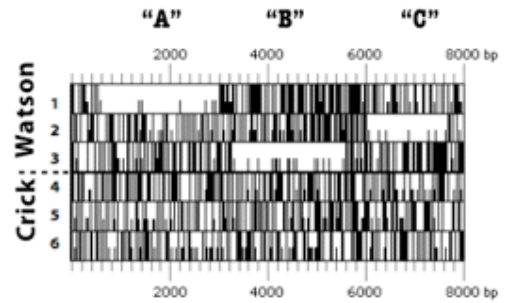


1. A 6-frame translation map of a segment of DNA is shown, with three open reading frames (A, B, and C). ORFs A and B are known to be in separate genes.

1a. Two transcription bubbles are shown, one in ORF A and one in ORF B. In the transcription bubble diagram, mark the following:

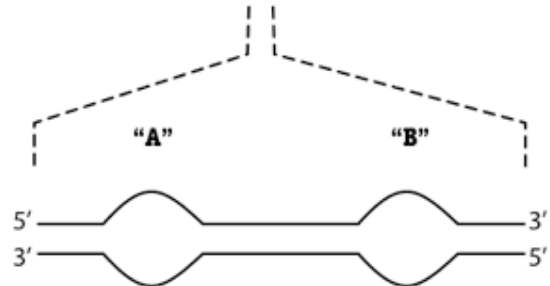
- the location of RNA polymerase on the appropriate strand in each bubble
- the RNA transcripts to show the relative lengths of RNA made by those two polymerases



1b. Are the promoters for ORFs A and/or B present in the DNA region shown in this diagram?

Promoter for A: Present? Yes **No** (circle one)  
If present, mark its location and label it.

Promoter for B: Present? **Yes** No (circle one)  
If present, mark its location and label it.



1c. Electron microscopy experiments failed to show RNA polymerases over the ORF "C" region of DNA. State whether each of the three explanations listed below is valid or not, explaining as necessary:

Explanation

If valid, just write "Valid." If invalid, BRIEFLY explain why.

ORFs B and C are exons of the same gene and a splicing error causes ORF C to be left out.

Splicing occurs after transcription.  
Incorrect splicing doesn't explain why transcription didn't happen.

ORF C has a mutation in its start (ATG) codon, preventing transcription.

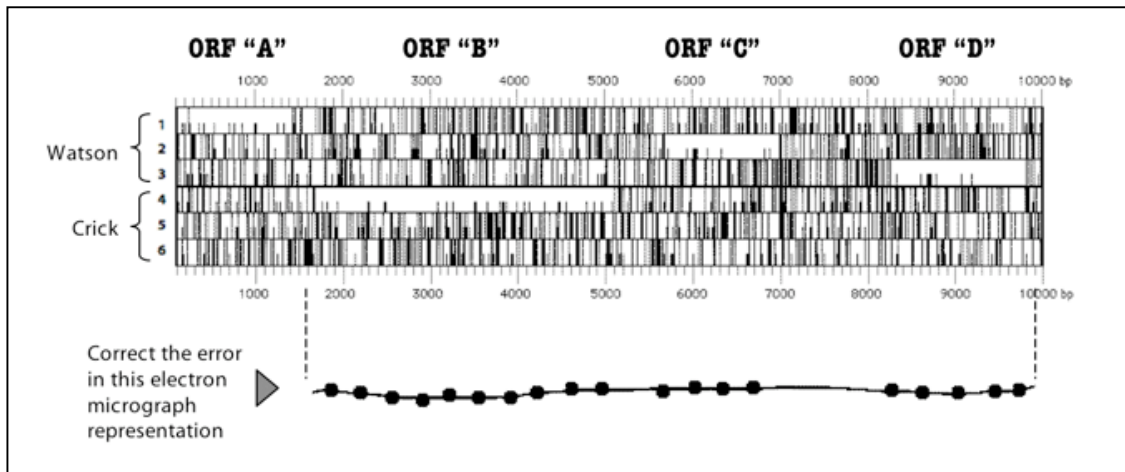
The start codon is used for translation, not transcription... whether or not the start

codon is intact, transcription could still happen.

ORF C has a promoter mutation preventing transcription.

VALID. (A promoter mutation is consistent with failure to transcribe the gene.)

2. A 6-frame translation map of a portion of a yeast genome is shown. The four potential open reading frames in this region (ORFs A, B, C, D) are indicated; ORFs C and D are known to be **exons of the same gene**.



2a. The diagram below the ORF map represents an electron micrograph of DNA from the region including ORFs B-D; black dots represent RNA polymerases. You will be asked to draw RNA transcripts next--but first, correct the error in the diagram and explain below why you think it is an error.

**Your explanation:**

The diagram doesn't show RNA polymerases over the intron -- but since the intron is going to be part of the transcript, there have to be RNA polymerases over the intronic region.

2b. Complete your corrected diagram to show RNA transcripts of relatively correct length on the RNA polymerases.

Transcription goes right-to-left through ORF B (because the Crick strand is the coding strand) so, the RNA transcripts will be smallest at the right (where transcription has just begun) and longest at the left (where it is about to end). For ORF C/D (Watson strand is coding) the situation reversed.

Note that the RNA lengths shown aren't quite accurate -- what we are looking for is relative proportions (which ones are short and which ones are longer).

2c. Several electron micrographs of ORF "A" DNA taken at the same time as that in part (a) did not show any RNA polymerases over ORF "A". Of the possible explanations (listed below) for this observation, cross out *all* the ones that you think are not reasonable, and BRIEFLY explain why [just for the unreasonable one(s)]:

Explanation

Why unreasonable (if unreasonable)

---

~~The promoter is not included in the region that is shown, so transcription could not occur~~

The promoter is still present on the DNA even if it is not included in this small window that is represented... so not having the promoter in the diagram is irrelevant for whether or not the gene is transcribed

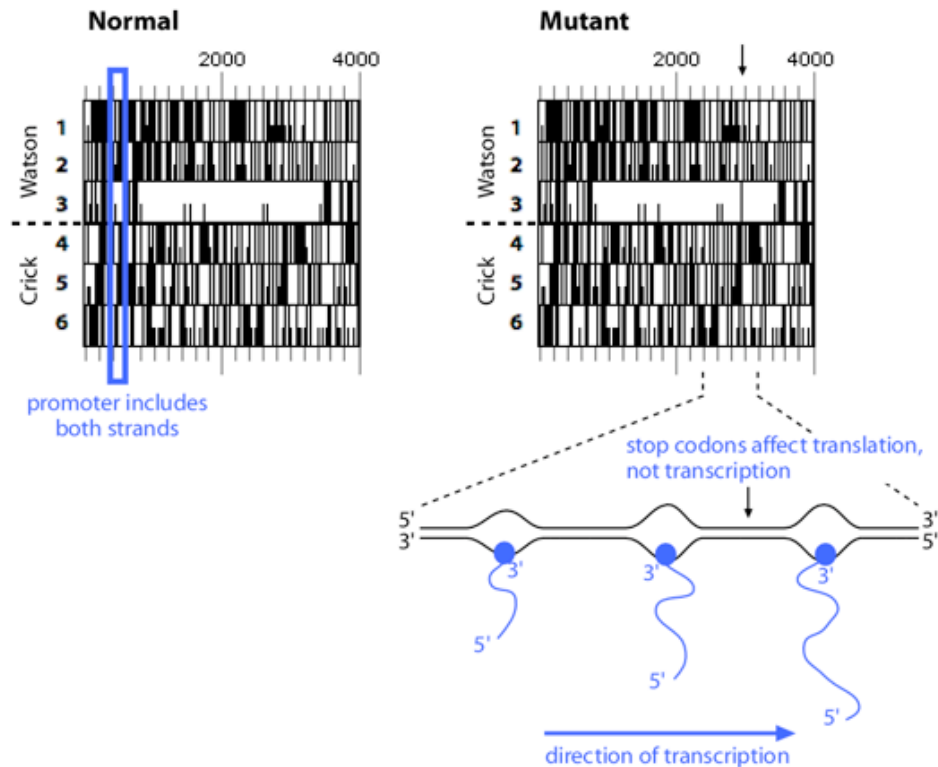
~~ORF "A" is actually a tRNA gene, so it will never have RNA polymerases on it~~

tRNA genes are transcribed also (that's how we get tRNAs), so that's not a reason why there aren't any polymerases over this region

ORF "A" is for a gene that was not being transcribed at the time that the electron microscopy was done.

[That's plausible... any given gene may be transcribed only some of the time, so it's quite possible that this gene was not being transcribed at the time the sample was collected.]

**3.** This question concerns a mutation in a gene that creates a premature stop codon. A 6-frame translation map was made of the region containing that gene from normal and from mutant cells as depicted below (arrow marks the location of premature stop codon; assume that the gene does not have an intron):



**(3a)** Three potential transcription bubbles are shown for the region containing the premature stop codon mutation (arrow marks the location of the mutation). In each bubble that you think could contain an active RNA polymerase, draw RNA polymerase and nascent transcripts on the appropriate strand and mark the 5' and 3' ends of the RNA.

**(3b)** Draw an arrow below the diagram to clearly indicate the direction of transcription.

**(3c)** Where is the promoter in relation to the open reading frame of this gene? On the "Normal" 6-frame translation map above, mark the approximate location of the promoter by drawing a box around the appropriate strand or strands.

**4.** Below is a 22 basepair sequence of DNA that is transcribed to make a 22 base mRNA:

```

5' AGGTAAAATGCATAAATAGCCA 3'
3' TCCATTTTACGTATTTATCGGT 5'
   |       |       |       |
   5       10      15      20

```

**(4a)** Write the mRNA sequence that could encode a peptide of 3 amino acids, and indicate with brackets the 3 codons for these amino acids.

AUG CAU AAA UAG

-----

**(4b)** A mutation occurs that adds a T at position 2 on the Watson strand between the A and G. What is the likely consequence on the translation of the peptide indicated in (a)?

Mutation creates new ATG in different reading frame and makes translation of peptide in (a) likely to be eliminated (or greatly reduced).

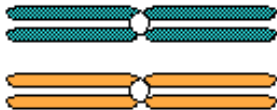
**(4c)** A different mutation to the original sequence changes base 2 on the Watson strand from G to T. Compared to the original sequence above, would the transcript from this mutant sequence likely have more or fewer associated ribosomes, and why?

Mutation creates the mRNA sequence AUGUAA which would initiate translation and immediately terminate it, releasing ribosomes, so likely to have fewer ribosomes associated.

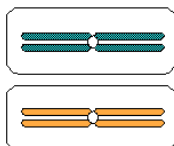
**(4d)** A different mutation to the original sequence changes base 10 on the Watson strand from a G to a C. What is the consequence for translation of the peptide indicated in (a)?

Mutation eliminates ATG and consequently translation of the peptide in (a).

**5.** Shown here is a pair of homologous chromosomes in a cell soon to undergo division: (only chromosomes are shown; crossovers, if present, are not shown).



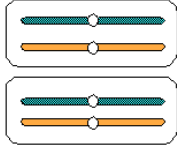
**5a.** After the ensuing anaphase and telophase, you find that the daughter cells have the following configuration (pretending for the sake of this question that you could actually detect chromosomes in telophase):



Was the division mitosis or meiosis? Explain.

The homologues have separated -- so it must be meiosis.

**5b.** Suppose, instead, that they had this configuration:



Again, was the division mitosis or meiosis? Explain.

Sister chromatids have separated, and there is one copy of each homologue -- so it must be a mitotic division.