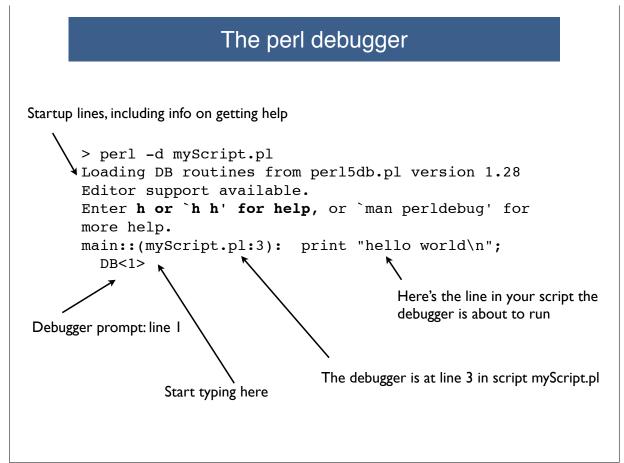
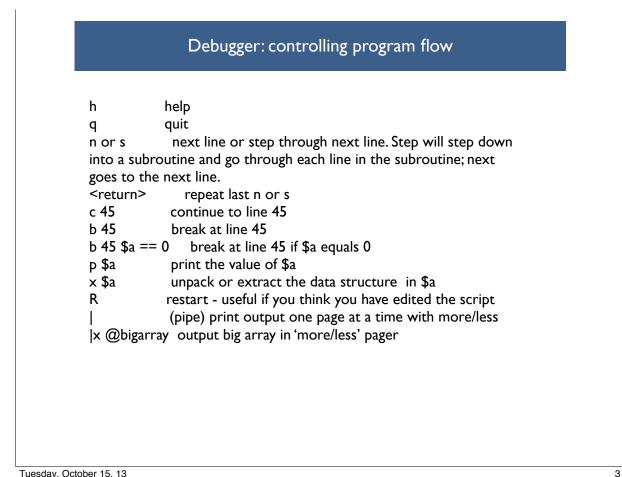
The Perl Debugger

- Perl has a built-in debugger.
- It runs perl scripts interactively, one command at a time.
- It will only run if your script is free of syntax errors.
- The debugger can help you find run-time errors.
- Also can run perl as an interactive shell
- These tools are excellent for exploring code snippets, regular expressions, finding bugs in code logic (=debugging)

Execute perl script normally with perl myScript.pl or ./myScript.pl etc Perl will try to run the script start to end. Easiest way to run a script in the debugger is with perl -d myScript.pl You can add any command line parameters to the script as normal perl -d myScript.pl infile.txt outfile.txt

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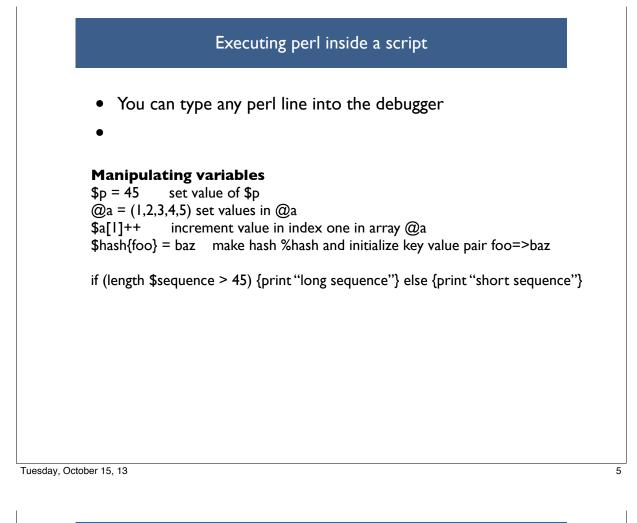


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- x expr evaluates expr in list context, returns formatted result.
- List context means elements are listed starting at index 0
- numbers are as is; strings are quoted and include new lines, tab characters etc.

```
DB<5> $a = 4
 DB<6> x $a
0 4
 DB<10> @a = (5,10,15)
 DB<11> x @a
0
   5
  10
1
2
   15
  DB<16> a = foo\nboo
  DB<17> x $a
0 'foo
               note string goes across new line
boo'
```

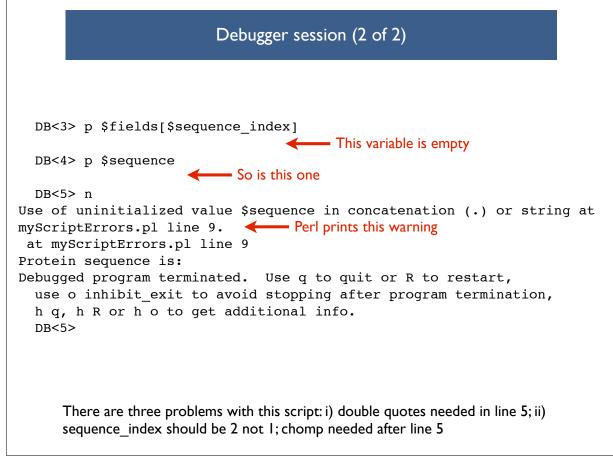


```
Script myScriptErrors.pl with logic errors and mistakes.
#!/usr/bin/perl
use warnings;
use strict;
my $data_line = 'ABC1\thuman\tMGTYIPLWQST\n';
my $sequence_index = 1;
my @fields = split /\t/, $data_line;
my $sequence = $fields[$sequence_index];
print "Protein sequence is: $sequence\n";
[Epinephrine:~] simonp% perl myScriptErrors.pl
Use of uninitialized value $sequence in concatenation
(.) or string at myScriptErrors.pl line 9.
Protein sequence is:
```

Debugger session to investigate run-time errors (1 of 2)

```
[Epinephrine:~] simonp% perl -d myScriptErrors.pl
Loading DB routines from per15db.pl version 1.33
Editor support available.
Enter h or `h h' for help, or `man perldebug' for more help.
main::(myScriptErrors.pl:5): my $data_line = 'ABC1\thuman
\tMGTYIPLWQST\n';
 DB<1> n
main::(myScriptErrors.pl:6): my $sequence_index = 1;
 DB<1> p $data line
DB<2>
main::(myScriptErrors.pl:7): my @fields = split /\t/, $data line;
 DB<2>
main::(myScriptErrors.pl:8): my $sequence = $fields[$sequence_index];
 DB<2> x @fields
0 'ABC1\\thuman\\tMGTYIPLWQST\\n' Constant Problem!! Only one array element
 DB<3> n
main::(myScriptErrors.pl:9): print "Protein sequence is: $sequence
\n";
```

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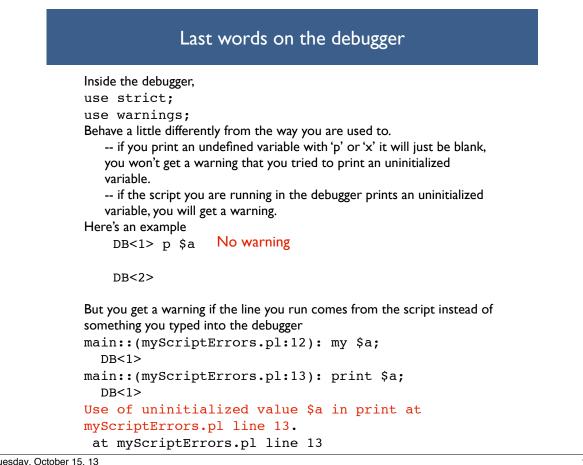


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The interactive perl debugger

```
> perl -de 4
Loading DB routines from per15db.pl version 1.28
Editor support available.
Enter h or `h h' for help, or `man perldebug' for more help.
main::(-e:1): 4
  DB<1> $a = {foo => [1,2], boo => [2,3], moo => [6,7]}
  DB<2> x $a
0
 HASH(0x8cd314)
   'boo' => ARRAY(0x8c3298)
      0
        2
      1
        3
   'foo' => ARRAY(0x8d10d4)
      0
        1
      1
         2
   'moo' => ARRAY(0x815a88)
      0
        6
      1
         7
```

```
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```



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