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CLIP2LE: A LABEL ENHANCEMENT FAIR REPRESEN-TATION METHOD VIA CLIP

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ABSTRACT

Label enhancement is a novel label shift strategy that aims to integrate the feature space with the logical label space to obtain a high-quality label distribution. This label distribution can serve as a soft target for algorithmic learning, akin to label smoothing, thereby enhancing the performance of various learning paradigms including multi-label learning, single positive label learning, and partial-label learning. However, limited by dataset type and annotation inaccuracy, the same label enhancement algorithm on different datasets struggles to achieve consistent performance, for reasons derived from the following two insights: 1) Differential Contribution of Feature Space and Logical Label Space: The feature space and logical label space of different datasets contribute differently to generating an accurate label distribution; 2) Presence of Noise and Incorrect Labels: Some datasets contain noise and inaccurately labeled samples, leading to divergent outputs for similar inputs. To address these challenges, we propose leveraging CLIP (Contrastive Language-Image Pre-training) as a foundational strategy, treating the feature space and the logical label space as two distinct modalities. By recoding these modalities before applying the label enhancement algorithm, we aim to achieve a fair and robust representation. In addition, we further explained the reasonableness of our motives in the discussion session. Extensive experimental results demonstrate the effectiveness of our approach to help existing label enhancement algorithms improve their performance on several benchmarks.

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1 INTRODUCTION

033 Currently, improving the performance of multi-label learning algorithms [30], single positive label 034 learning [26] and partial-label learning [29] by using the label shift become a common means, which is represented by the label enhancement method [21, 25]. Label enhancement (LE) employs both the feature space of the samples and the logical label space to generate a high-quality label distribution [7], 037 which is then enforced as a regularization term on a variety of learning paradigms (see Figure 1(a)). Despite impressive achievements, current LE algorithms have yet to deliver consistent performance across various benchmarks. Regarding this issue, we introduce two insights: 1) Many LE algorithms for label distribution generation assume equal importance between the feature space and the logical 040 label space, suggesting they make an equivalent impact. Indeed, the contribution of their features is 041 not fair. 2) Some LE datasets include noisy and inaccurate labels, potentially resulting in significantly 042 varied outputs for analogous inputs. 043

For the first insight, we give statistical evidence (see Figure 1(b)) that the difficulty of projecting the 044 feature space to the label distribution and the logical label space to the label distribution is different 045 on multiple benchmarks. Note that not in all datasets, logical label space moves to label distribution 046 space at the least cost. Here, the evaluated method considers the magnitude of the energy [11] of 047 the feature space X and the logical label space L projected to the label distribution space D with the 048 help of the matrix W, i.e., the matrix energy of W (the sum of the product of the matrix eigenvalues 049 and eigenvectors¹). W can be regarded as a cost matrix, and its higher energy indicates that the 050 projection of the matrix is more difficult, that is, the original matrix is further away from the target 051 matrix. Fig. 1(b) illustrates that the challenge of transforming logical labels \rightarrow label distributionis 052 significantly lower than that of feature space \rightarrow label distribution across the majority of datasets.

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¹https://wikiless.org/wiki/Eigenvalues_and_eigenvectors



Figure 1: This figure demonstrates the role of the label enhancement paradigm and also shows our motivation for why it is necessary to re-represent information from the feature space and the logical label space.

Current LE algorithms [6, 12, 13, 15, 22, 24, 27, 32] overlook this distinction. Indeed, this oversight often results in these algorithms generating label distributions that are biased towards either the feature space or the logical label space, which hinders their ability to perform universally well across various benchmark datasets (particularly when the feature space transformation is less complex). For the second insight, there is already a large body of literature [10, 14, 33, 34] supporting that these datasets contain noise and incorrect labels. These works primarily address the issue by identifying and tolerating noisy data in the label distribution space, without considering the constraint of similar feature space inputs on the similarity of outputs in the label distribution space.

To address the challenges posed by the above two insights, we propose in this paper an LE framework based on CLIP (Contrastive Language-Image Pre-training) [20] alignment. First, we develop a 081 pre-processing algorithm that harmonizes the transformation difficulty between the feature space and the logical label space, with the assistance of CLIP. In this context, we consider feature space vectors 083 and logical label vectors as distinct modalities that convey identical semantics, namely, the label 084 distribution to be derived. Significantly, this paper ensures that the dimensionality of the transformed 085 feature vectors aligns with that of the transformed logical label vectors. Second, to mitigate the impact of noisy data, we use the similarity matrix generated during the pre-training process of CLIP 087 for constraints i.e. by optimal transmission² [23] to move its distribution closer to the distribution of 880 the label distribution.

Based on the proposed novel LE framework, our contribution includes:

i) We propose a pre-processing algorithm that ensures fairness in the representation of the recoded feature space and the logical labeling space to help downstream LE algorithms achieve better performance.

We propose a novel regularization method to constrain the modeling process of CLIP to ensure
 that the semantic information of new features is not corrupted. Extensive experimental results and
 discussions demonstrate the importance of fairness representation, and there is also a significant
 performance improvement for downstream LE algorithms.

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2 CLIP2LE FRAMEWORK

2.1 Assumptions and notation

The concept of LE is first derived from label distribution learning [24]. The purpose of LE is to recover label distributions from logical labels as a novel type of supervised information that serves various learning paradigms. Currently, most LE algorithms can be divided into two categories, one is algorithmic adaptation [6, 7, 13] and the other is specialized algorithms [16, 22, 24]. These algorithms not only achieved SOTA results on label distribution learning, but also achieved impressive perfor-

²https://github.com/PythonOT/POT



Figure 2: This figure shows the framework of our method. Our method has two main components: 120 first, it starts with the feature space and the logical label space for contrast learning; second, the 121 coding distributions of the feature space and the coding distributions of the logical label space are both 122 close to the uniform distribution. The OT in the figure denotes the optimal transmission algorithm; the 123 aim is to have relatively smooth features after encoding. \mathbf{W}_i and \mathbf{W}_t denote the prototype matrices 124 which ensure that the output signals are in the same semantic space. 125

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mance on multi-label learning [30], partial-label learning [29], and single positive-label learning [26]. Nonetheless, the existence of biased characterizations and noise within these benchmarks prevents LE 128 algorithms from achieving consistently superior performance. We introduce a novel pre-processing 129 framework, termed CLIP2LE, designed to supply high-quality features to subsequent LE algorithms. 130

Assumptions. We have three critical assumptions for a CLIP2LE framework (see Figure 2). 131

a) We recognize the feature space and the logical label space as inherently misaligned modalities, 132 which can be reconciled using the assistance of CLIP. Moreover, fortunately, a large part of these 133 benchmarks are tabular data, and the model can gobble up a large number of samples in a single 134 batch, which ensures the performance of CLIP.

135 b) We identify a portion of the dataset that has noise and incorrect labels in the logical label space, 136 which may lead to instability in the output of the LE model, and CLIP ensures that similar inputs 137 generate similar outputs.

138 (c) Since both the feature space and the logical label space point to the semantics of the label 139 distribution, their similarity should also be consistent with the distributional morphology of the label 140 distribution. Here, we use optimal transmission to ensure the robustness of CLIP modeling.

141 Notation. Given a particular instance, the goal of our method is to learn the degree to which each 142 label describes that instance. Input matrix $\mathcal{X} \in \mathbb{R}^{M \times N}$, where M is the number of instances and 143 N is the dimension of features. x_i is the *i*-th instance in the dataset. The label distribution space is defined as $\mathcal{Y} \in \mathbb{R}^{M \times L}$, where y_j represents the *j*-th label. For each instance x_i , we define its 144 label distribution $\mathcal{D}_i = \{d_{x_i}^{y_1}, d_{x_i}^{y_2}, ..., d_{x_i}^{y_L}\}$, where $d_{x_i}^{y_j}$ is the description degree of the label y_j for 145 the instance x_i . The $d_{x_i}^{y_j}$ is constrained by $d_{x_i}^{y_j} \in [0, 1]$ and $\sum_{j=1}^{L} d_{x_i}^{y_j} = 1$. The label distribution that is predicted by the model is defined as $\mathcal{L}_i = \{l_{x_i}^{y_1}, l_{x_i}^{y_2}, ..., l_{x_i}^{y_L}\}$. The logical label is defined as 146 147 148 $\mathcal{G}_i = \{g_{x_i}^{y_1}, g_{x_i}^{y_2}, ..., g_{x_i}^{y_L}\}, \text{ where } g_{x_i}^{y_j} \in \{0, 1\}.$ 149

150 2.2 Method 151

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152 First, given a pairwise feature space vector x_i and a logical labeling vector \mathcal{G}_i , we input x_i and \mathcal{G}_i into 153 the feature encoder FE and the logical label encoder LLE, respectively, to obtain the re-encoded 154 features f_i and l_i . Here, both FE and LLE use MLP as an encoder where the activation function 155 uses ReLU. Next, we conduct joint embedding and regularization for features f_i and l_i . This step can 156 be written as follows:

$$\mathbf{I}_{e} = \text{Normalize}(\mathbf{f}_{i}\mathbf{W}_{i}), \mathbf{T}_{e} = \text{Normalize}(\mathbf{l}_{i}\mathbf{W}_{t}), \tag{1}$$

158 where \mathbf{W}_i and \mathbf{W}_t denote affine matrices (prototype matrix) and Normalize denotes normalization. 159 Finally, we compute the cosine similarity between features (I_e, T_e) and perform a contrast loss 160 function. This step can be written as follows: 161

$$logits = \mathbf{I}_e \mathbf{T}_e^{\mathrm{T}} \times \mathbf{E}^t, \tag{2}$$

loss = (CEL(logits, dim=0) + CEL(logits, dim=1))/2,(3)

where CEL denotes the cross-entropy function, t denotes temperature parameters for index E, and dim=0 and dim=1 denote computations done in a given dimension, respectively.

Feature distribution homogenization. So far, we expect features f_i and l_i to be smooth, which facilitates fast convergence of the downstream LE model during training. In general, we can use distribution measure formulas such as KL dispersion, J dispersion, etc., however, they are computationally expensive. Here, we use optimal transmission (OT) to make the distributions of f_i and l_i close to the uniform distribution at a small cost. Specifically, first, we need to compute the migration cost of these two distributions; in this paper, we use earth mover's distance (EMD)³. Next, we use Sinkhorn [5] to optimize this transmission cost. This step can be written as follows:

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Sinkhorn
$$\rightarrow \text{EMD}(\mathbf{f}_i, \mathcal{U}), \text{Sinkhorn} \rightarrow \text{EMD}(\mathbf{l}_i, \mathcal{U}),$$
 (4)

where Sinkhorn denotes the optimization method, \mathcal{U} denotes uniform distribution, and here the hyperparameter we set to the 10^{-3} .

High-quality feature generation. After N iterations we obtain high quality \mathbf{f}_i and \mathbf{l}_i . For the range of values of \mathbf{f}_i and \mathbf{l}_i , we use Tanh for constraints to avoid outliers. These two new features are used in downstream LE algorithms for inference to obtain accurate label distributions \mathcal{L}_i .

180 Logical label vectors with the help of TableGPT. Predictably, we struggle with treating the logical 181 label vector as a modality, due to the fact that the logical label vector contains less information and is sparser compared to the feature space \mathcal{X} . Simply increasing the neurons and depth of the LLE 182 can lead to pre-training that is difficult to converge and an imbalance between LLE and FE exists. 183 To address this problem, we attempt to introduce a prior on the large model (TableGPT) to precode 184 the logistic label vectors. We input it as tabular data into TableGPT's Table Encode to obtain a 185 high-quality representation. It is worth noting that we are frozen the parameters of TableGPT during the training process. We also try to input the logic label vectors into BERT as text, but it doesn't work 187 well. Here, we extracted the 256-dimensional vectors of the middle layer in Table Encoder as new 188 feature inputs to the MLP with only 3 layers. 189

Construction of the prototype matrix W_i and W_t . To make the output space of FE and LLE more compact, we construct a prototype matrix as the projection space. The prototype space consists of a set of representative vectors. Specifically, we begin by splicing the input space \mathcal{X} and the logical label space G into a matrix $\mathbf{Y} \in \mathbb{R}^{M \times (N+L)}$. Next, we use the nearest neighbor algorithm to obtain L clusters, the center of which is the representation vector. Finally, we concatenate these L cluster centers into a matrix $\hat{\mathbf{W}}$ and use PCA to compress it to the required dimensions. The whole step can be written as:

$$\mathbf{W}_{i} = \mathrm{PCA}(\mathrm{CONCAT}(\mathrm{KNN}(\mathrm{SPL}(\mathcal{X}, \mathbf{G})))), \tag{5}$$

where \mathbf{W}_i and \mathbf{W}_t are constructed in the same way.

3 EXPERIMENTS

Extensive experiments are conducted in this section to verify the effectiveness and competitiveness of CLIP2LE. We performed four sets of experiments demonstrating the impact of our approach on downstream LE algorithms, including the impact of our algorithms enforced on LE algorithms on label distribution learning, multi-label learning, partial-label learning, and single positive multi-label learning. In addition, we performed experiments evaluating CLIP2LE's robustness against noise and the effect of other CLIP algorithms (MaskCLIP and MetaCLIP) on the experiments.

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3.1 LE ALGORITHMS ON LABEL DISTRIBUTION LEARNING

Experimental setup. We use 13 real-world datasets [18, 24] for evaluation⁴. Our algorithm serves as a pre-processing algorithm for the 8 LE methods, including FCM [6], KM [13], LP [15], ML [12], GLLE [24], LESC [22], LIB [32], and LEVI [27]. To evaluate the recovery performance, we adopt 6 metrics, namely Chebyshev, Canberra, Clark, Kullback-Leibler, Cosine, and Intersection [7, 22, 24].

²¹⁴ 215

³https://encyclopedia.thefreedictionary.com/Earth+Mover%27s+Distance ⁴http://palm.seu.edu.cn/xgeng/LDL/index.htm

Here, we show only the performance of the metric functions Chebyshev and Clark. The rest is shown in the Supplementary Material.

Metric				Cheb	yshev ↓							Cla	ark↓			
Method	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB
Movie	0.230	0.234	0.161	0.164	0.122	0.121	0.110	0.107	0.859	1.766	0.913	1.140	0.569	0.564	0.551	0.517
SUB-3DFE	0.135	0.238	0.123	0.233	0.126	0.122	0.095	0.094	0.482	1.907	0.580	1.848	0.391	0.378	0.303	0.297
JAFFE	0.132	0.214	0.107	0.186	0.087	0.069	0.075	0.071	0.522	1.874	0.502	1.519	0.377	0.276	0.290	0.262
Yeast-alpha	0.044	0.063	0.040	0.057	0.020	0.015	0.012	0.017	0.821	3.153	1.185	3.088	0.337	0.253	0.319	0.275
Yeast-cdc	0.051	0.076	0.042	0.071	0.022	0.019	0.016	0.017	0.739	2.885	1.014	2.825	0.306	0.251	0.323	0.242
Yeast-cold	0.141	0.252	0.137	0.242	0.066	0.056	0.082	0.054	0.433	1.472	0.503	1.440	0.176	0.152	0.269	0.146
Yeast-diau	0.124	0.152	0.099	0.148	0.053	0.042	0.044	0.049	0.838	1.886	0.788	1.844	0.296	0.224	0.295	0.273
Yeast-dtt	0.097	0.257	0.128	0.244	0.052	0.043	0.084	0.034	0.329	1.477	0.499	1.446	0.143	0.119	0.294	0.092
Yeast-elu	0.052	0.078	0.044	0.072	0.023	0.019	0.017	0.018	0.579	2.768	0.973	2./11	0.295	0.241	0.317	0.224
Yeast-neat	0.109	0.175	0.080	0.105	0.049	0.040	0.052	0.039	0.580	1.802	0.508	1.769	0.213	0.199	0.288	0.105
Veest spo	0.150	0.175	0.090	0.171	0.002	0.000	0.055	0.055	0.320	1.011	0.338	1.708	0.200	0.238	0.277	0.224
Yeast-sopem	0.102	0.408	0.163	0.403	0.099	0.092	0.115	0.070	0.393	1.028	0.274	1.004	0.137	0.135	0.182	0.138
Metric				Cheb	vshev ↓				 			Cla	ark↓			
Ours + Method	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB
Movie	0 202	0.214	0.150	0.162	0.112	0.102	0.100	0.095	0 723	1 500	0.843	0.987	0.500	0 533	0.625	0.401
SUB-3DFE	0.121	0.209	0.104	0.222	0.131	0.100	0.099	0.082	0.481	1.807	0.410	1.222	0.201	0.335	0.312	0.250
JAFFE	0.112	0.198	0.095	0.155	0.090	0.066	0.056	0.069	0.521	1.588	0.487	1.322	0.229	0.256	0.232	0.229
Yeast-alpha	0.032	0.059	0.033	0.050	0.019	0.012	0.010	0.010	0.810	2.998	1.010	3.095	0.320	0.223	0.304	0.224
Yeast-cdc	0.050	0.056	0.041	0.080	0.010	0.018	0.015	0.010	0.539	2.288	0.982	2.547	0.222	0.237	0.310	0.238
Yeast-cold	0.123	0.233	0.106	0.214	0.055	0.051	0.088	0.050	0.399	1.256	0.666	1.425	0.168	0.110	0.260	0.139
Yeast-diau	0.111	0.143	0.095	0.144	0.052	0.041	0.049	0.050	0.776	1.566	0.789	1.654	0.122	0.205	0.300	0.266
Yeast-dtt	0.085	0.220	0.113	0.236	0.046	0.042	0.069	0.031	0.320	1.289	0.490	1.255	0.145	0.118	0.302	0.090
Yeast-elu	0.044	0.065	0.041	0.053	0.020	0.013	0.014	0.015	0.454	2.133	0.965	2.551	0.243	0.240	0.328	0.225
Yeast-heat	0.132	0.105	0.056	0.144	0.041	0.045	0.050	0.035	0.582	1.602	0.556	1.789	0.224	0.190	0.206	0.160
reast-spo	0.129	0.165	0.088	0.105	0.058	0.061	0.056	0.050	0.521	1.800	0.541	1.413	0.260	0.260	0.256	0.220
reast-spop	0.152	0.272	0.110	0.230	0.090	0.091	0.095	0.081	0.390	0.067	0.257	1.000	0.195	0.180	0.211	0.108
reast-sopeill	0.255	0.508	0.150	0.450	0.000	0.000	0.105	0.039	0.421	0.907	0.250	1.000	0.155	0.102	0.150	0.100

Table 1: Recovery results on 13 real-world datasets. \downarrow indicates that "the smaller the better" and \uparrow means that "the larger the better". The following two table blocks represent the 8 LE algorithms using our pre-processing steps. We highlight the best recovery results.

Result. We provide the detailed comparison results on 13 real-world datasets in Table 1. Overall, we found two interesting results: 1) our approach does not allow all algorithms to improve their performance, and 2) our approach is very friendly to non-deep algorithms, especially adaption ones. In addition, for the LIB algorithm, the ability of our method to help it boost is effective, probably due to the fact that the model capacity of LIB reaches its upper limit.

3.2 LE ALGORITHMS ON MULTI-LABEL LEARNING

Experimental setup. In this subsection, the efficiency and the performance of FLEM [31] + our method are evaluated in multiple multi-label learning datasets. All methods are implemented by PyTorch. All the computations are performed on a GPU server with NVIDIA Tesla V100. We use eight datasets, including two text datasets and six image datasets.

Metric				Hamm	ing loss ↓							Rank	ing loss↓			-
Dataset	AAPD	Reuters	VOC07	VOC12	COCO14	COCO17	CUB	NUS	AAPD	Reuters	VOC07	VOC12	COCO14	COCO17	CUB	NUS
FLEM-S	0.0276	0.0040	0.0239	0.0226	0.0191	0.0207	0.0850	0.0138	0.0522	0.0092	0.0194	0.0140	0.0239	0.0286	0.1058	0.0149
FLEM-T	0.0271	0.0040	0.0243	0.0228	0.0192	0.0209	0.0849	0.0139	0.0483	0.0094	0.0199	0.0138	0.0238	0.0286	0.1048	0.0148
FLEM-D	0.0271 0.0040 0.0243 0.0228 0.0192 0.0209 0.0849 0.0271 0.0041 0.0237 0.0231 0.0192 0.0209 0.0848							0.0137	0.0432	0.0091	0.0189	0.0139	0.0231	0.0279	0.1039	0.0139
Metric				Hamm	ing loss ↓							Ranki	ng loss ↓			
Dataset	AAPD	Reuters	VOC07	VOC12	COCO14	COCO17	CUB	NUS	AAPD	Reuters	VOC07	VOC12	COCO14	COCO17	CUB	NUS
FLEM-S + our method	0.0265	0.0038	0.0221	0.0220	0.0190	0.0203	0.0843	0.0139	0.0521	0.0098	0.0156	0.0131	0.0233	0.0285	0.1050	0.0145
FLEM-T + our method	0.0263	0.0043	0.0240	0.0222	0.0190	0.0213	0.0840	0.0135	0.0480	0.0093	0.0193	0.0122	0.0245	0.0283	0.1021	0.0140
FLEM-D + our method	0.0230	0.0033	0.0230	0.0221	0.0196	0.0201	0.0801	0.0133	0.0430	0.0090	0.0185	0.0130	0.0234	0.0278	0.1033	0.0121

Table 2: Recovery results on 8 real-world datasets. \downarrow indicates that "the smaller the better". The following two table blocks represent the 8 LE algorithms using our preprocessing steps.

Result. We provide the detailed comparison results on 8 real-world datasets in Table 2. Overall, we observe that our method does not uniformly enhance the performance of FLEM, particularly in scenarios with a fewer number of labels. Conversely, our approach demonstrates a substantial improvement in cases where there is a higher number of labels.

270 3.3 LE ALGORITHMS ON PARTIAL LABEL LEARNING271

Our method imposes an evaluation on PL-LE [25]. First, our method + PL-LE and PL-LE were
evaluated on 168 UCI data sets [1]. Our method + PL-LE achieves comparable performance against
PL-LE in 92.0% cases (150 out of 168) and 90.1% cases (147 out of 168) respectively. In addition,
PL-LE achieves superior performance against PL-LEAF and PL-ECOC in 8.0% cases (18 out of 168)
and 9.9% cases (21 out of 168) respectively.

Second, our method + PL-LE and PL-LE were evaluated in Real-World Data Sets. On all data sets, our method + PL-LE achieves superior or at least comparable performance against PL-LE. Our method improves 2%, 3.2%, 4.1%, 5.9%, 2.9%, and 3.3% compared to PL-LE on the FG-NET [19], Lost [4], MSRCv2 [17], BirdSong [3], Soccer Player [28], and Yahoo! News [8] dataset, respectively.

3.4 LE ALGORITHMS ON SINGLE-POSITIVE MULTI-LABEL LEARNING

Experimental setup. In the experiments, we adopt twelve widely-used multi-label learning datasets [9], which cover a broad range of cases with diversified multi-label properties. To evaluate the performance of our method + SPMLL [26] methods, we generate the single positive training data by randomly selecting one positive label to keep for each training example in the multi-label learning datasets. For each dataset, we run the comparing methods with 80%/10%/10% train/validation/test split. The validation and test sets are always fully labeled. Five popular multi-label metrics *Ranking* loss, Hamming loss, One-error, Coverage, and Average precision are employed for performance evaluation. Furthermore, for Average precision, the larger the values the better the performance. While for the other four metrics, the *smaller* the values the better the performance.

Result. Our method compared to SPMLL on CAL500, image, scene, yeast, core15k, revl-s1, core116k-s1, delicious, iaprtc12, espgame, mirfickr, tmc2007 dataset improves 3%, 4.1%, 1.0%, 0.92%, 8.9%, 12.6%, 1.1%, -2.1%, 3.9%, 4.4%, 15.8%, 6.6%, respectively, where the negative sign denotes performance degradation.

Metric				Cheb	yshev ↓							Cla	ırk↓			
w/o AS(i) + Method	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB
Movie	0.211	0.223	0.162	0.165	0.110	0.129	0.118	0.098	0.729	1.654	0.855	0.990	0.523	0.546	0.657	0.422
SUB-3DFE	0.120	0.210	0.105	0.228	0.141	0.133	0.102	0.091	0.499	1.944	0.430	1.229	0.221	0.339	0.310	0.290
JAFFE	0.113	0.201	0.123	0.166	0.091	0.063	0.059	0.077	0.543	1.589	0.498	1.400	0.222	0.299	0.243	0.230
Yeast-alpha	0.031	0.069	0.048	0.052	0.033	0.033	0.011	0.011	0.859	2.997	1.163	3.421	0.321	0.220	0.395	0.266
Yeast-cdc	0.059	0.068	0.055	0.093	0.012	0.025	0.033	0.012	0.599	2.489	1.177	2.643	0.221	0.255	0.319	0.256
Yeast-cold	0.124	0.289	0.133	0.225	0.059	0.056	0.087	0.052	0.455	1.432	0.678	1.566	0.232	0.115	0.261	0.144

Table 3: We removed the effect of homogenization of the feature distribution. Recovery results on 6 real-world datasets. \downarrow indicates that "the smaller the better". We highlight the best recovery results.

Metric				Cheb	yshev ↓							Cla	ırk↓			
w/o AS(ii) + Method	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB
Movie	0.241	0.252	0.174	0.165	0.129	0.120	0.109	0.110	0.887	1.767	0.947	1.156	0.570	0.561	0.587	0.512
SUB-3DFE	0.136	0.289	0.197	0.265	0.127	0.125	0.096	0.093	0.483	1.905	0.581	1.899	0.399	0.379	0.302	0.299
JAFFE	0.133	0.212	0.175	0.187	0.089	0.071	0.079	0.078	0.521	1.844	0.519	1.566	0.397	0.296	0.292	0.260
Yeast-alpha	0.049	0.065	0.041	0.055	0.029	0.033	0.027	0.065	0.820	3.159	1.192	3.222	0.322	0.250	0.336	0.278
Yeast-cdc	0.055	0.077	0.047	0.067	0.023	0.019	0.021	0.018	0.741	2.889	1.055	2.899	0.316	0.255	0.325	0.241
Yeast-cold	0.145	0.300	0.139	0.241	0.069	0.058	0.089	0.056	0.435	1.477	0.615	1.444	0.179	0.172	0.272	0.145

Table 4: We removed the effects of TabGP. Recovery results on 6 real-world datasets. \downarrow indicates that "the smaller the better". We highlight the best recovery results.

Metric				Cheb	yshev ↓							Cla	ark ↓			
w/o AS(iii) + Method	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB	FCM	KM	LP	ML	GLLE	LESC	LEVI	
Movie	0.249	0.267	0.173	0.195	0.177	0.121	0.111	0.119	0.889	1.766	0.933	1.157	0.571	0.569	0.582	
SUB-3DFE	0.137	0.292	0.195	0.264	0.123	0.133	0.097	0.095	0.485	1.910	0.589	1.912	0.397	0.388	0.313	
JAFFE	0.135	0.213	0.177	0.188	0.091	0.070	0.075	0.079	0.523	1.842	0.588	1.567	0.393	0.294	0.293	
Yeast-alpha	0.056	0.066	0.043	0.057	0.032	0.035	0.022	0.069	0.829	3.177	1.193	3.229	0.325	0.251	0.339	
Yeast-cdc	0.056	0.078	0.055	0.069	0.021	0.015	0.029	0.011	0.745	2.894	1.053	2.895	0.317	0.259	0.321	
Yeast-cold	0.147	0.314	0.135	0.245	0.072	0.063	0.094	0.059	0.436	1.466	0.619	1.474	0.184	0.173	0.274	

Table 5: We remove the effect of the prototype matrix. Recovery results on 6 real-world datasets. \downarrow indicates that "the smaller the better". We highlight the best recovery results.

324 3.5 ABLATION STUDY FOR CLIP2LE

To evaluate the effectiveness of our method, we conduct 3 experiments on the 3.1 task.

i) Remove the feature distribution homogenization. We remove the loss term that moves closer to the uniform distribution. As shown in Table 3, we find that the performance degradation is significant when the number of labels is greater than 6. This may be due to the principle of label distribution learning that as the number of labels increases, the lower the percentage of each label, the closer it is to a uniform distribution.

ii) Remove the TableGPT. To evaluate the effectiveness of recoding the logical label space by TableGPT, we removed TableEncoder. As shown in Table 4, we find that the performance degradation is significant when the number of labels is smaller than 6.

iii) Remove the prototype matrix. To demonstrate the effectiveness of the prototype matrices, the prototype matrices in our approach are replaced by learnable parameter matrices. As shown in Table 5, we find that the performance of the prototype matrix is almost homotopic to that of TableGPT and that the prototype matrix may be more important for labeling the role of logical vector encoding.

Metric				Cheb	yshev ↓							Cla	ırk↓			
Method without our method	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB
Movie SUB-3DFE	0.231 0.136	0.236 0.244	0.169 0.126	0.177 0.236	0.125 0.123	0.126 0.127	0.112 0.100	0.107 0.096	0.869 0.491	1.777 1.913	0.921 0.589	1.144 1.896	0.570 0.393	0.576 0.379	0.555 0.311	0.519 0.298
Metric				Cheb	yshev ↓							Cla	ırk↓			
Method with our method	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB
Movie SUB-3DFE	0.239	0.248	0.178	0.199	0.165	0.133	0.119	0.108	0.887	1.995 1.966	0.932	1.142	0.599	0.601	0.555	0.544

Table 6: Recovery results on 2 real-world datasets. \downarrow indicates that "the smaller the better". We highlight the best recovery results.

Metric				Cheb	yshev ↓							Cla	ırk↓			
Method without our method	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB
Movie SUB-3DFE	0.298 0.157	0.246 0.399	0.255 0.245	0.198 0.319	0.213 0.256	0.189 0.277	0.144 0.189	0.143 0.149	0.956 0.569	1.989 2.005	0.977 0.789	1.321 2.449	0.689 0.457	0.762 0.444	0.699 0.372	0.688 0.333
Metric				Cheb	yshev ↓							Cla	ırk↓			
Method without our method	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB
Movie SUB-3DFE	0.275 0.152	0.230 0.347	0.242 0.201	0.143 0.311	0.202 0.206	0.165 0.223	0.140 0.175	0.122 0.137	0.901 0.555	1.566 1.998	0.879 0.753	1.132 2.407	0.544 0.438	0.712 0.408	0.633 0.370	0.540 0.300

Table 7: Recovery results on 2 real-world datasets. \downarrow indicates that "the smaller the better". We highlight the best recovery results. These two datasets were injected with $0.5 \times$ Gaussian noise.

3.6 ROBUSTNESS EVALUATION OF CLIP2LE

To evaluate the ability of our method to tolerate noise, we present two experiments: one in which the labels in the logical label space are incorrect; and the other in which the logical label space carries Gaussian noise.

1) Since we assumed the problem of incorrect labels in the space of label distributions \mathcal{D} , we imposed 20% incorrect labels (for example, $[0.1, 0.2, 0.7] \rightarrow [0.7, 0.1, 0.2]$) on the training set in task 3.1 to validate the effectiveness of our method. As shown in Table 6, the interference of incorrect labels can be effectively eliminated by our method compared to the method without using preprocessing.

³⁶⁹ 2) As shown in Table 7, we inject 50% Gaussian noise $(0.5 \times)$ into the label labeling space, and the LE algorithm using CLIP2LE has better performance.

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3.7 PERFORMANCE OF DOWNSTREAM TASKS

To evaluate the effect of using the CLIP2LE method on the downstream prediction task, we select the LIB and LEVI algorithms as a baseline to be assessed on the SJAFFE dataset. Since the SJAFFE dataset is a face classification task, we employ ResNet-18 for prediction; where the cross-entropy function is used as the main loss term, and the label distributions predicted by LIB and LEVI are used as the regularization terms, where the weights of the regularization terms are all set to 0.15.

We found that the accuracy of pure LIB-based and LEVI-assisted prediction of facial emotion is 95.2% and 94.9%, respectively. While the accuracy of LIB and LEVI-assisted ResNet-18 prediction with CLIP2LE is 96.6% and 96.1%, respectively. It is worth noting that the prediction accuracy of ResNet-18 for facial emotions is 93.9%, without considering the regularization term. Here, our epochs are set to 200, the learning rate is 0.005, the batch size is set to 16, and the optimizer uses AdamW.

Metric				Cheb	yshev ↓							Cla	ırk↓			
Method without our method	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB	FCM	KM	LP	ML	GLLE	LESC	LEVI	LI
Movie SUB-3DFE	0.298	0.246 0.399	0.255 0.245	0.198 0.319	0.213 0.256	0.189 0.277	0.144 0.189	0.143 0.149	0.956	1.989 2.005	0.977 0.789	1.321 2.449	0.689 0.457	0.762 0.444	0.699 0.372	0.6 0.3
Metric				Cheb	yshev ↓							Cla	ark↓			
Method with our method	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB	FCM	KM	LP	ML	GLLE	LESC	LEVI	LI
Movie SUB-3DFE	0.275 0.152	0.230 0.347	0.242 0.201	0.143 0.311	0.202 0.206	0.165 0.223	0.140 0.175	0.122 0.137	0.901 0.555	1.566 1.998	0.879 0.753	1.132 2.407	0.544 0.438	0.712 0.408	0.633 0.370	0.5 0.3
Method with MaskCLIP	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB	FCM	KM	LP	ML	GLLE	LESC	LEVI	LI
Movie SUB-3DFE	0.272 0.151	0.228 0.338	0.245 0.202	0.144 0.313	0.200 0.201	0.162 0.215	0.138 0.170	0.121 0.133	0.899 0.554	1.562 1.995	0.877 0.742	1.130 2.402	0.542 0.433	0.711 0.402	0.629 0.365	0.53 0.29
Method with MetaCLIP	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB	FCM	KM	LP	ML	GLLE	LESC	LEVI	Ll
Movie SUB-3DFE	0.272 0.149	0.228 0.344	0.243 0.199	0.144 0.310	0.210 0.205	0.169 0.219	0.132 0.170	0.121 0.138	0.921 0.523	1.542 1.989	0.870 0.740	1.121 2.405	0.539 0.433	0.710 0.412	0.635 0.369	0.5 0.2

Table 8: Recovery results on 2 real-world datasets. \downarrow indicates that "the smaller the better". We highlight the best recovery results. We evaluated the effect of different CLIP versions.

EFFECT OF OTHER CLIP VERSIONS 3.8

To align the semantics of the logical label space and the feature space, we conduct experiments based on pure CLIP. Here, we investigate the effect of MaskCLIP and MetaCLIP on the experimental results. As shown in Table 8, MaskCLIP and MetaCLIP are essentially improved over pure CLIP on both datasets, with a decrease in very few algorithms. However, MaskCLIP and MetaCLIP consume much more computational resources than pure CLIP.

3.9 ESTIMATION ERROR BOUND

In this subsection, we estimate the error bounds of our method using the example of single positive multi-label learning. The empirical risk estimator (loss term for [26]) according to 3.4 can be rewritten as:

$$\mathcal{R}_{spmll}(f) = \frac{1}{n} \sum_{i=1}^{n} \sum_{j=1}^{L} \left(w_i^j \ell_i^j + \bar{w}_i^j \bar{\ell}_i^j \right),\tag{6}$$

where $w_i^j = \frac{d_i^j}{p(y^\gamma = 1|x_i)c}$ and $\bar{w}_i^j = \frac{1 - d_i^j}{p(y^\gamma = 1|x_i)c}$. Then the total loss function \mathcal{L}_{sp} is

$$\mathcal{L}_{sp} = \sum_{j=1}^{L} \left(w_i^j \ell_i^j + \bar{w}_i^j \bar{\ell}_i^j \right) + \left(\text{CEL}(\text{logits}, \text{dim=0}) + \text{CEL}(\text{logits}, \text{dim=1}) \right) / 2.$$
(7)

We define a function space as:

$$\mathcal{K}_{sp} = \left\{ (x, y) \mapsto \sum_{j=1}^{L} \left(w^{j} \ell^{j} + \bar{w}^{j} \bar{\ell}^{j} \right) + \left(\text{CEL}(\text{logits}, \text{dim}=0) + \text{CEL}(\text{logits}, \text{dim}=1) \right) / 2 | f \in \mathcal{F} \right\},$$
(8)

and denote the expected Rademacher complexity [2] of \mathcal{K}_{sp} as:

$$\widetilde{\mathfrak{R}}_{n}(\mathcal{K}_{sp}) = \mathbb{E}_{x,y,\sigma} \left[\sup_{g \in \mathcal{G}_{sp}} \frac{1}{n} \sum_{i=1}^{n} \sigma_{i} g\left(x_{i}, y_{i}\right) \right],$$
(9)

where $\boldsymbol{\sigma} = \{\sigma_1, \sigma_2, \dots, \sigma_n\}$ is *n* Rademacher variables with σ_i independently uniform variable taking value in $\{+1, -1\}$. We suppose that the SPMLL loss function \mathcal{L}_{sp} could be bounded by M,



Figure 3: This figure provides a comprehensive view of how difficult it is to transform information from a matrix across multiple benchmarks, with higher matrix energies representing more difficult information transformations.

i.e., $M = \sup_{x \in \mathcal{X}, f \in \mathcal{F}, y \in \mathcal{Y}} \mathcal{L}_{sp}(f(x), y)$, and for any $\delta > 0$, with probability at least $1 - \delta$, then we have

$$\sup_{f \in \mathcal{F}} R_{sp}(f) - \widehat{R}_{sp}(f) \le 2\widetilde{\mathfrak{R}}_n(\mathcal{K}_{sp}) + \frac{M}{2}\sqrt{\frac{\log\frac{2}{\delta}}{2n}}.$$

We suppose that the loss function $\ell(f(x), y)$ and $\bar{\ell}(f(x), y)$ are ρ^+ -Lipschitz and ρ^- -Lipschitz with respect to f(x) $(0 < \rho^+ < \infty$ and $0 < \rho^- < \infty)$ for all $y \in \mathcal{Y}$, respectively, and w^j and \bar{w}^j are both bounded in $[0, \kappa]$. Then, we have

$$\widetilde{\mathfrak{R}}_n(\mathcal{K}_{sp}) \le \sqrt{2}\kappa c(\rho^+ + \rho^-) \sum_{j=1}^c \mathfrak{R}_n(\mathcal{H}_{y_j}),$$

where $\mathcal{H}_y = \{h : x \mapsto f_y(x) | f \in \mathcal{F}\}$ and $\mathfrak{R}_n(\mathcal{H}_y) = \mathbb{E}_{x,\sigma} \left[\sup_{h \in \mathcal{H}_y} \frac{1}{n} \sum_{i=1}^n h(x_i) \right].$

We could obtain the following theorem: Assume the loss function $\ell(f(x), y)$ and $\ell(f(x), y)$ are ρ^+ -Lipschitz and ρ^- -Lipschitz with respect to f(x) $(0 < \rho^+ < \infty$ and $0 < \rho^- < \infty)$ for all $y \in \mathcal{Y}$ and the loss function \mathcal{L}_{sp} are bounded by M, i.e., $M = \sup_{x \in \mathcal{X}, f \in \mathcal{F}, y \in \mathcal{Y}} \mathcal{L}_{sp}(f(x), y)$, with probability at least $1 - \delta$,

$$R(\widehat{f}_{sp}) - R(f^*) \le 4\sqrt{2}\kappa c(\rho^+ + \rho^-) \sum_{j=1}^c \mathfrak{R}_n(\mathcal{H}_y) + M\sqrt{\frac{\log\frac{2}{\delta}}{2n}}.$$

Here, $f_{sp} = \min_{f \in \mathcal{F}} R_{sp}(f)$ and $f^* = \min_{f \in \mathcal{F}} R(f)$ are the empirical risk minimizer and the true risk minimizer, respectively. The proof can be found in the Appendix. This equation shows that f_{sp} would converge to f^* as $n \to \infty$ and $\mathfrak{R}_n(\mathcal{H}_y) \to 0$.

DISCUSSION AND ANALYSIS

In this section, we focus on why CLIP's methods are effective to echo our motivations. First, we visualize some matrix energies to represent the difficulty of transforming the feature space and the logical label space to the label distribution space (see Figure 3). In this paper matrix energies are computed as described below: First, we set a linear model with bias terms for the transformation of the feature space matrix to the label distribution matrix and the logical label matrix to the label distribution matrix, respectively. The linear model uses the nn.Linear operator in PyTorch 1.8. We used an evaluation platform with a Linux system, a single 3090 RTX GPU shader, the learning rate was uniformly set to 0.002, the batch size was set to throughput all the data at once, and the number of iterations was uniformly set to 1200.

486 SGD Adam 487 Logical label space Feature space 🔵 Logical label space 🛛 🔴 Feature space 488 120 80 489 40 490 491 JAFFE SUB-3DFE JAFFE Yeast-alpha Movie Yeast-cold SUB-3DFE Yeast-alpha Movie Veast-cold 492 WAdam Adagrad 493 Logical label space Feature space Logical label space
 Feature space 494 495 40 40 496 497 JAFFE SUB-3DFE Ye ast-alpha Movie Ye ast-cold JAFFE SUB-3DFE Yeast-alpha Movie Yeast-cold 498

Figure 4: This figure shows the effect of different optimizers on the generation of the energy matrix.

Maintaining fairness. The linear models are uniformly overfitted set to ensure fairness in information 501 migration, and they all have a training loss below 0.001. 502

503 **Learning rate's effect.** We attempt to obtain matrix energies at multiple learning rates ({0.001, 0.01, 504 (0.1), and we find that the learning rate interferes with the results by less than 3 percent and does not 505 affect the ordinal relationship.

506 Optimizer's effect. In addition, we also considered the effect of optimizers on our method and 507 we evaluated the effect of SGD, Adam, and Adagrad on our experiments. As shown in Figure 4, 508 these four optimizers are essentially homotopic though there are differences in the energy matrices 509 generated by them.

510 Before the linear model was trained, the transfer matrix energy of the feature space matrix and 511 the transfer matrix energy of the logical label space was essentially equal after using CLIP, with a 512 difference of no more than 2%. We also tried to perform the training of the linear model on the CPU, 513 due to the limited CPU storage, it is not possible to throughput the entire dataset, which can lead 514 to unfair comparisons. We also perform an exploratory experiment to consider the role of sample 515 weights based on the CLIP2LE algorithm. Specifically, each sample is assigned a learned parameter 516 during training, which is obtained through a 1D convolution and a pooling layer that acts on each 517 sample. We found an overall improvement of 2.4% in performance across CLIP2LE and will consider the role of sample weights in future work. 518

- In addition, in the Appendix we show the performance of some variants of CLIP.
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5 LIMITATIONS AND BROADER IMPLICATIONS

Since most of the evaluated datasets are tabular, their feature space dimensions are not uniform. For this, we need to pre-train a CLIP2LE for each dataset, which yields a great training cost. This may have led to a small amount of performance degradation on some datasets using our method. Moreover, in this paper, we do not compare with the SOTA method, which is because we focus on the preprocessing ability of CLIP2LE rather than obtaining the best LE results.

Our approach is a pre-processing algorithm that does not involve ethical and moral issues; it is a safe 529 and trustworthy machine-learning algorithm. 530

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6 CONCLUSION

534 In this paper, we propose a generalized label enhancement pre-processing method that can be applied 535 to tasks such as image, text, and speech. Here, we consider label enhancement as a multimodal fusion task, where the issues of fairness and consistency of representations are addressed by a customized 536 CLIP algorithm. In the discussion session, we further illustrate that extant label enhancement 537 algorithms that do not take into account the fairness of the representations result in not all-round 538 performance on multiple benchmarks. Extensive experimental results demonstrate that our proposed CLIP2LE is effective and robust.

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648 **APPENDIX / SUPPLEMENTAL MATERIAL** А 649

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693 694 This subsection is supplemented with details and data in the 3.1 task.

Details of the comparison methods. For the sake of fairness, we utilize the parameter settings recommended in their original works. Specifically, for FCM, we set the parameter $\beta = 2$. For KM, we leverage the Gaussian kernel. For LP, we set the parameter $\alpha = 0.5$. For ML, we set the number of neighbors k = c + 1. For GLLE, we select λ from $\{0.01, 0.1, ..., 100\}$ and set the number of neighbors k to c + 1. For LESC, λ_1 and λ_2 are selected from $\{0.0001, 0.1, ..., 10\}$. For LEVI, MLPs with two hidden layers and softplus activation functions are utilized, and the results are reported after 150 training epochs. For LIB, we select α and β from $\{0.001, 0.01, ..., 10\}$, and the fully connected networks with 3 layers and sigmoid activation function are leveraged in the proposed method.

659 **Experimental results.** Experimental results show that our method can effectively improve the 660 performance of existing LE algorithms (see Figure 9 and Figure 11). It is worth noting that the validity of our method is more outstanding in the Cosine metric. Furthermore, we find that consistent 662 with the insights in the main manuscript, our approach improves significantly on non-deep learning 663 algorithms.

665	Metric				Canb	erra ↓							Kullback	-Leibler	Ļ		
666	Method	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB
667	Movie SUB-3DFF	1.664	3.444	1.720	1.934	1.045	1.034	0.974	0.920 0.611	0.381	0.452	0.177	0.218	0.123	0.120	0.082	0.077 0.041
668	SJAFFE Vecet clabo	1.020	4.010	1.064	3.138	0.781	0.561	0.600	0.531	0.107	0.558	0.077	0.391	0.050	0.029	0.032	0.027
669	Yeast-cdc	2.885	9.875	3.644	9.695	0.959	0.765	1,148	0.893 0.747	0.100	0.630	0.121	0.602	0.013	0.010	0.011	0.009
670	Yeast-cold Yeast-diau	0.734 1.895	2.566 4.261	0.924 1.748	2.519 4.180	0.305 0.671	0.263 0.480	0.501 0.689	0.250 0.621	0.113 0.159	0.586 0.538	0.103 0.127	0.556 0.509	0.019 0.027	0.015 0.017	0.035 0.023	0.012 0.022
671	Yeast-dtt Yeast-elu	0.501	2.594 9.110	0.941 3.381	2.549 8.949	0.248 0.902	0.206 0.727	0.562 1.093	0.158 0.670	0.065	0.617 0.617	0.103 0.109	0.586 0.589	0.013 0.013	0.010 0.009	0.042 0.014	0.005 0.008
672	Yeast-heat Yeast-spo	1.157	3.849 3.854	1.293	3.779 3.772	0.430	0.401	0.646 0.605	0.327 0.454	0.147	0.586	0.089	0.556	0.017	0.015	0.027	0.011 0.019
673	Yeast-spo5 Yeast-sopem	0.563 0.534	1.382 1.253	0.401 0.365	1.355 1.226	0.305 0.183	0.284 0.180	0.311 0.248	0.241 0.144	0.123 0.208	0.334 0.531	0.042 0.067	0.317 0.503	0.034 0.027	0.031 0.027	0.028 0.036	0.021 0.018
674	Metric				Canb	erra ↓							Kullback	-Leibler	Ļ		
675	Ours + Method	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB
676	Movie SUB-3DFE	1.655	3.413 4.022	1.677	1.854 3.985	1.011	1.022 0.791	0.847	0.841 0.610	0.380	0.442	0.165	0.215	0.120	0.111	0.080	0.076 0.040
677	JAFFE Yeast-alpha	1.033	3.887	1.001	3.132	0.785	0.544	0.538	0.530 0.896	0.106	0.550	0.013	0.324	0.033	0.021	0.032	0.016
678	Yeast-cdc	2.410	9.863	3.643	9.610	0.921	0.753	1,145	0.740	0.087	0.611	0.110	0.599	0.013	0.010	0.012	0.007
679	Yeast-diau	1.890	4.245	1.733	4.101	0.290	0.280	0.480	0.621	0.110	0.580	0.102	0.509	0.010	0.013	0.032	0.009
680	Yeast-dtt Yeast-elu	0.500	2.585 9.022	0.941 3.305	2.549 8.888	0.248 0.912	0.201 0.720	0.560 1.064	0.155 0.566	0.053	0.601 0.610	0.096 0.056	0.544 0.523	0.011 0.031	0.010	0.041 0.014	0.002 0.004
681	Yeast-heat Yeast-spo	1.123 0.963	3.489 3.855	1.113 1.111	3.536 3.656	0.225 0.432	0.400 0.411	0.619 0.599	0.223 0.406	0.140	0.513 0.553	0.066 0.080	0.433 0.522	0.012 0.021	0.013 0.025	0.028 0.021	0.011 0.010
682	Yeast-spo5 Yeast-sopem	0.523 0.532	1.333 1.233	0.400 0.313	1.211 1.225	0.302 0.180	0.255 0.153	0.310 0.212	0.240 0.140	0.122 0.202	0.314 0.523	0.033 0.060	0.301 0.477	0.033 0.020	0.030 0.021	0.025 0.035	0.020 0.015
683					-					1	-			-			-

Table 9: Recovery results on 13 real-world datasets. \downarrow indicates that "the smaller the better". The following two table blocks represent the 8 LE algorithms using our pre-processing steps. We highlight the best recovery results.

Metric				Cos	ine ↑							Interse	ection \uparrow			
Method	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB
Movie (Ours)	0.773	0.880	0.929	0.919	0.936	0.937	0.954	0.955	0.677	0.649	0.778	0.779	0.831	0.833	0.849	0.859
Movie (CCLIP2LE)	0.775	0.856	0.925	0.912	0.934	0.937	0.965	0.967	0.675	0.644	0.772	0.770	0.811	0.815	0.810	0.866
Movie (TCLIP2LE)	0.770	0.888	0.931	0.922	0.934	0.941	0.956	0.959	0.683	0.666	0.779	0.781	0.834	0.835	0.852	0.879

Table 10: Recovery results on 1 real-world dataset. We highlight the best recovery results.

In this subsection, we discuss the role of other variants of CLIP on LE.

In fact, MLP is not necessarily a good choice as a CLIP encoder. Here, we propose two comparison 696 algorithms, one based on CNN (CCLIP2LE) and the other based on Transformer (TCLIP2LE). 697 CCLIP2LE used three-layer convolution and ReLU for the activation function; TCLIP2LE used a three-layer self-attention mechanism and GLU for the activation function. The remaining configura-699 tions such as learning rate, optimizer, and batchsize are consistent with the settings of CLIP2LE. 700

As shown in Table 10, we conducted a comparison experiment on the Movie dataset. We note that 701 TCLIP2LE performs the best, but also has the highest computational cost, and to trade-off speed and

702	Metric				Cos	sine ↑							Inters	ection \uparrow			
703	Method	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB	FCM	KM	LP	ML	GLLE	LESC	LEVI	LIB
704	Movie	0.773	0.880	0.929	0.919	0.936	0.937	0.954	0.955	0.677	0.649	0.778	0.779	0.831	0.833	0.849	0.859
705	JAFFE	0.912	0.812	0.922	0.815	0.927	0.932	0.956	0.958	0.827	0.579	0.810	0.587	0.850	0.855	0.882	0.887
706	Yeast-alpha	0.922	0.751	0.911	0.756	0.987	0.992	0.989	0.992	0.844	0.532	0.774	0.537	0.938	0.953	0.932	0.951
707	Yeast-cold	0.929	0.754	0.916	0.759	0.987	0.991	0.987	0.992	0.847	0.533	0.779	0.538	0.937	0.950	0.925	0.951
/0/	Yeast-diau	0.882	0.799	0.915	0.803	0.975	0.985	0.980	0.979	0.760	0.588	0.788	0.593	0.906	0.933	0.908	0.913
708	Yeast-dtt Yeast-elu	0.959	0.759	0.921	0.763	0.988 0.987	0.991	0.965 0.987	0.995 0.992	0.894	0.541	0.786	0.546	0.939	0.949 0.949	0.866	0.961
709	Yeast-heat	0.883	0.779	0.932	0.783	0.984	0.986	0.977	0.990	0.807	0.559	0.805	0.564	0.929	0.934	0.897	0.946
710	Yeast-spo Yeast-spo5	0.909	0.800	0.939	0.803	0.974	0.975	0.978	0.982	0.836	0.575	0.819	0.580	0.909	0.912	0.903	0.925
711	Yeast-sopem	0.878	0.812	0.950	0.815	0.978	0.978	0.972	0.985	0.767	0.592	0.837	0.597	0.912	0.913	0.885	0.931
712	Metric				Cos	sine ↑							Interse	ection \uparrow			
712	Metric Method	FCM	KM	LP	Cos ML	sine ↑ GLLE	LESC	LEVI	LIB	FCM	KM	LP	Interse ML	ection ↑ GLLE	LESC	LEVI	LIB
712 713	Metric Method Movie	FCM	KM 0.881	LP 0.955	Cos ML 0.933	sine ↑ GLLE 0.937	LESC 0.956	LEVI 0.959	LIB 0.966	FCM	KM 0.689	LP 0.789	Interse ML 0.796	GLLE 0.855	LESC 0.866	LEVI 0.874	LIB 0.884
712 713 714	Metric Method Movie SUB-3DFE JAFFE	FCM 0.785 0.915 0.910	KM 0.881 0.844 0.855	LP 0.955 0.929 0.946	Cos ML 0.933 0.856 0.869	sine ↑ GLLE 0.937 0.928 0.973	LESC 0.956 0.932 0.971	LEVI 0.959 0.956 0.979	LIB 0.966 0.958 0.985	FCM 0.678 0.826 0.829	KM 0.689 0.588 0.603	LP 0.789 0.819 0.856	Interse ML 0.796 0.599 0.669	ection ↑ GLLE 0.855 0.855 0.883	LESC 0.866 0.859 0.913	LEVI 0.874 0.888 0.899	LIB 0.884 0.898 0.926
712 713 714 715	Metric Method SUB-3DFE JAFFE Yeast-alpha	FCM 0.785 0.915 0.910 0.925 0.962	KM 0.881 0.844 0.855 0.756 0.788	LP 0.955 0.929 0.946 0.916	Cos ML 0.933 0.856 0.869 0.759 0.764	sine ↑ GLLE 0.937 0.928 0.973 0.988 0.988	LESC 0.956 0.932 0.971 0.993	LEVI 0.959 0.956 0.979 0.989 0.996	LIB 0.966 0.958 0.985 0.993 0.997	FCM 0.678 0.826 0.829 0.846 0.856	KM 0.689 0.588 0.603 0.545 0.545	LP 0.789 0.819 0.856 0.778 0.782	Interse ML 0.796 0.599 0.669 0.556 0.545	ection ↑ GLLE 0.855 0.855 0.883 0.945 0.942	LESC 0.866 0.859 0.913 0.956 0.958	LEVI 0.874 0.888 0.899 0.935 0.920	LIB 0.884 0.898 0.926 0.950
712 713 714 715 716	Metric Method Movie SUB-3DFE JAFFE Yeast-alpha Yeast-cdc Yeast-cold	FCM 0.785 0.915 0.910 0.925 0.963 0.923	KM 0.881 0.844 0.855 0.756 0.788 0.785	LP 0.955 0.929 0.946 0.916 0.930 0.933	Cos ML 0.933 0.856 0.869 0.759 0.764 0.795	sine ↑ GLLE 0.937 0.928 0.973 0.988 0.988 0.988 0.983	LESC 0.956 0.932 0.971 0.993 0.993 0.988	LEVI 0.959 0.956 0.979 0.989 0.996 0.972	LIB 0.966 0.958 0.985 0.993 0.997 0.989	FCM 0.678 0.826 0.829 0.846 0.856 0.856	KM 0.689 0.588 0.603 0.545 0.545 0.545 0.563	LP 0.789 0.819 0.856 0.778 0.783 0.798	Interse ML 0.796 0.599 0.669 0.556 0.545 0.575	ection ↑ GLLE 0.855 0.855 0.883 0.945 0.942 0.933	LESC 0.866 0.859 0.913 0.956 0.958 0.946	LEVI 0.874 0.888 0.899 0.935 0.929 0.885	LIB 0.884 0.898 0.926 0.950 0.955 0.947
712 713 714 715 716 717	Metric Method SUB-3DFE JAFFE Yeast-alpha Yeast-cdc Yeast-cold Yeast-diau Yeast-diau	FCM 0.785 0.915 0.910 0.925 0.963 0.923 0.899 0.963	KM 0.881 0.844 0.855 0.756 0.788 0.785 0.803 0.762	LP 0.955 0.929 0.946 0.916 0.930 0.933 0.918 0.923	Cos ML 0.933 0.856 0.869 0.759 0.764 0.795 0.811 0.795	sine ↑ GLLE 0.937 0.928 0.973 0.988 0.988 0.988 0.983 0.986 0.980	LESC 0.956 0.932 0.971 0.993 0.993 0.988 0.986 0.903	LEVI 0.959 0.956 0.979 0.989 0.996 0.972 0.982 0.972	LIB 0.966 0.958 0.985 0.993 0.997 0.989 0.981 0.906	FCM 0.678 0.826 0.829 0.846 0.856 0.854 0.765 0.903	KM 0.689 0.588 0.603 0.545 0.545 0.563 0.563 0.563	LP 0.789 0.819 0.856 0.778 0.783 0.798 0.798 0.789	Interse ML 0.796 0.599 0.669 0.556 0.545 0.575 0.594 0.556	ection ↑ GLLE 0.855 0.855 0.883 0.945 0.942 0.933 0.912 0.914	LESC 0.866 0.859 0.913 0.956 0.958 0.946 0.945 0.953	LEVI 0.874 0.888 0.899 0.935 0.929 0.885 0.912 0.860	LIB 0.884 0.898 0.926 0.950 0.955 0.947 0.919 0.962
712 713 714 715 716 717 718	Metric Movie SUB-3DFE JAFFE Yeast-alpha Yeast-cdc Yeast-cold Yeast-cliau Yeast-ditu Yeast-elu	FCM 0.785 0.915 0.910 0.925 0.963 0.923 0.899 0.963 0.955	KM 0.881 0.844 0.855 0.756 0.788 0.785 0.803 0.763 0.763	LP 0.955 0.929 0.946 0.916 0.930 0.933 0.918 0.933 0.935	Cos ML 0.933 0.856 0.869 0.759 0.764 0.795 0.811 0.789 0.763	sine ↑ GLLE 0.937 0.928 0.973 0.988 0.988 0.988 0.983 0.986 0.989 0.987	LESC 0.956 0.932 0.971 0.993 0.993 0.988 0.986 0.993 0.992	LEVI 0.959 0.956 0.979 0.989 0.996 0.972 0.982 0.972 0.982 0.972	LIB 0.966 0.958 0.985 0.993 0.997 0.989 0.981 0.996 0.992	FCM 0.678 0.826 0.829 0.846 0.856 0.854 0.765 0.903 0.889	KM 0.689 0.588 0.603 0.545 0.545 0.563 0.563 0.563 0.544 0.545	LP 0.789 0.819 0.856 0.778 0.783 0.798 0.798 0.799 0.794 0.789	Interse ML 0.796 0.599 0.669 0.556 0.545 0.575 0.594 0.556 0.563	ection ↑ GLLE 0.855 0.855 0.883 0.945 0.942 0.933 0.912 0.944 0.945	LESC 0.866 0.859 0.913 0.956 0.958 0.946 0.945 0.953 0.953	LEVI 0.874 0.888 0.899 0.935 0.929 0.885 0.912 0.869 0.933	LIB 0.884 0.898 0.926 0.950 0.955 0.947 0.919 0.962 0.959
712 713 714 715 716 717 718 719	Metric Method SUB-3DFE JAFFE Yeast-alpha Yeast-cdc Yeast-cdc Yeast-diu Yeast-diu Yeast-elu Yeast-heat	FCM 0.785 0.915 0.910 0.925 0.963 0.923 0.899 0.963 0.963 0.955 0.889 0.989	KM 0.881 0.844 0.855 0.756 0.788 0.785 0.803 0.763 0.763 0.762 0.783 0.762	LP 0.955 0.929 0.946 0.916 0.930 0.933 0.918 0.933 0.935 0.939	Cos ML 0.933 0.856 0.869 0.759 0.764 0.795 0.811 0.789 0.763 0.799	sine ↑ GLLE 0.937 0.928 0.973 0.988 0.988 0.988 0.983 0.986 0.989 0.987 0.991 0.971	LESC 0.956 0.932 0.971 0.993 0.993 0.988 0.986 0.993 0.992 0.986	LEVI 0.959 0.956 0.979 0.989 0.996 0.972 0.982 0.972 0.989 0.978 0.978	LIB 0.966 0.958 0.993 0.997 0.989 0.981 0.996 0.992 0.995	FCM 0.678 0.826 0.829 0.846 0.856 0.854 0.765 0.903 0.889 0.813 0.823	KM 0.689 0.588 0.603 0.545 0.545 0.563 0.563 0.563 0.544 0.545 0.556	LP 0.789 0.819 0.856 0.778 0.783 0.798 0.798 0.798 0.794 0.799 0.833 0.922	Interse ML 0.796 0.599 0.669 0.556 0.545 0.575 0.594 0.556 0.563 0.612 0.503	ection ↑ GLLE 0.855 0.855 0.883 0.945 0.942 0.933 0.912 0.944 0.945 0.935 0.912	LESC 0.866 0.859 0.913 0.956 0.958 0.946 0.945 0.953 0.953 0.939 0.915	LEVI 0.874 0.888 0.899 0.935 0.929 0.885 0.912 0.869 0.933 0.897 0.923	LIB 0.884 0.898 0.926 0.950 0.955 0.947 0.919 0.962 0.959 0.953 0.923
712 713 714 715 716 717 718 719	Metric Method SUB-3DFE JAFFE Yeast-cold Yeast-cold Yeast-diu Yeast-diu Yeast-du Yeast-heat Yeast-spo Yeast-spo5	FCM 0.785 0.915 0.910 0.925 0.963 0.923 0.923 0.963 0.955 0.889 0.955 0.889 0.913 0.925	KM 0.881 0.844 0.855 0.756 0.788 0.785 0.803 0.763 0.763 0.762 0.783 0.783 0.822 0.888	LP 0.955 0.929 0.946 0.916 0.930 0.933 0.933 0.933 0.935 0.939 0.945 0.968	Cos ML 0.933 0.856 0.869 0.759 0.764 0.795 0.811 0.789 0.763 0.799 0.821 0.892	sine ↑ GLLE 0.937 0.928 0.973 0.988 0.988 0.988 0.988 0.988 0.989 0.989 0.997 0.991 0.975 0.988	LESC 0.956 0.932 0.971 0.993 0.993 0.988 0.993 0.998 0.992 0.986 0.986 0.988	LEVI 0.959 0.956 0.979 0.989 0.996 0.972 0.982 0.972 0.982 0.972 0.989 0.978 0.978	LIB 0.966 0.958 0.985 0.993 0.997 0.989 0.981 0.996 0.992 0.995 0.989 0.989	FCM 0.678 0.826 0.829 0.846 0.856 0.854 0.765 0.903 0.889 0.813 0.837 0.845	KM 0.689 0.588 0.603 0.545 0.545 0.563 0.544 0.545 0.556 0.556 0.589 0.733	LP 0.789 0.819 0.856 0.778 0.783 0.783 0.798 0.798 0.794 0.789 0.833 0.822 0.889	Interse ML 0.796 0.599 0.669 0.556 0.545 0.545 0.575 0.594 0.556 0.612 0.593 0.612	ection ↑ GLLE 0.855 0.855 0.945 0.945 0.942 0.933 0.912 0.944 0.945 0.935 0.912 0.912 0.912	LESC 0.866 0.859 0.913 0.956 0.958 0.946 0.945 0.953 0.953 0.939 0.915 0.915	LEVI 0.874 0.888 0.899 0.935 0.929 0.885 0.912 0.869 0.933 0.897 0.933 0.897	LIB 0.884 0.898 0.926 0.955 0.947 0.919 0.962 0.959 0.953 0.939 0.935
712 713 714 715 716 717 718 719 720	Metric Method SUB-3DFE JAFFE Yeast-alpha Yeast-cold Yeast-cold Yeast-diu Yeast-diu Yeast-elu Yeast-elu Yeast-spo Yeast-spo5 Yeast-sopem	FCM 0.785 0.915 0.925 0.963 0.923 0.963 0.955 0.889 0.913 0.925 0.879	KM 0.881 0.844 0.855 0.756 0.788 0.785 0.803 0.763 0.763 0.763 0.763 0.783 0.762 0.783 0.822 0.888 0.815	LP 0.955 0.929 0.946 0.916 0.930 0.933 0.933 0.933 0.935 0.939 0.945 0.968 0.953	Cos ML 0.933 0.856 0.869 0.759 0.764 0.795 0.811 0.789 0.763 0.789 0.763 0.799 0.821 0.892 0.844	sine ↑ GLLE 0.937 0.928 0.973 0.988 0.988 0.983 0.986 0.989 0.987 0.987 0.991 0.975 0.988 0.979	LESC 0.956 0.932 0.971 0.993 0.988 0.986 0.993 0.992 0.986 0.986 0.986 0.986 0.981 0.991	LEVI 0.959 0.956 0.979 0.989 0.972 0.982 0.972 0.982 0.972 0.988 0.978 0.978 0.978 0.978	LIB 0.966 0.958 0.993 0.997 0.989 0.981 0.992 0.995 0.995 0.989 0.989 0.989	FCM 0.678 0.826 0.826 0.856 0.854 0.765 0.903 0.854 0.813 0.813 0.813 0.845 0.788	KM 0.689 0.588 0.603 0.545 0.545 0.563 0.545 0.556 0.556 0.556 0.589 0.733 0.598	LP 0.789 0.819 0.856 0.778 0.783 0.798 0.798 0.798 0.798 0.789 0.833 0.822 0.833 0.822 0.889 0.845	Interso ML 0.796 0.599 0.556 0.555 0.575 0.594 0.556 0.594 0.556 0.612 0.593 0.612 0.593 0.753 0.598	ection ↑ GLLE 0.855 0.885 0.945 0.945 0.942 0.933 0.912 0.944 0.935 0.912 0.925	LESC 0.866 0.859 0.913 0.956 0.958 0.946 0.945 0.953 0.953 0.939 0.915 0.915 0.933	LEVI 0.874 0.888 0.935 0.929 0.885 0.912 0.869 0.933 0.897 0.933 0.908 0.886	LIB 0.884 0.926 0.950 0.955 0.947 0.919 0.962 0.953 0.933 0.935 0.935

Table 11: Recovery results on 13 real-world datasets. ↑ means that "the larger the better". The following two table blocks represent the 8 LE algorithms using our pre-processing steps. We highlight the best recovery results.

accuracy, we use CLIP2LE in this paper. Moreover, the only potentially unfair point is the number of iterations; we find that TCLIP2LE converges more slowly, so we set it to have $2 \times$ as many iterations as CLIP2LE.