

Exercise 2: Calculating a weight matrix

- Open the “open_me_with_perl.txt” file and load the DNA sequences. Pass the filename as a command line argument!
- Check if the sequences contain valid nucleotides. If not, report it and exit.
- Create the Position Frequency Matrix. It should be similar to picture A.
- Print the Matrix and the “most frequent sequence” both in STDOUT and in a text file.

A

	1	2	3	4	5	6	7
A	1	4	1	2	0	17	13
C	28	5	5	0	3	3	2
G	0	0	4	0	25	1	7
T	2	22	21	29	4	10	9