

Statistics based computational methods for replication origin prediction in bacterial and viral genomes

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Abstract

Replication origins, which are places on DNA molecules where replication processes are initiated, are considered important sites for understanding the molecular mechanisms involved in DNA replication. Many computational methods have been developed for predicting their locations in archaeal, bacterial and eukaryotic genomes. However, a method designed for a particular kind of genomes might not work well for another. In this talk, we describe two complementary methods to predict the likely locations of replication origins in viral genomes. One approach is based on quantifying local abundance of DNA palindromes at or above a certain length, and the other approach is based on quantifying local abundance of bases A or T. This is based on joint works with David SH Chew and Ming-Ying Leung.