Perl practice problems for BNFO 601

1. Write a Perl program to read in two aligned DNA sequences in FASTA format and print the number of matches and mismatches. For example if the input in the file dna.fasta is

   ```
   >human
   ACG--TA
   >mouse
   ACTCCTC
   ```

   then your program should output matches=3 and mismatches=2.

2. Write a Perl program to read in two aligned DNA sequences in FASTA format and print the affine alignment score with m=5, mm=-4, gap open=-20 and gap extension = -1. For the above example your program should output 5+5-4-20-1+5-4=-14

3. Write a program to translate a DNA sequence in a FASTA file into amino acids. Hint: if you use a hashtable your program will be shorter than otherwise.