# Leveraging Ensemble Diversity for Robust Self-Training under Sample Selection Bias

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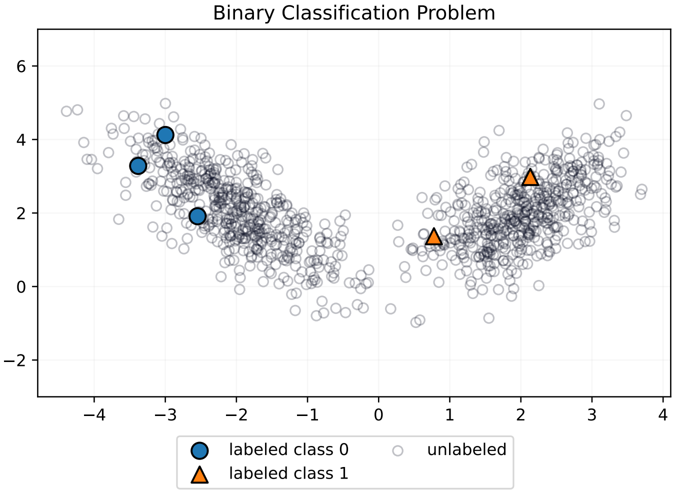
ENS DE LYON

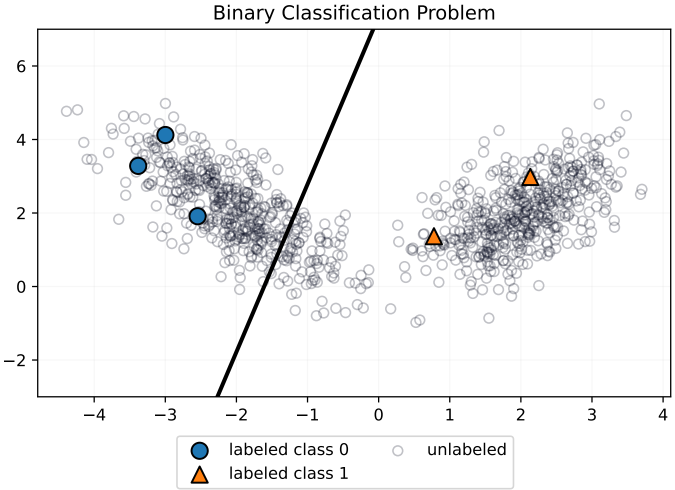
# Outline

1. Introduction
2. Failure of Self-Training
3. Learning with the $\mathcal{T}$-similarity
4. Numerical Experiments
5. Discussion

In some applications, data acquisition is cheaper than labeling . . .



. . . and supervised learning is inefficient.



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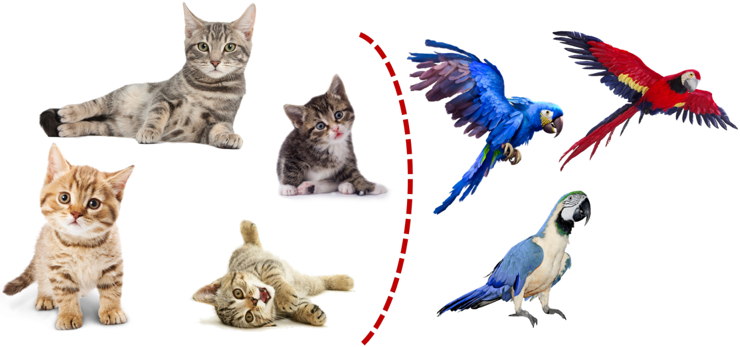

# Families of SSL Methods

- ⋆ Pseudo-labeling (Amini et al., 2023):
  - Unlabeled regularization (Feofanov et al., 2023)
  - Self-training (Feofanov et al., 2019)
- ⋆ Graph-based algorithms (van Engelen and Hoos, 2020):
  - Label propagation
  - Label spreading
- ⋆ Unsupervised preprocessing (van Engelen and Hoos, 2020):
  - Cluster-then-label
  - Feature extraction: auto-encoders, PCA
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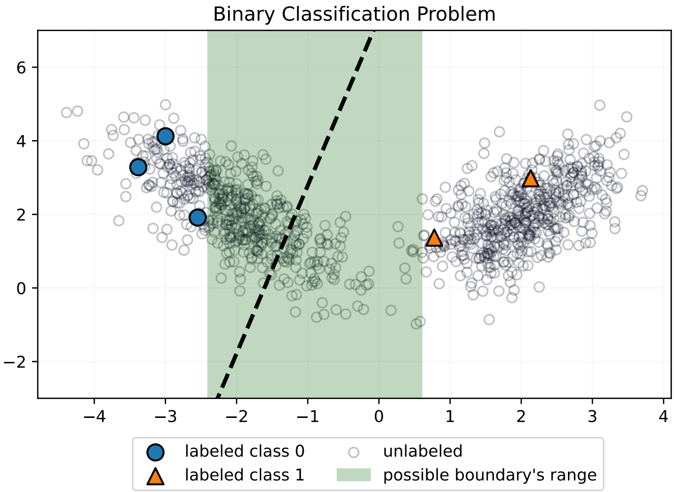
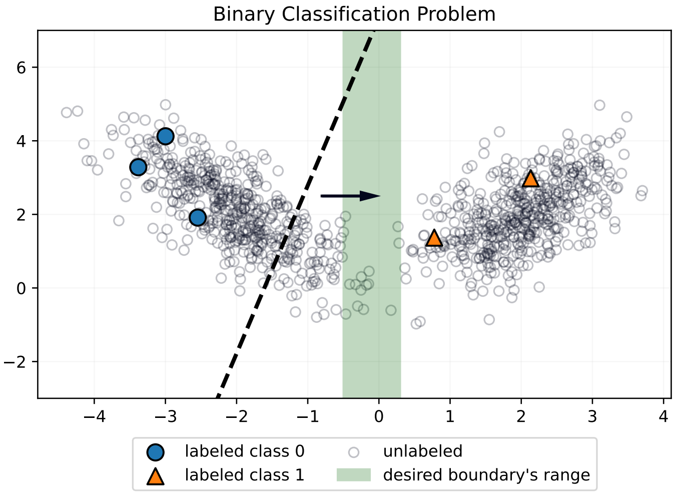
# Low Density Separation

Range of possible supervised classifiers is vast: we need to make assumptions.



Low Density Separation (LDS) assumption: push boundary away from regions of unlabeled data.



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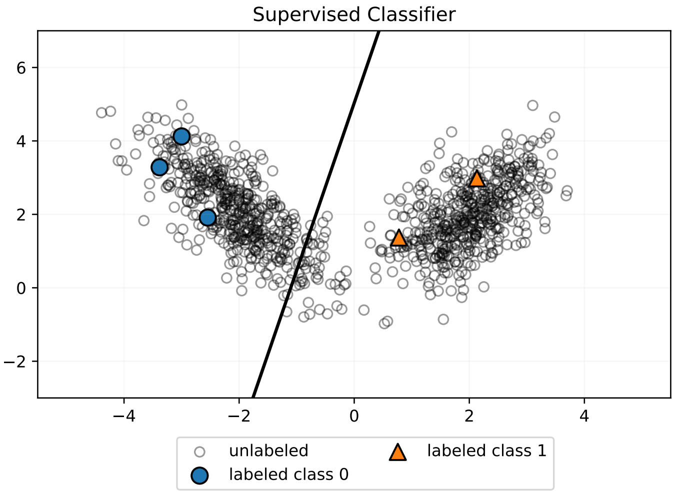
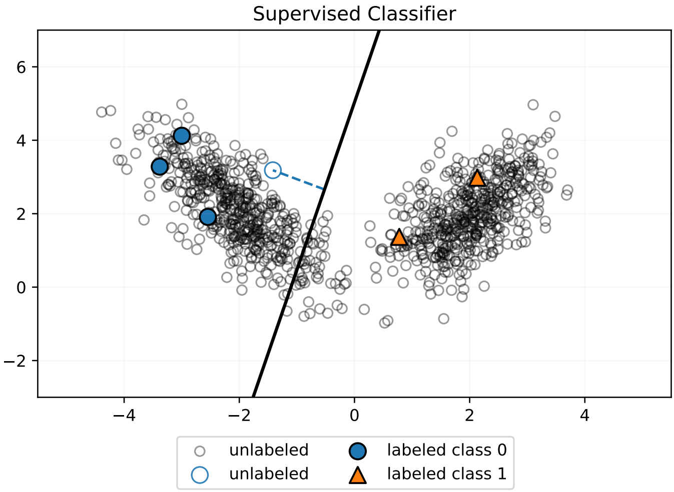
Start from a supervised classifier trained on the labeled set.

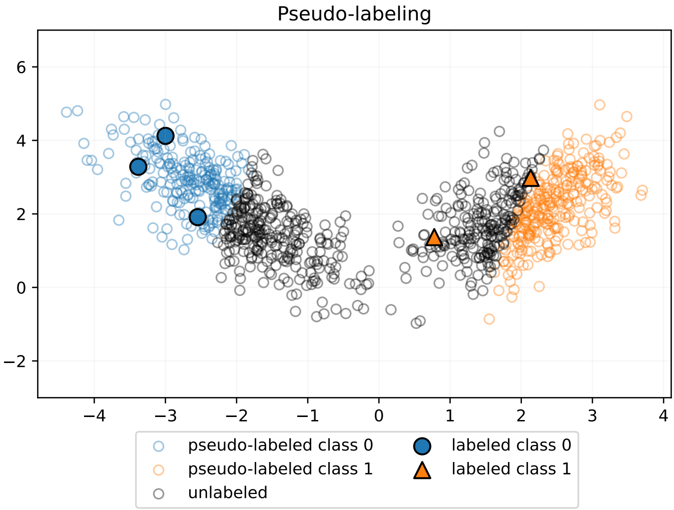


# Self-Training

Predict labels and confidence scores for unlabeled data.



Pseudo-label most confident data and include in the labeled set.



# Self-Training

Retrain the model and repeat the same procedure again.

And again. . .


Self-Training Iteration 2
6
4
2
0
−2
−4
−2
0
2
4
pseudo-labeled class 0
pseudo-labeled class 1
unlabeled
labeled class 0
labeled class 1

# Self-Training

Until there are no data to pseudo-label.

# Self-Training

Self-training pushed the boundary away from the confident data.

# Outline

# Two Fundamental Questions

$\star$ *Confidence Estimation* $\rightarrow$ How to rank unlabeled data?

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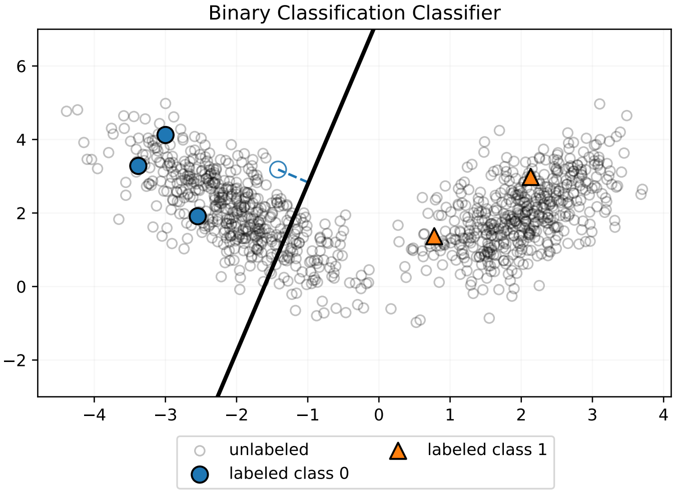
In this work, we focus on *Confidence Estimation*.

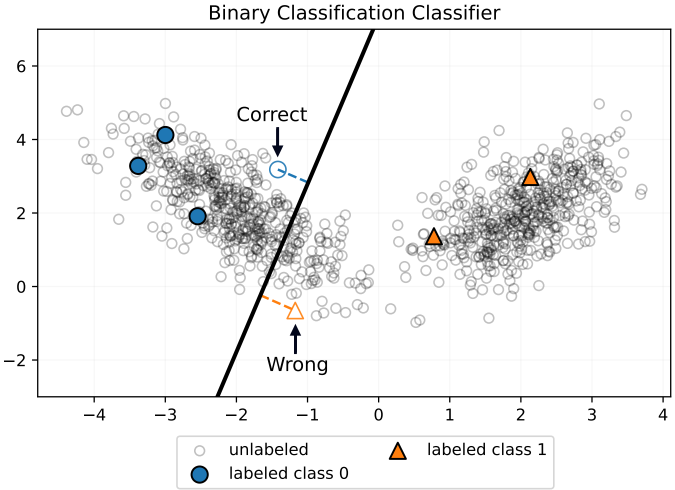
# Failure Cases

Requirements → trust the classifier's predictions.



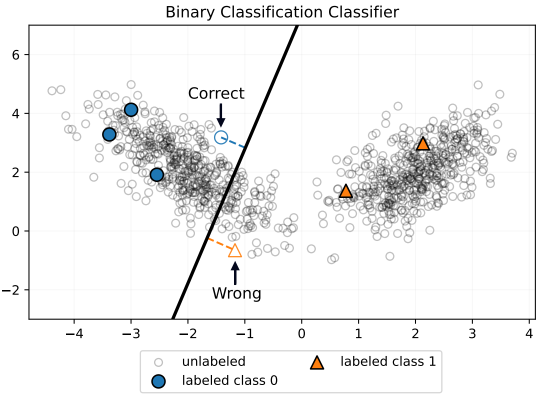
# Failure Cases

Problem $\rightarrow$ not safe since the prediction can be wrong.



# Failure Cases

Biased prediction confidence ⇒ wrong direction can be chosen.
→ This can occur when there is a distribution shift in the data.



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  - Creation of group study in clinical trials;
  - People with poor mobility less likely to be in street surveys;
  - Labeling can be constrained for privacy reasons.

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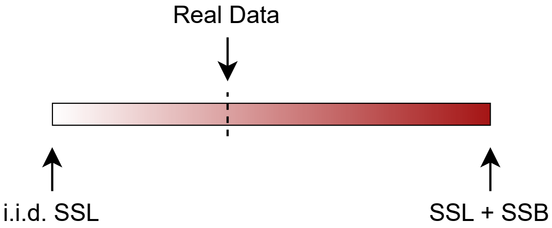
- Creation of group study in clinical trials;
- People with poor mobility less likely to be in street surveys;
- Labeling can be constrained for privacy reasons.

⋆ SSB has been studied but not in the case of SSL.

# SSL under Sample Selection Bias

SSL + SSB combines SSL and Sample Selection Bias (SSB):

1. Few labeled examples (SSL)
2. Biased labeling procedure (SSB)




Goal → obtain a method good on **both** i.i.d. SSL and SSL + SSB.

# Implementation of SSL + SSB

Select the labeled set to violate the i.i.d. assumption.

- Binary selection variable $s_i$ for each $\mathbf{x}_i$;
- $s_i = 1$ if $\mathbf{x}_i$ is labeled, $s_i = 0$ otherwise;
- Model $\mathbb{P}(s_i = 1|\mathbf{x}_i, y_i)$ to violate i.i.d. assumption.

# Implementation of SSL + SSB

Select the labeled set to violate the i.i.d. assumption.

`PCA-Bias` $\rightarrow$ for each class $c$,

1. Apply `PCA` on training data of class $c$;
2. Compute $\mathrm{proj}_1(\mathbf{x}_i)$, projection value on PC1;
3. $\mathbb{P}(s_i = 1 | \mathbf{x}_i, y_i = c) \propto \exp(r \cdot |\mathrm{proj}_1(\mathbf{x}_i)|), \quad r > 0.$

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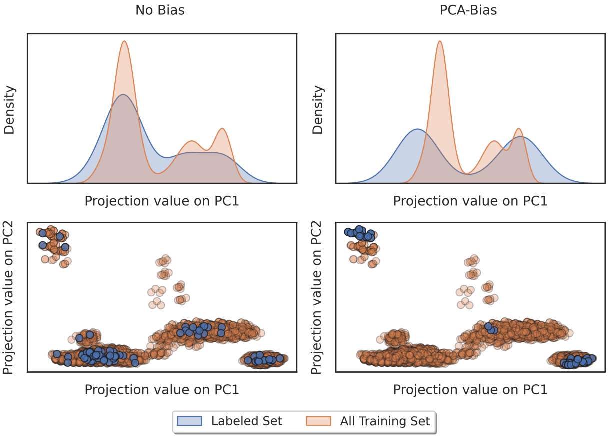

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- ⋆ `ERM` corresponds to supervised learning on the labeled set
- ⋆ $\texttt{PL}_{\theta=0.8}$ uses a fixed threshold $\theta = 0.8$ (Lee, 2013)
- ⋆ $\texttt{CSTA}_{\Delta=0.4}$ takes $\Delta\%$ most confident (Cascante-Bonilla et al., 2020)
- ⋆ `MSTA` optimizes the threshold to balance the error and the amount of data pseudo-labeled (Feofanov et al., 2019)

# Failure of Self-Training under SSL + SSB

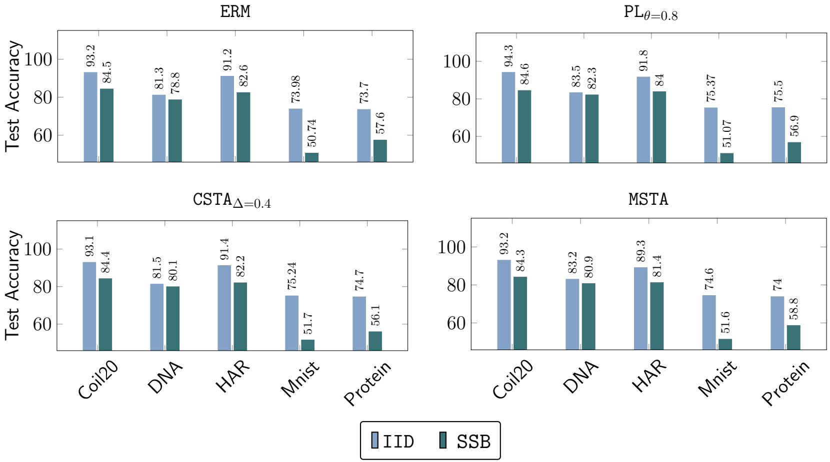



Figure: Test accuracies of the different baselines on $5$ datasets. Full results to be found here.

LOO over-optimistic w.r.t. generalization performance (Figure 1).

- Leave one labeled point out;
- Train on the remaining $n_\ell - 1$;
- Test on the one left out;
- Repeat for each labeled point.

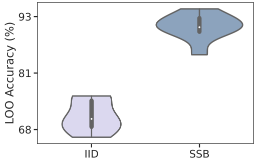


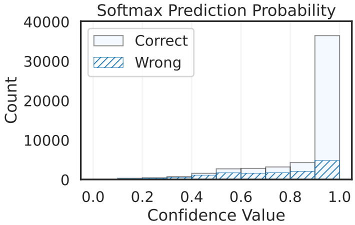

Figure: LOO on Mnist.

# Outline

# Motivation

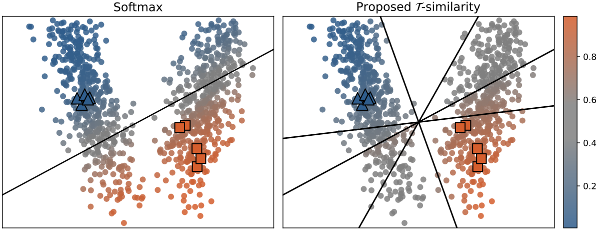
`softmax`-based confidence measure is unreliable in SSL + SSB.

- NNs are overconfident;
- `softmax` predictions biased towards the labeled set.




$\rightarrow$ We propose a novel confidence measure for NNs.

# Leveraging Ensemble Diversity




$$\min_{\mathcal{T}} \frac{1}{M} \sum_{h \in \mathcal{T}} \underbrace{\left( \frac{1}{n_\ell} \sum_{(\mathbf{x},y) \in \mathbf{X}_\ell \times \mathbf{y}_\ell} \ell(h(\mathbf{x}), y) \right)}_{\text{supervised loss}} + \underbrace{\frac{\gamma}{n_u M(M-1)} \sum_{h \neq \tilde{h} \in \mathcal{T}} \sum_{\mathbf{x} \in \mathbf{X}_u} h(\mathbf{x})^\top \tilde{h}(\mathbf{x})}_{\text{agreement loss}}$$

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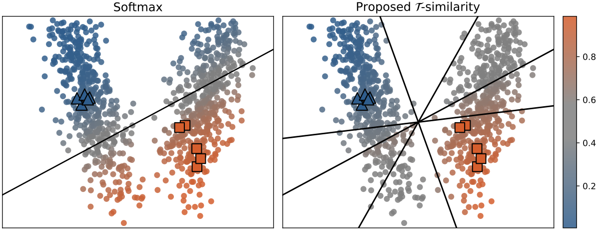


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We jointly train the ensemble to

1. Fit very well the labeled data
2. Disagree as much as possible on unlabeled data

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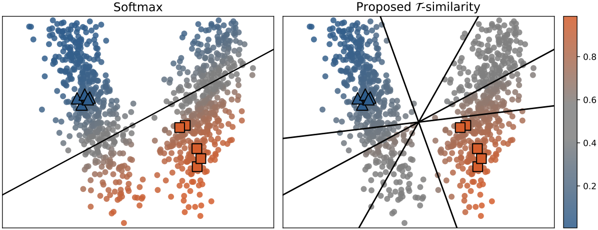


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We jointly train the ensemble to

1. Fit very well the labeled data
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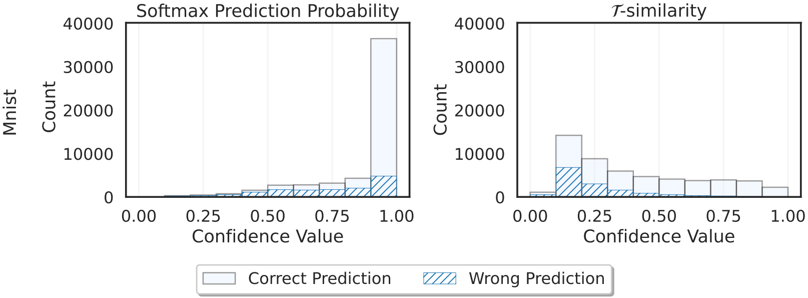
⋆ We define the $\mathcal{T}$-similarity as:

$$s_{\mathcal{T}}(\mathbf{x}) = \frac{1}{M(M-1)} \sum_{h \neq \tilde{h} \in \mathcal{T}} h(\mathbf{x})^\top \tilde{h}(\mathbf{x}).$$

⋆ For any $\mathbf{x}$, we have $0 \leq s_{\mathcal{T}}(\mathbf{x}) \leq 1$.



# Practical Implementation

1. Projection layers are learned through a classification head;
2. Confidence estimator is ensemble of $M = 5$ linear heads that don't affect representation.

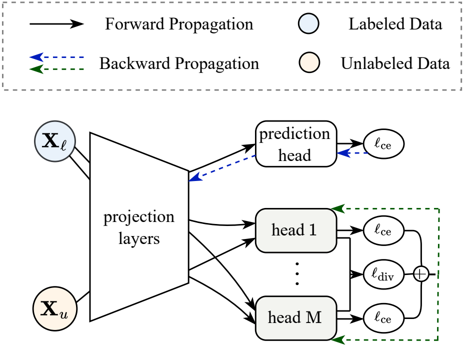



Figure: Architecture of the model.

# Binary Linear Case

- Fixed representation of dimension $d$, binary linear classification
- Linear ensemble $\mathbf{W} = \{\boldsymbol{w}_m \in \mathbb{R}^d | 1 \leq m \leq M\}$
- Prediction of $\boldsymbol{\omega}_m$ on $\mathbf{x}$ is $\operatorname{sign}(\boldsymbol{\omega}_m^\top \mathbf{x})$

$$\underset{\mathbf{W}\in\mathbb{R}^{d\times M}}{\operatorname{argmin}} \mathcal{L}(\mathbf{W}) := \underbrace{\frac{1}{Mn_\ell}\sum_{m=1}^{M}\sum_{i=1}^{n_\ell}\left(y_i - \boldsymbol{\omega}_m^\top \mathbf{x}_i\right)^2}_{\text{label fidelity term}} + \underbrace{\frac{1}{M}\sum_{m=1}^{M}\lambda_m \|\boldsymbol{\omega}_m\|^2}_{\text{regularization}}$$

$$+ \underbrace{\frac{\gamma}{n_u M(M-1)} \sum_{m\neq k} \sum_{i=n_\ell+1}^{n_\ell+n_u} w_m^\top \mathbf{x}_i w_k^\top \mathbf{x}_i,}_{\text{agreement term}} \qquad \textbf{(P)}$$

where $\gamma$ controls the influence of the diversity on the learning.

# Convergence to a Stationary Point

- Labeled set $(\mathbf{X}_\ell, \mathbf{y}_\ell) = (\mathbf{x}_i, y_i)_{i=1}^{n_\ell}$
- Unlabeled set $\mathbf{X}_u = (\mathbf{x}_i)_{i=n_\ell+1}^{n_\ell+n_u}$
- Assumption:

$$\forall m \in [\![1, M]\!], \lambda_m > \frac{\gamma(M+1)}{n_u(M-1)} \lambda_{max}(\mathbf{X}_u^\top \mathbf{X}_u) \qquad \textbf{(A)}$$

**Theorem (O., Feofanov, Redko)**

*Under Assumption **A**, $\mathcal{L}$ is strictly convex and coercive on $\mathbb{R}^{d\times M}$. Hence, the optimization problem (**P**) admits a unique solution $\mathbf{W}^*$ that verifies*

$$\nabla\mathcal{L}(\mathbf{W}^*) = 0. \qquad (1)$$

# Diversity of an Ensemble

$$\ell_{\text{div}}(\mathbf{W}, \mathbf{X}_u) = -\frac{1}{n_u M(M-1)} \sum_{m \neq k} \boldsymbol{\omega}_m^\top \mathbf{X}_u^\top \mathbf{X}_u \boldsymbol{\omega}_k.$$

**Theorem (O., Feofanov, Redko)**

$$\gamma \ell_{div}(\mathbf{W}^*, \mathbf{X}_u) \geq \frac{1}{2 n_\ell M} \sum_{m=1}^{M} \|\mathbf{y}_\ell - \mathbf{X}_\ell \boldsymbol{\omega}_m^*\|_2^2 + \frac{1}{2M} \sum_{m=1}^{M} (\boldsymbol{\omega}_m^*)^\top \left(\lambda_m \mathbf{I}_d + \frac{\mathbf{X}_\ell^\top \mathbf{X}_\ell}{n_\ell}\right) \boldsymbol{\omega}_m^*.$$

1. Trade-off between supervised performance and margin term
2. Assuming orthogonality, the predictors $\boldsymbol{\omega}_m$ span the $M$ directions of largest variance of the labeled data.

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**Theorem (O., Feofanov, Redko)**

$$\gamma \ell_{\textit{div}}(\mathbf{W}^*, \mathbf{X}_u) \geq \frac{1}{2M}\left(\lambda + \frac{1}{n_\ell}\lambda_{\min}\left(\mathbf{X}_\ell^\top \mathbf{X}_\ell\right)\right)\|\mathbf{W}^*\|_{\mathrm{F}}^2.$$

1. Direction of smallest variance is also important for diversity
2. Theorem shows the importance of representation learning

# Outline

# Diversity provides Calibrated Confidence Measure

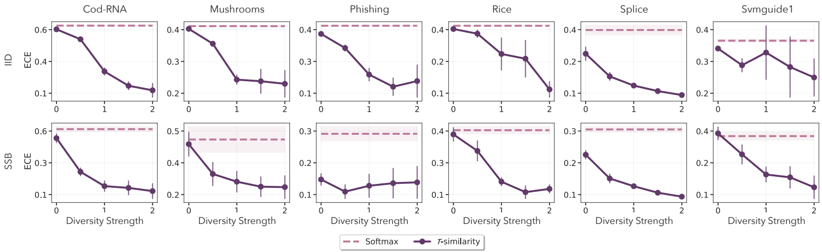


Figure: Increasing the diversity improves the classifier's calibration

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# Results in SSL+SSB

| Dataset | ERM | $\mathrm{PL}_{\theta=0.8}$ | | $\mathrm{CSTA}_{\Delta=0.4}$ | | MSTA | |
|---|---|---|---|---|---|---|---|
| | | softmax | $\mathcal{T}$-similarity | softmax | $\mathcal{T}$-similarity | softmax | $\mathcal{T}$-similarity |
| Cod-RNA | $74.51 \pm 8.86$ | $74.75 \pm 8.14$ | $\mathbf{80.06 \pm 3.55}$ | $73.39 \pm 7.36$ | $\mathbf{78.39 \pm 4.66}$ | $75.28 \pm 8.79$ | $\mathbf{76.88 \pm 7.67}$ |
| COIL-20 | $84.54 \pm 2.19$ | $\mathbf{84.69 \pm 3.56}$ | $84.57 \pm 2.85$ | $84.38 \pm 3.05$ | $\mathbf{84.57 \pm 3.16}$ | $\mathbf{84.32 \pm 2.34}$ | $84.07 \pm 2.85$ |
| Digits | $75.68 \pm 4.59$ | $\mathbf{80.47 \pm 3.8}$ | $78.2 \pm 3.34$ | $78.4 \pm 3.28$ | $\mathbf{79.14 \pm 3.5}$ | $78.02 \pm 5.15$ | $\mathbf{79.8 \pm 5.92}$ |
| DNA | $78.82 \pm 2.31$ | $\mathbf{80.29 \pm 2.24}$ | $79.06 \pm 2.31$ | $80.12 \pm 2.08$ | $\mathbf{80.76 \pm 2.24}$ | $80.89 \pm 2.64$ | $\mathbf{84.09 \pm 1.7}$ |
| DryBean | $64.6 \pm 3.89$ | $\mathbf{65.6 \pm 4.18}$ | $61.55 \pm 4.91$ | $\mathbf{64.91 \pm 3.72}$ | $64.6 \pm 3.53$ | $66.24 \pm 4.31$ | $\mathbf{67.0 \pm 3.96}$ |
| HAR | $82.57 \pm 1.96$ | $82.87 \pm 3.02$ | $\mathbf{83.12 \pm 2.27}$ | $82.19 \pm 2.61$ | $\mathbf{83.53 \pm 3.77}$ | $\mathbf{81.35 \pm 2.54}$ | $81.16 \pm 1.63$ |
| Mnist | $50.74 \pm 2.25$ | $51.08 \pm 2.55$ | $\mathbf{52.69 \pm 2.42}$ | $51.7 \pm 3.52$ | $\mathbf{54.26 \pm 1.82}$ | $51.6 \pm 2.58$ | $\mathbf{54.18 \pm 2.34}$ |
| Mushrooms | $69.45 \pm 7.29$ | $59.53 \pm 10.46$ | $\mathbf{71.36 \pm 6.63}$ | $62.98 \pm 7.25$ | $\mathbf{77.55 \pm 7.65}$ | $72.16 \pm 7.59$ | $\mathbf{76.16 \pm 13.04}$ |
| Phishing | $67.42 \pm 3.55$ | $66.08 \pm 5.66$ | $\mathbf{77.41 \pm 3.93}$ | $66.88 \pm 5.64$ | $\mathbf{76.17 \pm 8.58}$ | $69.48 \pm 4.37$ | $\mathbf{75.83 \pm 7.52}$ |
| Protein | $57.57 \pm 6.33$ | $57.45 \pm 6.36$ | $\mathbf{57.61 \pm 6.23}$ | $56.09 \pm 5.61$ | $\mathbf{57.74 \pm 7.8}$ | $58.81 \pm 6.54$ | $\mathbf{59.88 \pm 6.29}$ |
| Rice | $79.19 \pm 5.12$ | $80.54 \pm 4.31$ | $\mathbf{81.1 \pm 4.28}$ | $79.88 \pm 4.48$ | $\mathbf{81.56 \pm 3.61}$ | $80.35 \pm 4.89$ | $\mathbf{82.63 \pm 5.63}$ |
| Splice | $66.13 \pm 4.47$ | $67.14 \pm 2.62$ | $\mathbf{67.45 \pm 2.53}$ | $67.28 \pm 2.07$ | $\mathbf{68.05 \pm 2.17}$ | $66.08 \pm 4.98$ | $\mathbf{66.32 \pm 4.73}$ |
| Svmguide1 | $70.89 \pm 10.98$ | $70.35 \pm 11.74$ | $\mathbf{81.07 \pm 5.39}$ | $69.84 \pm 11.06$ | $\mathbf{74.46 \pm 7.23}$ | $71.04 \pm 11.11$ | $\mathbf{73.13 \pm 8.82}$ |

⋆ $\mathcal{T}$-similarity is better overall;

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| DNA | $78.82 \pm 2.31$ | $\mathbf{80.29 \pm 2.24}$ | $79.06 \pm 2.31$ | $80.12 \pm 2.08$ | $\mathbf{80.76 \pm 2.24}$ | $80.89 \pm 2.64$ | $\mathbf{84.09 \pm 1.7}$ |
| DryBean | $64.6 \pm 3.89$ | $\mathbf{65.6 \pm 4.18}$ | $61.55 \pm 4.91$ | $\mathbf{64.91 \pm 3.72}$ | $64.6 \pm 3.53$ | $66.24 \pm 4.31$ | $\mathbf{67.0 \pm 3.96}$ |
| HAR | $82.57 \pm 1.96$ | $82.87 \pm 3.02$ | $\mathbf{83.12 \pm 2.27}$ | $82.19 \pm 2.61$ | $\mathbf{83.53 \pm 3.77}$ | $\mathbf{81.35 \pm 2.54}$ | $81.16 \pm 1.63$ |
| Mnist | $50.74 \pm 2.25$ | $51.08 \pm 2.55$ | $\mathbf{52.69 \pm 2.42}$ | $51.7 \pm 3.52$ | $\mathbf{54.26 \pm 1.82}$ | $51.6 \pm 2.58$ | $\mathbf{54.18 \pm 2.34}$ |
| Mushrooms | $69.45 \pm 7.29$ | $59.53 \pm 10.46$ | $\mathbf{71.36 \pm 6.63}$ | $62.98 \pm 7.25$ | $\mathbf{77.55 \pm 7.65}$ | $72.16 \pm 7.59$ | $\mathbf{76.16 \pm 13.04}$ |
| Phishing | $67.42 \pm 3.55$ | $66.08 \pm 5.66$ | $\mathbf{77.41 \pm 3.93}$ | $66.88 \pm 5.64$ | $\mathbf{76.17 \pm 8.58}$ | $69.48 \pm 4.37$ | $\mathbf{75.83 \pm 7.52}$ |
| Protein | $57.57 \pm 6.33$ | $57.45 \pm 6.36$ | $\mathbf{57.61 \pm 6.23}$ | $56.09 \pm 5.61$ | $\mathbf{57.74 \pm 7.8}$ | $58.81 \pm 6.54$ | $\mathbf{59.88 \pm 6.29}$ |
| Rice | $79.19 \pm 5.12$ | $80.54 \pm 4.31$ | $\mathbf{81.1 \pm 4.28}$ | $79.88 \pm 4.48$ | $\mathbf{81.56 \pm 3.61}$ | $80.35 \pm 4.89$ | $\mathbf{82.63 \pm 5.63}$ |
| Splice | $66.13 \pm 4.47$ | $67.14 \pm 2.62$ | $\mathbf{67.45 \pm 2.53}$ | $67.28 \pm 2.07$ | $\mathbf{68.05 \pm 2.17}$ | $66.08 \pm 4.98$ | $\mathbf{66.32 \pm 4.73}$ |
| Svmguide1 | $70.89 \pm 10.98$ | $70.35 \pm 11.74$ | $\mathbf{81.07 \pm 5.39}$ | $69.84 \pm 11.06$ | $\mathbf{74.46 \pm 7.23}$ | $71.04 \pm 11.11$ | $\mathbf{73.13 \pm 8.82}$ |

- $\mathcal{T}$-similarity is better overall;
- Mushrooms and Phishing $\rightarrow$ from degradation to improvement;

# Results in SSL+SSB

| Dataset | ERM | $\text{PL}_{\theta=0.8}$ | | $\text{CSTA}_{\Delta=0.4}$ | | MSTA | |
|---|---|---|---|---|---|---|---|
| | | softmax | $\mathcal{T}$-similarity | softmax | $\mathcal{T}$-similarity | softmax | $\mathcal{T}$-similarity |
| Cod-RNA | $74.51 \pm 8.86$ | $74.75 \pm 8.14$ | $\mathbf{80.06 \pm 3.55}$ | $73.39 \pm 7.36$ | $\mathbf{78.39 \pm 4.66}$ | $75.28 \pm 8.79$ | $\mathbf{76.88 \pm 7.67}$ |
| COIL-20 | $84.54 \pm 2.19$ | $\mathbf{84.69 \pm 3.56}$ | $84.57 \pm 2.85$ | $84.38 \pm 3.05$ | $\mathbf{84.57 \pm 3.16}$ | $\mathbf{84.32 \pm 2.34}$ | $84.07 \pm 2.85$ |
| Digits | $75.68 \pm 4.59$ | $\mathbf{80.47 \pm 3.8}$ | $78.2 \pm 3.34$ | $78.4 \pm 3.28$ | $\mathbf{79.14 \pm 3.5}$ | $78.02 \pm 5.15$ | $\mathbf{79.8 \pm 5.92}$ |
| DNA | $78.82 \pm 2.31$ | $\mathbf{80.29 \pm 2.24}$ | $79.06 \pm 2.31$ | $80.12 \pm 2.08$ | $\mathbf{80.76 \pm 2.24}$ | $80.89 \pm 2.64$ | $\mathbf{84.09 \pm 1.7}$ |
| DryBean | $64.6 \pm 3.89$ | $\mathbf{65.6 \pm 4.18}$ | $61.55 \pm 4.91$ | $\mathbf{64.91 \pm 3.72}$ | $64.6 \pm 3.53$ | $66.24 \pm 4.31$ | $\mathbf{67.0 \pm 3.96}$ |
| HAR | $82.57 \pm 1.96$ | $82.87 \pm 3.02$ | $\mathbf{83.12 \pm 2.27}$ | $82.19 \pm 2.61$ | $\mathbf{83.53 \pm 3.77}$ | $\mathbf{81.35 \pm 2.54}$ | $81.16 \pm 1.63$ |
| Mnist | $50.74 \pm 2.25$ | $51.08 \pm 2.55$ | $\mathbf{52.69 \pm 2.42}$ | $51.7 \pm 3.52$ | $\mathbf{54.26 \pm 1.82}$ | $51.6 \pm 2.58$ | $\mathbf{54.18 \pm 2.34}$ |
| Mushrooms | $69.45 \pm 7.29$ | $59.53 \pm 10.46$ | $\mathbf{71.36 \pm 6.63}$ | $62.98 \pm 7.25$ | $\mathbf{77.55 \pm 7.65}$ | $72.16 \pm 7.59$ | $\mathbf{76.16 \pm 13.04}$ |
| Phishing | $67.42 \pm 3.55$ | $66.08 \pm 5.66$ | $\mathbf{77.41 \pm 3.93}$ | $66.88 \pm 5.64$ | $\mathbf{76.17 \pm 8.58}$ | $69.48 \pm 4.37$ | $\mathbf{75.83 \pm 7.52}$ |
| Protein | $57.57 \pm 6.33$ | $57.45 \pm 6.36$ | $\mathbf{57.61 \pm 6.23}$ | $56.09 \pm 5.61$ | $\mathbf{57.74 \pm 7.8}$ | $58.81 \pm 6.54$ | $\mathbf{59.88 \pm 6.29}$ |
| Rice | $79.19 \pm 5.12$ | $80.54 \pm 4.31$ | $\mathbf{81.1 \pm 4.28}$ | $79.88 \pm 4.48$ | $\mathbf{81.56 \pm 3.61}$ | $80.35 \pm 4.89$ | $\mathbf{82.63 \pm 5.63}$ |
| Splice | $66.13 \pm 4.47$ | $67.14 \pm 2.62$ | $\mathbf{67.45 \pm 2.53}$ | $67.28 \pm 2.07$ | $\mathbf{68.05 \pm 2.17}$ | $66.08 \pm 4.98$ | $\mathbf{66.32 \pm 4.73}$ |
| Svmguide1 | $70.89 \pm 10.98$ | $70.35 \pm 11.74$ | $\mathbf{81.07 \pm 5.39}$ | $69.84 \pm 11.06$ | $\mathbf{74.46 \pm 7.23}$ | $71.04 \pm 11.11$ | $\mathbf{73.13 \pm 8.82}$ |

- ⋆ $\mathcal{T}$-similarity is better overall;
- ⋆ Mushrooms and Phishing $\rightarrow$ from degradation to improvement.
- ⋆ Results in i.i.d. SSL: no significant improvement nor degradation.

# Outline

# Discussion

- $\star$ Practical and principled framework to study SSL + SSB;
- $\star$ Calibrated confidence measure;
- $\star$ $\mathcal{T}$-similarity good both in i.i.d. SSL and SSL + SSB.

Future work $\rightarrow$ use $\mathcal{T}$-similarity for iterative self-training, domain adaptation, or uncertainty modeling.

# To Know More

This work has been accepted to AISTATS 2024, Valencia, Spain. You may find the links to the paper and the code below. to know more about my research, see my website: ambroiseodt.github.io and feel free to contact me.

- ⋆ Paper: https://arxiv.org/abs/2310.14814
- ⋆ Code: https://github.com/ambroiseodt/tsim

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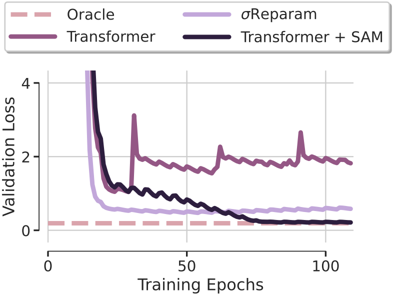
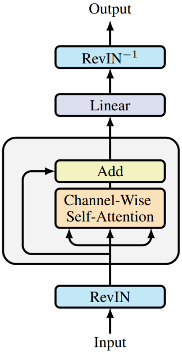
## SAMformer: Unlocking the Potential of Transformers in Time Series Forecasting - Oral ICML 2024




- ⋆ Paper: https://arxiv.org/pdf/2402.10198
- ⋆ Code: https://github.com/romilbert/samformer

Thanks for your attention !

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# Appendix: Datasets

| Dataset | Size | # of lab. examples $n_\ell$ | Dimension $d$ | # classes $C$ |
|---|---|---|---|---|
| Cod-RNA | 59535 | 99 | 8 | 2 |
| COIL-20 | 1440 | 200 | 1024 | 20 |
| Digits | 1797 | 99 | 64 | 10 |
| DNA | 3186 | 149 | 180 | 6 |
| DryBean | 13543 | 104 | 16 | 7 |
| HAR | 10299 | 299 | 561 | 3 |
| Mnist | 70000 | 100 | 784 | 10 |
| Mushrooms | 8124 | 79 | 112 | 2 |
| Phishing | 11055 | 99 | 68 | 2 |
| Protein | 1080 | 80 | 77 | 8 |
| Rice | 3810 | 29 | 7 | 2 |
| Splice | 3175 | 39 | 20 | 2 |
| Svgmguide1 | 3089 | 39 | 4 | 2 |

Table: Characteristics of datasets used in our experiments