Optimizing the Number of Sequencing Reads in Coding Schemes for DNA Data Storage

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DNA data storage is an emerging technology offering density and durability properties far superior to existing storage solutions. However, ensuring its reliability requires addressing diverse challenges, such as correcting errors introduced during the storage process (from sequencing and/or synthesis), and minimizing the number of sequencing reads needed to reconstruct the stored data.

Conventional coding schemes tackle these challenges through a pipeline combining three components: a consensus algorithm that produces a single consensus sequence from h reads, an error-correction code (ECC) to correct residual errors in each consensus sequence, and an erasure code to accelerate data retrieval. When Reed-Solomon codes are used as erasure codes, k source sequences are encoded into n coded sequences, each synthesized as a distinct DNA strand. After sequencing, it suffices to correctly recover any subset of k coded sequences to reconstruct the original data. According to the coupon collector problem [1], and assuming that the consensus algorithm reconstructs the sequences without error, the expected number of reads $E[T]$ required to recover the full information is upper bounded by [2]

$$E[T] \leq n \log \frac{n}{n-k} + nh \log \log n. \tag{1}$$

While this upper bound is not tight, it highlights the strong influence of both k and h on $E[T]$.

In practice, when storing V bits of information accross N DNA strands of length L bits each (with $V < N \times L$), a central design question arises: how should the ECC, the erasure code, and the consensus algorithm be jointly optimized to minimize $E[T]$? This work addresses this tradeoff by formulating an optimization problem over the ECC and erasure code rates, as well as the number of reads h retained after consensus.

To solve this problem, we first revisit the coupon collector framework to derive a more accurate yet tractable expression of $E[T]$, refining the upper bound in (1). We then extend this analysis to two practically relevant settings: (1) by taking into account consensus sequences that may be erroneous with probability $\mathbb{P}_e$, and (2) by considering erasure codes based on Raptor codes, which require more than k correct sequences for successful decoding. Building on these theoretical results, we numerically solve the optimization problem for various combinations of erasure codes (Reed-Solomon and Raptor) and ECCs (Reed-Solomon, LDPC, etc.), deriving in each case the optimal parameters and the corresponding minimum value of $E[T]$. Finally, we consider multiple channel models from [3] to illustrate how varying error rates lead to different optimal tradeoffs.

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