Lecture 3 Homework
http://thegrantlab.org/
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Q1. [4pts] Consider the following multiple alignment of Transcription Factor Binding site DNA sequences

	1	2	3	4	5
Sequence 1	-	G	A	G	C
Sequence 2	C	T	A	G	A
Sequence 3	C	G	A	-	A
Sequence 4	A	G	C	G	A

Give the average profile (frequency matrix) of the above alignment by filling out the table below. The first position of the first column (i.e. position in the alignment) has been done for your, now complete the rest. You will use this table for answering questions 2 and 3 below.

	1	2	3	4	5
A	0.25		0.75		0.75
C	0.5		0.25		0.25
T		0.25			
G		0.75		0.75	
-	0.25			0.25	

Q2. [2pts] What is the highest scoring sequence match to your profile above (question 1) and what is its score?

Sequence:	CGAGA

Score:	3.5

Q3. [2pts] Using your completed profile table above (from question 1) score the following two sequences (**S1** and **S2**):

S1. CTGGC	1.75

S2. AGCTA	2

Q4. [2pts] Following the heuristic threshold for a positive match proposed in Harbison et al. [Nature (2004) 431:99-104.] namely using the threshold for a positive match = 60% x Max Score

Are either of the two sequences in question 3 potential transcription factor binding sites? If so, why?

0.6 * 3.5 = 2.1

Neither sequence is a match, because they fall below the threshold of 60% x max score. S2 is very close to the cutoff of 2.1, but still below it.