Bioinformatics : Written Assignment 1

Q 1. Similarities between transcription and DNA replication are as listed below:

* Both processes take place within the nucleoplasm (nucleus) of the cell.

* Both processes depend on the original DNA strand, which is used as a template for the corresponding processes.

* Both processes are polymerisation reactions, with formation of phosphodiester bonds, giving polynucleotide strands as products.

* DNA helicase is responsible for unraveling the parent DNA, at specific sites, in both cases.

* Both processes use DNA-dependent polymerase for catalysing the polymerisation. Replication uses DNA-dependent DNA polymerase, while transcription involves DNA-dependent RNA polymerase.

* The polymerisation reaction in both cases occurs in the 5' to 3' direction.

Q 3.

Transcription	Translation
① Occurs in the nucleoplasm (within nucleus)	Occurs in the cytoplasm (outside nucleus)
② Polydiester polymerisation, with formation of poly-nucleotide (RNA) as product	Polymerisation occurs by formation of peptide bonds, with polypeptide (protien) as product.
③ Uses DNA strand as template	Uses processed mRNA as template
④ Nucleotides are "read" one a time from the template.	Nucleotides are "read" 3 at a time, in the form of codons
⑤ The process is not degenerate. Thus given a product RNA, it is possible to uniquely identify template DNA strand.	The process is degenerate. Hence, it is impossible to uniquely identify template RNA strand, given the product amino acid chain

Q 3 (i) DNA strand: 5′ AUGGUGGCCUAUCAUUAGGGGCUU 3′

⇒ Amino acid sequence: Met - Val - Ala - Tyr - His

(ii) DNA strand (after substitution): 5′ AUGGUGGCCUAACAUUAGGGGCUU 3′

⇒ Amino acid sequence: Met - Val - Ala

(iii) DNA strand (after insertion): 5′ AUGCGUGGCCUAUCAUUAGGGGCUU 3′

⇒ Amino acid sequence: Met - Arg - Gly - Leu - Ser - Leu - Gly - Ala

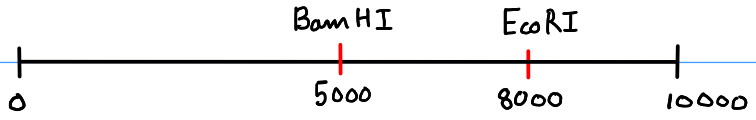
Q4. In theory, BamH1 is a good enzyme for SARS Cov-2 due to the following reasons:

* SARS Cov-2 has a very small number of nucleotide bases (around 30,000 bases). BamH1 is known to be very good at recognizing restriction sites within shorter sequences and cleaves well, post recognition of the target site.

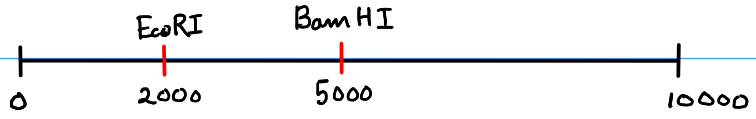
* Being a symmetric dimer, BamH1 is able to recognise and bind the DNA within the "cleft" between the two monomers, with large number of contacts. This is due to intensive water-aided H-bonding.

However, practically, BamH1 has only 1 recognition site in the Wuhan isolate genome, which is a major disadvantage as compared to other R.E. such as EcoR1. Thus, for practical purposes, BamH1 is not an ideal candidate for SARS Cov-2

Q5. There are 2 possible restriction maps for the given data. From the data, there is an ambiguity with respect to position of EcoR1. The 2 possible restriction maps are:



or



Q6. To insert the DNA strand in the vector, a linker molecule with restriction sites corresponding to either EcoRI or BamH1 must be ligated to both ends of the strand, with help of DNA ligase and the adapter molecule.

The restriction sites in the newly ligated molecule can be cut using the corresponding RE to obtain "sticky" ends (cohesive ends) required for insertion of the strand in the vector, to create the required recombinant DNA.

Q7. Advantages of PCR over cloning:

* PCR requires very small amounts of DNA sample for amplification
* PCR requires much less a priori information about the strand to be amplified.
* PCR process is much faster than cloning and create billions of copies in very little time. (in scale of hours).
* Much simpler process. Doesn't involve steps like isolation of vector, cutting with R.E., ligation of sample DNA within vector or transformation. The entire process is in-vitro
* The replicated DNA segment in cloning is within the cells of the culture and further within the vector. Thus extraction of DNA is much more complicated. On the other hand, output of PCR is the copies of the required DNA molecules making the process of extraction much simpler.

Advantages of Cloning over PCR:

* PCR process is very prone to errors, especially during the annealing stage. Contamination by foriegn genetic material is also more likely in PCR. On the other hand, cloning error is much lower.
* Cloning allows for further manipulation and propegation of the genetic material. This includes obtaining the protien product expressed by the strand.

Q8. Advantages of NGS over cDNA sequencing include:

* NGS is significantly quicker and inexpensive in comparison to other sequencing techniques.
* Requires very little amounts of genetic sample.
* Requires no a priori knowledge of the genetic material
* High throughput with single-nucleotide resolution, with high reproducibility
* Sequences both coding and non-coding RNA. cDNA sequencing, on the other hand, only sequences the coding RNA (mRNA).