Robust Composite DNA Storage under Sampling Randomness, Substitution, and Insertion–Deletion Errors

Busra Tegin[1], Tolga M Duman[2]

[1]IETR-UMR CNRS 6164, CentraleSupélec Rennes Campus, 35576 Cesson-Sevigne, France, Email: busra.tegin@centralesupelec.fr
[2]Department of Electrical and Electronics Engineering, Bilkent University, Ankara, Turkey, Email: duman@ee.bilkent.edu.tr

DNA storage offers a high-density, long-term alternative to traditional storage systems, addressing the exponential growth of digital data. Composite DNA extends this paradigm by leveraging mixtures of nucleotides to increase storage capacity beyond the four standard bases. These composite letters exploit the redundancies inherent in DNA synthesis and sequencing and are constructed by reading n copies of a DNA strand at a specific index. The resulting channel is referred to as a multinomial channel, whose output is a quartet of probabilities $\{p_A, p_C, p_T, p_G\}$ representing the expected frequency of each nucleotide in the n copies.

Each $L \in \mathbb{Z}^+$-bit segment of the codeword $\mathbf{c}$ is mapped to a composite symbol according to a fixed constellation diagram. The input constellation is defined on the three-dimensional probability simplex:

$$\Delta_L = \left\{ \boldsymbol{\rho}_s \in \mathbb{R}_+^3,\ \rho_{s,i} \in [0,1] \,\middle|\, \sum_{i=1}^{4} \rho_{s,i} = 1 \right\}, \tag{1}$$

for $s \in \{1, \dots, S\}$ with $S = 2^L$. This set can be viewed as analogous to constellation points in standard digital modulation schemes. From the perspective of DNA synthesis, this corresponds to producing many strands, where at each position the nucleotide is chosen independently from $\{A, C, T, G\}$ with probabilities $\rho_{s,i}$ associated with the s-th constellation point. Hence, a $\rho_{s,i}$ fraction of the readings corresponds to the i-th nucleotide.

To mitigate errors caused by sampling randomness, we derive transition probabilities and log-likelihood ratios (LLRs) for each constellation point and employ practical channel codes for error correction as follows. Let $u_{s,l}$ denote the l-th bit of the label of constellation point $\boldsymbol{\rho}_s$, corresponding to the L-bit segment defined by the mapping Δ_L. The LLR corresponding to the l-th bit of the i-th symbol, for $l \in \{1, \dots, L\}$, can be calculated as $LLR_{i,l} \propto \log \left(\frac{\sum_{s:u_{s,l}=0} P(\mathbf{d}_i|\boldsymbol{\rho}_s)}{\sum_{s:u_{s,l}=1} P(\mathbf{d}_i|\boldsymbol{\rho}_s)} \right)$.

We then extend this framework to substitution and insertion–deletion–substitution (IDS) channels. When the only source of error is sampling randomness, one can compute the exact LLR of the composite letter using our standard LLR formulation. However, when additional error types are present, such as substitution, deletion, or insertion errors, the nucleotide observed at a given strand position may differ from the expected set. We propose constellation update rules that account for these additional impairments as follows:

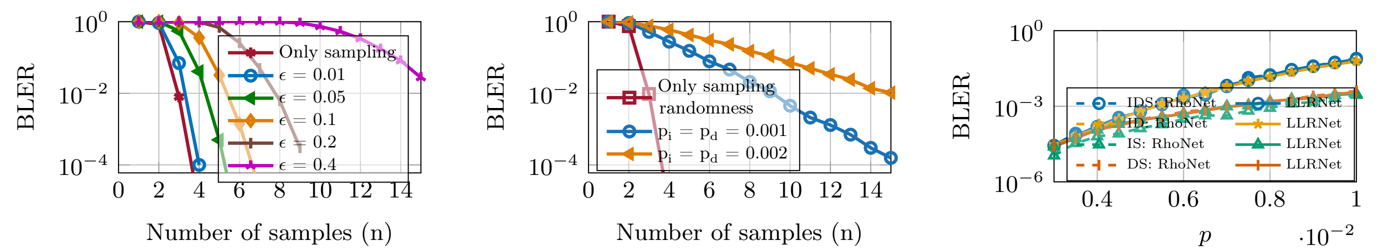
$$p_{\text{ns},i} = (1 - p_s) \left(\frac{(1 - p_i - p_d)^2}{(1 - p_i - p_d)^2 + 2p_i p_d \binom{E}{2}} + \frac{p_i p_d \left(2 \left(\binom{E-i}{2} + \binom{i-1}{2} \right) + E - i \right)}{(1 - p_i - p_d)^2 + 2p_i p_d \binom{E}{2}} \right), \tag{2}$$

where p_i, p_d, and p_s are the insertion, deletion, and substitution probabilities, respectively, and E is the length of the DNA strand after channel coding.

Accordingly, the constellation points are updated as

$$\hat{\boldsymbol{\rho}}_s = \sum_{t=0}^{\hat{n}} \binom{\hat{n}}{t} p_{\text{ns},i}^{\hat{n}-t} (1 - p_{\text{ns},i})^t \left[0.25 \frac{t}{\hat{n}} [1\ 1\ 1\ 1] + \frac{\hat{n} - t}{\hat{n}} \boldsymbol{\rho}_s \right]. \tag{3}$$

The results with analytical LLR update for the substitution-only channel and the insertion–deletion channel are provided in Figs. 1a and 1b, respectively. Furthermore, to address the limitations of analytical calculation, we further propose two learning-enhanced receiver architectures for composite DNA data storage systems: 1)RhoNet, a learning-assisted model-based approach that updates constellation points prior to analytical LLR computation; 2) LLRNet, which performs direct LLR estimation for composite letters, thereby bridging model-based and data-driven methodologies. The results are given in Fig. 1c, employing existing rate-0.5 LDPC codes with composite letter mapping for $L = 3$.



(a) Substitution channel with $\epsilon \in \{0.01, 0.05, 0.1, 0.2, 0.4\}$.

(b) ID channel with $p_i = p_d \in \{0.001, 0.002\}$.

(c) IDS/ID/IS/DS channels with RhoNet and LLRNet with $n = 14$.

[1] B. Tegin and T. M. Duman, "Robust composite DNA storage under sampling randomness, substitution, and insertion-deletion errors," 2026, https://arxiv.org/abs/2602.11951 *(Accepted for presentation in IEEE ICC 2026)*.