A Theory of Label Propagation for Subpopulation Shift

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Background

- of data we have are unlabeled.
- (x, y), target distribution T with unlabeled data x.

• In many machine learning tasks we encounter *distribution* shifts and often lots

Unsupervised domain adaptation: Source distribution S with labeled data

Example Dataset: Office-31

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desk chair

monitor

(Saenko, et al., 2010)

Example Dataset: BREEDS

goldfinch, brambling, water ouzel, chickadee

magpie, house finch, indigo bunting, bulbul



Source

Target

Entity30-Passerine



Source

Target

Entity30-Tableware

(Santurkar et al., 2021)



Classic Methods

- Traditional method: Reweight/resample based on the density ratio of S and T. • Caveat: Only works when the support of S and T are equal.
- Classic method for deep learning: Distributional matching¹, which learns a representation z on which the distribution of z(x) for $x \sim S$ and $x \sim T$ are the same, while performing classification by $x \to z \to \hat{y}$.
- Caveat: Forcing representation to match may not preserve the right information for y.

(¹Ben-David et al, 2010)

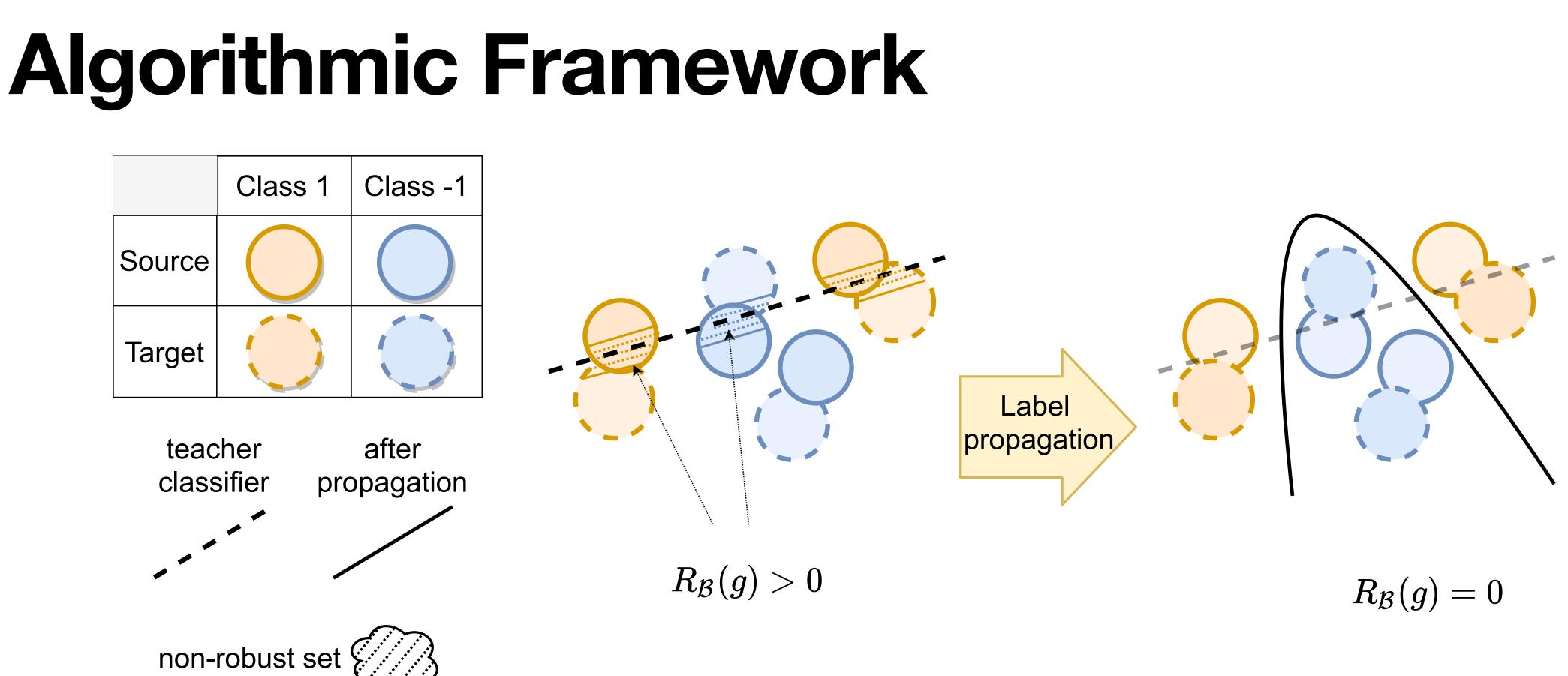
Our New Framework: Subpopulation Shift

- A new model and framework for distribution shift.
- where each S_i and T_i are correspondent in a certain sense.
- BREEDS is the classic dataset for subpopulation shifts of this form.

• Characterize source and target by $S = S_1 \cup \cdots \cup S_m$ and $T = T_1 \cup \cdots \cup T_m$,

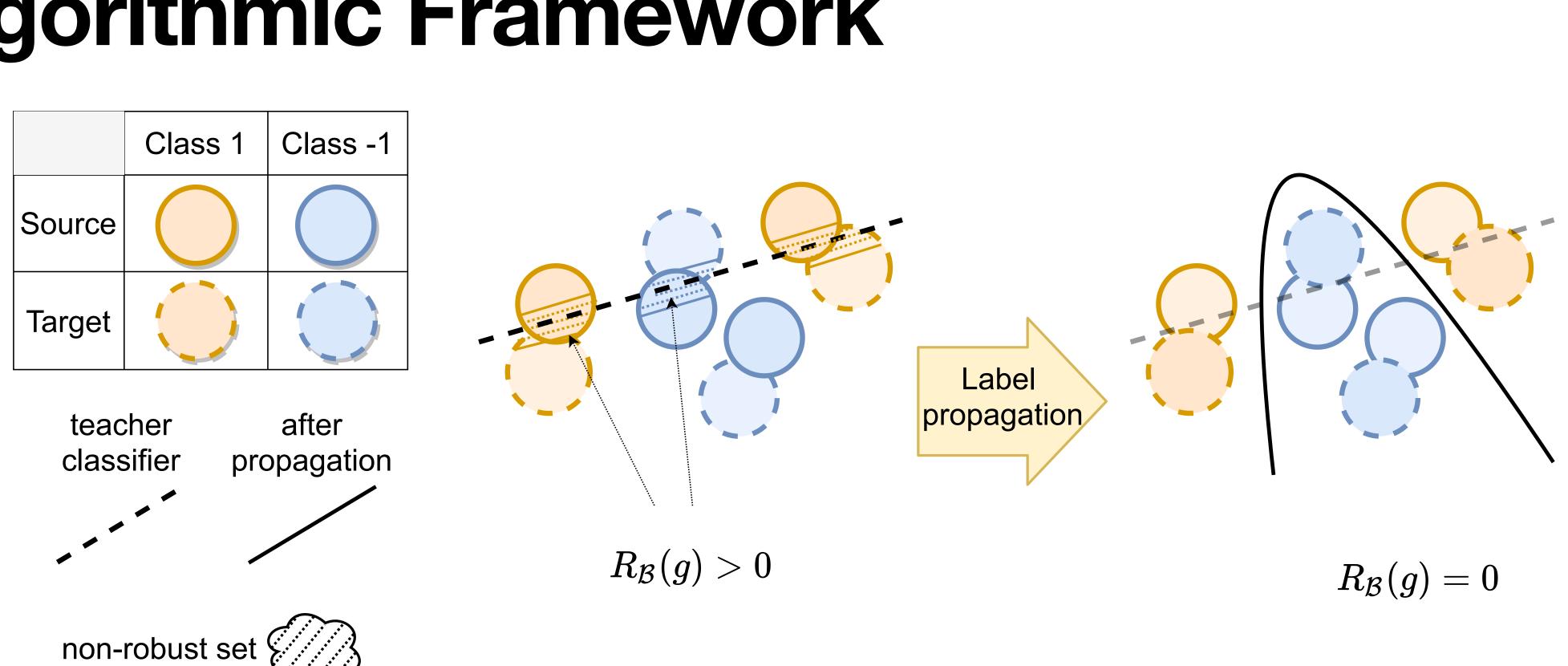
• Subpopulation shift is ubiquitous in practical tasks, e.g. "Poodles eating dog food" in the source and "Labradors eating meat" in the target. The previous

Subpopulation shift can also be more implicit and hard to describe by words.



- Suppose there is a (possibly noisy) teacher classifier g_{tc} on S. Goal: Propagate the label information from S to T based on unlabeled data.
- In this toy illustration, each $S_i \cup T_i$ forms a regular connected component.

Algorithmic Framework



- g_{tc} + A proper consistency regularization = Label propagation!

Consistency regularizer $R_{R}(g)$ measures the amount of non-robust set of g, i.e. points whose predictions by g is inconsistent in a small neighborhood.

Algorithm

- We expect the predictions to be stable under a suitable set of input transformations $B(x) \subset X$, and use the following consistency regularization: $R_B(g) := P_{x \sim \frac{1}{2}(S+T)}[\exists x' \in B(x), \text{ s.t. } g(x) \neq g(x')].$
- B can be a distance-based neighborhood set or some data augmentations A, and can take the general form $B(x) = \{x' : \exists A \text{ such that } d(x', A(x)) \leq r\}.$

• Define
$$L_{01}^{S}(g, g_{tc}) := P_{x \sim S}[g(x) \neq g_{tc}]$$

 $g = \operatorname{argmin}_{g:X \rightarrow Y, g \in G}$

- (x)], our algorithm is
- $_{G}L_{01}^{S}(g, g_{tc})$ s.t. $R_{B}(g) \leq \mu$,
- where μ is a constant satisfying $R_{R}(g^{*}) < \mu$, which is expected to be small.

Technical Assumption: Expansion

- The expansion property proposed in [1], some geometric regularity on $S_i \cup T_i$ w.r.t. B, is needed for local consistency regularization to propagate globally.
- Define the neighborhood set $N(x) := \{x' | B(x) \cap B(x') \neq \emptyset\}$ (informal), and for a set $A \subset X$ define $N(A) := \bigcup_{x \in A} N(x)$.
- Definition of (a, c)-multiplicative expansion: For $a \in (0,1), c > 1$, any i, any $A \in S_i \cup T_i \text{ with } P_{\frac{1}{2}(S+T)}[A] \leq a$, we have $P_{\frac{1}{2}(S_i+T_i)}[N(A)] \geq \min(cP_{\frac{1}{2}(S_i+T_i)}[A], 1)$.

networks on unlabeled data.

[1] Wei, C., Shen, K., Chen, Y., and Ma, T. (2021). Theoretical analysis of self-training with deep



Main Theorem

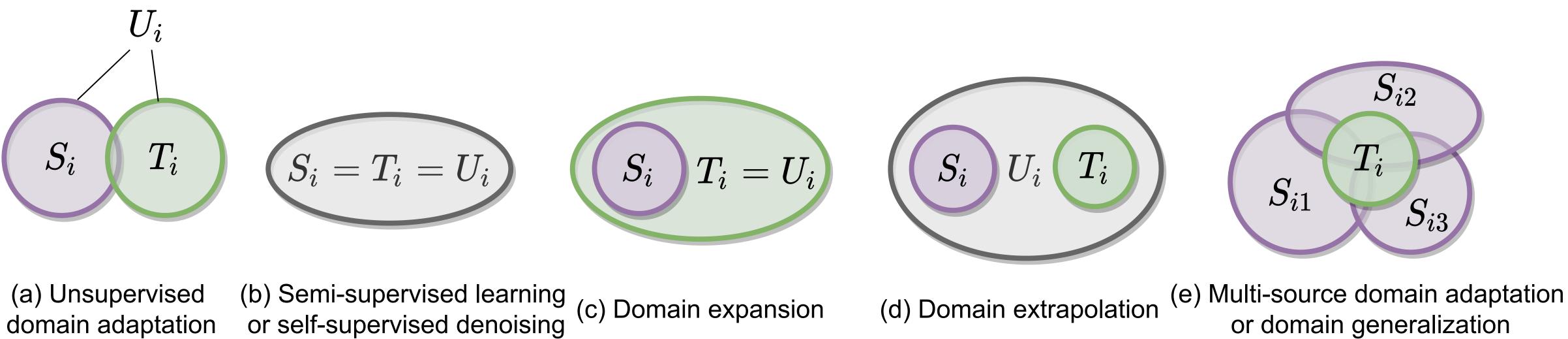
returned by the algorithm $\epsilon_T(g) = P_{x \sim T}[g(x) \neq g^*(x)]$ is bounded by

supposing μ is small.

• Based on (1/2,c)-multiplicative expansion, the target error of the classifier g $\epsilon_T(g) \leq O\left(\frac{\mu}{c-1}\right).$

• Remark: The accuracy of g can actually improve upon the accuracy on g_{tc} ,

Generalized Subpopulation Shift



• The previous result holds on the general setting where there is a general unlabeled dataset U that "covers" S and T, on which we perform label propagation.



Experiments: Subpopulation Shift Dataset

- ENTITY-30 task from BREEDS tasks.
- leverage SwAV, an existing unsupervised representation learned from

Method

Train on Source DANN (Ganin et al., 20 MDD (Zhang et al., 20) FixMatch (Sohn et al., 20

• We use FixMatch, an existing consistency regularization method. We also ImageNet, where there can be a better structure of subpopulation shift. We compare with popular distribution matching methods like DANN and MDD.

	Source Acc	Target Acc
	91.91±0.23	56.73±0.32
016)	$92.81{\pm}0.50$	$61.03{\pm}4.63$
)19)	$92.67{\pm}0.54$	$63.95 {\pm} 0.28$
2020)	90.87±0.15	$72.60{\pm}0.51$

Experiments: Classic Domain Adaptation Dataset

- Office-31 and Office-home.
- We add consistency regularization (FixMatch) to MDD, and observed improvement to the distribution matching method.

Method	$A \rightarrow W$	$\mathrm{D} ightarrow \mathrm{W}$	$W \rightarrow D$	$A \rightarrow D$	$D \rightarrow A$	$W \rightarrow A$	Average
MDD MDD+FixMatch		98.78±0.07 98.32±0.19		> 0	75.64±1.53 76.64±1.91	$72.82{\pm}0.52$ $74.93{\pm}1.15$	89.16 89.84

Table 2: Performance of MDD and MDD+FixMatch on Office-31 dataset.

Method	$Ar \rightarrow Cl Ar \rightarrow Pr$	$Ar \rightarrow Rw Cl \rightarrow A$	ar $Cl \rightarrow Pr Cl \rightarrow R$	w $\Pr \rightarrow Ar \Pr \rightarrow Cl$	$\Pr \rightarrow \operatorname{Rw} \operatorname{Rw} \rightarrow \operatorname{Ar}$	$\mathbf{R}\mathbf{w} \rightarrow \mathbf{Cl} \ \mathbf{R}\mathbf{w} \rightarrow \mathbf{Pr} \ \mathbf{Avera}$	age
MDD	54.9±0.7 74.0±0.3	77.7±0.3 60.6±0	.4 70.9±0.7 72.1±0	6 60.7±0.8 53.0±1.0) 78.0±0.2 71.8±0.4	59.6±0.4 82.9±0.3 68.0	.0
MDD+FixMatch	n 55.1 \pm 0.9 74.7 \pm 0.8	78.7±0.5 63.2±1	.3 74.1±1.8 75.3±0	$1 63.0 \pm 0.6 53.0 \pm 0.6$	$5\ 80.8{\pm}0.4\ 73.4{\pm}0.1$	59.4±0.7 84.0±0.5 69.0	.6

Table 3: Performance of MDD and MDD+FixMatch on Office-Home dataset.

Takeaway Message

Consistency-based methods (e.g. semi-supervised learning methods like FixMatch) can help domain adaptation, especially in the presence of subpopulation shift!