

# *Position-Aware Safe Boundary Interpolation Oversampling*

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# Outline

- **Background**
- **Literature**
- **Proposed Method**
- **Future Work**

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# Imbalance Data Classification

- Classification is a supervised learning task.
  - **Learn** from training data, then **predict** categorical classes on test data.
- **The imbalanced data sets**
  - The number of data in some classes are **extremely smaller** than other classes.
  - Widely existing in many applications, such as:
    - fraud detection, disease diagnosis, oil spill detection from satellite images, etc.
- Imbalanced data **significantly compromise** the performance of most standard learning algorithms.

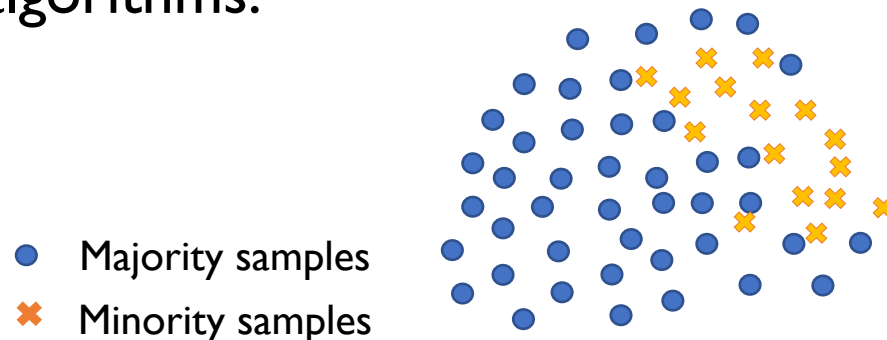


Fig. Imbalanced data

# Effects of Imbalance on SVM

- SVM works well on balanced datasets. But it towards the majority class and has low performance on the minority on imbalanced datasets.
- SVM has two objectives:
  - separating the two classes with the maximum margin
  - minimizing the number of misclassifications
- **Effects:** Margin is maximized with low total misclassification error

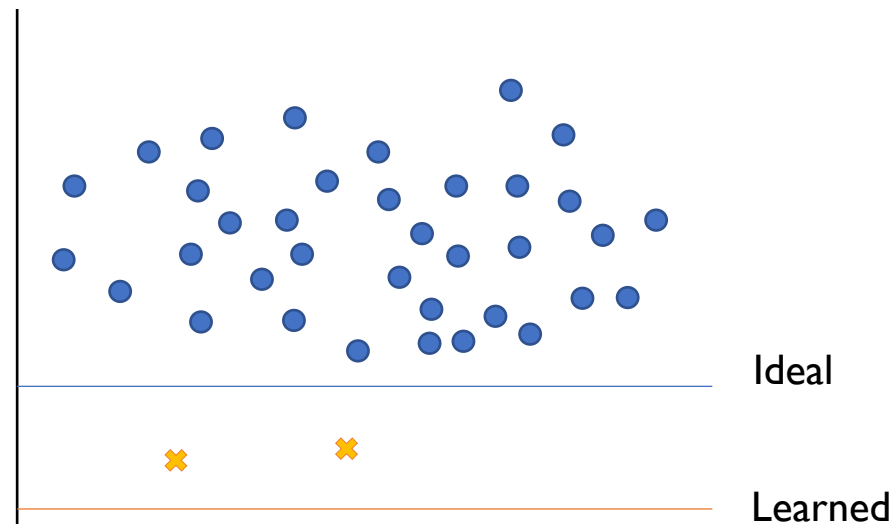


Fig. Effects of Imbalance on SVM

# Outline

➤ **Background**

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# Literature

- The existing solutions of class imbalance classification can be roughly divided into two types:
  - Algorithm-level methods: Modify learners, such as adding misclassification cost or modified loss function
    - Adaboost<sup>1</sup>, inducing the misclassification cost of the minority class to build an ensemble of weak learners
  - Data-level methods: Modify data distribution, create balanced dataset
    - Bootstrap<sup>2</sup>, sampling dataset with replacement in each iteration
    - Advantages:
      - more **universal** as they do not rely on any specific learner
      - more **flexible** combined with other techniques in machine learning.

1. P. Thanathamathee and C. Lursinsap, "Handling imbalanced data sets with synthetic boundary data generation using bootstrap re-sampling and adaboost techniques," PRL, 2013. 7

2. J. Han, J. Pei, and M. Kamber, Data mining: concepts and techniques. Elsevier, 2011.

# Literature: Data-level

- **Under-sampling:** sample part of **majority** data
  - **Issues:** probably will lose useful information by discarding the majority instances.
- **Over-sampling:** generate **more minority** data
  - **Issues:** more frequently used in data-level methods, as do not discard examples and would not lose useful information for classifier.
- **Cluster-based sampling:** integrate **clustering** algorithms with **over-sampling**.
  - Not only classify **between classes**, also handle samples **within classes**.
  - E.g. Cluster-SMOTE<sup>1</sup> (K-means), DBSMOTE<sup>2</sup> (DBSCAN)
  - **Issues:** introducing additional noise because of improper and non-robust clustering methods.

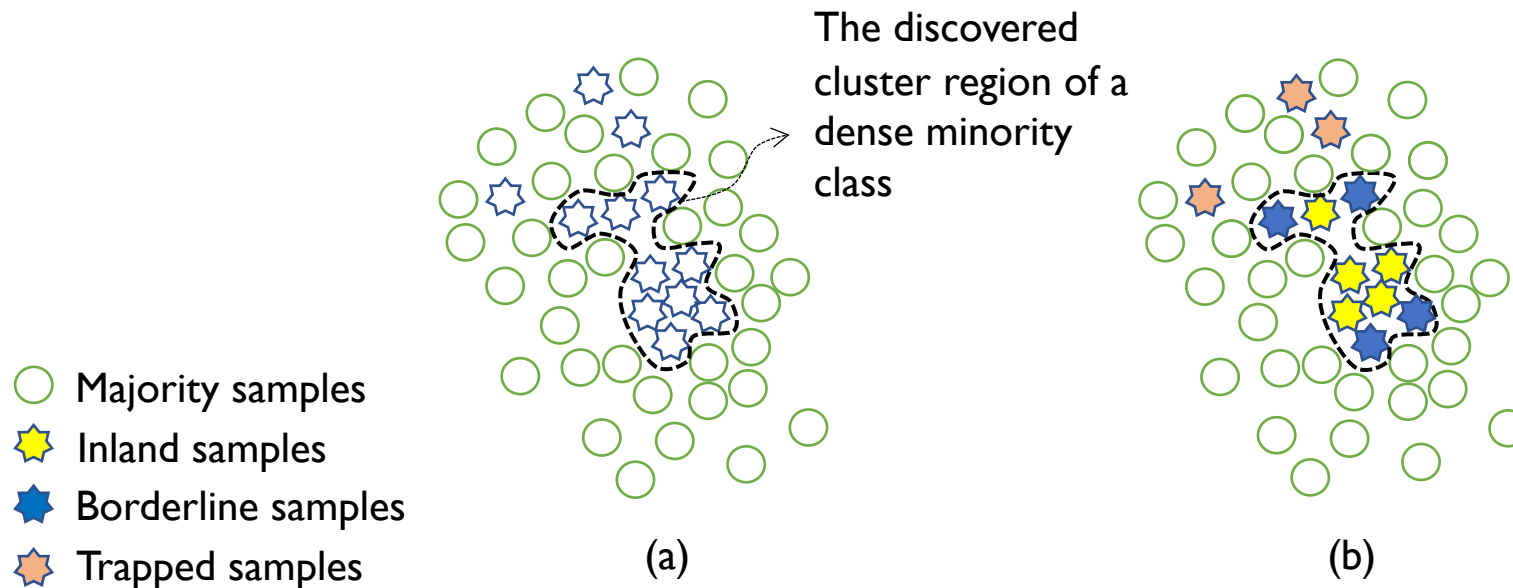
1. Nekooimehr and S. K. Lai-Yuen, "Adaptive semi-supervised weighted oversampling (a-suwo) for imbalanced datasets," Expert Systems with Applications, 2016.

2. D.A. Cieslak, N.V. Chawla, and A. Striegel, "Combating imbalance in network intrusion datasets." in GrC, 2006, pp. 732–737.



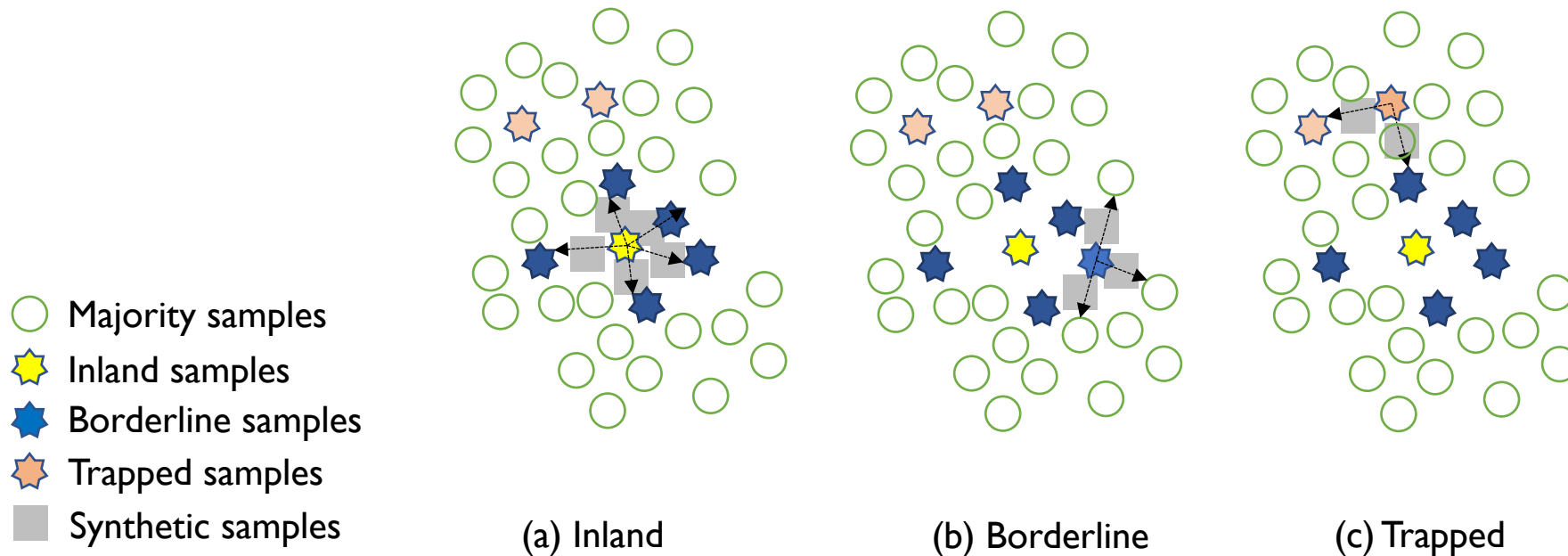
# Preliminary

- Recently, a position characteristic-aware interpolation over-sampling algorithm (PAIO) has been proposed to re-balance data sets.
- There are two main phases of this work:
  - I. **Cluster** the minority examples and identify them into inland, borderline, trapped points.



# Preliminary

- Recently, a position characteristic-aware interpolation over-sampling algorithm (PAIO) has been proposed to re-balance data sets.
- There are two main phases of this work:
  - 2. **Generate** synthetic examples accordingly.



# Outline

## ➤ **Background**

## ➤ **Literature**

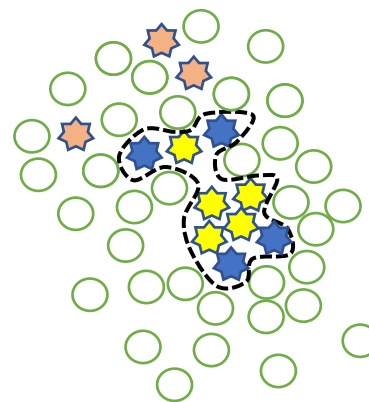
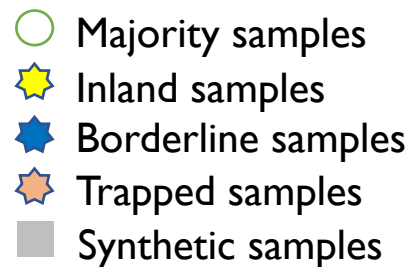
## ➤ **Proposed Method**

- Motivation
- Formulation
- Experiment

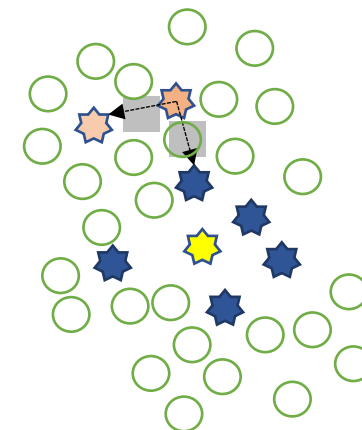
## ➤ **Future Work**

# Motivation

- **Issues of PAIO**
  - **Clustering Issue:** PAIO tends to group two dense minority samples into one cluster.
    - Leads the synthetic samples locate in majority sample.
  - **Generation Issue:** PAIO tries to generate synthetic points for trapped samples according to k-nearest neighbors
    - Easily causes the points close to majority samples.



(a) Clustering Issue



(b) Generation Issue

# Outline

## ➤ **Background**

## ➤ **Literature**

## ➤ **Proposed Method**

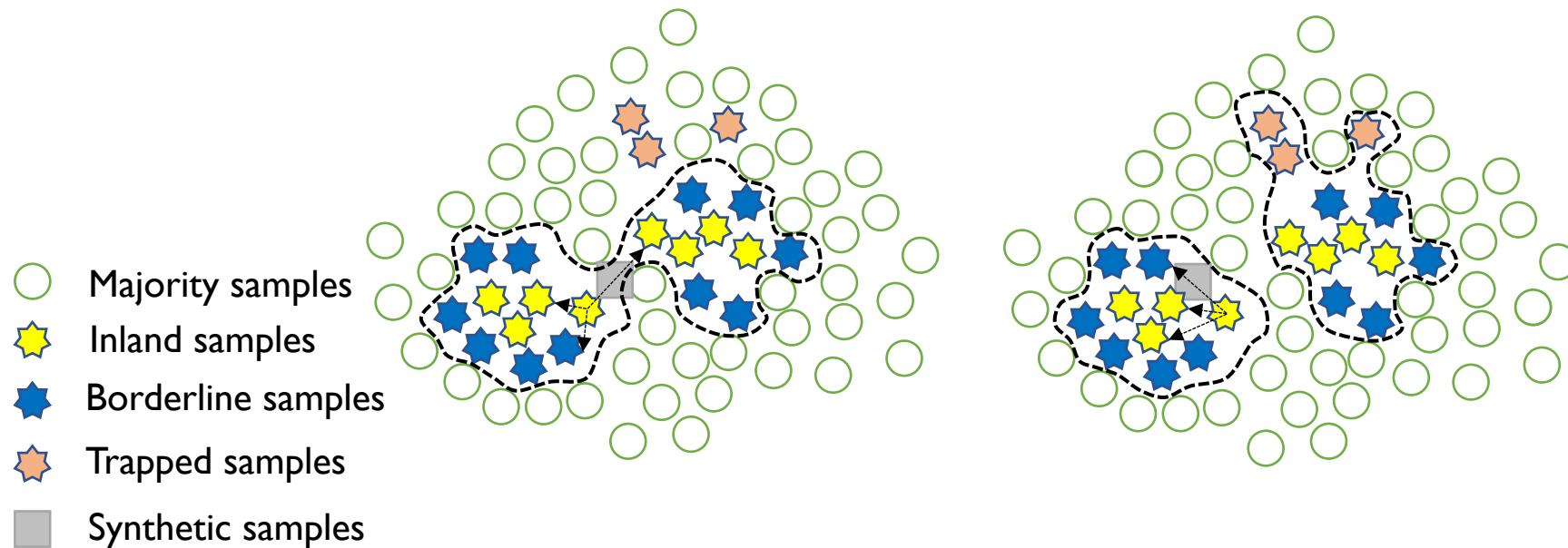
- Motivation
- **Formulation**
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## ➤ **Future Work**

# Proposed Method

## Clustering

- We employ one advanced clustering algorithm, CFSFDP, which is able to handle such scenario.



1. T. Zhu, Y. Lin, and Y. Liu, "Improving interpolation-based oversampling for imbalanced data learning," Knowledge-Based Systems, 2020.

2. A. Rodriguez and A. Laio, "Clustering by fast search and find of density peaks," Science, 2014.

# Proposed Method

## Clustering

- Given a distance matrix  $D = [d_{ij}]_{n \times n}$ , where  $d_{ij}$  denotes the distance between the minority samples  $x_i$  and  $x_j$ .
- For each minority sample  $x_i$  compute:
  - $\rho_i = \sum_{j:j \neq i} e^{-\left(\frac{d_{ij}}{d_c}\right)^2}$  (local density of minority points within a distance  $d_c$ )
  - $\delta_i = \min_{j:\rho_j > \rho_i} (d_{ij})$  (distance to the closest minority point with higher density)
- CFSFDP assumes that cluster centers are defined by a **high local density**  $\rho$  within a **relatively distance** between centers.

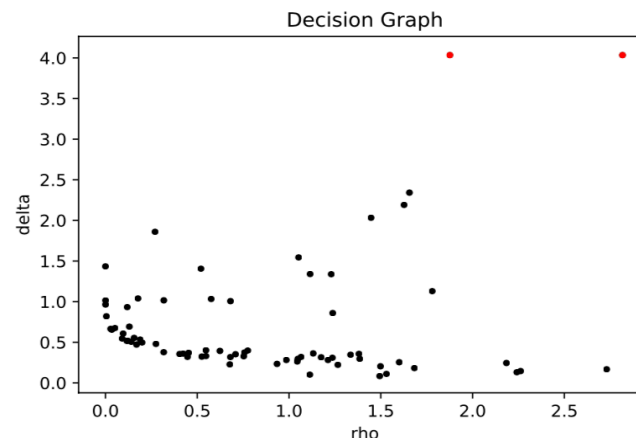


Fig. Decision Graph the imbalance dataset:Vowel dataset

# Proposed Method

## Division

- Given a set of minority examples  $X = \{x_1, \dots, x_n\}$  and a set of clusters from the clustering  $L = \{L_1, \dots, L_{n_L}\}$ , where  $L_c \subset X$ ,  $L_i \cap L_j = \emptyset$  for any  $i \neq j$ .
- For each minority example  $x_i$  compute its local density within its m-nearest neighbors  $N_m(x_i)$ :
  - $\kappa(x_i) = |N_m^*(x_i)|/m$ ,
  - where  $N_m^*(x_i) = \{x_j | x_j \in N_m(x_i) \cap L_c, x_i \in L_c, i \neq j\}$



# Proposed Method

## Division

- After clustering the minority examples, classify them into **inland, borderline, trapped examples**.
  - Inland:  $\kappa(x_i) > \rho TH$
  - Borderline:  $\kappa(x_i) \leq \rho TH$  and an inland sample exist in its  $N_m(x_i)$
  - Trapped:  $\kappa(x_i) \leq \rho TH$  and not a single inland sample exist in its  $N_m(x_i)$

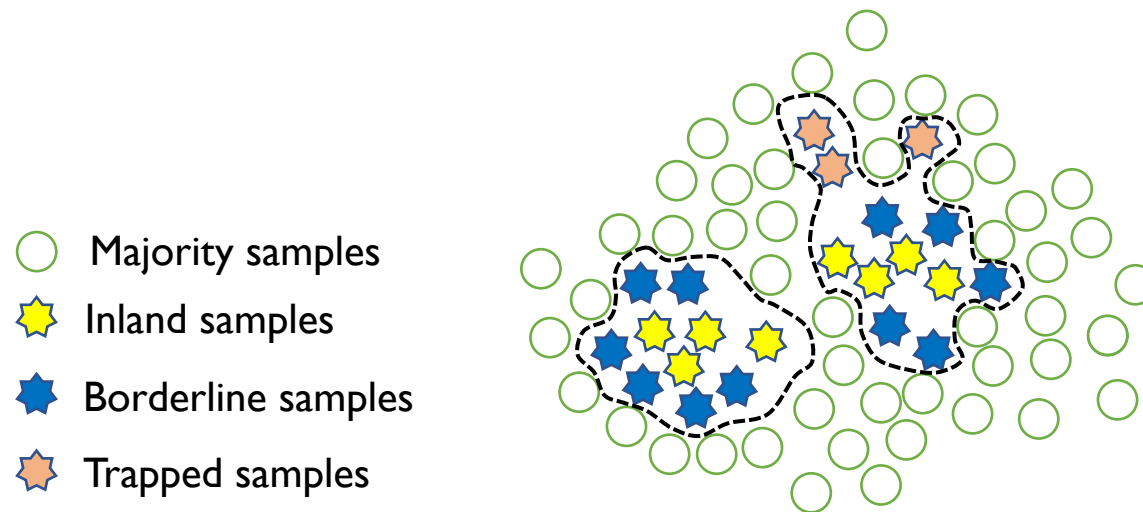


Fig. Our proposed classifying minority examples based on clustering

# Proposed Method

## Generation

- After grouping the minority examples, generate synthetic points for inland, borderline and trapped samples, respectively.
- We follow the interpolation-based method for **inland** and **borderline**, the same with PAIO.
- Given a point  $x_i$  and its candidate point  $x_j$ , the synthetic point  $s$  is calculated as:
$$s = x_i + \gamma(x_j - x_i),$$
 where  $\gamma$  is a constant vector.
- We propose a new method for **tapped points** to reduce noise.

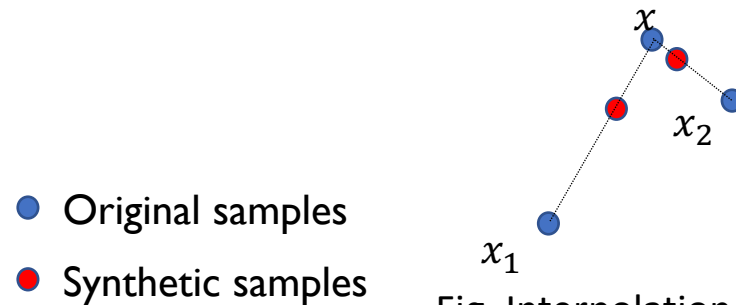
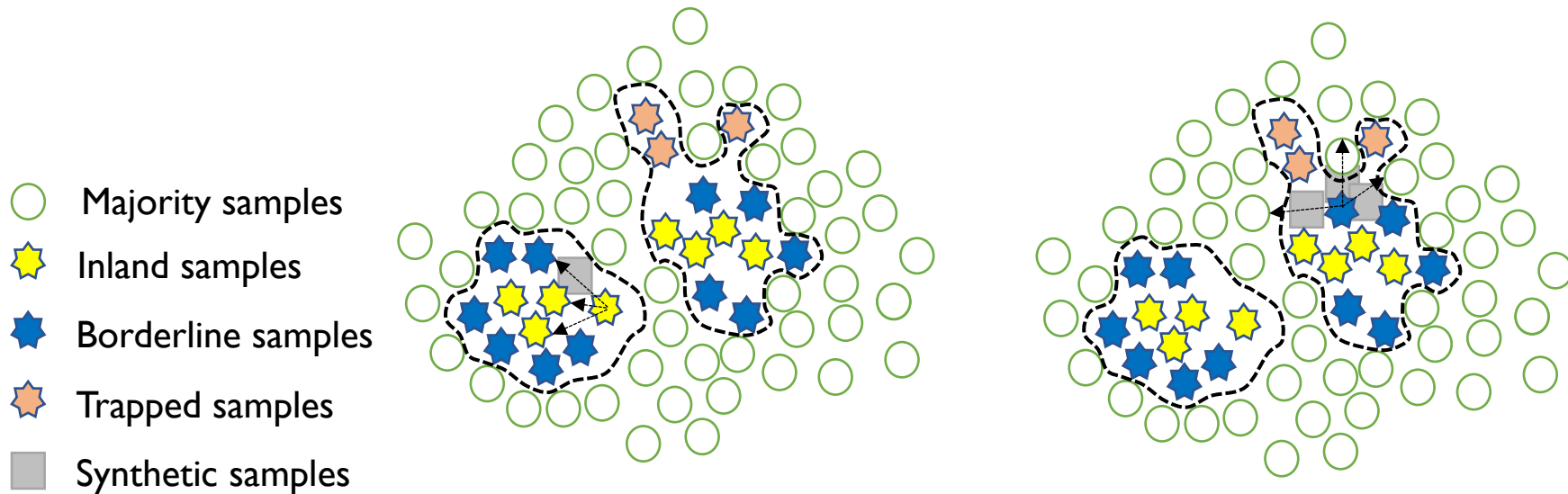


Fig. Interpolation-based Method

# Proposed Method

## Generation for inland and borderline

- For **inland** minority example  $x_i$ , its candidate point  $x_j$  chosen from the same cluster  $L_c \setminus x_i$ , where  $x_i \in L_c$ .
- For **borderline** minority example  $x_i$ , its candidate point  $x_j$  chosen from  $k_{maj}$  nearest majority neighbors  $N_{maj}(x_i)$ .



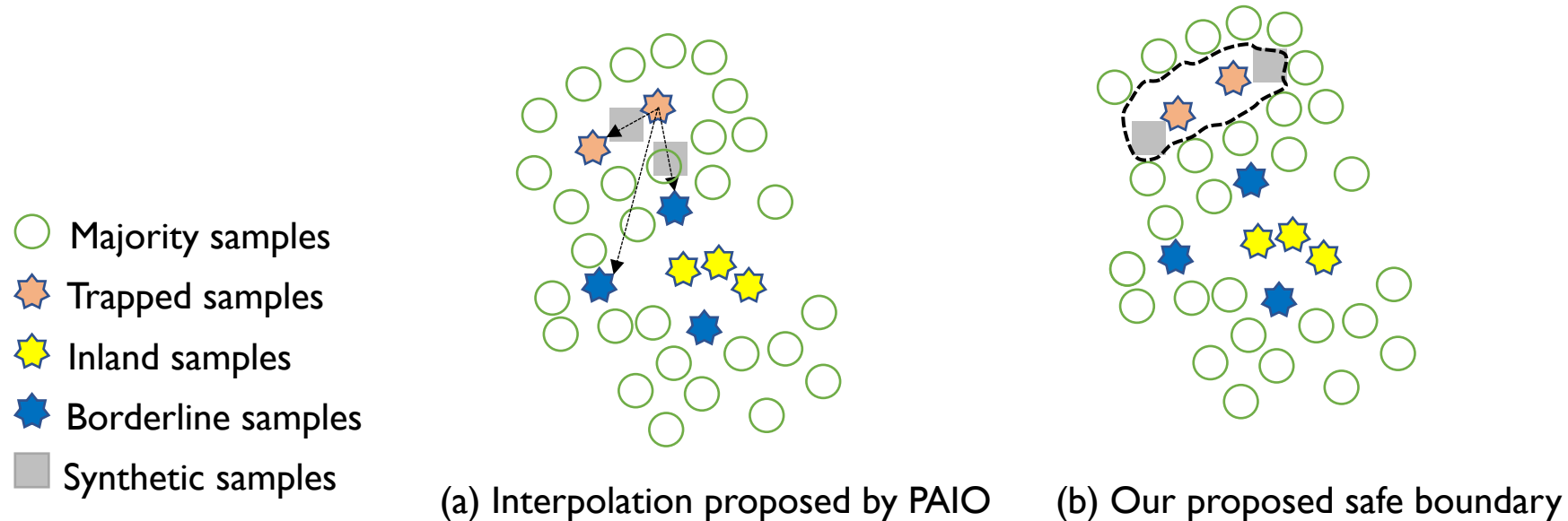
(a) Interpolation for Inland

(b) Interpolation for Borderline

# Proposed Method

## Generation for trapped

- We propose to learn the **safe boundary** of **trapped** samples to generate synthetic points with following hypothesis:
  - The embedding vectors of synthetic instances should be more similar to its corresponding trapped instance, than to any other majority instance.



# Proposed Method

## Generation

- We propose to learn the **safe boundary** of **trapped** samples to generate synthetic points with following hypothesis:
  - We define a partial loss  $l$  for a synthetic instance  $s$  as follows:

$$l = \max \left\{ 0, 2 - \left[ \max_{t' \in T} \phi(t', s) - \max_{m' \in M} \phi(m', s) \right] \right\}$$

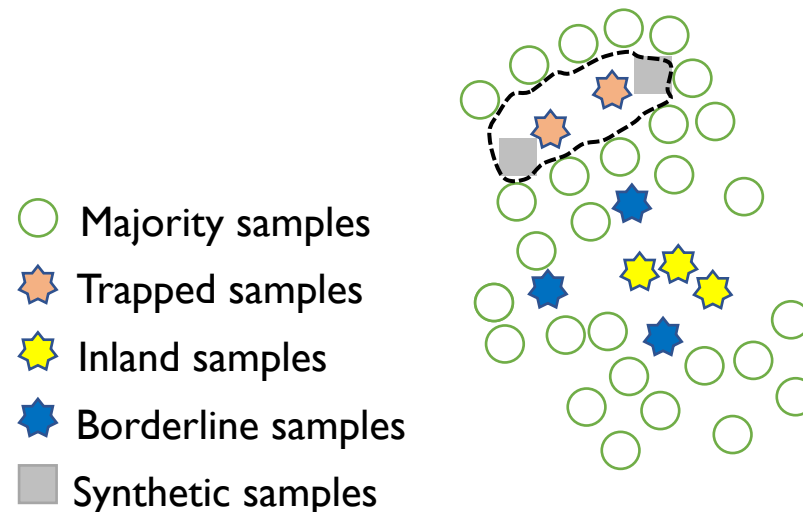


Fig. Our proposed safe boundary

# Proposed Method

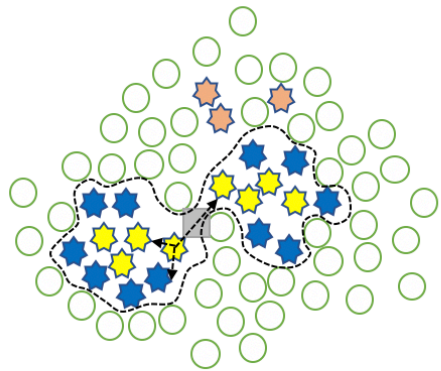
## Contribution

- **Clustering**

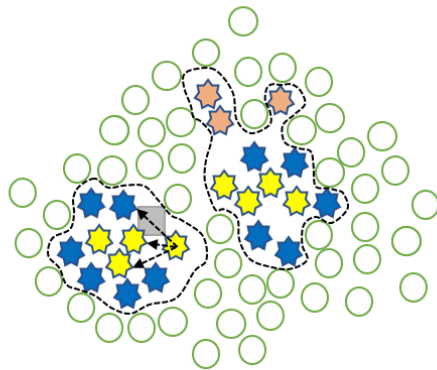
- We employ CFSFDP clustering algorithm to alleviate improper clustering in PAIO.

- **Generation**

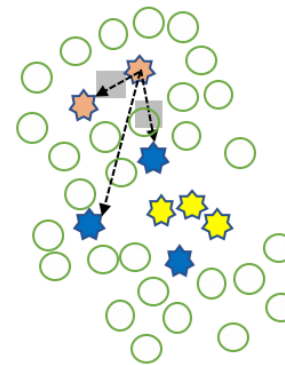
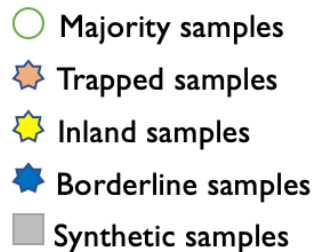
- We propose to learn the **safe boundary** of **trapped samples** to avoid noises.



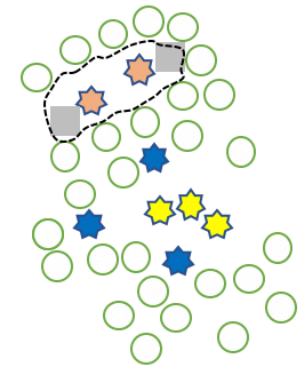
(a) Clustering adopted by PAIO



(b) CFSFDP clustering



(a) Interpolation proposed by PAIO



(b) Our proposed safe boundary

1. T. Zhu, Y. Lin, and Y. Liu, "Improving interpolation-based oversampling for imbalanced data learning," Knowledge-Based Systems, 2020.

2. A. Rodriguez and A. Laio, "Clustering by fast search and find of density peaks," Science, 2014.

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## ➤ **Future Work**

# Experiment

- Data sets:
  - Five classical Imbalanced data sets from UCI repository
- Compared with other nine oversampling algorithms:
  - ROS
  - SMOTE<sup>1</sup> and its variant: safe-SMOTE<sup>2</sup>
  - MWMO<sup>3</sup>
  - SMOM<sup>4</sup>
  - INOS<sup>5</sup>
  - MDO<sup>6</sup>
  - RACOG<sup>7</sup>
  - PAIO<sup>8</sup>
- Use two classical classifiers: Linear SVM and C4.5 decision tree



# Experiment

## Data sets:

Data	# Min class	# Maj class	# Min examples	# Maj examples	# numeric features	Imbalance ratio
Pima	1	1	268	500	8	1.866
Ecoli	5	3	64	272	7	4.25
Vowel	1	1	90	900	8	10
Yeast	2	8	81	1403	8	17.32
ABI	2	26	99	4078	7	41.19

- Description of inland, borderline and trapped and generated synthetic samples

Data	# I	# B	# T	# S <sub>I</sub>	# S <sub>B</sub>	# S <sub>T</sub>
Pima	135	12	9	135	57	76
Ecoli	43	12	9	69	68	761
Vowel	88	2	0	580	302	0
Yeast	10	14	57	72	180	1012
ABI	0	0	99	0	0	3930

# Experiment

## Metrics

- Precision and Recall
  - Precision =  $TP / (TP + FP)$
  - Recall =  $TP / (TP + FN)$
- F1-score: harmonic mean between precision and recall
  - F1-score =  $\frac{2 * precision * recall}{precision + recall}$
- G-mean: balance between the classification performance on both the majority and minority samples
  - G-mean =  $\sqrt{\frac{TP}{TP + FN} * \frac{TN}{TN + FP}}$
- AUC: area under the receiver operating characteristics curve

# Experiment

- F1-score, G-mean, and AUC values of all the oversampling methods on each numerical imbalanced dataset using **linear-svm**.

Data	Metrics	None	ROS	SMOTE	Safe-SMOTE	MWMO	SMOM	INOS	MDO	RACOG	PAIO	PABIO
pima	F1-score	0.6253	0.6188	0.6638	0.6609	0.6547	<u>0.6639</u>	0.6527	0.641	0.5339	0.6596	<b>0.6667</b>
	G-mean	0.6996	0.7002	<b>0.7384</b>	0.7359	0.731	<u>0.7383</u>	0.7282	0.7193	0.6248	0.7348	0.7070
	AUC	<b>0.8294</b>	0.7676	0.8274	0.8265	0.8202	<u>0.8275</u>	0.8239	0.8264	0.7304	0.8241	0.7500
Ecoli	F1-score	0.6935	0.7388	0.751	0.7478	0.7262	0.7526	0.7427	<u>0.758</u>	0.5998	0.7434	<b>0.7710</b>
	G-mean	0.7724	0.8849	<u>0.8866</u>	0.8778	0.8698	0.8857	0.8811	0.8807	0.7463	0.8855	<b>0.9000</b>
	AUC	<u>0.9392</u>	0.9372	0.9387	0.938	0.9314	<u>0.9392</u>	0.9389	0.9391	0.7929	<b>0.9405</b>	0.9000
vowel	F1-score	0.3106	0.5071	0.5071	0.5066	0.5031	0.5058	<u>0.509</u>	0.4934	0.4937	0.5061	<b>0.5385</b>
	G-mean	0.1805	<u>0.8765</u>	0.8701	0.8646	0.8614	0.8677	0.8677	0.8529	0.8151	0.873	<b>0.9090</b>
	AUC	0.8934	<u>0.9151</u>	0.9127	0.913	0.9116	0.913	0.9124	0.9092	0.8942	0.915	<b>0.9409</b>
Yeast	F1-score	0.2532	0.3282	0.3258	0.3801	0.3183	0.3219	0.3439	<u>0.4334</u>	0.3328	0.3337	<b>0.4715</b>
	G-mean	0.3202	0.8077	0.8029	0.7986	0.8016	0.8002	0.7991	0.75	0.7721	<u>0.8132</u>	<b>0.8320</b>
	AUC	0.7364	0.856	0.8583	0.8597	0.856	<u>0.86</u>	0.8525	0.8588	0.8216	0.8569	<b>0.8920</b>
Abalone	F1-score	NaN	0.1608	0.1614	<u>0.2021</u>	0.1599	0.1643	0.1977	0.1778	0.0855	0.1667	<b>0.2286</b>
	G-mean	0	0.7689	0.766	0.7194	0.7546	0.7607	0.7494	0.712	0.6625	<u>0.7719</u>	<b>0.8035</b>
	AUC	0.6635	0.8764	0.8782	0.8592	0.8645	0.8758	0.8796	0.8701	0.6974	<u>0.8803</u>	<b>0.9006</b>

# Experiment

- F1-score, G-mean, and AUC values of all the oversampling methods on each numerical imbalanced dataset using **C4.5 decision tree**.

Data	Metrics	None	ROS	SMOTE	Safe-SMOTE	MWMO	SMOM	INOS	MDO	RACOG	PAIO	PABIO
pima	F1-score	0.6061	0.6188	0.6378	0.635	0.6396	0.6407	0.6206	0.6397	0.5562	<u>0.6414</u>	<b>0.6968</b>
	G-mean	0.6879	0.7002	0.713	0.7139	<u>0.7166</u>	0.716	0.7021	<b>0.7174</b>	0.6452	0.7157	0.7097
	AUC	0.7619	0.7676	0.7708	<u>0.7728</u>	0.7644	0.7722	0.7632	<b>0.785</b>	0.7071	0.7689	0.7121
Ecoli	F1-score	0.648	0.6432	0.6847	0.6592	0.6698	0.6879	<u>0.694</u>	0.6657	0.5724	0.6725	<b>0.7539</b>
	G-mean	0.7453	0.776	0.8222	0.7925	0.8202	0.8275	<u>0.8286</u>	0.7637	0.7319	0.8239	<b>0.8606</b>
	AUC	0.8745	0.8961	0.9015	0.896	0.8832	<u>0.9052</u>	0.898	0.857	0.8076	0.8952	<b>0.9107</b>
vowel	F1-score	0.7943	0.783	0.7866	0.7934	<u>0.8043</u>	0.794	0.7589	0.7602	0.5113	0.7979	<b>0.8477</b>
	G-mean	0.8681	0.884	0.9061	0.9022	0.901	0.9144	<u>0.9399</u>	0.9333	0.8312	0.9241	<b>0.9763</b>
	AUC	0.9369	0.9487	0.954	0.9541	0.9496	0.9566	<u>0.9687</u>	0.9648	0.9002	0.9615	<b>0.9764</b>
Yeast	F1-score	0.3047	0.3552	0.3345	0.359	0.3142	0.3601	0.387	<u>0.3977</u>	0.3021	0.3637	<b>0.4286</b>
	G-mean	0.4403	0.629	0.6989	0.5956	0.7178	0.7531	0.6949	0.5627	<u>0.8068</u>	0.7296	<b>0.8314</b>
	AUC	0.7504	0.8433	0.833	0.8221	0.8333	0.851	<u>0.8674</u>	0.8125	0.8339	0.8523	<b>0.8926</b>
Abalone	F1-score	0.0769	0.0961	0.1331	0.1154	0.1251	0.1333	0.1253	0.1157	0.0833	<u>0.135</u>	<b>0.1753</b>
	G-mean	0.0045	0.3172	0.5021	0.3054	0.5009	0.5614	0.46	0.0109	<u>0.6508</u>	0.4816	<b>0.7062</b>
	AUC	0.5093	0.7783	0.7832	0.7688	0.7825	<u>0.79</u>	0.7852	0.5742	0.6946	0.787	<b>0.8351</b>

# Experiment

## Summary

- In terms of **F1-score**, our PABIO achieves the best results of all five data sets, either classified by linear SVM or decision tree.
- In terms of **G-mean**, our PABIO outperforms most of the five data sets.
  - Both high precision and recall
- In terms **robustness**:
  - Vowel dataset: no trapped example
    - Our proposed PABIO discovers more dense minority groups, which generates synthetic inland samples safely.
  - Abalone dataset: only has trapped examples
    - Our proposed PABIO learns safe boundary of interpolation, which can expand the minority region effectively and not introduce additional noise points.

# Experiment

## Hyperparameters

- To compare our proposed algorithm with PAIO, we adopt the recommended values of the common parameters in it.
  - The number of nearest neighbors  $m = 8$
  - The density threshold to divide minorities  $\rho Th = 0.5$
  - The number of majority nearest neighbors to generate synthetic borderline samples  $k_{maj} = 0.5$

# Experiment

## Hyperparameters

- Our proposed PABIO oversampling depends on the clustering of minorities, thus the cut-off distance:  $d_c$  of the clustering algorithm is crucial.
  - The value range of  $d_c$  is from 4% to 10%.
- **Findings:** Most of the five datasets have several the same F1-score, as if  $d_c$  falls into an appropriate range, it would result in the same clustering result, further, the same F1-score.

Data \ $d_c$	Pima	Ecoli	Vowel	Yeast	Abalone
4%	<b>0.6667</b>	0.7107	<b>0.5385</b>	<b>0.4715</b>	0.1544
6%	<b>0.6667</b>	<b>0.7710</b>	<b>0.5385</b>	<b>0.4715</b>	0.1851
8%	0.5991	0.6721	0.5008	0.3003	<b>0.2286</b>
10%	0.5991	0.6721	0.5008	0.3003	<b>0.2286</b>

Table. F1-score of Proposed PAIO Classified By Linear-SVM Varying Cut-off Distance.

# Outline

- **Introduction and background**
- **Literatures**
- **Proposed Method**
- **Future Work**



# Future Work

- Integrate proposed oversampling e.g. PABIO **with data cleaning, additional classifiers, or classifier ensembles** etc.
  - The majority class has the main concept of data, may also includes noise examples.
    - Integrate oversampling with the existing under-sampling.
    - Propose cluster-based under-sampling to identify overlapping borderline examples.
- Extend proposed oversampling on **data sets mixed with numerical and categorical variables**.
  - Distance metrics between categorical variables.
  - Interpolate meaningful synthetic categorical variables.
- Evaluate proposed oversampling on biological datasets, which usually have extreme high imbalance ratio, such as 10,000: 1.

# Reference

1. N.V. Chawla, K.W. Bowyer, L. O. Hall, and W. P. Kegelmeyer. SMOTE: synthetic minority over-sampling technique. *J. Artif. Int. Res. (JAIR)*, 16:321–357, 2002.
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Thank you!