

Scoring Schemes of Palindrome Clusters for More Sensitive Prediction of Replication Origins in Herpesviruses

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Many empirical studies show that there are unusual clusters of palindromes, closely spaced direct and inverted repeats around the replication origins of herpesviruses. In this talk, two new scoring schemes to quantify the spatial abundance of palindromes in a genomic sequence will be introduced. Based on these scoring schemes, a computational method to predict the locations of replication origins is developed. When our predictions are compared with 39 known or annotated replication origins in 19 herpesviruses, close to 80% of the replication origins are located within 2% of the genome length. Some ongoing work on accessing the statistical significance of these scores using Compound Poisson Approximation will also be discussed. If time permits, I will also talk about some other approaches to the problem that we are exploring at the moment.

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