Supplementary test
Introduction to Bioinformatics, 2014

Name, Neptun code:
I am attending the exam today: yes/no

The point value of each question is listed in parentheses.

Total points: 100

1. Give a narrow and broad **definition of bioinformatics**! (4)

Narrow: Science of biological data. Mostly molecular biology. Description, management, interpretation.

Broad: Science of biological knowledge. All computer applications in (molecular) biology including modeling. (simulation of behavior)

2. Describe **structured** and **unstructured** data representation! (4)

Structured: - We known the internal structure in terms of Entities and Relationships
- Information-rich, allows detailed comparisons
- need alignment for comparison
- example: sequences, graphs

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3. Fill in the **missing** elements! (4)

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Sometimes large number of dimensions
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Models	Entities	Relationships
Molecules	Atoms	Atomic interactions (chemical bonds)
Pathways	Enzymes	chemical reactions
Genetic networks	Genes	Co-regulation
Protein structure	Atoms	chemical bonds
Folds	Cα atoms	Peptide bond

4. Define **Levenshtein edit-distance** and **Hamming distance**! (4)

Levenshtein: edit distance between character string defined as a sum of costs assigned to matches, replacements and gaps.
2 strings do not need to be of the same length

number of exchanges necessary to turn one

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Levenshtein: edit distance between character string defined as a sum of costs assigned to matches, replacements and gaps.
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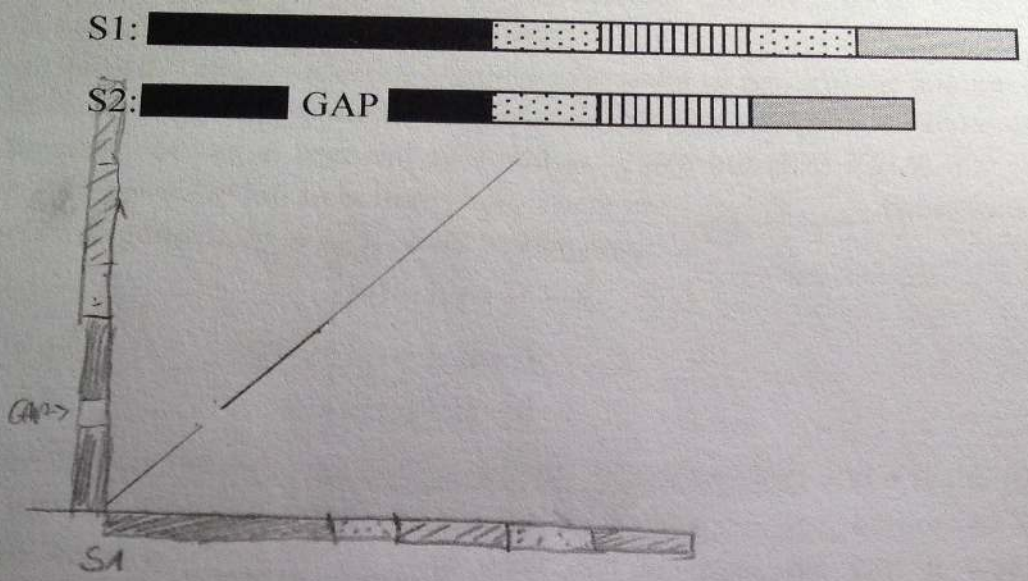
Hamming: number of exchanges necessary to turn one string of bits or characters into another one.
2 strings are of identical length and no alignment is done
- The exchanges in character strings can have different costs, stored in a lookup table.
In this case the value of the Hamming distance will be the sum of costs, rather than the number of exchanges



6. Calculate the **log odds ratio** of residues Alanine (A) and Valine (V) using the following multiple alignment! (4)

A	V	F	R	V	G
V	T	F	V	A	A
A	V	V	S	A	A
L	V	A	N	V	H

$g(A) = 7 \quad g(V) = 8 \quad g(A \wedge V) = 5$

$m(A/V) = \frac{g(A \wedge V)}{g(A) \cdot g(V)} = \frac{5}{7 \cdot 8} = \frac{5}{56}$

$M(A \wedge V) = \log(m(A/V)) = -1{,}05$

7. Define the following terms: (3)

running time: Defined as number of steps to be carried out.

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running time: Defined as number of steps to be carried out.

average case: using an average input problem-dependent, not trivial

worst case: inputs leading to an upper limit of running time / memory

8. Fill in the **missing** words! (9)

_____ algorithms find the best solution by constructing the solution from the stored optimal solutions of sub-problems. The Needleman-Wunsch algorithm is a well-known solution for global sequence alignment. In order to perform the alignment, a matrix is created which allows us to compare the two sequences. The score *F(i,j)* is the score of the best alignment between the initial segment $x_{1\ldots i}$ and $y_{1\ldots j}$. We initialize $F(0,0) = 0$. Then we proceed to fill the matrix from top left to bottom right. There are 3 possible ways that the best score *F(i,j)* of an alignment up to x_i, y_j could be obtained:

$$F(i,j) = \text{max}\begin{cases} F(i-1,j-1) + s(x_i, y_j) \\ F(i-1,j) - d \\ F(i,j-1) - d \end{cases}$$

where $s(x_i,y_j)$ is the score value for aligning x_i and y_j and *d* is the penalty for inserting a _____. The equation is applied repeatedly until we reach the bottom right corner. As we fill in the *F(i,j)* values we also keep a _____ in each cell showing the cell it was derived from. Using these _____ we can _____ the alignment of our sequences.

Smith-Waterman algorithm is a solution for local sequence alignment. The algorithm is similar to global alignment, there are two main differences. First, at calculating F matrix an extra possibility is added allowing *F(i,j)* to take the value 0 if all other options are negative _____. If the best alignment up to som

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9. How can you validate a multiple alignment using **3D structure** information? (2)

1. convert 3D structure into a series of secondary structure assignments, and write on top of the alignm

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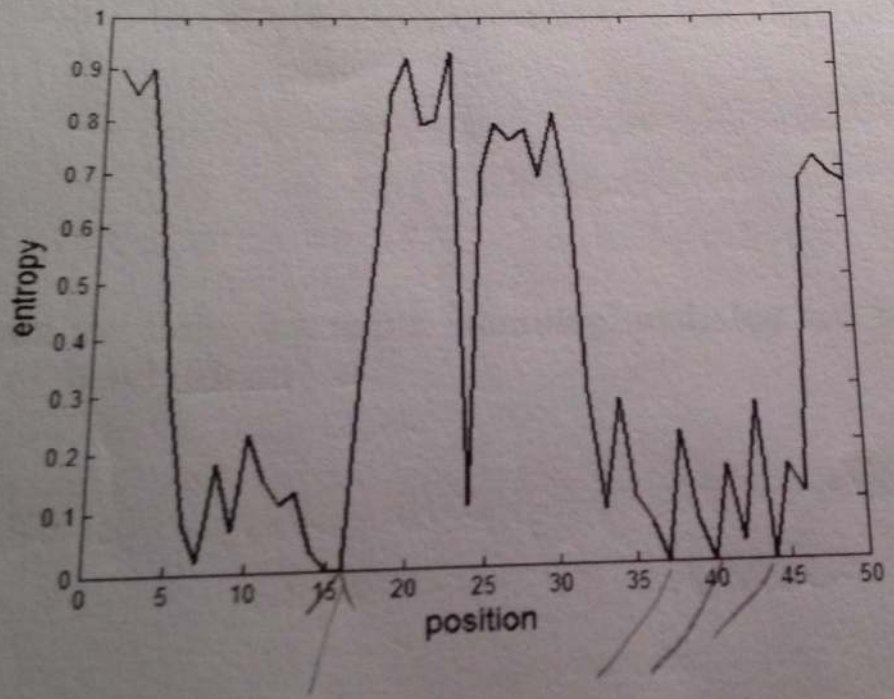
variable regions should maps to the surface of the protein, not in the buried parts

10. Which sequence has lower **complexity**? Support your statement by calculation! (3)
1. CGAGTAGCTCTGCTAA
2. GAGTGTCTTCTATTTG

Complexity: an empirical measure, proportional to the number of words (of arbitrary length) necessary to reproduce a sequence.

seq_1 seq_2 seq_3 seq_4 seq_5 seq_6 seq_7 seq_8 seq_9 seq_10
sequence name

12. What can you conclude from the multiple alignment that has generated the following normalized **entropy plot**? (2)



Best: 0
Worst: 2

dilages eset

conserved regions

WHAT THE FUCK?

16. Given the following distance matrix draw a dendrogram based on the **UPGMA** method and briefly explain your calculation! (6)

	A	B	C	D
B	8			
C	6	8		
D	8	2	8	
E	4	8	6	8

17. Explain how **BLAST** algorithm works (what are the BLAST tricks). List the main computational steps and briefly describe them! (8)

→ twice

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⇒ wait

18. List 5 applications of **next generation sequencing**! (5)

medical, microbiological

agricultural, such as only human cancer genes, only microbial genomes, etc

19. Compare traditional (**Sanger**) and **next generation sequencing** (list the advantages, disadvantages)! (4)

Sanger:

- Accurate
- Also works on few samples
- Expensive for data
- Small capital investment
- Slow

NSG:

- Less accurate
- Shorter reads
- Economical only with many samples
- ~1000 less expensive for data
- Large capital investment
- very fast

20. What is the order of the following steps/stages at **NGS** sequencing? (4)

(a) alignment (b) fragmented DNA (c) sample DNA (d) parallel sequencing (e) sequence (f) DNA fragments with sequencing adapters (g) PCR amplification

21. What are the future challenges of **NGS in clinical medicine**? Shortly explain at least 3 examples! (3)

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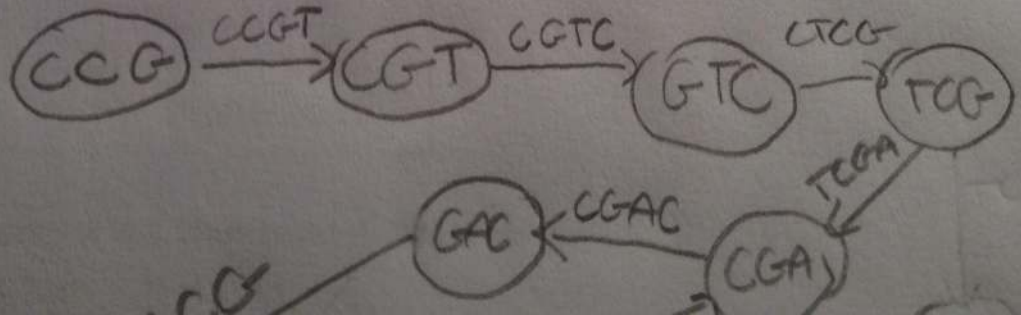
Interpretion of the variant we find

Storage and access in the medical record → each have ~4 million variant

22. Given the reads {CCGT, GAAA, AAAC, AACG, CGTC, GTCG, GACG, ACGA, TCGA, CGAC, CGAA}. What is the original sequence? Use the **de Bruijn graph** (k-mer = 3) based algorithm for the computation! Very briefly describe your computation! (6)

CCGTCGAAACGACG

CCGT
CGTC
GTCG
TCGA
CGAA
GAAA
AAAC
AACG



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