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Role of finite-size fragments in analysis of DNA replication JOHN BECHHOEFER, HAIYANG ZHANG, Dept. of Physics, Simon Fraser University — In higher organisms, DNA replicates simultaneously from many origins. Recent in-vitro experiments have yielded large amounts of data on the state of replication of DNA fragments. From measurements of the time dependence of the average size of replicated and non-replicated domains, one can estimate the rate of initiation of DNA replication origins, as well as the average rate at which DNA bases are copied. One problem in making such estimates is that, in the experiments, the DNA is broken up into small fragments, whose finite size can bias downwards the measured averages. Here, we present a systematic way of accounting for this bias by deriving theoretical relationships between the original domain-length distributions and fragment-domain length distributions. We also derive unbiased average-domain-length estimators that yield accurate results even in cases where the replicated (or non-replicated) domains are larger than the average DNA fragment. Then we apply these estimators to previously obtained experimental data to extract improved estimates of replication kinetics parameters.

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