1. Bioinformatics is:

a) a highly specialized area of biohazardous substances for public information.
b) a set of statistical methods for determining differences between groups of related individuals for production traits.
c) a scientific discipline that deals with the estimation of genetic parameters.
d) Scientific field that combines biology and computer science to analyze and interpret molecular biological data.

2. Which statement is correct?

a) Bioinformatics supports the protection and conservation of endangered species by analyzing the number of individuals in individual populations and managing their reproduction to maintain genetic diversity.
b) Bioinformatics does not deal with the conservation of endangered species.
c) Bioinformatics supports the conservation and preservation of endangered species by studying their genomes and identifying genetic markers for monitoring populations, assessing genetic diversity and assisting captive breeding programs.
d) Bioinformatic analyses cannot be applied in animal breeding.

3. For bioinformatic analysis, what not to have?

a) molecular genetic laboratory
b) computer
c) internet connection
d) on-line genomic databases

4. The most widely used method in bioinformatics analyses is BLAST. But what characteristic does not apply?

a) BLAST aligns two nucleotide or amino acid sequences
b) BLAST aligns more than two nucleotide or amino acid sequences
c) BLAST searches for local similarities in nucleotide or amino acid sequences
d) BLAST can search for structural and evolutionary relationships between two biological sequences

5. Genomic databases do not include:

a) GenBank
b) Uniprot
c) Ensebml
d) ENA

6. Local alignment uses the algorithm:

a) Needlman-Wunsch
b) Needlman- Waterman
c) Wunsch- Waterman
d) Smith-Waterman

7. A higher alignment score value means:

a) greater similarity between DNA sequences
b) less similarity between DNA sequences
c) conclusiveness of the difference between the DNA sequences
d) longer range of DNA sequence alignments

8. Tools for pairwise sequence alignment do not include:

a) EMBOS
b) BLAST
c) COBALT
d) LALIGN

9. Tools for multiple sequence alignment do not include:

a) CLUSTAL
b) T-Coffee
c) EMBOS
d) MUSCLE

10. The principle of multiple alignment is:

a) Same as BLAST
b) Based on the BLAST algorithm, but more complex
c) Alignment of more than two sequences simultaneously
d) Assembling multiple sequences into one.