Perl for Biologists

Session 6 April 8, 2015

Files, directories and I/O operations

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Session 6: Files, directories and I/O operations Perl for Biologists 1.2

Reminder: What is a Hash?

Array

Hash

Index	Value
0	apple
1	banana
2	cranberry
3	daikon
4	eggplant
5	81

Кеу	Value
red fruit	apple
yellow fruit	banana
red berry	cranberry
white tuber	daikon
purple veggie	eggplant
nine squared	81

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Reminder: Hash Syntax

- Declaring a variable to be a Hash, use "%" %hash;
- Can initialize a hash using an Array
 %hash = ('red fruit', 'apple',
 'yellow fruit', 'banana', 'nine
 squared', 81);

Reminder: Hash Syntax

• Accessing individual Hash element
 \$hash{'red fruit'};

• Equivalently

\$key = 'red fruit';
\$hash{\$key};

Reminder: Hash Syntax

- Assigning individual Hash element
 \$hash{'purple veggie'} =
 'eggplant';
- Can initialize a array using a Hash

@array = %hash;

Reminder: The Big Arrow

8hash = (

- 'red fruit'
- 'yellow fruit' => 'banana',
- 'red berry'
- 'white tuber'
- 'purple veggie' => 'eggplant', 'nine squared' => 81,

- => 'apple',
- => 'cranberry',

);

Reminder: Hash Functions

- keys(%hash): returns an Array of the Keys
 @hash_keys = keys (%hash);
 @hash_keys = keys %hash;
- values(%hash): returns an Array of the Values
 @hash_values = values (%hash);
 @hash_values = values %hash;

Reminder: Hash Functions

 each(%hash): returns the next Key Value pair as a 2 element array
 @pair = each (%hash);

print "\$pair[0] = \$pair[1]\n";

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Session 5 Exercises Review

- 1. Modify the code from session 3 exercise 3 to generate a 9kb long random DNA sequence. Save this sequence to a variable.
- 2. Create a hash where the keys are unique sequences of 3 base pairs and the values are the counts of how often the key appeared in the randomly generated sequence. Print out/save to a file these keys and values

Bonus: Print out/save keys and values sorted by values in decreasing order

/home/jarekp/perl_05/exercise1.pl

Person with the most number (at least 3) of distinct methods of populating a hash from a string wins 50 FREE CBSU computing hours!

/home/jarekp/perl_05/exercise2.pl
/home/jarekp/perl_05/exercise3.pl
/home/jarekp/perl_05/exercise4.pl
/home/jarekp/perl_05/exercise5.pl

Simple Line Input

Each program has three default input/output objects associated with it

- *input stream* usually keyboard input: STDIN
- *output stream* usually screen: STDOUT
- *error stream* usually screen: STDERR

```
#!/usr/local/bin/perl
```

```
$svar = <STDIN>; #get one line of std input
print STDOUT "1. [$svar]\n";
chomp($svar);
print STDERR "2. [$svar]\n";
print "3. [$svar]\n";
```

Opening files as streams

You can open file and create a stream with open function



the above opens the file for reading (default)

Opening files as streams

You can open file for writing:

```
open HANDLE, ">/path/filename";
```

The file will be created if it doesn't exist. If it does exist it will be overwritten.

Opening file for append requires '>>'

open HANDLE, ">>/path/filename";

Function **open** returns value indicating success or failure

```
$res = open HANDLE, ">/path/filename";
if($res)
{
    print "open successful\n";
}
```

or

```
if(!open HANDLE, ">/path/filename")
{
    print "open failed\n";
}
```

If there is an error special variable **\$!** is set to an error text message generated by the system (like "access denied")

```
if(!open HANDLE, ">/path/filename")
{
    print "open failed\nError is: $!";
}
```

There is a short version of **if**, especially useful in one-line statements:



There is a short version of **if**, especially useful in one-line statements:



Once opened, the file can be read the same way as <STDIN>

\$svar=<in>;

the file should be closed with close when not needed – it will flush the buffers

close(out);

script1.pl (1)

- Script to read file1 and copy the content to file2
- File names read from arguments of the script
- Every other new line replaced with a space

script1.pl (1)

```
#!/usr/local/bin/perl
```

```
#we want 2 file names as parameters
if($#ARGV != 1)
{
    print STDERR "USAGE: script1.pl file_name1 file_name2\n";
    exit;
}
```

```
#now try to open files
open in, $ARGV[0] or die "ERROR1: $!\n";
open out, ">" . $ARGV[1] or die "ERROR2: $!\n";
```

script1.pl (2)

```
#lets read file 1 and write file 2 in a loop
#lets replace line endings with space on every other line
#when writing to file 2
$n=1;
while ($txt=<in>)
{
        chomp $txt; #remove ending \n character
        print "line $n length is " . length($txt) . "\n";
        print out "$txt";
        if($n % 2 == 0)
        {
                print out "\n";
        }
        else
        {
                print out " ";
        }
        $n++;
}
#close files
close(in);
close(out);
```

What happens when we forget to open the file?

If reading, we will always get an empty string.

If writing, the data is ignored (goes to /dev/null).

What happens when we forget to close the file?

The file will be closed automatically when program exits, or when the handle is reused (opened again).

However, if the program crashes, the data being written to a file may be lost.

The data is written to a **buffer** first, then transferred to the disk later. This procedure speeds up read/write a lot, but if interrupted data may be lost.



.. yet the memory is almost full – here are the buffers

Very little memory used by processes

o ,				-		/						
top -	13:10:20	up 6	9 da	ays, 13	3:36,	2 us	ser	s, 1	Load at	verage: 8	.01, 8.03, 8.05	
Tasks	: 341 tot	al,	1 1	cunning	1, 330	slee	pi	ng,	2 sto	opped, () zombie	
Cpu (s	0.2%u	is, 0	.1%:	<u>sy, 0</u> .	0 % ni,	32.4	1%i	d, 67	7.4%wa,	, 0.0%hi,	, 0.0%si, 0.0%st	
Mem:	16336144	k tot	al	159954	108k 1	sed,		34073	36k fre	ee, 148	844k buffers	
Swap:	18579452	k tot	al,	3241	168k 1	ised,	18	25528	34k fre	ee, 145969	920k cached	
	TIOPP		177					ant			00100100	
PID	USER	PR	NI	VIRI	RES	SHR	5	\$CPU	*MEM	TIME+	COMMAND	
29689	Iee27	20	0	668m	10/m	26m	5	1.7		152:13.82	Ilreiox	
4193	root	20	0	0	0	0	1 1	0.3	0.0	0:03.70	kworker/6:3	
4341	Jarekp	20	0	1/336	1352	876	R	0.3	.0.0	0:00.17	top	
4996	root	20	0	516m	83m	1608	S	0.3	0.5	377:42.58	glusteris	
22790	mp6/3	20	0	322m	13m	9.8m	S	0.3	0.1	2:27.82	gnome-panel	
1	root	20	0	21512	420	212	S	0.0	0.0	0:01.61	init	
2	root	20	0	0	0	0	S	0.0	0.9	0:00.91	kthreadd	
3	root	20	0	0	0	0	S	0.0	0.0	0:01.57	ksoftirgd/0	
6	root	RT	0	0	0	0	S	0.0	0.0	0:00.00	migration/0	
7	root	RT	0	0	0	0	S	0.0	0.0	0:04.84	watchdog/0	
8	root	RT	0	0	0	0	S	0.0	0.0	0:00.00	migration/1	
10	root	20	0	0	0	0	S	0.0	0.0	0:00.50	ksoftirqd/1	
12	root	RT	0	0	0	0	S	0.0	0.0	0:04.20	watchdog/1	
13	root	RT	0	0	0	0	S	0.0	0.0	0:00.00	migration/2	
15	root	20	0	0	0	0	S	0.0	0.0	0:41.92	ksoftirqd/2	
16	root	RT	0	0	0	0	S	0.0	0.0	0:04.69	watchdog/2	
17	root	RT	0	0	0	0	S	0.0	0.0	0:00.00	migration/3	
19	root	20	0	0	0	0	S	0.0	0.0	0:00.78	ksoftirqd/3	
20	root	RT	0	0	0	0	S	0.0	0.0	0:04.08	watchdog/3	
21	root	RT	0	0	0	0	S	0.0	0.0	0:00.00	migration/4	
23	root	20	0	0	0	0	S	0.0	0.0	0:01.64	ksoftirqd/4	
24	root	RT	0	0	0	0	S	0.0	0.0	0:04.14	watchdog/4	
25	root	RT	0	0	0	0	S	0.0	0.0	0:00.00	migration/5	
27	root	20	0	0	0	0	S	0.0	0.0	0:00.46	ksoftirqd/5	
28	root	RT	0	0	0	0	S	0.0	0.0	0:08.67	watchdog/5	

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Buffering is a feature of both system and Perl interpreter, and it can be controlled by setting special variable \$|

\$| = 1; #don't buffer current stream \$| = 0; #do buffer current stream

A stream is made current by using select() function



A stream handle can be kept in a variable instead of bareword

open \$handle, "filename";

script2.pl (1)

Script printing random numbers to a file

File name is the argument

User decides to buffer the output or not

script2.pl (1)

```
#!/usr/local/bin/perl
```

```
if (\$ ARGV < 0)
{
        print STDERR "USAGE: script2.pl file name\n";
        exit;
}
print "Do you want to flush? (y/n) ";
while ($fl=<STDIN>)
{
        chomp $fl;
        if($fl ne "y" && $fl ne "n")
         {
                 print "error: invalid input $fl\n";
                 print "Do you want to flush? (y/n) ";
         }
        else
         {
                 last;
         }
}
```

script2.pl (2)

```
$n=0;
while($n<1000_000_000)
{
    $n++;
    if($n % 1000 == 0)
        {printf out "%010d %17.16f\n", $n, sqrt(rand(100));}
}
close(out);</pre>
```

Binary files

By default, any stream opened is treated as ASCII (text) stream.

Reading a file in ASCII (text) mode means some binary characters may be lost (converted) and in general the written binary file becomes corrupted.

See what happens when script1.pl is used for ~jarekp/perl_06/picture.jpg (you can view picture with eog).

File handle must be marked as binary in order to stop character conversion.

Binary files



open HANDLE2, ">/path/filename2"; binmode(HANDLE2); print HANDLE2 \$data;

script3.pl

Script copying binary file

Source file is argument 1, destination file argument 2

Print number of bytes copied

script3.pl

#!/usr/local/bin/perl

```
#we want 2 file names as parameters
if($#ARGV != 1)
{
        print STDERR "USAGE: script3.pl file name1 file name2\n";
        exit;
}
open in, $ARGV[0] or die "ERROR1: $!\n";
binmode(in);
open out, ">" . $ARGV[1] or die "ERROR2: $!\n";
binmode(out);
#lets read file 1 and write file 2 in a loop
$n=0;
while($cnt=read(in, $data, 1024))
{
        $n += $cnt;
        print "$n bytes total read so far, $cnt this iteration\n";
        print out $data or die "Error writing file\n$!";
}
print "$n bytes copied\n";
#close files
close(in);
close(out);
```

Opening pipelines

Perl can open output stream of a program and read it as a file.



The file handle will reach the end when program1 ends.



Perl can execute any program from inside a script:

system("program1 arg1 arg2");

STDOUT from program1 will go to script's STDOUT STDERR will go to script's STDERR

system("program1 arg1 arg2 1> out");

STDOUT from program1 will go to file out STDERR will go to script's STDERR

system("program1 arg1 arg2 1> out 2> err");

STDOUT from program1 will go to file out STDERR will go to file err

Perl script will WAIT until program1 finishes

system("program1 arg1 arg2 1> out 2> err &");

now Perl WILL NOT WAIT for program1 to finish, will continue immediately and program1 will run in parallel.

\$n = system("program1 arg1 arg2");

system() returns an integer representing completion code of the program

usually 0 for success and something else for error.

system("program1 arg1 arg2");

can be also written using back quotes, in this case the return is the OUTPUT of the command

\$str = `program1 arg1 arg2`

script4.pl

Script to find the number of sequences and

number of amino acids in *swissprot* BLAST database

script4.pl

#!/usr/local/bin/perl

```
open in, "fastacmd -d /shared data/genome db/BLAST NCBI/swissprot
-p T -D 1 | " or die "ERROR: $!\n";
$n=0;
$aa=0;
|=1;
while ($txt=<in>)
{
        if(substr($txt, 0, 1) eq ">")
         {
                 $n++;
                 if($n % 1000 == 0) {print "."; }
                 if ($n % 80 000 == 0) {print "\n"; }
         }
        else
         {
                 $aa += length($txt) - 1;
         }
}
if ($n % 80 000 != 0) {print "\n"; }
close(in);
print "swissprot contains $n sequences and $aa aa\n";
```

Logical operators for files and directories

- -e "name" file or directory exists
- -f "name" name is a file
- -d "name" *name* is a directory
- -s "name" name is non-zero size

-r "name"-w "name"-x "name"

name is readable *name* is writable *name* is executable

-z "name"

name exists and has zero size

... and more

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Functions operating on files and directories

- mkdir("name") create directory name
 rmdir("name") delete directory name
- chdir("name") change current SCRIPT directory to *name*
- unlink("name") delete file *name*
- rename("name") rename file or directory *name*
- ... and more

Functions operating on files and directories

Many Perl files and directories functions do the same as system functions:

chdir("name"); ⇔	system("cd name");	NOT THE SAME
changes cur directory of script	rent change Perl comma directo	es current directory of system and shell, Perl script current ory is NOT affected
mkdir("name"); ⇔	system("mkdir name")	OK, but system dependent
unlink("name"); 🗇	system("rm name")	OK, but system dependent

The most important difference between the functions and system calls is that the system calls will only work on one system (e.g. Linux if using "rm name", on Windows it should be "del name"), while the functions will work on ANY system

script4a.pl

```
#!/usr/local/bin/perl
$pwd = `pwd`;
print "1. Our curent directory is: $pwd";
mkdir("tmpdir");
if(!-e "tmpdir")
{
        print "ERROR!\n";
        exit;
}
else
{
        print "mkdir worked!\n";
}
chdir("tmpdir");
print "2. Our curent directory is: ";
system("pwd");
print "----\n";
system("cd /tmp; pwd ");
print "----\n";
print "3. Our curent directory is: ";
system("pwd");
chdir("/tmp");
print "4. Our curent directory is: ";
system("pwd");
```

Opening and reading a directory

Perl can open a directory and retrieve all its entries:

```
opendir DIRHANDLE, "/path/dirname";
```

Similar as to file **open**, **opendir** returns success or failure code

@ent = readdir(DIRHANDLE);

returns an array containing all entries in a directory – i.e. names of all files and directories it contains (including '.' and '..').

closedir DIRHANDLE;

script5.pl

```
#!/usr/local/bin/perl
```

```
opendir DIR, "/home/jarekp";
foreach $entry (readdir DIR)
{
        $fullentry = "/home/jarekp/$entry";
        if(-d $fullentry)
        {
                print "directory $entry\n";
        elsif(-x $fullentry)
        {
                print "executable $entry\n";
        elsif(-f $fullentry)
        {
                print "file $entry\n";
        else
        {
                print "other entry $entry\n";
        }
}
```

Exercises

- 1. Directory /home/jarekp/perl_06/files contains a set of fastq files with short reads. Write a script that lists all the files in this directory.
- 2. Modify the script from exercise 1 to open each file, read it, and produce a hash containing the distribution of sequence lengths in ALL files. Print the distribution out in descending order to a file. Plot it in Excel (no binning).

Hint 1: Fastq file contains 4 lines for each sequence: header (starting with @), sequence itself, '+' line, and quality score line. Check script4.pl – there we had two lines per sequence.

Hint 2: Create a hash where sequence lengths are the keys and values are frequencies of the lengths.

3. Modify the script from exercise 2 to produce <u>fasta</u> file containing ALL the sequences from ALL *fastq* files.

Hint: Open fasta file at the beginning, then write each header (replacing first @ with >) followed by sequence.