DNA-MGC+: A Codec for Reliable and Efficient DNA Data Storage

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Efficient and reliable data retrieval remains a major challenge in DNA data storage due to the inherent noisiness of the underlying biochemical processes, which lead to both base-level errors and sequence-level dropouts. We introduce DNA-MGC+ [1], a novel DNA storage codec designed to enable reliable and efficient data retrieval in the presence of insertion, deletion, and substitution (IDS) errors as well as dropouts. DNA-MGC+ combines an inner coding layer based on the Marker Guess & Check Plus (MGC+) code [2] for correcting IDS errors with an outer Reed-Solomon code that recovers from sequence dropouts and corrects residual errors.

We first evaluate the performance of DNA-MGC+ through extensive *in silico* simulations against six representative codecs from the literature. The results show that DNA-MGC+ achieves simultaneous gains across several key performance metrics under explicit reliability constraints, including sequencing depth requirements, read cost, decoding time, and error-correction capability. Notably, when paired with strong clustering and alignment tools, DNA-MGC+ enables reliable decoding under IDS error rates of up to 24%, as illustrated in Fig. 1a.

We further evaluate the performance of DNA-MGC+ through an *in vitro* experiment in which sequences encoded using multiple codec configurations were combined in a single oligonucleotide pool. Specifically, a 24-KB compressed file was encoded into oligonucleotides of length 170 bases using two configurations of DNA-MGC+: design A (1.03 bits/nt) and design B (0.71 bits/nt); as well as two codecs from the literature: DNA-Aeon [3] (1 bit/nt) and HEDGES [4] (0.61 bits/nt). The oligonucleotide pool was ordered from GenScript (electrochemical synthesis) and sequenced using both Illumina and Oxford Nanopore platforms, with multiple basecalling algorithms evaluated for the Nanopore data. The results in Fig. 1b show that, across all sequencing and basecalling setups, DNA-MGC+ consistently outperforms both DNA-Aeon and HEDGES in terms of the minimum sequencing depth required for reliable decoding, achieving depths below 3x under both Illumina and Nanopore sequencing.

Importantly, DNA-MGC+ achieves comparable sequencing depth requirements under both Illumina and Nanopore sequencing, despite the higher error rate of the latter. This stability can be attributed to the strong IDS error-correction capability of DNA-MGC+, which allows the decoder to compensate for elevated IDS error rates while preserving overall performance. In contrast, DNA-Aeon performs significantly better under Illumina sequencing than under Nanopore sequencing, indicating greater sensitivity to IDS errors. Notably, DNA-MGC+ achieves these performance levels without imposing any biochemical constraint on the sequence content (e.g., homopolymer length or GC content).

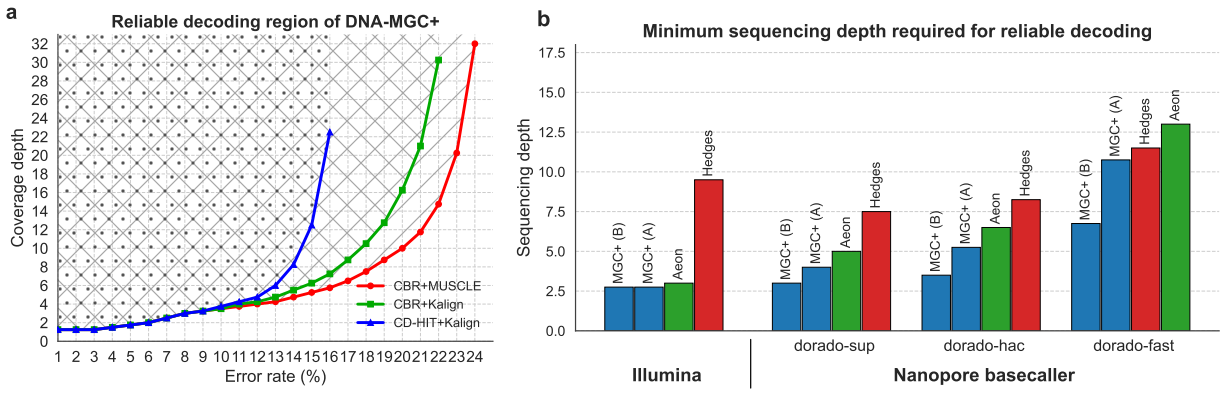

Figure 1: Performance of DNA-MGC+ under *in silico* and *in vitro* settings. (a) *In silico*: reliable decoding region of MGC+ under different clustering and alignment algorithms. (b) *In vitro*: minimum sequencing depth (estimated via progressive read downsampling) required by DNA-MGC+ and comparison codecs for reliable decoding under Illumina and Nanopore sequencing.

References

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