Paper Discussion Report

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I. Summary

A paper authored by Gunasekaran, et al. (2021) uses deep learning methods to perform classification of viruses from their DNA sequences. Since DNA is composed of strings of nucleotides, the problem amounts to classifying viruses according to samples of nucleotide strings. The authors collect data from the public nucleotide sequence database, The National Centre for Biotechnology Information (NCBI) https://www.ncbi.nlm.nih.gov. They then encode this data using label encoding and kmer encoding. For each encoding type, they run three different deep learning models: CNN, CNN-LSTM, and CNN-Bidirectional-LSTM. The architectures of all three models start with embedding layers, then convolutional layers, then max pooling layers, and then from there diverge to either add LSTM layers or bidirectional LSTM layers before finishing with dense layers and a final output layer. The authors compare all six combinations of the two encoding methods with the three model types using several performance metrics.

II. Problem Statement

All DNA and RNA is composed of a string of nucleotides. A nucleotide refers to one of four compounds for DNA (adenine, cytocine, guanine, thymine) or four compounds for RNA (adenine, cytocine, guanine, uracil). For double-helix DNA or RNA, each nucleotide bonds with one and only one other nucleotide, forming what is called a base pair (fig 1). Since these base pairs are fixed, then, a DNA or RNA sequence can be identified solely by one side of the double helix. Thus, every DNA virus can be identified by a single string of characters drawn from the set $\{A, C, G, T\}$ and every RNA virus can be identified by a string of characters drawn from the set $\{A, C, G, U\}$. The task, then, is to build highly accurate models to classify a virus from its DNA or RNA sample.

III. Related Work

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The authors are graduate students at NCA&T

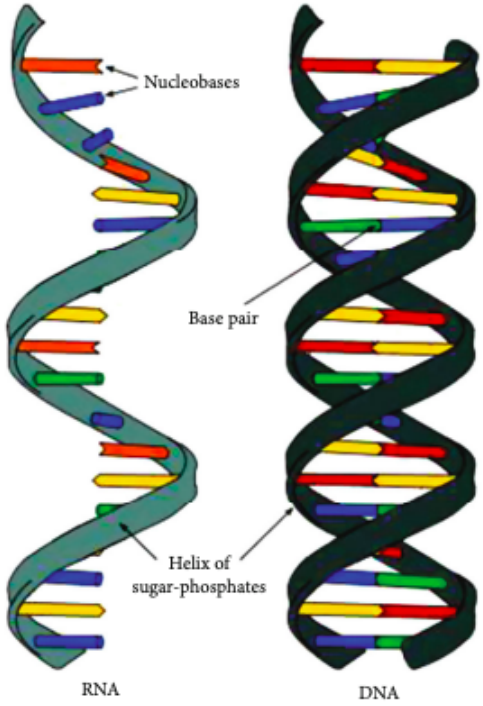

Fig. 1. Single or double-stranded DNA/RNA

A. Current Results on Proposed Problem

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IV. Data Collection

The authors obtain complete genomic sequences from the National Centre for Biotechnology Information (NCBI)

https://www.ncbi.nlm.nih.gov/. Sequence length ranges from 8 to 37971 nucleoids. They collected genomic sequences for six virus classes: COVID, MERS, SARS, Dengue, Hepatitus, and Influenza (Fig 2). Because the population of these viruses were unbalanced–for instance, there were 37272 samples of COVID and only 1418 samples of MERS–the authors opted to use Synthetic Minority Oversampling Technique (SMOTE) to get a more even distribution of all six classes in their dataset.

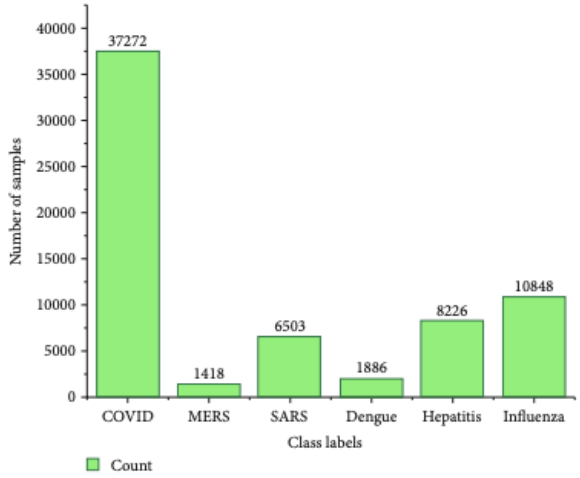

Fig. 2. Samples of virus classes retrieved from NCBI

V. Data Preprocessing

The authors encoded the data in two different formats for comparative analysis. In the first approach, they use label encoding, which replaces each nucleoid by a unique index value, preserving positional information (fig 3). In the second approach, they used kmer encoding, which generates all kmers from a sequence and forms an English-like sentence onto which natural language processing techniques can be applied (fig 4).

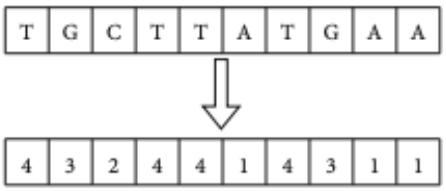

Fig. 3. Label encoding example

Once encoded, in both cases the input data is one-hot encoded and then fed into the first layer of the models, which is an embedding layer.

VI. Proposed Models

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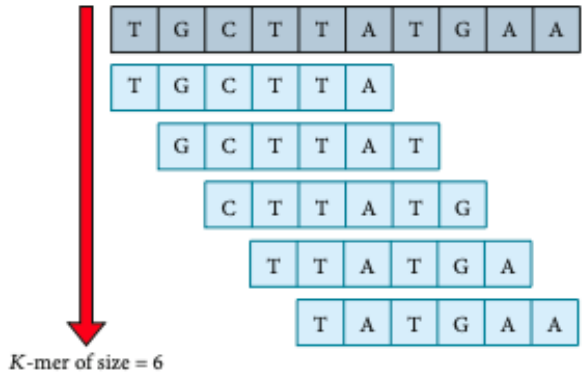

Fig. 4. Kmer encoding example, where k=6

A. Model Architecture

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B. Model Parameters

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VII. Paper Results

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A. Comparison Results

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VIII. Conclusion

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[1] H. Gunasekaran, K. Ramalakshmi, A. Rex Macedo Arokiaraj, S. Deepa Kanmani, C. Venkatesan, and C. Suresh Gnana Dhas. "Analysis of DNA Sequence Classification Using CNN and Hybrid Models." *Computational and mathematical methods in medicine*, 2021.