Article 5: answers

Nicolas E. Buchler, Ulrich Gerland, and Terence Hwa: On schemes of combinatorial transcription logic. *Proceedings of the National Academy of Sciences of the United States of America* (2003)

Question 1:

How is gene transcription quantified in the model described in the text?

Answer 1:

The degree of gene transcription is quantified by the equilibrium binding probability P of the RNAP to its DNA target, the promoter, given the cellular concentrations of all of the TFs. Given the binding strengths Ki and the cooperativity factors i,j for all the DNA sites, the binding probability P of the RNAP to the promoter can be computed straightforwardly.

Question 2:

What are the assumptions regarding protein-protein interactions in the model, and how are these interactions quantified?

Answer 2:

A weak glue-like interaction between two proteins (TFs andor RNAP) is assumed possible if the relative placements of the DNA-binding sites allow for direct contact of appropriate regions of the proteins.

Here we assume for simplicity the same interaction energy for all protein pairs and choose a conservative value of Eint = 2 kcal/mol

Question 3:

How are more complex regulatory functions, involving three or more inputs, implemented in the mode.

Answer 3:

Through the generalization of Fig 5. Combining different functions with distal regulation through DNA looping, getting a modular structure for the logic function.

Question 4:

How is the logic function "AND gate" implemented in the model, and what conditions enable its functionality?

Answer 4:

It can be obtained by choosing weak binding sites for both A and B and placing them adjacent to each other (see Fig. 2a) such that each TF alone cannot bind to its site, but when both are present binding occurs with the help of the additional cooperative interaction.