Bioinformatics Programming 2013

Perl – Basics

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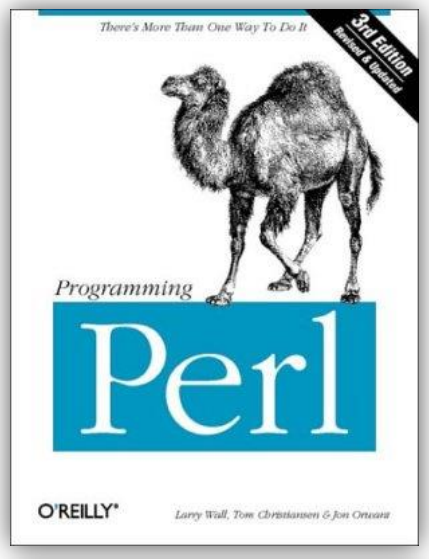
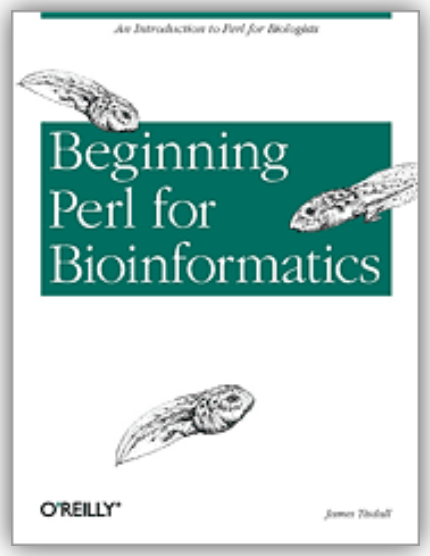
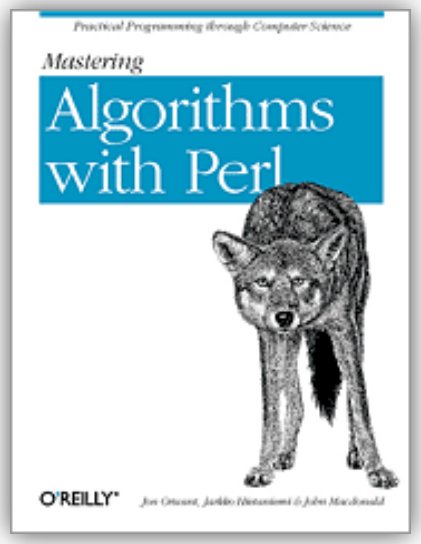
Why is Perl so heavily used in Bioinformatics ?

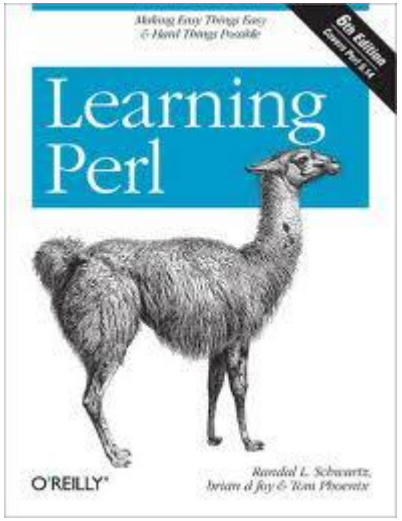
- **Perl is popular in bioinformatics because it is originally a text-processing language.**
- **Text is King** - Perl makes it easy to:
  - implement NLP and bio-informatics algorithms,
  - extract textual data,
  - generate textual data.
- **The Language Isn't (Half) Bad** - It also has the benefits of having:
  - a decent expressiveness,
  - a relatively low learning but also a decent performance.
- **Portability and Extensibility Made Easy**
  - is portable across many platforms,
  - comes with a very large library of extensions.

References







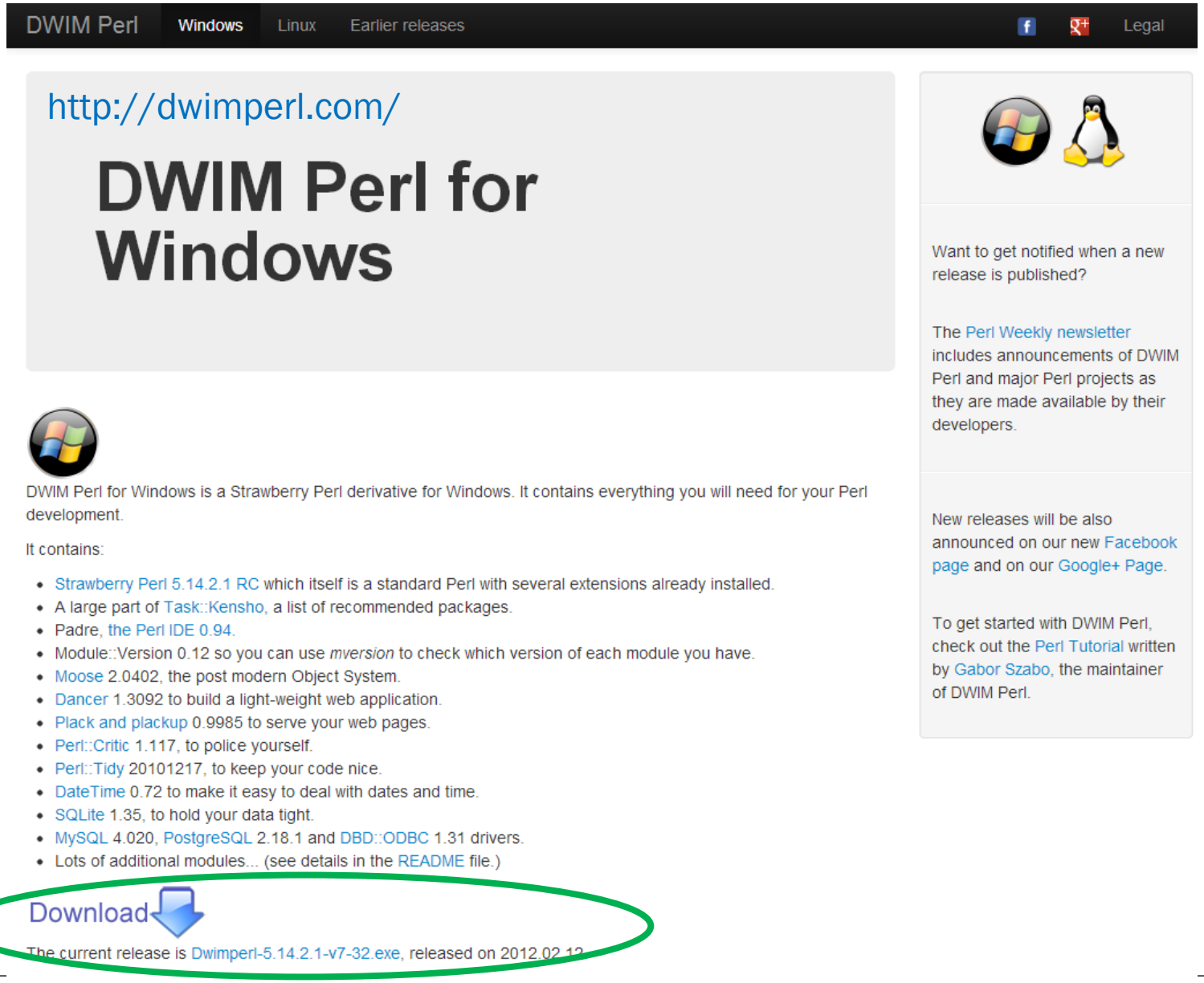


Google

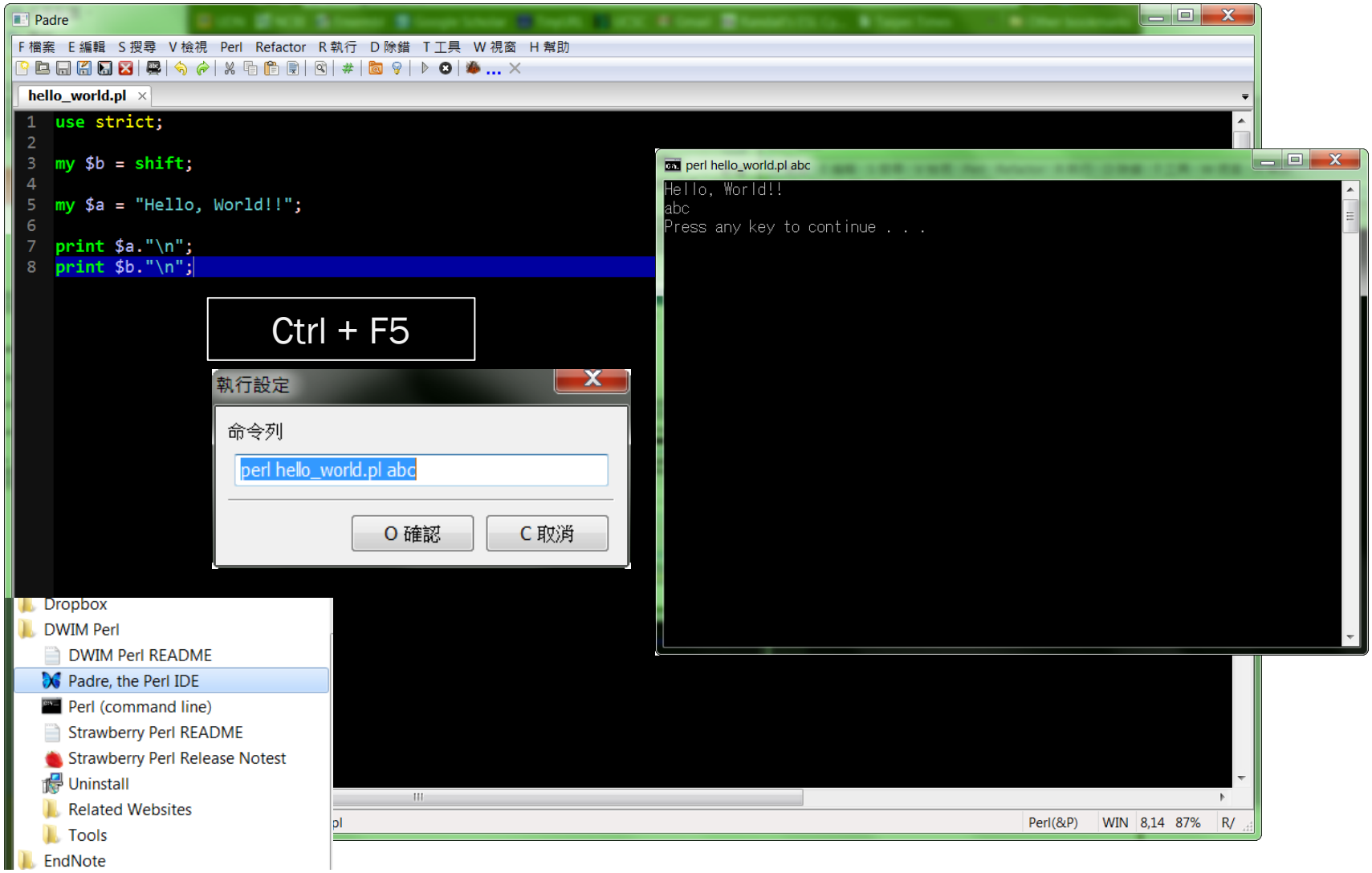
You will learn from this course …

- 2013/08/01:
  - Basic Perl data structure & statement
- 2013/08/20:
  - Regular Expression
- 2013/08/27:
  - Perl Packages
  - BioPerl
  - GD

Install Perl for Windows



Run Padre and execute my first perl script

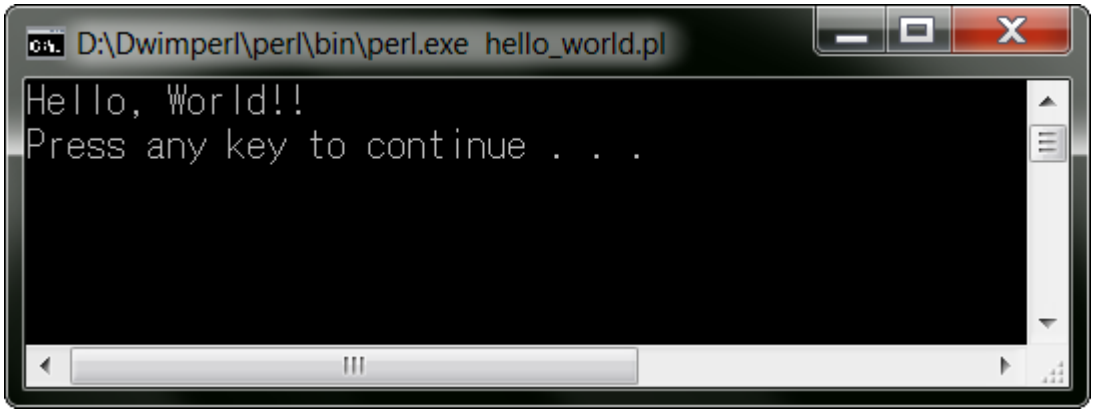


1st Perl script

```
use strict;

print “Hello, World!!\n”;
```

Save file as ***.pl** and Press **F5** to execute this script



You are familiar with Python, right?

其實PerI跟Python長得有點像，
但還是有點不一樣

Data type – string and numeric

Perl

- `my $a = 1;`
- `my $b = 'abc';`
- `my $c = "ABC";`
- `my $d = $b . $c;`
  `>> abcABC`
- `my $e = $b x 3;`
  `>> abcabcabc`

Python

- `a = 1`
- `b = 'abc'`
- `c = "ABC"`
- `d = b + c`
- `e = b * 3`

① A variable name starts with "$"
② Use "my" to declare variables to be local to the enclosing block .
③ Each command line ends with a semicolon (;)

What is the difference between ‘’ and “” ?

- Try to execute the following scripts:

```
use strict;

my $a = “John”;

print '$a is a good man.\n';
print "$a is a good mam.\n";
print $a . “ is a good man.\n”;
print "\$a is a good man.\n";
```

① Use “\” to print special characters (*i.e.* $, @, %, * and so on).

Data structure – list or array (1)

Perl

```
my @A1;
my @A2 = (‘a’,‘b’,’c’);
my @A3 = (1, 3, 5);
my $v = $A3[1];
$A3[2] = 0;
  >> (1, 3, 0)
my @A4 = (@A2, @A3);
  >> (1, 3, 0, ‘a’, ‘b’, ‘c’)
my @a = (1,3,5,7,9);
my @b = @a[1..3];
```

Python

```
A1 = []
A2 = [‘a’, ‘b’, ‘c’]
A3 = [1, 3, 5]
v = A3[1]
A3[2] = 0

A4 = A2 + A3

a = [1,3,5,7,9]
b = a[1:4]
```

① A array/list name starts with “@”.
② Use print join(“\s”, @array) to list the array elements.

Data structure – list or array (2)

Perl

- `my @a = (1, 7, 5, 3, 9)`
- `push(@a, 0);`
  `>> (1,7,5,3,9,0)`
- `scalar(@a);`
  `>> 6`
- `shift(@a);`
  `>> (7,5,3,9,0)`
- `pop(@A3);`
  `>> (7,5,3,9)`
- `@a = sort{$a<=>$b}(@a);`
  `>> (3,5,7,9)`
- `@a = sort{$b<=>$a}(@a);`
  `>> (9,7,3,5)`

Python

- `a = [1, 7, 5, 3, 9]`
- `a.append(0)`
- `len(a)`
- `a.pop(0)`
- `a.pop()`
- `a.sort()`
- `a.sort().reverse()`

① If the elements are string, using sort{$a cmp $b}@array

Data structure – list or array (3)

Perl

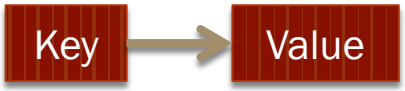
- `my @a = (1, 7, 5, 3, 9);`
- `@a = reverse(@a);`
  `>> (9,3,5,7,1)`
- `splice(@a, 2, 0);`
  `>> (9,3,7,1)`
- `splice(@a, 1, 2);`
  `>> (9,1)`
- `$#a`
  `>> 1 # the last index`

Python

- `a = [1, 7, 5, 3, 9]`
- `a.reverse()`
- `del a[2]`
- `a[1:3] = [] or del a[1:3]`

① splice(ARRAY, OFFSET, LENGTH)

Data structure – hash or dictionary



Perl

```
my %a;
my %a = ('spam' => 1,
         'eggs' => 3);
$a{'ice'} = 6;
my @k = keys(%a);
>> ('spam','eggs','ice')
my @v = values(%a);
>> (1, 3, 6)
scalar(keys(%a))
>> 3
delete($a{'eggs'});
>> ('spam' => 1,
    'ice' => 6)
```

Python

```
a = {}
a = {'spam': 1,
     'eggs': 3}
a['ice'] = 6
k = a.keys()

v = a.values()

len(a)

del a['eggs']
```

① Hash is designated with the symbol %

Print array and hash data

Array

```
my @a = (1, 7, 5, 3, 9);
foreach my $e (@a)
{
        print $e."\n";
}
```

Or

```
print join("\s", @a)."\n";
print join("\|", @a)."\n";
print join("\t", @a)."\n";
print join(undef, @a)."\n";
```

1|7|5|3|9

17539

Hash

```
my %a = ('spam' => 1,
         'eggs' => 3,
         'ice' => 6);
foreach my $key (keys %a)
{
     my $value = $a{$key};
       print "$key\t$value\n";
}
```

① "\n": 換行符號
② "\s": 空白(space)
③ "\t": Horizontal tab
④ join(DELIMITER, ARRAY) # convert array to string

Blocks

Perl

-
```
Block 1 {
      Block 2 {
            Block 3 {


                  } End Block 3
      } End Block 2
} # End Block 1
```

Indent is not required.

Python

-
```
Block 1 :
      Block 2 :
            Block 3 :


                  End Block 3
      End Block 2
End Block 1
```

Indent is required.

① Indents make scripts more readable.

Statements

if ... elsif ... else...

```
my $a = 10;
if ($a > 10)
{
    print “Block 1\n”;
}
elsif ($a == 10)
{
    print “Block 2\n”;
}
else
{
    print “Block 3\n”;
}
```

>> Block 2

unless ... elsif ... else

```
my $a = 10;
unless ($a > 10)
{
    print “Block 1\n”;
}
elsif ($a == 10)
{
    print “Block 2\n”;
}
else
{
    print “Block 3\n”;
}
```

>> Block 1

Loops – for, foreach, untill

for

- ```
  my @a = (2, 4, 6, 8, 10);
  ```
- ```
  for my $i (0 .. $#a)
  {
      print "$a[$i]\n";
  }
  ```

- ```
  for (my $i=0; $i<=$#a; $i++)
  {
      print "$a[$i]\n";
  }
  ```

foreach

- ```
  foreach my $i (@a)
  {
      print "$i\n";
  }
  ```

① $#array returns the last index of a array
② $a++ → $a+=1

Loops – while & until

while

```
my $a = 10;
while ($a > 0)
{
    print “Bingo!\n”;
    $a --;
}
```

until

```
until ($a == 0)
{
    print “Bingo!\n”;
    $a --;
}
```

① $a -- → $a-=1

File access

Read File

- `my $filename = “input.txt”;`
- `open(IN, “$filename”) or die (“Error!\n”);`
- Method 1:

```
my @input = <IN>;
```

- Method 2:

```
while (my $line = <IN>)
{
    do something …
}
```

- `close(IN);`

Write File

- `my $filename = “output.txt”;`
- `open(OUT, “>$filename”);`
- `print OUT “write something\n”;`
- `close(OUT);`

Example 1: counting DNA nucleotides

Input:
A DNA fasta file. For example,

```
>this is a fasta header
ATCGGCGGAGAAaacccttgggccccgggggTGGCG
aacccctggcgATGGTGACGATAGCAGATaagatag
TGGAGTaaGGTAT
```

Output:
For example,

A	22
T	14
C	17
G	32

Script for Example 1

```perl
use strict;

my $file = "example.fasta";

open IN, "$file";
my @seq = <IN>;
my $header = shift @seq; # remove the first element (fasta header) of the array

my %counter;
foreach my $seq (@seq)
{
        chomp($seq); # remove any newline character from the end of a string
        $seq = uc($seq); # convert string to uppercased version
                         # similar function "lc" => convert string to lowercased version
        my @dna = split(undef, $seq); # convert a string into a array
        foreach my $dna (@dna)
        {
                $counter{$dna} ++;
        }
}

while (my ($key, $value) = each %counter)
{
        print "$key\t$value\n";
}

```

Functions for processing string

- `my $s = “ATCGggta”;`
- `print uc($s)`
  `>> ATCGGGTA`
- `print lc($s)`
  `>> atcgggta`
- `print length($s);`
  `>> 8`

- `print ucfirst(“hello”);`
  `>> Hello`
- `print lcfirst(“HELLO”);`
  `>> hELLO`

- `my $a = “abcdefgfijklmnop”;`
- `my $b = substr($a, 3, 4);`
- `my $c = index($a, $b);`
  `>> 3`

- `my $url = “www.ym.edu.tw”;`
- `my @url = split(“\.”, $url);`
  `>> (‘www’,‘ym’,‘edu’,‘tw’)`
- `my $line = join(“\_”, @url);`
  `>> www_ym_edu_tw`

① substr(STR, OFFSET, LENGTH);
② Index(STR, SUBSTR, [POSITION]);

Example 2: counting common words

Input:
Two gene lists:
"TP53 NRG1 ATP5B ATF2 BIRC6 LARP7 EIF4H2 SFRS2"
"FBXL18 TLE3 DICS1 LARP7 ATAD2 NRG1 ATP2A TP53 PANK2"

Output:

Common genes include: TP53, LARP7, NRG1

Script for Example 2

```
use strict;

my $list1 = "TP53 NRG1 ATP5B ATF2 BIRC6 LARP7 EIF4H2 SFRS2";
my $list2 = "FBXL18 TLE3 DICS1 LARP7 ATAD2 NRG1 ATP2A TP53 PANK2";

my @list1 = split(" ", $list1);
my @list2 = split(" ", $list2);

my %list1;
my %commons;

foreach my $gene (@list1)
{
        $list1{$gene} = 0;
}

foreach my $gene (@list2)
{
        if (exists $list1{$gene}) ## used to check whether an key in hash exists.
        {
                $commons{$gene} = 0;
        }
}

print "Common genes include: ".join("\, ", keys(%commons))."\n";

```

Subroutine

Ex. 1

```
sub max
{
    my ($a, $b) = @_;
    if ($a > $b)
    {
        return($a);
    }
    else
    {
        return($b);
    }
}
```

```
my ($a, $b) = (10, 20);
my $max = max($a, $b);
```

Ex. 2

```
sub max
{
    my $a = shift; #等於shift @_
    my $b = shift;
    if ($a > $b)
    {
        return($a);
    }
    else
    {
        return($b);
    }
}
```

@_ is the default variable to contain the parameters passed to that subroutine.

Reference in Perl

A reference is a scalar value that points to a memory location that holds some type of data.

Array

- `my @a = (1, 2, 3);`
- `my $a = [1, 2, 3];`
  `# array ref`
- `$a[0] >> 1`
- `$a->[0] >> 1`
- `my @b = @$a 或 @{$a};`
- `my $b = \@a;`

Hash

- `my %a = ('a' => 1,`
  `'b' => 2);`
- `my $a = {'a' => 1,`
  `'b' => 2}; # ref`
- `$a{'a'} >> 1`
- `$a->{'a'} >> 1`
- `my %b = %$a 或 %{$a};`
- `my $b = \%a;`

① Use \ to reference assignment

Rewrite script for Example 2

```
1  use strict;
2
3  my $list1 = "TP53 NRG1 ATP5B ATF2 BIRC6 LARP7 EIF4H2 SFRS2";
4  my $list2 = "FBXL18 TLE3 DICS1 LARP7 ATAD2 NRG1 ATP2A TP53 PANK2";
5
6  my @list1 = split(" ", $list1);
7  my @list2 = split(" ", $list2);
8
9  my $list1 = {};
10 my $commons = {};
11
12 foreach my $gene (@list1)
13 {
14         $list1->{$gene} = 0;
15 }
16
17 foreach my $gene (@list2)
18 {
19         if (exists $list1->{$gene}) ## used to check whether an key in hash exists.
20         {
21                 $commons->{$gene} = 0;
22         }
23 }
24
25 print "Common genes include: ".join("\, ", keys(%{$commons}))."\n";
26
```

High dimensional array and has

Array in Array

- `my $a = [];`
- `$a->[0] = [“baseball”, “basketball”];`
- `$a->[1] = [“volleyball”, “football”];`
- `$a->[2] = [“soccer”, “swimming”];`

- `print $a->[1]->[1], “\n”;`

Hash in Hash

-
```
my $h = {
  ‘sales’ =>
  {
    ‘Brown’ => ‘Manager’,
    ‘Smith’ => ‘Salesman’,
    ‘Albert’ => ‘Salesman’,
  } ,
  ‘marketing’ =>
  {
    ‘Penfold’ => ‘Designer’,
    ‘Jurgenes’ => ‘Manager’
  }
}:
```

- `print $h->{‘sales’}->{‘Albert’}, “\n”;`

Example 3: query data

Input:

Search A gene's other information from a text file.

"database.txt" is a tab-delimited file.

```
1  Symbol   GeneID   MIM Location     Full name
2  TP53     7157     191170  17p13.1 tumor protein p53
3  MDM2     4193     164785  12q14.3-q15 MDM2 oncogene, E3 ubiquitin protein ligase
4  AKT1     207 164730  14q32.32     v-akt murine thymoma viral oncogene homolog 1
5  CDKN2A   1029     600160  9p21     cyclin-dependent kinase inhibitor 2A
6  PML 5371     102578  15q22   promyelocytic leukemia
7  RB1 5925     614041  13q14.2 retinoblastoma 1
8  RPL11    6135     604175  1p36.1-p35  ribosomal protein L11
```

Output:

Get the "Location" of "AKT1" >> 14q32.32

Script for Example 3

```perl
use strict;

my $db_file = "database.txt";

my $db = {};

open IN, $db_file;
my @data = <IN>;
chomp @data;
my $head = shift @data;
my @head = split("\t", $head);

### Database construction
foreach my $line (@data)
{
        my @list = split("\t", $line);
        for my $i (1 .. $#head)
        {
                $db->{$list[0]}->{$head[$i]} = $list[$i];
        }
}

### Query
my $query = "AKT1";
my $col = "Location";

print $db->{$query}->{$col}, "\n";
```