Software project – BT 3172

RNN for protein classification using amino acid sequence

Documentation

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15214

❖ Introduction

An application of a deep learning model that can predict whether the given protein does the Ubiquitin transferase activity (binary classification) using its fasta file as input.

❖ Features and functionalities

- Take the records in fasta format of which the transferase activity is unknown as a fasta file
- Store the uniportID and amino acid sequence of each fasta record
- Remove the amino acids from original sequence that have less impact of protein
- Vectorization of amino acid sequences to a fixed length
- Dropping the vectorized sequences that are longer than 1000 amino acids
- Perform binary classification using pre-trained model on vectorized sequences
- Output results as a table

❖ Future improvements

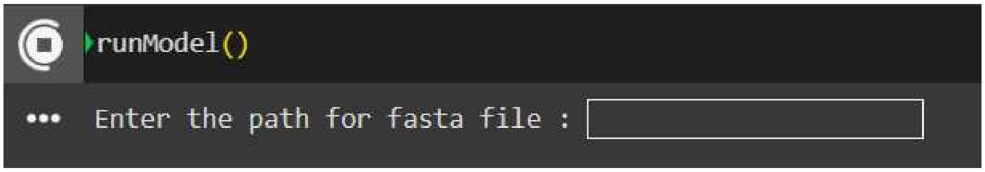
- Improve the accuracy of the model more
- Input protein structure data for better results
- Use transfer learning approach for better training and fine tuning
- Create new features using raw features for dimension reduction
- Use appropriate data augmentation techniques to expand the data set
- Improve the neural network architecture more but without preventing being overfitted
- Develop a GUI to upload the fasta file to make more user friendly
- Develop the model to predict a specific function of a protein out of parent class of proteins of that function to reduce the bias of the model
  E.g.: predict whether the given sequence is doing Ubiquitin transferase activity out of all the known transferase activities

❖ Compatible environment of application

- Tensorflow 2.15.0
- Pandas 2.2.1
- Numpy 1.23.4
- Biopython 1.76
- Keras 3.1.1
- Prettytable 3.10.0

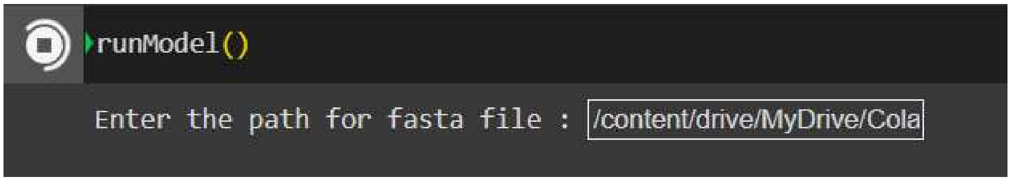
❖ User interface and how to use

- The runModel() method should be called and the prompt will be;



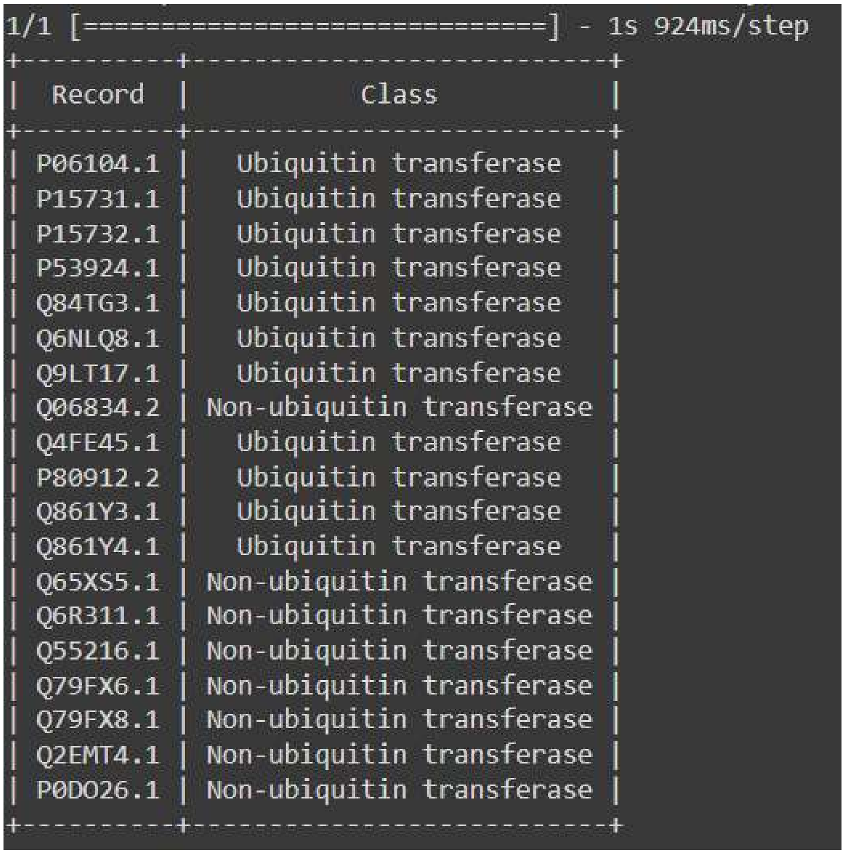
```
runModel()
••• Enter the path for fasta file :
```

- Then the path of the fasta file should pass as the user input and then press Enter



```
runModel()
Enter the path for fasta file : /content/drive/MyDrive/Cola
```

- The predictions will be on a table



```
1/1 [==============================] - 1s 924ms/step
+----------+--------------------------+
|  Record  |          Class           |
+----------+--------------------------+
| P06104.1 |   Ubiquitin transferase  |
| P15731.1 |   Ubiquitin transferase  |
| P15732.1 |   Ubiquitin transferase  |
| P53924.1 |   Ubiquitin transferase  |
| Q84TG3.1 |   Ubiquitin transferase  |
| Q6NLQ8.1 |   Ubiquitin transferase  |
| Q9LT17.1 |   Ubiquitin transferase  |
| Q06834.2 | Non-ubiquitin transferase |
| Q4FE45.1 |   Ubiquitin transferase  |
| P80912.2 |   Ubiquitin transferase  |
| Q861Y3.1 |   Ubiquitin transferase  |
| Q861Y4.1 |   Ubiquitin transferase  |
| Q65XS5.1 | Non-ubiquitin transferase |
| Q6R311.1 | Non-ubiquitin transferase |
| Q55216.1 | Non-ubiquitin transferase |
| Q79FX6.1 | Non-ubiquitin transferase |
| Q79FX8.1 | Non-ubiquitin transferase |
| Q2EMT4.1 | Non-ubiquitin transferase |
| P0DO26.1 | Non-ubiquitin transferase |
+----------+--------------------------+
```

❖ Source code

https://github.com/Sachintha125/RNN-for-proteins