**Abstract and Introduction summary**

* To Process biological data we need many resources and a lot of time, which are costly.
* The problem is biological data is very big and complex, we need efficient way to analyze it.
* We will analyze it with pattern matching, we will search for a specific pattern for disease or mutation.
* The paper will study different kinds of algorithms for pattern matching, complexity and performance.
* Keyword search and matching are techniques to discover patterns inside specific strings. Algorithms for matching, are used to discover matches between patterns and input strings.
* We will consider the pattern is p and text is t, pattern is shorter than t, and we need to find all occurrence of p in t.
* There are two main approaches for string matching, first is exact matching, for instance: Smith-Waterman (SW); Needleman Wunsch (NW); Boyer Moore Horspool (BMH); Dynamic Programming; Knuth Morris Pratt (KMP). Second approach, is approximate matching, also known by Fuzzy string searching, for instance: Rabin Karp; Brute Force.
* In this paper is analyzed the similarity measures on Protein, DNA and RNA, using for that effect, different types of string matching algorithms.