

Abstract

One of more wide which to worry about source code plagiarism is academic wide, specially practicum activity of informatics because it related with algorithm and programming and it is implemented with source code. Assistent as corrector has found misery to detect plagiarism indicator which happen on student's tasks which is collected. Needleman-Wunsch algorithm as tools to detect source code plagiarism should be can ascertain equality level between two source code or more.

In bioinformatics, Needleman-Wunsch algorithm is first method which is discovered to find equally between two junction of DNA (Deoxyribo Nucleic Acid). This Algorithm is extension from string matching which is included one of more dynamic programming technics. Concept of this algorithm is junctions of carbon (A,T,G,C) which construct both DNA is made parallel with way to pin up and move them, so we can find maximal of equally level globally (Global Alignment). In implementation, to make source code is parallel, every line or token from source code will be analogy as junctions carbon in DNA parallelism. The result of observation is got conclusion that Needleman-Wunsch algorithm can ascertain equally level accuratly and know plagiarism source code with process continued.

Keywords: Needleman-Wunsch, source code, plagiarism, parallelism