Learning Deep Latent Spaces for Multi-Label Classification

Chih-Kuan Yeh[1*], Wei-Chieh Wu[2*], Wei-Jen Ko[2], Yu-Chiang Frank Wang

[1]Research Center for IT Innovation, Academia Sinica, Taipei, Taiwan

[2]Department of Electrical Engineering, National Taiwan University, Taipei, Taiwan

Introduction

Multi-Label Learning

Person, Sports Ball, Tennis Racket

Person, Tie

Person, Ski

- Label Embedding

  It transforms the label vectors into subspace with latent embedding of the corresponding information.

Motivation

Problems in existing works:

- Only consider linear embedding functions
- Few works jointly utilize the input space for label embedding.
- Separate label embedding and prediction into two tasks.

The proposed Canonical-Correlated Autoencoder(C2AE) jointly performs

feature-aware label embedding & label-correlation aware prediction

by advancing deep canonical correlation analysis(DCCA)

Method

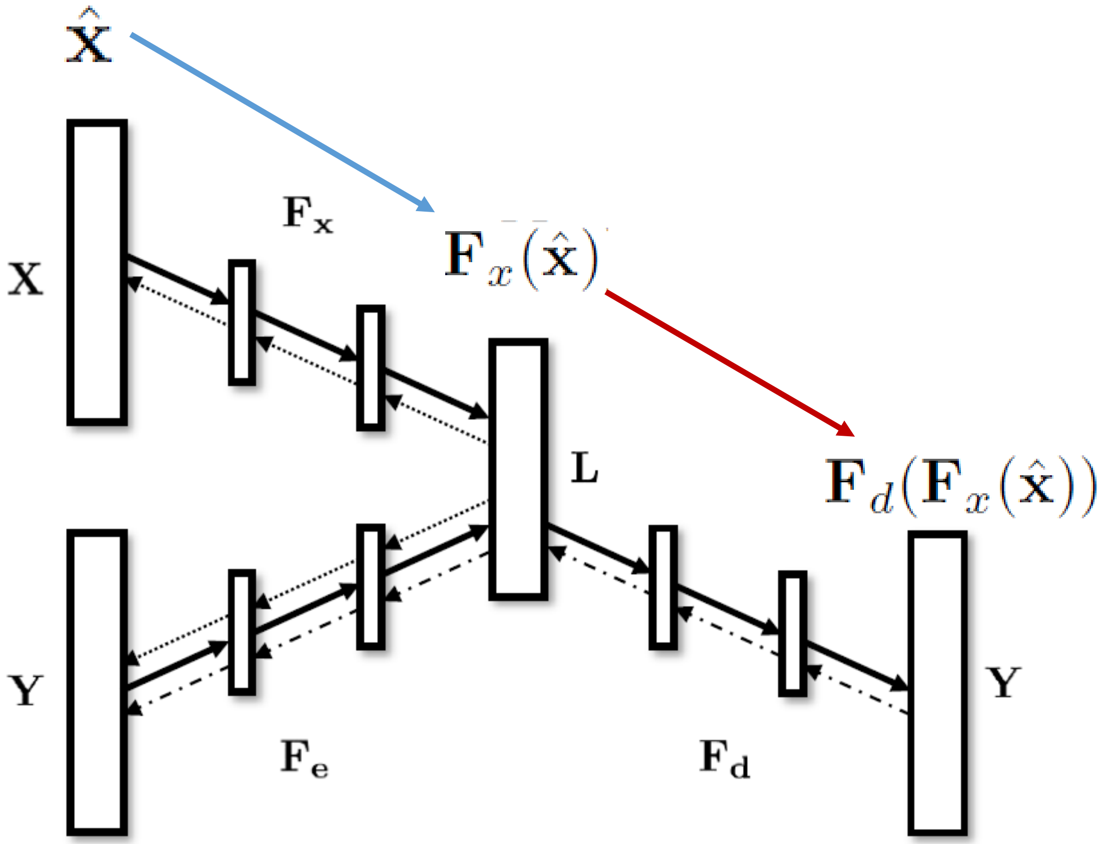
Canonical-Corelated Autoencoder(C2AE)

The objective function

$$\Theta = \min_{\mathbf{F}_x,\mathbf{F}_e,\mathbf{F}_d} \boxed{\mathbf{\Phi}(\mathbf{F}_x, \mathbf{F}_e)} + \alpha \boxed{\mathbf{\Gamma}(\mathbf{F}_e, \mathbf{F}_d)}$$

Encoder

Decoder



CCA and DCCA

Canonical correlation analysis (CCA) is a standard statistical technique for relating cross-domain data

Input feature data $\mathrm{X} \longleftrightarrow$ Label data Y

$$\mathrm{W}_1 \;\Big\downarrow\; \mathrm{W}_2$$

Maximize $\mathit{corr}\left(\mathrm{W}_1^T\mathrm{X}, \mathrm{W}_2^T\mathrm{Y}\right)$

Subspace

DCCA: replaces the two linear projections by DNNs and solves the same objective function with gradient descent techniques.

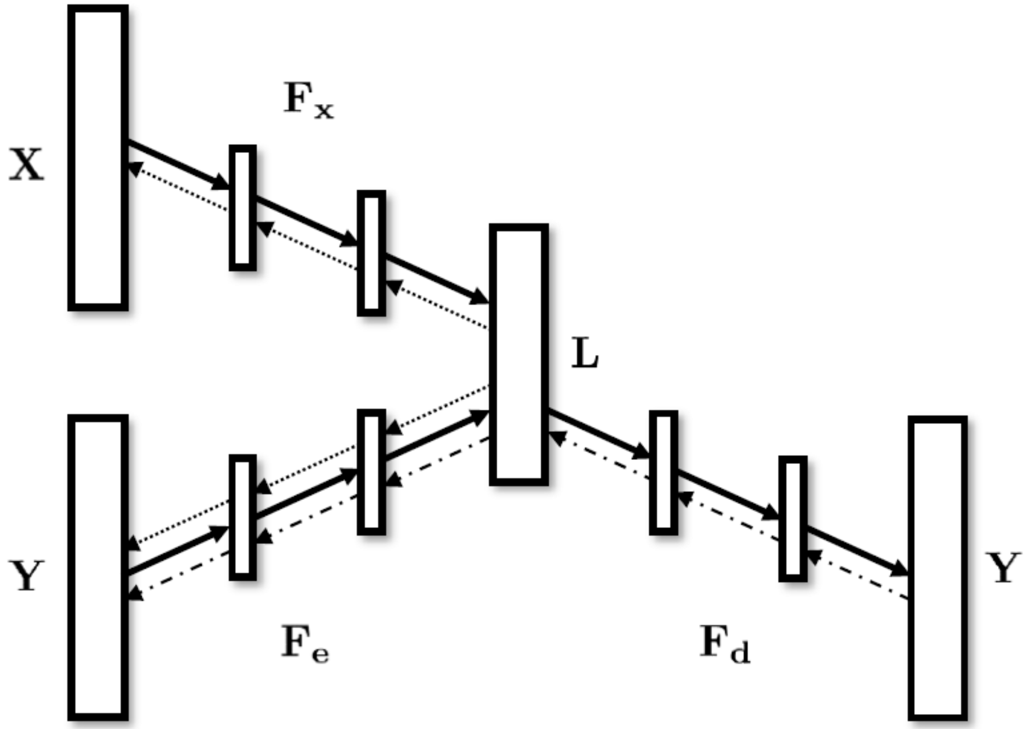
Method

The objective function

$$\min_{\mathbf{F}_x,\mathbf{F}_e} \quad \|\mathbf{F}_x(\mathbf{X}) - \mathbf{F}_e(\mathbf{Y})\|_F^2$$

$$\text{s.t.} \quad \mathbf{F}_x(\mathbf{X})\mathbf{F}_x(\mathbf{X})^T = \mathbf{F}_e(\mathbf{Y})\mathbf{F}_e(\mathbf{Y})^T = \mathbf{I},$$

The above identity constraint would make the above formulation equivalent to the standard CCA objective function.

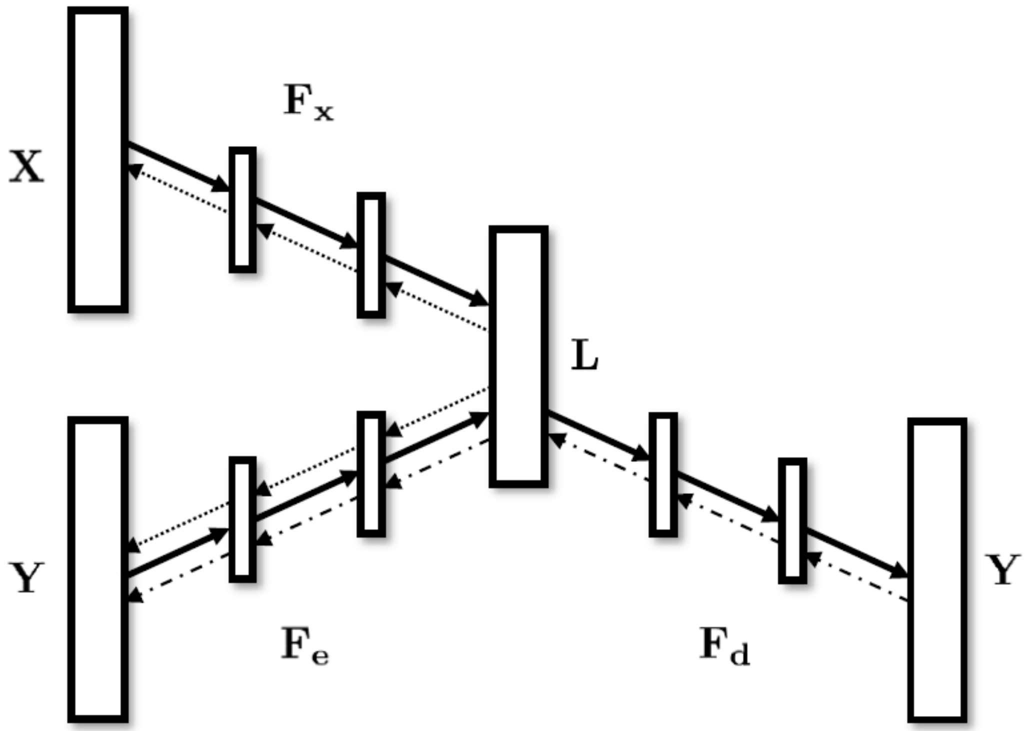


Method

The objective function

$$\Gamma(\mathbf{F}_e, \mathbf{F}_d) = \sum_{i=1}^{N} E_i$$

$$E_i = \frac{1}{|\mathbf{y}_i^1||\mathbf{y}_i^0|} \sum_{(p,q)\in \mathbf{y}_i^1 \times \mathbf{y}_i^0} \exp(-(\mathbf{F}_d(\mathbf{F}_e(\mathbf{x}_i))^q - \mathbf{F}_d(\mathbf{F}_e(\mathbf{x}_i))^p))$$



Minimizing the above loss function is equivalent to maximizing the prediction outputs of all positive-negative label attribute pairs.

Experiment

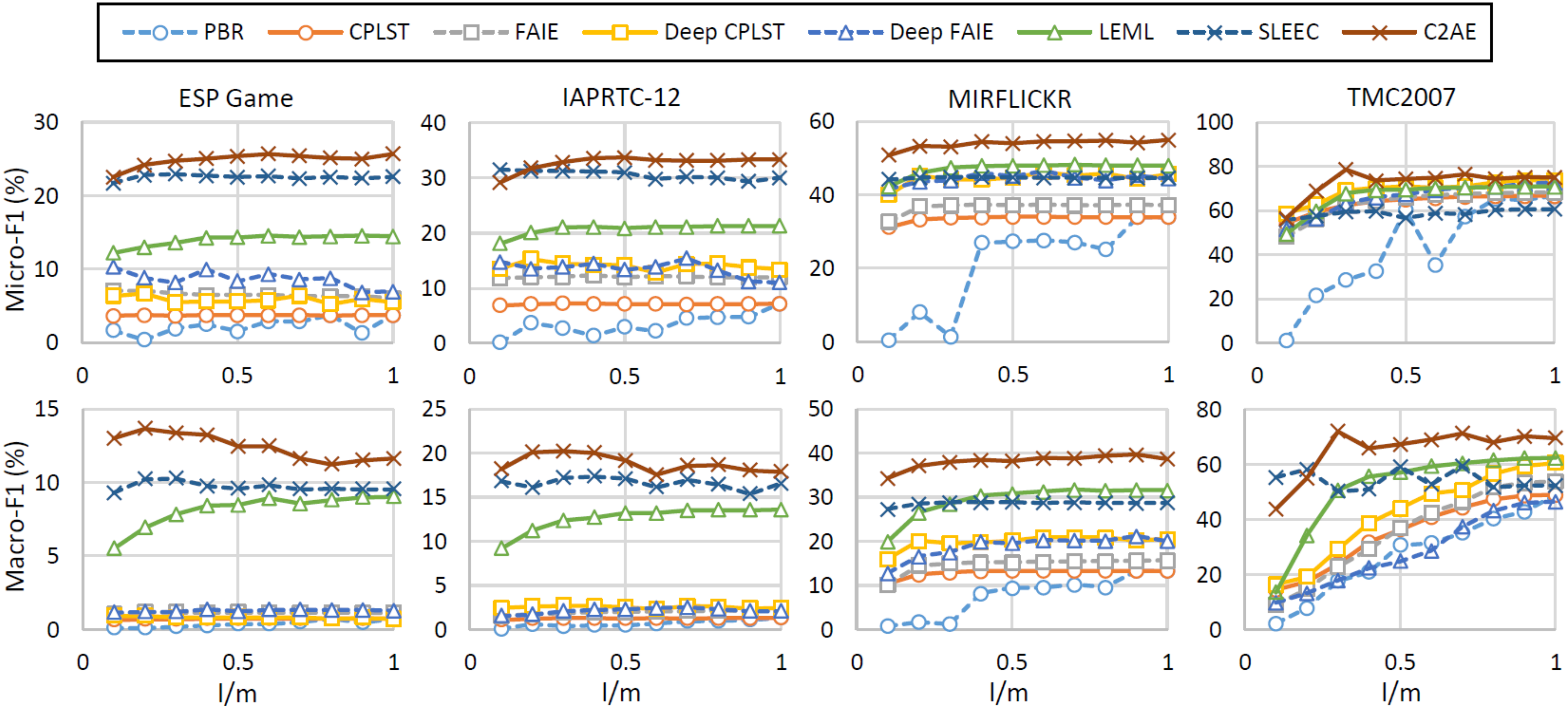
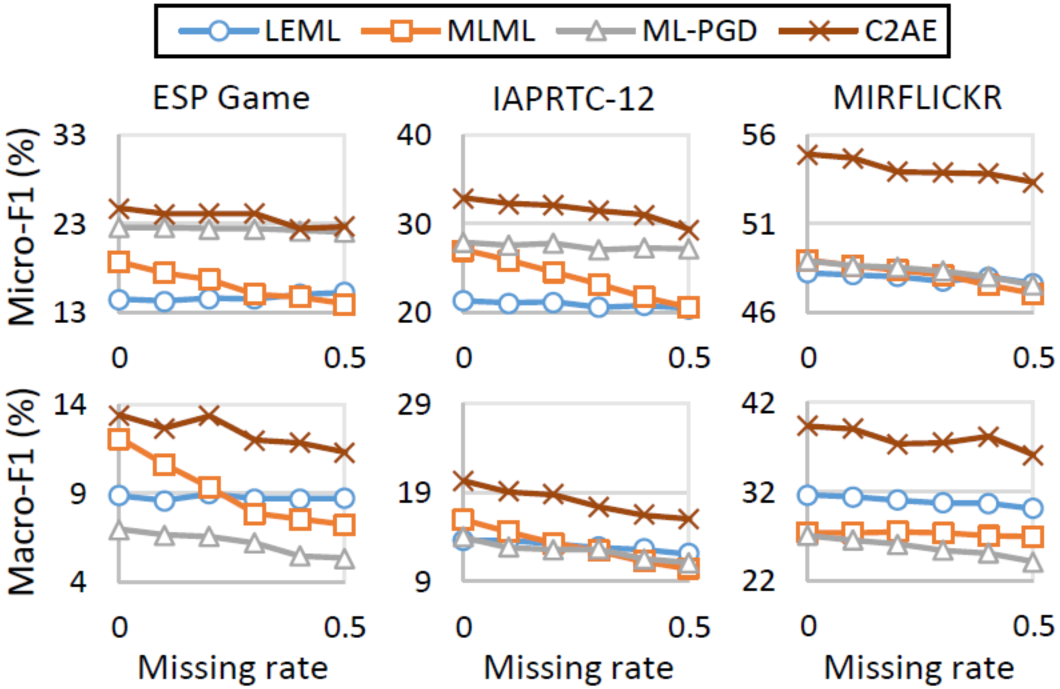


Figure 2: Performance comparisons in terms of Micro-F1 and Macro-F1 with different latent space dimension ratios (l/m).

Experiment

Table 2: Performance comparisons of DNN-based approaches on NUS-WIDE. Macro-F1 and Micro-F1 are abbreviated as as C-F1 and O-F1, respectively.

Method	C-P	C-R	C-F1	O-P	O-R	O-F1
CNN-WARP	31.7	35.6	33.5	48.6	60.5	53.9
CNN-RNN	40.5	30.4	34.7	49.9	61.7	55.2
DNN-BCE	42.2	23.7	21.7	56.6	67.0	61.4
BP-MLL	44.5	39.8	38.3	57.3	68.9	62.5
C2AE	**55.8**	**45.3**	**48.6**	**66.2**	**69.1**	**67.6**



C-P: per-class precision
O-P: overal precision

C-R: per-class recall
O-R: overal recall

Experiment

Hamming Loss

	PMLSP	PARVLS	PMLLRS	PML-lc	PML-fp
emotions	**0.211**	0.242	0.243	0.247	0.252
scene	**0.105**	0.213	0.550	0.170	0.170
yeast	0.220	**0.208**	**0.208**	0.215	0.215
cal500	**0.280**	**0.280**	[illegible]	[illegible]	[illegible]
genbase	**0.006**	0.033	[illegible]	[illegible]	[illegible]
medical	**0.052**	0.120	[illegible]	[illegible]	[illegible]
corel5k	**0.116**	0.242	[illegible]	[illegible]	[illegible]

Ranking Loss

	PMLSP	PARVLS	PMLLRS	PML-lc	PML-fp
emotions	**0.184**	0.243	0.261	0.202	0.212
scene	**0.100**	0.227	0.174	0.215	0.214
yeast	0.184	0.192	**0.180**	0.189	0.189
[illegible]	[illegible]	[illegible]	0.320	0.329	0.328
[illegible]	[illegible]	[illegible]	0.090	0.007	0.008
[illegible]	[illegible]	[illegible]	0.088	0.113	0.113
[illegible]	[illegible]	[illegible]	0.376	0.383	**0.315**

	PMLSP	PARVLS	PMLLRS	PML-lc	PML-fp
emotions	**0.787**	0.752	0.710	0.769	0.762
scene	**0.846**	0.725	0.742	0.699	0.694
yeast	0.742	**0.743**	**0.743**	0.738	0.738
cal500	**0.593**	0.587	0.577	0.567	0.568
genbase	**0.987**	0.887	0.710	0.969	0.967
medical	**0.794**	0.737	0.759	0.695	0.697
corel5k	**0.426**	0.333	0.362	0.355	0.420

One Error

	PMLSP	PARVLS	[illegible]	[illegible]	[illegible]
emotions	**0.264**	0.314	[illegible]	[illegible]	[illegible]
scene	**0.242**	0.372	0.399	0.455	0.467
yeast	0.252	**0.244**	0.246	0.245	0.249
cal500	0.401	**0.341**	0.480	0.450	0.446
genbase	**0.012**	0.111	0.411	0.044	0.045
medical	**0.303**	0.311	0.342	0.426	0.423
corel5k	**0.693**	0.743	0.775	0.782	0.714

	[illegible]	[illegible]	PMLLRS	PML-lc	PML-fp
[illegible]	[illegible]	[illegible]	0.395	0.336	0.347
scene	**0.103**	0.174	0.166	0.197	0.198
yeast	0.479	0.467	**0.466**	0.492	0.488
cal500	0.654	**0.632**	0.652	0.650	0.648
genbase	**0.016**	0.058	0.103	0.021	0.021
medical	**0.082**	0.116	0.103	0.130	0.130
corel5k	0.426	0.494	0.462	0.469	0.**410**

Experiment

emotions	3/0/0	2/1/0	3/0/0	3/0/0
scene	3/0/0	3/0/0	3/0/0	3/0/0
yeast	3/1/4	2/2/4	3/5/0	3/4/1
cal500	3/5/0	7/1/0	8/0/0	8/0/0
genbase	8/0/0	8/0/0	7/1/0	6/2/0
medical	8/0/0	4/2/2	7/1/0	8/0/0
corel5k	8/0/0	8/0/0	8/0/0	8/0/0

emotions	3/0/0	2/1/0	3/0/0	3/0/0
scene	3/0/0	3/0/0	3/0/0	3/0/0
yeast	3/1/4	2/2/4	3/5/0	3/4/1
cal500	3/5/0	7/1/0	8/0/0	8/0/0
genbase	8/0/0	8/0/0	7/1/0	6/2/0
medical	8/0/0	4/2/2	7/1/0	8/0/0
corel5k	8/0/0	8/0/0	8/0/0	8/0/0

emotions	2/1/0	3/0/0	3/0/0	3/0/0
scene	3/0/0	3/0/0	3/0/0	3/0/0
yeast	0/6/2	0/6/2	1/4/3	1/5/2
cal500	0/3/5	3/5/0	6/2/0	6/2/0
genbase	5/3/0	8/0/0	5/3/0	4/4/0
medical	4/4/0	3/5/0	8/0/0	8/0/0
corel5k	7/1/0	7/1/0	7/1/0	1/7/0

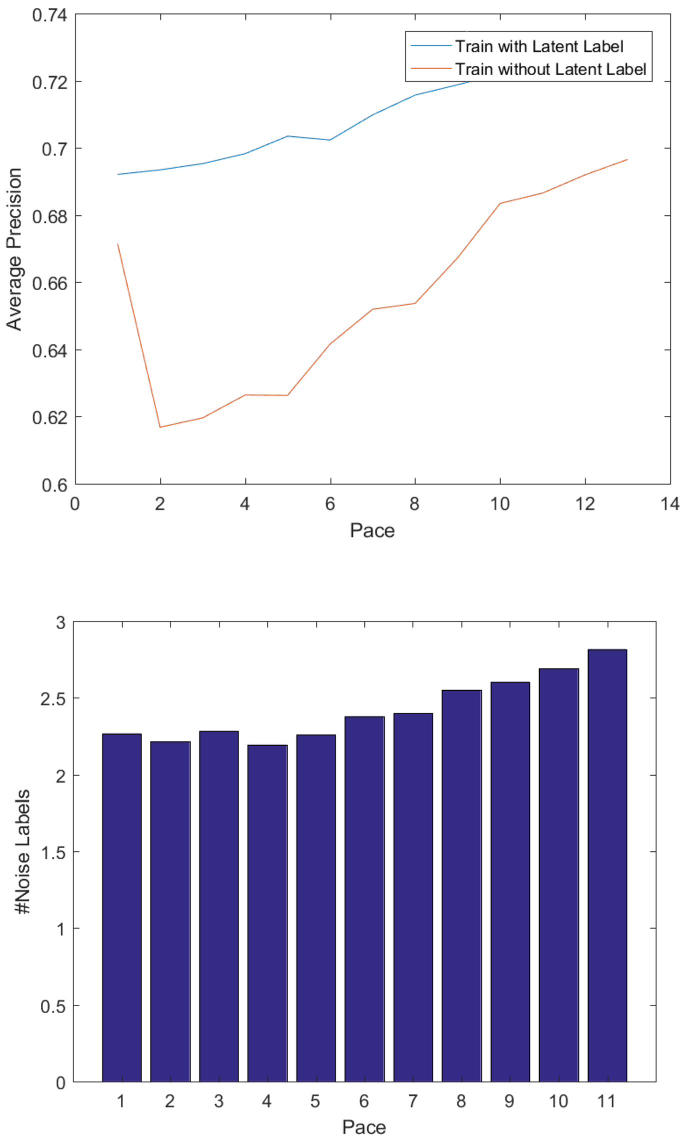
emotions	1/2/0	2/1/0	1/2/0	1/2/0
scene	3/0/0	3/0/0	3/0/0	3/0/0
yeast	2/1/5	1/3/4	4/3/1	3/3/2
cal500	0/7/1	3/4/1	2/6/0	2/6/0
genbase	7/1/0	8/0/0	0/8/0	0/8/0
medical	7/1/0	5/3/0	8/0/0	8/0/0
corel5k	8/0/0	7/0/1	7/0/1	0/2/6

emotions	3/0/0	3/0/0	3/0/0	3/0/0
scene	3/0/0	3/0/0	3/0/0	3/0/0
yeast	1/6/1	1/7/0	1/6/1	1/6/1
cal500	7/1/0	1/7/0	8/0/0	8/0/0
genbase	7/1/0	8/0/0	5/3/0	4/4/0
medical	7/1/0	4/4/0	8/0/0	8/0/0
corel5k	8/0/0	7/1/0	7/1/0	0/4/4

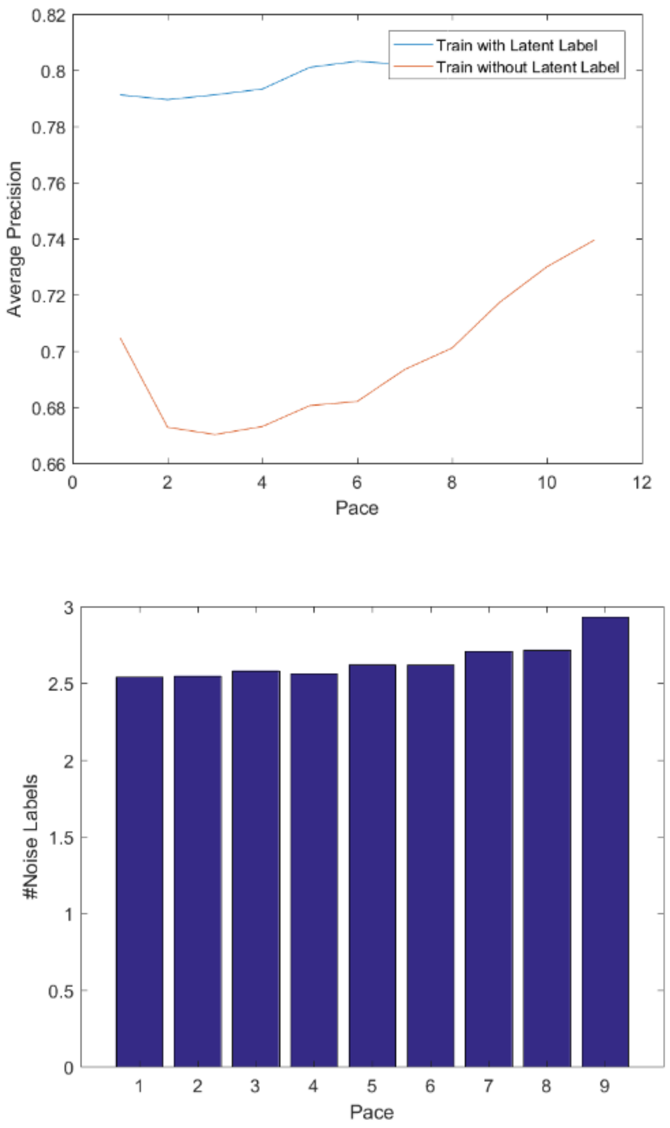
Hamming loss	36/ 6/4	34/ 6/6	39/ 7/0	39/ 6/1	148/25/11
Ranking loss	41/ 5/0	30/13/3	34/ 9/3	24/15/7	129/42/13
One-error	21/18/7	27/17/2	33/10/3	26/18/2	107/63/14
Coverage	28/12/6	29/11/6	25/19/2	17/21/8	99/63/22
Average precision	36/ 9/1	27/19/0	35/10/1	27/14/5	125/52/7
total	162/50/18	147/66/17	166/55/9	133/74/23	

- On seven datasets across all evaluation metrics, PMLSP ranks *1st* in 74.3% cases and ranks *2nd* in 11.4% cases.
- Out of 230 statistical tests (46 data sets 5 evaluation metrics), PMLSP is comparable to the counterpart PARVLS, PMLLRS, PML-lc and PML-fp in 92.2%, 92.6%, 96.1% and 90% cases.
- Furthermore, PMLSP significantly outperforms the counterpart PARVLS, PMLLRS, PML-lc and PML-fp in 70.4%, 63.9%, 72.1 and 57.8% cases.
- PMLSP achieves optimal performance in datasets emotions, scene, genbase and medical in almost all cases over five metrics(except on medical where PMLLRS outperforms PMLSP in term of *ranking loss*).

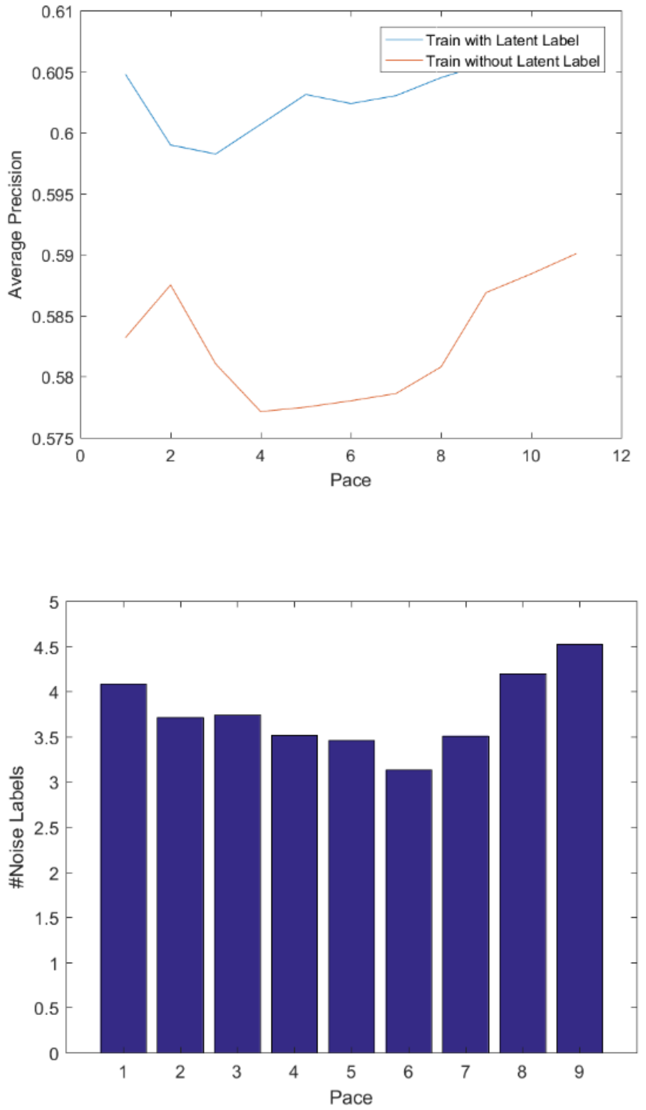
Experiment



emotions

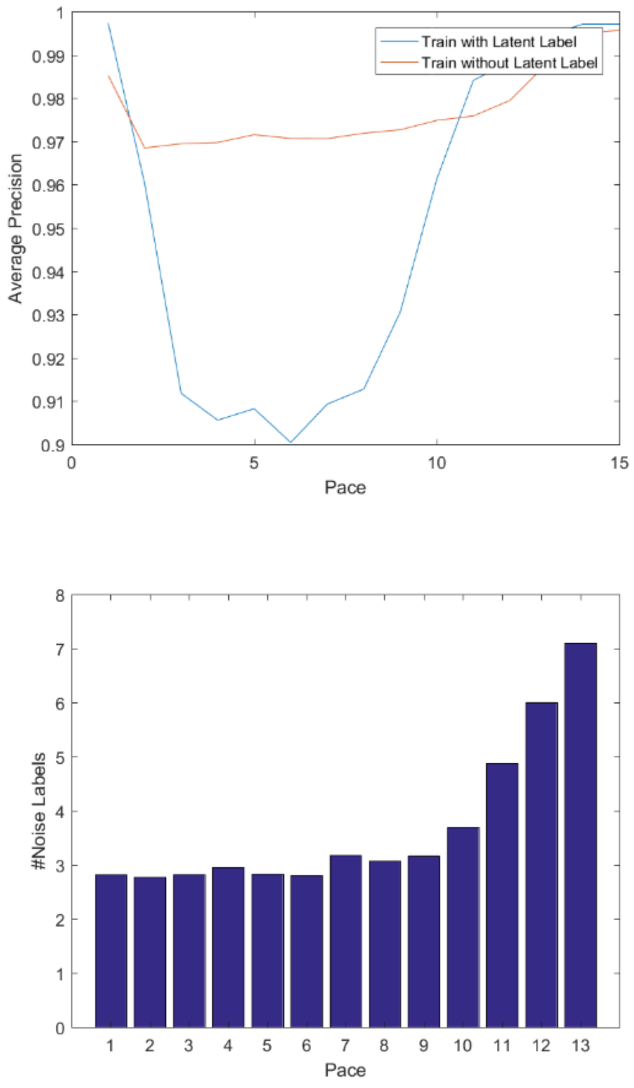


scene

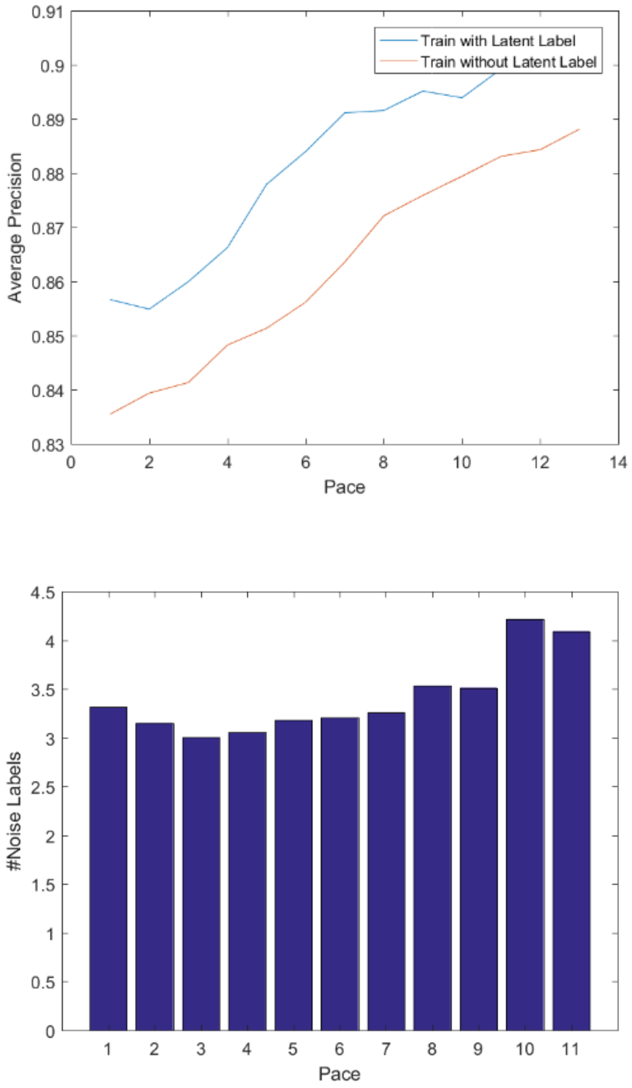


Cal500

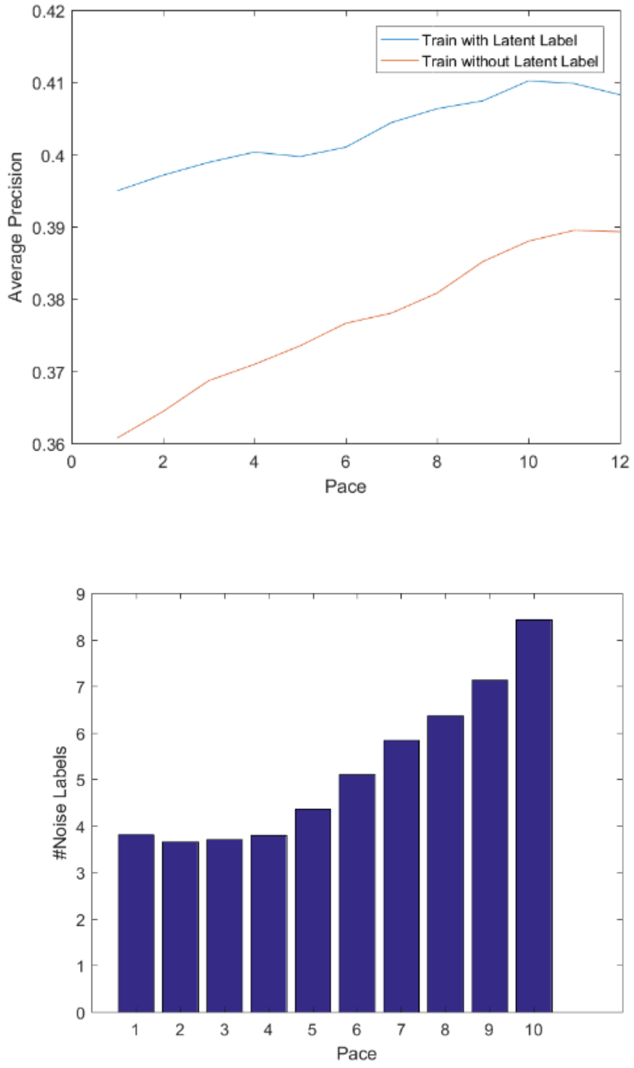
Experiment



genbase



medical



Corel5K

Thanks