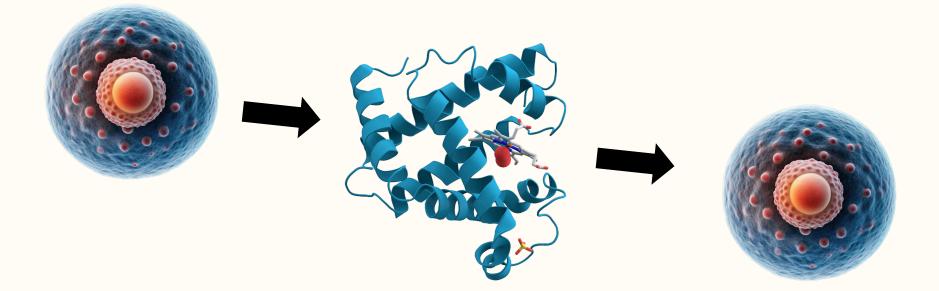
## Learning from Imperfect and Missing Information

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## **Proteins Involved in Signaling**

**Goal:** Classify proteins that are involved in signaling across cellular membranes [ Sair Tran Barabote '06, Elkan Noto '08 ]



**Classical Learning Theory Approach** Collect positive and negative samples and train a classifier

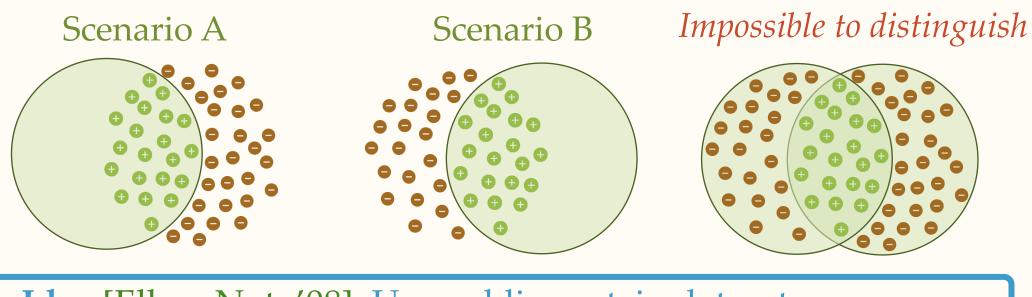
**Issue** [Elkan Noto'08]

- "...TCDB is a database containing information about over 4000 proteins that <u>are involved</u> in signaling..."
- "If we ask a biologist for proteins that are <u>not involved</u> in this process, the only answer is <u>"all other proteins"</u>

We have a good quality data set with samples of the form  $(x_i, 1)$ But, we do not have collected data of the form  $(x_i, -1)!$ 

**Q.** Can we solve classification problems using only positive data?

**Theorem** [Natarajan 1987] [Lee M. Zampetakis] Binary classification with only positive samples can be solved only for very restricted function classes

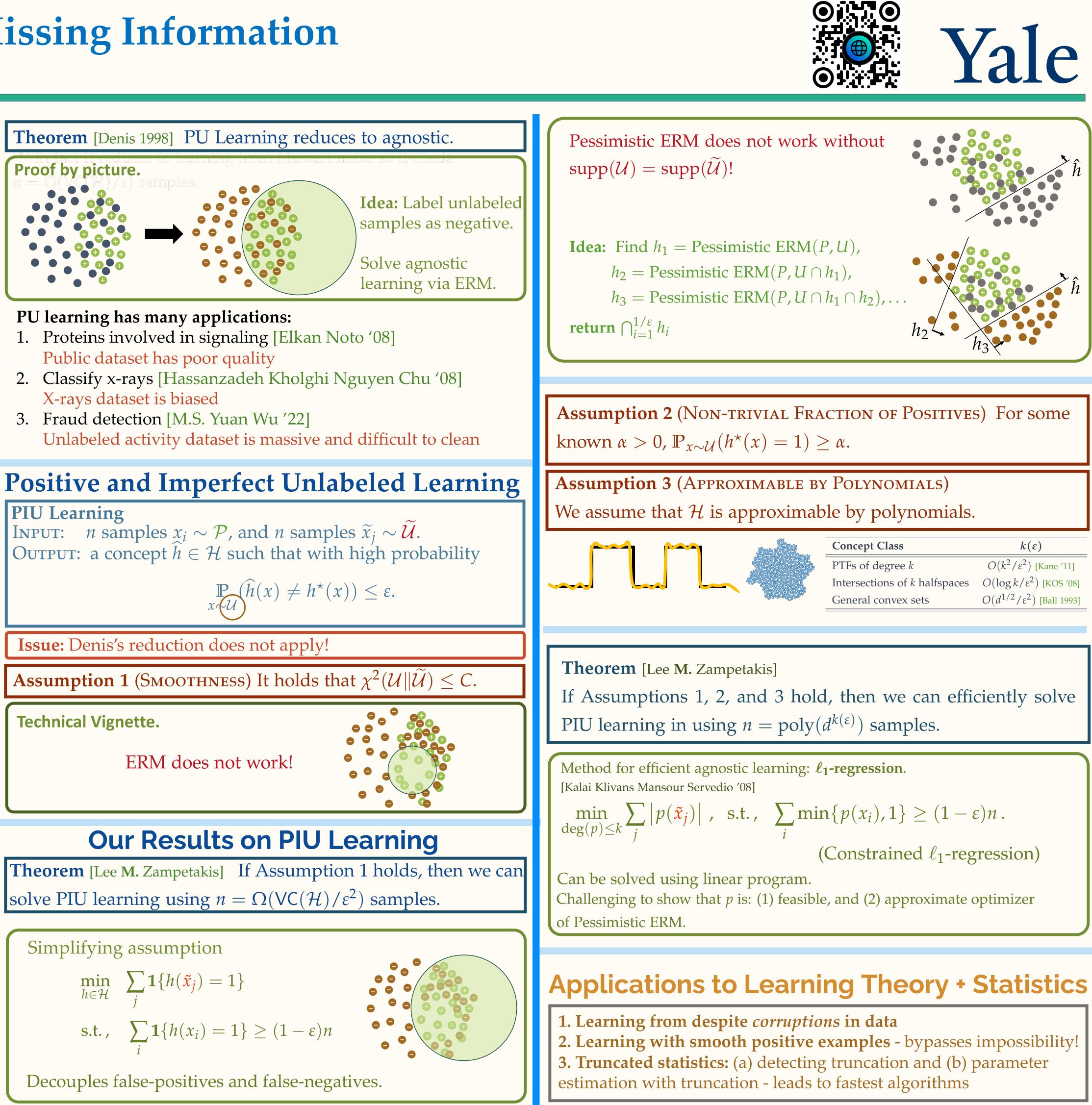


Idea [Elkan Noto'08]. Use public protein dataset as a proxy **Issues**. Some proteins in this data may impact signaling

## **PU Learning – Prior Work**

**INPUT:** *n* samples  $x_i \sim \mathcal{P}$ , and *n* samples  $\widetilde{x}_j \sim \mathcal{U}$ . OUTPUT: a concept  $\hat{h} \in \mathcal{H}$  such that with high probability

 $\mathbb{P}_{x \sim \mathcal{U}}(\widehat{h}(x) \neq h^{\star}(x)) \leq \varepsilon.$ 



Concept Class
PTFs of degree <i>k</i>
Intersections of $k$ halfspaces
General convex sets

$$\min_{|p|\leq k}\sum_{j} |p(\tilde{x}_{j})|, \quad \text{s.t.}, \quad \sum_{i} \min\{p(x_{i}), 1\} \geq (1-\varepsilon)n.$$