

Bioinformatics for Biologists

Spring 2021

Study guide for quiz 1-2

1. Know the full name, 3-letter and 1-letter abbreviation of the 20 amino acids.
2. Know the physicochemical properties (hydrophobicity, size, and charge) of the amino acids.
3. Know how different amino acids approximately relate to each other based on hydrophobicity, size, and charge
4. Be familiar with the amino acid Venn diagram
5. Why are some amino found classified in opposing categories, such as both hydrophobic and charged?

6. How do genomes evolve?
7. What are homologs?
8. What are orthologs?
9. What are paralogs?
10. What are common scenarios for different gene copies after gene duplication?
11. What is an isoform and what is a homolog? How can you tell them apart?
12. What is alternative splicing?

13. What does FASTA format look like?

14. What information does a substitution matrix hold?
15. Give an example of a substitution matrix
16. What is a local alignment?
17. What is a global alignment?
18. Which matrix does BLAST use as default?

19. Why is BLAST faster than Smith-Waterman?
20. What does it mean for an algorithm to be heuristic?
21. What does it mean for an algorithm to be exhaustive?
22. How do gap penalties influence your BLAST results?
23. Know the different databases and query data types for the 5 blast algorithms

blastn: Search a **nucleotide** database using a **nucleotide** query

blastp: Search **protein** database using a **protein** query

blastx: Search **protein** database using a **translated nucleotide** query

tblastn: Search **translated nucleotide** database using a **protein** query

tblastx: Search **translated nucleotide** database using a **translated nucleotide** query

24. What do you need to evaluate which of the following alignments is better?

PARIS

PARIS

PA--S

or

PAS--

