

1. EXERCISE (5.1.pl)

Write a program that will ask the user for a first name and report the corresponding family name. Use the names of the following people: George Bush, Barak Obama, Bill Clinton, Jimmy Carter.

2. EXERCISE (5.2.pl)

Modify 5.1.pl so the program only prints the last name if that person actually exists in the hash. Otherwise print "Person not known".

3. EXERCISE (5.3.pl)

Fill an array with a couple of words and make sure that some words appear more than once. Then write a program that counts the number of occurrences of each word in the array and reports it back to the screen. HINT: Loop through the array using a foreach loop and save the occurrences in a hash. Make use of the fact that uninitialized variables are assumed to be 0 when doing maths.

4. EXERCISE (5.4.pl)

Read the sequence file (big.fas). Search for the first occurrence of the DNA motif "ACCTGT". Print the position of the motif to the screen.

5. EXERCISE (5.5.pl)

Try applying your last exercise script to the file big2.fas. It doesn't work yet, even though the sequences are the same. The reason is the format of the big2.fas file. The actual sequence data is organized in multiple lines of 50 nucleotides! Update your script to account for this. HINT: Try reading the file into an array and then concatenate the multiple lines into one big string.

6. EXERCISE (5.6.pl)

Read the big.fas file. Search for the first and the last occurrence of the motif "ACCTGT" and return the substring between the two motifs (excluding the motifs themselves). Print the substring to the screen and also report its length.

7. EXERCISE (5.7.pl)

Fill an array with the following strings: "fred", "barney", "wilma" and "betty". Sort the array alphabetically, but looking at the words backwards.