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# Enhanced SS-DBSCAN Clustering Algorithm for High-Dimensional Data

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Abstract. This research introduces an enhanced SS-DBSCAN, a scalable and robust density-based clustering algorithm de-signed to tackle challenges in high-dimensional and complex data analysis. The algorithm integrates advanced parameter op-timization techniques to improve clustering accuracy and interpretability. Key innovations include a Fast Grid Search (FGS) method for optimizing the search of optimal MinPts by keeping the  $\epsilon$  parameter obtained constant. Notably, this study emphasizes the often-overlooked MinPts parameter, introducing a dynamic approach that initiates by calculating density metrics within a specified  $\epsilon$  distance and adjusting the MinPts range based on the standard deviation of these metrics. This approach identifies optimal MinPts values based on the maximum allowed range. Comprehensive experiments on five real-world datasets 2.2 demonstrate SS-DBSCAN's superior performance compared to DBSCAN, HDBSCAN, and OPTICS, evidenced by higher silhouette and Davies-Bouldin Index scores. The results highlight SS-DBSCAN's ability to capture intrinsic clustering structures accurately, providing deeper insights across various research domains. SS-DBSCAN's scalability and adaptability to diverse data densities make it a valuable tool for analyzing large, complex datasets. 

Keywords: SS-DBSCAN Clustering, High-Dimensional, Fast Grid Search, Scalability, Adaptability

## 1. Introduction

Data mining is an interdisciplinary field that merges database technology, statistics, machine learning, and pattern recognition, benefiting from each of these areas [1]. While still not extensively adopted in many research domains, numerous studies have highlighted the potential of data mining in developing predictive models, evaluating risks, and assisting with decision-making [2]. Data mining utilizing large datasets can generate crucial and impactful insights that are vital for precise decision-making and risk evaluation [3]. Algorithms designed for data mining facilitate the achievement of these objectives.

The advent of large and complex datasets has ushered in a new era of data-driven insights across various domains. Among the myriad available datasets, those that encompass extensive and highdimensional data like medical information stand out due to their comprehensive and detailed collection of information [4], [5]. The complexity, volume, and high dimensionality of these datasets pose significant challenges for clustering and data analysis, necessitating advanced methodologies for effective data preprocessing and clustering parameter optimization.

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When managing datasets characterized by high density, arbitrary shapes, and irregular distribution, DBSCAN (Density-Based Spatial Clustering of Applications with Noise) is recommended as a robust algorithm specifically designed to address these complex scenarios [6]-[9]. However, DBSCAN has its limitations, particularly in the selection of its two primary parameters, which can affect its performance and accuracy [10]. Despite its effectiveness in handling complex datasets, DBSCAN faces challenges, particularly in the selection and tuning of its two key parameters: the minimum number of points required to form a dense region (MinPts) and the maximum distance between two points for one to be considered as in the neighborhood of the other ( $\epsilon$ ) [11]. Among the two parameters,  $\epsilon$  has been the subject of extensive research, whereas MinPts has often been overlooked, with its selection frequently relying on rule-of-thumb methods or manual estimation based on data size. However, both parameters play a crucial role in determining clustering outcomes. In particular, improper determination of MinPts can significantly affect clustering results, especially as the data size of the same dataset increases. 

Other variants of DBSCAN, such as HDBSCAN (Hierarchical Density-Based Spatial Clustering of Applications with Noise) and OPTICS (Ordering Points To Identify the Clustering Structure), have been developed to address some of these limitations. HDBSCAN extends DBSCAN by converting it into a hierarchical clustering algorithm that does not require the user to specify a fixed value for  $\epsilon$ , aiming to find clusters of varying densities. However, HDBSCAN still struggles with high-dimensional datasets, as the hierarchical approach can become computationally expensive and less effective in distinguishing between closely spaced clusters in such complex data [12], [13]. Similarly, OPTICS improves upon DB-SCAN by ordering points to identify the clustering structure and handling clusters of varying densities more effectively. Nevertheless, OPTICS also faces challenges in high-dimensional spaces, where the complexity of data can lead to suboptimal clustering results and increased computational costs [14]. 2.2

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This paper elaborates on the enhancements introduced to the SS-DBSCAN algorithm from our previ-ous work, focusing on its innovative approach to automatically select DBSCAN parameters [11], [12]. The methodology presented here is specifically tailored to navigate the complexities inherent in high-dimensional datasets, providing a more nuanced and effective clustering solution for the unique chal-lenges posed by these extensive datasets. We introduce a more convenient and improved grid search method, named Fast Grid Search (FGS) for determining MinPts. By leveraging automatic parameter selection, SS-DBSCAN aims to improve the precision and applicability of clustering techniques, en-hancing the potential for actionable insights in various research domains. Additionally, we demonstrate the pivotal role of Principal Component Analysis (PCA) and t-Distributed Stochastic Neighbor Embed-ding (t-SNE) in preprocessing, alongside a modified approach to SS-DBSCAN parameter optimization, in enhancing clustering accuracy and interpretability within complex datasets. SS-DBSCAN is tested against other DBSCAN variant algorithms to demonstrate its robustness and resilience. 

# 2. Related Works

<sup>39</sup> Clustering algorithms, particularly Density-Based Spatial Clustering of Applications with Noise (DB-<sup>40</sup> SCAN), have been extensively studied for their capability to identify natural groupings in data without <sup>41</sup> requiring a predefined number of clusters. The original DBSCAN algorithm, introduced by Ester et al. <sup>42</sup> (1996), [9] demonstrated effectiveness in discovering clusters of arbitrary shapes and handling noise. <sup>43</sup> Still, its performance heavily relies on the appropriate selection of two key parameters:  $\epsilon$  and MinPts. <sup>44</sup> Numerous subsequent studies have attempted to address these challenges through various enhance-

ments to the DBSCAN algorithm. Schubert et al. (2017) revisited DBSCAN and discussed that DB-

SCAN is still a practical and effective clustering algorithm, especially when applied with careful consideration of parameters and indexing strategies [10]. Selecting the  $\epsilon$  parameter for DBSCAN in highdimensional data is still challenging due to diminished contrast in distances [15]-[17]. This issue persists irrespective of the indexing method, making DBSCAN parameterization difficult in high-dimensional contexts. Algorithms like OPTICS and HDBSCAN eliminate the need for the  $\epsilon$  parameter, making them more user-friendly. However, they also face challenges when dealing with high-dimensional data. [18]-[20].

Other modifications of the DBSCAN algorithm have been proposed to enhance its clustering per-8 8 formance. Liu et al. (2010) introduced DBSCAN-DLP, which uses a dynamic approach to select the 9 9  $\epsilon$  value by calculating it for each data point based on the local density and mean distance, although 10 10 this increases computational complexity [21]. Karami & Johansson (2014) developed BDE-DBSCAN, 11 11 combining Binary Differential Evolution with DBSCAN to fine-tune its parameters [22], while Ren et 12 12 al. (2012) created DBCAMM, which uses Mahalanobis distance and an innovative merging strategy for 13 13 better image segmentation. [23] Lai et al. (2019) proposed an optimization technique using the MVO 14 14 algorithm to iteratively refine DBSCAN parameters, [24] and Khan et al. (2018) introduced adaptive 15 15 DBSCAN to automate parameter selection [25]. Despite these advancements, there is still a need for 16 16 more adaptable and user-friendly methods for attaining better clusters with DBSCAN, which the current 17 17 paper aims to address. 18 18 Other experiments conducted by Gan and Tao were performed on datasets, and their parameter settings 19 19

were not well-suited for cluster analysis. Gan & Tao's (2015) choice of the  $\epsilon$  ( $\epsilon$ ) parameter was unusually large, set at a minimum of  $\epsilon$  = 5,000 for all their experiments [26]. Their results only demonstrated better performance under certain questionable settings. In contrast, more realistic parameter choices showed that SS-DBSCAN implementations by Monko & Kimura (2023) with an effective selection of both parameters (i.e.  $\epsilon$  & MinPts) result in the best results [11].

In high-dimensional datasets, the complexity and volume of data present significant challenges for traditional clustering algorithms [27]-[29]. These datasets often contain intricate patterns that are not readily apparent, necessitating the use of advanced dimensionality reduction techniques like Principal Component Analysis (PCA) and t-Distributed Stochastic Neighbor Embedding (t-SNE) [30]-[33]. In practice, applying PCA to reduce the dimensionality to a smaller number of components (e.g., 30-50) before running t-SNE is a common approach. This ensures that t-SNE works more efficiently and effectively, especially with very large or complex datasets [34], [35].

Various studies have also highlighted the potential of data mining and clustering in the medical domain. For instance, Zhang et al. (2016) explored big data mining in clinical medicine, emphasizing the utility of clustering techniques in identifying meaningful patterns in patient data [36]. Ngiam and Khor (2019) discussed the role of machine learning algorithms in healthcare delivery, underscoring the importance of robust clustering methods for clinical decision-making [2].

From the above-discussed related works, we realized a need to address the existing gaps by building 37 upon SS-DBSCAN, a new variant of DBSCAN that we developed in our previous studies that incorpo-38 rates stratified sampling for  $\epsilon$  estimation and a novel grid search method for determining MinPts. We put 39 more emphasis on the MinPts which most algorithms tend to use the rule of thumb 2 for 2 dimension 40 or 2\* D for high dimension where D is the dimension of the data. Abdulhameed et al. (2024) offers 41 significant improvements over traditional DBSCAN (Semi Supervised-DBSCAN) by incorporating a 42 pre-specified condition or constraint to better identify core points, the authors determined the MinPts 43 parameter based on whether the dataset is noisy or not [37]. For noisy data, the MinPts is set to 2\*D, 44 45

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where D is the number of features and for noiseless data, the MinPts is set to D+1 [37]. These ap-proaches still doesnt work well with complex real world data with high dimension. And upon increasing the data size it usually result into poorer clusters. In this work the MinPts determination is improved and offers better results than all other algorithms. The dual optimization of  $\epsilon$  and MinPt sensures that SS-DBSCAN is finely tuned to the intrinsic clustering structures within the high-dimensional datasets, enhancing clustering accuracy and interpretability. 

# 3. Contribution

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This paper makes four main contributions to the field of data mining and clustering high-dimensional datasets:

- (1) We enhanced the original DBSCAN to SS-DBSCAN to address the complexities of highdimensional data through advanced parameter optimization techniques, ensuring precise and reliable clustering results.
- (2) We developed a novel adaptive range method based on local density estimates. This method dynamically adjusts the range for MinPts to improve adaptability of SS-DBSCAN to varying data densities.
  - (3) We enhanced the grid search technique to significantly reduce the computational time required to determine the optimal MinPts in any DBSCAN variant that utilizes this parameter.
  - (4) With enhancement and improvement listed above, we realized scalable and adaptable DBSCAN, SS-DBSCAN, which is a valuable tool for analyzing large and complex datasets across various research domains.

# 4. Methodology

4.1. Overview and Motivation

Clustering high-dimensional data remains a significant challenge, particularly in cases where data density varies across different regions, making parameter selection for traditional clustering algorithms difficult. **DBSCAN** (Density-Based Spatial Clustering of Applications with Noise) is a well-known density-based clustering method that detects arbitrarily shaped clusters and identifies noise. However, its performance is highly sensitive to the choice of parameters ( $\epsilon$  and MinPts), significantly impacting clustering quality. 

The main limitations of DBSCAN include:

- Global  $\epsilon$  estimation A single fixed  $\epsilon$  value may not work well for datasets with varying densities.
- **Rule-based MinPts selection** Traditional DBSCAN often relies on heuristics like MinPts = 2D, which do not always yield optimal clusters, especially in high-dimensional data.
- Noise misclassification Poor parameter selection can incorrectly classify valid data points as noise or merge distinct clusters.

To address these challenges, we propose SS-DBSCAN (Stratified Sampling-DBSCAN), an enhanced version of DBSCAN that automates parameter tuning and improves clustering accuracy in high-dimensional datasets. SS-DBSCAN introduces two key enhancements: 

- Adaptive  $\epsilon$  Estimation: Instead of using a fixed global  $\epsilon$ , SS-DBSCAN applies stratified sampling to estimate  $\epsilon$  dynamically, improving sensitivity to variations in local density.
  - **Optimized MinPts Selection**: Instead of relying on a heuristic formula, SS-DBSCAN performs a fast grid search using the *Silhouette Score* to determine the best MinPts value, ensuring well-separated clusters with minimal noise.

These modifications enable SS-DBSCAN to handle noisy, high-dimensional datasets more robustly, ensuring that clusters are accurately formed without excessive noise classification. The following sections explain how SS-DBSCAN selects parameters, handles noise, and improves clustering performance.



## Fig. 1. Impoved MinPts for SS-DBSCAN Architecture

# 4.2. Data Preprocessing

Our methodological pipeline begins with the application of Multi-Head Self-Attention (MHSA) and Standard Scaler, followed by Principal Component Analysis (PCA) and t-Distributed Stochastic Neigh-bor Embedding (t-SNE) as part of data pre-processing. Then, it proceeds with the strategies for achiev-ing high-quality clustering using SS-DBSCAN. Fig. 1 illustrates the process through data pre-processing techniques and parameter selection, particularly emphasizing the MinPts parameter, which has histori-cally been the most challenging to optimize in previous research. The datasets used in our experiments were mainly text data (i.e., Emotion-Sentiment, Coronavirus-Tweets, Cancer-Docand MIMIC III) and one numerical dataset (Sonar). The text data comprised sequences ranging from a minimum of 50 to a maximum of 500, with an average sequence length of 250. The average length of 250 reflects the natural distribution within the selected datasets. Therefore, we used the all-mpnet-base-v2 pre-trained 

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model from Sentence-BERT to generate embeddings [38]-[40]. This pre-trained model has a maximum
 sequence length of 384, which can accommodate the sequence length of our data, has dimensions of
 768, and has been trained over 1 billion training pairs [41]. By generating high-quality embeddings us ing Setence-BERT, we enhanced the representational capacity of our data, facilitating more accurate and
 meaningful clustering.

MHSA was crucial in handling high-dimensional text embeddings, particularly in long-form text datasets, which helped enhance feature representations and capture contextual relationships between words and sentences through simultaneous attention to different parts of the text. The Standard Scaler, in this case, was employed to prevent the dominance of high-variance features and to ensure that all features contribute proportionally to the clustering process. It also helped improve the interpretabil-ity of the data and reduce computational complexity. PCA is applied to retain the maximum variance while reducing the number of dimensions, thereby simplifying the data while preserving the essential characteristics necessary for effective clustering. In our experiments, we retained 95% of the variance through PCA to minimize information loss before applying t-SNE. Subsequently, we used t-SNE to project the high-dimensional data into a two-dimensional space, facilitating better visualization and analysis. We employed the default hyperparameters for t-SNE:  $TSNE(n\_components=2, perplexity =$ 30, learning\_rate = "auto", n\_iter=300). Applying PCA before t-SNE was essential for several rea-sons. Firstly, PCA reduced the dimensionality of the data, making t-SNE more computationally efficient and faster. Additionally, by retaining only the most significant features, PCA helped minimize noise, thereby enhancing the quality of input data for t-SNE. Furthermore, it played a crucial role in preventing 2.0 t-SNE from overfitting to noise in high-dimensional data, resulting in more stable and robust clustering outcomes. By preprocessing the data with PCA, t-SNE was better able to reveal and preserve the under-2.2 2.2 lying structure of the dataset, particularly in cases that involved complex data. This step was vital for both visualization and clustering, as it facilitated the identification of patterns that might not be evident in higher-dimensional representations. 

## *4.3.* SS-DBSCAN Parameter Selection

For the clustering component, our algorithm, Stratified Sampling DBSCAN (SS-DBSCAN), incorporates a novel stratified sampling technique for estimating the  $\epsilon$  parameter. This approach was thoroughly discussed in our previous conference paper [12] and is depicted in Fig. 1 as the second step following data pre-processing. The stratified sampling technique effectively accommodates the varying density distributions within the datasets, ensuring that  $\epsilon$  is optimally set to capture the spatial distribution of data points accurately. As a result, this enhancement strengthens the natural clustering tendency of SS-DBSCAN, leading to more precise and well-defined clusters.

# <sup>36</sup> 4.3.1. Fast Grid Search for MinPts

To optimize the selection of the minimum points (MinPts), which dictate the core points in the DB-SCAN algorithm, we implement a Fast Grid Search strategy. This approach tests a range of MinPts values to pinpoint the optimal number that maximizes cluster validity, as measured by silhouette scores. This metric assesses how similar an object is to its own cluster compared to other clusters [42]-[44]. In our previous work, we employed a grid search technique to determine the optimal value for MinPts. We manually established a range, starting from 3 and extending to a maximum value, iterating by 1 or in steps of *n*, while maintaining the  $\epsilon$  value derived from the k-distance graph, which varied based on the data size and number of neighbors, k [11]. This approach enabled partial automation in selecting MinPts; however, we still had to manually define the range. This process not only increased execution time due 

to multiple iterations but also introduced the risk of overlooking critical values that could yield optimal
 silhouette scores, as the manual range setting might exclude such values.

Our novel method for selecting a single, optimal value for MinPts overcomes these limitations. It em-ploys an adaptive range based on local density estimates. By calculating the density metrics  $\rho_i$  for points within a specified  $\epsilon$  distance and computing the standard deviation ( $\sigma$ ) of these metrics, we dynamically adjust the range for MinPts by defining lower and upper bound. The lower bound is the average density minus the standard deviation, while the upper bound is the average density plus the standard deviation. This method significantly improves the adaptability of SS-DBSCAN to varying data densities and sizes. It provides a robust criterion for other analytical methods that require dynamic adjustments of sample sizes based on data density. Attaining the optimal value for MinPts involves a process described as follows: 

#### Calculating Density Metrics

This function calculates the density metric for each point in a dataset by counting how many points lie within a certain distance  $\epsilon$  of each point (1). For a dataset *D* with points  $x_i$ , the density metric  $\rho_i$ for point  $x_i$  is given by:

$$\rho_i = \sum_{x_{j \in D}} 1\left( \|x_i - x_j\| \leqslant \epsilon \right),\tag{1}$$

where,

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 1 is the indicator function, which is 1 if the condition is true and 0 otherwise, and  $||x_i - x_j||$  is the Euclidean distance between points  $x_i$  and  $x_j$ .

$$\overline{\rho} = \frac{1}{n} \sum_{i=1}^{n} \rho_i,\tag{2}$$

where,  $\overline{\rho}$  is the mean of the density metrics, and *n* is the total number of points (2)

#### Computing Standard Deviation

We then compute the standard deviation of the density metrics to understand the variability or spread of the density metrics across the dataset (3). If  $\rho$  represents the vector of density metrics across all points, the standard deviation  $\sigma$  is computed as:

$$\sigma = \sqrt{\frac{1}{n} \sum_{i=1}^{n} (\rho_i - \overline{\rho})^2},\tag{3}$$

#### • Computing the Range for Minimum Samples

Equation (4) computes a range for the MinPts parameter in SS-DBSCAN clustering based on the average density  $\overline{\rho}$  and the computed standard deviation  $\sigma$ . The range is defined by a lower and upper bound, adjusted to ensure that the samples are at least 2.

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2	Lower Bound = max $(2   \overline{\alpha} - \sigma )$	(4a)
4	$H_{\text{rest}} = \frac{1}{1000} \left[ \frac{1}{1000} \left[ \frac{1}{1000} \right] \right]$	(11)
5	Upper Bound = $\lfloor \rho + \sigma \rfloor$ .	(4b)
4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45	Upper Bound = $[\overline{\rho} + \sigma]$ . Here, [.] denotes the floor function, which rounds down to the nearest integer, that the lower bound is not less than 2, reflecting a minimum practical constration. After determining the optimal range for MinPts defined in Equation (4) a arf ast grid search technique to identify the best value by utilizing the silhoud shown in Algorithm 1. This approach was enhanced by iterating through the crucially, addressing the previous issue of unnecessarily printing all values optimize the process, we introduced a stopping criterion: after identifying the the iteration continues for five additional steps. If the silhoute score show consistently decreases during these iterations, the loop is terminated. This significant reduction in computational time, decreasing execution from as lon as short as 4 seconds in certain datasets, as demonstrated in Table 1. The exe increases proportionally with the data size, type and the number of neighbor directly influence the computation of the range. Through this dual optimization strategy ( $\epsilon$ & MinPts), SS-DBSCAN is finely sensitivity and adherence to the intrinsic clustering structures, thus promisi reliable clustering outcomes.	(4b) The function ensures and (4)b, we employ a et escore as a metric identified range and, within this range. To e current best MinPts, s no improvement or modification led to a g as 2,158 seconds to cution time, however, or (k), both of which the tuned to improve its ing more precise and
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2:	<b>Input:</b> <i>eps</i> : The epsilon value for SS-DBSCAN
3:	<b>Input:</b> <i>start_min_samples</i> : The starting value of MinSamples
4:	<b>Input:</b> <i>end_min_samples</i> : The ending value of MinSamples
5:	<b>Output:</b> <i>best_min_samples</i> : The optimal MinSamples value
6:	Initialize $best_silhouette\_score \leftarrow -\infty$
7:	Initialize $decrease\_counter \leftarrow 0$
8:	Initialize <i>last_silhouette_score</i> $\leftarrow -\infty$
9:	for $i \leftarrow start_min_samples$ to end_min_samples do
10:	Perform DBSCAN clustering on <i>features_array_tsne</i> with parameters:
11:	$eps \leftarrow eps$
12:	$min\_samples \leftarrow i$
13:	Calculate labels $\leftarrow db.labels_{-}$
14:	if number of unique clusters in <i>labels</i> > 1 then
15:	Calculate silhouette score $current_silhouette\_score$ $\leftarrow$
	silhouette_score(features_array_tsne, labels)
16:	Print: "For min_samples value = " + str( $i$ ) + ", Total no of clusters = " + str(len(set( <i>labels</i> ))))
	+ ", Silhouette Score: " + str( <i>current_silhouette_score</i> )
17:	if current_silhouette_score > best_silhouette_score then
18:	Update $best_silhouette\_score \leftarrow current\_silhouette\_score$
19:	Update $best_min_samples \leftarrow i$
20:	Reset $decrease\_counter \leftarrow 0$
21:	else
22:	Increment decrease_counter $\leftarrow$ decrease_counter + 1
23:	if decrease_counter $\geq 5$ then
24:	break
25:	end if
26:	end if
27:	else
28:	Print: "Insufficient clusters for min_samples value = " + $str(i)$
29:	end if
30:	end for
31:	Calculate $time\_elapsed \leftarrow time.time() - since$
32:	Print: "Time taken for training: :.0fm : :.0fs".format( <i>time_elapsed</i> //60, <i>time_elapsed</i> %60)
	return best_min_samples

# 5. Experiment Setup

We designed a comprehensive experimentation process to rigorously compare the effectiveness of var-ious clustering algorithms across multiple datasets. In this research, we primarily worked with real-world text and numerical data of varying sizes and complexity to evaluate the effectiveness of SS-DBSCAN and other DBSCAN variants in clustering high-dimensional embeddings. The datasets selected for our 

experiments included Emotion-Sentiment, Coronavirus-Tweets, Cancer-Doc, Sonar, and MIMIC III, covering various applications. The datasets were chosen based on the following criteria: (1) Diversity - They include different domains such as medical records (MIMIC-III, Cancer-Doc), sentiment analy-sis (Emotion-Sentiment, Coronavirus-Tweets), and structured data (Sonar). (2) Data Complexity – The data selected vary in structure, ensuring SS-DBSCAN's applicability across different data types. (3) High-Dimensionality Challenges – Each dataset presents clustering challenges that standard DBSCAN struggles with, making them ideal for benchmarking our method. The performance of each clustering algorithm was evaluated using the silhouette score and Davies-Bouldin Index, whereas the silhouette score measures the quality of clustering [42]-[44]. A higher sil-houette score indicates better-defined and more distinct clusters, thereby validating the effectiveness of the clustering technique. Davies-Bouldin Index (DBI) was another metric used to evaluate the quality of clustering algorithms based on cluster compactness and separation [45]. Lower DBI values (close to 0) indicate good clustering, while higher DBI values (much greater than 1) indicate poorer clustering. Table 1 Comparison of Grid Search and Fast Grid Search at Various Data Sizes Data size Search Range **Grid Search Fast Grid Search** MinPts Time(secs) **MinPts** Time(secs) 525-1509 1210-3150 1225-3506 755-1825 2.2 2.2 95-557 77-317 345-1225 50-184 5.1. Clustering Algorithms Applied in Different Data Sizes To evaluate the effectiveness of our preprocessing and clustering methodologies, we performed com-parative analyses of several algorithms across varying data sizes within the MIMIC III dataset. The primary objective of this experiment was to demonstrate the robustness of SS-DBSCAN, particularly in managing complex datasets, and to assess its performance consistency as data size increases, an area where other algorithms often exhibit limitations as seen in Table 2. The MIMIC dataset used in this study primarily consists of two distinct clusters: Adverse Drug Reaction (ADR) and Non-ADR cases. Among the algorithms tested, only SS-DBSCAN consistently identified the correct number of clusters, regardless of increasing data size. In contrast, the other algorithms produced varying numbers of clus-ters with inconsistent results as the dataset expanded. These findings demonstrate that the enhanced 

SS-DBSCAN algorithm delivers superior clustering accuracy and robustness compared to the other al-gorithms evaluated in this experiment. Clustering results are also visualized in Fig. 2, Fig. 3, Fig. 4 and Fig. 5 

#### 5.1.1. Clustering Results with SS-DBSCAN

SS-DBSCAN employs stratified sampling for precise estimation of the  $\epsilon$  parameter and utilizes a Fast Grid Search method for optimizing MinPts, allowing for the dynamic adjustment of DBSCAN's parameters to better align with the inherent structure of the data. The resulting parameter values vary 

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DataSize      SS-DBSCAN      DBSCAN      HDBSCAN      HDBSCAN      OPTICS $ips$ MinPt Clusters $eps$ MinPt Clusters      ClusterSize Clusters $xi$ MinPt Clusters        1000      4.1189      93      2      1.7438      4      3      30      3      0.001      9      5        2000      3.3084      75      2      1.3950      4      10      20      3      0.001      7      5        3000      3.1629      59      2      1.0884      4      6      14      4      0.001      7      4        4000      3.2177      64      2      0.9509      4      16      15      4      0.001      8      4        5000      2.1996      102      2      0.8634      4      41      20      4      0.001      7      4        vidingly based on the characteristics of the dataset. Figure 2 presents the clustering results ge S-DBSCAN.	DataSize			CAN		DBGC	A BT	IIDDO	CAN		0.0	TICC
eps      MinPt Clusters      eps      MinPt Clusters      Clustersize Clusters      Xi      MinPt Clusters        1000      4.1189      93      2      1.7438      4      3      30      3      0.001      9      5        2000      3.3084      75      2      1.3950      4      10      20      3      0.001      7      5        3000      3.1629      59      2      1.0884      4      6      14      4      0.001      7      4        4000      3.2177      64      2      0.9509      4      16      15      4      0.001      7      4        5000      2.1996      102      2      0.8634      4      41      20      4      0.001      7      4        vdingly based on the characteristics of the dataset. Figure 2 presents the clustering results gets-DBSCAN.      S-DBSCAN.      S-DBSCAN. <td< th=""><th>Dutubilit</th><th></th><th>S-DBS</th><th></th><th></th><th>DBSC</th><th></th><th>HDBS</th><th></th><th>·</th><th>OP</th><th></th></td<>	Dutubilit		S-DBS			DBSC		HDBS		·	OP	
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$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	2000	3.3084	75	2	1.3950	4	10	20	3	0.001	7	5
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	3000	3.1629	59	2	1.0884	4	6 16	14	4	0.001	/	4
solution of the dataset. Figure 2 presents the clustering results ge S-DBSCAN.	4000	3.2177	04 102	2	0.9509	4	10	15	4	0.001	8	4
rdingly based on the characteristics of the dataset. Figure 2 presents the clustering results ge S-DBSCAN.	5000	2.1990	102	4	0.8034	4	41	20	4	0.001	/	4

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<sup>41</sup> DBSCAN utilizes manually selected parameters based on established practices, specifically setting <sup>42</sup> MinPts to 4 and  $\epsilon$  to the knee value. The  $\epsilon$  parameter is determined by identifying the knee point, which <sup>43</sup> corresponds to the location of a significant bend in the curve. The MinPts parameter is chosen according <sup>44</sup> to the rule that suggests MinPts should be set to 2 times the dimensionality of the data (2\*dim). Fig. 3 <sup>45</sup> illustrates the clusters obtained.

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<sup>45</sup> algorithm.



Coronavirus-Tweets, Cancer-Doc, and Sonar. Our comprehensive evaluation demonstrated that SS DBSCAN consistently outperformed the other algorithms across all datasets and data sizes by the use of

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parameter values indicated in Table 3. The results of these experiments are presented in Fig. 8, providing a quantitative comparison of clustering performance. Additionally, the clustering outcomes are visual-ized better in Fig. 6, which illustrates the superior clustering quality achieved by SS-DBSCAN. These visualizations highlight the algorithm's ability to effectively manage varying data densities and complex structures, reinforcing its robustness and applicability across different types of high-dimensional data. Table 3 Parameter Values and Cluster Results of Different Algorithms on Various Datasets SS-DBSCAN DBSCAN HDBSCAN **OPTICS** Dataset eps MinPt Clusters Min Cluster Size Clusters xi MinPt Clusters eps MinPt Clusters 3.7833 466 0.001 Emotion Sentiment 1.0365 Corona Tweets 3.2270 1.1366 0.001 1.8789 CancerDoc 3.5805 0.001 MIMIC III 3.2177 0.9509 0.001 Sonar 5.0213 1.5947 \_ 0.001 2.2 

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Table 4 and Table 5. The stratified sampling approach for  $\epsilon$  estimation and the FGS for MinPts signifi-cantly enhance the robustness and resilience of the clustering process. This highlights the scalability of SS-DBSCAN and its adaptability to varying data densities and sizes and high dimensional data making it a valuable tool for complex data and decision-making. 

	Table 4									
	Silhoue	tte and DBI	Scores of	Different A	lgorithms	at Various E	Data Size	s of MIMIC	Π	
	Data Size SS-DBSC		CAN	AN DBSCAN			AN	OPTIC	-	
		Silhouette	DBI	Silhouette	DBI	Silhouette	DBI	Silhouette	DBI	
	1000	0.64	0.39	0.24	1.41	0.54	1.51	0.02	1.37	-
	2000	0.62	0.48	-0.22	1.36	0.40	1.59	-0.11	1.25	
	3000	0.61	0.44	-0.40	1.45	0.38	1.50	-0.16	1.23	
	4000	0.61	0.44	-0.46	1.54	0.34	1.59	-0.22	1.22	
	5000	0.61	0.45	-0.04	1.52	0.09	1.57	-0.35	1.25	_
		Silhouette an	nd DBI Sc	T ores of Dif	able 5 ferent Alg	orithms on V	/arious D	Datasets		
Data		D ( C!						CAN OPTICS		
Dutu	set	Data Size	SS-DI	BSCAN	DBS	CAN	HDBS	CAN	OPTIC	CS
Dutu	set	Data Size	SS-DI Silhouet	BSCAN te DBI	DBS( Silhouette	CAN e DBI Sil	HDBS(	CAN DBI Silhe	OPTI( )uette	CS DBI
Emot	ionsSentiment	s 4000	SS-DI Silhouet 0.55	BSCAN te DBI 5 0.79	DBS Silhouette 0.40	CAN <b>DBI Sil</b> 4.26	HDBSC houette 0.18	CAN DBI Silho 4.67 -0	OPTIC Duette	CS DBI 6.30
Emot	set ionsSentiment navirusTweets	Data Size s 4000 4000	SS-DI Silhouet 0.55 0.43	BSCAN te DBI 3 0.79 0.83	DBS0 Silhouette 0.40 0.25	CAN <b>DBI</b> Sil 4.26 1.89	HDBS0 houette 0.18 0.18	CAN DBI Silhe 4.67 -0 2.42 -0	OPTIC Duette	CS DBI 6.30 1.56
Emot	ionsSentiment navirusTweets erDoc	Data Size s 4000 4000 4000	SS-DI Silhouet 0.55 0.43 0.45	BSCAN te DBI 3 0.79 0.83 0.71	DBS0 Silhouette 0.40 0.25 0.35	CAN <b>DBI</b> Sil 4.26 1.89 1.62	HDBS0 houette 0.18 0.18 0.09	CAN DBI Silhe 4.67 -0 2.42 -0 1.47 -0	<b>OPTIC</b> <b>Duette</b> 0.23 0.16 0.16	CS DBI 6.30 1.56 1.65
Emot Coro Canc MIM	ionsSentiment navirusTweets erDoc IC III	Data Size s 4000 4000 4000 4000	SS-DI Silhouet 0.55 0.43 0.45 0.61	BSCAN te DBI 5 0.79 0.83 0.71 0.44	DBS0 Silhouette 0.40 0.25 0.35 -0.46	CAN 2 DBI Sil 4.26 1.89 1.62 1.54	HDBS0 houette 0.18 0.18 0.09 0.34	CAN      Silh        DBI      Silh        4.67      -0        2.42      -0        1.47      -0        1.59      -0	<b>OPTIC</b> <b>Duette</b> 0.23 0.16 0.16 0.22	CS DBI 6.30 1.56 1.65 1.22

#### 6. Result Interpretation

Our implementation of SS-DBSCAN significantly enhances the clustering process by allowing us to precisely select the optimal values for  $\epsilon$  (the maximum radius of the neighborhood) and MinPts (the minimum number of points in a neighborhood to form a cluster). This method ensures that we consistently achieve reliable clustering outcomes, distinctly improving upon the approach used by other density-based clustering algorithms.

In the standard DBSCAN framework, the MinPts parameter is typically determined using a heuristic based on the dataset's dimensionality, often set at twice the number of dimensions. In our study, after reducing the data's dimensionality from 768 to 2, we applied a MinPts value of 4 following this rule of thumb. However, this approach is somewhat arbitrary and fail to accurately reflect the true density distribution in more complex datasets. Consequently, this led to suboptimal clustering results as shown in our experiments.

On the other hand, HDBSCAN, another variation of DBSCAN, adjusts its sensitivity based on several parameters such as min\_cluster\_size, min\_samples, and alpha. The performance of HDBSCAN hinges significantly on the appropriate selection of min\_cluster\_size. Ineffective choices for this parameter can lead to poor clustering results, whereas optimal parameter tuning can considerably enhance the clustering quality. However, as the data size increases, the performance of HDBSCAN reduces, often returning meaningless clusters, as seen in Fig. 4.

OPTICS (Ordering Points To Identify the Clustering Structure) was also included in our experiment
 to explore its potential advantages over traditional density-based methods like DBSCAN and HDB SCAN. OPTICS attempts to uncover the clustering structure of data by ordering points based on their
 density-reachability. However, in our experiments, OPTICS underperformed in all datasets, as illus trated in Figure 5 and Figure 8. The algorithm's sensitivity to initial parameter settings (min\_samples,

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Fig. 7. Algorithms' Performances in Different Data Sizes of MIMIC III

xi, min\_cluster\_size, metric), coupled with its computational complexity, resulted in very poor clusters. OPTICS struggled to adapt to the intricate density variations in the data, ultimately producing less meaningful clustering outcomes.

Therefore, SS-DBSCAN distinguishes itself from other algorithms by incorporating stratified sam-pling to determine the best values for  $\epsilon$  and FGS to determine MinPts without arbitrary estimations. This approach allows SS-DBSCAN to adapt effectively across different sizes and complexities of datasets, including complex and noisy datasets. SS-DBSCAN delivers consistent results and underscores our algorithm's robustness, making it highly effective for diverse applications. 

# 7. Discussion

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In this paper, we enhanced the SS-DBSCAN and evaluate its performance in different data sizes and on different datasets. Our findings underscore the adaptability and robustness of SS-DBSCAN, especially in handling large and complex data. The unique parameter optimization approach of SS-DBSCAN enhances its efficacy in identifying meaningful clusters vital for data mining and decision-making. Below, we discuss several aspects of SS-DBSCAN's application and the implications of our results: 

7.1. Noise Sensitivity

SS-DBSCAN performed better in managing noise in all datasets used for the experiment than tradi-tional DBSCAN, HDBSCAN, and OPTICS. In contrast to standard DBSCAN, which relies on a fixed 

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Fig. 8. Algorithms' Performance in Different Datasets of 4000 size

global  $\epsilon$  estimation, SS-DBSCAN utilizes stratified sampling to determine  $\epsilon$  adaptively, ensuring better sensitivity to local density variations and reducing the risk of misclassifying sparse regions as noise. Ad-ditionally, SS-DBSCAN improves MinPts selection through a Fast Grid Search approach, where MinPts is optimized based on the Silhouette Score, excluding noise points from the computation. This pre-vents misclassified noise from distorting cluster validity, leading to a more robust and noise-resistant clustering process. Unlike DBSCAN, where MinPts is often set based on a rule of thumb (e.g., 2D for high-dimensional data), SS-DBSCAN dynamically selects the best-fitting MinPts, ensuring that the clustering structure is well-defined with fewer noise points. These enhancements collectively enable SS-DBSCAN to produce higher-quality clusters with better-defined boundaries, particularly in complex and high-dimensional datasets. 

# 7.2. Scalability

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The scalability of SS-DBSCAN was rigorously evaluated using the MIMIC III dataset, a large and complex real-world dataset. The results demonstrate the algorithm's efficiency in handling extensive data volumes while maintaining high-quality clustering performance. This establishes SS-DBSCAN as a highly suitable solution for large-scale datasets where computational efficiency and time constraints are critical factors. Furthermore, the algorithm's flexibility in determining both the  $\epsilon$  and MinPts param-eters consistently yields more accurate and reliable results, regardless of dataset size. This adaptability underscores SS-DBSCAN's robustness across varying data densities, further enhancing its applicability in diverse research and real-world scenarios.

#### 7.3. Parameter Adaptivity and Robusteness

Our methodology dynamically adjusts  $\epsilon$  and MinPts based on the dataset's intrinsic characteristics. This adaptivity allows SS-DBSCAN to respond flexibly to variations in data density and distribution, ensuring optimal clustering across different datasets. We also explored how variations in  $\epsilon$  and MinPts in different datasets affect the stability of the clusters. Our results show that SS-DBSCAN maintains consistent clustering quality even with minor parameter adjustments, highlighting its reliability for clustering applications where precision is paramount.

## 7.4. Cluster Validation

We employed a silhouette statistical measure and Davies-Bouldin Index (DBI) to validate the clusters generated by SS-DBSCAN. Both silhouette and DBI scores confirm the distinctiveness and relevance of the clusters. In comparison with other algorithms used in our experiment, SS-DBSCAN stands out for its robustness and precision. Unlike methods that require extensive parameter tuning and may not form clusters effectively, SS-DBSCAN adapts its parameters automatically, offering more reliable clustering even in complex datasets. 

#### 7.5. Importance of Dimensionality Reduction

Dimensionality reduction is essential in clustering high-dimensional data, as it enhances cluster sep-arability, reduces noise, and improves computational efficiency. While the choice of technique is not 2.2 limited to a specific method, our research found that the combination of PCA and t-SNE yielded the best results for all algorithms used in our experiments. PCA removes noise and extracts principal features, while t-SNE preserves local structure and adapts to varying cluster densities, leading to better-defined clusters across different dataset sizes. Other techniques, such as UMAP [46], can also be used, but our experiments showed key differences. UMAP performed well on smaller datasets, producing compact clusters, but as dataset size increased, it introduced significant noise and fragmented clusters. In con-trast, PCA + t-SNE maintained consistent clustering performance and better noise handling across all dataset sizes. While UMAP emphasizes local manifold learning, t-SNE's perplexity parameter provided better cluster separation, making it a more suitable choice for our research. Future work can explore alternative combinations, such as PCA before UMAP or t-SNE after UMAP, to balance local and global structure preservation. 

## 7.6. Future Work

Future research could explore the applicability of our technique to a broader range of datasets beyond those considered in this study. Our work primarily focused on text-based and structured (numerical) realworld data, where the proposed approach demonstrated effectiveness in handling high-dimensional and complex data distributions. However, its performance on other datasets, such as image, audio, or multi-modal data, remains an open question. Investigating how our method adapts to different data structures and domains would be a valuable direction for future work, potentially enhancing its generalizability and robustness across diverse applications. 

## 8. Conclusion

In this study, we introduced an enhanced SS-DBSCAN algorithm designed to improve parameter selection and noise handling in complex and high-dimensional datasets. By leveraging adaptive  $\epsilon$  estimation through stratified sampling and an optimized MinPts selection with the Fast Grid Search technique, SS-DBSCAN overcomes key limitations of traditional DBSCAN and other density-based clustering, making it particularly effective for high-dimensional, noisy, and non-spherical datasets.

Our experiments demonstrate that SS-DBSCAN excels in clustering diverse datasets, including text embeddings and structured numerical data. The algorithm dynamically adapts to varying density distri-butions, ensuring more accurate cluster formations while reducing the risk of misclassification. Addi-tionally, its efficiency in handling large data volumes makes it a valuable tool for real-world clustering applications in domains such as biomedical informatics, social media analysis, and anomaly detection. Beyond improving clustering accuracy, these enhancements strengthen the interpretability of cluster

structures, providing deeper, actionable insights into complex datasets. Such insights are crucial for data-driven decision-making in research and industry. 

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