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Data Mining

Course Project

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Group 10

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### Report on Collaborative Filtering for Protein-Ligand Activity Prediction

#### Introduction

Collaborative filtering is a popular technique used in recommendation systems to predict user preferences based on past interactions. In this project, we apply collaborative filtering to predict the activities of protein-ligand interactions. The dataset consists of activities measured between various proteins and ligands (ChEMBL IDs). This report details the implementation, evaluation, and results of the collaborative filtering approach using Singular Value Decomposition (SVD) and Stochastic Gradient Descent (SGD) for optimization.

The code for this report can be seen in <https://github.com/bgbigberna/DP_2324/tree/main/Project_RandomForest>

## Dataset

The dataset used for training the model is activity\_train.csv, which contains the following columns:

* ProteinID: Identifier for the protein.
* ChemblID: Identifier for the chemical.
* Activity: Activity value representing the interaction strength between the protein and the chemical.

The test dataset, activity\_test\_blanked.csv, contains the same columns but with some activity values missing, which need to be predicted.

## Data Preparation

The first step involves reading the datasets and creating a matrix where rows represent proteins, columns represent chemicals, and the values represent activity levels. This matrix is then used for matrix factorization. A function create\_rankingMatrix is defined to transform the dataset into a matrix format. Ranking Matrix can be observed below.

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#### Matrix Factorization using SVD

The core of the prediction model involves matrix factorization using SVD. The function make\_init\_PQ initializes the matrices P and Q, which will be factorized iteratively.

A mask matrix is created to identify the locations of the known values, which helps in calculating the error during training.

The function calc\_error computes the Mean Squared Error (MSE) for the predictions.

#### Optimization using Stochastic Gradient Descent (SGD)

SGD is used to iteratively update the matrices P and Q to minimize the prediction error. The function run\_epoch\_reg performs a single epoch of SGD with regularization.

The function RecSys\_SGD runs the SGD algorithm for a specified number of epochs, regularization parameters, and learning rate.

## Training the Model

The model is trained with different learning rates, and the MSE for each epoch is plotted to observe the convergence of the algorithm.

#### Uma imagem com file, Gráfico, diagrama, captura de ecrã Descrição gerada automaticamenteHyperparameter Tuning

Hyperparameters for regularization (Lp and Lq) are tuned by trying different combinations and selecting the one with the lowest MSE.

The best combination found was:

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#### Evaluation and Results

The model was evaluated on a separate test dataset. The test data matrix was created similarly to the training data matrix. The predicted values were compared to the actual values to calculate the MSE.

The optimal regularization parameters were found by iterating through different combinations and selecting the ones that resulted in the lowest MSE.

Below you can observe the image of the activity\_test\_blanked.csv but with the activity already predicted.

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#### Conclusion

The collaborative filtering approach using SVD and SGD successfully predicted protein-ligand activities with a reasonably low MSE. The hyperparameter tuning process was crucial in improving the model's performance. The final model can be used to predict activities for new protein-ligand pairs, aiding in drug discovery and related fields.

Further improvements could involve experimenting with different factorization techniques, incorporating additional features, or using more advanced optimization algorithms.