# Pairwise sequence alignment using dialign algoritm

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Abstrak

This skripsi discusses a method known DIALIGN to find the best alignment of two DNA sequences. This algorithm is based on segment-tosegment comparison instead of the commonly used residue-to-residue comparison. Also, this algorithm avoids the wellknown difficulties concerning the choice of appropriate gap penalties. In DIALIGN, all possible diagonals of the input sequences will be weighted and compared to find the diagonals which compose optimal alignment. Diagonal weight is based on match probability of residues in the diagonal. Having the maximum score, the alignment will be constructed by tracing back the components which produce the maximum score. The resulted alignment can be considered as consistent collections of diagonals. In the final, the algorithm is implemented in a program. According to the simulation of the program, DIALIGN algorithm is able to produce optimal sequence alignment from a pair of sequence. And the program performs well on short sequences.