

CATSyn: Predicting Synergistic Drug Combinations through Context-Aware Heterogeneous Graph Convolution Model Supplementary Materials

1 Classification Results

The task of drug synergy prediction can not only be formulated as a regression task to predict synergy scores but also as a classification task to predict synergy categories. Specifically, it involves classifying drug combinations into one of three categories: synergistic, additive, or antagonistic. This classification approach is applicable in certain scenarios, and we conducted experiments to evaluate its performance. Following the threshold settings for synergy scores proposed by MGAE, combinations with synergy scores below 0 were classified as antagonistic, scores between 0 and 30 as additive, and scores above 30 as synergistic. Experiments were conducted using the O’Neil dataset.

Table 1 and 2 shows the results of the classification task. In the classification task, CATSyn again demonstrates superior performance in comparison with the baseline models. It obtains remarkable scores across several key metrics under the 10-fold random CV setting. In particular, CATSyn achieves the highest AUC with an outstanding score of 0.96, indicating its exceptional ability in distinguishing between synergistic and non-synergistic drug pairs. Similar performance is also observed in terms of AUPR, where CATSyn achieves the highest score of 0.68, suggesting its superior balance between precision and recall in synergy prediction. The results underscore our method’s robustness and reliability on the classification task of drug synergies, highlighting its potential as a powerful tool in the domain of drug interaction analysis. This is likely due to CATSyn’s comprehensive approach in embedding drug dynamically based on cell line features, enhancing both the accuracy and the generalizability of the predictions.

Table 1: The Classification Performance on The O’Neil dataset Using Four Scores Under the 10-fold random CV Setting

Method	AUC	AUPR	ACC	Kappa
Loewe				
DeepSynergy	0.90	0.60	0.93	0.56
Matchmaker	0.91	0.61	0.93	0.56
TranSynergy	0.89	0.58	0.93	0.48
Hypergraph	0.92	0.63	0.93	0.57
MGAE-DC	0.94	0.67	0.95	0.61
CATSyn (ours)	0.95	0.71	0.95	0.65
Bliss				
DeepSynergy	0.90	0.71	0.86	0.61
Matchmaker	0.92	0.73	0.87	0.63
TranSynergy	0.90	0.71	0.87	0.66
Hypergraph	0.91	0.77	0.88	0.68
MGAE-DC	0.92	0.77	0.88	0.68
CATSyn (ours)	0.93	0.84	0.87	0.69
ZIP				
DeepSynergy	0.88	0.69	0.86	0.59
Matchmaker	0.90	0.71	0.86	0.61
TranSynergy	0.90	0.71	0.86	0.58
Hypergraph	0.91	0.74	0.87	0.63
MGAE-DC	0.92	0.76	0.88	0.63
CATSyn (ours)	0.92	0.77	0.88	0.66
HSA				
DeepSynergy	0.91	0.77	0.84	0.67
Matchmaker	0.91	0.78	0.84	0.67
TranSynergy	0.91	0.78	0.85	0.68
Hypergraph	0.92	0.83	0.85	0.70
MGAE-DC	0.93	0.85	0.86	0.71
CATSyn (ours)	0.93	0.86	0.86	0.71

Table 2: The Classification Performance on The NCI-ALMANAC dataset Using Four Scores Under the 10-fold random CV Setting

Method	AUC	AUPR	ACC	Kappa
Loewe				
DeepSynergy	0.93	0.60	0.94	0.57
Matchmaker	0.92	0.60	0.94	0.57
TranSynergy	0.90	0.61	0.95	0.58
Hypergraph	0.94	0.62	0.96	0.58
MGAE-DC	0.95	0.66	0.97	0.61
CATSyn (ours)	0.96	0.65	0.97	0.64
Bliss				
DeepSynergy	0.93	0.72	0.90	0.62
Matchmaker	0.93	0.73	0.91	0.61
TranSynergy	0.93	0.72	0.91	0.63
Hypergraph	0.93	0.76	0.92	0.66
MGAE-DC	0.94	0.78	0.93	0.68
CATSyn (ours)	0.96	0.80	0.93	0.69
ZIP				
DeepSynergy	0.89	0.71	0.89	0.62
Matchmaker	0.89	0.72	0.90	0.62
TranSynergy	0.90	0.72	0.91	0.63
Hypergraph	0.92	0.76	0.93	0.65
MGAE-DC	0.93	0.77	0.93	0.65
CATSyn (ours)	0.94	0.78	0.94	0.65
HSA				
DeepSynergy	0.92	0.80	0.86	0.66
Matchmaker	0.93	0.81	0.86	0.67
TranSynergy	0.93	0.82	0.86	0.68
Hypergraph	0.93	0.84	0.87	0.70
MGAE-DC	0.94	0.86	0.87	0.70
CATSyn (ours)	0.94	0.86	0.87	0.70