

QUANTIFYING STATISTICAL SIGNIFICANCE FOR DEEP SEMI-SUPERVISED ANOMALY DETECTION VIA SELECTIVE INFERENCE

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What ?

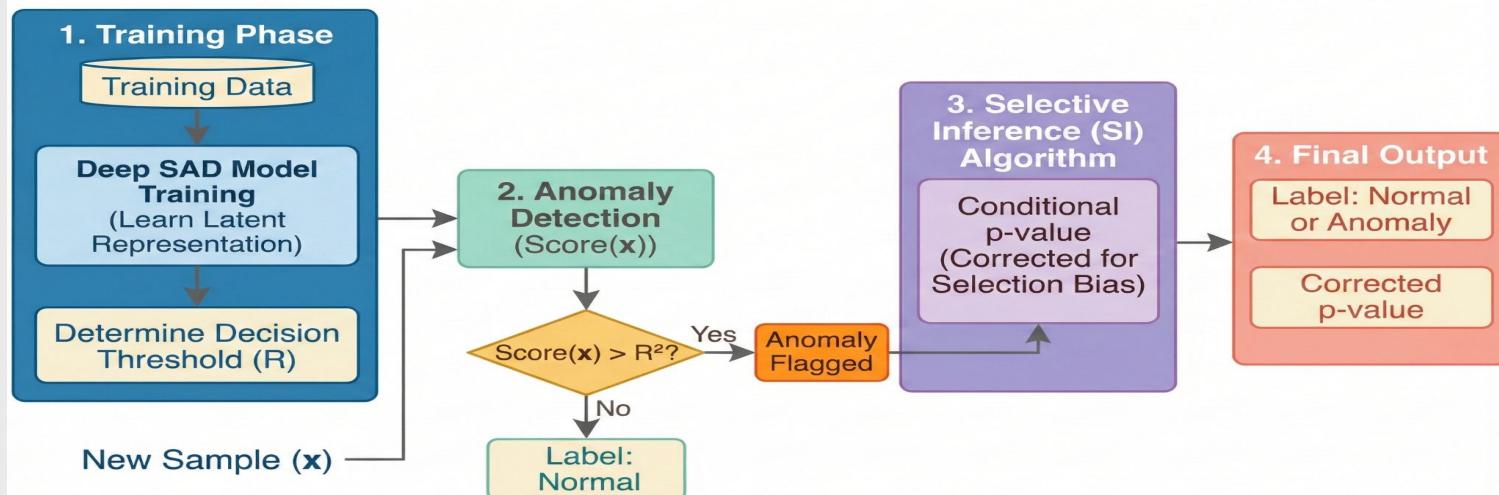
- Core Objective:** Develop a statistical inference framework to quantify the reliability of predictions from "black-box" Deep SAD models.
- Novelty:** Integrate Selective Inference to compute **valid p-values**, ensuring rigorous control of the **False Positive Rate** (FPR) at the significance level α .
- Efficacy:** Demonstrate that the proposed method achieves superior **Statistical Power** compared to traditional correction techniques (e.g., Bonferroni correction) on benchmark datasets.

Why ?

- Practical Necessity:** In **safety-critical domains** (e.g., healthcare, industry), false alarms (false positives) can lead to severe **financial and psychological consequences**.
- Research Gap:** Current **SOTA models** like Deep SAD operate as "black boxes" providing predictions without **quantitative reliability metrics**, thereby preventing operators from accurately assessing risks.
- Project Objective:** Integrate **Selective Inference** to "transparentize" decisions, providing precise **statistical significance** to rigorously control the False Positive Rate.

Overview

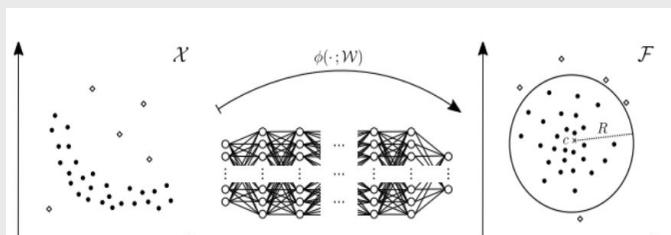
SI-DeepSAD: Selective Inference for Deep SAD System



Description

1. Deep SAD Training

- The Deep SAD model (Ruff et al., 2020) is trained in a semi-supervised manner to learn how to distinguish between normal and anomalous samples with an objective function of minimizing the distance of normal samples to the center c and maximizing the distance of anomalous samples.
- After training is complete, a threshold R is determined as the boundary for detecting anomalies.



2. Testing New Samples

- The model predicts "anomaly" if the score $Score(x) = ||f(x) - c||^2 > R^2$
 - $f(x)$: Representation in the latent space.
 - R : Decision radius (calculated from the quantile of the normal set and the unlabeled set in the training set).

3. Selective Inference

- Technique:** Parametric Selective Inference
- P-value calculation process:**
 - Parameterization:** Construct a line $X(z) = a + bz$ passing through the suspected sample (x_{test}).
 - Constraints Tracking:** Find the set of value intervals of z such that:
 - Statistical sign preservation:** Ensure the sign of the Test statistic between x_{test} and x_{ref} does not change so that the test direction vector η is fixed - Solve system of linear inequalities.
 - Invariant network structure:** Leaky ReLU and MaxPool neurons keep their activation state - Solve system of linear inequalities.
- The model still predicts as anomaly:** $Score(X(z)) > R^2$ - solve quadratic inequality.
- Statistical calculation:** Calculate the conditional probability (p-value) based on the Truncated Gaussian distribution within the intervals found in step 2.

