An overview of search and match algorithms complexity and performance

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ABSTRACT

DNA extracted from cells has huge amount of information about us. It distinguishes creatures and make them different. So, to do sequence matching that helps us to understand evaluation and genetic relationships, we have a lot of algorithms each of them has its performance and complexity.

INTRODUCTION

When we discover pattern in a specific string ,we have two main approaches of matching:

    a. Exact matching:

    1. For instance: Smith-waterman(SW),Needleman wunsch (NW), Boyer moore horspool(BMH).

    2. Dynamic programming: Knuth morris pratt(KMP).

    b. Approximate matching (fuzzy string searching):for instance like Rabin karp and Brute force.

We will analyze in this paper matching in protein, DNA and RNA.