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CSE 428 Computational Biology

Replacing Graph Inputs with Gemini-Based Image–Text Embeddings for Drug Synergy Prediction in Pisces

In this project, I explored the question, can we replace Pisces original graph-based molecular representations with image-text embeddings generated by Gemini and still get good performance in drug synergy prediction? Pisces normally uses GNNs to process molecular graphs, but I wanted to see if a large vision-language model could do a similar job using 2D molecular images and textual descriptions instead. My prediction was that Gemini was going to underperform compared to GNNs, but I was hoping the results would be at least close.

Pisces is a framework for predicting drug synergy. It takes Drug A, Drug B, and a cell line as input, encoding each drug using a graph neural network (GNN) based on its molecular graph structure. The goal is to predict whether the two drugs will work synergistically in the given cell line. Instead of using graphs, I generated 2D molecular images from SMILES strings using RDKit, then passed those through Gemini Vision to get embeddings. I also experimented with using Gemini to generate natural language descriptions of the molecules and used text embeddings as input. These new representations replaced the original GNN embeddings in Pisces.

The overall training setup was mostly unchanged, using binary classification with BCEWithLogitsLoss. But to improve performance, I made a few key changes. Compared to the evaluation I presented in class, I ended up doing some changes that surprisingly resulted in dramatically better results. First, I added weighted sampling to help with class imbalance, since the dataset has a lot more non-synergistic pairs than synergistic ones. I also applied class weighting using pos_weight in the loss function to penalize mistakes on the minority class more. This helped the model improve recall without sacrificing too much overall performance. I also added gradient clipping and used a learning rate scheduler to stabilize training. Finally, I saved the best model based on F1 score after each epoch so I could avoid overfitting.

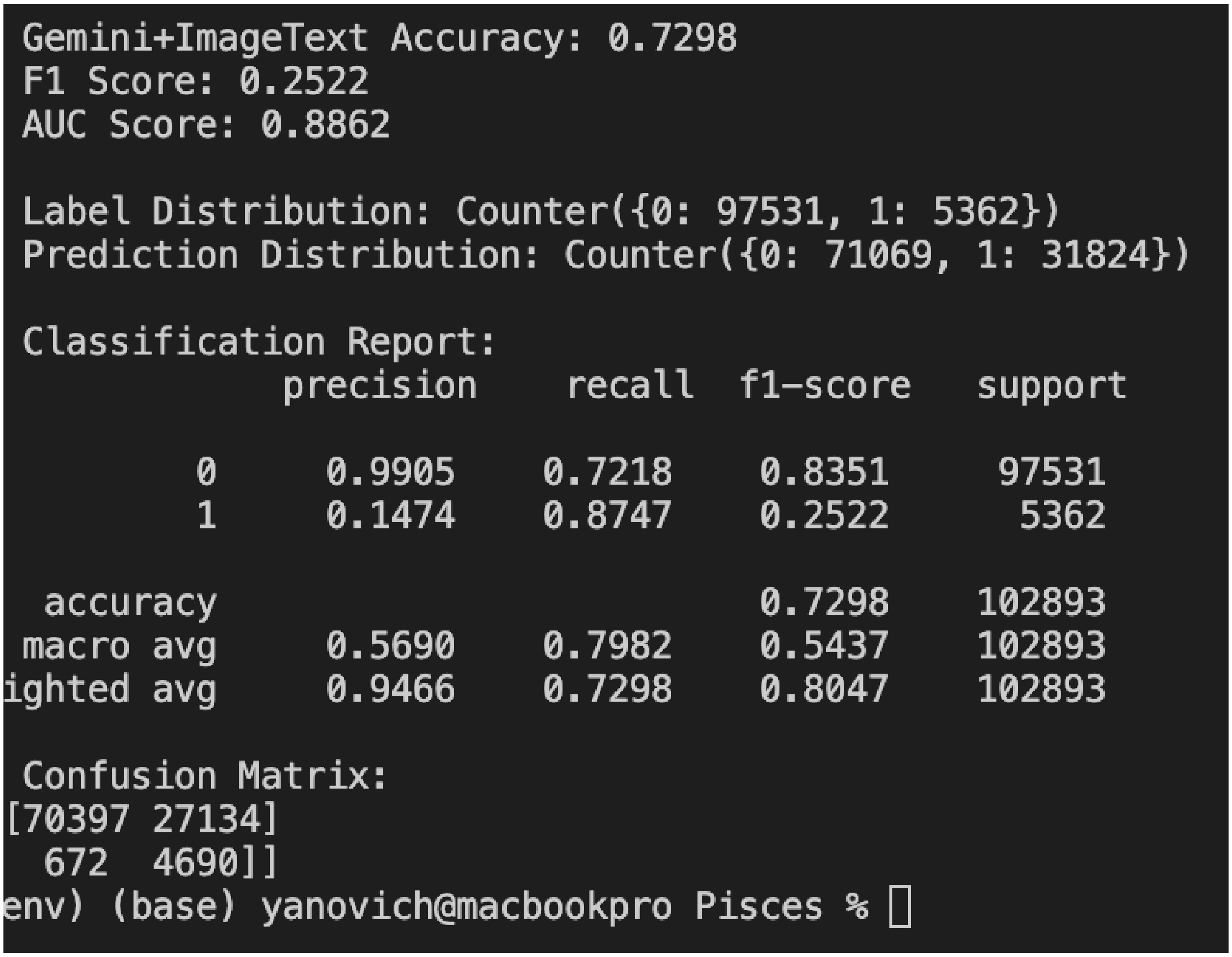
Each epoch took about an hour to train, so I experimented with different epoch ranges. I found that training for 24 epochs caused overfitting, and the sweet spot was around 15–18 epochs. Using the model checkpoint saved at epoch 15, I got my best results.

For my best Gemini run, I got an accuracy of 72.98%, an F1 score of 0.2522, and an AUC of 0.8862. The model did especially well on recall, hitting 87.5% on the synergistic class, which means it was really good at catching true positives, useful if the goal is to discover potentially synergistic drug pairs. The downside was low precision, so there were quite a few false positives, making it less reliable for confident predictions.

Compared to the original Pisces GNN model from the paper, which had an accuracy of around 78–82%, an F1 score between 0.42–0.48, and AUC around 0.85–0.88, the

Gemini-based model still lagged behind in overall performance. But I was honestly surprised that it came relatively close in terms of AUC and did even better than I expected on recall. The GNN version is still more balanced and trustworthy overall, but Gemini has potential as a lightweight alternative, especially since it avoids the complexity of building and processing molecular graphs.

This project showed that with the right training tweaks like class weighting, balanced sampling, and smart optimizer tuning, even a non-graph-based model like Gemini can get surprisingly decent results on drug synergy prediction. There's still room to improve precision, but overall, it was a fun experiment and a promising step toward making these kinds of models more flexible. Following the class presentation I looked at ways I could try to even come closer to pisces original results and I tried with just training it more with 24 epoch but that got me way worse results so I tried looking in ways I could try and just improve the way the model is trained and to my surprise it worked



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 Gemini+ImageText Accuracy: 0.7298
 F1 Score: 0.2522
 AUC Score: 0.8862

 Label Distribution: Counter({0: 97531, 1: 5362})
 Prediction Distribution: Counter({0: 71069, 1: 31824})

 Classification Report:
             precision    recall  f1-score   support

         0     0.9905    0.7218    0.8351     97531
         1     0.1474    0.8747    0.2522      5362

  accuracy                         0.7298    102893
 macro avg     0.5690    0.7982    0.5437    102893
ighted avg     0.9466    0.7298    0.8047    102893

 Confusion Matrix:
[70397 27134]
  672  4690]]
env) (base) yanovich@macbookpro Pisces %
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