

分子生物计算

(*Perl* 语言编程)

天津医科大学
生物医学工程与技术学院

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第 10..13 章 GenBank、PDB、BLAST、其他

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教学提纲

- 1 模式匹配
- 2 输入记录分隔符
- 3 读取文件
- 4 文件夹处理
- 5 格式化输出

- 6 与外部程序进行交互
- 7 浮点数比较
- 8 引用
- 9 模块
- 10 BioPerl

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```
1 my $name = "manfred";
2
3 if ($name =~ /fred/) {
4     print "You could be fred\n";
5 }
6 #You could be fred
7
8 if ($name =~ /\bfred\b/) {
9     print "You ARE fred\n";
10 }
```



```
1 if ( $line =~ /^\/\\\/\n/ ) {  
2     last;  
3 }  
4  
5 if ( $line =~ m!//\n! ) {  
6     last;  
7 }
```



模式匹配 | 修饰符 | /m

```
1 #!/usr/bin/perl
2
3 use warnings;
4
5 "AAC\nGTT" =~ /^.*$/;
6 print "Without /m:\n", $&, "\n";
7 #Without /m:
8 #Use of uninitialized value $& in print at
   XXX.pl line N.
9
10 "AAC\nGTT" =~ /^.*$/m; # 开启多行模式
11 print "With /m:\n", $&, "\n";
12 #With /m:
13 #AAC
```



模式匹配 | 修饰符 | /s

```
1 #!/usr/bin/perl
2
3 use warnings;
4
5 "AAC\nGTT" =~ /^.*$/;
6 print "Without /s:\n", $&, "\n";
7 #Without /s:
8 #Use of uninitialized value $& in print at
   XXX.pl line N.
9
10 "AAC\nGTT" =~ /^.*$/s; # .能够匹配\n了!
11 print "With /s:\n", $&, "\n";
12 #With /s:
13 #AAC
14 #GTT
```



模式匹配 | 捕获

```
1 #!/usr/bin/perl
2
3 use strict; use warnings;
4
5 my $alphabet = join "", 'a' .. 'z';
6 $alphabet =~ /k(lmnop)q/;
7 print $1, "\n\n";
8 #lmnop
9
10 $alphabet =~ /((a)b)c/;
11 print "First pattern = ", $1, "\n";
12 print "Second pattern = ", $2, "\n";
13 print "Third pattern = ", $3, "\n";
14 #First pattern = abc
15 #Second pattern = ab
16 #Third pattern = a
```



模式匹配 | 捕获

```
1 my $string = "File code=123 name=test.txt";
2 if ($string =~ /code=(\d+)\s+name=( [\w\.] +) /) {
3     print "Code is $1\nName is '$2'\n";
4 }
```

```
1 my %q_count;
2 while (<>) {
3     while (/ \b (Q \w +) \b /g) {
4         ++$q_count{$1};
5     }
6 }
7 foreach my $word (sort {$q_count{$b} <=> $q_count{$a}
8     } keys %q_count) {
9     print "The word $word appeared ", $q_count{
10         $word}, " times\n";
11 }
```



When not to use Regular Expressions

- Splitting delimited data: `split`
- Swapping single characters: `tr`
- Extracting fixed position data: `substr`
- Finding the position of an exact string: `index`



模式匹配 | index

```
1 my $string = "xxxxxxhixxxxxxxxxxhixxxxxxxxhi";
2 my $lastpos = 0;
3
4 while (1){
5     my $pos = index($string,"hi",$lastpos);
6     last if ($pos == -1); # Substring not
    found
7     print "Found hi at index $pos\n";
8     $lastpos = ++$pos;
9 }
10
11 # Found hi at index 6
12 # Found hi at index 17
13 # Found hi at index 27
```



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输入记录分隔符

```
1 my $save_input_separator = $/;  
2  
3 $/ = "//\n";  
4 $record = <GBFILE>;  
5  
6 $/ = $save_input_separator;
```



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读取文件 | tell & seek

```
1 for (;;) {  
2     for ($curpos = tell(FILE); $_ = <FILE>;  
3         $curpos = tell(FILE)) {  
4         # search for some stuff and put it  
5         into files  
6     }  
7     sleep($for_a_while);  
8     seek(FILE, $curpos, 0);  
9 }
```



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文件夹处理 | 递归

```
1 #!/usr/bin/perl
2 use strict; use warnings;
3 list_recursively('pdb');
4
5 sub list_recursively {
6     my ($directory) = @_ ;
7     my @files = ();
8     unless ( opendir( DIRECTORY, $directory ) ) {
9         print "Cannot open directory $directory!\n";
10        exit;
11    }
12    @files = grep ( !/^\.\.?$/ , readdir(DIRECTORY) );
13    closedir(DIRECTORY);
14    foreach my $file (@files) {
15        if ( -f "$directory/$file" ) {
16            print "$directory/$file\n";
17        }
18        elsif ( -d "$directory/$file" ) {
19            list_recursively("$directory/$file");
20        }
21    }
22 }
```



```
1 #!/usr/bin/perl
2
3 use strict;
4 use warnings;
5 use File::Find;
6 #perldoc File::Find
7
8 find( \&my_sub, ('pdb') );
9
10 sub my_sub {
11     -f and ( print $File::Find::name, "\n" );
12 }
```



文件夹处理 | 通配

```
1 # <*>
2 my @files = <*.doc>;
3 print "I have ", scalar @files, " doc files in
   my work directory\n";
4
5 # glob
6 my @files2 = glob("*.rtf");
7 print "I have ", scalar @files2, " rtf files in
   my work directory\n";
8
9 chdir ("/home") or die "Can't move to work
   directory: $!";
10 while (my $file = <*.doc>) {
11     print "Found file $file\n";
12 }
```



文件夹处理 | 定位

```
1 #!/usr/bin/perl
2 use warnings; use strict;
3
4 # If you want to open a file in a location
  relative to the location of your script
  then you can use the FindBin module to get
  the filesystem location of your Perl
  program.
5 use FindBin qw($Bin);
6
7 # This code will add the ExtraModules
  directory to the module search path.
8 use lib "$Bin/ExtraModules";
9
10 print "Script is located in $Bin\n";
```



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格式化输出 | printf

```
1 while(<>) {
2     /^ATOM/ or next;
3
4     my($n, $x, $y, $z, $element)
5         = ($_ =~ /^.{6}(.{5}).{19}(.{8})(.{8})
6             (.{8}).{22}(..)/);
7
8     $n      =~ s/^\\s*//;
9     $element =~ s/^\\s*//;
10
11     if (($n == 1) or ($n == 1078)) {
12         printf "%8.3f%8.3f%8.3f %2s\\n", $x, $y,
13             $z, $element;
14     }
15 }
```



格式化输出 | printf

```
1 my $first  = '3.14159265';
2 my $second = 76;
3 my $third  = "Hello world!";
4
5 printf STDOUT "A float: %6.4f An integer: %-5
   d and a string: %s\n", $first, $second,
   $third;
6 #A float:  3.1416 An integer: 76      and a
   string: Hello world!
```



格式化输出 | here 文档

```
1 #!/usr/bin/perl
2 use strict; use warnings;
3 my $DNA = 'AAACCCCCCGGGGGGGGTTTTTT';
4 for ( my $i = 0 ; $i < 2 ; ++$i ) {
5     print <<HEREDOC;
6         On iteration $i of the loop!
7         $DNA
8
9 HEREDOC
10 }
11 #     On iteration 0 of the loop!
12 #     AAACCCCCCGGGGGGGGTTTTTT
13 #
14 #     On iteration 1 of the loop!
15 #     AAACCCCCCGGGGGGGGTTTTTT
16 #
```



格式化输出 | format & write

```
1 #!/usr/bin/perl
2 use strict; use warnings;
3 my $id          = 'A0000';
4 my $description = 'Highly weird DNA.  This DNA is so
   unlikely!';
5 my $DNA = '
   AAAAAACCCCCCCCCCCCCCGGGGGGGGGGGGGGGGGGGGGGGGGGGTTT
   TTTT';
6 # Define the format
7 format STDOUT =
8 # The header line
9 >@<<<<<<<< @<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<...
10 $id,          $description
11 # The DNA lines
12 ^<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<<~
13 $DNA
14 .
15 # Print the fasta-formatted DNA output
16 write;
```



```
1 >A0000      Highly weird DNA.  This DNA is so un...  
2 AAAAAACCCCCCCCCCCCCCGGGGGGGGGGGGGGGGGGGGGGGGGTTTTTTTT  
3 TTTTTTTTTTTTTT
```



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用途

Using the functions described in this next slide it is straightforward to either pass data through an external program as part of your Perl script, use Perl as a glue language to automate the execution of other programs, or simply use Perl as a convenient way to launch another program.

三种方法

There are three different functions you can use within Perl to launch an external program. These are `system`, backticks (`` ``) and `exec` and they all have slightly different purposes.



用途

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三种方法

There are three different functions you can use within Perl to launch an external program. These are `system`, backticks (`` ``) and `exec` and they all have slightly different purposes.



system

System is used where you want to launch an external program and check that it worked, but you don't need to collect any data back from it.

backticks

If you want to get hold of the output of programs then you need to use backticks rather than system.

exec

Exec is a somewhat unusual function in perl as it causes execution of your perl program to end immediately, and your running perl program is replaced by whatever program you specify.



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外部程序 | 运行 | 举例

```
1 my $filename = $ARGV[0];
2 my $stride = '/usr/local/bin/stride';
3 my $options = '';
4 # 捕获输出
5 my @results = `$stride $options $filename`;
6 my $now = `date`;
7 my @functions = qw( int rand length );
8 my %about;
9 foreach (@functions) {
10     # $about{$_} = `perl doc -t -f $_`;
11     $about{$_} = qx(perl doc -t -f $_);
12 }
13
14 # 不捕获输出, 返回值为程序退出状态
15 system "$stride $options $filename";
16 system 'date';
17 system 'tar', 'cvf', $starfile, @dirs;
```



Piping data out of an external program

```
1 open (my $log, "tail -f /var/log/httpd/  
  access_log |") or die "Can't open pipe to  
  web logs: $!";  
2  
3 while (<$log>) {  
4     if (/Safari/) {  
5         print "Oooh, a Mac user...\n";  
6     }  
7 }
```



Piping data into an external program

```
1 open (my $zip, "| zip compress.zip -") or die  
    "Can't open pipe to zip: $!";  
2  
3 print $zip "I want to be smaller...";  
4  
5 close $zip or die "Can't close pipe to zip :  
    $!";
```



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浮点数比较

```
1 #!/usr/bin/perl
2
3 if ( 10 / 3 == ( ( 1 / 3 ) * 10 ) ) {
4     print "Success!\n";
5 }
6 else { print "Failure!\n"; }
7 #Failure!
8
9 if ( abs( 10/3 - ( ( 1/3 ) * 10 ) ) < 1e-10 ) {
10     print "Right!\n";
11     print "E=", abs(10/3 - ( (1/3) * 10 ) ), "\n";
12 }
13 else { print "Wrong!\n"; }
14 #Right!
15 #E=4.44089209850063e-16
```



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```
1 my @array = (1, 2, 3, 4);
2 my $slow_arrayref = \@array;
3 my $quick_arrayref = [1, 2, 3, 4];
4
5 my %hash = (
6     dog => 'woof',
7     cat => 'meow',
8 );
9 my $slow_hashref = \%hash;
10 my $quick_hashref = {
11     dog => 'woof',
12     cat => 'meow',
13 };
```




```
1 my $arrayref = [10, 20, 30];
2 print "First element is ", $$arrayref[0], "\n";
3 print "First element is ", $arrayref->[0], "\n";
4
5 my $hashref = {
6     duck => 'quack',
7 };
8 print "The duck says ", $$hashref{duck}, "\n";
9 print "The duck says ", $hashref->{duck}, "\n";
```



```
1 my @original = (2, 4, 6, 8);
2 my @copy = @original;
3 for (0..$#copy){ $copy[$_] *= 10; }
4 print "Copy says ", $copy[1], " but original
   was ", $original[1];
5 # The copy is altered so the second element
   is 40, but the original still says 4.
6
7 my $original = [2, 4, 6, 8];
8 my $copy = $original;
9 for (0..(@$copy-1)){ $copy->[$_] *= 10; }
10 print "Copy says ", $copy->[1], " but original
    was ", $original->[1];
11 # Both the original and copy references point
    to an array whose second element is 40.
```



Country	Population	Language	Currency
UK	60,441,457	English	Pounds
France	60,656,178	French	Euros
Ireland	4,015,676	English/Irish	Euros



```
1 my %countries;
2 my %uk_info = (
3     population => 60441457,
4     language => 'English',
5     currency => 'Pounds',
6 );
7 my %france_info = (
8     population => 60656178, language => 'French',
9     currency => 'Euros',
10 );
11
12 $countries{uk} = \%uk_info;
13 $countries{france} = \%france_info;
14 #$countries{ireland} = \%ireland_info;
15
16 print "Population of France is ",
17     $countries{france}->{population}, "\n";
```



```
1 my %countries = (  
2     uk => {  
3         population => 60441457,  
4         language => 'English',  
5         currency => 'Pounds',  
6     },  
7     france => {  
8         population => 60656178,  
9         language => 'French',  
10        currency => 'Euros',  
11    },  
12    ireland => {  
13        ...  
14    },  
15 );  
16  
17 print "Population of France is ",  
18     $countries{france}->{population}, "\n";
```



```
1 my %countries;
2
3 $countries{uk}      -> {population} = 60441457;
4 $countries{france} -> {population} = 60656178;
5 $countries{france} -> {currency}   = 'Euros';
6
7 print "Population of France is ",
8       $countries{france}->{population}, "\n";
```



Data: country.txt

```
1 |-----+-----+-----+-----|
2 | Country | Population | Language      | Currency |
3 |-----+-----+-----+-----|
4 | UK      | 60,441,457 | English       | Pounds   |
5 | France  | 60,656,178 | French        | Euros    |
6 | Ireland | 4,015,676  | English/Irish | Euros    |
7 |-----+-----+-----+-----|
```

Task

Q: Population of France

A: 60,656,178



Data: country.txt

1	-----+-----+-----+-----
2	Country Population Language Currency
3	-----+-----+-----+-----
4	UK 60,441,457 English Pounds
5	France 60,656,178 French Euros
6	Ireland 4,015,676 English/Irish Euros
7	-----+-----+-----+-----

Task

Q: Population of France

A: 60,656,178



shell

```
1 grep -i -w France country.txt | cut -f2
```

csvkit

```
1 # Method 1
2 csvsql --query "select Population from
  country where Country=='France'" country.
  txt | csvlook
3 # Method 2
4 csvgrep -t -c Country -m France country.txt |
  csvcut -c Population | csvlook
```

shell

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1 grep -i -w France country.txt | cut -f2
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```
1 # Method 1
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3 # Method 2
4 csvgrep -t -c Country -m France country.txt |
  csvcut -c Population | csvlook
```

Perl-hash

```
1 #!/usr/bin/perl
2 use strict; use warnings;
3 my $fi = "country.txt";
4 my ( @header, @fields, %countries);
5 open my $IN, '<', $fi or die "$0 : failed to open input file '
    $fi' : $!\n";
6 while (<$IN>) {
7     chomp;
8     if ( $. == 1 ) {
9         @header = map { lc } split /\t/;
10    }
11    else {
12        @fields = map { lc } split /\t/;
13        for ( my $i = 1 ; $i < @header ; $i++ ) {
14            $countries{$fields[0]}->{$header[$i]}=$fields[$i];
15        }
16    }
17 }
18 close $IN or warn "$0: failed to close input file '$fi': $!\n";
19 print "Population of France is ", $countries{france}->{
    population}, "\n";
```

Perl-Data::Table

```
1 #!/usr/bin/perl
2
3 use strict;
4 use warnings;
5 use Data::Table;
6
7 my $countries = Data::Table::fromFile("country.txt
  ");
8
9 print "Population of France is ",
10   $countries->
11   match_pattern_hash('$_{Country} eq "France"')->
12   col('Population'),
13   "\n";
```

R

```
1 #!/usr/bin/Rscript
2
3 library(readr)
4 library(dplyr)
5
6 countries <- read_tsv("country.txt")
7 countries %>%
8   filter(Country=="France") %>%
9   select(Population) %>%
10  pull()
```



```
1 my @experiments = (  
2     {  
3         sample_id => 1,  
4         sample_name => 'kidney',  
5         sample_measures => [12,56,34,65,76],  
6     },  
7     {  
8         sample_id => 4,  
9         sample_name => 'liver',  
10        sample_measures => [24,66,12,17,26],  
11    },  
12    { ... },  
13 );  
14  
15 foreach my $expt (@experiments) {  
16     print "The first measure for sample ",  
17         $expt->{sample_id},  
18         " (", $expt->{sample_name}, ") was ",  
19         $expt->{sample_measures}->[0], "\n";  
20 }
```



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```
1 # METHOD 1: cpan
2 #Open cpan shell
3 sudo cpan #Or
4 perl -MCPAN -e shell
5 #Install modules
6 cpan>install Date::Calc
7
8 # METHOD 2: cpanm
9 #Install cpanm
10 #perlbrew is an admin-free perl installation
    management tool
11 perlbrew install-cpanm
12 #Install modules
13 cpanm Bio::Perl
14
15 # METHOD 3: manual
```




```
1 #!/usr/bin/perl
2
3 use warnings;
4 use strict;
5
6 use Date::Calc qw(:all);
7 #use Date::Calc qw(Days_in_Year Days_in_Month
8   );
9 print "In Feb 2020 there are ",Days_in_Month
   (2020,2)," days";
```



```
1 #!/usr/bin/perl
2
3 use warnings; use strict;
4
5 use LWP::UserAgent;
6
7 my $ua = LWP::UserAgent->new;
8 $ua->timeout(10);
9 $ua->env_proxy;
10
11 my $response=$ua->get('http://search.cpan.org/');
12
13 if ($response->is_success) {
14     print $response->decoded_content;
15 }
16 else {
17     die $response->status_line;
18 }
```



```
1 #!/usr/bin/perl
2
3 use warnings;
4 use strict;
5
6 package Example::Module;
7
8 # Module code goes here
9
10 1;
```



```
1 #!/usr/bin/perl
2 use warnings; use strict;
3
4 use Exporter;
5 our @ISA = qw(Exporter);
6 our @EXPORT_OK = qw(will_be_exported);
7
8 sub public {
9     # This is designed to be seen, but can only be addressed by
10    using its fully qualified name eg Example::Functional::public
11    ()
12 }
13
14 sub _private {
15     # This is only for internal use and shouldn't be used from
16     outside the module.
17 }
18
19 sub will_be_exported {
20     # This can be exported into the namespace of the calling
21     program
22 }
23
24 1;
```



```
1 #!/usr/bin/perl
2
3 use warnings;
4 use strict;
5
6 package Example::Object_oriented;
7
8 sub new {
9     # This creates the refernece which is going to be
10    our object
11    my $hashref = {};
12    # We then call bless to associate it with this
13    module.
14    bless $hashref;
15    # Finally we return it so the calling program can
16    start using it.
17    return $hashref;
18 }
```



```
16 sub save_value {
17     # This subroutine takes a single argument which it
    stores in the hash reference. The $object is provided
    automatically as the first argument to every object
    oriented subroutine (other than 'new').
18     my ($object, $new_value) = @_;
19     $object->{value} = $new_value;
20 }
21 sub get_value {
22     # This subroutine retrieves a value which was
    previously stored via the save_value subroutine. If
    there isn't a value to retrieve it returns the
    undefined value.
23     my ($object) = @_;
24     if (exists $object->{value}) {return $object->{value}
    };}
25     else { return undef; }
26 }
27
28 1;
```



```
1 #!/usr/bin/perl
2
3 use warnings;
4 use strict;
5
6 use Example::Object_oriented;
7
8 my $object = Example::Object_oriented->new();
9
10 $object->save_value("Hello");
11
12 print "The object says '". $object->get_value
    () . "'\n";
```



教学提纲

- 1 模式匹配
- 2 输入记录分隔符
- 3 读取文件
- 4 文件夹处理
- 5 格式化输出

- 6 与外部程序进行交互
- 7 浮点数比较
- 8 引用
- 9 模块
- 10 BioPerl




```
1 use Bio::SeqIO;
2
3 my $string = ">SEQ1\nacgt\n>revseq1\ntgca ";
4 my $format = "fasta";
5
6 my $stringfh = IO::String->new($string);
7 open($stringfh, "<", $string) or die "Could not open
   string for reading: $!";
8
9 my $seqio = Bio::SeqIO-> new(-fh      => $stringfh,
10                             -format => $format,
11                             );
12
13 while( my $seq = $seqio->next_seq ) {
14     print $seq->id . ' = ' . $seq->seq() . "\n";
15 }
```



```
1 use strict; use Bio::SeqIO;
2 my $input_file = shift;
3 my $seq_in = Bio::SeqIO->new( -format => 'embl',
4                               -file   => $input_file,
5                               );
6 my @seq_array;
7 while ( my $seq = $seq_in->next_seq() ) {
8     push(@seq_array,$seq);
9 }
10 @seq_array = sort { $a->length <=> $b->length }
    @seq_array;
11 my $total = 0;
12 my $count = 0;
13 for my $seq ( @seq_array ) {
14     $total += $seq->length;
15     $count++;
16 }
17 print "Mean length ", $total/$count, " Median ",
18       $seq_array[$count/2]->length, "\n";
```



```
1 use Bio::SeqIO;
2
3 my $usage = "x2y.pl infile informat outfile outformat ";
4 my $infile = shift or die $usage;
5 my $informat = shift or die $usage;
6 my $outfile = shift or die $usage;
7 my $outformat = shift or die $usage;
8
9 my $seq_in = Bio::SeqIO->new( -file    => "$infile",
10                               -format => $informat,
11                               );
12 my $seq_out = Bio::SeqIO->new( -file    => ">$outfile",
13                               -format => $outformat,
14                               );
15 while (my $inseq = $seq_in->next_seq) {
16     $seq_out->write_seq($inseq);
17 }
```



```
1 use Bio::SeqIO;
2 my $usage = "splitgb.pl infile "; my $infile = shift or die $usage;
3 my $inseq = Bio::SeqIO->new( -file => "<$infile", -format => 'Genbank',);
4 my %outfiles = ( human => {
5     Genbank => Bio::SeqIO->new(
6         -file => '>human.gb',
7         -format => 'Genbank',
8     ),
9     Fasta   => Bio::SeqIO->new(
10        -file => '>human.fa',
11        -format => 'Fasta',
12    ),
13 },
14 other => {
15     Genbank => Bio::SeqIO->new(
16         -file => '>other.gb',
17         -format => 'Genbank',),
18     Fasta   => Bio::SeqIO->new(
19         -file => '>other.fa',
20         -format => 'Fasta',),
21 },
22 );
23 while (my $seqin = $inseq->next_seq) {
24     if ($seqin->species->binomial =~ m/Homo sapiens/) {
25         $outfiles{'human'}->{'Genbank'}->write_seq($seqin);
26         $outfiles{'human'}->{'Fasta'}->write_seq($seqin);
27     } else {
28         $outfiles{'other'}->{'Genbank'}->write_seq($seqin);
29         $outfiles{'other'}->{'Fasta'}->write_seq($seqin);
30     }
31 }
```



```
1 use Bio::DB::GenBank;
2 use Bio::DB::Query::GenBank;
3
4 $query = "Arabidopsis[ORGN] AND topoisomerase[TITL] and
   0:3000[SLEN]";
5 $query_obj = Bio::DB::Query::GenBank->new(-db => '
   nucleotide',
6                                           -query =>
   $query );
7
8 $gb_obj = Bio::DB::GenBank->new;
9
10 $stream_obj = $gb_obj->get_Stream_by_query($query_obj);
11
12 while ($seq_obj = $stream_obj->next_seq) {
13     # do something with the sequence object
14     print $seq_obj->display_id, "\t", $seq_obj->length,
       "\n";
15 }
```



```
1 #!/usr/bin/perl
2 use strict; use warnings;
3 use Bio::DB::Query::GenBank; use Bio::DB::GenBank;
4 use Bio::SeqIO;
5
6 my $query_string = $ARGV[0];
7 my $fo_fa=$query_string.".fa"; my $fo_gb=$query_string.".gb";
8 my $query = Bio::DB::Query::GenBank->new(
9     -db => 'nucleotide', -query => $query_string
10 );
11 my $gb = Bio::DB::GenBank->new;
12 my $stream = $gb->get_Stream_by_query($query);
13
14 my %outfiles = (
15     Fasta => Bio::SeqIO->new( -file => ">$fo_fa", -format => '
16     Fasta',),
17     Genbank => Bio::SeqIO->new( -file => ">$fo_gb", -format => '
18     Genbank',),
19 );
20 while ( my $seq = $stream->next_seq ) {
21     $outfiles{'Fasta'}->write_seq($seq);
22     $outfiles{'Genbank'}->write_seq($seq);
23 }
```





TEX

LATEX

X_YTEX

Beamer

