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## Unit 6 - Week 4: Comparative Genomics

### Course outline

#### How to access the portal

#### Pre-requisite Assignment

#### Week 1: Introduction to Functional Genomics

#### Week 2: Genome Analysis (Part 1)

#### Week 3: Genome Analysis (Part 2)

#### Week 4: Comparative Genomics

- Lecture 15: Genomic Insight into Evolution (unit? unit=30&lesson=31)
- Lecture 16: Genome sequence: Different Questions,

## Assignment week 4

The due date for submitting this assignment has passed. **Due on 2019-09-25, 23:59 IST.**  
As per our records you have not submitted this assignment.

1) Which one of the following options is INCORRECT with regard to comparative genomics? **1 point**

- Use information from several genomes to learn more about the individual genes
- The sequences of a gene are compared against all other known genes of the same species
- The entire genome of a species can be compared with the entire genome of an another species
- Use of computational tools to predict the evolutionary rates of a family of genes

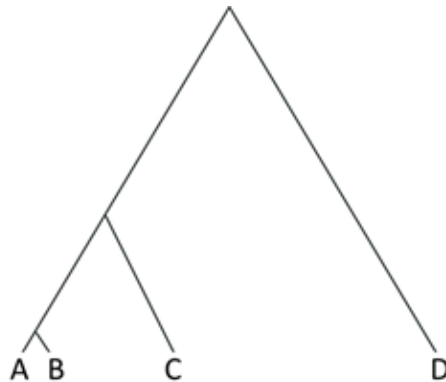
No, the answer is incorrect.

Score: 0

Accepted Answers:

*The sequences of a gene are compared against all other known genes of the same species*

2) Given below is a phylogenetic tree plotted based on the comparisons between genomes of 4 **1 point** different species, named A, B, C and D. If you were to identify genes contributing to some unique feature of species A, then your analyses would include the genome sequence of



Different Comparisons (unit? unit=30&lesson=32)

Lecture 17: Outcome of Comparative Genomics (unit? unit=30&lesson=33)

Lecture 18: Laboratory Session 1 (unit? unit=30&lesson=34)

Lecture 19: Laboratory Session 2 (unit? unit=30&lesson=35)

Quiz : Assignment week 4 (assessment? name=54)

Feedback For Week 4 (unit? unit=30&lesson=61)

Assignment Solution - Week 4 (unit? unit=30&lesson=62)

Text Transcripts

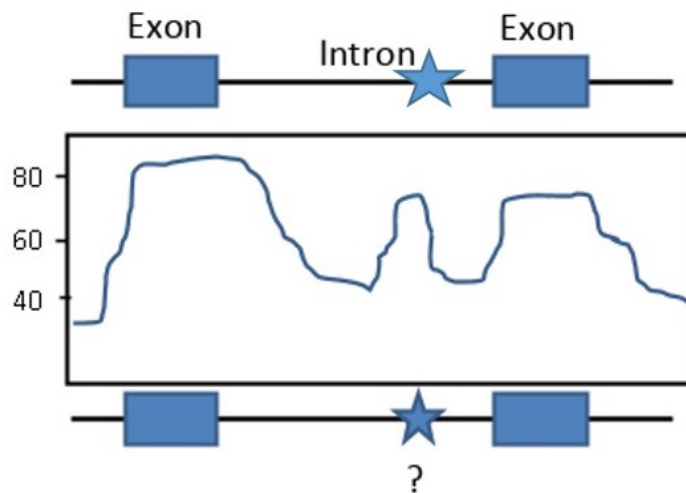
Live Session

- species A only
- species A and B
- species A, B, and C
- species A, B, C and D

No, the answer is incorrect.  
Score: 0

Accepted Answers:  
*species A, B, C and D*

3) Shown below is a pictorial representation of a conserved gene having two exons and the nucleotide sequence of the gene from human and mouse was compared. The Y-axis of the line diagram shows the percent similarity across the gene sequence. The star [★] symbol represents a conserved segment of the intronic region. Based on these data, identify the option that correctly interpret the observations: **1 point**



- Conserved regions indicate the likely functional segment of the genome regardless they are coding or non-coding for a protein
- Changes in nucleotide sequences that are not critical for the gene function are most often passed on to the next generation (since the offspring survive), and hence lower levels of similarity
- The segment of the DNA identified by the star symbol could be critical for the gene function though it is not located in the exonic region
- All of these

No, the answer is incorrect.  
Score: 0

Accepted Answers:  
*All of these*

4) The term "syntenic region" refers to a chromosomal segment: **1 point**

- where preserved co-localization of genes on chromosomes of different species are observed
- modified using recombinant DNA approach
- that shows the densely stained region in the karyotype
- which is prone to recombination

No, the answer is incorrect.  
Score: 0

Accepted Answers:  
*where preserved co-localization of genes on chromosomes of different species are observed*

5) Array-based comparative genomic hybridization (arrayCGH) is a popular method of analysing (whole) genome content. ArrayCGH can be used to detect: **1 point**

- balanced chromosomal translocation
- copy number variations (CNVs)
- single nucleotide variations (SNP)
- all of these

No, the answer is incorrect.

Score: 0

Accepted Answers:

*copy number variations (CNVs)*

6) BLAST is a bioinformatics tool to compare the sequences of DNA, RNA and amino acids. Which one of the following combinations is NOT TRUE about the BLAST tool? **1 point**

- blastp | compares protein query sequence with protein sequence database
- blastx | compares nucleotide query sequence with protein sequence database
- tblastn | Compares nucleotide query sequence with protein sequence database
- blastn | DNA query sequence with DNA sequence database

No, the answer is incorrect.

Score: 0

Accepted Answers:

*tblastn | Compares nucleotide query sequence with protein sequence database*

7) Which one of the following statements is NOT TRUE regarding the transposable elements? **1 point**

- Gene disruption caused by the transposable element can be reversed
- A class of transposable elements involve the RNA intermediate for its integration on to the genome
- The integration of transposable elements on to the genome, regardless of their classes, is a random process and not dependent on the sequence of the target site
- The integration of transposable element on to the genome requires the enzymes transposase, DNA polymerase and DNA ligase

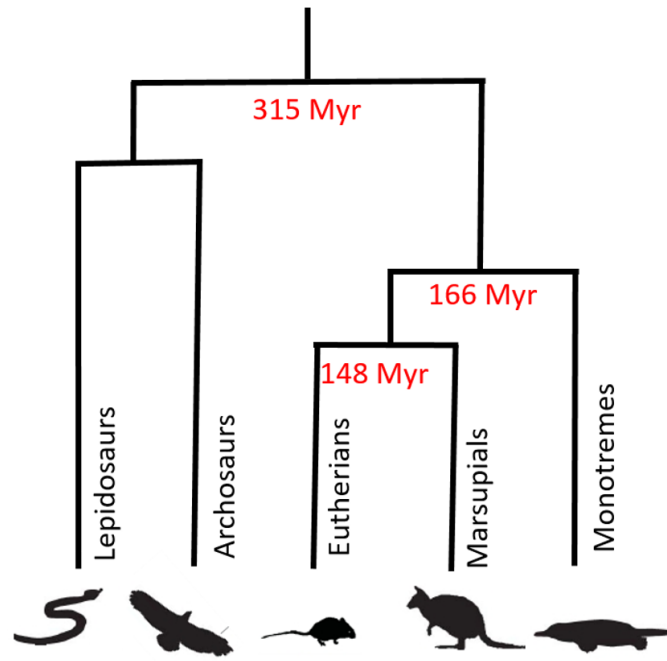
No, the answer is incorrect.

Score: 0

Accepted Answers:

*The integration of transposable elements on to the genome, regardless of their classes, is a random process and not dependent on the sequence of the target site*

8) Review the phylogenetic tree given below and identify the option that lists the most closely related species **1 point**

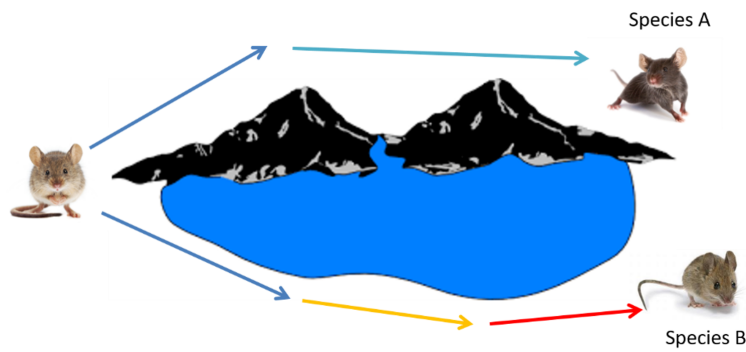


- Eutherians, Archosaurs
- Marsupial, Monotremes
- Lepidosauurs, Monotremes
- Eutherian, Marsupials

No, the answer is incorrect.  
Score: 0

Accepted Answers:  
*Eutherian, Marsupials*

9) The term “speciation” refers to the evolutionary process by which populations evolve to become distinct species. Review the figure given and identify the option that depicts the mode of speciation that the figure represents. **1 point**



- Allopatric speciation
- Peripatric speciation
- Parapatric speciation
- Sympatric speciation

No, the answer is incorrect.  
Score: 0

Accepted Answers:  
*Allopatric speciation*

10 Biological sequence databases are repositories that houses the annotated sequence of the various species and are useful for the comparative genomic analyses. Among the options given below, identify the option that INCORRECTLY matches the database name with the groups of organisms **1 point**

- UCSC genome browser | Mammals and worms
- Ensemble | Mammals, fish, insects and worms
- VISTA | Human, mouse and rat
- EnteriX | enteric bacteria and fungus

No, the answer is incorrect.

Score: 0

Accepted Answers:

*EnteriX | enteric bacteria and fungus*