Chapter 15 Assignments

1. In-Class Assignments

Background
The Central Dogma

Once the structure of DNA was understood, it took many years to learn *how* DNA codes for making a protein. In its most basic form, it is a two-step process.

Transcription ***Translation***
DNA ----------------------------> RNA ----------------------------> protein

(primary structure = amino acid chain)

Transcription is the process of using DNA as a template to make a piece of RNA. Transcription is a good name for this first step: a nucleotide-for-nucleotide RNA copy of DNA is made. In other words, the 'language' has not changed; the process simply copies from the language of nucleotides in DNA to the language of nucleotides in RNA.

Translation is the process of using a piece of RNA (specifically messenger RNA or mRNA) as a template to make an amino acid chain. This is a good term to use because the language has changed, from the language of nucleotides in RNA to the language of amino acids in a protein.

These two steps were first described in bacteria. As you might predict, things are a bit more complicated in eukaryotic cells. For example, RNA goes through a process called RNA processing before it is translated. But for now we will focus on the basics, omitting many details. You will use the puzzles to model the two processes of transcription and translation.
Transcription

RNA polymerase is the name of the enzyme that is responsible for the polymerization of a piece of RNA using DNA as a template. In this case, polymerization means the formation of a covalent bond between one RNA nucleotide and the next. This piece of RNA is complementary and anti-parallel to the DNA template. Because of the

3-dimensional nature of the molecules, RNA polymerase works only one way: it can read DNA 3' ---> 5' and make RNA 5' ---> 3'. So only one of the two strands is read and transcribed.

Here's an example.

DNA	Sense strand	………5' ATTGGCATCGGACT 3' ……...
	Antisense strand	………3' TAACCGTAGCCTGA 5'………
RNA		………5' AUUGGCAUCGGACU 3'………

The strand that is used as a template is called the antisense strand because the RNA that is produced is identical to the other, so-called sense strand. It's not exactly identical though. For one thing the 5-carbon sugar is ribose in RNA instead of deoxyribose in DNA. And there is no thymine base in DNA. In RNA there is uracil (U) instead. So the DNA to RNA pair-bonding rules C to G, G to C, T to A and A to U. Create the following transcripts.

1. DNA – GGTACGTCCGACCGGTTT

RNA –

2. DNA – TTACGTACGTACCTCGTCA

RNA –

3. DNA – ACGTCATCTAGCGTACCGT

RNA –

4. DNA – GTACCGCATTGCATCCTTA

RNA -

Translation

Translation is much more complicated than transcription. Recall that we're translating from the language of nucleotides in RNA to the language of amino acids in protein.

How to translate? By using the genetic code, which is a triplet code. A series of three nucleotides in RNA, called a codon, codes for one amino acid.

With 4 nucleotides, and using a triplet code, there are 4^3, or 64 unique triplet combinations. But there are only 20 amino acids. So there is more than one way to 'say' a particular amino acid; the genetic code is said to be redundant. You don't need to memorize the genetic code; just look it up.

Second letter

First letter	U	C	A	G	Third letter
U	UUU } Phe UUC UUA } Leu UUG	UCU } Ser UCC UCA UCG	UAU } Tyr UAC **UAA Stop** **UAG Stop**	UGU } Cys UGC **UGA Stop** UGG Trp	U C A G
C	CUU } Leu CUC CUA CUG	CCU } Pro CCC CCA CCG	CAU } His CAC CAA } Gln CAG	CGU } Arg CGC CGA CGG	U C A G
A	AUU } Ile AUC AUA **AUG Met**	ACU } Thr ACC ACA ACG	AAU } Asn AAC AAA } Lys AAG	AGU } Ser AGC AGA } Arg AGG	U C A G
G	GUU } Val GUC GUA GUG	GCU } Ala GCC GCA GCG	GAU } Asp GAC GAA } Glu GAG	GGU } Gly GGC GGA GGG	U C A G

A couple of important points to note. First, AUG, which codes for methionine, is the 'start signal.' Translation of a piece of mRNA does not start until the first AUG codon. But in our puzzle model, we're in the midst of a gene; imagine that the start codon has already been reached. Second, there are several ways to say 'stop.' When one of these codons is reached, translation ceases; the amino acid chain is complete. In our puzzle model, we won't encounter a stop signal.

Doing the actual translation is a big job and requires several other 'players.' In addition to mRNA, two other types of RNA are needed: ribosomal RNA (rRNA) and transfer RNA (tRNA). Both of these types of RNA are transcribed but never translated. They are used, 'as is' in other ways. rRNA combines with certain proteins to make ribosomal subunits. There are two subunits, the large and the small. These come together to create functional ribosomes. (In eukaryotes, ribosomal subunits are made in the nucleus and then exit to the cytoplasm before coming together.)

Original antisense DNA	***3' C T A C T A G G C T A G C T A C T A 5'***
mRNA	
Amino acid sequence	

Original antisense DNA	***3' T A G C C T C A T C G G T A C T T C 5'***
mRNA	
Amino acid sequence	

Original antisense DNA	***3' G A T C C T A G G A T C A T G C A T 5'***
mRNA	
Amino acid sequence	

Original antisense DNA	***3' T T T C A G C T A A A T C G A C T G 5'***
mRNA	
Amino acid sequence	

2. ***Transcription, Translation and Mutations***

Mutations are changes in DNA that occur during DNA replication. Are all mutations deleterious (harmful)? Because of the redundancy of the genetic code, a change from one nucleotide to another may not even cause a change in the amino acid sequence. On the other hand, it might lead to a change in the amino acid 'called for' by a given codon. This might be deleterious, or beneficial. Clearly some mutations must have been beneficial, to have led to all the biological diversity in the world. Mutation is the source of all new genetic variation; it is the raw material upon which natural selection acts.

There are several ways to categorize mutations. You'll look at two main types of mutations: point mutations, and reading frame shifts. A point mutation in one in which there is a base substitution. Reading frame shifts are caused by insertions or deletions.

Use your knowledge of base pairing and mRNA to transcribe the sequences below. After determining the mRNA sequence, use the codon table below to determine the amino acid sequence.

Second letter

First letter	U	C	A	G	Third letter
U	UUU Phe	UCU Ser	UAU Tyr	UGU Cys	U
	UUC Phe	UCC Ser	UAC Tyr	UGC Cys	C
	UUA Leu	UCA Ser	**UAA Stop**	**UGA Stop**	A
	UUG Leu	UCG Ser	**UAG Stop**	UGG Trp	G
C	CUU Leu	CCU Pro	CAU His	CGU Arg	U
	CUC Leu	CCC Pro	CAC His	CGC Arg	C
	CUA Leu	CCA Pro	CAA Gln	CGA Arg	A
	CUG Leu	CCG Pro	CAG Gln	CGG Arg	G
A	AUU Ile	ACU Thr	AAU Asn	AGU Ser	U
	AUC Ile	ACC Thr	AAC Asn	AGC Ser	C
	AUA Ile	ACA Thr	AAA Lys	AGA Arg	A
	AUG Met	ACG Thr	AAG Lys	AGG Arg	G
G	GUU Val	GCU Ala	GAU Asp	GGU Gly	U
	GUC Val	GCC Ala	GAC Asp	GGC Gly	C
	GUA Val	GCA Ala	GAA Glu	GGA Gly	A
	GUG Val	GCG Ala	GAG Glu	GGG Gly	G

Original antisense DNA	***3' TAC GGT TTA CTA TGC ……… 5'***
mRNA	
Amino acid sequence	

Point mutation ***3' T A C G G T T T A C T A <u>C</u> G C ……… 5'***	
mRNA	
Amino acid sequence	

What is the effect of this mutation?

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Point mutation ***3' T A C G G T T T A C T <u>G</u> T G C ……… 5'***	
mRNA	
Amino acid sequence	

What is the effect of this mutation?

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Insertion ***3' T A C G G T T T <u>C</u> A C T A T G C ……… 5'***	
mRNA	
Amino acid sequence	

What is the effect of this mutation?

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Deletions ***3' T A C G G T T T A T A T G C ……… 5'***	
mRNA	

Amino acid sequence

What is the effect of this mutation?

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Which type of mutation, point or reading frame, is likely to have the greatest impact? Why?

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