Pattern matching is one of the most important research

subjects that have been studied in computer science. Over

the years, pattern matching algorithms have been extensively applied in various computer applications, for example, in retrieval of information, information security,

and searching nucleotide or amino acid sequence patterns

in biological sequence databases. Pattern matching problem can be defined as finding one or more usually all the

occurrence of a given pattern ( 01 1 m Pppp− = … ) of

length min a text ( 01 1 n Tttt− = … ) of length n, which

are built over a finite alphabet set Σof size σ.

The aim of a good algorithm is to minimize the work

done during each attempt and to maximize the length of

the shifts. Hence, some well-known algorithms have been

presented to get a better shift value, for example, Boyer-Moore (BM) [1], Quick Search (QS) [2] and Berry–

Ravindran (BR) [3].

In this paper, a fast hybrid algorithm (called BRFS) by

combining the ideas of BR and FS [5] is presented. It

turns out that the proposed algorithm, though not linear,

achieves good results especially in the case of small alphabets and long patterns.

The rest of the paper is organized as follows. Section 2

gives the review of several efficient algorithms in practice. Section 3 describes the BRFS algorithm in detail. In

section 4, the experiment results of comparisons between

the proposed algorithm and the other five algorithms are

given. And section 5 is the conclusion.

With the development of sequencing techniques, it has become easy to obtain the sequence, i.e. the linear arrangement of residues (nucleotides or

amino-acids), of DNA, RNA, or protein molecules. However, determining the

function of a molecule remains difficult and is often bound to find a sequence

similarity to another molecule whose role in the cell is at least partially known.

Then, the biologist can predict that both molecules share the same function

and try to check this experimentally. Functional annotations are transferred

from one sequence to the other provided that their similarity is high enough.

This procedure is also applied to molecules subparts, whose sequences are

shorter: protein domains, DNA/RNA motifs, etc.

Depending on the sequence lengths and expected level of evolutionary relatedness, the sequence similarity can be found using alignment or pattern

matching procedures. A quest in bioinformatics has been to design more sensitive sequence similarity searching methods to push further the limit or gray