



模式分析与机器智能  
工业和信息化部重点实验室  
MIT Key Laboratory of  
Pattern Analysis & Machine Intelligence

ParNeC | 模式识别与神经计算研究组  
Pattern Recognition and Neural Computing

# Boosting Semi-Supervised Learning by Exploiting All Unlabeled Data

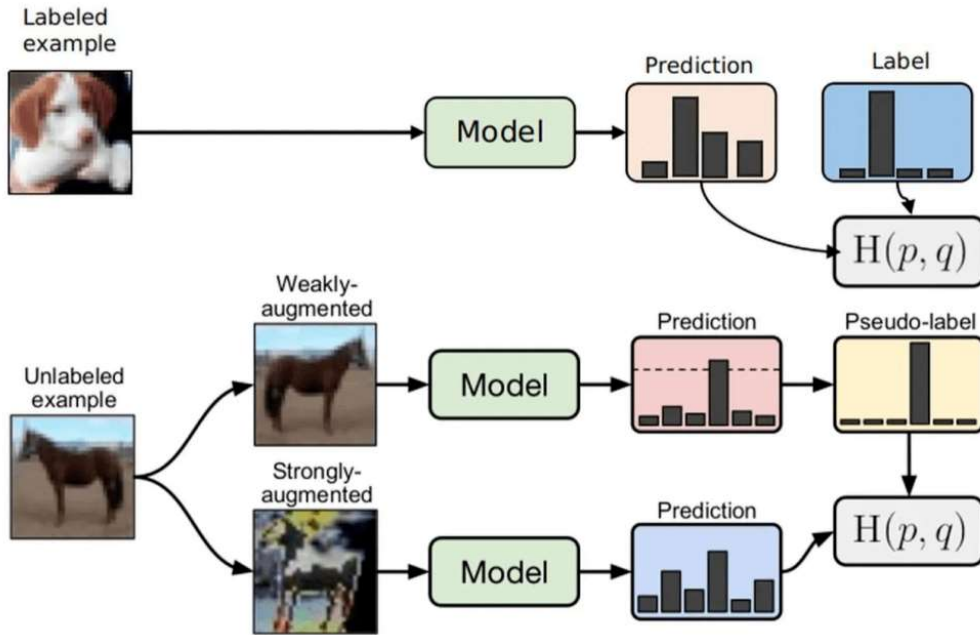
---

Yuhao Chen<sup>1</sup> Xin Tan<sup>2</sup> Borui Zhao<sup>1</sup> Zhaowei Chen<sup>1</sup> Renjie Song<sup>1</sup> Jiajun Liang<sup>1</sup> Xuequan Lu<sup>3</sup>  
<sup>1</sup>MEGVII Technology      <sup>2</sup>East China Normal University      <sup>3</sup>Deakin University  
{yhao.chen0617, zhaoborui.gm, chaoweichan}@gmail.com, xtan@cs.ecnu.edu.cn  
{songrenjie, liangjiajun}@megvii.com, xuequan.lu@deakin.edu.au

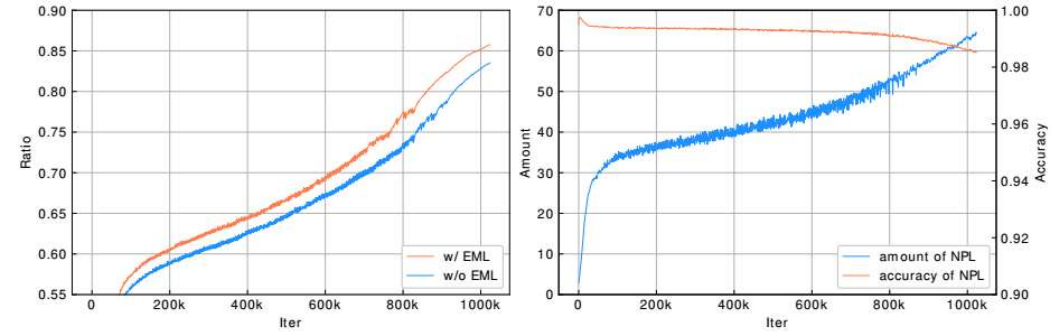
CVPR 2023

# Background

## How to utilize all unlabeled examples?

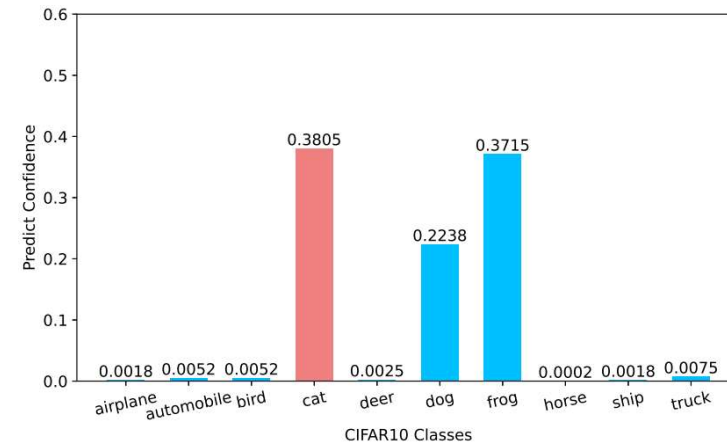


FixMatch



(a)

(b)



FullMatch = EML + ANL

## Entropy Meaning Loss(EML)

weakly-augmented:  $Q^{(i)} = [q_1^{(i)}, \dots, q_C^{(i)}]$

soft label:  $y_c^{(i)} = \frac{1 - \mathbb{1}(u_c^{(i)} = 0) \cdot p_c^{(i)}}{\sum_c \mathbb{1}(u_c^{(i)} = 1)}$

strongly-augmented:  $P^{(i)} = [p_1^{(i)}, \dots, p_C^{(i)}]$

mask:  $s_c^{(i)} = \mathbb{1}(q_c^{(i)} \geq \tau)$   
 $u_c^{(i)} = \mathbb{1}(\max(Q^{(i)}) \geq \tau) \cdot \mathbb{1}(s_c^{(i)} = 0)$

---

### EML\_loss

---

1. **Input:** pred\_w, pred\_s, k.

2. Generate Pseudo-label Mask mask\_p.

3. Generate top\_k-1 mask excluding max(pred\_w) from weakly augmented predictions.

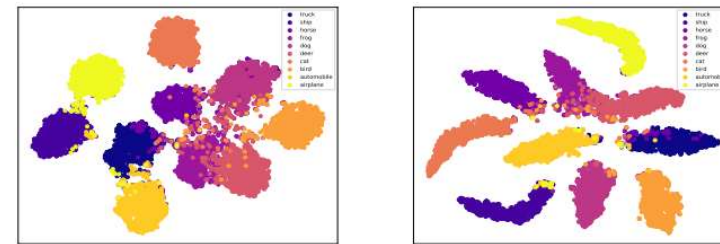
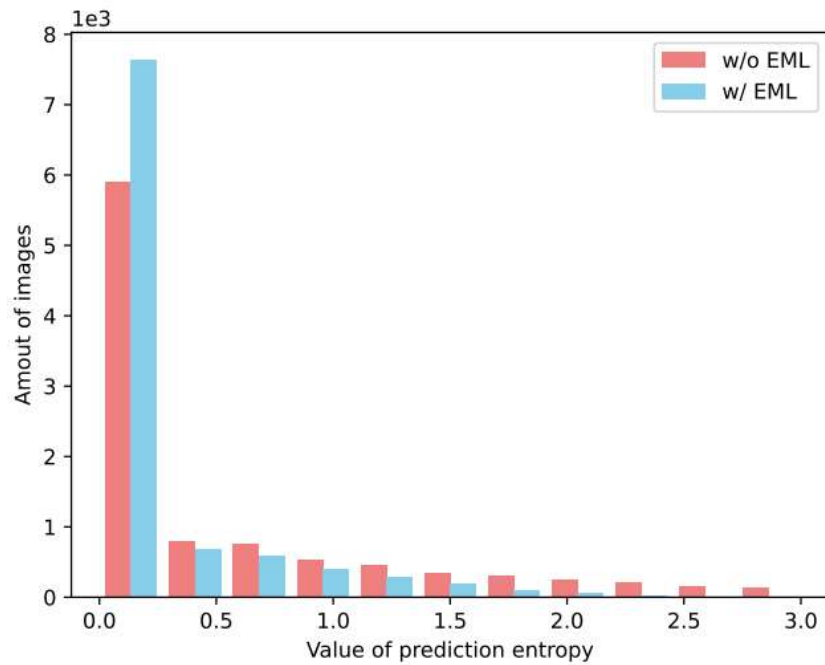
4. Compute the value of  $\sum_{i=1}^n \text{pred}_{s_c} / \sum_{c=1}^C \text{pred}_{s_c}$  using the mask.

5. compute cross-entropy.

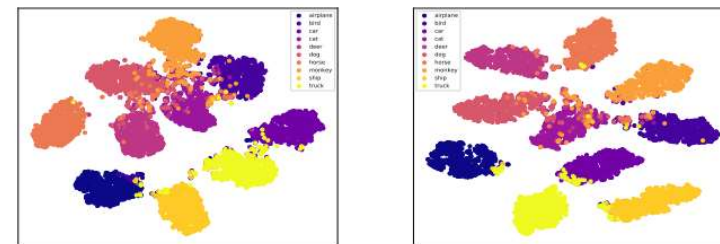
---

# Method

## Entropy Meaning Loss(EML)



(a) CIFAR-10

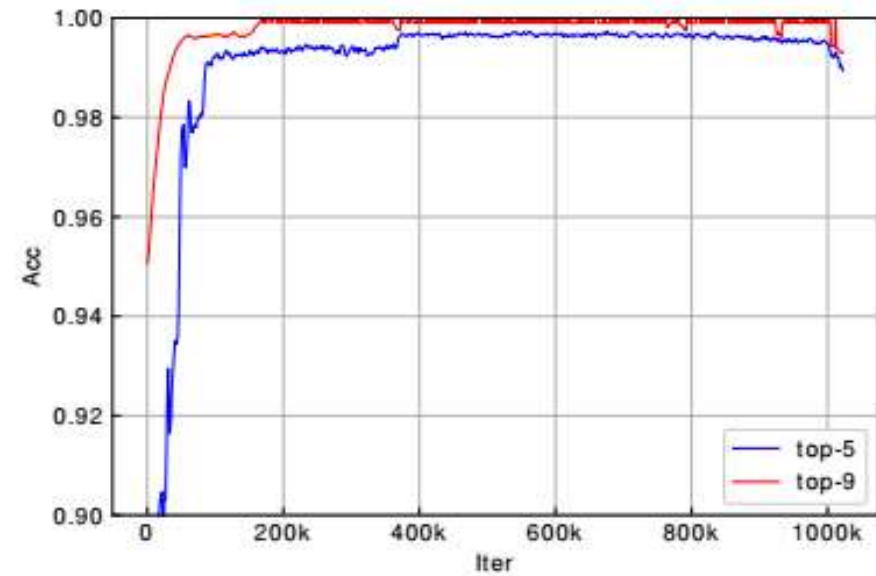


(b) STL-10

## Method

### top\_k & ANL

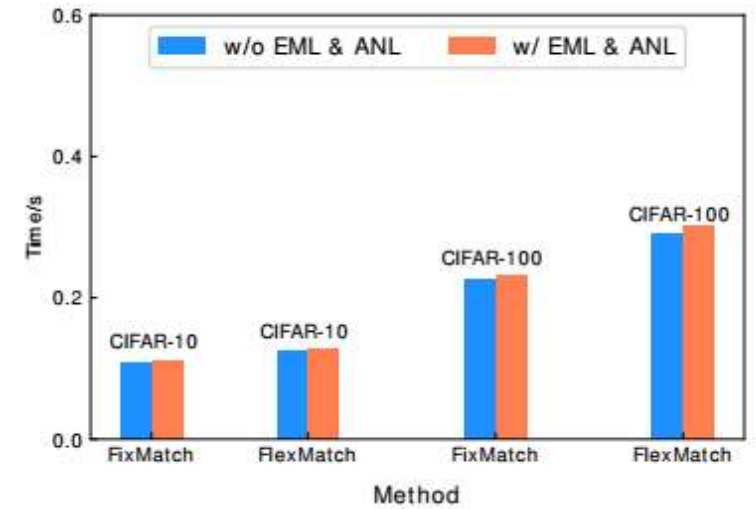
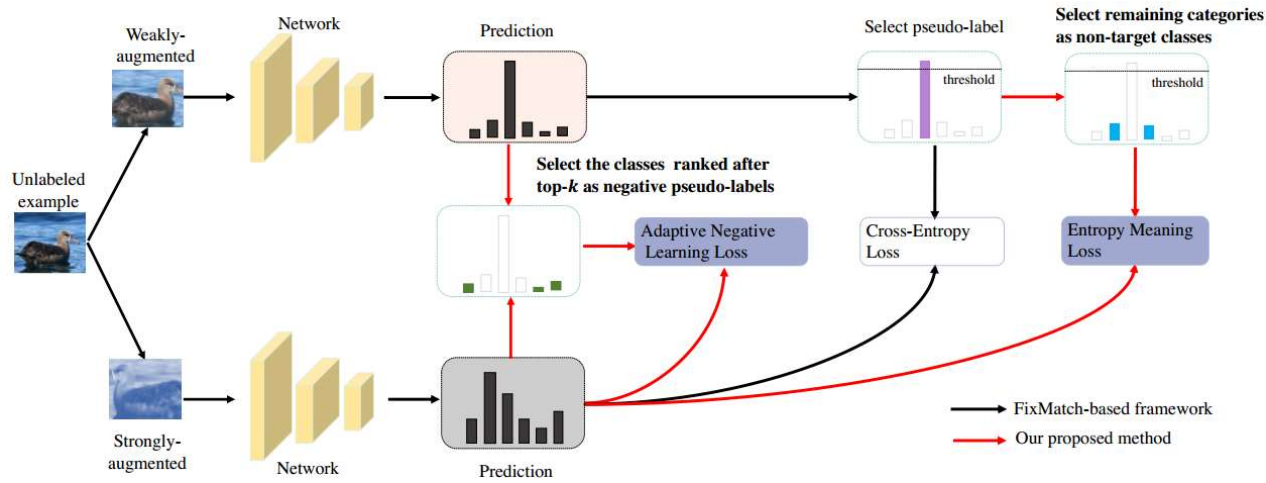
$$k = \arg \min_{\theta \in [2, C]} (Acc(P_t, \hat{Q}_t, \theta) = 100\%)$$



$$- \frac{1}{B} \sum_{i=1}^B \sum_{c=1}^C \mathbb{1}[\text{Rank}(q_c^{(i)}) > k] \log(1 - p_c^{(i)})$$

# Method

## FullMatch



# Experiment

Label Amount	CIFAR-10			CIFAR-100			SVHN		STL-10
	40	250	4000	400	2500	10000	40	1000	1000
UDA [33]	89.38±3.75	94.84±0.06	95.71±0.07	53.61±1.59	72.27±0.21	77.51±0.23	94.88±4.27	<b>98.11</b> ±0.01	93.36±0.17
RemixMatch [2]	90.12±1.03	93.7±0.05	95.16±0.01	57.25±1.05	73.97±0.35	<b>79.98</b> ±0.27	75.96±9.13	94.84±0.31	93.26±0.14
Semco <sup>†</sup> [21]	92.13±0.22	94.88±0.27	96.20±0.08	55.89±1.18	68.07±0.01	75.55±0.12	-	-	92.51±0.29
Dash [34]	86.78±3.75	95.44±0.13	95.92±0.06	55.24±0.96	72.82±0.21	78.03±0.14	96.97±1.59	97.97±0.06	92.74±0.40
UPS [24]	94.74±0.29	94.89±0.08	95.75±0.05	58.93±1.66	72.86±0.24	78.03±0.23	-	-	93.98±0.28
AlphaMatch <sup>†</sup> [11]	91.35±3.38	95.03±0.29	-	61.26±3.13 <sup>†</sup>	<b>74.98</b> ±0.27 <sup>†</sup>	-	97.03±0.26	-	90.36±0.75
CoMatch [18]	93.12±0.92	95.10±0.35	95.94±0.03	59.98±1.11	72.99±0.21	78.17±0.23	-	-	91.34±0.41
SimMatch <sup>†‡</sup> [41]	94.40±1.37	95.16±0.39	96.04±0.01	62.19±2.21	74.93±0.32	79.42±0.11	-	-	-
CR [9]	94.31±0.9	94.96±0.3	95.84±0.13	50.77±0.79	72.42±0.37	78.97±0.23	96.33±1.84	97.61±0.06	93.04±0.42
NP-Match [30]	95.09±0.04	95.04±0.06	95.89±0.02	61.08±0.99	73.97±0.26	78.78±0.13	-	-	94.41±0.24
FixMatch [26]	92.53±0.28	95.14±0.05	95.79±0.08	57.45±1.76	71.97±0.16	77.8±0.12	96.19±1.18	<b>98.04</b> ±0.03	93.75±0.33
FullMatch (ours)	<b>94.11</b> ±1.01	<b>95.36</b> ±0.12	<b>96.25</b> ±0.08	<b>59.42</b> ±1.40	<b>73.06</b> ±0.40	<b>78.56</b> ±0.10	<b>97.65</b> ±0.10	98.01±0.03	<b>94.26</b> ±0.09
FlexMatch [38]	95.03±0.06	95.02±0.09	95.81±0.01	60.06±1.62	73.51±0.2	78.1±0.15	96.08±1.24	97.37±0.06	94.23±0.18
FullFlex (ours)	<b>95.56</b> ±0.15	<b>95.61</b> ±0.04	<b>96.28</b> ±0.03	<b>62.60</b> ±0.64	<b>74.60</b> ±0.42	<b>79.26</b> ±0.21	<b>97.48</b> ±0.04	<b>97.58</b> ±0.02	<b>94.50</b> ±0.12

Table 1. **Top-1 accuracy (%) for CIFAR-10/100, SVHN and STL-10 datasets on 3 different folds.** *FullFlex* indicates applying our method to FlexMatch. <sup>†</sup> indicates introducing an additional technique named DA (Distribution Alignment) [2]. <sup>‡</sup> represents the result comes from the original paper.

	Top-1	Top-5
UPS [24]	57.31	79.77
NP-Match [30]	58.22	80.67
FixMatch [26]	56.34	78.20
FullMatch (ours)	<b>57.44 (+1.1)</b>	<b>79.26 (+1.06)</b>
FlexMatch [38]	58.15	80.52
FullFlex (ours)	<b>59.58 (+1.43)</b>	<b>81.38 (+0.86)</b>

Table 2. **Top-1 and Top-5 accuracy (%) on ImageNet.** In green are the values of performance improvement over the baselines.

# Experiment

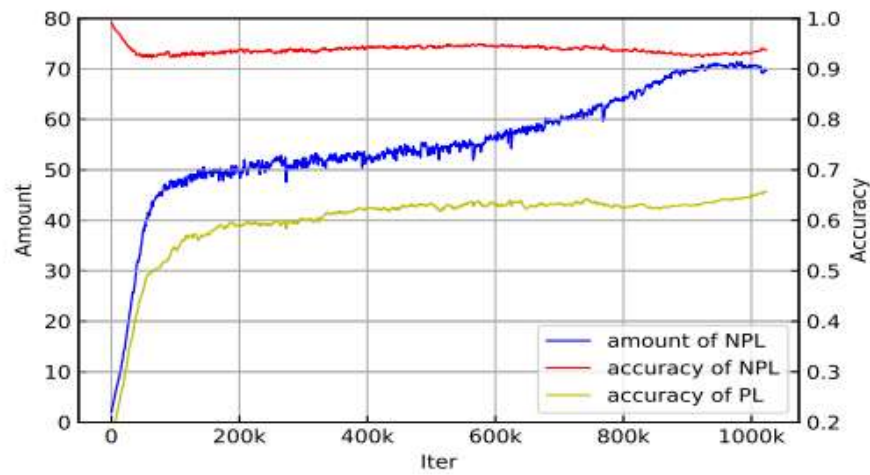


Figure 1. Visualize the experimental results on CIFAR-100 with 400 label samples.

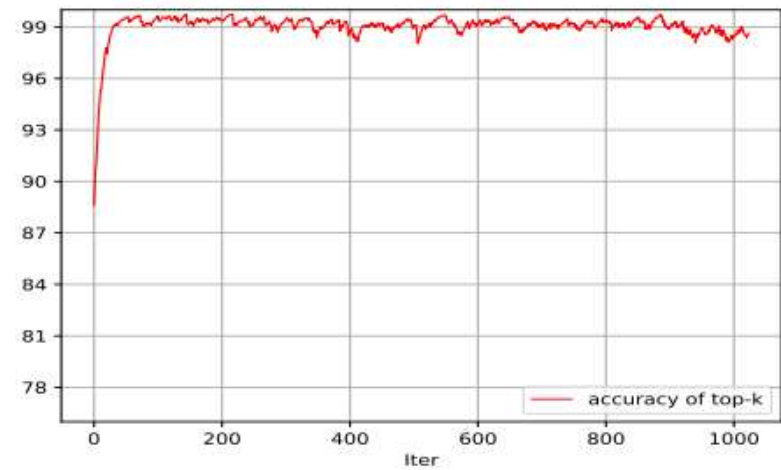


Figure 2. Visualizations the accuracy of top- $k$  in the first 1K iterations on CIFAR-100 with 400 label samples.

# Ablation Study

	CE	BCE	w PL	w/o PL	Accuracy	$\Delta$
FixMatch					57.68	-
EML	✓				58.35	+0.67
		✓			<b>58.47</b>	<b>+0.79</b>
ANL			✓		57.83	+0.15
				✓	58.59	+0.91
			✓	✓	<b>58.67</b>	<b>+0.99</b>
FullMatch		✓	✓	✓	<b>59.32</b>	<b>+1.64</b>

Table 3. Ablation study of FullMatch on 400-label split from CIFAR-100. CE and BCE represent the loss implementation of EML. “w PL” and “w/o PL” means applying ANL on examples with/without pseudo-label, respectively.  $\Delta$  represents the performance improvement over the baseline.

$\alpha$	0.5			1.0			2.0		
$\beta$	0.5	1.0	2.0	0.5	1.0	2.0	0.5	1.0	2.0
acc	78.43	78.36	78.50	78.38	78.46	78.48	78.49	78.31	78.47

Table 4. Ablation study on  $\alpha$  and  $\beta$ . All experiments are conducted on CIFAR-100 with 10000-label.

**Thanks**