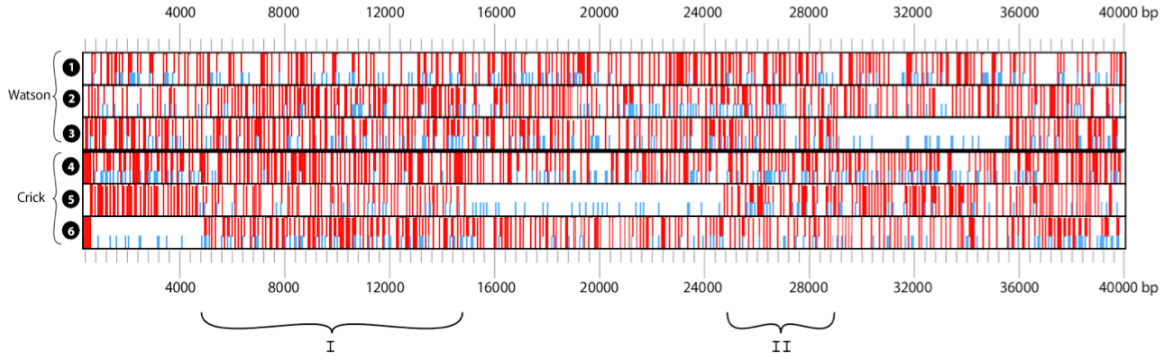
QS1 Practice -- Answers

1. A 6-frame translation map of a portion of the human genome is shown below. This portion contains ONLY TWO genes, "A" and "B".



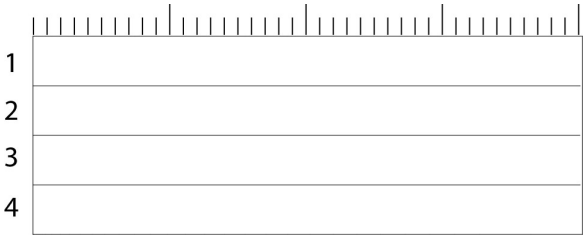
It is known that Gene A has an intron and that Gene B does not. Of the regions marked "I" and "II" below the map, which do you think corresponds to the intron?

Intron is region I

Why can the other region not be the intron? Outline your reasoning:

Both exons have to be on the same pre-mRNA. Look at the ORFs on either side of region II. The template strand for the ORF just left of region II is the Watson strand, while the template for the ORF to the right of region II is the Crick strand... so those two ORFs would be on separate transcripts, transcribed in opposite directions.

2. On an alien planet, as on earth, life is based on DNA chemically just like ours: with four types of bases, with 5' - 3' polarity, and transcribed and translated using similar mechanisms to ours. However, we do not know how many strands are present in alien DNA, nor do we know how many bases make up a codon. But, we do know that translation maps of the alien DNA show the following general pattern (i.e., four rows instead of the six you have seen in quiz section):



(a) Based on what you've been told so far, which of the following hypotheses are not consistent with the translation map? For JUST the one(s) that you state as being inconsistent, give a very brief explanation.

Hypothesis	Explanation for rejected hypothesis
Single-stranded DNA; 3 bases per codon	would only need 3 rows in the translation map (1 strand, 3 reading frames)
Double-stranded DNA; 3 bases per codon	would need 6 rows (2 strands, 3 reading frames per strand)
Single-stranded DNA, 2 bases per codon	would only need 2 rows (one strand, two reading frames)
Double-stranded DNA, 2 bases per codon	[consistent -- two strands, 2 reading frames per strand]
Single-stranded DNA, 4 bases per codon	[consistent -- 1 strand, 4 reading frames per strand]
Double-stranded DNA, 4 bases per codon	would need 8 rows (2 strands, 4 reading frames per strand)

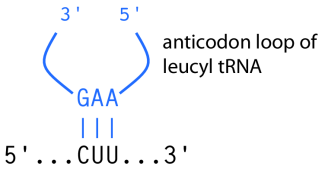
(b)

Later on, it is found that the aliens have 44 different kinds of amino acids in their proteins. Given this new information, which of the above hypotheses do you think is most likely correct, and why?

Need 44 codons (plus stop codons), for which a 2-base genetic code would not suffice (only 16 codons possible with a 2-base code). Four bases per codon, could easily encode 44 amino acids, so the best fit is single-stranded DNA with 4 bases per codon.

3. As you saw in quiz section, tRNAs are transcribed from genes in the genome much like with any other gene; but unlike with protein-coding genes, the transcript itself is the product in the case of tRNA genes. This question is about the potential consequences of mutations in tRNA genes.

(a) Drawn on the right is a leucine codon. Assume that this codon is part of an mRNA (in the correct reading frame) and draw the anticodon of the leucyl tRNA correctly base-paired to this codon.



(b)

Now consider a single base change (mutation) in a particular tRNA gene such that the tRNA made from this mutated gene can base-pair with the CUU codon drawn above. In a cell that is making this mutant tRNA, the following portion of an mRNA:

5'... AUU CCU CAU ACC GAC CUU UAC CGU UUG CAC ...3'

...is translated as:

... ile pro his thr asp phe tyr arg leu his ...

• In what way is this outcome not what you would normally expect? (Refer to the codon table on p.1-23 of lecture notes if necessary.)

CUU should be translated as leucine, but it is being translated as phenylalanine.

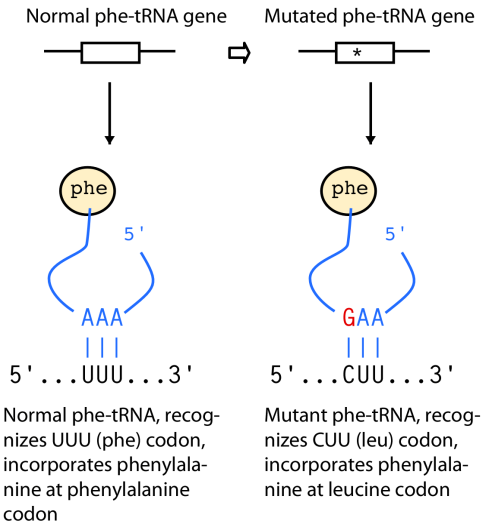
• Assuming that aminoacylation by tRNA synthetase is unchanged in this cell, explain how the mutation in the tRNA gene could give this outcome:

What was the tRNA gene? __phenylalanyl tRNA_____

Which specific codon does it normally recognize? ____UUU_____

What specifically has changed to allow the translation outcome shown above? (A base-pairing diagram would help!)

The base corresponding to the 3'-most position of the anticodon of the phe-tRNA gene has changed, such that the phe-tRNA's anticodon sequence now basepairs with a CUU codon. Thus, in place of leucine, a phenylalanine gets incorporated.



• In general terms, what do you think the repercussions of having this mutation could be for the cell?

First, the normal leucyl-tRNA is still there in the cell, so there will be competition for CUU codons between the normal leu-tRNA and the mutant phe-tRNA, so depending on their relative abundances in the cell and their efficiency at accessing the codon, there will be different amounts of misincorporation.

Second, if the original UUU-detecting tRNA gene has been mutated, will there be any tRNA to recognize UUU codons? How would that affect translation?