Sequencing by Hybridization (SBH) [19], also called “sequencing by k-tuple composition” is a method to determine the order in which nucleotides appear in a strand of DNA. It uses a matrix, or chip, with a fixed number of features and each one can accommodate one probe, consisting of smaller sequences of k nucleotides, to be searched in the DNA strand. This leads to a combinatorial constraint that limits the use of classical algorithms to piece together the entire sequence of the DNA strand of interest. Usually k is between 8 and 10, so a chip with k=8 will have 48 = 65 536 probes on it that will allow researchers to reconstruct only 200 nucleotides long sequences.

In SBH, an appropriate length probe must be used to unambiguously determine a target sequence of length N. When the sequence is larger than 40 nucleotides, a probe of length k=4 cannot be used to reconstruct the target with a high probability of success. As N increases, the probability of redundancy in the target increases, making unambiguous reconstruction difficult. Hence the AI methods are well suited to solve the DNA sequencing problem and obtain a near optimal solution. DIMANTS [19] is a multi-casts ant system that uses a heuristic approach based on social insects’ organization. Also, evolutionary programming has been applied for DNA sequencing with very good results after numerous simulations. A hybrid genetic algorithm that had a greedy improvement managed to have over 95% optimal results when tested on sequences to up to 500 nucleotides and probes of length 10 [19].