A COMPARATIVE STUDY OF CROSS−CORRELATION METHODS FOR ALIGNMENT OF DNA SEQUENCES CONTAINING REPETITIVE PATTERNS (WedPmOR2)

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Abstract :

In this work we consider the problem of global DNA sequence alignment. One of the best known and most efficient computational techniques used for this task is the cross−correlation method. We compare efficacy of evaluating periodic DNA sequence misalignment using the standard magnitude−and−phase cross−correlation method with the lesser known phase−only cross−correlation method. We prove that for a periodic DNA sequence whose length is a prime number the standard approach leads to significant sidelobes in the cross−correlation, the magnitude of which increases with the length of the sequence, while the phase−only approach allows attaining a perfect cross−correlation with zero sidelobes. Numerical experiments are included and robustness of the phase−only method to random DNA insertions and imperfect DNA fragment matches is discussed.

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