Ime in priimek (s tiskanimi črkami) / Name (please print): _____

Vpisna številka / Student ID: _____

Osnove bioinformatike / Introduction to Bioinformatics

1. izpitni rok / First Examination Period

24. januar 2014 / January 24, 2014

Naloga / Exercise	1	2	3	4	5	Vsota / Sum
Vrednost / Max	6	6	6	5	6	29
Točk / Points						

[6] 1. Given are two sequences

```
CAGA
CATAGG
```

and a scoring function

$$\sigma(a,b) = \begin{cases} 1 & a = b \\ -2 & a = - \text{ or } b = - \\ 0 & \text{otherwise} \end{cases}$$

Propose all possible global alignments with a maximal score. Do this by computing the dynamic programming table, highlight all trace-backs, report on alignment score and show the aligned sequences for all alignments with a maximal score.

Dani sta zaporedji:

```
CAGA
CATAGG
```

in ocenjevalna funkcija

$$\sigma(a,b) = \begin{cases} 1 & a = b \\ -2 & a = - \text{ ali } b = - \\ 0 & \text{v ostalih primerih} \end{cases}$$

Globalno poravnaj zaporedji tako, da bo ocena poravnave maksimalna, in izpiši vse poravnave z najvišjo oceno: pripravi in izračunaj tabelo dinamičnega programiranja, označi “trace-back” za vse poravnave z najvišjo oceno, poročaj o oceni poravnave in prikažite vse poravnave zaporedij z najvišjo oceno.

$$M_{i,j} = \max\left(M_{i-1,j} + \sigma(s_i, -), M_{i,j-1} + \sigma(-, t_j), M_{i-1,j-1} + \sigma(s_i, t_j)\right)$$

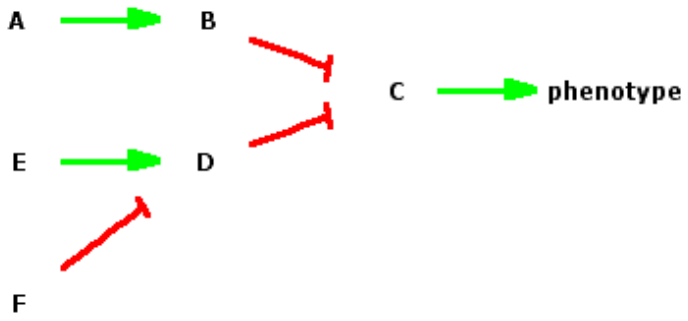
Page for your solutions. / Stran za vaše rešitve.

[6] 2. Gene regulation networks can be inferred through epistasis, where one gene can block the other one in the pathway for a specific phenotype.

Given is a set of 9 experiments, where we have observed a phenotype for the wild type organism (E1), different single mutants (E2 to E5), and different double mutants (E6 to E9). Genes were either knocked-out (e.g, B-) or over-expressed (e.g., A+). The phenotype can have tree values: n (decreased), 0, p (increased), where phenotype 0 is a wild-type phenotype.

ID	Gene 1	Gene 2	phenotype	Confidence	Comments	Ignore	Edit	Delete
E1			0	1.00		I	E	D
E2	A+		n	0.50		I	E	D
E3	B-		p	0.50		I	E	D
E4	D-		p	0.50		I	E	D
E5	E+		n	0.50		I	E	D
E6	B-	C-	n	0.20		I	E	D
E7	D-	C-	n	0.20		I	E	D
E8	E+	D-	p	0.20		I	E	D
E9	F-	D-	p	0.20		I	E	D

We are still missing (at least) three crucial experiments to confirm our hypothesis about what the network should look like:



Which are the three missing experiments (on single or double mutants) that we should perform? What should the outcome (phenotype) of those experiments be?

Pri gradnji genskih regulacijskih mrež iz fenotipskih podatkov o mutantih smo govorili o epistazi, pojavu, kjer en gen lahko blokira druge na regulacijski poti do fenotipa.

Razpredelnica podaja nabor devetih eksperimentov, kjer smo opazovali fenotip pri nemutiranem organizmu (E1), enojnih (E2 do E5) in dvojnih mutantih (E6 do E9). Gene smo pri eksperimentih ali izničili (npr. B-) ali jih čezmerno izrazili (npr. A+). Opazovani fenotip smo zajeli kvalitativno z vrednostmi n (znižan), 0, p (povečan). Fenotip divjega osebka je 0.

Kateri so trije manjkajoči eskperimenti (enojni ali dvojni mutanti in njihovi fenotipi), s katerimi bi lahko dokazali prikazano mrežo genske regulacije (slika).

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3. Given are short sequences of DNA fragments from four hypothetical species.

[2] (a) Explain Jukes-Cantor (JC) correction in one or two sentences.

[2] (b) Compute a pairwise distance matrix (mismatch frequency) between the sequences. Correct the matrix using JC correction. Answer should include both the original and the corrected matrix.

[2] (c) Draw a dendrogram of the four sequences, using the JC-corrected matrix. Use the single linkage method (see image).

Podana so kratka zaporedja fragmetov DNA štirih hipotetičnih vrst.

(a) V enem ali dveh stavkih razložite Jukes-Cantorjev (JC) popravek.

(b) Izračunajte matriko medsebojnih razdalj (frekvenco različnih nukleotidov) med zaporedji. Popravite vrednosti z uporabo popravka JC. Odgovor naj vključuje tako prvotno kot popravljeno matriko.

(c) Narišite dendrogram štirih sekvenc na osnovi popravljene matrike. Pri združevanju merite razdaljo med dvema najbližjima točkama dveh skupin (slika).

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ATTCCATTTA
GATTCATTTC
TTTCCATTTT
GTTCCATTTA
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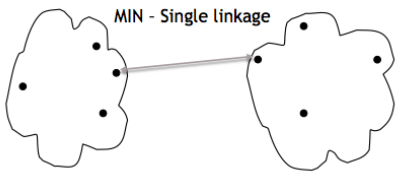

$d_{\mathrm{JC}} = -\frac{3}{4}\ln(1 - \frac{4}{3}d)$

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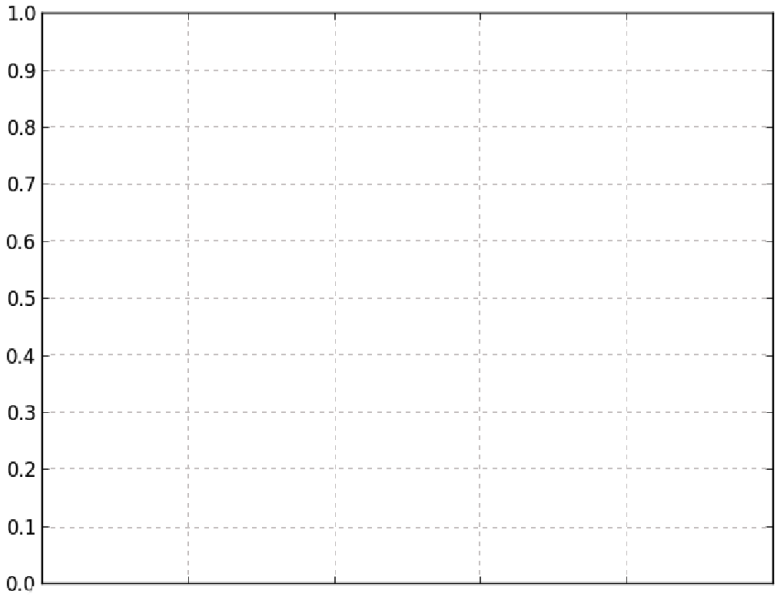

[5] 4. Explain how would you use a genetic algorithm to solve

$$\sum_{i=0}^{n} a_i x_i = 0,$$

where constants a_i are real numbers. Define encoding of individuals, mutations, crossover and fitness function for this problem.

Razložite, kako bi z genetskim algoritmom rešili

$$\sum_{i=0}^{n} a_i x_i = 0,$$

kjer so kontante a_i realna števila. Definirajte kodiranje osebkov, mutacije, križanje in oceno uspešnosti posameznika za ta problem.

[2] 5. (a) What are pseudocounts and why do we use them?

[4] (b) Construct a hidden Markov model from hidden and observable (here DNA) sequences given below. Use a pseudocount of 2.

(a) Kaj so "pseudocount"-i in zakaj jih uporabljamo?

(b) Zgradite skriti Markov model iz skritega in vidnega zaporedja, ki sta zapisani spodaj. Uporabite "pseudocount" 2.

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IIIIGGGGGGGGGGGGGGGGIIIIIIIIIIII
GTATATGGTAGAACGATATTGATAACAATTCTAT
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