

ORIS: An interactive software tool for prediction of replication origin in prokaryotic genomes

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Software

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Summary

The origin of replication is a small segment in the genome at which the DNA replication process is initiated (Alberts et al., 2013). Bacterial genomes generally have a single origin of DNA replication whereas archaea and eukaryotes have multiple replication sites (Egan, Fogel, & Waldor, 2005; O'Donnell, Langston, & Stillman, 2013). The accurate identification of the origin of replication sequences is important to understand the complex replication process and could also provide new effective drug targets (Grimwade & Leonard, 2017).

Here, we present a standalone software tool, ORIS, for finding the origin of replication sites in the genome. ORIS is a novel tool that lets the user interactively explore the whole genome sequence data using several computational methods and charts. ORIS is developed particularly for biologists and researchers who are working in the area of DNA replication. ORIS allows users with little or no programming background to interactively explore whole genome sequences and identify the putative origin of replication sites in the genome of interest.

ORIS is well suited for origin finding across bacteria, archaea and to some extent eukaryotes. The origin of replication sites in *Plasmodium falciparum* were computationally predicted using ORIS and experimentally verified (Agarwal, Bhowmick, Shah, Krishnamachari, & Dhar, 2017).

There are a few online tools/databases which may help in finding the origin of replication sites for a few species (Frank & Lobry, 2000; Gao & Zhang, 2008). These tools are limited by the type of computational approaches they take and are not interactive. Whereas, ORIS is a comprehensive software suite that can take any genome as input. It can perform context-based analysis, which includes DSP (digital signal processing) based correlation measures, all types of skew measures and entropy-based methods for predicting the origin of replication (Beauchamp & Yuen, 1979; Shah & Krishnamachari, 2012). Features such as pattern matching, generating sequence logo, DNA bending profiles, and composition statistics are also available as part of the analysis.

An obvious advantage of using ORIS is that all the computational methods implemented in ORIS are accessible through a simple and intuitive GUI but the user has to manually document/log the metadata associated with the results (e.g., the method used, method parameters, and input files). We plan to implement automatic logging in future releases of ORIS so that this information is easily recorded along with the results, which will make it, even more, easier to reproduce the results while minimizing user efforts.

We have tested and validated our tool by performing a case study (available as a supplementary document from ORIS' GitHub repository). The method details are also included in the supplementary document. A user guide is available from ORIS' GitHub repository.

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