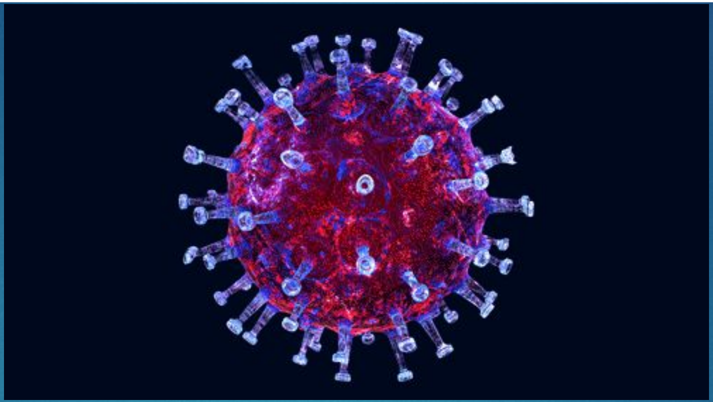

COVID-19 mRNA Vaccine Degradation Prediction

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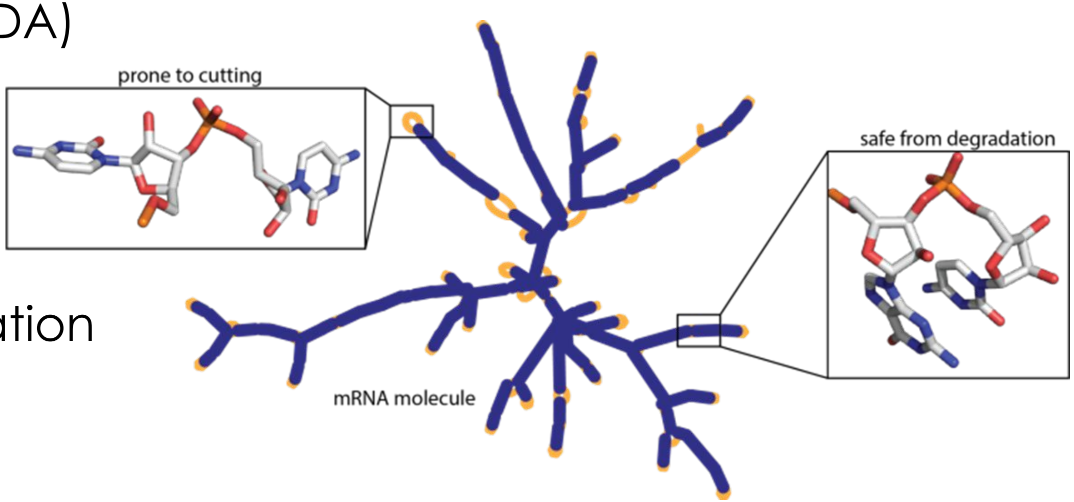


Background

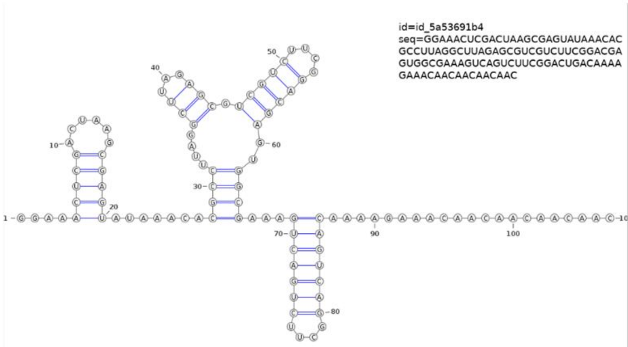
- mRNA (messenger RNA) carry a string of information from DNA. This message will instruct our body to produce the corresponding protein
- Advantages: easy development process, low time required to develop, reduced risk of pre-existing immunity against the vaccine and a less expensive process.
- Disadvantage: mRNA molecules tend to degrade quickly. Therefore, vaccine are kept under intense refrigeration.

Problem Statement

- To help researchers to understand how are the reactivity and degradation rates of mRNA at different conditions.
- To design model which can predict the degradation rates at each base (A, C, G or U) of mRNA molecule
- To develop models and design rules for mRNA degradation to accelerate mRNA vaccine research and deliver a refrigerator-stable vaccine against COVID-19

Dataset

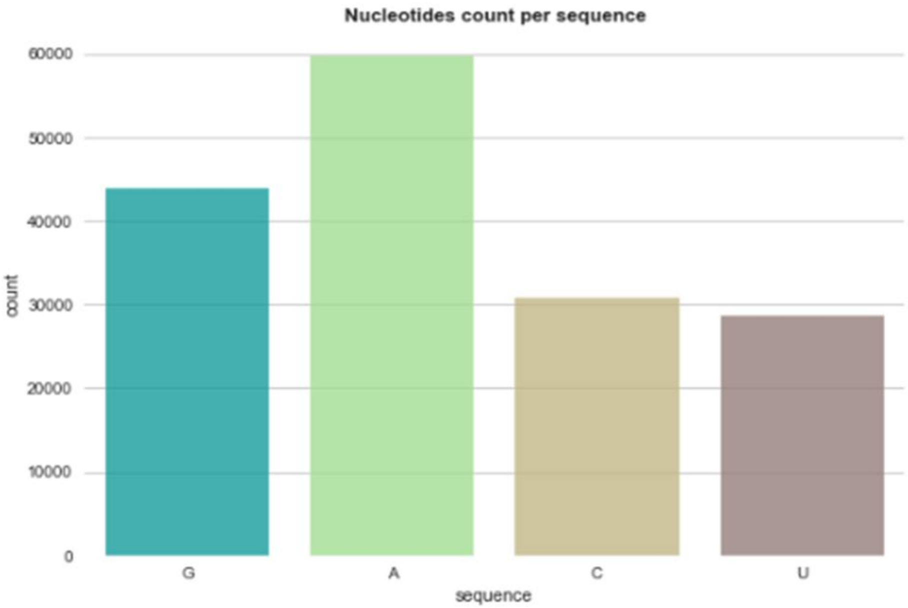
- Data source: Kaggle competition OpenVaccine
- Training Data: 17 columns, 2400 rows
- Testing Data: 5 columns, 3634 rows
- The feature fields (X) are:
- sequence: describe the RNA sequence
- structure: whether a base is paired or unpaired
- predicted_loop_type: the structure context


id=id_5a53691b4
seq=GGAAACUCGACUAAGCGAGUAUAAACAC
GCCUUAGGCUUAGAGCGUCGUCUUCGGACGA
GUGGCGAAAGUCAGUCUUCGGACUGACAAAA
GAAACAACAACAACAAC
1
10
20
30
40
50
60
70
80
90
100

Dataset (continued)

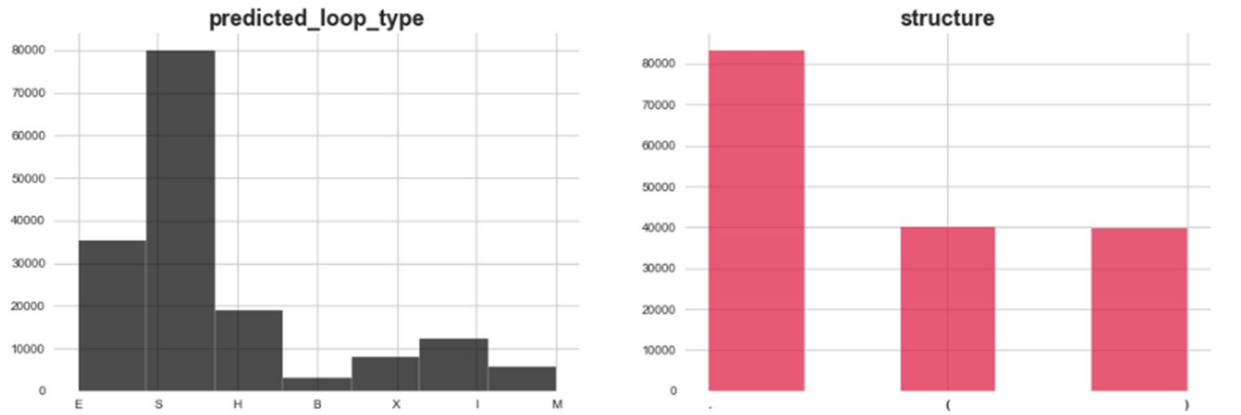
- The predicted fields(y) are:
- reactivity: determine the likely secondary structure of RNA
- deg_Mg_pH10 and deg_pH10: determine the probability of degradation at the base after incubating with/without Mg at pH10
- deg_Mg_50C and deg_50C: determine the probability of degradation at the base after incubating with/without Mg at 50C

Exploratory Data Analysis (EDA)



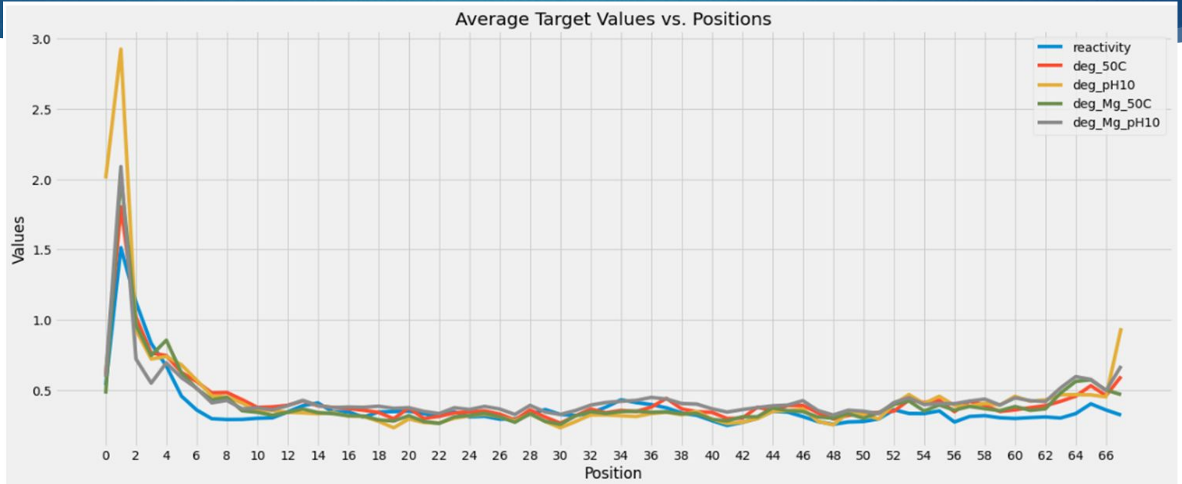
- A and G nucleotides are highly present in the sequences compared to C and U.

EDA (Continued)



- ➢ S (Paired "Stem") is the dominant loop type.
- ➢ E (Dangling End) and H (Hairpin Loop) are also highly represented in comparison with the rest.
- ➢ . structure (unpaired) is dominating, the paired structures) and (are equally represented (sicne their pair together).

EDA (continued)



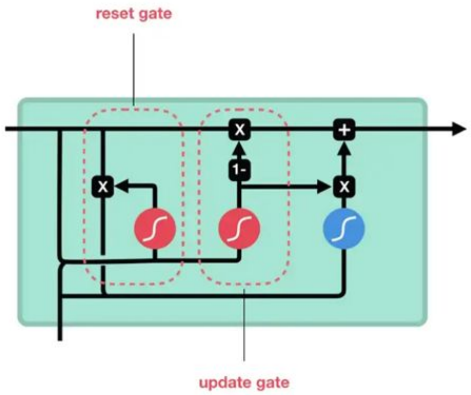
- High values of Degradation & Reactivity at the beginning of the sequence.
- There is high degradation because of pH10 at the beginning but no such pattern for rest of the positions.

Model Selection

- ➢ mRNA is a sequence of bases and each base is dependent on the bases that come before it.
- ➢ RNN suffers from short-term memory and thus often suffer from vanishing gradients problem. One of the solution for this is GRU.
- ➢ Gated Recurrent Unit (GRU) has two gates.

- **Reset gate** determines how to combine new input to previous memory.

- **Update gate** determines how much of the previous state to keep.



Model Pre-processing

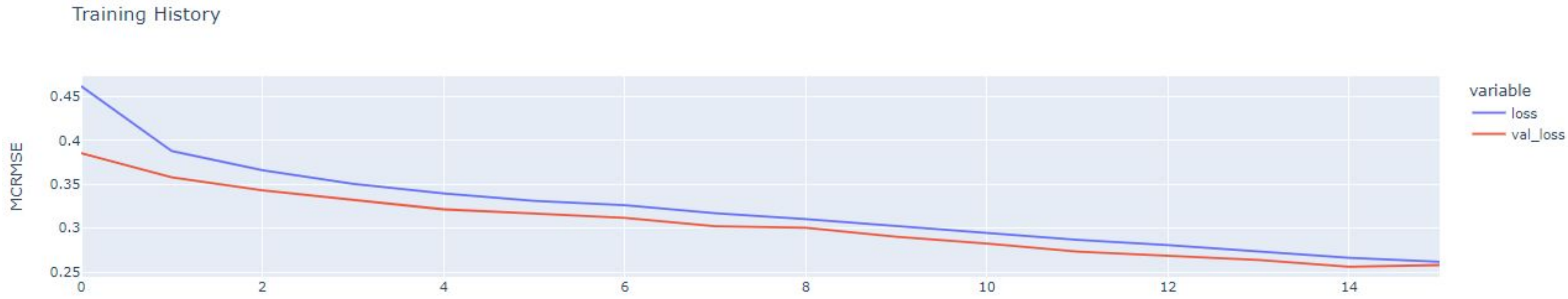
- Train-Test Split: 90% and 10%
- Use stratify to filter the training data with ‘signal_to_noise’ feature to exclude the noisy samples that have values ≤ 1 (outlier)

Modelling

- Embedding layer: The categorical features are encoded by numbers, and then, the features are extracted for learning.
- Hidden layer: Bidirectional GRU layer is used to optimize the results as the data are passed in the forward and backward directions to better capture the information in the sequence data.
- Dense layer: The dense layer has 5 outputs (five target columns of reactivity) and the activation = ‘linear' because the problem is a regression problem.
- loss = 'MCRMSE’: there are multiple outputs that we are trying to predict. The MCRMSE is simply an average across all RMSE values.

Evaluation

- Train and test loss are similar. Loss curve of both train set and test set follow each other closely and decreases overtime. Hence our model is not overfit.
- Loss: 0.2614 vs Val_loss: 0.2578



Conclusion & Recommendation

- GRU model is adopted for model deployment.
- Finding: high values of degradation & reactivity at the beginning of the sequence.
- By combining the finding with the prediction model that we developed, we are able to help researchers in designing more stable covid-19 mRNA vaccine.
- Future work: Tune parameters, Stack bidirectional GRU with bidirectional LSTM, try CNN

Thank you