General Framework for Classification at the Top

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Motivation

Binary classification

- Two group of samples:
 - negative samples with label y = 0,
 - positive samples with label y = 1.

Binary classification

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 - model f maps a sample x to its classification score $s \in \mathbb{R}$,
 - ullet decision threshold $t\in\mathbb{R}$ decides whether a sample is classified as positive or not

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 Usually, the model returns the probability that the sample is from the positive class and the threshold is 0.5.

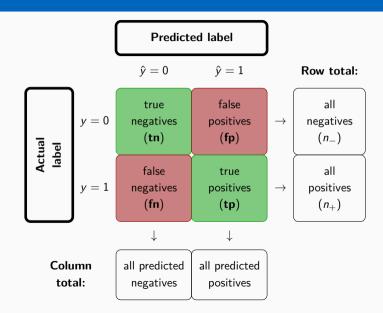
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- Usually, the model returns the probability that the sample is from the positive class and the threshold is 0.5.
- Goal: find classifier which predicts labels for unknown samples with the lowest possible error.

Confusion matrix



Binary Classification

General form of binary classification

minimize
$$\frac{1}{n_{-}} \sum_{i \in \mathcal{I}_{-}} \mathbb{1}_{[s_{i} \geq t]} + \frac{1}{n_{+}} \sum_{i \in \mathcal{I}_{+}} \mathbb{1}_{[s_{i} < t]}$$
subject to
$$s_{i} = f(\mathbf{x}_{i}; \mathbf{w}), \quad i \in \mathcal{I},$$

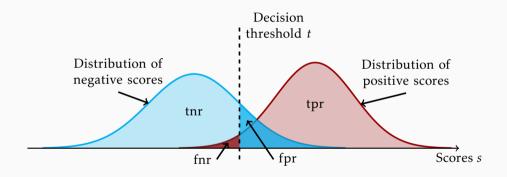
• $\mathcal{I} = \mathcal{I}_- \cup \mathcal{I}_+$ is a set of indices of all sample where

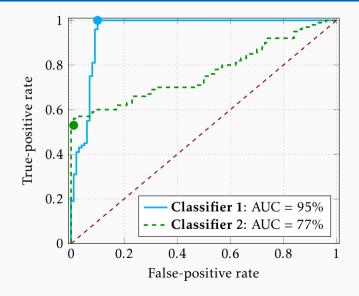
$$\begin{split} \mathcal{I}_{-} &= \left\{ i \mid i \in \left\{ 1, 2, \ldots, n \right\} \; \land \; y_i = 0 \right\}, \\ \mathcal{I}_{+} &= \left\{ i \mid i \in \left\{ 1, 2, \ldots, n \right\} \; \land \; y_i = 1 \right\}, \end{split}$$

1_[·] is Iverson function defined by

$$1_{[x]} = \begin{cases} 0 & \text{if } x \text{ is false,} \\ 1 & \text{if } x \text{ is true.} \end{cases}$$

ROC curves





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- What if some samples are more relevant than others?
 - Search engines: relevant results should be on the first few pages.
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 - Expensive post-processing: development of new drugs.

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- In such cases, Classifier 2 may be better.

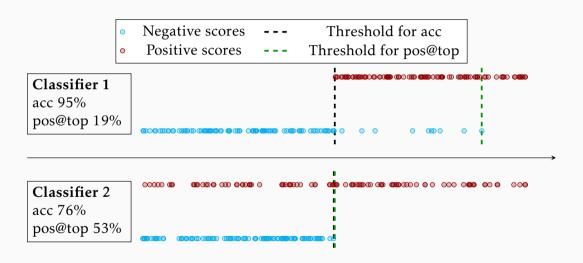
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- In such cases, Classifier 2 may be better.
- Classifier 1 maximizes accuracy

$$\operatorname{acc}(\boldsymbol{s}) = \frac{1}{n} \sum_{i \in \mathcal{I}} \mathbb{1}_{[y_i = \hat{y}_i]}.$$

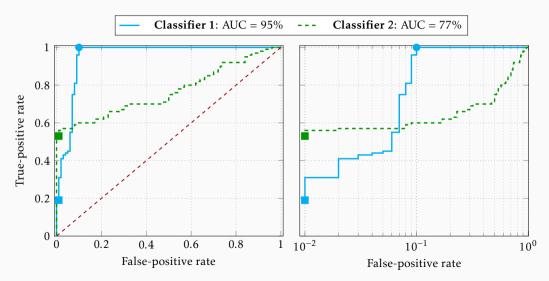
Classifier 2 maximizes the number of positive samples at the top

$$\mathsf{pos@top}(oldsymbol{s}) = rac{1}{n_+} \sum_{i \in \mathcal{I}_+} \mathbb{1}_{\left[s_i \geq \mathsf{max}_{j \in \mathcal{I}_-} \ s_j
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Classification at the Top

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- General formulation

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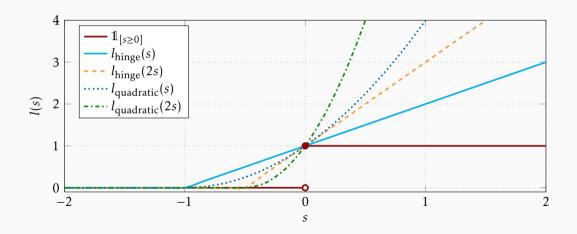
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Difficult problem: constrained, discontinuous, non-convex, and non-decomposable.

ROC curves



Surrogate approximation

General surrogate formulation

minimize
$$\frac{1}{2} \| \boldsymbol{w} \|^2 + \frac{1}{n_+} \sum_{i \in \mathcal{I}_+} I(t - s_i)$$
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Pat&Mat-NP maximizes true-positive rate with fixed false-positive rate

t solves
$$\frac{1}{n_{-}}\sum_{i\in\mathcal{I}_{-}}I\left(\vartheta(s_{i}-t)\right)=\tau.$$

Classification at the Top:

Linear Model

- Linear model $f(\mathbf{x}; \mathbf{w}) = \mathbf{w}^{\top} \mathbf{x}$.
- General surrogate formulation with linear model

minimize
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subject to
$$s_i = \boldsymbol{w}^\top \boldsymbol{x}_i, \quad i \in \mathcal{I},$$
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- Properties that we are interested in:
 - Convexity of the objective function.
 - Robustness to outliers.

Convexity of the objective function

Theorem

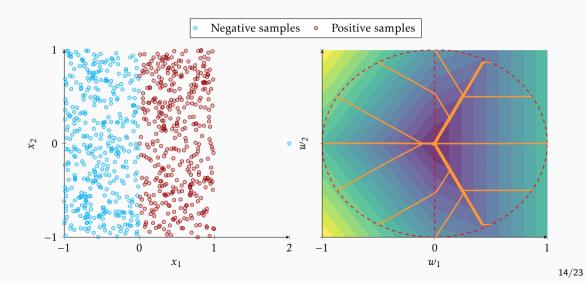
If the threshold t is a convex function of the weights \boldsymbol{w} , then function

$$L(\mathbf{w}) = \frac{1}{2} \|\mathbf{w}\|^2 + \frac{1}{n_+} \sum_{i \in \mathcal{T}_+} I(t - s_i)$$

is convex.

- Both formulations TopPush and Pat&Mat-NP have convex thresholds.
- Both formulations are convex and continuous.

When convexity is not enough...



How to solve it?

Using gradient descent

$$\mathbf{w}^{k+1} \leftarrow \mathbf{w}^k - \alpha^k \cdot \nabla L(\mathbf{w}^k),$$

where $\alpha^k > 0$ is a learning rate, and $\nabla L(\mathbf{w}^k)$ is a gradient of the objective function

$$\nabla L(\mathbf{w}) = \mathbf{w} + \frac{1}{n_+} \sum_{i \in T_+} I'(t(\mathbf{w}) - f(\mathbf{x}_i; \mathbf{w})) (\nabla t(\mathbf{w}) - \nabla f(\mathbf{x}_i; \mathbf{w})).$$

Classification at the Top:

Non-linear Model

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 - Non-linear models are usually large and expensive to train.

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- What to do if the dataset is too large to fit in memory?

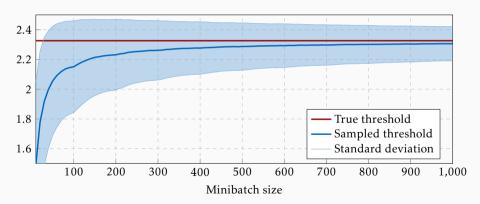
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- Disadvantages:
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- What to do if the dataset is too large to fit in memory?
- Stochastic gradient descent: the gradient is computed only on a small subset of all data called minibatch.

Issues when passing to mini-batches

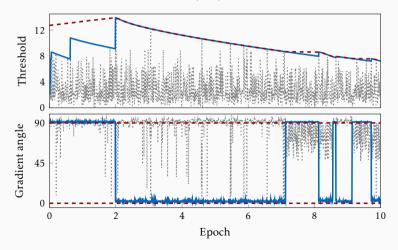
Problems:

- ullet The threshold is a function of all scores o the loss function is non-decomposable.
- As a result, stochastic gradient descent provides a biased gradient estimate.



How to reduce bias?

- Increase size of minibatch → Pat&Mat-NP.
- Add threshold from last minibatch \rightarrow *DeepTopPush*.

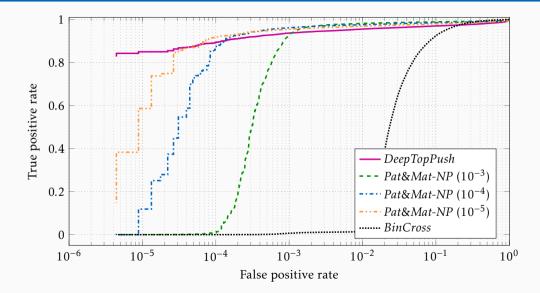


How does it work?

Steganography

- Dataset: 205 579 samples, 9% of samples are positive.
- Each sample consists of 22 510 features.
- Only linear model.
- Goals:
 - Maximize the true-positive rate at extremely low levels of the false-positive rate.

Steganography



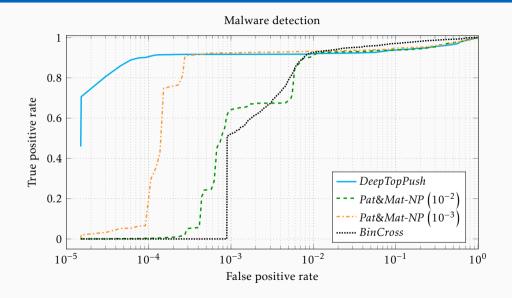
AVAST: Malware detection

- Dataset: 6 580 166 samples, 87% of samples are positive.
- Hierarchical data structure:
 - Each sample is a JSON file, which may consist of other JSON files.
 - Each sample is of a different size (from 1 KB to 2.5 MB).
 - DeepTopPush and Pat&Mat-NP used as an extension for hierarchical multi-instance learning (HMIL).

Goals:

- Maximize the true-positive rate at extremely low levels of the false-positive rate.
- The false-positive rate must be as low as possible to avoid disruptive false alarms for the end-user.

AVAST: Malware detection



Thank you for your attention.