

Origin of DNA replication: positioning and strength, from bulk to single cell experiment

The positioning and strength of origin of DNA replication in human are still poorly defined. Origins are licensed in G1 phase and fired in S phase of the cell cycle. Experiments can independently profile mean replication timing (MRT) and replication fork directionality (RFD) genome-wide. Such profiles contain information on multiple origins' properties and on fork speed. Due to possible origin inactivation by passive replication, however, observed and intrinsic origin efficiencies can markedly differ. Thus, there is a need for methods to infer intrinsic from observed origin efficiency, which is context-dependent. Here, we show that MRT and RFD data are highly consistent with each other. Using neural networks, we infer an origin licensing landscape that, when inserted in an appropriate simulation framework, jointly predicts MRT and RFD data with unprecedented precision. We furthermore uncover an analytical formula that predicts intrinsic from observed origin efficiency combined with MRT data. While this formula has been derived using various approximation, we show that it can be exact for a specific type of firing and can be also used to study single cell experiments.

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