfile ».



- A pattern-action language, like sed
- Looks a little like C but automatically handles input, field splitting, initialization, and memory management:
- A great prototyping language
 - awk 'programme' file1 file2 ... :
 instructions between « ' »
 - awk 'programme' : with standard input
 - awk -f pfile file1 file2 ...: instructions are in « pfile ».



Bioinfo Structure of an awk program

```
BEGIN { action } Optional BEGIN segment : for processing to run prior to reading input pattern { action } pair(s) « pattern-action »: For each pattern matched, the corresponding {action} is done. At least one of the pattern or {action} has to be given. If pattern is not given, {action} is done for each line. Default pattern is to match all lines. If {action} is not given, the line is printed.
```

```
pattern { action }
END { action } Optionnel END segment: for processing to run at the end
```

- Search pattern in the input, line after line
- Run action on the line where pattern is found

```
awk '{print;}' FILENAME
```

→ Because pattern is not specified, each line will be printed



Patterns in awk

- « pattern » acts as a selector
- Patterns can be :
 - specific patterns : « BEGIN » or « END »
 - regular expression : /regexpr/
 - A predicate : $\langle x \rangle > 0$
 - A combination of patterns with « && » or « || »
 - /NYU/ matches if the string "NYU" is in the line
 - x > 0 matches if the condition is true
 - /NYU/ && (x > 0)



Operators in awk

Relational operators

- « < » : Less than
- « <= » : Less than or equal to
- « > » : Greater than
- $\ll >= >$: Greater than or equal to
- « == » : Equal to
- « != » : Not equal to
- ~ » : Matches (compares a string to a regular expression)
- « !~ » : Does not match



Operators in awk

Logic operators

- « && » : And (reports "true" if both sides are true)
- « || » : Or (reports "true" if either side, or both, are true)
- «! »: Not (Reverses true/false of the following expression)

Arithmetic operators

- « + » : Addition

- « - » : Subtraction

- « * » : Multiplication

- « I » : Division

- « ^ » : Exponentiation (** may also work)

- « % » : Remainder

Concatenation

BEGIN {string = "Super" "power"; print string}



Actions in awk

- action may include a list of one or more C like statements, as well as arithmetic and string expressions and assignments and multiple output streams.
- action is performed on every line that matches pattern.
 - If pattern is not provided, action is performed on every input line
 - If action is not provided, all matching lines are sent to standard output.
- Since *patterns* and *actions* are optional, *actions* must be enclosed in braces to distinguish them from *pattern*.



ls | awk 'BEGIN { print "List of fasta files with name
beginning with h:" } /^h.*\.fa\$/ { print } END { print
"done!" }'

```
Terminal
Fichier Édition Affichage Rechercher Terminal Aide
cgaspin@belloc:~$
cgaspin@belloc:~$ ls *fa
hs_alt_CHM1_1.1_chr1.fa hs_ref_GRCh38.p7_chr1.fa ncRNA.fa
cgaspin@belloc:~$ ls | awk 'BEGIN { print "List of fasta files with name beginni
ng with h:" } /^h.*\.fa$/ { print } END { print "done!" }'
List of fasta files with name beginning with h:
hs alt CHM1 1.1 chr1.fa
hs_ref_GRCh38.p7_chr1.fa
done!
cgaspin@belloc:~$
```



- Awk reconizes the concepts of « file », « record », and « field »
- A file consists of records, which by default are the lines of the file
- A record consists of fields, which by defaults are separated by spaces (or tabs)



awk - record

- Default record separator is newline
 - By default, awk processes its input a line at a time.
- Could be any other regular expression.
- **RS**: record separator
 - Can be changed in **BEGIN** action
- NR is the variable whose value is the number of the current record.



awk - field

- Each input line is split into fields.
 - FS: field separator: default is space (1 or more spaces or tabs)
 - awk -Fc option sets FS to the character c
 - Can also be changed in BEGIN
 - **\$0** is the entire line
 - \$1 is the first field, \$2 is the second field,
- Only fields begin with \$



awk - variable

- awk allows to define and use variables
 - BEGIN { sum = 0 } { sum++ } END { print sum }
- awk variables take on numeric (floating point) or string values according to context
- User-defined variables are unadorned (they need not be declared)
- By default, user-defined variables are initialized to the null string which has numerical value 0



awk - variable

- awk allows to define and use variables
 - BEGIN { sum = 0 } { sum++ } END { print sum }
- Some variables are predefined :
 - RS, ORS: record separators in input and output, respectively
 - NR: current number of records when processing
 - FNR: number of record in the file
 - FS, OFS: field separators in input and output, respectively
 - NF: Number of fields on the current record



A program which counts the number of lines in nf:

```
awk 'BEGIN { total = 0 } { total ++ } END { print
total }' nf
```

- total: a variable initialized to '0' at the beginning
- total: is incremented for each read
- The value of total is printed at the end



Terminal _ _ _ X
Fichier Édition Affichage Rechercher Terminal Aide

CTACCCTAACCCTAACCCTAACCCTAACCCTAACCCCTAACCCCTAACCCCTAACCCCTAACCCCTAACCCCTAACCCCTAACCCCTAACCCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCTAACCCCTAACCCCTAACCCCTAACCTAACCTAACCCCTAACCCCTAACCTAACCCCTAACCTAACCCCTAACCTAACCCTAACCCCTAACCTAACCCCTAACCTAACCCCTAACCCCTAACCTAACCCCTAACCCCTAACCTAACCCCTAACCTAACCCCTAACCTAACCCCTAACCCCTAACCTAACCCCTAACCTAACCCCTAACC

==> ncRNA.fa <==

>HACA::KI0AEA23Y021AHM1:153-304

AAACATATTAGACTTCATGAAGGGTTTACTTAAAAATGCTCCTTTCAGGCTCCGATTTTACTTTTATTGGAA

>U6::KI0AEA4YJ21FM1:76-172

AGGTTGCCTGTTGTGAT

>U2::KI0ARB19YN08FM1:1720-1905

ATCAAAGCTATAAGCTTTGAGAGGTGA
>U6::KI0AFA4DA08FM1:355-451

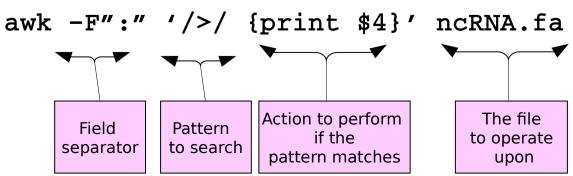
AGGTTGCCTGTTGTGAT

>RNaseMRP_RNA::KIOAIA24YL10AHM1:633-793

GTAATCCCAAAGAACAGCTACGGAGTGCTTAGGCACTCTGGGGAAAGTCCTCGGACATACTGCAGAAATGCGTCCTGAA AGGGGTATTCTAGTCATGTGATAAAGTTATGCTGTTAGGTATTGGTCTACTGAACACAATGAGGCTTACTCTTGGGAGT

AC

cgaspin@belloc:~\$





- awk 'NR==2, NR==5' FILE
 - → Write the lines from the second one to the fifth
- awk 'NR==50' FILE
 - → write only the 50th line
- awk 'NR < 26' FILE
 - → writhe the first 25 lines
- awk 'NF > 0' FILE > NEWFILE
 - → Only non empty lines are printed, the result is in NEWFILE
- awk 'NF > 4' FILE
 - → Only the lines with more than 4 fields are printed
- awk 'END { print \$NF } ' FILE
 - → Only print the value of the last field in a record



What do the following commands?

```
- awk 'NR > 25' FILE
- awk 'END { print NR } ' FILE
- awk '{ print NF ":" $0 }' FILE
- awk '{ print NR ":" $0 }' FILE
- awk '$5 == "abc123"' FILE
- awk '{ print $1, $2 }' FILE
- awk '{ print $2, $1 }' FILE
- awk '{ $2 = ""; print }' FILE
- awk '/REGEX/' FILE
- awk '!/REGEX/' FILE
- awk '/AAA|BBB|CCC/' FILE
- awk '{print NF, $1 }' FILE
```



Functions on strings

• length(s): give the length of the string. Default s is \$0.

```
awk 'BEGIN{nc=0}{nc=nc+length; nw=nw+NF} END {print
NR,"lines,",nw,"words,",nc,"chars"}' FILE
```

- substr(s,i,len): returns the substring of string s, starting at index i of length len. If length is omitted, the suffix of s starting at index i is returned.
- sub(s,sub,string): performs single substitution. It replaces the first occurrence of s with sub. The third parameter is optional. If it is omitted, \$0 is used.
- tolower(s): returns a copy of string s with all upper-case characters converted to lower-case.
- toupper(s): returns a copy of string s with all upper-case characters converted to upper-case.
- split(s,arr,regex): This function splits the string s into fields by regular expression regex and the fields are loaded into the array arr. If regex is omitted, then FS is used.



Loops statements

If

```
awk 'BEGIN {num = 10; if (num % 2 == 0) printf "%d is even number.\n", num }'
```

• If-Then-Else

```
awk 'BEGIN {num = 11; if (num % 2 == 0) printf "%d is even
number.\n", num; else printf "%d is odd number.\n", num }'
```



Bioinfo Control flow statements

for loop

```
awk 'BEGIN {for (i = 1;i <= 5;++i) print I}'
echo "1 2 3 4"|awk '{for (i=1;i<=NF;i++) total=total+$i}; END
{print total}'</pre>
```

while loop

```
awk 'BEGIN {i= 1; while (i < 6) {print i; ++i}}'
awk 'BEGIN {while (1) print "forever"}'
awk 'BEGIN {x=1; while (1) {print "Iteration"; if (x==10) break; x++;}}'</pre>
```

Do-while loop

```
awk 'BEGIN {i = 1; do {print i; ++i} while (i < 6)}'
awk 'BEGIN{count=1; do print "This gets printed at least once";
while(count!=1)}'</pre>
```



Control flow statements

If

```
awk 'BEGIN {num = 10; if (num % 2 == 0) printf "%d is even number.\n", num }'
```

• If-Then-Else

```
awk 'BEGIN {num = 11; if (num % 2 == 0) printf "%d is even
number.\n", num; else printf "%d is odd number.\n", num }'
```



Arrays in awk

- Array elements are not declared
- Array can have any value:
 - Numbers
 - Strings (associative arrays)
- Example

```
awk 'BEGIN {fruits["mango"]="yellow";fruits["orange"]=
"orange";print fruits["orange"]}'
```



What do the following programs?

```
awk '{line[NR]=$0} END {for (i=NR; (i>0); i=i-1) {print
line[i]}}' file
```

```
Awk 'BEGIN {item[101]="HD
Camcorder";item[102]="Refrigerator";item[103]="MP3
Player";item[104]="Tennis Racket";item[105]="Laser
Printer";item[1001]="Tennis Ball";item[55]="Laptop";
item["na"]="Not Available"; for (x in item) print item[x];}
```



What do the following program ?

```
awk '{line[NR]=$0} END {for (i=NR; (i>0); i=i-1) {print line[i]}}' file
```

```
Terminal
                                                                             х
Fichier Édition Affichage Rechercher Terminal Aide
SUSA
cgaspin@belloc:~/TP/TP_REGEX$ cat fich2
SUSA
SUSSS
SUS
SUAD
UAD-DUA
SUAD
cgaspin@belloc:~/TP/TP_REGEX$ awk '{ line[NR] = $0 } END { for (i=NR; (i > 0);
i=i-1) {print line[i]} }' fich2
SUAD
UAD - DUA
$UAD
SUS
SUSSS
SUSA
cgaspin@belloc:~/TP/TP REGEX$
```



What can you do with awk?

Question files: give the list of chromosomes in file file1.bed

```
74711
chr2
             127472363
                        Pos1
chr3
     74723
             127473530
                        Pos2
chr1
     73530
             127474697
                        Pos3
     17469
                               0
chr2
                        Pos4
             127475864
                               0
                        Neg1
chr3
     12747
             127477031
                        Neg2
                               0
chr5
     17477
            127478198
                        Neg3
chr7
     74781
             127479365
                        Pos5
             127480532
chr7
     74795
             127481699
                        Neg4
\mathsf{chr}1
     12748
```

```
awk '{print $1}' file1.bed | sort | uniq
```



Part III

TP3

Exercises



Used material

- https://www.powershow.com/view1/18c06e-ZDc1Z/CSCI_20330_20The_20UNIX_20System_powerpoint_ppt_presentation
- http://www.grymoire.com/Unix/Sed.html#uh-5
- https://www.tutorialspoint.com/awk/awk_quick_guide.htm