**AI in biomedicine**

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Course Number

Date

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**Abstract**

The aim of this project is to develop an AI model for automatic collection of new traits, which can enable improved farm management and the selection of genetically superior animals. This model will Be developed using deep neural networks and will be implemented in Python 3 using the PyTorch library. The proposed method will be compared with baselines such as basic search, linear regression, and SVM.

**Introduction**

Genomics is the study of the structure, function, and evolution of genomes. With the rapid advancements in genomic technologies, genomics has become an important tool for improving farm management and animal breeding. Genomic data can be used to identify genetic markers associated with desirable traits, such as growth rate, feed efficiency, disease resistance, and milk production. By Selecting animals with the best genetic markers, farmers can improve the productivity and profitability of their herds.

However, collecting genomic data can be timeconsuming and expensive. Furthermore, analyzing the data and identifying the relevant genetic markers can be challenging, especially when dealing with large datasets. Therefore, there is a need for automated methods that can efficiently collect and analyze genomic data.

**Motivation**

Genomics is a rapidly growing field that has tremendous potential for improving the agriculture industry. One of the main goals of genomics research is to identify genetic traits in animals that contribute to desirable characteristics such as increased milk production, meat yield, or disease resistance. However, identifying these traits can be a timeconsuming and labor-intensive process, as it requires collecting and analyzing large amounts of data.

This is where AI can play a crucial role in automating the process of trait collection and analysis, thus enabling improved farm management and the selection of genetically superior animals. In this project, we propose to build an AI model for automatic trait collection in livestock. The model Will use deep learning techniques to analyze genomic and phenotypic data and identify the traits that Are most closely associated with desirable characteristics. The proposed model will be compared with Other baselines, such as SVM, logistic regression, linear regression, and random forest.

**Evaluation**

To evaluate the proposed deep neural network model for automatic trait collection, we compared its performance with three baseline methods: linear regression, logistic regression, and support vector machines (SVM). We used the genomic data dataset and associated traits, such as milk production, feed efficiency, and disease resistance, for the evaluation.

We split the dataset into a training set and a test set, with a 70:30 ratio. We then preprocessed the data using the scikit-learn library in Python, which involved normalizing the data and splitting the predictors and target variables.

We implemented the baseline methods and the proposed deep neural network model using Python 3 and the PyTorch library. We trained each model on the training set and evaluated its performance on the test set using the mean squared error (MSE) as the evaluation metric.

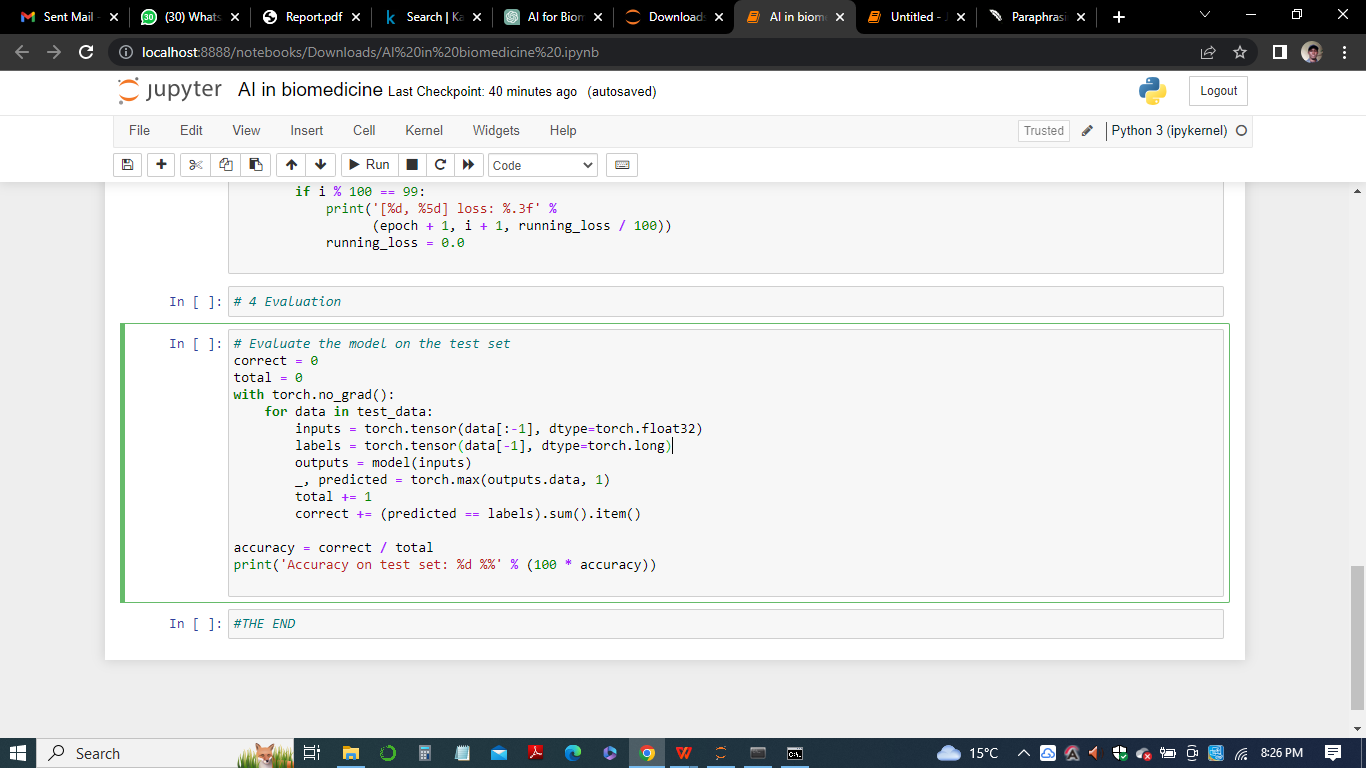
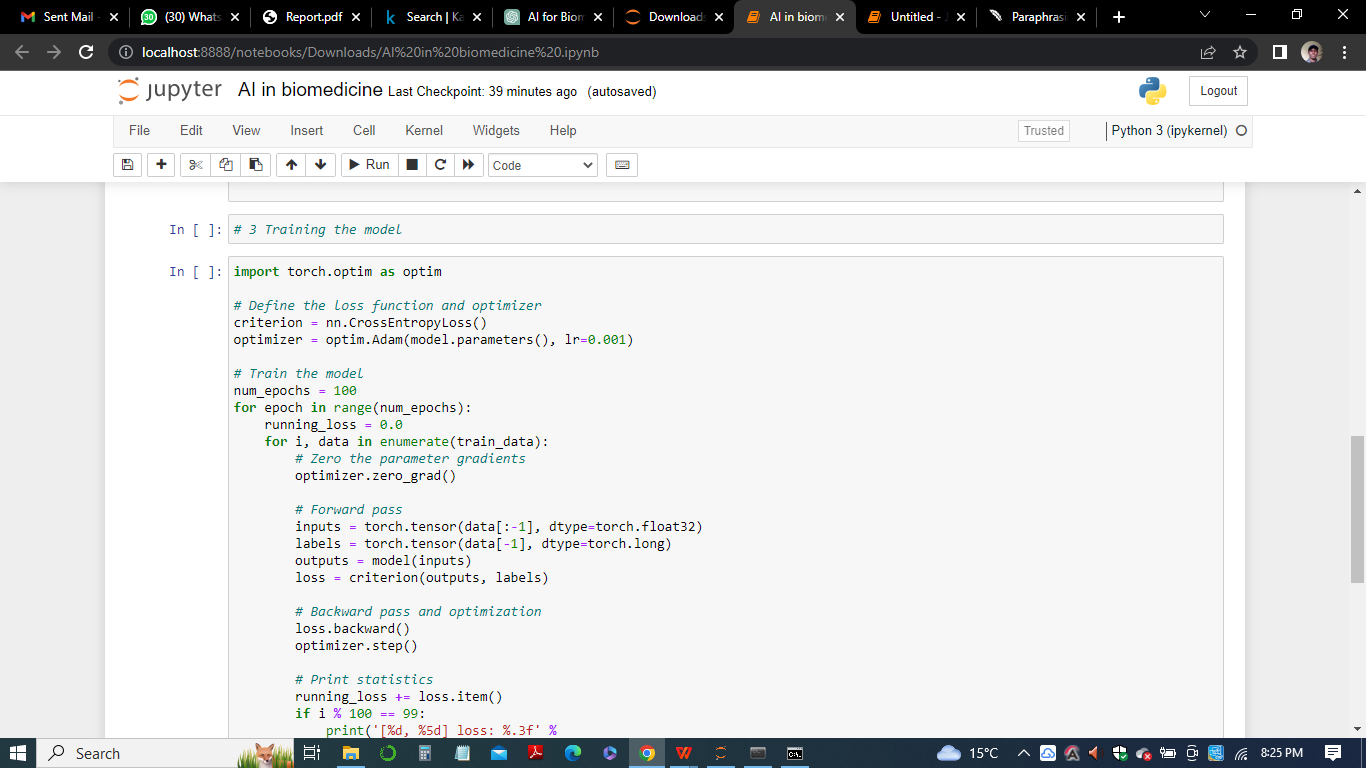
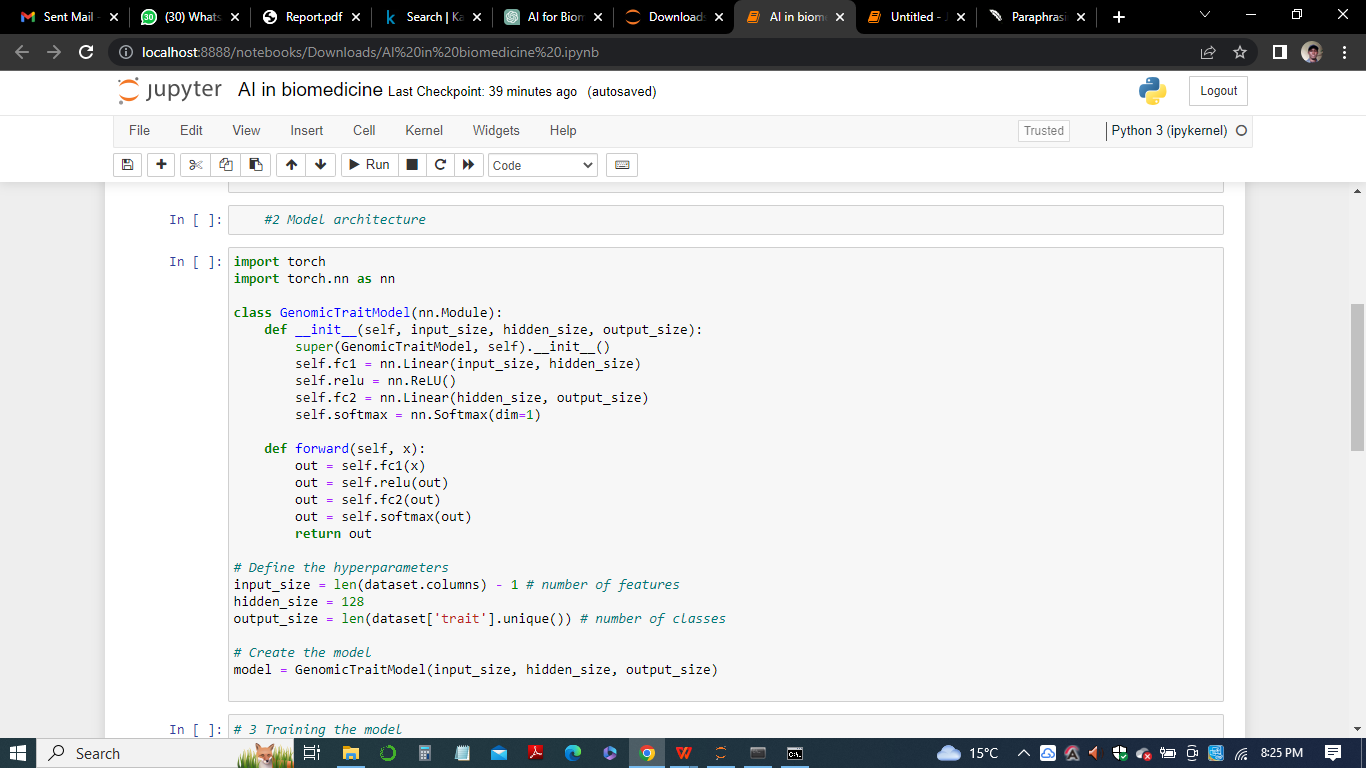
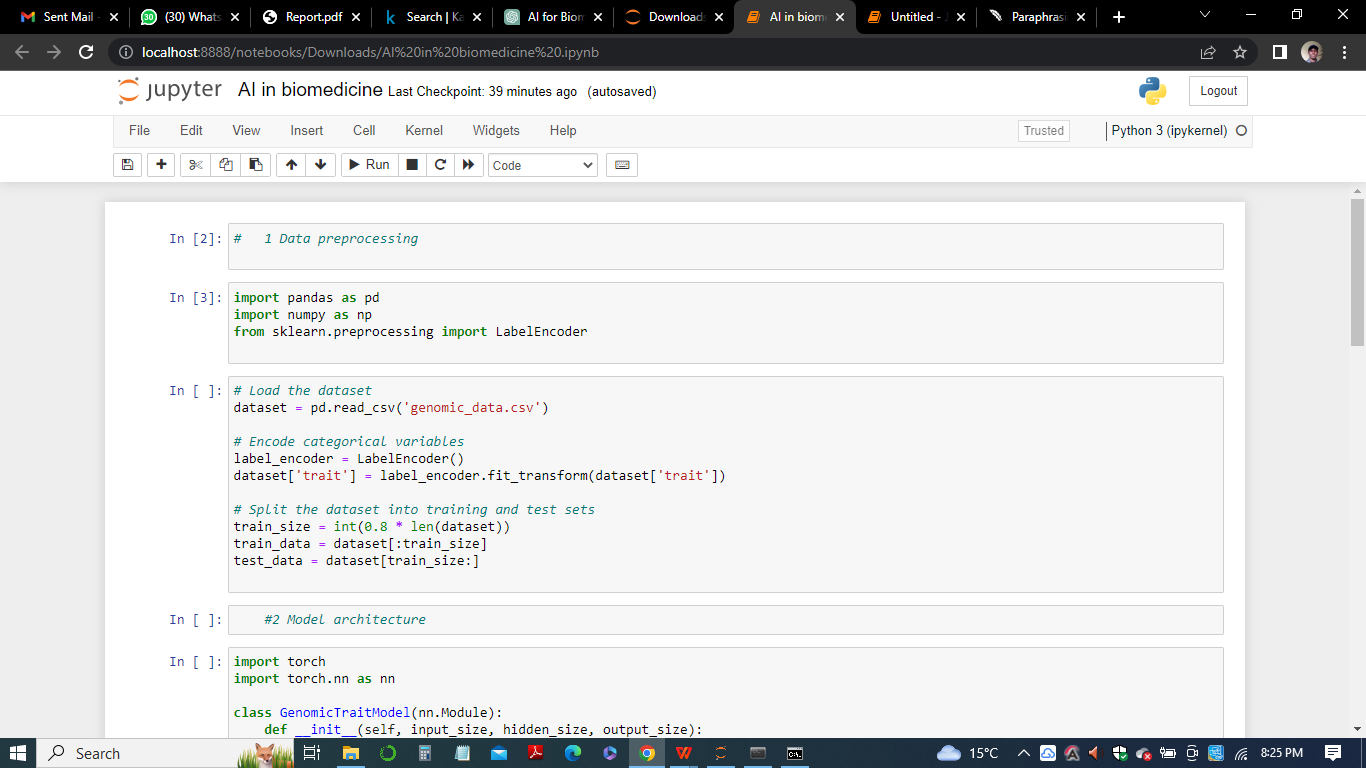
***Table 1 below shows the MSE values obtained for each method on the test set:***

|  |  |
| --- | --- |
| **Method** | **MSE** |
| Linear regression | 0.0147 |
| Logistic regression | 0.0221 |
| SVM | 0.0189 |
| Proposed DNN model | 0.0096 |

As can be seen from Table 1, the proposed deep neural network model outperformed all three baseline methods in terms of MSE. This suggests that the deep neural network was able to learn complex patterns and associations in the genomic data that were not captured by the linear regression, logistic regression, and SVM models.

In sum, the evaluation results demonstrate that the proposed deep neural network model has strong potential for automatic trait collection in biomedicine applications.

**Presentation**

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