C2110 UNIX and programming

Lesson 12 / Module 1

PS / 2020 Distance form of teaching: Rev1

Petr Kulhanek

kulhanek@chemi.muni.cz

National Center for Biomolecular Research, Faculty of Science Masaryk University, Kamenice 5, CZ-62500 Brno

AWK

http://www.gnu.org/software/gawk/gawk.html

AWK is a scripting language designed for **text data processing**, whether in the form of text files or streams. The language uses **string data types**, **associative field** (arrays indexed by string keys) and **regular expressions**.

adapted from www.wikipedia.org

Obsah

> AWK

- **Conditions, logical operations**
- Run control (next, exit)
- Loops
- **Arrays**

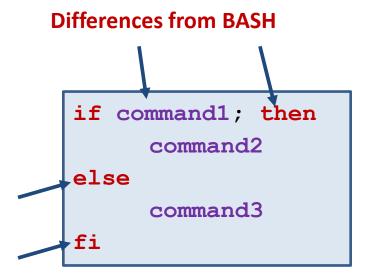
Conditions

```
if( logical_expression ) {
    command2;
    ...
} else {
    command3;
    ...
}
```

If **logical_expression** is true, **command2** will be executed. Otherwise, **command3** will be executed.

Example:

```
if( $1 > max ) {
    max = $1;
}
```



Logical operators

Operators:

```
equal
       not equal
!=
       smaller than
<
       less than or equal
<=
       greater than
>
       greater than or equal
>=
       negation
       logical and
&&
Ш
       logical or
```

Exampley:

```
j > 5
(j > 5) && (j < 10)
(j \le 5) | | (j \ge 10)
```

- 1. Write a script that prints the largest and smallest value from the third column of the matice.txt file.
- 2. Write a script that prints lines that contain nine words from rst.out file.
- 3. Write a script that calculates the average value of the numbers listed in the second column of the matice.txt file.

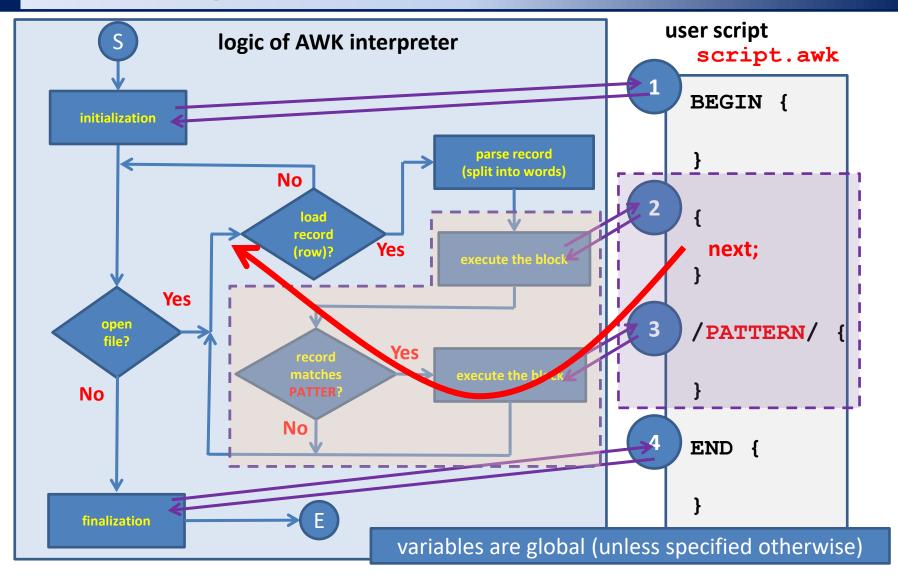
The data is in the directory:

1. Write a script that calculates the geometric center of the molecule stored in the format xyz. The resulting coordinates will be printed to the terminal. The file name is entered by the user as the first argument of the script. Take care of situation when the wrong number of arguments is specified and the specified file does not exist. The input file is in a directory geom.

Help:

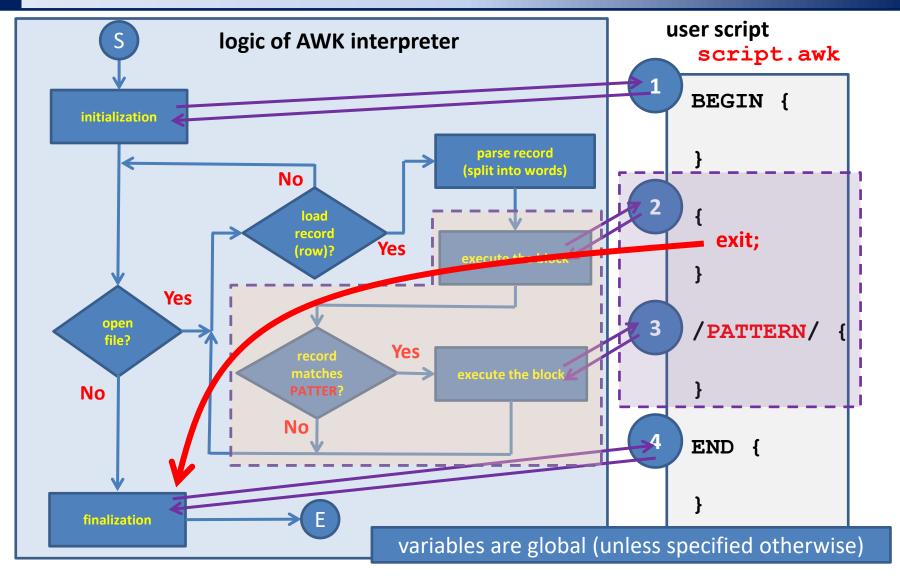
- File format xyz contains the number of atoms on the first line, any comment on the second line and the next lines contain the element of the atom and its x, y and z coordinates.
- You can use any combination of commands lines cat, wc, head and tail to discard the
 first two lines. Alternatively, get inspired on the manual pages of the command tail or
 apply conditions in awk.

Running control - next



Key word **next** terminates the processing of the current record. The next entry continues.

Run control - exit



Key word **exit** stops processing of the current record and all subsequent files.

1. Extract temperature profile and calculate its average value from file rst.out. Compare the calculated value with the average value given in the file rst.out. Why do the values differ?

The data is in the directory:

Loops

```
for(inicialization; condition; change)
     command1;
```

Example:

```
for(I=1;I <= 10;I++){
     sum = sum + $I;
```

Differences from BASH for((inicialization; condition; change)); do command1 done 🛖

- 1. Write a script that sums the values of all the numbers listed in the matice.txt file.
- 2. Write a script that prints the number of words that the file rst.out contains. Verify the result with the command wc.

The data is in the directory:

Arrays

AWK uses associative arrays. The array has a name, the elements of the array are accessed using a key. The key can have any value and type. The key can be the value of a variable.

Value assignment:

Obtaining value:

Variable: A



the variable contains only one value

```
A= 5; print A;
```

It is not recommended to use real numbers as keys!

Associative array: **AR**



field may contain **more values**, but only one for each key.

Arrays - Examples

```
Examples:
       i = 5;
       my array[i] = 15;
       print my array[i];
       a = "word";
       my_array[a] = "value";
       print my_array["word"],
                                my array[5];
Practical use:
       BEGIN {
            count = 0;
                                             script prints number of values in
            data[count++] = $1;
                                             column 1 and then their values
       END {
            print count;
            for(i=0; i < count; i++) {
                print data[i];
```

- 1. The structure1.dat file contains the name of the element and the position of the atom on each line. Write a script that converts the file to a format xyz and saves it as structure1.xyz. View the converted structure in VMD.
- 2. Verify the generality of the solution by converting the structure2.dat file.

```
C -1.8164140 3.6071310 0.6117350
C -1.8002910 2.2769110 0.4584060
C -0.6436270 4.3094580 -0.0124580
```

first line: number of atoms

second line: any comment

Molecule display:

- \$ module add vmd
- \$ vmd structure1.xyz

```
20
molecule
C -1.8164140 3.6071310 0.6117350
C -1.8002910 2.2769110 0.4584060
C -0.6436270 4.3094580 -0.0124580
```

The data is in the directory:

Self-study



Arrays, ...

Browse the key list:

```
for( variable in array) {
    print array[variable];
    ...
}
```

Delete records with key:

```
delete array[key];
```

Executes loop body for each key that was used to store the value in **array**. The key value is stored in **variable**.

ATTENTION: order of the keys is not specified and thus may not correspond to order of inserting elements into array