GMM for Anomaly Detection
Group 22

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Abstract—This work extends DAGMM, an unsupervised anomaly detection framework, by replacing the Gaussian mixture model with Laplace and Student's t-distributions. Experimental results demonstrate that Laplace improves detection performance on the KDDCUP99 dataset, while Student-t offers modest gains on smaller, noisier datasets such as Arrhythmia and Thyroid. Although Gaussian mixtures remain effective when anomalies are well-separated, heavy-tailed distributions provide a simple and interpretable improvement in more complex or variable settings.

Index Terms—Anomaly Detection, Deep Autoencoding Gaussian Mixture Model (DAGMM), Laplace Distribution, Student's t-Distribution, Unsupervised Learning, KDDCUP99.

I. INTRODUCTION

Anomaly detection plays a critical role across domains such as cybersecurity, healthcare, fraud detection, and fault monitoring, where identifying rare or unexpected events is essential. However, traditional approaches often struggle when applied to high-dimensional data, where sparse clustering, ambiguous distance measures, and the curse of dimensionality make modeling normal behavior increasingly difficult.

Deep Autoencoding Gaussian Mixture Model (DAGMM) addresses these challenges by jointly learning a compressed latent representation of the data through a deep autoencoder and modeling this compressed space using a Gaussian Mixture Model (GMM). This integrated framework enables the system to align feature learning directly with anomaly scoring, improving robustness and detection accuracy compared to methods that treat compression and density estimation separately.

While the original DAGMM assumes that normal data distributions can be well-modeled using Gaussian mixtures, this assumption may not always hold particularly when normal data exhibits heavy tails, outliers, or complex variability. Motivated by this, we investigate extending DAGMM by replacing the Gaussian mixture with Laplace and Student's t-distributions, aiming to better capture irregular patterns in complex datasets while retaining the simplicity and interpretability of the original model.

II. RELATED WORK

Traditional anomaly detection methods, such as Principal Component Analysis (PCA), One-Class SVM, and Isolation Forest, often struggle when applied to high-dimensional or complex datasets. These techniques typically rely on assumptions about proximity or simple density structures, which break down in sparse, high-dimensional feature spaces where distance measures lose their meaning.

Reconstruction-based models, particularly autoencoders, aim to detect anomalies by assuming that anomalous samples will reconstruct poorly. However, this assumption is not always reliable, as deep models may inadvertently generalize well even on outliers, leading to low reconstruction errors for anomalous data.

Density estimation methods such as Gaussian Mixture Models (GMMs) offer another approach but similarly face challenges in high dimensions due to the "concentration of distances" problem.

DAGMM addresses these issues by jointly learning latent feature representations and modeling their density in a unified framework, aligning compression with anomaly scoring. By combining feature learning and probabilistic estimation end-to-end, DAGMM improves anomaly detection performance across diverse datasets. Building on this foundation, our work investigates whether moving beyond the Gaussian assumption—using heavier-tailed distributions like Laplace and Student's t—can further enhance detection robustness in more complex settings.

III. PROPOSED METHOD

We build upon the original Deep Autoencoding Gaussian Mixture Model (DAGMM) framework for unsupervised anomaly detection. DAGMM consists of two key components: a deep autoencoder that compresses high-dimensional inputs into a low-dimensional latent space, and an estimation network that models this latent space using a Gaussian Mixture Model (GMM).

During training, DAGMM jointly optimizes the autoencoder and the GMM-based density estimator end-to-end. The final anomaly score for a sample is based on its energy value, computed as the negative log-likelihood under the estimated mixture distribution. This tight integration between compression and probabilistic modeling improves robustness compared to methods that separate these steps.

In this work, we extend DAGMM by replacing the Gaussian mixture model with alternative heavy-tailed distributions: Laplace and Student's t-distributions. Laplace mixtures use L1 distance and are more tolerant of moderate deviations, while Student's t-distributions introduce an explicit degree-of-freedom parameter, allowing even greater tail flexibility.

Our extensions modify only the energy computation step. The autoencoder architecture, estimation network, and overall training procedure remain unchanged. By isolating the impact of the distributional assumption, we aim to assess whether heavier-tailed models provide measurable benefits in capturing complex or irregular data patterns without compromising DAGMM's interpretability and simplicity.

IV. DATASETS

We evaluate the models on four publicly available benchmark datasets commonly used for anomaly detection: KD-DCUP99, KDDCUP-Rev, Thyroid, and Arrhythmia. Each dataset presents different challenges in terms of dimensionality, anomaly ratio, and data complexity.

KDDCUP99 (10% subset): A large-scale network intrusion detection dataset containing mostly attack traffic. It has 494,021 samples across 118 features, with approximately 80% of the samples being anomalous (attacks).

KDDCUP-Rev: A resampled version of KDDCUP99 designed to reflect a more realistic anomaly rate of approximately 20%. It contains 121,597 samples across the same 118 features.

Thyroid: A low-dimensional medical dataset with six features and 3,772 samples, where anomalies correspond to cases of hyperfunctioning thyroid. Anomalies make up about 2.5% of the data.

Arrhythmia: A small but high-dimensional dataset with 452 samples and 279 features, representing various arrhythmia types. About 15% of the samples are labeled as anomalies.

Due to the unavailability of the exact versions used in the original DAGMM paper, substitute versions of the Arrhythmia and Thyroid datasets were used, which contained fewer samples and increased the challenge for model training and evaluation.

A summary of dataset characteristics is provided in Table I.

TABLE I
OVERVIEW OF DATASETS USED FOR EVALUATION.

Dataset	# Samples	# Features	Anomaly %
KDDCUP99 (10%)	494,021	118	80%
KDDCUP-Rev	121,597	118	20%
Thyroid	3,772	6	2.5%
Arrhythmia	452	279	15%

V. EXPERIMENTAL SETUP

All models were implemented in Python using the PyTorch framework and trained on standard computing environments without specialized hardware acceleration.

The autoencoder architecture followed the original DAGMM design, with progressively reducing layer sizes leading to a 3-dimensional latent space. Reconstruction errors were captured through relative Euclidean distance and cosine similarity, appended to the latent representations and fed into the estimation network. The estimation network modeled these features using either a Gaussian, Laplace, or Student's t-mixture distribution.

Training was conducted using the Adam optimizer with a learning rate of 1×10^{-3} and a batch size of 1024. Models were trained for 50–100 epochs depending on the dataset size and convergence behavior. All models were trained in an unsupervised manner using only normal samples; anomaly labels were used solely for evaluation.

Following the DAGMM paper, energy thresholds were selected to match the known anomaly ratios for each dataset. For Student's t models, a fixed degrees-of-freedom parameter $\nu = 4$ was used across all experiments, providing moderately heavy tails without overfitting. Laplace models required no additional hyperparameters. Results were averaged across multiple runs to ensure robustness against random initialization effects.

A. Implementation Details

The full source code, including preprocessing, model training, and evaluation scripts, is available at this GitHub repository for reproducibility. Preprocessing involved one-hot encoding of categorical features and normalization based on statistics computed from the normal class. Thresholding for anomaly detection was based on the 80th percentile of energy scores computed from the training set.

VI. RESULTS

We evaluate the performance of Gaussian, Laplace, and Student's t-based DAGMM models across four datasets: KD-DCUP99, KDDCUP-Rev, Arrhythmia, and Thyroid. Performance is assessed using precision, recall, F1-score, and accuracy, with thresholds selected to match the known anomaly ratios.

Table II summarizes the precision, recall, and F1-scores achieved by each model across the datasets.

TABLE II
PERFORMANCE METRICS FOR EACH MODEL ACROSS DATASETS.

Dataset	Model	Precision	Recall	F1-Score	Accuracy
KDDCUP99	Gaussian	0.8950	0.8245	0.8583	0.9104
	Laplace	0.9364	0.8939	0.9146	0.9451
	Student's t	0.9384	0.8982	0.9179	0.9471
KDDCUP-Rev	Gaussian	0.5153	0.2934	0.3739	0.6725
	Laplace	0.3212	0.1921	0.2404	0.5954
	Student's t	0.4379	0.2816	0.3428	0.6401
Thyroid	Gaussian	0.1846	0.8495	0.3033	0.8122
	Laplace	0.0681	0.2796	0.1095	0.7812
	Student's t	0.1752	0.8065	0.2879	0.8081
Arrhythmia	Gaussian	0.5156	0.5000	0.5077	0.7529
	Laplace	0.4442	0.2838	0.3463	0.6429
	Student's t	0.5000	0.4848	0.4923	0.7452

In addition to the tabular results, Figures 1, 2, and 3 provide a visual comparison of precision, recall, and F1-score across the datasets for all three models.
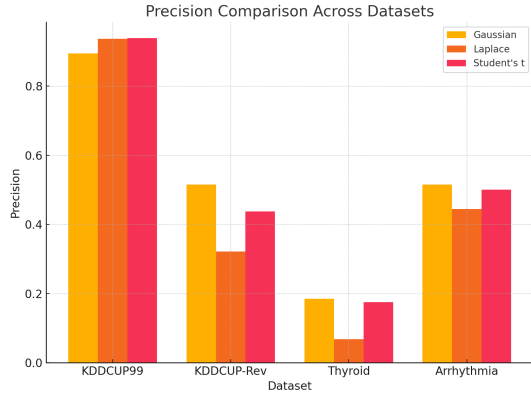
Fig. 1. Precision comparison across datasets for Gaussian, Laplace, and Student's t models.

Fig. 2. Recall comparison across datasets for Gaussian, Laplace, and Student's t models.
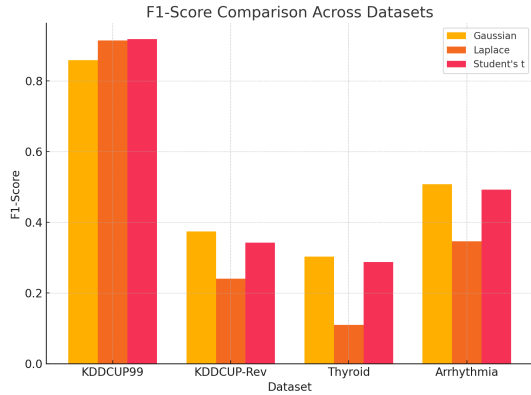

Fig. 3. F1-score comparison across datasets for Gaussian, Laplace, and Student's t models.

As shown in Table II and Figures 1–3, the Laplace-based DAGMM achieved the highest precision and F1-score on KDDCUP99, outperforming both the original Gaussian and Student's t models. On KDDCUP-Rev, the Student's t model performed comparably to Gaussian, while Laplace underperformed significantly. On the Thyroid and Arrhythmia datasets, all models struggled due to limited sample sizes and variability; however, Student's t consistently achieved marginal improvements over Gaussian by reducing false positives without hurting recall.

These results highlight that while Gaussian mixtures remain a strong baseline when anomalies are well-separated, heavier-tailed mixtures can offer practical benefits in more complex or imbalanced settings.

VII. ANALYSIS AND INSIGHTS

The results show that DAGMM's autoencoder effectively compresses normal data into a compact latent space, making Gaussian mixture modeling highly competitive when anomalies are clearly separated. In such cases, such as KDDCUP99, the Gaussian-based model already achieves strong precision and recall without requiring heavier-tailed modifications.

Laplace-based DAGMM demonstrated advantages in capturing moderate deviations and outliers, particularly on the high-dimensional KDDCUP99 dataset. Its heavier tails allowed for better separation of attack samples from normal traffic, leading to improved F1-scores. However, Laplace mixtures struggled on smaller datasets like Thyroid and Arrhythmia, where the limited number of samples and higher noise levels likely led to poorer density estimation and higher false positive rates.

Student's t-based DAGMM consistently achieved slightly better F1-scores compared to Gaussian across the more challenging datasets, notably Thyroid and Arrhythmia. Its flexible tails helped reduce false positives without significantly sacrificing recall, striking a better balance between sensitivity and specificity in noisier, more irregular settings.

Overall, while heavy-tailed models occasionally offered measurable improvements, the Gaussian assumption remained reliable when anomalies were distinct and well-separated. The improvements with Student's t were modest but consistent, suggesting that moving beyond Gaussian mixtures is beneficial primarily for complex or highly variable datasets.

VIII. CONCLUSION

This work explored extending DAGMM for unsupervised anomaly detection by replacing its Gaussian mixture assumption with heavier-tailed alternatives: Laplace and Student's t-distributions.

Experiments across four benchmark datasets showed that Gaussian DAGMM already performs reliably when anomalies are well-separated. Laplace mixtures provided clear improvements on high-dimensional data like KDDCUP99 but struggled on smaller, noisier datasets. Student's t models consistently offered modest gains across more complex datasets by reducing false positives without sacrificing recall.

Overall, replacing the Gaussian mixture offers a simple and effective way to enhance DAGMM's flexibility, particularly in settings where data distributions are irregular or heavy-tailed. These extensions maintain the model's end-to-end simplicity and interpretability while improving detection robustness in challenging cases.

IX. FUTURE WORK

Several directions exist to extend this work further. First, dynamically learning the degrees-of-freedom parameter ν in Student's t-distributions could adapt the tail behavior to better match specific datasets.

Second, exploring alternative non-Gaussian mixtures such as skewed distributions, multimodal densities, or normalizing flows could enhance DAGMM's flexibility in capturing complex anomaly structures.

Finally, extending DAGMM to domains such as time-series anomaly detection, spatial anomaly localization, or combining it with variational inference and Bayesian uncertainty estimation could open new avenues for robust unsupervised anomaly detection.

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