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## A novel algorithm for finding imperfect palindromes in long sequences

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A sequence is called a perfect palindrome if it is equal to its inverse complement. Other sequences are classified as imperfect palindromes. The identification of both perfect and imperfect palindromes that are close to the perfect ones is a significant problem in computational biology, as these structures are often associated with genomic instability and regulatory elements. While perfect palindromes can be found in linear time, the efficient computational search for imperfect palindromes, allowing mismatches, deletions and insertions, remains an open problem in bioinformatics. We propose a new algorithm SIPAM for efficient identification of imperfect palindromes in long sequences. We've conducted extensive testing of the algorithm's performance on both synthetic and real biological data.

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