Name:_____ Dr. Reichler's Bio 325-uex Summer 2008 Quiz 7/2

1) You are interested to see if two genes, pizzagood and tacosgood, that are transcribed in response to the same stimuli. What information from DNA might help you determine this?

2) Regarding question #1, in relation to the location of the gene, where would you expect to find this information?

3) We looked at data showing conservation and differences in alternative splicing. Give an example of each situation.

4) How can the data about conservation of alternative splicing isoforms in different individuals be useful in diagnosing disease?

5) What information can be coded for in the 3' UTR of an mRNA?

6) What mechanism might explain the presence of plentiful mRNA but little protein being present?

7) How could looking at the sequence of a gene tell you where the protein was located? How could where in the gene you found this information tell you about where the protein might be located?

8) What is the connection between fetuses who are exposed to poor nutrition and smoking?

9) What is different about the genes of a totipotent cell versus a pluripotent cell?

10) What evidence suggests that DNA packaging is different between animal and plant cells?

11) What is the function of many of the hox proteins?

12) If you were studying the SRY gene, coded on the Y chromosome. Could you tell when SRY begins to be expressed using a reporter gene? Would a reporter gene allow you to determine the stability of SRY protein?

13) Would you expect the chimpanzee or human version of the huntingtin gene to be larger?

14) Do B-cells have more or less DNA than other cells in your body? How is this related to the function of B-cells?

15) By looking at the DNA sequence, how would you identify a hox pseudogene?

16) What different information can be gleaned from comparing transposons between humans and chimps or different people? Why is this information partially dependent on knowing the time since the last common ancestor?

Answers:

1) You are interested to see if two genes, pizzagood and tacosgood, that are transcribed in response to the same stimuli. What information from DNA might help you determine this?
Look in the promoters and see if there are similar sequences that would bind to transcription factors thereby activating transcription.

2) Regarding question #1, in relation to the location of the gene, where would you expect to find this information?
Within a few thousand nucleotides of the transcription start site, or further away as enhancers.

3) We looked at data showing conservation and differences in alternative splicing. Give an example of each situation.
Alternative splicing is conserved in mice of different genetic backgrounds. It is different in male and female fruit flies and in different tissues, heart and kidney, of mice.

4) How can the data about conservation of alternative splicing isoforms in different individuals be useful in diagnosing disease?
Since there seems to be such similiarity in splicing for some genes in different individuals, abnormalities in splicing may indicate a disease state.

5) What information can be coded for in the 3' UTR of an mRNA?
Binding of miRNA and transport of mRNA

6) What mechanism might explain the presence of plentiful mRNA but little protein being present?
Binding of miRNA that blocks translation or the binding of a regulatory protein that blocks translation, as in the ferritin protein.

7) How could looking at the sequence of a gene tell you where the protein was located? How could where in the gene you found this information tell you about where the protein might be located?
Amino acids sequences can code for information about where a protein needs to be transported. Signal peptides are always at the beginning of the protein, while nuclear localization signals can be anywhere.

8) What is the connection between fetuses who are exposed to poor nutrition and smoking?
Both may lead to the adaptation to thriftiness as adults due to poor fetal nutrition.

9) What is different about the genes of a totipotent cell versus a pluripotent cell?
A pluripotent cell has already irreversibly packaged some of its DNA, none of the totipotent cell's DNA has been irreversibly packages yet.

10) What evidence suggests that DNA packaging is different between animal and plant cells?
Most mature plant cells are totipotent while few mature animal cells are.

11) What is the function of many of the hox proteins?

They are transcription factors.

12) If you were studying the SRY gene, coded on the Y chromosome. Could you tell when SRY begins to be expressed using a reporter gene? Would a reporter gene allow you to determine the stability of SRY protein?
Reporter genes can tell when or where transcription of a gene is activated, but since the reporter gene protein is different from the SRY gene, no information about the SRY protein can be determined.

13) Would you expect the chimpanzee or human version of the huntingtin gene to be larger?
If we use the puffer fish-human comparison combined with the general sense that humans have more transposons then chimpanzees, we could surmise that the human huntingtin gene should have more transposons.

14) Do B-cells have more or less DNA than other cells in your body? How is this related to the function of B-cells?
Less, the rearrangement and splicing out of certain DNA allows each B-cell to make a unique antibody protein.

15) By looking at the DNA sequence, how would you identify a hox pseudogene?
It will have some sequence similarity to active hox genes, but will lack some critical component, like a functional promoter, that keeps it from being expressed.

16) What different information can be gleaned from comparing transposons between humans and chimps or different people? Why is this information partially dependent on knowing the time since the last common ancestor?
Between chimps and people we see how active transposons have been in the last 6 million years. Between different people, we can see how active transposons have been since the people shared a common ancestor. The time of the last common ancestor will allow an estimation of transposon movement per given time.