RETABAD: A BENCHMARK FOR RESTORING SEMAN-TIC CONTEXT IN TABULAR ANOMALY DETECTION

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ABSTRACT

In tabular anomaly detection (AD), textual semantics often carry critical signals, as the definition of an anomaly is closely tied to domain-specific context. However, existing benchmarks provide only raw data points without semantic context, overlooking rich textual metadata such as feature descriptions and domain knowledge that experts rely on in practice. This limitation restricts research flexibility and prevents models from fully leveraging domain knowledge for detection. **ReTabAD** addresses this gap by **Re**storing textual semantics to enable context-aware **Tab**ular Anomaly Detection research. We provide (1) 20 carefully curated tabular datasets enriched with structured textual metadata, together with implementations of stateof-the-art AD algorithms—including classical, deep learning, and LLM-based approaches—and (2) a zero-shot LLM framework that leverages semantic context without task-specific training, establishing a strong baseline for future research. Furthermore, this work provides insights into the role and utility of textual metadata in AD through experiments and analysis. Results show that semantic context improves detection performance and enhances interpretability by supporting domain-aware reasoning. These findings establish ReTabAD as a benchmark for systematic exploration of context-aware AD. The resource is publicly released at https://yoonsanghyu.github.io/ReTabAD/.

1 Introduction

Anomaly detection (AD), the task of identifying patterns that diverge from the distribution of normal data, represents a fundamental challenge across diverse domains such as finance (Al-Hashedi & Magalingam, 2021), cybersecurity (Landauer et al., 2023), manufacturing (Kharitonov et al., 2022), and healthcare (Fernando et al., 2021). In particular, anomaly detection in tabular data, i.e., tabular AD, is of critical importance, as structured datasets—including sensor logs, transaction records, and clinical measurements—form the backbone of real-world operational systems. Despite its practical importance, tabular AD remains a challenging problem due to the heterogeneous nature of tabular datasets, which often combine numerical, categorical, and even textual attributes with rich semantic meaning.

DAMI Repository (Campos et al., 2016) and ADBench (Han et al., 2022) have made significant contributions to tabular AD by establishing standardized benchmarks that enabled fair and rigorous comparisons across AD algorithms. Despite this contribution, these benchmarks were developed under earlier detection paradigms that prioritized only numerical features with conventional machine learning pipelines—for instance, converting categorical values into arbitrary integer codes, or discarding non-numerical fields (as shown in Figure 1). More critically, they excluded textual metadata that practitioners routinely rely on in real-world applications, *e.g.*, feature descriptions, domain context, categorical semantics, measurement units, and operational constraints. This omission is particularly problematic because the definition of an anomaly is inherently "context-dependent" (Chandola et al., 2009; Pang et al., 2021)—without understanding feature semantics and domain constraints, models may misclassify benign deviations as anomalies or fail to detect subtle but critical abnormalities.

Table 1: **Comparison of ReTabAD with Existing Resources.** Prior work can be categorized into benchmarks that mainly provide datasets for evaluation, and libraries that offer algorithm implementations and pipelines. ReTabAD uniquely combines both: raw tabular values, structured metadata, and ready-to-use pipelines for classical, deep learning, and LLM-based AD models.

	Coverag	ge (number)	Data T	Гуре	Alge	orithn	1 Туре	Information Used		
Resource Type	Datasets	Algorithms	Tabular data	Metadata	ML	DL	LLM	Statistic	Semantic	
Benchmark										
DAMI Repository (Campos et al., 2016)	23	12	✓	X	/	X	X	✓	Х	
ADBench (Han et al., 2022)	47	14	1	X	✓	1	X	✓	X	
Library										
PyOD (Zhao et al., 2019)	-	10+	X	X	/	1	X	✓	Х	
DeepOD (Xu et al., 2023a)	-	9	X	X	X	1	X	✓	X	
ReTabAD (ours)	20	17	1	/	1	1	1	/	1	

Recent advances in Large language models (LLMs) demonstrate improved capabilities for handling textual representations of numerical data, particularly in contextual reasoning (Kojima et al., 2022; Fons et al., 2024). These advances suggest new opportunities for leveraging semantic metadata in tabular AD that has been missing from traditional approaches. In particular, such textual metadata can serve as valuable domain priors—enabling models to form more plausible decision boundaries, better interpret anomalous behavior, and generalize more effectively in small-data settings. Early efforts such as AnoLLM (Tsai et al., 2025) have begun to explore this direction, revealing the potential of LLM-based approaches in tabular settings. However, their application remains constrained to utilizing only column names, due to the lack of richer textual annotations in existing benchmarks. This disconnect underscores the need for a new benchmark that restores semantic context, allowing researchers to meaningfully evaluate and advance context-aware tabular AD.

Motivated by these considerations, we introduce ReTabAD, the first context-aware tabular AD benchmark that incorporates rich textual metadata into AD, enabling models to ground their predictions in semantic context rather than purely numerical patterns. As highlighted in Table 1, our benchmark prioritizes quality by curating 20 tabular datasets with rich textual metadata and carefully validated anomaly definitions. This design stands in contrast to ADBench (Han et al., 2022), which achieves broader coverage by simply transforming CV/NLP datasets into tabular format—an approach that increases dataset quantity but lacks the semantic context necessary for context-aware AD. Alongside these curated datasets, ReTabAD enables comprehensive evaluation across 17 algorithms, ranging from classical and deep learning methods to the latest LLM-based approach. Furthermore, we also propose a zero-shot LLM baseline that leverages the provided metadata without any task-specific training to establish a fair starting point for context-aware AD. Empirically, incorporating textual metadata improves zero-shot LLM performance by an average of +7.6% AUROC across multiple models (see Table 4). As a result, our zero-shot LLM approach achieves performance comparable to state-of-the-art training-based methods, despite never being trained on task-specific data. Together, these contributions position ReTabAD as a unified and forward-looking benchmark that enables systematic study of tabular AD in both traditional and context-aware paradigms.

To sum up, our contributions are summarized as follows:

- The first context-aware tabular AD benchmark: We present ReTabAD, which provides 20 carefully curated tabular datasets enriched with textual metadata and faithful anomaly definitions, and enables standardized evaluation across 16 unsupervised algorithms, including classical, deep learning, and LLM-based approaches.
- Zero-shot tabular AD framework leveraging textual metadata: We introduce and evaluate a zero-shot LLM framework that establishes not only a strong and competitive baseline but also a new evaluation paradigm for context-aware tabular AD. By leveraging semantic context without task-specific training, ReTabAD provides a standardized reference point for future research.
- Insights into context-aware tabular AD: We systematically analyze how incorporating textual metadata affects not only model performance but also reasoning quality. Specifically, we evaluate alignment between predicted key features and supervised attributions, and qualitatively examine model-generated reasoning texts, providing insights into how context enhances interpretability and anomaly attribution.

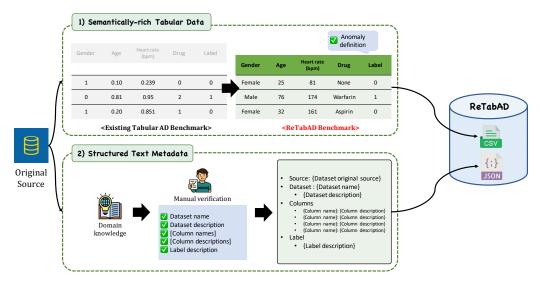


Figure 1: **Overall Data Collection and Annotation Process of ReTabAD.** We preserve semantically rich tabular values and augment them with structured textual metadata, enabling rigorous evaluation of context-aware AD.

Overall, our work emphasizes the importance of semantic information (*e.g.*, textual metadata) in AD for tabular data. We hope that this perspective, together with our new benchmark, will guide future research toward developing context-aware approaches.

2 LIMITATIONS ON PREVIOUS TABULAR AD BENCHMARKS

Benchmarking efforts in tabular AD have primarily aimed to provide reproducible and systematic comparisons of algorithms across diverse datasets. The comparative studies (Goldstein & Uchida, 2016; Campos et al., 2016; Ruff et al., 2021b) established the first generation of evaluation resources, offering systematic comparisons of a broad range of algorithms on real-world datasets. In particular, the DAMI Repository (Campos et al., 2016) introduced semantically meaningful tabular datasets with well-defined anomaly classes, demonstrating the importance of defining anomalies in a way that reflects meaningful deviations. With the rise of deep learning, ADBench (Han et al., 2022) further advanced the field by integrating both classical and deep anomaly detection algorithms, collecting datasets from multiple domains, and analyzing them from diverse perspectives. Together with open-source libraries such as PyOD (Zhao et al., 2019) and DeepOD (Xu et al., 2023a), these resources have substantially advanced the field by enabling standardized protocols and large-scale experimental studies.

Despite these contributions, existing benchmarks lack textual metadata that makes semantic context explicit. Although anomaly classes are often well defined, the datasets are typically provided only in numerical form, and the conversion processes—such as one-hot encoding, text embedding, or dimensionality reduction—inevitably discard important semantic information. Some benchmarks also incorporate datasets from non-tabular modalities like images and speech, where feature-level semantics cannot be clearly specified. As a result, most prior research has been confined to improving performance within these numeric-only settings, focusing on better modeling of given datasets rather than leveraging the rich textual information that practitioners use in real-world anomaly detection.

3 RETABAD: TABULAR AD BENCHMARK RESTORING SEMANTIC CONTEXT

To overcome these limitations as described in Section 2, we introduce ReTabAD, a next-generation benchmark that focuses exclusively on genuinely tabular datasets while systematically integrating rich semantic information. This design enables the systematic evaluation of context-aware AD.

Table 2: **Text Metadata Structure.** Example from the Cardiotocography (Campos & Bernardes, 2000) dataset in ReTabAD.

Dataset: Cardiotocography
Source: https://archive.ics.uci.edu/dataset/193/cardiotocography
Description: Measurements from fetal heart rate (FHR) and uterine contractions (UC) from 2126 cardiotocograms.

Column	Type	Logical Type	Description
LB	int	numerical	FHR baseline (bpm)
AC	float	numerical	Accelerations per second
UC	float	numerical	Uterine contractions per second
ASTV	int	numerical	% time with abnormal short term variability
:	:	:	
Tendency	string	categorical	Histogram tendency (Left-skewed, Symmetric)

Label: Binary label (0: Normal, 1: Suspect/Pathologic)

3.1 Datasets

Data Collection and Annotation. ReTabAD covers 20 tabular datasets drawn from widely used repositories and real-world application domains. Building upon the comprehensive coverage of ADBench (Han et al., 2022), we curate a subset of datasets and enrich them with textual metadata according to the following criteria: (1) datasets must have a clearly defined domain and ground-truth anomaly labels, (2) dataset size should be manageable for diverse models while reflecting real-world class imbalance, (3) sufficient documentation should exist to recover reliable semantic descriptions, and (4) datasets that are too easy, where performance is already saturated, should be discarded. In addition, we incorporate new datasets by inspecting their class label definitions and class-wise sample ratios, and then annotating anomalies accordingly to construct well-posed AD tasks. A complete list of the datasets and their description is summarized in Table 7 in the Appendix A and an overview of the data collection and annotation process is illustrated in Figure 1.

Semantically-rich Tabular Data. To incorporate rich semantic information into tabular data, we consider the following two principles:

- Raw Numerical Preservation: ReTabAD preserves numerical features in their original scales rather than applying unspecified normalization or standardization. Maintaining raw values retains domain-meaningful interpretations that support intuitive reasoning about anomalies. For instance, a resting heart rate of 200 bpm in an adult is directly recognizable as a critical medical anomaly, whereas its normalized counterpart only conveys statistical rarity without clinical significance.
- Categorical Text Restoration: Existing benchmarks often provide categorical features in inconsistent formats (e.g., integer-encoded, text-embeddings) or apply inappropriate normalization that discards semantic meaning. Contrary to this practice, ReTabAD restores categorical attributes to their original textual values instead of applying such transformations. This restoration enables models, particularly language-based approaches, to reason over human-interpretable categories rather than arbitrary numerical surrogates.

Structured Text Metadata. We provide each dataset supplemented with a JSON-formatted metadata file, containing structured semantic descriptions omitted in previous benchmarks. To ensure reliability, we provide direct links to the original data sources, enabling researchers to verify our interpretations. The metadata is organized into three categories:

- Dataset-Level Descriptions: High-level descriptors, including dataset name, purpose, origin, and collection methodology. Each entry includes links to original publications or repositories to enhance credibility.
- *Column-Level Descriptions*: For each column, ReTabAD provides its name, human-readable description, logical type (*e.g.*, numerical, categorical, ordinal, binary), measurement units, if available. All descriptions are cross-referenced with the original dataset documentation.
- Label-Level Descriptions: For each dataset, ReTabAD clearly specifies which classes are considered normal and which are treated as anomalies. These anomaly definitions are derived directly from the original dataset documentation, with full source attribution.

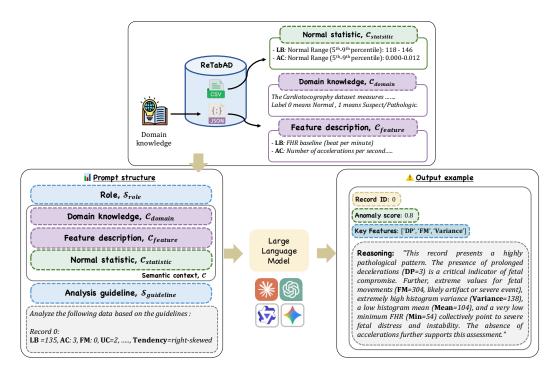


Figure 2: **Zero-shot LLM Baseline Overivew.** We design prompts to evaluate the role of semantic metadata by incorporating domain knowledge (\mathcal{C}_{domain}), feature descriptions ($\mathcal{C}_{feature}$), and normal statistics ($\mathcal{C}_{statistic}$). The LLM generates outputs including anomaly scores, key features, and anomaly reasoning.

3.2 Algorithms

To provide a comprehensive comparison, we evaluate 16 representative *unsupervised AD models*, with full algorithmic details provided in Appendix B. These models are grouped into three categories: (1) **Classical methods**: We include a diverse range of foundational algorithms that remain widely used. These encompass distance-based (*e.g.*, KNN (Ramaswamy et al., 2000)), density-based (*e.g.*, LOF (Breunig et al., 2000)), boundary-based (*e.g.*, OCSVM (Schölkopf et al., 1999)), and ensemble techniques (*e.g.*, Isolation Forest (Liu et al., 2008)). (2) **Deep learning methods**: We consider representative deep models designed to capture complex, non-linear representations of normality beyond classical heuristics. These include methods based on deep one-class classification (*e.g.*, DeepSVDD (Ruff et al., 2018)), reconstruction (*e.g.*, RCA (Liu et al., 2021), MCM (Yin et al., 2024)), and contrastive learning (*e.g.*, GOAD (Bergman & Hoshen, 2020), NeuTraL (Qiu et al., 2021)). (3) **LLM-based methods**: We include AnoLLM (Tsai et al., 2025), which leverages semantic information but is constrained to using only column names as context. To further leverage rich and structured metadata, we propose a new zero-shot LLM framework that directly utilizes context data as input for AD. This investigation illustrates the potential of applying LLMs to AD tasks when comprehensive semantic cues are available. Implementation details are provided in Section 3.3.

3.3 ZERO-SHOT LLM FRAMEWORK FOR CONTEXT-AWARE AD

Motivation. Despite the importance of textual metadata in real-world tabular datasets, there has been no systematic attempt to leverage such information. Conventional training-based AD models are designed to process data as numerical or categorical vectors, making it structurally difficult to directly integrate textual descriptions that contain the semantic information of features. Although there have been attempts to utilize textual metadata, most have remained limited—for instance, relying only on column name without capturing the broader context. As a consequence, such approaches fail to leverage critical signals for AD conveyed by metadata, including inter-feature relationships and domain-specific contextual cues. To address this limitation, we propose a zero-shot LLM-based AD framework that explores the potential of semantic context through context-aware reasoning over tabular data. By enabling the LLM to interpret feature semantics and relationships in natural language,

our framework shifts the focus from purely statistical patterns to high-level contextual understanding and points toward a new paradigm for context-aware AD.

Our Design. To utilize LLMs for tabular AD, we propose a zero-shot LLM framework as a strong baseline for context-aware AD, as illustrated in Figure 2. We employ a carefully designed prompt that integrates domain knowledge and structured reasoning guidelines. The prompt for each data instance x_i consists of three key components: a **System Prompt** (\mathcal{S}), a **Data Input Formatter** ($\mathcal{T}(x_i)$), and a **Structured Output Query** (\mathcal{Q}).

- 1. **System Prompt** (\mathcal{S}): The system prompt provides the necessary context for the task. It is constructed by concatenating the following information(detailed templates are in the Appendix D.3):
 - Role and Task Definition (S_{role}): Assigns the LLM an expert persona for each dataset's domain (e.g., "You are a domain expert in finance").
 - Semantic Context (\mathcal{C}): Supplies essential metadata \mathcal{M} about the dataset, including:
 - **Domain Knowledge** (C_{domain}): A brief background of dataset and label information.
 - Feature Description ($C_{features}$): Descriptions, units, and meanings of each feature.
 - **Normal Statistic** ($C_{\text{statistical}}$): Normal ranges or distributional context derived from the training data.
 - Analysis Guidelines ($S_{guidelines}$): Provides general principles for identifying anomalies based on the given context.
- 2. **Data Input Formatter** $(\mathcal{T}(x_i))$: Each data instance x_i is serialized into a human-readable text format to serve as input. For example, a record is formatted as:

```
"Record i: [feature_name_1=value_1], [feature_name_2=value_2], ...".
```

This use of feature names, rather than generic indices, provides essential semantic context. For efficiency, multiple instances are processed in a single batch.

3. **Structured Output Query** (\mathcal{Q}): To ensure consistent and automatically parsable responses, the final part of the prompt queries the LLM to return its analysis in a structured JSON format. The required format is:

```
{ "anomaly_score": s, "key_features": F, "reasoning": e } where s is the anomaly score in [0, 1], F is a list of key features, and e is the explanation in text.
```

3.4 EVALUATION

Problem Setup. The concept of normality, a ground-truth law of normal behavior for a given task (Ruff et al., 2021a), is modeled through a probability distribution $\mathcal P$ with corresponding density function p(x). Conventional tabular anomaly detectors map each data instance $x \in \mathbb R^K$ to a class label $y \in \{0,1\}$ by learning this distribution, where K denotes the feature dimension, and 0 and 0 indicate normal and anomalous status, respectively. ReTabAD extends this traditional setup by incorporating semantic metadata M, which encompasses domain knowledge, feature descriptions, and contextual information about normal behavior patterns. The primary objective is to model a conditional distribution $p(x|\mathcal M)$ that leverages semantic context for enhanced AD. This work focuses on analyzing the impact of semantic context $\mathcal M$ on detection performance.

Hyperparameter Optimization. We follow the default model architectures and tune key hyperparameters, including preprocessing settings. Hyperparameters for training-based methods are faithfully searched, and detailed configurations are provided in the Appendix C for reproducibility.

Evaluator LLMs. We evaluate a set of leading LLMs in a zero-shot AD setting to assess their general semantic reasoning capabilities. Specifically, we include state-of-the-art reasoning-oriented models—GPT-4.1 (Fachada et al., 2025), Claude-3.7-sonnet (Anthropic, 2025), Qwen3-235B (Yang et al., 2025), and Gemini-2.5-pro (Comanici et al., 2025)—as well as a lightweight yet competitive model, GPT-40-mini (OpenAI, 2024). For consistency and clarity, we report detailed ablation and qualitative analyses with Gemini-2.5-pro.

Evaluation Protocol. ReTabAD follows the *one-class classification setting*, where the training set consists of 50% of the normal samples, while the test set consists of the remaining normal samples and all anomalous samples, as in previous studies (Bergman & Hoshen, 2020; Livernoche et al., 2023). For performance evaluation, we primarily report the Area Under the Receiver Operating Characteristic Curve (AUROC), a standard metric in AD (Ruff et al., 2018). To mitigate randomness, each experiment is run five times with different seeds, and Full results with the Area Under the

Table 3: **AUROC Performance on the ReTabAD.** This table compares training-based methods and our zero-shot LLM (Gemini-2.5-pro, best performing LLM). Results are averaged over 5 runs, with standard deviations reported in Appendix **F**.

				Trair	ing-based l	Methods					Zero-shot LLM
Dataset	IForest	OCSVM	LOF	DeepSVDD	NeuTraL	SLAD	DIF	MCM	DRL	AnoLLM	Ours
automobile	0.648	0.645	0.688	0.845	0.810	0.780	0.647	0.801	0.762	0.625	0.767
backdoor	0.888	0.876	0.702	0.800	0.948	0.935	0.973	0.961	0.902	0.885	0.827
campaign	0.732	0.700	0.669	0.721	0.760	0.717	0.677	0.761	0.737	0.738	0.813
cardiotocography	0.830	0.868	0.826	0.813	0.791	0.764	0.740	0.843	0.847	0.735	0.829
census	0.620	0.647	0.596	0.712	0.686	0.687	0.726	0.729	0.728	0.737	0.895
churn	0.506	0.651	0.465	0.573	0.651	0.571	0.494	0.580	0.553	0.557	0.809
cirrhosis	0.849	0.823	0.843	0.807	0.831	0.810	0.820	0.830	0.814	0.850	0.850
covertype	0.968	0.998	0.980	0.971	0.998	0.999	0.998	0.998	0.995	0.990	0.961
credit	0.639	0.717	0.590	0.638	0.690	0.691	0.689	0.671	0.680	0.495	0.681
equip	0.980	0.987	0.987	0.984	0.985	0.981	0.987	0.986	0.984	0.986	0.978
gallstone	0.650	0.671	0.704	0.731	0.780	0.758	0.649	0.757	0.745	0.574	0.667
glass	0.944	0.959	0.974	0.963	0.968	0.952	0.936	0.966	0.949	0.907	0.919
glioma	0.722	0.725	0.711	0.766	0.784	0.886	0.686	0.790	0.764	0.708	0.895
quasar	0.915	0.930	0.966	0.804	0.954	0.952	0.793	0.950	0.897	0.957	0.961
seismic	0.710	0.710	0.615	0.729	0.716	0.727	0.736	0.716	0.714	0.746	0.741
stroke	0.679	0.716	0.625	0.722	0.703	0.678	0.705	0.753	0.727	0.687	0.776
vertebral	0.500	0.638	0.540	0.581	0.697	0.679	0.340	0.615	0.477	0.597	0.755
wbc	0.961	0.969	0.960	0.969	0.785	0.938	0.679	0.957	0.954	0.871	0.968
wine	0.987	0.957	0.974	0.974	0.988	0.980	0.760	0.979	0.958	0.933	0.991
yeast	0.838	0.875	0.803	0.820	0.841	0.846	0.815	0.856	0.841	0.809	0.861
Average Rank Average AUROC	7.43 0.778	5.45 0.803	7.53 0.761	6.38 0.796	4.40 0.818	5.45 0.817	7.73 0.742	4.03 0.825	6.30 0.801	7.25 0.769	4.08 0.847

Precision-Recall Curve (AUPRC) (Saito & Rehmsmeier, 2015) and standard deviations are in the Appendix E, F.

4 EXPERIMENTS ON RETABAD BENCHMARK

This section explores the potential of context-aware approaches in tabular AD. Specifically, we design our experiments to investigate the following research questions:

- Does semantic context \mathcal{M} improve AD performance? (§4.1)
- Which types of semantic information contribute most to detection performance? (§4.2)
- Can LLMs leverage domain-specific knowledge to identify specialized anomaly patterns? (§4.3)

4.1 Context-aware AD Performance

Table 3 presents a detailed comparison across 20 datasets. For clarity, we report representative AD methods in the main table; the complete per-dataset results for all evaluated models are provided in Appendix F. Despite requiring no training, our zero-shot LLM framework with textual metadata achieves an average rank of 4.08, approaching the state-of-the-art training-based method, MCM (Yin et al., 2024), demonstrating that semantic context can serve as a strong signal for AD. Notably, the benefit of semantic context is especially pronounced in datasets such as glioma, where 20 out of 21 features are categorical and primarily expressed as binary (yes/no) attributes. In such settings, raw tabular values (e.g., ATRX=1, IDH1=0) carry little meaning without domain-specific descriptions. By leveraging column-level metadata (e.g., "ATRX mutation present"), the LLM can better interpret the clinical implications of these attributes, leading to a substantial performance gain. This highlights how semantic context is crucial when features are categorical or domain-specific, providing not only improved detection accuracy but also guidance for developing future AD models that are semantically grounded.

We quantify the overall effect of incorporating textual metadata on zero-shot LLMs. As summarized in Table 4, enriching the tabular input with semantic context consistently yields substantial gains across all evaluator models, where *No Desc.* refers to the setting that provides only normal statistics without metadata and *Full Desc.* includes all available textual information. On average, we observe a +7.6 percentage point improvement in AUROC over the *No Desc.* baseline, indicating that models are better able to

Table 4: **Effect of Textual Metadata on Zero-shot LLMs.** We report average AU-ROC across 20 datasets of ReTabAD.

Evaluator LLM	No Desc.	Full Desc.
GPT-4o-mini	0.692	0.726
GPT-4.1	0.696	0.735
Claude-3.7-sonnet	0.725	0.777
Qwen3-235B	0.665	0.747
Gemini-2.5-pro	0.691	0.847

Table 5: Win Rate Comparison across Different Context Types on the ReTabAD. Win rates are computed based on AUROC performance, where each type represents different combinations of contextual information: Domain knowledge, Feature description, and Normal statistics.

	Conte	xt Informa	tion			Win Rate		
Type	$\overline{\mathcal{C}_{statistical}}$	$C_{feature}$	\mathcal{C}_{domain}	GPT-4o-mini	GPT-4.1	Claude-3.7-Sonnet	Qwen3-235B	Gemini-2.5-pro
A (No Desc.)	1	Х	Х	0.15	0.20	0.00	0.05	0.05
В	✓	1	X	0.05	0.15	0.20	0.20	0.00
C	X	1	1	0.25	0.30	0.10	0.10	0.15
D (Full Desc.)	✓	✓	✓	0.55	0.35	0.70	0.65	0.80

ground their predictions when provided with feature descriptions and dataset semantics. Interestingly, the performance gap is even more pronounced for reasoning-oriented LLMs such as GPT-4.1 and Gemini-2.5-pro, which show the largest relative gains among all models. This suggests that these models are particularly capable of leveraging structured textual cues to form more contextually grounded anomaly judgments, whereas lighter models still benefit but to a lesser extent.

4.2 ABLATION STUDY ON CONTEXTUAL INFORMATION

To evaluate the relative contribution of different information sources, we design an ablation study with four prompt variants (Type A–D) in our ReTabAD benchmark as follows:

- Type A (No Desc.): Normal statistic only (anonymized column names e.g., AA, AB, ...)
- Type B: Normal statistic + Feature Description
- Type C: Feature description + Domain knowledge
- Type D (Full Desc.): Normal statistic + Feature description + Domain knowledge

The ablation results (Table 5) clearly demonstrate that combining all three sources of semantic information yields the highest win rate across all LLMs. Column descriptions generally improve performance when added to normal statistics (Type A \rightarrow B) (see Table 11 in the Appendix E), while domain descriptions alone (Type C) produce mixed results—highlighting the necessity of numerical context for stable reasoning. Type D exhibits strong synergistic effects, indicating that LLMs benefit from both statistical grounding and domain-level priors to accurately detect anomalies. Overall, these findings show that even without domain knowledge, the inclusion of feature descriptions already leads to clear performance gains, and that semantic information (both domain and feature) becomes substantially more powerful when coupled with statistical context.

4.3 FEATURE ATTRIBUTION AND REASONING ANALYSIS

Key Feature Alignment with Supervised Attributions. We design a quantitative evaluation to measure whether LLMs identify features that truly drive anomaly classification, focusing exclusively on *anomalous instances*. Normal instances are not evaluated individually, as they are primarily used to establish the decision boundary and represent expected behavior. Hence, our metric specifically measures whether the model's reasoning highlights features that explain *why* a sample is anomalous. Specifically, we train an XGBoost (Chen &

Table 6: **Impact of Textual Metadata on Reasoning Alignment.** We report F1-Score@K (K=1,3) on anomalous instances for Type A (No Desc.) and Type D (Full Desc.).

Dataset	F1	@1	F1	@3
	Type A	Type D	Type A	Type D
campaign churn glioma	0.086 0.133 0.009	0.344 0.288 0.551	0.159 0.160 0.044	0.466 0.400 0.589

Guestrin, 2016) on ground-truth labels and compute SHAP (Lundberg & Lee, 2017) values for each instance. For a given anomalous instance x_i , we define the reference set $R_i^{(K)}$ as the top-K features ranked by absolute SHAP values, and compare it with the LLM's predicted top-K features $\hat{F}_i^{(K)}$ using F1@K, which serves as a *proxy metric* for domain-informed reasoning. Table 6 illustrates representative datasets where textual metadata provides clear benefits, while full results across all 20 datasets are reported in the Appendix E. These examples show that semantic context can help LLMs

recover the features that drive anomalous behavior. This improvement is especially pronounced in glioma and campaign, where key biomarkers (IDH1, TP53) and key determinants of campaign success (poutcome (outcome of the previous campaign), duration (length of the last contact)) are consistently recovered, yielding large F1 gains. These results demonstrate that textual metadata alone enables LLMs to account for much of the explanatory signal behind anomalies, allowing them to identify the key features that drive abnormal behavior without any task-specific training.

Qualitative Analysis of Reasoning Text. To quantitatively explore reasoning quality, we measure detection AUROC improvement when reasoning texts of detected anomalies are provided as contextual examples in the prompt, prioritizing samples with higher anomaly scores. As shown in Figure 3, we observe that performance initially fluctuates with very few examples, improves steadily up to five examples, and then saturates, confirming that our evaluation captures meaningful variations in reasoning quality. This suggests that the quality of reasoning can meaningfully affect detection outcomes. Importantly, the effect is more pronounced when comparing against Type A explanations: higher-quality reasoning (Type D) offers richer, domain-relevant insights and leads to greater performance gains.

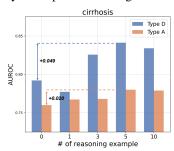


Figure 3: Quantitative Evaluation of LLM Reasoning via Performance Gain. Results are reported on the representative cirrhosis dataset.

To illustrate further, Figure 4 presents an example from the cirrhosis dataset. Type A explanation merely states a numeric deviation, offering little insight into why the sample is anomalous. In contrast, Type D explanation highlights "The elevated Prothrombin time (11.50) indicates compromised liver synthetic function". Importantly, the notion of liver synthetic function is not provided in the metadata itself; rather, it emerges as an intermediate diagnostic step derived from the model's prior knowledge. This shows that, when enriched with textual metadata, the LLM not only grounds its reasoning in the observed feature but also extends beyond the given descriptions to provide domain meaningful interpretation. This contrast demonstrates how textual metadata can elevate shallow observations into domain-aware explanations that incorporate both provided context and external knowledge.

Cirrhosis.json Type A (w/ $C_{statistic}$) GT label: 1 (Anomaly) Metadata: Anomaly score: 0.6 "dataset_name": "cirrhosis", Reasoning: Feature AP is above the normal range "description": "The dataset includes clinical features for predicting survival states of patients with liver cirrhosis.", "columns": I Type D (w/ $c_{statistic}$, $c_{feature}$, c_{domain}) "name": "*Prothrombin*", GT label: 1 (Anomaly) "dtype": "float", "logical_type": "numerical", Anomaly score: 0.68 "description": "Prothrombin time in seconds" Reasoning: The elevated Prothrombin time (11.50) is the key anomaly, indicating *compromised liver synthetic function*. While other markers are currently stable, impaired coagulation is a direct measure of liver $"label_description": "In this dataset, the normal/abnormal classification is a constant of the constant of t$ failure and a significant predictor of *mortality*, warranting an abnormal based on patient survival status. classification

Figure 4: **Reasoning Text Examples on the cirrhosis dataset.** Left: JSON example. Right: Comparison of Type A (numeric deviation only) and Type D (domain grounded explanation).

5 CONCLUSION AND FUTURE WORK

We present ReTabAD, a benchmark that restores textual semantics for context-aware tabular AD. By pairing raw tabular data with textual metadata, ReTabAD enables models not only to detect anomalies but to reason about why they occur. Our results show that semantic context improves performance and interpretability, allowing zero-shot LLMs to approach state-of-the-art training-based detectors. Beyond benchmarking, ReTabAD can serve as a foundation for diverse applications including semantic-guided data augmentation and hybrid approaches that combine statistical and semantic cues. We hope this resource accelerates research toward context-aware, interpretable anomaly detection that is robust and deployable in real-world systems.

REFERENCES

- Khaled Gubran Al-Hashedi and Pritheega Magalingam. Financial fraud detection applying data mining techniques: A comprehensive review from 2009 to 2019. *Computer Science Review*, 40: 100402, 2021.
- Anthropic. Claude opus 4.1. https://www.anthropic.com/news/claude-opus-4-1, August 2025. Accessed: 2025-08-20.
- Liron Bergman and Yedid Hoshen. Classification-based anomaly detection for general data. *arXiv* preprint arXiv:2005.02359, 2020.
- Markus M Breunig, Hans-Peter Kriegel, Raymond T Ng, and Jörg Sander. Lof: identifying density-based local outliers. In *Proceedings of the 2000 ACM SIGMOD international conference on Management of data*, pp. 93–104, 2000.
- D. Campos and J. Bernardes. Cardiotocography. UCI Machine Learning Repository, 2000. DOI: https://doi.org/10.24432/C51S4N.
- Guilherme O Campos, Arthur Zimek, Jörg Sander, Ricardo JGB Campello, Barbora Micenková, Erich Schubert, Ira Assent, and Michael E Houle. On the evaluation of unsupervised outlier detection: measures, datasets, and an empirical study. *Data mining and knowledge discovery*, 30 (4):891–927, 2016.
- Varun Chandola, Arindam Banerjee, and Vipin Kumar. Anomaly detection: A survey. ACM computing surveys (CSUR), 41(3):1–58, 2009.
- Tianqi Chen and Carlos Guestrin. Xgboost: A scalable tree boosting system. In *Proceedings of the 22nd acm sigkdd international conference on knowledge discovery and data mining*, pp. 785–794, 2016.
- Gheorghe Comanici, Eric Bieber, Mike Schaekermann, Ice Pasupat, Noveen Sachdeva, Inderjit Dhillon, Marcel Blistein, Ori Ram, Dan Zhang, Evan Rosen, et al. Gemini 2.5: Pushing the frontier with advanced reasoning, multimodality, long context, and next generation agentic capabilities. arXiv preprint arXiv:2507.06261, 2025.
- Nuno Fachada, Daniel Fernandes, Carlos M Fernandes, Bruno D Ferreira-Saraiva, and João P Matos-Carvalho. Gpt-4.1 sets the standard in automated experiment design using novel python libraries. *arXiv* preprint arXiv:2508.00033, 2025.
- Tharindu Fernando, Harshala Gammulle, Simon Denman, Sridha Sridharan, and Clinton Fookes. Deep learning for medical anomaly detection—a survey. *ACM Computing Surveys (CSUR)*, 54(7): 1–37, 2021.
- Elizabeth Fons, Rachneet Kaur, Soham Palande, Zhen Zeng, Tucker Balch, Manuela Veloso, and Svitlana Vyetrenko. Evaluating large language models on time series feature understanding: A comprehensive taxonomy and benchmark. *arXiv preprint arXiv:2404.16563*, 2024.
- Markus Goldstein and Seiichi Uchida. A comparative evaluation of unsupervised anomaly detection algorithms for multivariate data. *PloS one*, 11(4):e0152173, 2016.
- Songqiao Han, Xiyang Hu, Hailiang Huang, Minqi Jiang, and Yue Zhao. Adbench: Anomaly detection benchmark. *Advances in neural information processing systems*, 35:32142–32159, 2022.
- Stefan Hegselmann, Alejandro Buendia, Hunter Lang, Monica Agrawal, Xiaoyi Jiang, and David Sontag. Tabllm: Few-shot classification of tabular data with large language models. In *International conference on artificial intelligence and statistics*, pp. 5549–5581. PMLR, 2023.
- Andrey Kharitonov, Abdulrahman Nahhas, Matthias Pohl, and Klaus Turowski. Comparative analysis of machine learning models for anomaly detection in manufacturing. *Procedia Computer Science*, 200:1288–1297, 2022.
- Takeshi Kojima, Shixiang Shane Gu, Machel Reid, Yutaka Matsuo, and Yusuke Iwasawa. Large language models are zero-shot reasoners. *Advances in neural information processing systems*, 35: 22199–22213, 2022.

- Max Landauer, Sebastian Onder, Florian Skopik, and Markus Wurzenberger. Deep learning for anomaly detection in log data: A survey. *Machine Learning with Applications*, 12:100470, 2023.
- Boyang Liu, Ding Wang, Kaixiang Lin, Pang-Ning Tan, and Jiayu Zhou. Rca: A deep collaborative autoencoder approach for anomaly detection. In *IJCAI: proceedings of the conference*, volume 2021, pp. 1505, 2021.
- Fei Tony Liu, Kai Ming Ting, and Zhi-Hua Zhou. Isolation forest. In 2008 eighth ieee international conference on data mining, pp. 413–422. IEEE, 2008.
- Victor Livernoche, Vineet Jain, Yashar Hezaveh, and Siamak Ravanbakhsh. On diffusion modeling for anomaly detection. *arXiv preprint arXiv:2305.18593*, 2023.
- Scott M. Lundberg and Su-In Lee. A unified approach to interpreting model predictions. In *Proc. the Advances in Neural Information Processing Systems (NeurIPS)*, 2017.
- OpenAI. Gpt-4o mini: Advancing cost-efficient intelligence. https://openai.com/index/gpt-4o-mini-advancing-cost-efficient-intelligence/, 2024. Accessed: 2024-08-13.
- Guansong Pang, Longbing Cao, Ling Chen, and Huan Liu. Learning representations of ultrahigh-dimensional data for random distance-based outlier detection. In *Proceedings of the 24th ACM SIGKDD international conference on knowledge discovery & data mining*, pp. 2041–2050, 2018.
- Guansong Pang, Chunhua Shen, Longbing Cao, and Anton Van Den Hengel. Deep learning for anomaly detection: A review. *ACM computing surveys (CSUR)*, 54(2):1–38, 2021.
- Chen Qiu, Timo Pfrommer, Marius Kloft, Stephan Mandt, and Maja Rudolph. Neural transformation learning for deep anomaly detection beyond images. In *International conference on machine learning*, pp. 8703–8714. PMLR, 2021.
- Sridhar Ramaswamy, Rajeev Rastogi, and Kyuseok Shim. Efficient algorithms for mining outliers from large data sets. In *Proceedings of the 2000 ACM SIGMOD international conference on Management of data*, pp. 427–438, 2000.
- Lukas Ruff, Robert Vandermeulen, Nico Goernitz, Lucas Deecke, Shoaib Ahmed Siddiqui, Alexander Binder, Emmanuel Müller, and Marius Kloft. Deep one-class classification. In *International* conference on machine learning, pp. 4393–4402. PMLR, 2018.
- Lukas Ruff, Jacob R. Kauffmann, Robert A. Vandermeulen, Grégoire Montavon, Wojciech Samek, Marius Kloft, Thomas G. Dietterich, and Klaus-Robert Müller. A unifying review of deep and shallow anomaly detection. *Proc. IEEE*, 109(5):756–795, 2021a.
- Lukas Ruff, Jacob R Kauffmann, Robert A Vandermeulen, Grégoire Montavon, Wojciech Samek, Marius Kloft, Thomas G Dietterich, and Klaus-Robert Müller. A unifying review of deep and shallow anomaly detection. *Proceedings of the IEEE*, 109(5):756–795, 2021b.
- Takaya Saito and Marc Rehmsmeier. The precision-recall plot is more informative than the roc plot when evaluating binary classifiers on imbalanced datasets. *PloS one*, 10(3):e0118432, 2015.
- Bernhard Schölkopf, Robert C Williamson, Alex Smola, John Shawe-Taylor, and John Platt. Support vector method for novelty detection. *Advances in neural information processing systems*, 12, 1999.
- Bernhard Schölkopf, John C Platt, John Shawe-Taylor, Alex J Smola, and Robert C Williamson. Estimating the support of a high-dimensional distribution. *Neural computation*, 13(7):1443–1471, 2001
- Mei-Ling Shyu, Shu-Ching Chen, Kanoksri Sarinnapakorn, and LiWu Chang. A novel anomaly detection scheme based on principal component classifier. Technical report, University of Miami, Department of Electrical and Computer Engineering, 2003.
- Che-Ping Tsai, Ganyu Teng, Phillip Wallis, and Wei Ding. AnoLLM: Large language models for tabular anomaly detection. In *The Thirteenth International Conference on Learning Representations*, 2025. URL https://openreview.net/forum?id=7VkHffT5X2.

- Hu Wang, Guansong Pang, Chunhua Shen, and Congbo Ma. Unsupervised representation learning by predicting random distances. *arXiv preprint arXiv:1912.12186*, 2019.
- Hongzuo Xu, Guansong Pang, Yijie Wang, and Yongjun Wang. Deep isolation forest for anomaly detection. *IEEE Transactions on Knowledge and Data Engineering*, 35(12):12591–12604, 2023a. doi: 10.1109/TKDE.2023.3270293.
- Hongzuo Xu, Yijie Wang, Juhui Wei, Songlei Jian, Yizhou Li, and Ning Liu. Fascinating supervisory signals and where to find them: Deep anomaly detection with scale learning. In *International Conference on Machine Learning*, pp. 38655–38673. PMLR, 2023b.
- An Yang, Anfeng Li, Baosong Yang, Beichen Zhang, Binyuan Hui, Bo Zheng, Bowen Yu, Chang Gao, Chengen Huang, Chenxu Lv, et al. Qwen3 technical report. *arXiv preprint arXiv:2505.09388*, 2025.
- Hangting Ye, He Zhao, Wei Fan, Mingyuan Zhou, Dan dan Guo, and Yi Chang. Drl: Decomposed representation learning for tabular anomaly detection. In *The Thirteenth International Conference on Learning Representations*, 2025.
- Jiaxin Yin, Yuanyuan Qiao, Zitang Zhou, Xiangchao Wang, and Jie Yang. Mcm: Masked cell modeling for anomaly detection in tabular data. In *The Twelfth International Conference on Learning Representations*, 2024.
- Yue Zhao, Zain Nasrullah, and Zheng Li. Pyod: A python toolbox for scalable outlier detection. *Journal of machine learning research*, 20(96):1–7, 2019.

A RETABAD DATASET DETAILS

ReTabAD benchmark consists of 20 datasets, each accompanied by a JSON text metadata file. This comprehensive collection encompasses a wide range of domains and data characteristics, as summarized in Table 7. Our benchmark spans critical application areas including healthcare (7 datasets: cardiotocography, cirrhosis, gallstone, glioma, stroke, vertebral, wbc), finance (2 datasets: campaign, credit), cybersecurity (backdoor), and various scientific domains such as biology (yeast), astronomy (quasar), and geophysics (seismic). This broad domain representation is particularly valuable for evaluating context-aware tabular anomaly detection, as it enables assessment of whether algorithms can leverage domain-specific knowledge to improve detection performance. The diversity allows researchers to investigate how contextual understanding of different application areas—such as medical diagnostic patterns in healthcare datasets versus fraud detection patterns in financial datasets—can enhance anomaly detection capabilities beyond traditional domain-agnostic approaches.

A.1 DATA COLLECTION

The datasets were carefully curated by selecting genuine tabular datasets from ADBench (Han et al., 2022) and tracing back to their original sources, with the majority sourced from the UCI Machine Learning Repository¹. By accessing the original data sources, we identified and corrected erroneous preprocessing steps present in ADBench and verified the appropriate definitions of anomalies for each dataset. This rigorous validation process resulted in datasets that differ from their ADBench counterparts, ensuring higher quality and more reliable anomaly labels. We additionally filtered out datasets lacking sufficient metadata or showing performance saturation across methods to maintain benchmark discriminative power. We further enriched our collection by incorporating additional high-quality datasets from Kaggle² to ensure broader domain coverage. We provide both raw data and preprocessing code to ensure reproducibility and transparency. Complete source information, dataset access links, and preprocessing scripts are available in our benchmark repository, and all datasets are publicly accessible.

Dataset Name Normal Count Domain **Datapoints** Columns Anomaly Count Anomaly Ratio (%) 26.42 automobile Manufacturing 159 26 117 42 backdoor Network 50,000 42 48,780 1,220 2.44 7,842 6,056 1,786 22.77 campaign Finance 16 1.655 22.15 cardiotocography Healthcare 2.126 471 21 50,000 47,121 census Demographics 41 2.879 5.76 churn Telecommunications 7,032 20 5,163 1,869 26.6 cirrhosis Healthcare 247 17 165 82 33.20 50,000 12 49,520 480 0.96 covertype Environment credit Finance 30,000 23 23,364 6,636 22.12 7,672 6,905 767 10.00 Manufacturing 6 eauip Healthcare 241 38 161 80 33 20 gallstone 214 9 glass Forensics 163 51 23.83 23 glioma Healthcare 730 487 243 33 29 50,000 8 40,520 9,480 18.96 quasar Astronomy seismic Geophysics 2.584 18 2,414 170 6.58 Healthcare 4,909 10 4,700 209 4.26 stroke 310 210 100 32.26 vertebral Healthcare 6 30 535 178 33.27 whc Healthcare 357 26.97 wine Chemistry 178 13 130 48 Biology 1,484 1.389 95 6.40 yeast

Table 7: Dataset Statistics with Domain Information

A.2 TABULAR DATA PREPROCESSING

To ensure fair and consistent evaluation across models, we apply a standardized preprocessing pipeline to all datasets. We provide both raw data and comprehensive preprocessing code for each dataset to guarantee reproducibility and transparency in our benchmark. This systematic approach addresses common inconsistencies found in existing benchmarks and ensures that all datasets maintain their

¹https://archive.ics.uci.edu/

²https://www.kaggle.com/

inherent characteristics while providing a unified foundation for algorithm comparison. The main preprocessing steps are as follows:

• Dataset size standardization:

 Datasets exceeding 50,000 samples are randomly downsampled to 50,000 instances using np.random.choice with seed 42 for reproducibility and also provide csv file.

• Anomaly definition verification:

- Anomaly labels are verified against original dataset documentation to ensure correct interpretation.
- Ambiguous or incorrectly defined anomaly classes from processed versions are corrected based on domain knowledge and source specifications.
- For newly incorporated datasets, anomaly classes are carefully defined following domainspecific criteria and established conventions in the respective fields.

• Anomaly ratio balancing:

- Anomaly class proportions are capped at a maximum of 1/3 of the total dataset.
- Test sets maintain approximately balanced anomaly ratios for reliable evaluation metrics.

• Missing value handling:

- Any instance containing missing values in input features or target labels is completely removed.
- No imputation is applied to avoid introducing artificial patterns or bias.

• Feature value restoration:

- Categorical features are strictly identified and restored based on original metadata from the UCI Machine Learning Repository and other data sources.
- Original categorical values are recovered from encoded representations to preserve semantic meaning.
- Numerical features are restored to their original scales by referencing source documentation, as normalization criteria applied in existing benchmarks were often unclear or undocumented.
- Each column is assigned column names based on original dataset documentation.

Table 8: Dataset Information Summary

Dataset Name	Description	Label Definition
automobile	Car specifications and insurance risk ratings from the 1985 Auto Imports Database.	High-risk cars with symboling +2 or +3 are considered anomalies, while normal-risk cars with other symboling values are normal.
backdoor	Network traffic data for detecting backdoor attacks.	Backdoor attacks are considered anomalies, while normal network traffic is normal.
campaign	Bank marketing data with client demographics and outcomes.	Clients who subscribed to term deposits are considered anomalies, while those who did not subscribe are normal.
cardiotocography	Fetal heart rate and uterine contraction measurements from CTGs.	Suspect or Pathologic fetal states are considered anomalies, while Normal states are normal.
census	U.S. Census data with demographic and socioeconomic attributes.	High-income individuals (>\$50K) are considered anomalies, while low-income individuals (<=\$50K) are normal.
churn	Telco customer data with demographics, service usage, and account details.	Customers who churned are considered anomalies, while customers who stayed are normal.
cirrhosis	Mayo Clinic study data on primary biliary cirrhosis patients.	Patients who died are considered anomalies, while censored patients or those who survived are normal.
covertype	Forest cover type data with ecological and cartographic variables.	Cottonwood/Willow forests (low elevation deciduous riparian) are considered anomalies, while Lodgepole Pine forests (mid to high elevation coniferous) are normal.
credit	Credit card dataset with demographics and payment history.	Customers who defaulted on their credit card payment are considered anomalies, while customers who did not default are normal.
equip	Industrial equipment sensor data for fault detection.	Faulty equipment states are considered anomalies, while normal operation states are normal.
gallstone	Clinical data of patients with gallstone disease including lab results.	Patients with gallstones present are considered anomalies, while patients without gallstones are normal.
glass	Forensic glass dataset with oxide content measurements for type identification.	Less common or specialized glass types (containers, tableware, headlamps) are considered anomalies, while common architectural glass types are normal.
glioma	Clinical and genetic data of glioma patients with tumor grades.	Glioblastoma Multiforme (GBM) cases are considered anomalies, while Lower-Grade Glioma (LGG) cases are normal.
quasar	SDSS dataset with spectral features of stars, galaxies, and quasars.	Quasars (QSO) are considered anomalies as rare astronomical objects, while stars and galaxies are normal common objects.
seismic	Mining dataset of seismic bumps for hazardous event prediction.	Hazardous states with high energy seismic bumps are considered anomalies, while non-hazardous states are normal.
stroke	Patient data with demographics, health risks, and stroke outcomes.	Patients who had a stroke are considered anomalies, while patients who did not have a stroke are normal.
vertebral	Biomechanical features from spinal X-rays of vertebral conditions.	Original 'Normal' class samples are considered anomalies, while pathological classes (Hernia and Spondy-Iolisthesis) are normal.
wbc	Breast cancer dataset from digitized cell nuclei features.	Malignant breast cancer cases are considered anomalies, while benign cases are normal.
wine	Chemical analysis of Italian wines from three cultivars.	Wine cultivar 3 is considered an anomaly as it differs from the other two typical cultivars.
yeast	Protein features for predicting subcellular localization in yeast.	Proteins localized to endoplasmic reticulum membrane (ME1/ME2) are considered anomalies due to rare localization.

A.3 METADATA FORMAT

We newly establish structured metadata to provide comprehensive dataset information for evaluating context-aware tabular AD. The metadata follows a standardized format designed for extensibility to accommodate future datasets and evolving research needs. This structured approach enables seamless integration of new datasets while maintaining consistency across the benchmark. Table 2 illustrates the metadata structure using the Cardiotocography dataset as an example from the ReTabAD benchmark.

- **Dataset Description:** The metadata begins with essential dataset identifiers including the dataset name, original source URL, and a concise description of the data collection context. This information provides the foundational context necessary for domain information.
- **Feature Description:** Each feature is systematically documented with four key attributes: (1) *Feature name* the original column identifier, (2) *Type* the raw data type (int, float, string), (3) *Logical type* the semantic classification (numerical, categorical, ordinal, binary), and (4) *Description* a detailed explanation of the feature's meaning and measurement units. This multilayered typing system enables our prompt generator to apply appropriate analysis strategies for different feature characteristics.
- Label Description: The metadata explicitly defines the anomaly detection target, specifying the label column name, data type, and semantic interpretation. For binary classification tasks, the mapping between numeric values (0/1) and semantic labels (Normal/Anomaly) is clearly established to ensure consistent interpretation across different prompt types.

This structured metadata format enables our system to automatically generate contextually appropriate prompts while maintaining consistency across diverse datasets. The standardized schema supports both domain-specific analysis (using feature descriptions and dataset context) and domain-agnostic analysis (using only statistical properties and logical types), facilitating comprehensive evaluation of contextual information impact on anomaly detection performance. Additionally, our metadata-driven approach can automatically recommend appropriate data preprocessing strategies based on logical types—for instance, suggesting standardization for numerical features, one-hot encoding for categorical features, and ordinal encoding for ordinal features—even when provided with only raw tabular data, as demonstrated in Table 9.

Table 9: Recommended preprocessing methods for each logical_type.

logical_type	Details
numerical	Meaning: Continuous or discrete numeric values Recommended Preprocessing: StandardScaler (z-score), MinMaxScaler, log transform (if skewed), clipping or winsorization Notes: Improves stability in statistical and deep models
categorical	Meaning: Unordered categories Recommended Preprocessing: One-hot encoding (low cardinality), learned embedding (high cardinality), label encoding (for trees) Notes: Prefer embedding for many categories
ordinal	Meaning: Ordered categories Recommended Preprocessing: Ordinal encoding (e.g., Low=0, Medium=1, High=2) Notes: Numeric mapping should preserve order
binary	Meaning: Two distinct values Recommended Preprocessing: 0/1 encoding Notes: Single column usually sufficient

B RETABAD ALGORITHM DETAILS

Our benchmark covers a comprehensive set of unsupervised anomaly detection algorithms. For methods that are not available in existing libraries, we directly implemented them based on the original sources to ensure their faithful integration into our benchmark. In addition, we include all implementations available in widely used libraries (PyOD³ and DeepOD⁴). To ensure consistency, we standardize every algorithm to follow a unified fit/predict interface in the scikit-learn style,

³https://pyod.readthedocs.io/

⁴https://deepod.readthedocs.io/en/latest/

enabling seamless comparison across methods. Furthermore, we expose the core hyperparameters of each algorithm, making them tunable within our framework so that hyperparameter optimization (HPO) can be conducted fairly and reproducibly across all categories of models.

B.1 CLASSICAL METHODS

IForest. Isolation Forest (IForest) (Liu et al., 2008) detects anomalies by recursively partitioning the feature space using random decision trees. Since anomalies are typically easier to isolate than normal instances, they yield shorter average path lengths in the trees. This property enables efficient detection with linear time complexity, making IForest suitable for high-dimensional datasets.

KNN. The k-Nearest Neighbors (KNN) method (Ramaswamy et al., 2000) identifies anomalies based on the distance between a data point and its neighbors. Anomalous points tend to reside far from dense clusters of normal samples, leading to larger distance-based scores. Variants such as average or median distance to the k neighbors are commonly used to improve robustness.

OCSVM. One-Class Support Vector Machine (OCSVM) (Schölkopf et al., 2001) learns a decision boundary that encloses the majority of the data while maximizing the margin in a high-dimensional feature space. Samples falling outside this boundary are flagged as anomalies. Despite its sensitivity to kernel and parameter choices, OCSVM remains a widely adopted baseline for one-class anomaly detection.

LOF. The Local Outlier Factor (LOF) (Breunig et al., 2000) algorithm measures the local deviation of a point's density relative to its neighbors. Instances with significantly lower local density are considered anomalous. LOF is effective in detecting context-dependent anomalies but can be sensitive to neighborhood size and parameter selection.

PCA. Principal Component Analysis (PCA) for anomaly detection (Shyu et al., 2003) projects data into a lower-dimensional subspace that captures the majority of variance. Reconstruction error or the residual in the discarded components is then used as the anomaly score. This approach is effective when anomalies do not conform to the dominant low-dimensional structure of normal data.

B.2 DEEP LEARNING METHODS

DeepSVDD. Deep Support Vector Data Description (DeepSVDD) (Ruff et al., 2018) extends the classic one-class classification paradigm to deep neural networks. It learns a feature representation that maps normal samples into a compact hypersphere in the latent space, while anomalies lie farther away. This method is a widely used baseline for deep one-class anomaly detection.

REPEN. REPEN (Pang et al., 2018) proposes a random distance-based framework for anomaly detection in ultrahigh-dimensional data. By learning representations that preserve relative distances between randomly sampled triplets, the method improves the effectiveness of distance-based outlier detectors applied on the learned embedding space.

RDP. Random Distance Prediction (RDP) (Wang et al., 2019) trains a Siamese neural network to predict distances in a randomly projected space, learning representations that preserve data proximity. These learned embeddings significantly improve anomaly detection and clustering performance without using any labels.

RCA. The RCA method (Liu et al., 2021) introduces a collaborative autoencoder framework where multiple autoencoders jointly learn reconstructions. Anomalous samples tend to disrupt collaboration, yielding higher reconstruction errors. This collaborative structure enhances robustness against complex anomaly patterns.

GOAD. GOAD (Bergman & Hoshen, 2020) frames anomaly detection as a self-supervised classification task. By applying diverse geometric transformations to data and predicting transformation labels, the model learns discriminative representations of normality. Anomalies fail to conform to the learned classification boundaries, enabling detection.

NeuTraL. NeuTraL (Qiu et al., 2021) introduces neural transformation learning, where input samples are transformed via trainable mappings. The model learns to distinguish normality based on consistency across multiple transformations, making it applicable to non-image domains such as tabular data.

DIF. Deep Isolation Forest (DIF) (Xu et al., 2023a) integrates the principles of Isolation Forest with deep representation learning. The method first learns embeddings that capture salient data characteristics, followed by isolation-based partitioning to detect anomalies more effectively in high-dimensional settings.

SLAD. Scale Learning for Anomaly Detection (SLAD) (Xu et al., 2023b) introduces auxiliary supervisory signals derived from scale consistency. By enforcing scale-invariant representations, SLAD enhances the generalization capability of deep anomaly detection models, especially for complex tabular datasets.

MCM. Masked Cell Modeling (MCM) (Yin et al., 2024) learns feature correlations by reconstructing randomly masked cells with a trainable mask generator. Anomalies are detected via high reconstruction errors, and a diversity loss ensures complementary masks.

DRL. Decomposed Representation Learning (DRL) (Ye et al., 2025) remaps tabular data into a constrained latent space by decomposing each normal sample into a weighted combination of randomly generated orthogonal basis vectors. A novel discrepancy constraint further amplifies the separation between normal and anomalous patterns, resulting in strong detection performance across diverse tabular benchmarks.

B.3 LLM BASED METHODS

AnoLLM. AnoLLM (Tsai et al., 2025) employs large language models for unsupervised tabular anomaly detection by serializing mixed-type rows into text and fine-tuning an LLM to model the data distribution. Anomaly scores are derived from negative log-likelihoods, offering strong performance on mixed-feature benchmarks and competitive results on predominantly numerical datasets.

Zero-shot LLM. We additionally introduce a zero-shot baseline that leverages large language models for tabular anomaly detection. Each data row is serialized into a textual prompt together with semantic metadata, and the LLM assigns anomaly scores based on its contextual reasoning without any fine-tuning. This setting highlights the potential of LLMs as strong baselines for semantic-aware anomaly detection.

C EXPERIMENTAL DETAILS OF BASELINE METHODS

C.1 Hyperparameter settings

Table 10 summarizes the hyperparameter search ranges for each model. By default, each configuration searches over scaling_type $\in \{std, minmax\}$ and cat_encoding $\in \{int, onehot\}$.

Model	Default Parameters	Hyperparameter Search Range
OCSVM	kernel: rbf contamination: 0.1	nu: {0.1, 0.2, 0.3, 0.4, 0.5} contamination: {0.1, 0.2, 0.3}
LOF	novelty: True metric: euclidean p: 2	n_neighbors: {10, 20, 30, 50} contamination: {0.01, 0.05, 0.1} leaf_size: {10, 30, 50}
KNN	leaf_size: 30 metric: minkowski p: 2	n_neighbors: {10, 20, 30, 50} contamination: {0.01, 0.05, 0.1}
IForest	max_features: 1.0 bootstrap: False	n_estimators: {50, 100, 200, 300, 500} contamination: {0.05, 0.1, 0.15, 0.2, 0.25, 0.3}
PCA	svd_solver: auto weighted: True n_selected_components: null	n_components: {null, 2, 3, 5, 10, 15, 20, 25, 30} contamination: {0.1, 0.2, 0.3} whiten: {True, False}
DeepSVDD	bias: False	lr: {0.005, 0.001, 0.0005, 0.0001} rep_dim: {32, 64, 128} hidden_dims: {100,50; 128,64; 256,128; 512,256,128}
REPEN	act: ReLU init_score_ensemble_size: 50 init_score_subsample_size: 8	lr: {0.001, 0.0001} rep_dim: {128, 256} hidden_dims: {100,50; 256,128}
RDP	rep_dim: 128 hidden_dims: 100,50	Ir: {0.001, 0.0001} hidden_dims: {100,50; 256,128} rep_dim: {32, 128}
RCA	bias: False act: LeakyReLU alpha: 0.5 inference_ensemble: 10	Ir: {0.005, 0.001, 0.0005, 0.0001} rep_dim: {32, 128, 256} hidden_dims: {100,50; 128,64; 256,128; 512,256,128}
GOAD	act: LeakyReLU n_layers: 5 n_trans: 256 hidden_dim: 8	lr: {0.001, 0.0001} trans_dim: {32, 128} n_trans: {256, 512}
NeuTraL	act: LeakyReLU trans_type: residual trans_hidden_dims: 50 n_trans: 11	lr: {0.001, 0.0001} rep_dim: {32, 128} hidden_dims: {100,50; 256,128}
SLAD	act: LeakyReLU n_slad_ensemble: 20 magnify_factor: 200 subspace_pool_size: 50 dist_size: 10	lr: {0.001, 0.0001} hidden_dims: {100, 200} n_unified_feature: {128, 256}
DeepIsolationForest	bias: False lr: 0.001 act: ReLU max_samples: 256	rep_dim: {32, 128, 256} hidden_dims: {100,50; 256,128; 512,256} n_ensemble: {50, 200} n_estimators: {6, 10}
MCM	enc_layers, dec_layers: 3 hidden_dim: 256 z_dim: 128 mask_layers: 3	lr: {0.005, 0.001, 0.0005, 0.0001} mask_number: {10, 15} lambda: {1, 5, 10}
DRL	enc_layers, dec_layers: 3 hidden_dim: 128 input_info_ratio: 0.1 contrastive_learning_ratio: 0.06 n_basis_vec: 5	lr: {0.005, 0.001, 0.0005, 0.0001} input_info_ratio: {0.05, 0.1, 0.15} contrastive_learning_ratio: {0.03, 0.06, 0.09}
AnoLLM	lr:0.00005 training_steps: 2000 n_permutations: 21	model: {SmolLM-135M, SmolLM-360M}

Table 10: Default parameters and hyperparameter search ranges for baselines.

D DETAILED DESCRIPTION OF ZERO-SHOT LLM BASELINE

D.1 EVALUATOR LLMS

GPT-4o-mini (OpenAI). A lightweight variant of OpenAI's GPT-4o, designed for cost-efficient inference while retaining strong reasoning capabilities. It is optimized for practical deployment scenarios where efficiency is prioritized over maximum performance. (gpt-4o-mini-2024-07-18)

GPT-4.1 (OpenAI). The successor to GPT-4, providing enhanced reasoning ability, improved tooluse integration, and stronger multimodal alignment. It represents OpenAI's flagship model as of late 2024. (gpt-4.1)

Claude-3.7-sonnet (**Anthropic**). A mid-sized model in Anthropic's Claude family, optimized for balanced reasoning and efficiency. The "sonnet" variant is designed to offer strong performance on structured tasks while maintaining lower inference cost compared to larger Claude models. (claude-3-7-sonnet-20250219)

Gemini-2.5-pro (**Google DeepMind**). Google's flagship multimodal model, capable of processing text, images, and structured inputs. The "pro" version provides stronger reasoning than lighter variants, and is designed for research and production-scale applications. (gemini-2.5-pro)

Qwen3-235B (Alibaba DAMO Academy). A large-scale autoregressive language model trained on multilingual and multimodal data. With 235 billion parameters, Qwen3 represents Alibaba's third-generation LLM, aiming to provide competitive performance on both English and Chinese benchmarks. (qwen3-235b-a22b)

D.2 IMPLEMENTATION DETAILS OF ZERO-SHOT LLMS

Data parameters. By default, tabular inputs are serialized in raw form without normalization or discretization. However, both normalization (serialize_normalize_method) and discretization into a user-defined number of buckets (serialize_n_buckets) are available as options. For normal statistics, we provide 5th/95th percentiles derived from the training data, which serve as representative ranges for contextual grounding.

Model parameters. We use large language models in a zero-shot setting, where the backbone LLM (llm_model) can be selected flexibly (e.g., GPT-4o). The inference batch size is set to 15, with a maximum of 5 retries per query. For prompt construction, we adopt the Type D format (prompt_type=D), which incorporates full textual metadata (domain, feature, and normal statistics).

D.3 PROMPT TEMPLATE

To systematically assess the role of semantic context in anomaly detection, we design a dedicated PromptGenerator that produces four distinct prompt types (A–D). Each type selectively incorporates different levels of contextual information—ranging from raw numerical inputs to full metadata descriptions—allowing controlled ablations of the information available to the LLM. All numerical attributes are consistently formatted by rounding to three decimal places, ensuring clarity and reproducibility in prompt construction.

- Type A (No Desc.): Normal statistic only (anonymized column names e.g., AA, AB, ...)
- Type B: Normal statistic + Feature Description
- **Type C**: Feature description + Domain knowledge
- Type D (Full Desc.): Normal statistic + Feature description + Domain knowledge

```
Type A Prompt

Analyze the data for anomaly detection.

## Statistical Context

## Numerical features- Normal Ranges:

AA: Normal Range (5<sup>th</sup>-9<sup>th</sup> percentile): A - B

AB: Normal Range (5<sup>th</sup>-9<sup>th</sup> percentile): A - B

### Categorical features - Normal Values:

AK: D, E, F

Analyze the following data:
Record 0: AA={feature_1 value}, _ , AK={feature_k value}

Record B: AA={feature_1 value}, _ , AK={feature_k value}

Return valid JSON array:
[{"record_id':"0", "anomaly_score":0.0, "reasoning":"Analysis result",
    "key_features":["feature1", "feature2"},

[{"record_id':"1", "anomaly_score":0.0, "reasoning":"Analysis result",
    "key_features":["feature1", "feature2"}]
```

Figure 5: Type A Prompt Examples

Figure 6: Type B Prompt Examples

Figure 7: Type C Prompt Examples

```
Type D Prompt
 You are a senior {dataset name} expert analyzing data for anomaly detection.
## Dataset: {dataset_name} {dataset_description}
## Target Label: {target_description}
 ## Features:
 ### Numerical features:
 {feature_1 name}: {feature_1 description}
{feature_2 name}: {feature_1 description}
### Categorical features:
{feature_K name} {feature_K description}
 ## Statistical Context
### Numerical features- Normal Ranges:
 ### Categorical features - Normal Values:
  {feature K name}:D, E, F
# Analysis Guidelines:
### Numerical Analysis:
- Compare each numerical feature to the normal distribution baselines above.
- Identify values beyond 95th percentile OR below 5th percentile (likely abnormal).
- Consider cumulative effect of multiple borderline values.
- **Individual normal values do not guarantee normal overall patterns - evaluate holistic combinations.**
### Categorical Pattern Analysis:
    -**Don't just check if categorical values are 'in-distribution**'.
    - Look beyond individual categorical validity - assess contextual appropriateness given other features.
    - Identify contradictory categorical combinations or misalignment with numerical severity indicators.
    Use dataset context and feature descriptions to guide analysis.
- Use Gataset context and reduce descriptions to guide dialysis.

- Look for meaningful patterns across multiple features.

- Consider how features relate based on domain knowledge and semantic context.

- Evaluate logical consistency between categorical and numerical features.

- Assess whether feature combinations make domain-specific logical sense.

- Leverage target label definition
 Analyze the following data based on the guidelines provided above: Record 0: \{feature_1 name\} = \{feature_1 value\}, \dots, \{feature_k name\} = \{feature_k value\}\}
 Record B: {feature_1 name}={feature_1 value}, ..., {feature_k name}={feature_k value}
 Return valid JSON array:
 [{"record_id":"0","anomaly_score":0.0,"reasoning":"Analysis result", "key_features":["feature1", "feature2"},
 [{"record_id":"1","anomaly_score":0.0,"reasoning":"Analysis result", "key_features":["feature1", "feature2"}]
```

Figure 8: Type D Prompt Examples

E COMPARISON OF THE LLMS

Table 11: Comparison of the LLMs' AUROC performance across four context types (Type A–D). Each column represents a different LLM evaluated under four prompt conditions: Type A, Type B, Type C, and Type D.

Dataset		GPT-4	o-mini			GP	Г-4.1			Claude-3	3.7-sonnet			Qwen	3-235B			Gemini-	2.5-pro	
Dittiect	Type A	Type B	Type C	Type D	Type A	Type B	Type C	Type D	Type A	Type B	Type C	Type D	Type A	Type B	Type C	Type D	Type A	Type B	Type C	Type D
automobile	0.584	0.568	0.537	0.554	0.684	0.610	0.540	0.606	0.781	0.778	0.647	0.807	0.590	0.556	0.642	0.660	0.806	0.751	0.546	0.767
	(± 0.036)	(± 0.041)	(± 0.047)	(± 0.043)	(± 0.020)	(± 0.034)	(± 0.046)	(± 0.033)	(± 0.015)	(± 0.016)	(± 0.029)	(± 0.012)	(± 0.035)	(± 0.042)	(± 0.026)	(± 0.023)	(± 0.012)	(± 0.017)	(± 0.044)	(± 0.016)
backdoor	0.759	0.806	0.819	0.762	0.743	0.763	0.793	0.709	0.812	0.855	0.835	0.776	0.780	0.797	0.824	0.792	0.804	0.762	0.553	0.827
	(± 0.017)	(± 0.012)	(± 0.010)	(± 0.016)	(± 0.018)	(± 0.016)	(± 0.013)	(± 0.019)	(±0.011)	(± 0.007)	(± 0.009)	(±0.015)	(± 0.014)	(± 0.013)	(± 0.010)	(± 0.013)	(± 0.012)	(±0.016)	(±0.041)	(±0.010)
campaign	0.526	0.505	0.458	0.493	0.562	0.581	0.502	0.595	0.554	0.555	0.522	0.618	0.508	0.530	0.479	0.557	0.596	0.558	0.528	0.813
	(± 0.038)	(± 0.042)	(± 0.048)	(± 0.044)	(± 0.032)	(±0.029)	(± 0.043)	(± 0.027)	(± 0.037)	(± 0.037)	(± 0.041)	(± 0.025)	(± 0.043)	(±0.040)	(± 0.046)	(± 0.035)	(± 0.027)	(± 0.035)	(± 0.040)	(±0.011)
cardiotocography	0.771	0.778	0.724	0.781	0.741	0.764	0.686	0.776	0.686	0.798	0.827	0.834	0.587	0.689	0.650	0.753	0.643	0.685	0.784	0.829
	(± 0.016)	(± 0.015)	(± 0.019)	(± 0.015)	(± 0.018)	(± 0.016)	(± 0.021)	(± 0.015)	(± 0.021)	(± 0.013)	(± 0.010)	(± 0.009)	(± 0.032)	(±0.020)	(± 0.024)	(± 0.017)	(± 0.025)	(± 0.021)	(± 0.015)	(±0.010)
census	0.655	0.669	0.672	0.654	0.656	0.706	0.710	0.709	0.657	0.674	0.665	0.662	0.635	0.713	0.564	0.677	0.662	0.721	0.686	0.895
	(±0.023)	(±0.022)	(±0.022)	(±0.023)	(±0.023)	(±0.019)	(±0.018)	(±0.018)	(±0.023)	(±0.021)	(±0.022)	(±0.022)	(±0.025)	(±0.018)	(±0.034)	(±0.021)	(±0.022)	(±0.018)	(±0.020)	(±0,006)
churn	0.532	0.470	0.478	0.572	0.577	0.479	0.475	0.527	0.486	0.463	0.743	0.805	0.524	0.533	0.612	0.687	0.499	0.481	0.483	0.809
Cildin	(±0.040)	(±0.046)	(±0.045)	(±0.036)	(±0.033)	(±0.046)	(±0.046)	(±0.040)	(±0.044)	(±0.047)	(±0.018)	(±0.012)	(±0.041)	(±0.040)	(±0.033)	(±0.021)	(±0.043)	(±0.045)	(±0.045)	(±0.012)
cirrhosis	0.760	0.730	0.761	0.806	0.665	0.745	0.594	0.811	0.796	0.762	0.803	0.823	0.742	0.738	0.588	0.854	0.694	0.775	0.650	0.850
Cirinosis	(±0.016)	(±0.019)	(±0.016)	(±0.012)	(±0.022)	(±0.017)	(±0.032)	(±0.011)	(±0.013)	(±0.016)	(±0.012)	(±0.010)	(±0.018)	(±0.018)	(±0.032)	(±0.007)	(±0.020)	(±0.015)	(±0.024)	(±0.007)
covertype	0.884	0.883	0.864	0.892	0.932	0.886	0.694	0.942	0.884	0.898	0.875	0.916	0.785	0.867	0.700	0.932	0.861	0.931	0.860	0.961
covertype	(±0.006)	(±0.006)	(±0.007)	(±0.005)	(±0.003)	(±0.006)	(±0.020)	(±0.003)	(±0.006)	(±0.005)	(±0.007)	(±0.004)	(±0.012)	(±0.007)	(±0.019)	(±0.003)	(±0.007)	(±0.003)	(±0.007)	(±0.002)
	0.540		0.522			0.475		0.613	0.524	0.518	0.500		0.522	0.550	0.560	0.552		0.507	0.516	
credit	(±0.046)	0.508 (±0.049)	(±0.048)	0.511 (±0.049)	0.504 (±0.050)	(±0.053)	0.496 (±0.050)	(±0.033)	(±0.048)	(±0.048)	(±0.050)	0.573 (±0.036)	(±0.048)	(±0.045)	(±0.044)	(±0.045)	0.501 (±0.050)	(±0.049)	(±0.048)	0.681 (±0.021)
	0.972	0.969	0.923	0.977	0.941	0.927	0.833	0.943	0.970	0.977	0.902	0.972	0.929	0.957	0.888	0.967	0.975	0.973	0.890	0.978
equip																				
	(± 0.001)	(± 0.002)	(± 0.004)	(± 0.001)	(± 0.003)	(± 0.004)	(± 0.009)	(± 0.003)	(± 0.002)	(± 0.001)	(± 0.005)	(± 0.001)	(± 0.004)	(± 0.002)	(± 0.006)	(± 0.002)	(± 0.001)	(± 0.001)	(± 0.006)	(± 0.001)
gallstone	0.540	0.547	0.573	0.589	0.563	0.624	0.531	0.599	0.574	0.590	0.574	0.601	0.556	0.672	0.592	0.623	0.615	0.625	0.468	0.667
	(± 0.046)	(± 0.044)	(± 0.036)	(± 0.034)	(± 0.035)	(± 0.025)	(± 0.047)	(± 0.033)	(± 0.036)	(± 0.034)	(± 0.036)	(± 0.033)	(± 0.037)	(± 0.022)	(± 0.031)	(± 0.025)	(± 0.026)	(± 0.025)	(± 0.049)	(± 0.022)
glass	0.897	0.895	0.916	0.913	0.868	0.882	0.953	0.944	0.871	0.891	0.906	0.916	0.872	0.903	0.841	0.867	0.832	0.909	0.934	0.919
	(± 0.005)	(± 0.005)	(± 0.004)	(± 0.004)	(± 0.007)	(± 0.006)	(± 0.002)	(± 0.003)	(± 0.007)	(± 0.005)	(± 0.005)	(± 0.004)	(± 0.007)	(± 0.005)	(± 0.008)	(± 0.007)	(± 0.009)	(± 0.004)	(± 0.003)	(± 0.004)
glioma	0.545	0.638	0.700	0.729	0.628	0.624	0.776	0.755	0.717	0.692	0.778	0.676	0.568	0.903	0.841	0.867	0.586	0.651	0.598	0.895
	(± 0.044)	(± 0.025)	(± 0.019)	(± 0.017)	(± 0.025)	(± 0.025)	(± 0.015)	(± 0.017)	(± 0.018)	(± 0.020)	(± 0.015)	(± 0.021)	(± 0.036)	(± 0.005)	(± 0.008)	(± 0.007)	(± 0.033)	(± 0.024)	(± 0.033)	(± 0.005)
quasar	0.576	0.820	0.585	0.770	0.810	0.859	0.226	0.846	0.908	0.882	0.649	0.940	0.736	0.890	0.435	0.919	0.816	0.875	0.269	0.961
	(± 0.035)	(± 0.010)	(± 0.033)	(± 0.015)	(± 0.011)	(± 0.007)	(± 0.051)	(± 0.008)	(± 0.004)	(± 0.006)	(± 0.024)	(± 0.003)	(± 0.018)	(± 0.005)	(± 0.038)	(± 0.004)	(± 0.011)	(± 0.007)	(± 0.053)	(± 0.002)
seismic	0.602	0.603	0.640	0.654	0.630	0.745	0.557	0.653	0.642	0.651	0.621	0.653	0.626	0.625	0.571	0.689	0.646	0.625	0.642	0.741
	(± 0.033)	(± 0.033)	(± 0.025)	(± 0.023)	(± 0.026)	(± 0.017)	(± 0.037)	(± 0.023)	(± 0.025)	(± 0.024)	(± 0.026)	(± 0.023)	(± 0.026)	(± 0.026)	(± 0.036)	(± 0.020)	(± 0.024)	(± 0.026)	(± 0.025)	(± 0.018)
stroke	0.571	0.583	0.571	0.586	0.562	0.576	0.586	0.628	0.574	0.590	0.570	0.589	0.574	0.594	0.520	0.637	0.562	0.584	0.569	0.776
	(± 0.036)	(± 0.034)	(± 0.036)	(± 0.033)	(± 0.037)	(± 0.035)	(± 0.033)	(± 0.025)	(± 0.035)	(± 0.034)	(± 0.036)	(± 0.034)	(± 0.035)	(± 0.032)	(± 0.041)	(± 0.025)	(± 0.037)	(± 0.033)	(± 0.036)	(± 0.015)
vertebral	0.531	0.479	0.730	0.612	0.427	0.416	0.264	0.407	0.485	0.518	0.759	0.679	0.468	0.390	0.221	0.261	0.461	0.403	0.872	0.755
	(±0.040)	(±0.046)	(±0.017)	(±0.033)	(±0.050)	(±0.052)	(±0.069)	(±0.055)	(±0.044)	(±0.041)	(±0.016)	(±0.021)	(±0.047)	(±0.054)	(±0.077)	(±0.068)	(±0.047)	(±0.055)	(±0.007)	(±0.017)
wbc	0.949	0.948	0.942	0.957	0.868	0.912	0.953	0.944	0.950	0.950	0.951	0.953	0.849	0.885	0.770	0.919	0.861	0.950	0.943	0.968
	(± 0.002)	(± 0.003)	(± 0.003)	(± 0.002)	(± 0.007)	(±0.004)	(± 0.002)	(± 0.003)	(± 0.003)	(± 0.003)	(± 0.002)	(± 0.002)	(±0.008)	(±0.006)	(± 0.015)	(± 0.004)	(±0.007)	(± 0.003)	(± 0.003)	(±0.002)
wine	0.893	0.923	0.946	0.946	0.743	0.865	0.995	0.896	0.879	0.916	0.949	0.960	0.686	0.788	0.656	0.920	0.663	0.943	0.999	0.991
	(±0.005)	(±0.004)	(±0.003)	(±0.003)	(±0.018)	(±0.007)	(±0.000)	(±0.005)	(±0.006)	(±0.004)	(±0.003)	(±0.002)	(±0.020)	(±0.012)	(±0.023)	(±0.004)	(±0.022)	(±0.003)	(±0.000)	(±0,000)
veast	0.746	0.737	0.731	0.760	0.819	0.806	0.470	0.798	0.752	0.747	0.746	0.778	0.762	0.745	0.675	0.807	0.731	0.718	0.672	0.861
,	(±0.017)	(±0.018)	(±0.018)	(±0.016)	(±0.010)	(±0.012)	(±0.046)	(±0.013)	(±0.017)	(±0.017)	(±0.017)	(±0.015)	(±0.016)	(±0.017)	(±0.022)	(±0.012)	(±0.018)	(±0.019)	(±0.022)	(±0.007)
	(((,,	,	,	,			,,			,,	,	,,	((,	
Average	0.692	0.703	0.705	0.726	0.696	0.712	0.632	0.735	0.725	0.735	0.741	0.777	0.665	0.716	0.631	0.747	0.691	0.721	0.673	0.847

Table 12: Comparison of the LLMs' AUPRC performance across four context types (Type A–D). Each column represents a different LLM evaluated under four prompt conditions: Type A, Type B, Type C, and Type D.

Dataset		GPT-4	o-mini			GP	Γ-4.1			Claude-3	3.7-sonnet			Qwen:	3-235B			Gemini-	2.5-pro	
	Type A	Type B	Type C	Type D	Type A	Type B	Type C	Type D	Type A	Type B	Type C	Type D	Type A	Type B	Type C	Type D	Type A	Type B	Type C	Type D
automobile	0.517	0.450	0.428	0.457	0.568	0.477	0.449	0.606	0.683	0.702	0.544	0.733	0.478	0.468	0.574	0.606	0.701	0.672	0.440	0.683
	(± 0.042)	(± 0.036)	(± 0.051)	(± 0.028)	(± 0.021)	(± 0.039)	(± 0.044)	(± 0.018)	(± 0.019)	(± 0.025)	(± 0.048)	(± 0.014)	(± 0.037)	(± 0.041)	(± 0.022)	(± 0.031)	(± 0.016)	(± 0.023)	(± 0.052)	(± 0.015)
backdoor	0.098	0.125	0.149	0.096	0.114	0.103	0.186	0.083	0.154	0.178	0.175	0.144	0.138	0.241	0.248	0.186	0.123	0.116	0.051	0.161
	(± 0.031)	(± 0.038)	(± 0.024)	(± 0.042)	(± 0.033)	(± 0.041)	(± 0.019)	(± 0.046)	(± 0.027)	(± 0.021)	(± 0.034)	(± 0.039)	(± 0.035)	(± 0.018)	(± 0.016)	(± 0.028)	(± 0.040)	(± 0.044)	(± 0.049)	(± 0.023)
campaign	0.387	0.378	0.349	0.369	0.407	0.412	0.375	0.434	0.398	0.415	0.389	0.448	0.370	0.392	0.363	0.413	0.440	0.413	0.390	0.683
	(± 0.026)	(± 0.033)	(± 0.045)	(± 0.019)	(± 0.024)	(± 0.017)	(± 0.041)	(± 0.013)	(± 0.035)	(± 0.022)	(± 0.038)	(± 0.015)	(± 0.029)	(± 0.020)	(± 0.046)	(± 0.011)	(± 0.018)	(± 0.027)	(± 0.043)	(± 0.008)
cardiotocography	0.411	0.573	0.534	0.573	0.585	0.621	0.551	0.653	0.518	0.671	0.699	0.708	0.434	0.577	0.526	0.610	0.502	0.322	0.412	0.711
	(± 0.037)	(± 0.014)	(± 0.026)	(± 0.031)	(± 0.019)	(± 0.025)	(± 0.043)	(± 0.012)	(± 0.040)	(± 0.017)	(± 0.021)	(± 0.009)	(± 0.034)	(± 0.028)	(± 0.047)	(± 0.016)	(± 0.039)	(± 0.051)	(± 0.044)	(± 0.007)
census	0.114	0.083	0.078	0.080	0.180	0.176	0.177	0.179	0.211	0.210	0.244	0.187	0.233	0.269	0.120	0.204	0.228	0.194	0.169	0.188
	(± 0.044)	(± 0.047)	(± 0.049)	(± 0.046)	(± 0.018)	(± 0.020)	(± 0.016)	(± 0.022)	(± 0.013)	(± 0.015)	(± 0.009)	(± 0.024)	(± 0.011)	(± 0.006)	(± 0.041)	(± 0.017)	(± 0.012)	(± 0.019)	(± 0.025)	(± 0.021)
churn	0.436	0.410	0.408	0.463	0.479	0.479	0.412	0.411	0.420	0.411	0.406	0.629	0.699	0.428	0.438	0.533	0.541	0.415	0.412	0.703
	(± 0.023)	(± 0.035)	(± 0.036)	(± 0.017)	(± 0.020)	(± 0.020)	(± 0.038)	(± 0.039)	(± 0.031)	(± 0.037)	(± 0.040)	(± 0.011)	(± 0.008)	(± 0.033)	(± 0.024)	(± 0.014)	(± 0.013)	(± 0.036)	(± 0.038)	(± 0.007)
cirrhosis	0.629	0.697	0.667	0.707	0.649	0.730	0.610	0.813	0.792	0.783	0.741	0.845	0.737	0.753	0.639	0.848	0.750	0.749	0.662	0.846
	(± 0.032)	(± 0.016)	(± 0.021)	(± 0.015)	(± 0.029)	(± 0.012)	(± 0.036)	(± 0.009)	(± 0.010)	(± 0.011)	(± 0.018)	(± 0.006)	(± 0.014)	(± 0.013)	(± 0.033)	(± 0.005)	(± 0.013)	(± 0.013)	(± 0.024)	(± 0.006)
covertype	0.038	0.076	0.048	0.067	0.135	0.077	0.213	0.145	0.200	0.193	0.108	0.533	0.097	0.253	0.043	0.194	0.090	0.186	0.122	0.279
	(± 0.021)	(± 0.026)	(± 0.023)	(± 0.027)	(± 0.015)	(± 0.025)	(± 0.008)	(± 0.017)	(± 0.012)	(± 0.013)	(± 0.030)	(± 0.004)	(± 0.028)	(± 0.007)	(± 0.041)	(± 0.011)	(± 0.029)	(± 0.010)	(± 0.019)	(± 0.006)
credit	0.391	0.410	0.425	0.421	0.367	0.345	0.364	0.427	0.344	0.393	0.421	0.507	0.387	0.391	0.408	0.401	0.370	0.364	0.377	0.526
	(± 0.025)	(± 0.019)	(± 0.016)	(± 0.018)	(± 0.033)	(± 0.039)	(± 0.036)	(± 0.014)	(± 0.041)	(± 0.024)	(± 0.017)	(± 0.009)	(± 0.026)	(± 0.025)	(± 0.021)	(± 0.022)	(± 0.034)	(± 0.036)	(± 0.030)	(± 0.007)
equip	0.649	0.640	0.630	0.552	0.687	0.625	0.659	0.712	0.924	0.907	0.754	0.920	0.718	0.842	0.703	0.867	0.918	0.806	0.705	0.919
	(± 0.030)	(± 0.032)	(± 0.034)	(± 0.042)	(± 0.017)	(± 0.029)	(± 0.022)	(± 0.013)	(± 0.005)	(± 0.006)	(± 0.020)	(± 0.004)	(± 0.015)	(± 0.008)	(± 0.018)	(± 0.007)	(± 0.004)	(± 0.010)	(± 0.019)	(± 0.004)
gallstone	0.498	0.588	0.522	0.537	0.544	0.594	0.520	0.551	0.592	0.595	0.558	0.584	0.542	0.615	0.592	0.576	0.596	0.591	0.497	0.615
	(± 0.033)	(± 0.018)	(± 0.027)	(± 0.024)	(± 0.022)	(± 0.016)	(± 0.028)	(± 0.021)	(± 0.015)	(± 0.014)	(± 0.020)	(± 0.017)	(± 0.023)	(± 0.010)	(± 0.012)	(± 0.019)	(± 0.013)	(± 0.014)	(± 0.032)	(± 0.010)
glass	0.615	0.655	0.707	0.608	0.846	0.837	0.928	0.836	0.836	0.812	0.887	0.850	0.800	0.839	0.762	0.820	0.754	0.891	0.895	0.886
	(± 0.031)	(± 0.027)	(± 0.019)	(± 0.033)	(± 0.008)	(± 0.009)	(± 0.003)	(± 0.009)	(± 0.009)	(± 0.010)	(± 0.005)	(± 0.007)	(± 0.011)	(± 0.009)	(± 0.016)	(± 0.010)	(± 0.017)	(± 0.005)	(± 0.004)	(± 0.005)
glioma	0.576	0.569	0.480	0.594	0.605	0.605	0.758	0.773	0.624	0.556	0.509	0.846	0.548	0.613	0.557	0.725	0.594	0.640	0.577	0.865
	(± 0.020)	(± 0.021)	(± 0.036)	(± 0.018)	(± 0.017)	(± 0.017)	(± 0.012)	(± 0.011)	(± 0.015)	(± 0.022)	(± 0.030)	(± 0.007)	(± 0.025)	(± 0.016)	(± 0.022)	(± 0.013)	(± 0.018)	(± 0.015)	(± 0.021)	(± 0.006)
quasar	0.359	0.635	0.376	0.534	0.586	0.670	0.261	0.663	0.843	0.791	0.438	0.899	0.537	0.809	0.279	0.848	0.586	0.715	0.296	0.918
	(± 0.039)	(± 0.013)	(± 0.037)	(± 0.020)	(± 0.017)	(± 0.011)	(± 0.044)	(± 0.012)	(± 0.007)	(± 0.009)	(± 0.033)	(± 0.004)	(± 0.021)	(± 0.008)	(± 0.041)	(± 0.006)	(± 0.017)	(± 0.013)	(± 0.042)	(± 0.003)
seismic	0.161	0.200	0.163	0.238	0.427	0.228	0.105	0.197	0.173	0.174	0.177	0.208	0.200	0.188	0.149	0.227	0.210	0.182	0.176	0.214
	(± 0.032)	(± 0.026)	(± 0.031)	(± 0.019)	(± 0.010)	(± 0.018)	(± 0.035)	(± 0.027)	(± 0.030)	(± 0.030)	(± 0.029)	(± 0.024)	(± 0.026)	(± 0.028)	(± 0.034)	(± 0.020)	(± 0.023)	(± 0.029)	(± 0.031)	(± 0.022)
stroke	0.106	0.098	0.083	0.096	0.586	0.670	0.261	0.663	0.098	0.090	0.109	0.143	0.103	0.108	0.083	0.124	0.103	0.101	0.096	0.206
	(± 0.029)	(± 0.032)	(± 0.035)	(± 0.031)	(± 0.017)	(± 0.011)	(± 0.044)	(± 0.012)	(± 0.032)	(± 0.034)	(± 0.028)	(± 0.022)	(± 0.030)	(± 0.028)	(± 0.035)	(± 0.025)	(± 0.030)	(± 0.031)	(± 0.033)	(± 0.016)
vertebral	0.493	0.447	0.430	0.433	0.442	0.429	0.364	0.421	0.430	0.401	0.453	0.419	0.462	0.429	0.379	0.378	0.460	0.420	0.802	0.694
	(± 0.027)	(± 0.032)	(± 0.035)	(± 0.033)	(± 0.033)	(± 0.035)	(± 0.041)	(± 0.037)	(± 0.035)	(± 0.038)	(± 0.031)	(± 0.037)	(± 0.030)	(± 0.035)	(± 0.040)	(± 0.040)	(± 0.030)	(± 0.037)	(± 0.011)	(± 0.018)
wbc	0.779	0.814	0.551	0.834	0.860	0.906	0.958	0.944	0.920	0.932	0.953	0.965	0.858	0.862	0.746	0.894	0.837	0.940	0.925	0.963
	(± 0.012)	(± 0.009)	(± 0.028)	(± 0.008)	(± 0.006)	(± 0.004)	(± 0.002)	(± 0.003)	(± 0.004)	(± 0.003)	(± 0.002)	(± 0.001)	(± 0.007)	(± 0.006)	(± 0.015)	(± 0.005)	(± 0.008)	(± 0.003)	(± 0.003)	(± 0.001)
wine	0.450	0.564	0.399	0.520	0.678	0.794	0.993	0.828	0.709	0.880	0.994	0.995	0.612	0.719	0.576	0.858	0.611	0.887	0.999	0.985
	(± 0.036)	(± 0.021)	(± 0.043)	(± 0.028)	(± 0.016)	(± 0.010)	(± 0.001)	(± 0.009)	(± 0.014)	(± 0.006)	(± 0.001)	(± 0.001)	(± 0.025)	(± 0.014)	(± 0.022)	(± 0.007)	(± 0.025)	(± 0.005)	(± 0.000)	(± 0.001)
yeast	0.294	0.269	0.170	0.301	0.403	0.356	0.114	0.334	0.404	0.343	0.248	0.414	0.296	0.269	0.262	0.390	0.286	0.276	0.190	0.449
	(± 0.035)	(± 0.038)	(± 0.047)	(± 0.033)	(± 0.023)	(± 0.027)	(± 0.041)	(± 0.031)	(± 0.023)	(± 0.030)	(± 0.043)	(± 0.022)	(± 0.035)	(± 0.038)	(± 0.039)	(± 0.026)	(± 0.037)	(± 0.036)	(± 0.046)	(± 0.019)
Average	0.400	0.434	0.380	0.424	0.507	0.507	0.463	0.534	0.514	0.522	0.490	0.599	0.462	0.503	0.422	0.535	0.485	0.494	0.460	0.625

F FULL BASELINE RESULTS

Table 13: AUROC Performance across all baselines.

Dataset	OCSVM	LOF	KNN	IForest	PCA	DeepSVDD	REPEN	RDP	RCA	GOAD	NeuTraL	SLAD	DIF	MCM	DRL	AnoLLM
automobile	0.645	0.688	0.656	0.648	0.497	0.845	0.611	0.774	0.679	0.676	0.810	0.780	0.647	0.801	0.762	0.624
	(±0.025)	(±0.029)	(±0.015)	(± 0.034)	(±0.028)	(±0.030)	(± 0.059)	(± 0.017)	(± 0.025)	(± 0.065)	(±0.012)	(± 0.030)	(± 0.023)	(± 0.013)	(±0.066)	(±0.021)
backdoor	0.876	0.702	0.934	0.888	0.822	0.800	0.856	0.897	0.915	0.889	0.948	0.935	0.973	0.961	0.902	0.885
	(±0.004)	(±0.008)	(±0.004)	(±0.004)	(±0.003)	(±0.116)	(±0.013)	(±0.001)	(±0.003)	(±0.007)	(±0.001)	(±0.001)	(±0.002)	(±0.003)	(±0.017)	(±0.010)
campaign	0.700	0.669	0.754	0.732	0.750	0.721	0.697	0.693	0.722	0.740	0.760	0.717	0.677	0.761	0.737	0.738
	(± 0.004)	(±0.005)	(± 0.007)	(±0.006)	(±0.003)	(±0.014)	(± 0.010)	(± 0.010)	(± 0.010)	(± 0.002)	(±0.008)	(± 0.002)	(± 0.004)	(± 0.005)	(± 0.018)	(±0.012
cardiotocography	0.868	0.826	0.780	0.830	0.840	0.813	0.759	0.766	0.858	0.788	0.791	0.764	0.740	0.843	0.847	0.735
	(±0.006)	(±0.010)	(± 0.011)	(±0.006)	(±0.005)	(±0.015)	(± 0.035)	(± 0.008)	(± 0.005)	(±0.012)	(±0.016)	(± 0.018)	(±0.007)	(± 0.012)	(±0.019)	(±0.014)
census	0.647	0.596	0.738	0.620	0.627	0.712	0.811	0.717	0.745	0.708	0.686	0.687	0.726	0.729	0.728	0.737
	(±0.001)	(± 0.002)	(±0.001)	(± 0.009)	(±0.002)	(±0.048)	(±0.007)	(±0.002)	(± 0.002)	(±0.002)	(±0.002)	(±0.002)	(± 0.005)	(±0.007)	(±0.036)	(±0.009)
churn	0.651	0.465	0.532	0.506	0.579	0.573	0.546	0.523	0.616	0.683	0.651	0.571	0.494	0.580	0.553	0.557
	(±0.007)	(±0.007)	(± 0.003)	(± 0.010)	(±0.023)	(±0.071)	(±0.058)	(± 0.004)	(± 0.030)	(±0.006)	(± 0.004)	(±0.014)	(± 0.005)	(± 0.024)	(±0.012)	(±0.018)
cirrhosis	0.823	0.843	0.843	0.849	0.822	0.807	0.876	0.795	0.834	0.816	0.831	0.810	0.820	0.830	0.814	0.850
	(±0.012)	(± 0.013)	(±0.012)	(± 0.013)	(±0.017)	(±0.018)	(±0.010)	(±0.023)	(±0.012)	(±0.022)	(±0.022)	(±0.018)	(±0.011)	(±0.020)	(±0.012)	(±0.015)
covertype	0.998	0.980	0.991	0.968	0.976	0.971	0.986	0.992	0.998	0.998	0.998	0.999	0.998	0.998	0.995	0.990
	(±0.000)	(± 0.003)	(± 0.000)	(± 0.003)	(±0.001)	(±0.007)	(±0.006)	(±0.001)	(± 0.000)	(±0.002)	(±0.003					
credit	0.717	0.590	0.692	0.639	0.684	0.638	0.661	0.593	0.702	0.682	0.690	0.691	0.689	0.671	0.680	0.495
	(±0.003)	(± 0.007)	(±0.007)	(± 0.003)	(± 0.003)	(±0.039)	(±0.012)	(±0.009)	(±0.002)	(±0.005)	(±0.016)	(± 0.002)	(±0.002)	(± 0.004)	(±0.020)	(±0.019
equip	0.987	0.987	0.987	0.980	0.986	0.984	0.986	0.973	0.986	0.983	0.985	0.981	0.987	0.986	0.984	0.986
	(±0.000)	(± 0.000)	(± 0.000)	(± 0.000)	(± 0.000)	(±0.000)	(± 0.000)	(±0.001)	(± 0.000)	(±0.001)	(± 0.000)	(± 0.001)	(± 0.000)	(±0.001)	(±0.001)	(±0.002
gallstone	0.671	0.704	0.702	0.650	0.637	0.731	0.621	0.725	0.720	0.734	0.780	0.758	0.649	0.757	0.745	0.574
	(±0.047)	(± 0.032)	(±0.040)	(±0.021)	(±0.026)	(±0.020)	(±0.049)	(±0.029)	(± 0.033)	(±0.034)	(±0.019)	(±0.028)	(±0.026)	(± 0.034)	(±0.029)	(±0.028
glass	0.959	0.974	0.953	0.944	0.938	0.963	0.936	0.965	0.959	0.967	0.968	0.952	0.936	0.966	0.949	0.907
	(±0.010)	(± 0.010)	(± 0.014)	(±0.016)	(±0.011)	(±0.012)	(±0.018)	(±0.011)	(± 0.014)	(±0.011)	(±0.010)	(±0.011)	(±0.012)	(±0.012)	(±0.013)	(±0.016)
glioma	0.725	0.711	0.787	0.722	0.715	0.766	0.727	0.739	0.787	0.772	0.784	0.886	0.686	0.790	0.764	0.708
	(±0.012)	(±0.016)	(±0.006)	(±0.013)	(±0.012)	(±0.012)	(±0.039)	(±0.015)	(± 0.008)	(±0.009)	(±0.013)	(±0.005)	(±0.012)	(±0.009)	(±0.040)	(±0.022)
quasar	0.930	0.966	0.969	0.915	0.894	0.804	0.931	0.953	0.950	0.901	0.954	0.952	0.793	0.950	0.897	0.961
	(±0.008)	(±0.009)	(±0.004)	(±0.007)	(± 0.013)	(±0.135)	(± 0.014)	(± 0.004)	(±0.012)	(±0.014)	(±0.006)	(±0.009)	(±0.042)	(±0.007)	(±0.024)	(±0.014)
seismic	0.710	0.615	0.741	0.710	0.671	0.729	0.739	0.719	0.729	0.717	0.716	0.727	0.736	0.716	0.714	0.741
	(±0.002)	(±0.007)	(±0.005)	(±0.006)	(± 0.003)	(±0.015)	(±0.005)	(±0.006)	(±0.005)	(±0.003)	(±0.007)	(±0.006)	(±0.005)	(±0.019)	(±0.016)	(±0.011
stroke	0.716	0.625	0.732	0.679	0.678	0.722	0.745	0.674	0.764	0.709	0.703	0.678	0.705	0.753	0.727	0.687
	(±0.004)	(±0.022)	(±0.005)	(± 0.003)	(± 0.004)	(±0.005)	(±0.017)	(±0.009)	(±0.011)	(±0.002)	(±0.005)	(±0.007)	(±0.007)	(±0.005)	(±0.025)	(±0.010
vertebral	0.638	0.540	0.469	0.500	0.524	0.581	0.340	0.551	0.566	0.687	0.697	0.679	0.340	0.615	0.477	0.597
	(±0.043)	(±0.021)	(±0.038)	(±0.019)	(±0.013)	(±0.062)	(±0.100)	(±0.018)	(±0.020)	(±0.037)	(±0.040)	(±0.020)	(±0.008)	(±0.128)	(±0.042)	(±0.014
wbc	0.969	0.960	0.961	0.961	0.960	0.969	0.879	0.924	0.964	0.947	0.785	0.938	0.679	0.957	0.954	0.871
	(±0.006)	(±0.006)	(±0.006)	(±0.004)	(±0.006)	(±0.005)	(±0.026)	(±0.010)	(±0.007)	(±0.009)	(±0.024)	(±0.023)	(±0.016)	(±0.006)	(±0.010)	(±0.031
wine	0.957	0.974	0.976	0.987	0.980	0.974	0.657	0.939	0.973	0.973	0.988	0.980	0.760	0.979	0.958	0.933
	(±0.012)	(±0.014)	(±0.012)	(±0.006)	(±0.007)	(±0.011)	(±0.053)	(±0.032)	(±0.011)	(±0.009)	(±0.002)	(±0.010)	(±0.033)	(±0.012)	(±0.012)	(±0.020
yeast	0.875	0.803	0.831	0.838	0.861	0.820	0.826	0.786	0.866	0.836	0.841	0.846	0.815	0.856	0.841	0.809
,	(±0.008)	(±0.010)	(±0.007)	(±0.014)	(±0.009)	(±0.015)	(±0.049)	(±0,004)	(±0.008)	(±0.007)	(±0,009)	(±0.019)	(±0.004)	(±0.014)	(±0.033)	(±0.018)

Table 14: AUPRC Performance across all baselines.

Dataset	OCSVM	LOF	KNN	IForest	PCA	DeepSVDD	REPEN	RDP	RCA	GOAD	NeuTraL	SLAD	DIF	MCM	DRL	AnoLLM
automobile	0.578	0.618	0.534	0.543	0.419	0.762	0.496	0.637	0.566	0.620	0.718	0.665	0.544	0.675	0.661	0.553
backdoor	(±0.039) 0.043	(±0.031) 0.052	(±0.017) 0.092	(±0.039) 0.032	(±0.040) 0.019	(±0.065) 0.131	(±0.043) 0.168	(±0.049) 0.276	(±0.035) 0.054	(±0.094) 0.245	(±0.021) 0.908	(±0.060) 0.867	(±0.029) 0.494	(±0.038) 0.188	(±0.069) 0.132	(±0.025) 0.319
	(±0.002)	(±0.006)	(±0.005)	(±0.001)	(±0.000)	(±0.039)	(±0.011)	(±0.007)	(±0.003)	(±0.027)	(±0.000)	(±0.003)	(±0.044)	(±0.029)	(±0.033)	(±0.012)
	0.539	0.524	0.572	0.559	0.580	0.561	0.523	0.517	0.560	0.563	0.593	0.563	0.507	0.588	0.561	0.573
campaign	(±0.007)	(±0.004)	(±0.009)	(±0.010)	(±0.005)	(±0.013)	(±0.013)	(±0.011)	(±0.012)	(±0.006)	(±0.015)	(±0.006)	(±0.007)	(±0.007)	(±0.018)	(±0.011)
cardiotocography	0.788	0.735	0.707	0.730	0.750	0.767	0.691	0.697	0.774	0.733	0.738	0.712	0.678	0.757	0.767	0.630
	(±0.012)	(±0.013)	(±0.016)	(±0.008)	(±0.008)	(±0.025)	(±0.022)	(±0.011)	(±0.016)	(±0.016)	(±0.016)	(±0.017)	(±0.009)	(±0.021)	(±0.025)	(±0.018)
census	0.354	0.168	0.335	0.136	0.153	0.346	0.411	0.304	0.395	0.352	0.281	0.308	0.371	0.315	0.348	0.222
census	(±0.005)	(±0.003)	(±0.003)	(±0.002)	(±0.001)	(±0.060)	(±0.015)	(±0.003)	(±0.004)	(±0.006)	(±0.003)	(±0.005)	(±0.005)	(±0.012)	(±0.022)	(±0.010)
churn	0.520	0.395	0.420	0.407	0.486	0.477	0.464	0.430	0.505	0.563	0.527	0.471	0.406	0.463	0.463	0.429
CHUIII	(±0.010)	(±0.007)	(±0.003)	(±0.005)	(±0.014)	(±0.071)	(±0.048)	(±0.002)	(±0.034)	(±0.005)	(±0.003)	(±0.010)	(±0.005)	(±0.025)	(±0.005)	(±0.016)
cirrhosis	0.836	0.850	0.850	0.866	0.834	0.819	0.883	0.792	0.845	0.818	0.836	0.826	0.835	0.841	0.822	0.824
CITHOSIS	(±0.014)	(±0.014)	(±0.013)	(±0.012)	(±0.016)	(±0.018)	(±0.014)	(±0.020)	(±0.013)	(±0.024)	(±0.028)	(±0.018)	(±0.013)	(±0.016)	(±0.016)	(±0.017)
	0.871	0.802	0.874	0.320	0.304	0.825	0.468	0.743	0.915	0.890	0.940	0.914	0.923	0.880	0.781	0.654
covertype	(±0.011)	(±0.011)	(±0.004)	(±0.023)	(±0.010)	(±0.031)	(±0.114)	(±0.016)	(±0.012)	(±0.026)	(±0.003)	(±0.009)	(±0.015)	(±0.027)	(±0.062)	(±0.020)
credit	0.610	0.412	0.556	0.483	0.547	0.540	0.559	0.410	0.600	0.575	0.576	0.583	0.566	0.545	0.525	0.352
	(±0.005)	(±0.006)	(±0.014)	(±0.003)	(±0.005)	(±0.033)	(±0.012)	(±0.008)	(±0.004)	(±0.008)	(±0.027)	(±0,003)	(±0.003)	(±0.006)	(±0.037)	(±0.018)
equip	0.972	0.971	0.972	0.950	0.970	0.965	0.969	0.941	0.971	0.969	0.967	0.954	0.970	0.970	0.966	0.972
equip	(±0.000)	(±0.001)	(±0.000)	(±0.001)	(±0.001)	(±0.001)	(±0.001)	(±0.002)	(±0.001)	(±0.000)	(±0.001)	(±0.003)	(±0.000)	(±0.001)	(±0.004)	(±0.002)
gallstone	0.667	0.702	0.691	0.637	0.630	0.724	0.642	0.727	0.710	0.721	0.775	0.746	0.649	0.744	0.733	0.580
ganstone	(±0.052)	(±0.036)	(±0.046)	(±0.008)	(±0.036)	(±0.031)	(±0.035)	(±0.023)	(±0.037)	(±0.038)	(±0.009)	(±0.032)	(±0.036)	(±0.035)	(±0.022)	(±0.027)
glass	0.920	0.942	0.894	0.869	0.878	0.918	0.850	0.919	0.907	0.923	0.928	0.900	0.881	0.917	0.896	0.808
grass	(±0.027)	(±0.021)	(±0.038)	(±0.049)	(±0.035)	(±0.041)	(±0.043)	(±0.035)	(±0.043)	(±0.036)	(±0.035)	(±0.029)	(±0.029)	(±0.042)	(±0.038)	(±0.024)
glioma	0.761	0.673	0.785	0.706	0.703	0.753	0.712	0.718	0.801	0.781	0.741	0.863	0.684	0.802	0.702	0.688
gnoma	(±0.013)	(±0.025)	(±0.007)	(±0.014)	(±0.016)	(±0.023)	(±0.038)	(±0.016)	(±0.009)	(±0.010)	(±0.024)	(±0,006)	(±0.011)	(±0.008)	(±0.034)	(±0.022)
quasar	0.918	0.949	0.952	0.758	0.863	0.707	0.891	0.932	0.937	0.860	0.932	0.926	0.776	0.927	0.850	0.936
quana	(±0.006)	(±0.009)	(±0.002)	(±0.022)	(±0.025)	(±0.191)	(±0.016)	(±0.002)	(±0.010)	(±0.036)	(±0.003)	(±0,005)	(±0.020)	(±0.006)	(±0.040)	(±0.013)
seismic	0.248	0.168	0.257	0.247	0.204	0.256	0.261	0.231	0.253	0.246	0.236	0.239	0.253	0.249	0.246	0.283
scisinic	(±0.004)	(±0.005)	(±0,006)	(±0.010)	(±0.004)	(±0.005)	(±0.006)	(±0.009)	(±0.006)	(±0.005)	(±0.012)	(±0.007)	(±0,006)	(±0.016)	(±0.009)	(±0.009)
stroke	0.228	0.116	0.227	0.214	0.179	0.178	0.244	0.153	0.247	0.202	0.171	0.185	0.217	0.242	0.206	0.163
SHOKE	(±0.011)	(±0.004)	(±0.008)	(±0.009)	(±0.006)	(±0.007)	(±0.013)	(±0.007)	(±0.012)	(±0.007)	(±0.007)	(±0.010)	(±0.013)	(±0.010)	(±0.004)	(±0.010)
vertebral	0.545	0.513	0.446	0.463	0.485	0.584	0.421	0.518	0.504	0.597	0.636	0.605	0.385	0.582	0.461	0.551
renconn	(±0.032)	(±0.021)	(±0.021)	(±0.013)	(±0.010)	(±0.049)	(±0.121)	(±0.013)	(±0.012)	(±0.030)	(±0.044)	(±0.028)	(±0.002)	(±0.117)	(±0.037)	(±0.028)
wbc	0.970	0.962	0.962	0.956	0.959	0.974	0.856	0.922	0.962	0.955	0.761	0.936	0.781	0.955	0.950	0.827
	(±0.007)	(±0.007)	(±0,008)	(±0.009)	(±0.010)	(±0.005)	(±0.031)	(±0.013)	(±0.011)	(±0.007)	(±0.028)	(±0.019)	(±0.014)	(±0.010)	(±0.025)	(±0.019)
wine	0.933	0.957	0.960	0.980	0.967	0.959	0.505	0.889	0.954	0.952	0.981	0.967	0.714	0.969	0.926	0.874
WIIIC	(±0.022)	(±0.027)	(±0.021)	(±0.010)	(±0.015)	(±0.021)	(±0.039)	(±0.051)	(±0.022)	(±0.033)	(±0.008)	(±0.019)	(±0.062)	(±0.019)	(±0.021)	(±0.023)
yeast	0.427	0.311	0.369	0.435	0.384	0.359	0.370	0.299	0.420	0.390	0.351	0.384	0.361	0.455	0.381	0.369
yeasi	(±0.027)	(±0.018)	(±0.004)	(±0.055)	(±0.022)	(±0.030)	(±0.102)	(±0.019)	(±0.029)	(±0.013)	(±0.018)	(±0.045)	(±0,008)	(±0.051)	(±0.061)	(±0.040)
	(±0.027)	(±0.018)	(±0.004)	(±0.055)	(±0.022)	(±0.030)	(±0.102)	(±0.019)	(±0.029)	(±0.013)	(±0.018)	(±0:043)	(±0.008)	(±0.051)	(±0.001)	(±0.040)

G PERFORMANCE DETAILS OF KEY FEATURE ESTIMATION

To support the results in Table 6, this section details the procedure used to measure the key feature alignment metric. Building on the insight from TabLLM (Hegselmann et al., 2023), which emphasized the importance of feature attribution analysis for interpreting model reasoning, we adopt a similar perspective for evaluating LLM explanations. Concretely, we assess whether the key features predicted by an LLM align with attribution scores derived from a supervised reference model. To this end, we train an XGBoost classifier using ground-truth labels and compute SHAP (Lundberg & Lee, 2017) values for each test instance. For a given anomalous instance x_i , the top-K features ranked by absolute SHAP values define the reference set:

$$R_i^{(K)} = \text{TopK}(|\phi(x_i)|),$$

where $\phi(x_i)$ denotes the SHAP value vector for instance x_i . In parallel, the LLM outputs a set of key features for x_i , which we denote as \hat{F}_i . We then measure alignment between the two sets using the F1 score at K:

$$F1@K(x_i) = \frac{2 \cdot |R_i^{(K)} \cap \hat{F}_i|}{|R_i^{(K)}| + |\hat{F}_i|}.$$

The final metric is averaged over all anomalous instances:

$$F1@K = \frac{1}{|\mathcal{A}|} \sum_{x_i \in \mathcal{A}} F1@K(x_i),$$

where \$\mathcal{A}\$ denotes the set of anomalous samples. Overall, providing textual metadata (Type D) leads to clear improvements in F1 alignment compared to the no-description setting (Type A) (see Table 15). Strong improvements are observed in datasets such as glioma, wine, equip, and glass, where domain-specific semantics play a critical role and textual descriptions allow the LLM to better capture SHAP-derived ground truth. Moderate improvements appear in datasets including campaign, churn, gallstone, wbc, and vertebral, with consistent but smaller gains. In contrast, limited or negative effects are found in datasets like backdoor, covertype, quasar, and stroke. In some cases, such as quasar, baseline alignment is already high, so additional metadata may introduce noise rather than provide further benefit. In others, such as covertype, the complex multi-class structure can confuse the LLM's reasoning and reduce the effectiveness of textual cues. It is also worth noting that for the automobile dataset, the number of anomalous samples is too small to yield statistically reliable estimates, and thus alignment results should be interpreted with caution. In summary, textual metadata provides strong semantic cues that improve reasoning alignment across datasets, with particularly notable benefits in domain-specific settings (e.g., healthcare, equipment).

Table 15: Impact of Textual Metadata on Reasoning Alignment across 20 Datasets. We report F1-Score@K (K = 1, 3) on anomalous instances for Type A (No Desc.) and Type D (Full Desc.).

Dataset	F1	@1	F1@3			
	Type A	Type D	Type A	Type D		
automobile	0.000	0.000	0.000	0.042		
backdoor	0.452	0.356	0.397	0.413		
campaign	0.129	0.344	0.224	0.466		
cardiotocography	0.092	0.083	0.210	0.199		
census	0.177	0.196	0.165	0.257		
churn	0.133	0.288	0.160	0.400		
cirrhosis	0.127	0.281	0.155	0.212		
covertype	0.488	0.322	0.542	0.350		
credit	0.111	0.140	0.253	0.349		
equip	0.367	0.621	0.358	0.619		
gallstone	0.071	0.228	0.050	0.174		
glass	0.000	0.361	0.000	0.361		
glioma	0.009	0.551	0.044	0.589		
quasar	0.762	0.497	0.825	0.514		
seismic	0.236	0.301	0.224	0.332		
stroke	0.479	0.394	0.493	0.482		
vertebral	0.233	0.350	0.425	0.422		
wbc	0.110	0.259	0.170	0.340		
wine	0.367	0.773	0.367	0.773		
yeast	0.600	0.624	0.631	0.707		

H EXPERIMENTAL DETAILS FOR REASONING TEXT ANALYSIS

To assess the impact of reasoning quality on AD performance, we conduct a controlled experiment using test-time prompting. For each dataset, we split the test set in half: one half is used to extract reasoning texts from detected anomalies (based on high anomaly scores), and the other half is used to evaluate the effect of injecting these reasoning examples. Specifically, we vary the number of reasoning examples $\{1, 3, 5, 10\}$ included in the prompt in descending order of anomaly score.

As a metric, we compute the AUROC difference between the baseline (zero-shot prompt without examples) and the model performance after injecting reasoning examples. We further compare the impact of different reasoning types (e.g., Type A vs. Type D) and anomaly score levels (e.g., top-scoring vs. uncertain cases). We observe that high-quality reasoning (Type D) leads to more consistent and larger performance gains, particularly in semantically rich domains like cirrhosis.

ETHICS STATEMENT

This work utilizes several publicly available healthcare datasets (e.g., CTG, cirrhosis, glioma) that contain sensitive clinical information. We emphasize that all experiments are conducted strictly for research purposes and do not involve direct patient interaction. While our benchmark and methods are designed to advance anomaly detection research, false alarms in healthcare applications may lead to unnecessary interventions, patient anxiety, or resource misallocation. Therefore, the models and results reported here should not be interpreted as ready for clinical deployment. Any practical adoption in healthcare settings must be accompanied by rigorous validation, ethical review, and close collaboration with medical professionals.