Algorithms in Genome Research
Winter 2013/2014

Exercises

Number 8, Discussion: 2014 Jan 10

1. Define new similarities and dissimilarities to compare 2 or more genomes. Are they relevant from a biological point of view?

2. Define constraints allowing the definition of the variables of type a and b (see slide 23 of the lecture).

   $a(i,k)$ denotes a **matching** between two genes;

   $b_x(i)$ denotes the **saturation** of a gene in genome G_x;

3. Resolve the following linear program with the solver miniSat+ (http://minisat.se/MiniSat+.html):
   Objective $\max(z); \ z = x_1 + 2x_2 - x_3$

   Constraints
   $$
   \begin{aligned}
   x_1 - 2x_2 + 3x_3 &\geq 1 \\
   x_1 + x_2 + x_3 &= 1 \\
   2x_1 + x_2 + x_3 &< 3
   \end{aligned}
   $$

   Boolean variables $x_i \in \{0,1\} \qquad \forall i = 1,2,3.$

4. What are the advantages and defaults of exemplar, intermediate and maximum matching models during genomics comparison?

5. What are the advantages and defaults of the free family assignment model?