A DNA Data Storage Channel Model Trained on Genomic Data with Nanopore Sequencing

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Abstract

Data storage on DNA molecules is currently a promising technology because of its higher density, increased durability, and reduced energy consumption compared to conventional data storage. The MinION is currently the most used sequencer in DNA storage, however its main drawback is its (roughly) 10% error rate, which can be potentially overcome thanks to bioinformatics algorithms and channel coding. These error-correction solutions are usually first evaluated with numerical simulations (in-silico) and then validated through experiments (in-vitro), the latter still being very costly and time-consuming. State-of-the-art DNA storage channel simulators are based on three different approaches: independent and identically distributed models [1], black-box deep learning techniques [2] and empirical parameters [3]. A comparison of these models with experimental datasets shows that they are not accurate enough when it comes to the MinION [4]. For this reason, we recently introduced [5] a novel DNA storage channel model that relies on Markov models with memory. However, in [5] our model was trained on a *small* amount of experimental data. Although this small dataset leads to a more accurate model than existing solutions, there is still a risk that it introduces undesired bias due to insufficient k-mer coverage. In this work, we introduce a novel methodology to train our channel model on a genomic dataset, which provides a significantly larger amount of data compared to our prior experiments. In particular, we discuss the choice of efficient alignment techniques for genomic data and address the key issue of selecting only relevant genomic reads to accurately train the model. We also present the results of training our model onto the genome of the streptococcus thermophilus bacteria. In future works, we will rely on our channel model to develop efficient and accurate source and channel coding solutions for DNA data storage.

References

[1] W. Song, K. Cai, M. Zhang, and C. Yuen, "Codes With Run-Length and GC-Content Constraints for DNA-Based Data Storage," *IEEE Communications Letters*, vol. 22, no. 10, pp. 2004–2007, 2018.

[2] S. Chandak, J. Neu, K. Tatwawadi, J. Mardia, B. Lau, M. Kubit, R. Hulett, P. Griffin, M. Wootters, T. Weissman, and H. Ji, "Overcoming High Nanopore Basecaller Error Rates for DNA Storage via Basecaller-Decoder Integration and Convolutional Codes," in *ICASSP*, pp. 8822–8826, 2020.

[3] R. R. Wick, "Badread: simulation of error-prone long reads," *Journal of Open Source Software*, vol. 4, no. 36, p. 1316, 2019.

[4] R. Heckel, G. Mikutis, and R. N. Grass, "A Characterization of the DNA Data Storage Channel," *Scientific Reports*, vol. 9, no. 1, p. 9663, 2019.

[5] B. Hamoum, E. Dupraz, L. Conde-Canencia, and D. Lavenier, "Channel Model with Memory for DNA Data Storage with Nanopore Sequencing," in *2021 11th International Symposium on Topics in Coding (ISTC)*, pp. 1–5, 2021.