

Perl's plain ole documentation (pod)

See the onCourse site for URLs with more help with Perl's pod.

```
#!/usr/bin/perl  
  
use strict;  
use warnings;
```

```
=pod
```

```
=head1 NAME
```

```
my_a1.pl
```

```
=head1 DESCRIPTION
```

```
=head2 SUMMARY
```

This Perl program splits a sequence of DNA into the upstream and genic regions. It then performs a number of string manipulations on both those sequences. A report (see Output below) is printed.

```
=head2 INPUT
```

No input. A string of DNA is manually set in a variable.

```
=head2 OUTPUT
```

To CONSOLE (screen):

A report of the first three codons and their bp locations, the upstream and genic regions and their lengths, the reverse complement of the genic portion, and the number of As and Ts in the upstream region.

```
=head1 AUTHORS
```

your name goes here

```
=head1 MODIFICATION HISTORY
```

```
=head3 August 4, 2009 (mdl) --
```

back from fishin', just getting started

```
=head3 August 11, 2009 (mdl) --
```

finished the starter kit

```
=head3 (add your modification dates and notes here)
```

```
=cut
```

```
# include a blank line after =cut  
# your Perl program continues below this point
```

- (1) include your "pod" labels and documentation into your perl file
- (2) Windows command-line: > **pod2pdf a1.pl > a1README.pdf**