

DNA computing by Splicing

DNA computing (or more generally, molecular computation) is a research area combining biochemistry and computer science, in an attempt to find alternative modes and models of computation. It was Initiated by Leonard Adleman in 1994 [Adleman1994].

The first part of the talk will be a short introduction to the area of DNA computing. We will see some properties of DNA and some DNA operations. We then discuss Adleman's experiment as an example of how these operations can be used to perform computations. This new paradigm of computing also calls for new mathematical models of computation.

In the second part, we focus on a specific subfield of DNA computing, called *Splicing*. The biochemical basis of splicing is the cutting and recombination of DNA molecules using restriction enzymes. Roughly speaking, these enzymes can cause two molecules to recombine in the following way: The first part of molecule 1 is attached to the second part of molecule 2 and the first part of molecule 2 to the second of molecule 1.

Tom Head [Head87], observed that this behaviour can be regarded as a string rewriting operation, specified by a rule of four elements, called splicing rule and usually written as follows ([PaRoSa1998]):

$$r = u_1\#u_2\$u_3\#u_4$$

This rule means that if a string contains u_1u_2 as a substring, it can be cut between u_1 and u_2 , and recombined with a string containing u_3u_4 in the way described above.

This operation can be used to define a computational model (language generating device) called *Splicing system* or *H system*, which consists of an alphabet, a set of splicing rules and an initial language. The language is obtained by iteratively applying the splicing rules to the initial language.

We will see some classic results and some new directions in the theory of splicing.

References

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