

# AWK programming



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# Course organization

- 9:00 AM to 5:00 PM
- Lunch break 12:00 AM till 2:00 PM
- Five minutes breaks every hour 10:00 AM to 10:05 AM...
- BBB includes :
  - Chat public or private
  - Shared notes (location of the course notes and solutions)
  - Polls
- The idea is to adapt to all participants. Therefore feel free to ask question, to give other solutions, to interact.
- We will learn from your questions and our errors.

# Do you have command line access?

- Use your local machine or a distant server
  - Local :
    - \*nix or mac open a terminal
    - MS-Windows open mobaxterm
  - Distant : <https://mobaxterm.mobatek.net/>
    - \*nix or mac open a terminal and connect to server using ssh
    - MS-Windows open putty or mobaxterm and connect to server
- Paste the result of the date command in the shared notes followed by you name.

# Self presentation

- Name
- Laboratory
- Research field or object
- What are you expecting from this day?

# What you are going to learn about awk?

- How to use build in variables.
- How to create set and delete a variable.
- How to create and use loops.
- How to create and use tests.
- How to create and populate an array.

# Why should you use AWK?

- 1) Because it enables to make reproducible file processing.
- 2) Because it is quite simple and can process large files.
- 3) Because it is installed on close to all Unix servers.
- 4) Because it exists in mobaXterm on MS-Windows.
- 5) Because it has a lot of useful functions.

# Write an AWK script in vi

**To create a new file or edit a existing :**

**vi myfile.awk or vi and then in vi "w myfile.awk"**

**Once in vi :**

i to insert

A to append

[ESC] to stop to insert

d to delete

yy to copy and p to paste a line

[ESC] : nu to present the line numbers

[ESC] : 1,\$s/before/after/

/mysearch to search in the file

[ESC] : wq to write and quit

[ESC] : q! to force to quit

## invoking AWK

```
awk '$2 == 5' myfile.txt
```

```
cat myfile.txt | awk '$2 == 5'
```

```
awk '$2 == 5' < myfile.txt
```

**If the file filter.awk contains '\$2 == 5' then**

```
cat myfile.txt | awk -f filter.awk
```

```
awk -f filter.awk myfile.txt
```

```
awk -f filter.awk < myfile.txt
```

If your programme is longer than the line or has a complicated structure use an awk script file.

# AWK command structure

```
awk 'awk command string' filename.txt
```

awk command string structure :

```
'BEGIN{statements} FILTER{statements}END{ statements}'
```

- **BEGIN** runs before reading the input file
- *FILTER* RE to select the processed lines
- **END** runs after reading the input file
- Statements are separated by « ; »

Use simple or double quotes at command ends.

# AWK built-in variables

## Built-in variables

\$0	Whole line,
\$1, \$2 ... \$NF	first, second... last field
ARGC	Number of command line arguments
ARGV	Array of command line arguments
FILENAME	Name of current input file
FS, RS	Input field / record separator (def: one space, \n)
NF	Number of fields in current record
NR, FNR	Number of record read so far / in current file
OFMT	Output format for numbers (default: %.6g)
OFS, ORS	Output field / rec. separator (def: one space, \n)
RESTART, RLENGTH	Start / Length of string matched by match function (see below)
SUBSEP	Subscript separator (default: \034)

# Data files used for the exercises

- Fasta : sequence file
- GFF3 : gene transfer format
- VCF : variant call format
- Expression measurements : text file with counts
  
- Files have headers and content
- File can be structured in columns
  
- <http://genoweb.toulouse.inra.fr/~klopp/SedAwk2021/Data/>

# Exercises : using built-in variables

- Extract header lines from the gtf file
- Extract the second column from the expression measurement file
- Print input file name
- Print number of blocks in each row of the expression measurement file

# AWK operators

## Operators

&&		!				Logical operators. Ex: !(\$2<4    \$3<20)
<	<=	==	!=	>=	>	Comparing operators
~	!~					matched by, not
selector?if-true-exp:if-false-exp						

# Exercises : using operators

- Extract lines from the expression measurement file where the third block value is between 5 and 7
- Extract lines from the expression measurement file where the fourth block value is like '5...'

# AWK functions

## Main built-in functions

r: regex ; s,t: strings ; n,p: integers

---

**int**(n), **sqrt**(n), **exp**(n), **log**(n),  
**sin**(n), **cos**(n)

---

**rand**() Random number between 0 and 1

---

**close**(file or command)

---

**getline** [var] Read next line from input file,  
**getline** [var] < file from a specific file,  
command | **getline** [var] or from a pipe  
Return 1 (record found), 0 (end of file), -1 (error)

---

**gsub**(r,s) Substitute s for r globally in \$0 / string t;  
**gsub**(r,s,t) return # of subs made

---

**index**(s,t) Return first position of string t in s, or 0  
if t is not present

---

**length**(s) Return number of characters in s

---

**match**(s,r) Test whether s contains a substring  
matched by r; return index or 0; sets  
RSTART and RLENGTH

---

**split**(s,a) Split s into array a on FS / field  
**split**(s,a,fs) separator fs; return # of fields

---

**sprintf**(fmt,expr-list)  
Return expr-list formatted according to format string fmt

---

**sub**(r,s) Substitute s for the leftmost longest  
**sub**(r,s,t) substring of \$0 / t matched by r; return #  
of subs made

---

**substr**(s,p) Return substring of s (of length n)  
**substr**(s,p,n) starting at position p

---

**tolower**(s), **toupper**(s) Lower and upper cases

---

**srand**() to set the random number generation

# Exercises : using functions

- Print a random value
- Print length of "ABCDEFGHJIJ" string
- Print substring of "ABCDEFGHJIJ" from position 3 to 7
- Split string "ABCDEFGHJIJ" in characters and print second cell

# AWK data structures : arrays and dictionaries

**Variable** : `a = 10; var = "var"; tt =1.36`

**Array** : `a[1]=1; a[2]=3; a[3]="eight"`

Quick way to produce an array : `split("123",a,"")`

**Hash table, dictionary** :

`h["one"]=1; h["two"]=3; h["three"]="eight"`

Delete function removes an element from an array or a hash table.

`Delete(a[1]); delete(h["two"])`

# Exercise 1 : follow up

- What are these programs doing?

1) 

```
BEGIN{  
    print "this is the beginning"  
}
```

2) 

```
{  
    print "print"  
}
```

3) 

```
END{  
    print .NR  
}
```

4) 

```
/^A/  
{  
    print .NR  
}
```

5) 

```
BEGIN{  
    print "#this is the header"  
}  
{  
    print "line number " .NR  
}  
END{  
    print "#end"  
}
```

# How does this program work?

- mel.awk file contains and uses a gff file as input

```
BEGIN{
    cnt = 0;
    totlen =0
}
$3 == "exon" {
    cnt = cnt + 1;          #cnt++;
    totlen = totlen + ($5-$4+1); #totlen += ($5-$4+1);
}
END{
    print "cnt " cnt " m1 " (totlen/cnt)
}
```

# Exercises : using data structures

- Create variable a, attribute value 10 to a and print a
- Create array t, attribute value 10 to t[1] and value 24 to t[2] and print t[1] and t[2]
- Create dictionary d, attribute value 10 to d["ten"] and value 24 to d["twenty"] and print d["ten"] and d["twenty"]

# AWK control structure

**if** (expression) statement1 **else** statement2

**while** (expression) statement

**for** (expr1;expr2;expr3) statement

**do** statement **while** (expression)

**break** / **continue** : immediately leave / start next iteration  
of innermost enclosing loop

**exit** / **exit** expression : go immediately to the END  
action; if within the END action, exit program

# Loop exercise

- What is this program doing?

```
{
    for (i=1; i<=$NF; i++){a=a+$i;}
}
END{
    print "sum of all values = "a
}
```

# awk parameters passing

- To pass an awk command or an awk script generic we can transmit parameter.
- Two parameters
  - ARGC (argument count) and ARGV (argument array)
  - -v option

```
awk -f myscript.awk file "A" "B"
```

```
awk -f myscript.awk file A B
```

```
awk -v param1="A" -v param2="B" -f myscript.awk file
```

# Exercises : using control structures

- Create a loop from 1 to 10 with step 1 and print the result
- Create a loop from 1 to 10 with step 1 and print the result only if the values are 4 or 8
- Create a loop from 1 to 10 with step 1 and print the result until 6 and leave the loop

# What is programming?

- Starting from an idea or a question
- Write code which produces the expected result
- Before writing the code
  - Define your **inputs and outputs**
  - Define your **program structure** (loops, tests, functions...)
  - Decide what **data structure** you need (variable, array,...)
- Add tests to your inputs to make your code more **robust**
- Add documentation to make your code **maintainable** (document inputs and outputs, functions,...)

## Exercise 2 : creating a sample file

- With AWK,
  - Create a file of 100 lines,
  - Each line contains one random number between 0 and 1
- Transform your program to print random characters instead of numbers
- Transform you program to print 10 random characters per line
- Transform you program to print 3 blocks of numeric values and 3 blocks of characters per line

# Creating novel function in awk

- Awk has built-in functions but you can extend these by creating your own functions.
- Functions are used to replace parts of codes which are repeated in the program or to make the program more readable.
- Functions can be grouped in a function file which is loaded before using the functions. Loading is performed with `@include "functions.awk"`.
- To create a function you use the 'function' function and define inputs and outputs.

```
function print_concatenate(str1, str2) {  
    print str1 "_" str2  
}
```

```
Function square(val) {  
    return(val * val)  
}
```

# Commenting an awk program

- To make you programs more readable for others or yourself you should add comments.
- Comment are lines which do not change the program behavior.
- Comment are lines starting with a hashtag '#'

```
# print_concatenate concatenates two strings with "_"
function print_concatenate(str1, str2) {
    print str1 "_" str2
}
```

# Running awk scripts

- You can run an awk scripts without invoking “awk -f” .
- For this you have to add a **shebang** at the first line of you script.
- A **shebang** is a line starting with `#!` indicating the location of the awk interpreter. For example `/usr/bin/awk`.  
You can get it using the `which awk` command.
- Then you render your script executable with `chmod +x myscript.awk`

```
#!/usr/bin/awk -f  
  
{  
    print NR"\t"$0  
}
```

## Exercise 3 : follow up

- Change your program in order to run if from the command line without calling “awk -f myprogram.awk” but “myprogram.awk”
- Create a function in your program to build the character strings. Function input = number of character, function return = string
- Move you function to a function file and include this function file in a new program which only runs the main part of the code.
- Add comments to the function and the program to help maintenance

# Exercise 4 : processing the file

- With AWK,
  - For each column of the file : to\_be\_processed.txt  
[http://genoweb.toulouse.inra.fr/~klopp/awk/to\\_be\\_processed.txt](http://genoweb.toulouse.inra.fr/~klopp/awk/to_be_processed.txt)
  - Count the number of columns per line.
- For each numerical column find minimum and maximum values.
- Count the number of distinct elements per column.
- Count the number of occurrences of each element in the fourth column for all lines of the file.

# Exercise 5 : join files

- With AWK
  - Join both files :  
[http://genoweb.toulouse.inra.fr/~klopp/awk/to\\_be\\_joined1.txt](http://genoweb.toulouse.inra.fr/~klopp/awk/to_be_joined1.txt)  
[http://genoweb.toulouse.inra.fr/~klopp/awk/to\\_be\\_joined2.txt](http://genoweb.toulouse.inra.fr/~klopp/awk/to_be_joined2.txt)  
Using the first column