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LoRAS: An oversampling approach for imbalanced datasets

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Abstract

The Synthetic Minority Oversampling Technique (SMOTE) is widely-used for the analysis of imbalanced datasets. It is known that SMOTE frequently overgeneralizes the minority class, leading to misclassifications for the majority class, and effecting the overall balance of the model. In this article, we present an approach that overcomes this limitation of SMOTE, employing Localized Random Affine Shadowsampling (LoRAS) to oversample from an approximated data manifold of the minority class. We benchmarked our algorithm with 14 publicly available imbalanced datasets using three different Machine Learning (ML) algorithms and compared the performance of LoRAS, SMOTE and several SMOTE extensions that share the concept of using convex combinations of minority class data points for oversampling with LoRAS. We observed that LoRAS, on average generates better ML models in terms of F1-Score and Balanced accuracy. Another key observation is that while most of the extensions of SMOTE we have tested, improve the F1-Score with respect to SMOTE on an average, they compromise on the Balanced accuracy of a classification model. LoRAS on the contrary, improves both F1 Score and the Balanced accuracy thus produces better classification models. Moreover, to explain the success of the algorithm, we have constructed a mathematical framework to prove that LoRAS oversampling technique provides a better estimate for the mean of the underlying local data distribution of the minority class data space.

Index terms— Imbalanced datasets, Oversampling, Synthetic sample generation, Data augmentation, Manifold learning

1 Introduction

Imbalanced datasets are frequent occurrences in a large spectrum of fields, where Machine Learning (ML) has found its applications, including business, finance and banking as well as bio-medical science. Oversampling approaches are a popular choice to deal

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with imbalanced datasets (Barua et al., 2014, Bunkhumpornpat et al., 2009, Chawla et al., 2002, Haibo et al., 2008, Han et al., 2005). We here present Localized Randomized Affine Shadowsampling (LoRAS), which produces better ML models for imbalanced datasets, compared to state-of-the art oversampling techniques such as SMOTE and several of its extensions. We use computational analyses and a mathematical proof to demonstrate that drawing samples from a locally approximated data manifold of the minority class can produce balanced classification ML models. We validated the approach with 12 publicly available imbalanced datasets, comparing the performances of several state-of-the-art convex-combination based oversampling techniques with LoRAS. The average performance of LoRAS on all these datasets is better than other oversampling techniques that we investigated. In addition, we have constructed a mathematical framework to prove that LoRAS is a more effective oversampling technique since it provides a better estimate for local mean of the underlying data distribution, in some neighbourhood of the minority class data space.

For imbalanced datasets, the number of instances in one (or more) class(es) is very high (or very low) compared to the other class(es). A class having a large number of instances is called a majority class and one having far fewer instances is called a minority class. This makes it difficult to learn from such datasets using standard ML approaches. Oversampling approaches are often used to counter this problem by generating synthetic samples for the minority class to balance the number of data points for each class. SMOTE is a widely used oversampling technique, which has received various extensions since it was published by Chawla et al. (2002). The key idea behind SMOTE is to randomly sample artificial minority class data points along line segments joining the minority class data points among k of the minority class nearest neighbors of some arbitrary minority class data point. In other words, SMOTE produces oversamples by generating random convex combinations of two close enough data points.

The SMOTE algorithm, however has several limitations for example: it does not consider the distribution of minority classes and latent noise in a data set (Hu et al., 2009). It is known that SMOTE frequently over-generalizes the minority class, leading to misclassifications for the majority class, and effecting the overall balance of the model (Puntumapon and Waiyamai, 2012). Several other limitations of SMOTE are mentioned in Blagus and Lusa (2013). To overcome such limitations, several algorithms have been proposed as extensions of SMOTE. Some are focusing on improving the generation of synthetic data by combining SMOTE with other oversampling techniques, including the combination of SMOTE with Tomek-links (Elhassan et al., 2016), particle swarm optimization (Gao et al., 2011, Wang et al., 2014), rough set theory (Ramentol et al., 2012), kernel based approaches (Mathew et al., 2015), Boosting (Chawla et al., 2003), and Bagging (Hanifah et al., 2015). Other approaches choose subsets of the minority class data to generate SMOTE samples or cleverly limit the number of synthetic data generated (Santoso et al., 2017). Some examples are Borderline1/2 SMOTE (Han et al., 2005), ADAPtive SYNthetic (ADASYN) (Haibo et al., 2008), Safe Level SMOTE (Bunkhumpornpat et al., 2009), Majority Weighted Minority Oversampling TEchnique

(MWMOTE) (Barua et al., 2014), Modified SMOTE (MSMOTE), and Support Vector Machine-SMOTE (SVM-SMOTE) (Suh et al., 2017) (see Table 1) (Hu et al., 2009). Another recent method, G-SMOTE, generates synthetic samples in a geometric region of the input space, around each selected minority instance (Douzas and Bacao, 2019). Voronoi diagrams have also been used in recent research for improving classification tasks for imbalanced datasets. Because of properties inherent to Voronoi diagrams, a newly proposed algorithm V-synth identifies exclusive regions of feature space where it is ideal to create synthetic minority samples (Carvalho and Prati, 2018, Young et al., 2015).

Related research and novelty: A more recent trend in the research on imbalanced datasets is to generate synthetic samples, aiming to approximate the latent data manifold of the minority class data space. In Bellinger et al. (2018), a general framework for manifold-based oversampling, especially for high dimensional datasets, is proposed for synthetic oversampling. The method has been successfully applied in Bellinger et al. (2016) to deal with gamma-ray spectra classification. It produces a synthetic set S of n instances in the manifold-space by randomly sampling n instances from the PCA-transformed reduced data space. In order to produce unique samples on the manifold, they apply i.i.d. additive Gaussian noise to each sampled instance prior to adding it to the synthetic set S , controlling the distribution of the noise through the Gaussian distribution parameters. The synthetic Gaussian instances are then mapped back to the feature space to produce the final synthetic samples (Bellinger et al., 2018). Another scheme, using auto-encoders to oversample from an approximated manifold, has also been discussed in Bellinger et al. (2018). This approach selects random minority class samples by adding Gaussian noise to them, and using the auto-encoder framework first maps them non-orthogonally off the manifold and then maps them back orthogonally on the manifold Bellinger et al. (2018). It remains unclear from this research how the approach would perform in terms of improving F1-Scores of imbalanced classification models as it focuses on relative improvement in the Area Under the (ROC) Curve (AUC) as a performance measure. According to Saito and Rehmsmeier (2015), AUC of the Receiver Operating Characteristic Curve (ROC) curve might not be informative enough for imbalanced datasets. This issue has also been addressed in Davis and Goadrich (2006). Unlike the work of Bellinger et al. (2018) LoRAS relies on locally approximating the manifold by generating random convex combination of noisy minority class data points. Our oversampling strategy LoRAS, rather aims at improving the precision-recall balance (F1-Score) and class wise average accuracy (Balanced accuracy) of the ML models used. The F1-Score can measure how well the classification model handled the minority class classification, whereas Balanced accuracy provides us with a measure of how both majority and minority classes were handled by the classification model. Thus, these two measures together can give us a holistic understanding of a classifier performance on a dataset.

Notably, in the pre-SMOTE era of research, related to oversampling there has been works aiming to enrich minority classes of imbalanced datasets by adding Gaussian

noise Lee (2000) and using the noisy data itself, as oversampled data. The strategy of generating oversamples with convex combinations of minority class samples is also well known, SMOTE itself being an example of such a strategy. Our oversampling strategy LoRAS leverages from a combination of these two strategies. Unlike Lee (2000), we generate Gaussian noise in small neighbourhoods around the minority class samples and create our final synthetic data with convex combinations of multiple noisy data points (shadowsamples) as opposed to SMOTE based strategies, that consider combination of only two minority class data points. Adding the shadowsamples allows LoRAS to produce a better estimate for local mean of the latent minority class data distribution.

We also provide a mathematical framework to show that convex combinations of multiple shadowsamples can provide a proper estimate for the local mean of a neighbourhood in the minority class data space. To be specific, an LoRAS oversample is an unbiased estimator of the mean of the underlying local probability distribution, followed by a minority class sample (assuming that it is some random variable) such that the variance of this estimator is significantly less than that of a SMOTE generated oversample, which is also an unbiased estimator of the mean of the underlying local probability distribution, followed by a minority class sample. In addition to this, LoRAS provides an option of choosing the neighbourhood of a minority class data point by performing prior manifold learning over the minority class using t-Stochastic Neighbourhood Embedding (t-SNE) (van der Maaten and Hinton, 2008). t-SNE is a state-of the art algorithm used for dimension reduction maintaining the underlying manifold structure in a sense that, in a lower dimension t-SNE can cluster points, that are close enough in the latent high dimensional manifold. It uses a symmetric version of the cost function used for it’s predecessor technique Stochastic Neighbourhood Embedding (SNE) and uses a Student-t distribution rather than a Gaussian to compute the similarity between two points in the low-dimensional space. t-SNE employs a heavy-tailed distribution in the low-dimensional space to alleviate both the crowding problem and the optimization problems of SNE (Hinton and Roweis, 2003, van der Maaten and Hinton, 2008).

Till date there are at least eighty five extension models built on SMOTE (Kovács, 2019). Considering a large number of benchmark datasets explored in our study, it was necessary to shortlist certain oversampling algorithms for a comparative study. We found quite a few studies that have applied or explored SMOTE and extension of SMOTE such as Borderline1/2 SMOTE models, ADASYN, and SVM-SMOTE (Aditsania et al., 2017, Ah-Pine et al., 2016, Chiamanusorn and Sinapiromsaran, 2017, Le et al., 2019, Suh et al., 2017, Wang et al., 2014). Moreover all these oversampling strategies are focused on oversampling from the convex hull of small neighbourhoods in the minority class data space, a similarity that they share with our proposed approach. Considering these factors, we choose to focus on these five oversampling strategies for a comparative study with our oversampling technique LoRAS.

Table 1: Popular algorithms built on SMOTE.

Extension	Description
-----------	-------------

Borderline1/2 SMOTE (Han et al., 2005)	Identifies borderline samples and applies SMOTE on them
ADASYN (Haibo et al., 2008)	Adaptively changes the weights of different minority samples
SVM-SMOTE (Suh et al., 2017)	Generates new minority samples near borderlines with SVM
Safe-Level-SMOTE (Bunkhumpornpat et al., 2009)	Generates data in areas that are completely safe
MWMOTE (Barua et al., 2014)	Identifies and weighs ambiguous minority class samples

2 LoRAS: Localized Randomized Affine Shadowsampling

In this section we discuss our strategy to approximate the data manifold, given a dataset. A typical dataset for a supervised ML problem consists of a set of *features* $F = \{f_1, f_2, \dots\}$, that are used to characterize patterns in the data and a set of *labels* or ground truth. Ideally, the number of instances or samples should be significantly greater than the number of features. In order to maintain the mathematical rigor of our strategy we propose the following definition for a *small dataset*.

Definition 1. Consider a class or the whole dataset with n samples and $|F|$ features. If $\log_{10}(\frac{n}{|F|}) < 1$, then we call the dataset, a *small dataset*.

The LoRAS algorithm is designed to learn from a dataset by approximating the underlying data manifold. Assuming that F is the best possible set of features to represent the data and all features are equally important, we can think of a data oversampling model to be a function $g : \prod_{i=1}^l R^{|F|} \rightarrow R^{|F|}$, that is, g uses l parent data points (each with $|F|$ features) to produce an oversampled data point in $R^{|F|}$.

Definition 2. We define a random affine combination of some arbitrary vectors as the affine linear combination of those vectors, such that the coefficients of the linear combination are chosen randomly. Formally, a vector v , $v = \alpha_1 u_1 + \dots + \alpha_n u_n$, is a random affine combination of vectors u_1, \dots, u_m , ($u_j \in R^{|F|}$) if $\alpha_1 + \dots + \alpha_m = 1$, $\alpha_j \in R^+$ and $\alpha_1, \dots, \alpha_m$ are the coefficients of the affine combination chosen randomly from a Dirichlet distribution.

The simplest way of augmenting a data point would be to take the average (or random affine combination with positive coefficients as defined in Definition 2) of two data points as an augmented data point. But, when we have $|F|$ features, we can assume that the hypothetical manifold on which our data lies is $|F|$ -dimensional. An $|F|$ -dimensional manifold can be locally approximated by a collection of $(|F|-1)$ -dimensional planes.

Given $|F|$ sample points we could exactly derive the equation of an unique $(|F|-1)$ -dimensional plane containing these $|F|$ sample points. Note that, a small neighbourhood of a dataset can itself be considered as a small dataset. A small neighbourhood of k points around a data point in a dataset, given sufficiently small k , satisfies Definition 1, that is k and $|F|$ satisfies, $\log_{10}(\frac{k}{|F|}) < 1$. Thus, considering k to be sufficiently small we can assume that this small neighbourhood is a small dataset. To enrich this small dataset, we create *shadow data points* or *shadowsamples* from our k parent data points in the minority class data point neighbourhood. Each shadow data point is generated by adding noise from a normal distribution, $\mathcal{N}(0, h(\sigma_f))$ for all features $f \in F$, where

$h(\sigma_f)$ is some function of the sample variance σ_f for the feature f . For each of the k data points we can generate m shadow data points such that, $k \times m \gg |F|$. Now it is possible for us to choose $|F|$ shadow data points from the $k \times m$ shadow data points even if $k < |F|$. We choose $|F|$ shadow data points as follows: we first choose a random parent data point p and then restrict the domain of choice to the shadowsamples generated by the parent data points in N_k^p .

For high dimensional datasets, choosing k-nearest neighbours of data point using simple Euclidean, Manhattan or general Minkowski distance measures can be misleading in terms of approximating the latent data manifold. To avoid this, we propose to adopt a manifold learning based strategy. Before choosing the k-nearest neighbours of a data point, we perform a dimension reduction on the data points of the minority class using the well-known dimension reduction and manifold learning technique t-SNE (van der Maaten and Hinton, 2008). Once we have a two dimensional t-embedding of the minority class data, we choose the k-nearest neighbours of a particular data point consistent to its k-nearest neighbours (measured as per usual distance metrics) in the 2-dimensional t-SNE embedding of the minority class.

Once we choose our neighbourhood and generate the shadowsamples, we take a random affine combination with positive co-efficients (Convex combination) of the $|F|$ chosen shadowsamples to create one augmented Localized Random Affine Shadowsample or a LoRAS sample as defined in Definition 2. Considering the arbitrary low variance that we can choose for the Normal distribution from which we draw our shadowsamples, we assume that our shadowsamples lie in the latent data manifold itself. It is a practical assumption, considering the stochastic factors leading to small measurement errors. Now, there exists an unique $(|F| - 1)$ -dimensional plane, that contains the $|F|$ shadowsamples, which we assume to be an approximation of the latent data manifold in that small neighbourhood. Thus, a LoRAS sample is an artificially generated sample drawn from an $(|F| - 1)$ -dimensional plane, which locally approximates the underlying hypothetical $|F|$ -dimensional data manifold. It is worth mentioning here, that the effective number of features in a dataset is often less than $|F|$. In high dimensional data there are often correlated features or features with low variance. Thus, for practical use of LoRAS one might consider generating convex combinations of effective number of features which might be less than $|F|$.

In this article, all imbalanced classification problems that we deal with are binary classification problems. For such a problem, there is a minority class C_{\min} containing a relatively less number of samples compared to a majority class C_{\max} . We can thus consider the minority class as a small dataset and use the LoRAS algorithm to oversample. For every data point p we can denote a set of shadowsamples generated from p as S_p . In practice, one can also choose $2 \leq N_{\text{aff}} \leq |F|$ shadowsamples for an affine combination and choose a desired number of oversampled points N_{gen} to be generated using the algorithm. We can look at LoRAS as an oversampling algorithm as described in Algorithm 1.

Algorithm 1: Localized Random Affine Shadowsample (LoRAS) Oversampling

Inputs:

C_{maj} : Majority class parent data points
 C_{min} : Minority class parent data points

Parameters:

k : Number of nearest neighbors to be considered per parent data point
 (default value : 30 if $|C_{min}| \geq 100$, 5 otherwise)
 $|S_p|$: Number of generated shadow samples per parent data point
 (default value : $\max\left(\left\lceil \frac{2|F|}{k} \right\rceil, 40\right)$)
 L_σ : List of standard deviations for normal distributions for adding noise to each feature
 (default value : $[0.005, \dots, 0.005]$)
 N_{aff} : Number of shadow points to be chosen for a random affine combination
 (default value : $|F|$)
 N_{gen} : Number of generated LoRAS points for each nearest neighbors group
 (default value : $\frac{|C_{maj}| - |C_{min}|}{|C_{min}|}$)
 $embedding$: Type of Embedding used to choose minority class neighbourhood (regular or t-embedding)
 (default value : 'regular')
 $perplexity$: Perplexity of t-embedding (applicable only if $embedding = \text{'t-embedding'}$)
 (default value : 30)

Constraint:

$$N_{aff} < k * |S_p|$$

Initialize `loras_set` as an empty list

For each minority class parent data point p in C_{min} **do**

$neighborhood \leftarrow$ calculate k -nearest neighbors of p , as per selected **Embedding** parameter and
 append p

 Initialize `neighborhood_shadow_sample` as an empty list

For each parent data point q in $neighborhood$ **do**

$shadow_points \leftarrow$ draw $|S_p|$ shadow samples for q drawing noises from normal
 distributions with corresponding standard deviations L_σ containing elements for every
 feature
 Append $shadow_points$ to `neighborhood_shadow_sample`

Repeat

$selected_points \leftarrow$ select N_{aff} random shadow points from `neighborhood_shadow_sample`
 $affine_weights \leftarrow$ create and normalize random weights for $selected_points$
 $generated_LoRAS_sample_point \leftarrow selected_points \cdot affine_weights$
 Append $generated_LoRAS_sample_point$ to `loras_set`

Until N_{gen} resulting points are created;

Return resulting set of generated LoRAS data points as `loras_set`

The LoRAS algorithm thus described, can be used for oversampling of minority classes in case of highly imbalanced datasets. Note that the input variables for our algorithm are: number of nearest neighbors per sample k , number of generated shadow points per parent data point $|S_p|$, list of standard deviations for normal distributions for adding noise to every feature and thus generating the shadow samples L_σ , number of shadow samples to be chosen for affine combinations N_{aff} , number of generated points for each nearest neighbors group N_{gen} and embedding strategy **embedding**. There is a conditional input variable **perplexity** which takes a positive numerical value if one

chooses a t-embedding. The perplexity parameter of the t-SNE algorithm is quite crucial. The perplexity parameter can influence the t-Embedding calculated by the t-SNE algorithm. There have been several studies that address the issue on finding a right perplexity parameter for a given problem (Kobak and Berens, 2019). That is why, we recommend careful choice of this parameter in order to leverage more from our algorithm. Another important parameter of our algorithm is the N_{aff} . For this parameters an ideal choice would be the number of effective features in a dataset since this number would be a reasonable approximation to the dimension of the underlying data manifold. One could employ a feature selection technique to find out a good estimate for this. A simple random grid search is also very helpful to get reasonably good estimates of these parameters. We have mentioned all the default values of the LoRAS parameters in Algorithm 1, showing the pseudocode for the LoRAS algorithm. As an output, our algorithm generates a LoRAS dataset for the oversampled minority class, which can be subsequently used to train a ML model.

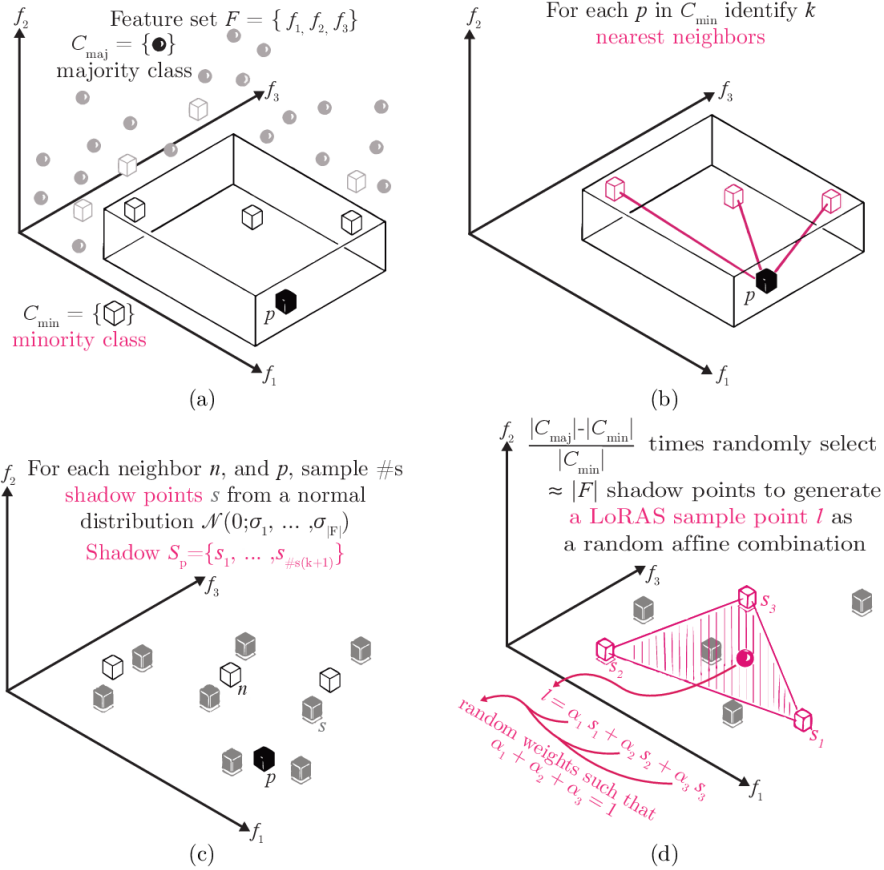


Figure 1: Visualization of the workflow demonstrating a step-by-step explanation for LoRAS oversampling. (a) Here, we show the parent data points of the minority class points C_{min} . For a data point p we choose three of the closest neighbors (using knn) to build a neighborhood of p , depicted as the box. (b) Extracting the four data points in the closest neighborhood of p (including p). (c) Drawing shadow points from a normal distribution, centered at these parent data point n . (d) We randomly choose three shadow points at a time to obtain a random affine combination of them (spanning a triangle). We finally generate a novel LoRAS sample point from the neighborhood of a single data point p .

3 Case studies

For testing the potential of LoRAS as an oversampling approach, we designed benchmarking experiments with a total of 14 datasets which are either highly imbalanced, high dimensional or with a small number of data points. With this number of diverse case studies we should have a comprehensive idea of the advantages of LoRAS over the other oversampling algorithms of our interest.

3.1 Datasets used for validation

Here we provide a brief description of the datasets and the sources that we have used for our studies.

Scikit-learn imbalanced benchmark datasets: The `imblearn.datasets` package is complementing the `sklearn.datasets` package. It provides 27 pre-processed datasets, which are imbalanced. The datasets span a large range of real-world problems from several fields such as business, computer science, biology, medicine, and technology. This collection of datasets was proposed in the `imblearn.datasets` python library by Lemaître et al. (2017) and benchmarked by Ding (2011). Many of these datasets have been used in various research articles on oversampling approaches (Ding, 2011, Saez et al., 2016). A statistically reliable benchmarking analysis of all 27 datasets in a stratified cross validation framework involves a lot of computational effort. We thus choose 11 datasets out of these two depending on two criteria:

- **Highly imbalanced:** We choose datasets with imbalance ratio more than 25:1. This category includes `abalone_19`, `letter_image`, `mammography`, `ozone_level`, `webpage`, `wine_quality`, `yeast_me2` datasets.
- **High dimensional:** We choose the datasets with more than 100 features. This category includes `arrhythmia`, `isolet`, `scene`, `webpage` and `yeast_ml8`.

Note that the `webpage` dataset is common in both the criteria, giving us a total of 11 datasets. We choose these two categories because they are of special interest in research related to imbalanced datasets and have received extensive attention in this research area (Anand et al., 2010, Blagus and Lusa, 2013, Hooda et al., 2018, Jing et al., 2019).

Credit card fraud detection dataset: We obtain the description of this dataset from the website. <https://www.kaggle.com/mlg-ulb/creditcardfraud>. “The dataset contains transactions made by credit cards in September 2013 by European cardholders. This dataset presents transactions that occurred in two days, where there are 492 frauds out of 284,807 transactions. The dataset is highly unbalanced, the positive class (frauds) account for 0.00172 percent of all transactions. The dataset contains only numerical input variables, which are the result of a PCA transformation. Feature variables f_1, \dots, f_{28} are the principal components obtained with PCA, the only features that have not been transformed with PCA are the ‘Time’ and ‘Amount’. The feature ‘Time’ contains the seconds elapsed between each transaction and the first transaction in the dataset. The feature ‘Amount’ consists of the transaction amount. The labels are encoded in the

‘Class’ variable, which is the response variable and takes value 1 in case of fraud and 0 otherwise” (Dal Pozzolo et al., 2017).

Small datasets: We were also interested to check the performance of LoRAS on small datasets. We obtained two such datasets: ar1, ar3. Both of these datasets have very few data points and less than 10 points in the minority class.

Thus, in total we benchmark our oversampling algorithms against the existing algorithms on a total of 14 datasets. We provide relevant statistics on these datasets in Table 2

Dataset	Imbalance ratio	Number of samples	Number of features
abalone_19	130:1	4177	10
arrythmia	17:1	452	278
isolet	12:1	7797	617
letter-img	26:1	20000	16
mammography	42:1	11183	6
scene	13:1	2407	294
ozone_level	34:1	2536	72
webpage	33:1	34780	300
wine-quality	26:1	4898	11
yeast-me2	28:1	1484	8
yeast-ml8	13:1	2417	103
credit fraud	577:1	284807	28
ar1	12.44:1	121	30
ar3	6.8:1	63	30

Table 2: Table showing some statistics for the datasets we study in this article. For each dataset, we mark in bold the feature of the dataset that led us to its choice for our study.

3.2 Methodology

For every dataset we have analyzed, we used a consistent workflow. Given a dataset, for every machine learning model, we judge the model performances based on a 5×10 -fold stratified cross validation framework. However, for the two small datasets ar1 and ar3 we use a 5×3 -fold stratified cross validation framework, since there are less than 10 samples in the minority class. First we randomly scuffle the dataset. For a given dataset, we first split the dataset into 10 folds, each one distinct from the other maintaining the imbalance ratio for every fold. We then train the machine learning models on the dataset without any oversampling with 10-fold cross validation. This means that we train and test the model 10 times, each time considering a fold as a test fold and rest 9 folds as training folds. However, while training the ML models with oversampled data, we oversample only on the training folds and leave the test fold as they are for each training session. For each dataset we repeat the whole process five times to avoid the stochastic effects as much as possible.

For the oversampling algorithms, for a given dataset, we chose the same neighbourhood size for every oversampling model. If there were less than 100 data points in the minority class the neighbourhood size was chosen to be 5. Otherwise we chose a neighbourhood

size of 30. Given a large number of datasets we are analyzing, we did not customize this for every dataset and rather chose to stick to the above mentioned general rule. For LoRAS oversampling however, we performed a preliminary study to find out customized parameter values for every dataset, since the LoRAS algorithm is highly parametrized in nature. We tried several combinations of parameters N_{aff} , **embedding** and **perplexity** employing random grid search. For our initial study involving the parameter optimization of LoRAS, given a dataset, we performed a simple train-test split of the dataset (1:1 train-test split ratio), and then applied LoRAS with parameter grids on the training data to oversample and test the classifier performances on the test data. The training set is kept relatively small, so that the classifier does not gain much experience on the data while parameter estimation and gets prone to overfitting. This study was kept completely independent from our main cross-validation based results so that the samples from the test sets of our cross validation have minimum effect on parameter tuning. For parameter N_{aff} the grid interval is $[2, |F|]$, $|F|$ being the number of features. We choose five numbers while forming a search grid from this interval. Three of them are randomly chosen and the numbers 2 and $|F|$ are always included in this set of 5 numbers. For parameter **embedding** we the grid values are the two possible entries that the parameter adopts. For the **perplexity** parameter, we used grid values $[0.01, 0.1, 1, 10, 30, 100]$.

We emphasize here, that for all the algorithms including LoRAS, for a given dataset, we keep the neighbourhood size for every oversampling model fixed. For every oversampling model that we considered, the neighbourhood size for the oversampling model is the parameter that the model is highly sensitive to, since it contributes the most in determining the distribution of the oversampled minority class. For LoRAS, there are three (out of seven parameters in total) parameters designed to better model/approximate the minority class data manifold (for example: the ones involving the t-SNE on the minority class), which are tuned to show the applicability of manifold approximation to improve convex combination based oversampling. However, as suggested, we keep all parameters related to the original distribution of the minority class, for all oversampling models fixed for all comparisons.

However, considering the philosophy of LoRAS and a comparatively large number of parameters it use, we take liberty to tune the other parameters for LoRAS, since the other parameters are the key to a proper approximation or modelling of the minority class data manifold, which we argue to be the key factor behind the success of LoRAS.

For LoRAS oversampling every dataset we use an unique value for N_{aff} as presented in Table 3. For individual ML models we use different settings for the LoRAS parameters **embedding** and **perplexity** which we mention explicitly in our supplementary materials while presenting the results for each ML model for each dataset. To ensure fairness of comparison, we oversampled such that the total number of augmented samples generated from the minority class was as close as possible to the number of samples in the majority class as allowed by each oversampling algorithm. Speaking of other parameters of the LoRAS algorithm, for L_{σ} , we chose a list consisting of a constant value of .005 for each

dataset and for the parameter N_{gen} we chose the value as: $\frac{|C_{\text{maj}}| - |C_{\text{min}}|}{|C_{\text{min}}|}$. We provide a detailed list of parameter settings used by us for the oversampling algorithms in Table 3

Table 3: In this table we present the details of parameter settings for the oversampling algorithms used by us for our experiment. The second column is the size of the oversampling neighbourhood and we have chosen the same size for all the oversampling models for each dataset in our analysis. The last three columns are specific to LoRAS parameters.

Dataset	Minority samples	Oversampling nbd	LoRAS N_{aff}
abalone19	32	5	10
arrythmia	25	5	100
isolet	600	30	179
letter-img	734	30	16
mammography	260	30	6
scene	177	30	2
ozone_level	73	5	10
webpage	981	30	94
wine-quality	183	30	2
yeast-me2	51	5	2
yeast-ml8	178	30	3
credit fraud	492	30	30
ar1	9	3	30
ar3	8	3	10

To choose ML models for our study we first did a pilot study with ML classifiers such as k-nearest neighbors (knn), Support Vector Machine (svm) (linear kernel), Logistic regression (lr), Random forest (rf), and Adaboost (ab). As inferred in (Blagus and Lusa, 2013) we found that knn was quite effective for the datasets we used. We also noticed that lr and svm performed better compared to rf and ab in most cases. We thus chose knn, svm and lr for our final studies. We used lbfgs solver for our logistic regression model and a linear kernel for our svm models. For our knn models, we choose 10 nearest neighbours for our prediction if there are less than 100 samples in the minority class and 30 nearest neighbours otherwise. For ‘arrythmia’, ‘abalone-19’, ‘ar1’ and ‘ar3’ however we use only 5 nearest neighbours for the knn model since it has only 25, 32, 9 and 8 minority class samples respectively. We choose this parameter to be consistent to the neighbourhood size of the oversampling models, since the neighbourhood size directly influences the distribution of the training data and hence the model performance.

In our analysis we take special notice of the credit card fraud detection dataset. This dataset is not included in the `imblearn.datasets` Python library. However, the main reason why we want to pay a special attention to this dataset is that, it is by far the most imbalanced publicly available dataset that we have come across. The extreme imbalance ratio of 577:1 is incomparable to any of the datasets in `imblearn.datasets`. Also, this dataset has received special attention of researchers attempting to use ML in Credit fraud detection (Varmedja et al., 2019). In this article we see that lr and rf have good prediction accuracies on the dataset. Thus we chose these two ML models for the credit

fraud dataset. Varmedja et al. (2019) has also not provided cross validated analysis of their models, while our models have been trained and tested with the usual 10-fold cross validation framework as discussed before. Also, for two small datasets with a critically small minority class, we used only knn and lr classifiers, with parameter settings as specified before. The reason is, for all the 12 other datasets, svm did not stand out to be the best performer in terms of F1-Score in any of them.

For computational coding, we used the `scikit-learn` (V 0.21.2), `numpy` (V 1.16.4), `pandas` (V 0.24.2), and `matplotlib` (V 3.1.0) libraries in Python (V 3.7.4).

4 Results

For imbalanced datasets there are more meaningful performance measures than *Accuracy*, including *Sensitivity* or *Recall*, *Precision*, and *F1-Score* (*F-Measure*), and *Balanced accuracy* that can all be derived from the *Confusion Matrix*, generated while testing the model. For a given class, the different combinations of recall and precision have the following meanings:

- High Precision & High Recall: The model handled the classification task properly
- High Precision & Low Recall: The model cannot classify the data points of the particular class properly, but is highly reliable when it does so
- Low Precision & High Recall: The model classifies the data points of the particular class well, but misclassifies high number of data points from other classes as the class in consideration
- Low Precision & Low Recall: The model handled the classification task poorly

F1-Score, calculated as the harmonic mean of precision and recall and, therefore, balances a model in terms of precision and recall. These measures have been defined and discussed thoroughly by M. Abd Elrahman and Abraham (2013). Balanced accuracy is the mean of the individual class accuracies and in this context, it is more informative than the usual accuracy score. High Balanced accuracy ensures that the ML algorithm learns adequately for each individual class.

In our experiments we have noticed an interesting behaviour of oversampling models in terms of their average F1-Score and Balanced accuracy. Once we present our experiment results, we will discuss why considering F1-Score and Balanced accuracy can give us a clearer idea about model performances. We will use the above mentioned performance measures wherever applicable in this article.

Selected model performances for all datasets: We provide the detailed results of our experiments for all machine learning models as supplementary material. To be precise, for every combination of datasets, ML models and oversampling strategies we provide the mean and variance of the 10-fold cross validation process over 5 repetitions.

For judging the performance of the oversampling models we follow the following scheme:

- First, for a given dataset, we choose the ML model trained on that dataset that provides the highest average F1-Score over all the oversampling models and training without oversampling. The F1-Score reflects the balance between precision and recall and considered as a reliable metric for imbalanced classification task.
- We then consider the Balanced accuracy and F1- score of the chosen model as an evaluation of how well the oversampling model performs on the considered dataset. Following this evaluation scheme we present our results in Table 4.

Table 4: Table showing Balanced accuracy/F1-Score for several oversampling strategies (Baseline, SMOTE, SVM-SMOTE, Borderline1 SMOTE, Borderline2 SMOTE, ADASYN and LoRAS column-wise respectively) for all 14 datasets of interest for ML learning models producing best average F1 score over all oversampling strategies and baseline training for respective datasets.

Dataset	ML	Baseline	SMOTE	Bl-1	Bl-2	SVM	ADASYN	LoRAS
abalone19	knn	.534/.000	.644/.054	.552/.044	.552/.044	.556/.045	.571/.055	.675/.059
arrythmia	lr	.679/.37	.666/.345	.672/.352	.709/.307	.679/.350	.667/.362	.694/. 380
isolet	lr	.900/. .826	.898/.806	.899/.802	.906/.693	.911/.799	.898/.806	.904/.809
letter-img	knn	.927/. .915	.988/.781	.984/.768	.977/.687	.986/.724	.985/.732	.989/.833
mammography	knn	.703/. .549	.911/.413	.909/.414	.899/.326	.909/.467	.905/.353	.896/.511
scene	lr	.551/.168	.616/.222	.619/.230	.620/.223	.616/. .235	.620/.224	.616/.226
ozone_level	lr	.517/.062	.800/.190	.777/.212	.781/.183	.738/. .215	.803/.192	.809/.207
webpage	knn	.805/. .711	.906/.267	.901/.274	.903/.287	.904/.267	.903/.264	.923/.613
wine-quality	lr	.517/.067	.718/.179	.715/.182	.711/.171	.712/. .216	.721/.180	.734/.197
yeast-ml8	knn	.500/.000	.558/.152	.561/.153	.563/.153	.572/.158	.558/.151	.559/.152
yeast-me2	knn	.523/.074	.834/.331	.797/.373	.79/.304	.785/. .388	.825/.315	.842/.354
credit fraud	rf	.669/.775	.922/.359	.919/.645	.919/.556	.913/.741	.923/.350	.904/. .820
ar1	knn	.340/.071	.561/.306	.549/.298	.594/.338	.550/.324	.583/.320	.563/. .349
ar3	rf	.634/.259	.810/.531	.809/. .584	.819/.582	.755/.479	.781/.457	.823/.563
Average	-	.636/.338	.775/.352	.764/.380	.771/.346	.759/.386	.777/.340	.783/.433
Average rank	-	6.53/4.64	3.57/4.75	4.35/3.46	3.39/5.10	4.07/3.17	3.5/4.71	2.57/2.14

Calculating average performances over all datasets, LoRAS has the best Balanced accuracy and F1-Score. As expected, SMOTE improved Balanced accuracy compared to model training without any oversampling. Surprisingly, it lags behind in F1-Score, for quite a few datasets with high baseline F1-Score such as letter_image, isolet, mammography, webpage and credit fraud. Interestingly, the oversampling approaches SVM-SMOTE and Borderline1 SMOTE also improved the average F1-Score compared to SMOTE, but compromised for a lower Balanced accuracy. On the other hand, applying ADASYN increased the Balanced accuracy compared to SMOTE, but again compromises on the F1-Score. In contrast, our LoRAS approach produces the best Balanced accuracy on average by maintaining the highest average F1-Score among all oversampling techniques. We want to emphasize that, even considering stochastic factors, LoRAS can improve both the Balanced accuracy and F1-Score of ML models significantly compared to SMOTE, which makes it unique.

Datasets with high imbalance ratio: To verify the performance of LoRAS on highly imbalanced datasets we present average of the selected model performances for the datasets with highest imbalance ratios (among the ones we have tested) in Table 5.

Table 5: Table showing the average Balanced accuracy/F1-Score of the selected models for datasets with the highest imbalance ratios and high dimensional datasets separately

Average	Baseline	SMOTE	BI-1	BI-2	SVM	ADASYN	LoRAS
Highly imbalanced datasets	.662/.381	.840/.321	.819/.364	.817/.319	.814/.382	.841/.305	.846/.449
High dimensional datasets	.687/.415	.728/.358	.730/.362	.740/.332	.736/.361	.729/.361	.739/ .436

From our results we observe that LoRAS oversampling can significantly improve model performances for highly imbalanced datasets. LoRAS provides the highest F1-Score and Balanced accuracy among all the oversampling models. The results here show similar properties for SMOTE, Borderline-1 SMOTE, SVM SMOTE, ADASYN and LoRAS as discussed before. Note that, for the credit fraud dataset, which is the most imbalanced among all, LoRAS has significant success over the other oversampling models in terms of Balanced accuracy. For the webpage dataset as well it improves the Balanced accuracy significantly, compromising minimally on the baseline F1-Score. The same trend follows for the letter_image dataset. Notably, these three datasets have the highest number of overall samples as well, implying that with more data LoRAS can significantly outperform compared convex combination based oversampling models.

High dimensional datasets: It is also of interest to us to check how LoRAS performs on high dimensional datasets. We therefore select five datasets with highest number of features among our tested datasets and present the performances of the selected ML methods in Table 5. From our results for high dimensional datasets, we observe that LoRAS produces the best F1-Score and second best Balanced accuracy on average among all oversampling models as Borderline-2 SMOTE beats LoRAS marginally. SMOTE improves both Balanced accuracy with respect to the baseline score here. Borderline-1 SMOTE and SVM SMOTE further increases SMOTE’s performance both in terms of F1-Score and Balanced accuracy. Borderline-2 SMOTE, although improves the Balanced accuracy of SMOTE compromises on the F1-Score. Note that, even excluding the webpage dataset, where LoRAS has an overwhelming success, LoRAS still has the best average F1-Score and third highest Balanced accuracy marginally behind SVM-SMOTE and Borderline-2 SMOTE. We thus conclude, that for high dimensional datasets LoRAS can outperform the compared oversampling models in terms of F1-Score, while compromising marginally for Balanced accuracy.

Small datasets: For the two small datasets (with less than 10 samples in minority class) we have explored, we observed that LoRAS performs reasonably well. For the ‘ar1’, LoRAS produces the best F1-Score and third best Balanced accuracy. For the ‘ar2’ dataset LoRAS produces the best Balanced accuracy and the third best F1-Score. Note that LoRAS performs quite well for the ‘abalone’ and ‘arrhythmia’ datasets, which also have a small number of data points in the minority class.

Statistical Analysis: Following Tarawneh et al. (2020), we use the Wilcoxon’s signed rank test to compare LoRAS against the other convex-combination based oversampling algorithms, in terms of both the performance measures we have used: F1-Score and Balanced accuracy. Tarawneh et al. (2020) chose this test for comparative studies since it is safer than parametric tests as it refrains from assuming homogeneity or normal distribution of data. Therefore, it can be applied to any classifier evaluation measure. Tarawneh et al. (2020) further confirms: ‘The Wilcoxon test aims to find if a null hypothesis is true or not. The null hypothesis H_0 assumes that there is no significant difference between the classification results (observations) obtained from two different methods. We assume that the null hypothesis is rejected if the p-value of the Wilcoxon test is less than $\alpha = 0.05$ ’(Tarawneh et al., 2020).

Table 6: Table showing p-values for comparison of LoRAS against the other oversampling algorithms, in terms of both the performance measures we have used: F1-Score and Balanced accuracy.

Measure	Baseline	SMOTE	BI-1	BI-2	SVM	ADASYN
F1-Score	0.0303	0.0009	0.0479	.0035	0.0479	0.0009
Balanced accuracy	0.0009	0.0354	0.0258	0.5095	0.0382	0.1670

From Table 6 we observe that the p-values for all the paired tests are less than 0.05 for the F1-Score, and therefore, the H_0 is rejected for all the paired tests in case of the F1-Score. Thus, the F1-Scores LoRAS produce have a big enough difference compared to the other compared algorithms, to be statistically significant. For Balanced accuracy, the algorithms Borderline-2 SMOTE and ADASYN do not show significant statistical difference to LoRAS. However, since F1-Score is a more reliable and widely used metric for imbalanced datasets, we conclude that overall results generated by LoRAS are significantly different from the compared oversampling algorithms.

Tarawneh et al. (2020) also remarks that the p-value alone is informative enough and does not provide information about the relationship strength between variables. The p-values do not reveal whether the results are significantly different in favour of LoRAS or against LoRAS. For that following Tarawneh et al. (2020) we use the metrics W_+ , W_- and R . These are calculated using the following stpng:

- For each data pair (involving LoRAS and some other oversampling algorithm) of model predictions , the difference between both predictions is calculated and stored in a vector D , excluding the zero difference values.
- The signs of the difference is recorded in a sign vector S .
- The entries in $|D|$ are ranked, forming a vector R' . In case of tied ranks, an average ranking scheme is adopted. This means, after ranking the entries of $|D|$ are ranked using integers and then, in case of tied entries the average of the integer ranks are considered as the average rank for all the respective tied entries with a specific tied value.

- Component-wise product of S and R' provides us with the vector W , the vector of the signed ranks. The sum of absolute values of the positive entries in W is W_+ and the sum of absolute values of the negative entries in W is W_- . After this we define, $W_R = \min\{W_+, W_-\}$
- Then the test statistic Z is calculated by the equation

$$Z = \frac{W_R - \frac{n(n+1)}{4}}{\sqrt{\frac{n(n+1)(2n+1)}{24} - \frac{\sum t^3 - \sum t}{48}}} \quad (1)$$

where n is the number of components in D and t is the number of times some i -th entry occurs in R' , summed over all such repeated instances.

- Finally R is calculated using $R = \frac{|Z|}{\sqrt{N}}$, where N is the total number of datasets compared, which is 14 in our case.

Note that a higher value W_+ for LoRAS indicates towards a superior performance of LoRAS and the value of R indicates towards how superior(with a higher W_+)/ inferior(with a higher W_-) the performance of LoRAS is, compared to the other oversampling model for the tested datasets. Tarawneh et al. (2020) have considered ranges of $R \leq 0.1$, $0.1 < R \leq 0.5$ and $R > 0.5$ to be indicators for small, medium and high degree of change (improvement or deterioration) in the predictive performance respectively.

Table 7: Table showing $W_+/W_- /R$ for comparison of LoRAS against the other oversampling algorithms, in terms of both the performance measures we have used: F1-Score and Balanced accuracy.

Measure	Baseline	SMOTE	Bl-1	Bl-2	SVM	ADASYN
F1-Score	95/10/.713	105/0/.880	90/15/.629	102/3/.830	80/15/.629	105/0/.880
Balanced accuracy	105/0/.880	102/3/.830	95/10/.715	69/36/.286	95/10/.722	95/10/.837

From Table 7 we note that, LoRAS has a higher W_+ value for both F1 Score and Balanced accuracy in comparison to each of the other convex combination based oversampling methods in consideration. Moreover for the F1 Score measure, the R value is also more than 0.5, indicating a high degree of improvement in F1-Score for LoRAS, over the considered oversampling models. Similarly, for Balanced accuracy, we find high degree of improvement for LoRAS, over all considered oversampling models except the Borderline-2 SMOTE, for which there is a medium degree of improvement. Overall, we thus conclude that LoRAS provides a significant improvement in performance over the compared convex combination based oversampling methods.

5 Discussion

We have constructed a mathematical framework to prove that LoRAS is a more effective oversampling technique since it provides a better estimate for the mean of the underlying local data distribution of the minority class data space. Let $X = (X_1, \dots, X_{|F|}) \in C_{\min}$ be an arbitrary minority class sample. Let N_k^X be the set of the k -nearest neighbors

of X , which will consider the neighborhood of X . Both SMOTE and LoRAS focus on generating augmented samples within the neighborhood N_k^X at a time. We assume that a random variable $X \in N_k^X$ follows a shifted t-distribution with k degrees of freedom, location parameter μ , and scaling parameter σ . Note that here σ is not referring to the standard deviation but sets the overall scaling of the distribution (Jackman, 2009), which we choose to be the sample variance in the neighborhood of X . A shifted t-distribution is used to estimate population parameters, if there are less number of samples (usually, ≤ 30) and/or the population variance is unknown. Since in SMOTE or LoRAS we generate samples from a small neighborhood, we can argue in favour of our assumption that locally, a minority class sample X as a random variable, follows a t-distribution. Following Blagus and Lusa (2013), we assume that if $X, X' \in N_k^X$ then X and X' are independent. For $X, X' \in N_k^X$, we also assume:

$$\begin{aligned}
\mathbf{E}[X] &= \mathbf{E}[X'] \\
&= \mu = (\mu_1, \dots, \mu_{|F|}) \\
\text{Var}[X] &= \text{Var}[X'] \\
&= \sigma^2 \left(\frac{k}{k-2} \right) \\
&= \sigma'^2 = (\sigma_1'^2, \dots, \sigma_{|F|}'^2)
\end{aligned} \tag{2}$$

where, $\mathbf{E}[X]$ and $\text{Var}[X]$ denote the expectation and variance of the random variable X respectively. However, the mean has to be estimated by an estimator statistic (i.e. a function of the samples). Both SMOTE and LoRAS can be considered as an estimator statistic for the mean of the t-distribution that $X \in C_{\min}$ follows locally.

Theorem 1. *Both SMOTE and LoRAS are unbiased estimators of the mean μ of the t-distribution that X follows locally. However, the variance of the LoRAS estimator is less than the variance of SMOTE given that $|F| > 2$.*

Proof. A shadow sample S is a random variable $S = X + B$ where $X \in N_k^X$, the neighborhood of some arbitrary $X \in C_{\min}$ and B follows $\mathcal{N}(0, \sigma_B)$.

$$\begin{aligned}
\mathbf{E}[S] &= \mathbf{E}[X] + \mathbf{E}[B] \\
&= \mu \\
\text{Var}[S] &= \text{Var}[X] + \text{Var}[B] \\
&= \sigma'^2 + \sigma_B^2
\end{aligned} \tag{3}$$

assuming S and B are independent. Now, a LoRAS sample $L = \alpha_1 S^1 + \dots + \alpha_{|F|} S^{|F|}$, where $S^1, \dots, S^{|F|}$ are shadow samples generated from the elements of the neighborhood of X , N_k^X , such that $\alpha_1 + \dots + \alpha_{|F|} = 1$. The affine combination coefficients $\alpha_1, \dots, \alpha_{|F|}$ follow a Dirichlet distribution with all concentration parameters assuming equal values

of 1 (assuming all features to be equally important). For arbitrary $i, j \in \{1, \dots, |F|\}$,

$$\begin{aligned}\mathbf{E}[\alpha_i] &= \frac{1}{|F|} \\ \text{Var}[\alpha_i] &= \frac{|F| - 1}{|F|^2(|F| + 1)} \\ \text{Cov}(\alpha_i, \alpha_j) &= \frac{-1}{|F|^2(|F| + 1)}\end{aligned}$$

where $\text{Cov}(A, B)$ denotes the covariance of two random variables A and B . Assuming α and S to be independent,

$$\mathbf{E}[L] = \mathbf{E}[\alpha_1]\mathbf{E}[S^1] + \dots + \mathbf{E}[\alpha_{|F|}]\mathbf{E}[S^{|F|}] = \mu \quad (4)$$

Thus L is an unbiased estimator of μ . For $j, k, l \in \{1, \dots, |F|\}$,

$$\begin{aligned}\text{Cov}[\alpha_k S_j^k, \alpha_l S_j^l] &= \mathbf{E}[\alpha_k S_j^k \alpha_l S_j^l] - \mathbf{E}[\alpha_k S_j^k] \mathbf{E}[\alpha_l S_j^l] \\ &= \mathbf{E}[\alpha_k \alpha_l] \mu_j^2 - \frac{\mu_j^2}{|F|^2} \\ &= \left[\text{Cov}(\alpha_k, \alpha_l) + \frac{1}{|F|^2} \right] \mu_j^2 - \frac{\mu_j^2}{|F|^2} = \mu_j^2 \text{Cov}(\alpha_k, \alpha_l)\end{aligned} \quad (5)$$

since $\alpha_k \alpha_l$ is independent of $S_j^k S_j^l$. For an arbitrary j , j -th component of a LoRAS sample L_j

$$\begin{aligned}\text{Var}(L_j) &= \text{Var}(\alpha_1 S_j^1 + \dots + \alpha_{|F|} S_j^{|F|}) \\ &= \text{Var}(\alpha_1 S_j^1) + \dots + \text{Var}(\alpha_{|F|} S_j^{|F|}) + \sum_{k=1}^{|F|} \sum_{l=1, l \neq k}^{|F|} \text{Cov}(\alpha_k S_j^k, \alpha_l S_j^l) \\ &= \frac{\mu_j^2(|F| - 1) + 2(\sigma_j'^2 + \sigma_{Bj}^2)|F|}{|F|(|F| + 1)} - \frac{\mu_j^2(|F| - 1)}{|F|(|F| + 1)} \\ &= \frac{2(\sigma_j'^2 + \sigma_{Bj}^2)}{(|F| + 1)}\end{aligned} \quad (6)$$

For LoRAS, we take an affine combination of $|F|$ shadowsamples and SMOTE considers an affine combination of two minority class samples. Note, that since a SMOTE generated oversample can be interpreted as a random affine combination of two minority class samples, we can consider, $|F| = 2$ for SMOTE, independent of the number of features. Also, from Equation 4, this implies that SMOTE is an unbiased estimator of the mean of the local data distribution. Thus, the variance of a SMOTE generated sample as an estimator of μ would be $\frac{2\sigma'^2}{3}$ (since $B = 0$ for SMOTE). But for LoRAS as an estimator of μ , when $|F| > 2$, the variance would be less than that of SMOTE. \square

This implies that, locally, LoRAS can estimate the mean of the underlying t-distribution better than SMOTE. To visualize the key aspects of LoRAS oversampling, we provide the PCA plots for oversampled data from the ozone_level dataset several oversampling methods we have studied in Figure 2. From Figure 2 we can observe that SMOTE and ADASYN oversamples highly on the neighbourhood of the outliers, depicted by a blue box in each subplot. While this is somewhat controlled in Borderline1-SMOTE and

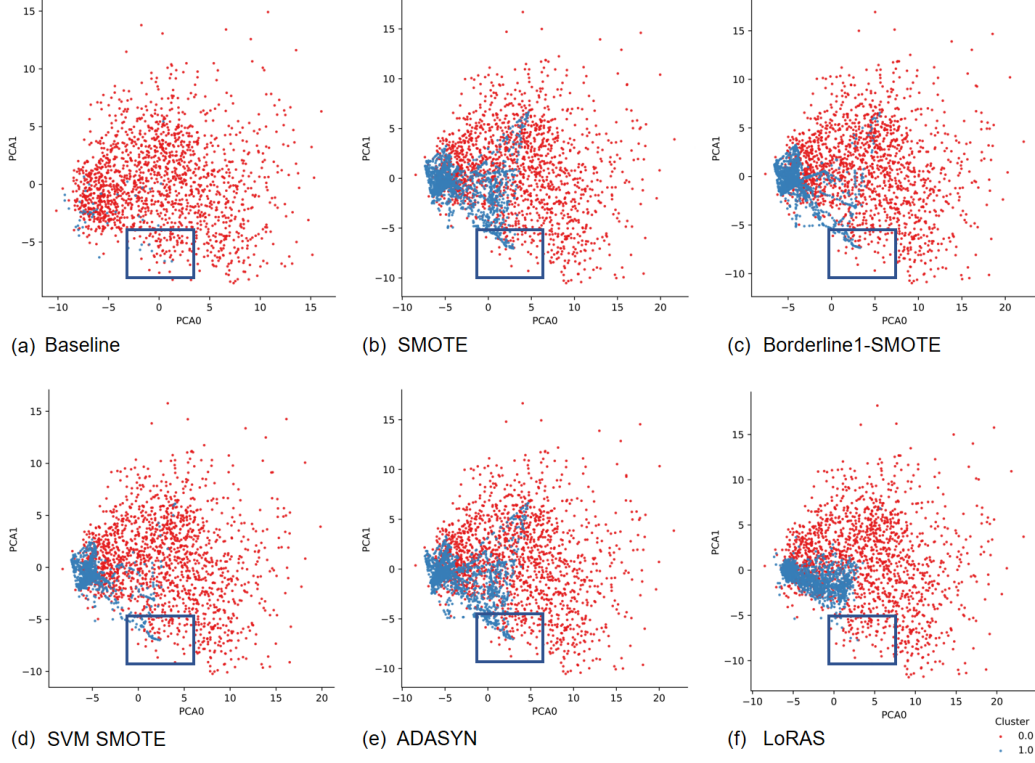


Figure 2: Figure showing for Principal Component Analysis plot of ozone dataset for baseline data and oversampled data with several oversampling strategies for the ozone_level dataset. The boxed region in each subplot shows a neighbourhood of outliers and how each oversampling strategy generates synthetic samples in that neighbourhood.

SVM SMOTE, they still generate some synthetic samples in this neighbourhood. LoRAS on the other hand refrains, leveraging on its strategy to produce a better estimate for local mean of the underlying local data distribution. This enables LoRAS to ignore the outliers and to oversample more uniformly resulting in a better approximation of the data manifold. Note that, the average F1-Scores of the oversampling models as presented in Table 4 has a direct correlation to how the oversampling strategy oversamples in this neighbourhood. SMOTE and ADASYN generates the lowest F1-Scores and show a tendency of oversampling excessively from this neighbourhood. Borderline-SMOTE and SVM improves the F1-Score compared to SMOTE and ADASYN, again, consistent to their behaviour of oversampling lesser in this neighbourhood. LoRAS, has the highest average F1-Score and oversampling very sparsely from this neighbourhood.

6 Conclusions

Oversampling with LoRAS produces comparatively balanced ML model performances on average, in terms of Balanced Accuracy and F1-Score among the compared convex-combination strategy based oversampling techniques. This is due to the fact that, in most cases LoRAS produces lesser mis-classifications on the majority class with a reasonably small compromise for mis-classifications on the minority class. From our study

we infer that for tabular high dimensional and highly imbalanced datasets our LoRAS oversampling approach can better estimate the mean of the underlying local distribution for a minority class sample (considering it a random variable) and can improve Balanced accuracy and F1-Score of ML classification models. However, the scope of such convex combination based strategies including LoRAS, might be limited for heterogeneous image based imbalanced datasets.

The distribution of both the minority and majority class data points is considered in the oversampling techniques such as Borderline1 SMOTE, Borderline2 SMOTE, SVM-SMOTE, and ADASYN (Gosain and Sardana, 2017). SMOTE and LoRAS are the only two techniques, among the oversampling techniques we explored, that deal with the problem of imbalance just by generating new data points, independent of the distribution of the majority class data points. Thus, comparing LoRAS and SMOTE gives a fair impression about the performance of our novel LoRAS algorithm as an oversampling technique, without considering any aspect of the distributions of the minority and majority class data points and relying just on resampling. Other extensions of SMOTE such as Borderline1 SMOTE, Borderline2 SMOTE, SVM-SMOTE, and ADASYN can also be built on the principle of LoRAS oversampling strategy. According to our analyses LoRAS already reveals great potential on a broad variety of applications and evolves as a true alternative to SMOTE, while processing highly unbalanced datasets.

Availability of code: A preliminary implementation of the algorithm in Python (V 3.7.4) and an example Jupyter Notebook for the credit card fraud detection dataset is provided on the GitHub repository <https://github.com/sbi-rostock/LoRAS>. This version does not yet include the t -embedding parameter. In our computational code, $|S_p|$ corresponds to `num_shadow_points`, L_σ corresponds to `list_sigma_f`, N_{aff} corresponds to `num_aff_comb`, N_{gen} corresponds to `num_generated_points`.

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Supplementary data

We provide the detailed individual results for each dataset and each ML model for our analysis as supplementary data. Here, we use the acronyms bl1, bl2, SVM and ADA for the oversampling models Borderline-1 SMOTE, Borderline-2 SMOTE, SVM-SMOTE and ADASYN respectively. We mark in bold for each dataset, the ML model with the highest average F1-Score, a criteria by which we select the model results to include in our further analysis.

Dataset: abalone_19

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Baseline	0	0	0	0	0	0	0
SMOTE	0.045	0.046	0.048	0.049	0.049	0.0474	0.00181659
bl1	0.048	0.05	0.04	0.051	0.043	0.0464	0.00472229
bl2	0.044	0.047	0.04	0.056	0.051	0.0476	0.0061887
SVM	0.057	0.062	0.049	0.057	0.051	0.0552	0.00521536
ADA	0.045	0.046	0.049	0.05	0.048	0.0476	0.00207364
LoRAS (Em=t,p=10)	0.055	0.055	0.056	0.057	0.057	0.056	0.001
F1-Score average						0.04288571	

Table 8: F1-Scores for the logistic regression model for 5 runs of 10-fold cross validation for abalone_19 dataset

Oversampling model	lr1	lr2	lr3	lr4	lr5	mean	sd
Baseline	0.5	0.5	0.499	0.499	0.499	0.4994	0.00054772
SMOTE	0.709	0.73	0.725	0.734	0.729	0.7254	0.00971082
bl1	0.677	0.686	0.623	0.696	0.659	0.6682	0.02870017
bl2	0.657	0.687	0.64	0.733	0.701	0.6836	0.03661694
SVM	0.662	0.689	0.631	0.667	0.659	0.6616	0.02075572
ADA	0.71	0.729	0.727	0.735	0.726	0.7254	0.00928978
LoRAS (Em=t,p=10)	0.728	0.747	0.733	0.735	0.743	0.7372	0.00769415

Table 9: Balanced accuracies for the lr model for 5 runs of 10-fold cross validation for abalone_19 dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Baseline	0	0	0	0	0	0	0
SMOTE	0.032	0.03	0.028	0.028	0.031	0.0298	0.00178885
bl1	0.023	0.025	0.024	0.027	0.027	0.0252	0.00178885
bl2	0.023	0.025	0.024	0.027	0.027	0.0252	0.00178885
SVM	0.035	0.039	0.035	0.039	0.025	0.0346	0.00572713
ADA	0.031	0.03	0.028	0.028	0.031	0.0296	0.00151658
LoRAS (Em=t,p=10))	0.032	0.033	0.029	0.033	0.032	0.0318	0.00164317
F1-Score average						0.02517143	

Table 10: F1-Scores for the svm model for 5 runs of 10-fold cross validation for abalone_19 dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Baseline	0.5	0.5	0.5	0.5	0.5	0.5	0
SMOTE	0.766	0.733	0.701	0.727	0.74	0.7334	0.02343715
bl1	0.615	0.662	0.635	0.703	0.684	0.6598	0.03563285
bl2	0.615	0.662	0.635	0.703	0.684	0.6598	0.03563285
SVM	0.686	0.728	0.684	0.737	0.702	0.7074	0.02416195
ADA	0.757	0.733	0.699	0.726	0.753	0.7336	0.02334095
LoRAS (Em=t,p=10)	0.745	0.758	0.703	0.768	0.752	0.7452	0.02505394

Table 11: Balanced accuracies for the svm model for 5 runs of 10-fold cross validation for abalone_19 dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Baseline	0	0	0	0	0	0	0
SMOTE	0.056	0.05	0.053	0.047	0.066	0.0544	0.00730068
bl1	0.044	0.059	0.035	0.052	0.034	0.0448	0.01080278
bl2	0.044	0.062	0.042	0.039	0.031	0.0436	0.0114149
SVM	0.046	0.062	0.037	0.045	0.035	0.045	0.01065364
ADA	0.057	0.049	0.053	0.054	0.063	0.0552	0.00521536
LoRAS (Em=r,p=NA)	0.058	0.062	0.055	0.061	0.063	0.0598	0.00327109
F1-Score average						0.04325714	

Table 12: F1-Scores for the knn model for 5 runs of 10-fold cross validation for abalone_19 dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Baseline	0.677	0.5	0.5	0.5	0.5	0.5354	0.07915681
SMOTE	0.555	0.652	0.661	0.635	0.72	0.6446	0.05943316
bl1	0.572	0.569	0.522	0.564	0.537	0.5528	0.02210656
bl2	0.555	0.594	0.541	0.543	0.545	0.5556	0.02213143
SVM	0.678	0.57	0.523	0.548	0.538	0.5714	0.06199032
ADA	0.656	0.651	0.668	0.669	0.71	0.6708	0.02323144
LoRAS (Em=r,p=NA)	0.666	0.683	0.664	0.667	0.698	0.6756	0.01463899

Table 13: Balanced accuracies for the knn model for 5 runs of 10-fold cross validation for abalone_19 dataset

Dataset: arrhythmia

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Baseline	0.36	0.39	0.354	0.35	0.396	0.37	0.02140093
SMOTE	0.346	0.34	0.249	0.35	0.44	0.345	0.06762396
bl1	0.356	0.347	0.38	0.309	0.372	0.3528	0.0277074
bl2	0.334	0.362	0.317	0.27	0.252	0.307	0.04540925
SVM	0.403	0.426	0.244	0.326	0.351	0.35	0.07141078
ADA	0.398	0.306	0.336	0.336	0.435	0.3622	0.05270863
LoRAS (Em=t,p=1)	0.429	0.43	0.288	0.353	0.403	0.3806	0.06045908
F1-Score average						0.35251429	

Table 14: F1-Scores for the lr model for 5 runs of 10-fold cross validation for arrhythmia dataset

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Baseline	0.688	0.701	0.646	0.673	0.687	0.679	0.02094039
SMOTE	0.674	0.673	0.624	0.673	0.686	0.666	0.02411431
bl1	0.686	0.676	0.676	0.654	0.672	0.6728	0.01171324
bl2	0.729	0.766	0.697	0.68	0.673	0.709	0.03850325
SVM	0.713	0.723	0.621	0.671	0.668	0.6792	0.04074555
ADA	0.696	0.642	0.649	0.656	0.695	0.6676	0.02594802
LoRAS (Em=t,p=1)	0.718	0.725	0.639	0.695	0.694	0.6942	0.03377425

Table 15: Balanced accuracies for the lr model for 5 runs of 10-fold cross validation for arrhythmia dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Baseline	0.259	0.381	0.387	0.376	0.321	0.3448	0.05475582
SMOTE	0.259	0.381	0.387	0.376	0.321	0.3448	0.05475582
bl1	0.259	0.381	0.387	0.376	0.321	0.3448	0.05475582
bl2	0.259	0.381	0.387	0.376	0.321	0.3448	0.05475582
SVM	0.259	0.381	0.387	0.376	0.321	0.3448	0.05475582
ADA	0.259	0.381	0.387	0.376	0.321	0.3448	0.05475582
LoRAS (Em=t,p=1)	0.259	0.381	0.387	0.376	0.321	0.3448	0.05475582
F1-Score average						0.3448	

Table 16: F1-Scores for the svm model for 5 runs of 10-fold cross validation for arrhythmia dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Baseline	0.659	0.676	0.686	0.697	0.694	0.6824	0.01540454
SMOTE	0.659	0.676	0.686	0.697	0.694	0.6824	0.01540454
bl1	0.659	0.676	0.686	0.697	0.694	0.6824	0.01540454
bl2	0.659	0.676	0.686	0.697	0.694	0.6824	0.01540454
SVM	0.659	0.676	0.686	0.697	0.694	0.6824	0.01540454
ADA	0.659	0.676	0.686	0.697	0.694	0.6824	0.01540454
LoRAS (Em=t,p=1)	0.659	0.676	0.686	0.697	0.694	0.6824	0.01540454

Table 17: Balanced accuracies for the svm model for 5 runs of 10-fold cross validation for arrhythmia dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Baseline	0	0	0	0	0.5	0.1	0.2236068
SMOTE	0.185	0.191	0.202	0.192	0.22	0.198	0.01372953
bl1	0.187	0.195	0.182	0.194	0.158	0.1832	0.01505656
bl2	0.176	0.194	0.163	0.169	0.154	0.1712	0.01508973
SVM	0.213	0.224	0.178	0.206	0.191	0.2024	0.01814663
ADA	0.196	0.196	0.202	0.169	0.206	0.1938	0.01449828
LoRAS (Em=t,p=1)	0.179	0.179	0.168	0.192	0.207	0.185	0.01494992
F1-Score average						0.17622857	

Table 18: F1-Scores for the knn model for 5 runs of 10-fold cross validation for arrhythmia dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Baseline	0.5	0.5	0.5	0.5	0.5	0.5	0
SMOTE	0.674	0.688	0.72	0.728	0.755	0.713	0.03234192
bl1	0.665	0.677	0.66	0.691	0.658	0.6702	0.01377316
bl2	0.666	0.689	0.642	0.666	0.658	0.6642	0.01697645
SVM	0.684	0.681	0.609	0.69	0.689	0.6706	0.03463091
ADA	0.712	0.693	0.719	0.727	0.73	0.7162	0.01475466
LoRAS (Em=t,p=1)	0.664	0.673	0.67	0.728	0.715	0.69	0.02930017

Table 19: Balanced accuracies for the knn model for 5 runs of 10-fold cross validation for arrhythmia dataset

Dataset: isolet

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Base	0.901	0.792	0.819	0.811	0.807	0.826	0.0430581
SMOTE	0.799	0.798	0.808	0.817	0.809	0.8062	0.00785493
bl1	0.792	0.797	0.805	0.812	0.804	0.802	0.00771362
bl2	0.695	0.698	0.694	0.7	0.681	0.6936	0.0074364
SVM	0.796	0.795	0.813	0.795	0.8	0.7998	0.00766159
ADA	0.806	0.793	0.815	0.813	0.803	0.806	0.00877496
LoRAS (Em=t,p=30)	0.809	0.793	0.821	0.816	0.81	0.8098	0.01056882
F1-Score average						0.79191429	

Table 20: F1-Scores for the lr model for 5 runs of 10-fold cross validation for isolet dataset

Ovesampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
baseline	0.901	0.89	0.906	0.903	0.903	0.9006	0.0061887
SMOTE	0.894	0.892	0.901	0.904	0.902	0.8986	0.00527257
bl1	0.892	0.894	0.903	0.906	0.9	0.899	0.00591608
bl2	0.906	0.907	0.905	0.912	0.902	0.9064	0.00364692
SVM	0.907	0.908	0.92	0.909	0.911	0.911	0.00524404
ADA	0.899	0.891	0.901	0.904	0.897	0.8984	0.00487852
LoRAS (Em=t,p=30)	0.905	0.894	0.909	0.908	0.906	0.9044	0.00602495

Table 21: Balanced accuracies for the lr model for 5 runs of 10-fold cross validation for isolet dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	variance
Base	0.791	0.788	0.797	0.798	0.793	0.7934	0.00415933
SMOTE	0.457	0.459	0.458	0.463	0.46	0.4594	0.00230217
bl1	0.49	0.489	0.486	0.494	0.498	0.4914	0.00466905
bl2	0.49	0.489	0.486	0.494	0.498	0.4914	0.00466905
SVM	0.476	0.479	0.473	0.474	0.475	0.4754	0.00230217
ADA	0.483	0.477	0.48	0.483	0.486	0.4818	0.00342053
LoRAS (Em=t,p=30)	0.505	0.501	0.501	0.486	0.507	0.5	0.00824621
F1-Score average						0.52754286	

Table 22: F1-Scores for the svm model for 5 runs of 10-fold cross validation for isolet dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Baseline	0.893	0.893	0.906	0.9	0.904	0.8992	0.00605805
SMOTE	0.894	0.893	0.895	0.897	0.895	0.8948	0.00148324
bl1	0.905	0.902	0.904	0.906	0.908	0.905	0.00223607
bl2	0.905	0.902	0.904	0.906	0.908	0.905	0.00223607
SVM	0.899	0.901	0.899	0.899	0.897	0.899	0.00141421
ADA	0.903	0.898	0.902	0.903	0.904	0.902	0.00234521
LoRAS (Em=t,p=30)	0.91	0.906	0.909	0.908	0.911	0.9088	0.00192354

Table 23: Balanced Accuracies for the svm model for 5 runs of 10-fold cross validation for isolet dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Base	0.874	0.881	0.87	0.873	0.871	0.8738	0.00432435
SMOTE	0.496	0.496	0.498	0.492	0.495	0.4954	0.00219089
bl1	0.506	0.507	0.508	0.508	0.508	0.5074	0.00089443
bl2	0.46	0.464	0.463	0.462	0.468	0.4634	0.00296648
SVM	0.525	0.526	0.527	0.528	0.53	0.5272	0.00192354
ADA	0.486	0.487	0.488	0.485	0.487	0.4866	0.00114018
LoRAS (Em=t,p=30)	0.421	0.424	0.42	0.422	0.422	0.4218	0.00148324
F1-Score average						0.53937143	

Table 24: F1-Scores for the knn model for 5 runs of 10-fold cross validation for isolet dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Baseline	0.914	0.92	0.91	0.915	0.913	0.9144	0.00364692
SMOTE	0.915	0.915	0.915	0.913	0.913	0.9142	0.00109545
bl1	0.917	0.918	0.918	0.918	0.918	0.9178	0.00044721
bl2	0.905	0.903	0.902	0.902	0.904	0.9032	0.00130384
SVM	0.923	0.923	0.924	0.924	0.925	0.9238	0.00083666
ADA	0.911	0.912	0.912	0.911	0.911	0.9114	0.00054772
LoRAS (Em=t,p=30)	0.883	0.884	0.882	0.884	0.883	0.8832	0.00083666

Table 25: Balanced accuracies for the knn model for 5 runs of 10-fold cross validation for isolet dataset

Dataset: letter_image

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Baseline	0.743	0.745	0.745	0.744	0.742	0.7438	0.00130384
SMOTE	0.581	0.587	0.582	0.585	0.583	0.5836	0.00240832
bl1	0.477	0.499	0.497	0.488	0.487	0.4896	0.00882043
bl2	0.331	0.337	0.337	0.339	0.339	0.3366	0.00328634
SVM	0.463	0.468	0.47	0.467	0.468	0.4672	0.00258844
ADA	0.52	0.52	0.521	0.522	0.518	0.5202	0.00148324
LoRAS(Em=r,p=NA)	0.666	0.643	0.636	0.638	0.644	0.6454	0.01199166
F1-Score average						0.54091429	

Table 26: F1-Scores for the lr model for 5 runs of 10-fold cross validation for letter_image dataset

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Baseline	0.831	0.833	0.833	0.831	0.83	0.8316	0.00134164
SMOTE	0.953	0.956	0.954	0.955	0.953	0.9542	0.00130384
bl1	0.928	0.921	0.926	0.926	0.92	0.9242	0.00349285
bl2	0.912	0.907	0.905	0.91	0.906	0.908	0.00291548
SVM	0.945	0.947	0.945	0.944	0.944	0.945	0.00122474
ADA	0.948	0.949	0.948	0.949	0.948	0.9484	0.00054772
LoRAS (Em=r,p=NA)	0.915	0.942	0.942	0.944	0.946	0.9378	0.01285302

Table 27: Balanced accuracies for the lr model for 5 runs of 10-fold cross validation for letter_image dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Baseline	0.753	0.757	0.757	0.762	0.761	0.758	0.00360555
SMOTE	0.166	0.166	0.165	0.165	0.165	0.1654	0.00054772
bl1	0.174	0.173	0.174	0.174	0.174	0.1738	0.00044721
bl2	0.174	0.169	0.174	0.174	0.174	0.173	0.00223607
SVM	0.168	0.177	0.169	0.169	0.17	0.1706	0.00364692
ADA	0.177	0.186	0.177	0.177	0.177	0.1788	0.00402492
LoRAS (Em=t,p=1)	0.204	0.206	0.204	0.204	0.203	0.2042	0.00109545
F1-Score average						0.26054286	

Table 28: F1-Scores for the svm model for 5 runs of 10-fold cross validation for letter_image dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Base	0.829	0.831	0.831	0.833	0.832	0.8312	0.00148324
SMOTE	0.809	0.809	0.808	0.807	0.807	0.808	0.001
bl1	0.819	0.819	0.819	0.819	0.819	0.819	0
bl2	0.819	0.819	0.819	0.819	0.819	0.819	0
SVM	0.812	0.813	0.813	0.812	0.814	0.8128	0.00083666
ADA	0.823	0.823	0.823	0.823	0.823	0.823	1.2413E-16
LoRAS (Em=t,p=1)	0.851	0.852	0.851	0.85	0.849	0.8506	0.00114018

Table 29: Balanced accuracies for the svm model for 5 runs of 10-fold cross validation for letter_image dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Base	0.913	0.914	0.914	0.916	0.919	0.9152	0.00238747
SMOTE	0.78	0.782	0.782	0.782	0.782	0.7816	0.00089443
bl1	0.757	0.769	0.773	0.769	0.775	0.7686	0.0069857
bl2	0.757	0.675	0.659	0.674	0.672	0.6874	0.03943729
SVM	0.662	0.741	0.738	0.741	0.738	0.724	0.0346915
ADA	0.732	0.729	0.732	0.735	0.734	0.7324	0.00230217
LoRAS (Em=r,p=NA)	0.839	0.831	0.832	0.83	0.833	0.833	0.00353553
F1-Score average						0.77745714	

Table 30: F1-Scores for the knn model for 5 runs of 10-fold cross validation for letter_image dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Base	0.926	0.927	0.926	0.928	0.93	0.9274	0.00167332
SMOTE	0.989	0.989	0.988	0.989	0.989	0.9888	0.00044721
bl1	0.984	0.983	0.984	0.986	0.985	0.9844	0.00114018
bl2	0.978	0.977	0.973	0.98	0.977	0.977	0.00254951
SVM	0.986	0.986	0.986	0.986	0.986	0.986	0
ADA	0.985	0.985	0.986	0.986	0.986	0.9856	0.00054772
LoRAS (Em=r,p=NA)	0.99	0.989	0.989	0.99	0.989	0.9894	0.00054772

Table 31: Balanced accuracies for the knn model for 5 runs of 10-fold cross validation for letter_image dataset

Dataset: mammography

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Base	0.532	0.535	0.524	0.533	0.533	0.5314	0.00427785
SMOTE	0.283	0.286	0.282	0.282	0.288	0.2842	0.00268328
bl1	0.244	0.245	0.243	0.243	0.244	0.2438	0.00083666
bl2	0.218	0.217	0.216	0.216	0.217	0.2168	0.00083666
SVM	0.32	0.315	0.314	0.312	0.314	0.315	0.003
ADA	0.207	0.21	0.21	0.209	0.209	0.209	0.00122474
LoRAS (Em=t,p=.01)	0.366	0.362	0.355	0.363	0.366	0.3624	0.00450555
F1-Score average						0.30894286	

Table 32: F1-Scores for the lr model for 5 runs of 10-fold cross validation for mammography dataset

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Base	0.702	0.704	0.7	0.702	0.702	0.702	0.00141421
SMOTE	0.885	0.884	0.88	0.881	0.886	0.8832	0.00258844
bl1	0.881	0.881	0.878	0.879	0.88	0.8798	0.00130384
bl2	0.872	0.87	0.868	0.87	0.872	0.8704	0.00167332
SVM	0.883	0.88	0.88	0.882	0.88	0.881	0.00141421
ADA	0.864	0.865	0.867	0.867	0.868	0.8662	0.00164317
LoRAS (Em=t,p=.01)	0.853	0.853	0.863	0.856	0.859	0.8568	0.00426615

Table 33: Balanced accuracies for the lr model for 5 runs of 10-fold cross validation for mammography dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Base	0.458	0.435	0.412	0.437	0.418	0.432	0.01806931
SMOTE	0.097	0.096	0.097	0.0096	0.096	0.07912	0.03886608
bl1	0.098	0.102	0.103	0.103	0.103	0.1018	0.00216795
bl2	0.098	0.102	0.103	0.103	0.103	0.1018	0.00216795
SVM	0.1	0.096	0.096	0.096	0.096	0.0968	0.00178885
ADA	0.1	0.096	0.095	0.095	0.095	0.0962	0.00216795
LoRAS (Em=t,p=.01)	0.108	0.106	0.108	0.106	0.106	0.1068	0.00109545
F1-Score average						0.14493143	

Table 34: F1-Scores for the svm model for 5 runs of 10-fold cross validation for mammography dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Base	0.66	0.649	0.637	0.647	0.639	0.6464	0.00915423
SMOTE	0.751	0.754	0.759	0.756	0.756	0.7552	0.00294958
bl1	0.748	0.768	0.771	0.771	0.771	0.7658	0.01003494
bl2	0.748	0.768	0.771	0.771	0.771	0.7658	0.01003494
SVM	0.763	0.754	0.756	0.755	0.753	0.7562	0.00396232
ADA	0.764	0.755	0.754	0.753	0.753	0.7558	0.00465833
LoRAS (Em=t,p=.01)	0.78	0.774	0.78	0.773	0.775	0.7764	0.00336155

Table 35: Balanced accuracies for the svm model for 5 runs of 10-fold cross validation for mammography dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Base	0.557	0.554	0.545	0.544	0.54	0.548	0.00717635
SMOTE	0.408	0.417	0.411	0.416	0.416	0.4136	0.00391152
bl1	0.417	0.413	0.416	0.417	0.411	0.4148	0.00268328
bl2	0.324	0.33	0.331	0.326	0.323	0.3268	0.00356371
SVM	0.473	0.469	0.463	0.463	0.467	0.467	0.00424264
ADA	0.356	0.354	0.353	0.352	0.354	0.3538	0.00148324
LoRAS (Em=r,p=NA)	0.515	0.512	0.505	0.511	0.512	0.511	0.00367423
F1-Score average						0.43357143	

Table 36: F1-Scores for the knn model for 5 runs of 10-fold cross validation for mammography dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Base	0.706	0.706	0.701	0.702	0.7	0.703	0.00282843
SMOTE	0.909	0.914	0.913	0.912	0.91	0.9116	0.00207364
bl1	0.91	0.908	0.912	0.908	0.908	0.9092	0.00178885
bl2	0.898	0.9	0.901	0.9	0.899	0.8996	0.00114018
SVM	0.913	0.91	0.91	0.906	0.908	0.9094	0.00260768
ADA	0.903	0.91	0.905	0.904	0.906	0.9056	0.00270185
LoRAS (Em=r,p=NA)	0.9	0.894	0.899	0.896	0.894	0.8966	0.00279285

Table 37: Balanced accuracies for the knn model for 5 runs of 10-fold cross validation for mammography dataset

Dataset: scene

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Base	0.178	0.181	0.173	0.172	0.138	0.1684	0.01738678
SMOTE	0.236	0.231	0.222	0.216	0.205	0.222	0.01226784
bl1	0.246	0.242	0.244	0.224	0.198	0.2308	0.02032732
bl2	0.227	0.24	0.226	0.221	0.205	0.2238	0.01263725
SVM	0.234	0.243	0.237	0.24	0.224	0.2356	0.00730068
ADA	0.231	0.242	0.233	0.216	0.2	0.2244	0.01653179
LoRAS (Em=t,p=30)	0.239	0.234	0.233	0.22	0.206	0.2264	0.01339029
F1-Score average						0.21877143	

Table 38: F1-Scores for the lr model for 5 runs of 10-fold cross validation for scene dataset

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Base	0.554	0.559	0.553	0.553	0.536	0.551	0.00874643
SMOTE	0.628	0.629	0.613	0.612	0.6	0.6164	0.01217785
bl1	0.632	0.632	0.631	0.613	0.589	0.6194	0.01882286
bl2	0.625	0.638	0.621	0.616	0.603	0.6206	0.01277889
SVM	0.611	0.622	0.616	0.618	0.607	0.6148	0.00589067
ADA	0.625	0.64	0.626	0.613	0.596	0.62	0.01647726
LoRAS (Em=t,p=30)	0.631	0.628	0.625	0.61	0.6	0.6188	0.01325519

Table 39: Balanced accuracies for the lr model for 5 runs of 10-fold cross validation for scene dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Base	0.333	0.189	0.149	0.169	0.158	0.1996	0.0760513
SMOTE	0.226	0.198	0.203	0.188	0.194	0.2018	0.01460137
bl1	0.222	0.214	0.204	0.199	0.193	0.2064	0.01163185
bl2	0.222	0.214	0.204	0.199	0.193	0.2064	0.01163185
SVM	0.269	0.203	0.208	0.189	0.189	0.2116	0.03317831
ADA	0.241	0.205	0.195	0.191	0.195	0.2054	0.0205621
LoRAS (Em=t,p=30)	0.239	0.211	0.209	0.191	0.197	0.2094	0.01851486
F1-Score average						0.2058	

Table 40: F1-Scores for the svm model for 5 runs of 10-fold cross validation for scene dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Base	0.507	0.516	0.539	0.552	0.545	0.5318	0.01935717
SMOTE	0.633	0.63	0.639	0.613	0.624	0.6278	0.00988433
bl1	0.622	0.657	0.64	0.631	0.619	0.6338	0.01535252
bl2	0.622	0.657	0.64	0.631	0.619	0.6338	0.01535252
SVM	0.644	0.64	0.652	0.617	0.615	0.6336	0.01665233
ADA	0.649	0.643	0.624	0.619	0.624	0.6318	0.01329286
LoRAS (Em=t,p=30)	0.639	0.651	0.645	0.616	0.627	0.6356	0.01409965

Table 41: Balanced accuracies for the svm model for 5 runs of 10-fold cross validation for scene dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Base	0.011	0	0.011	0	0.011	0.0066	0.00602495
SMOTE	0.217	0.209	0.217	0.215	0.218	0.2152	0.00363318
bl1	0.232	0.235	0.234	0.238	0.236	0.235	0.00223607
bl2	0.234	0.235	0.238	0.233	0.232	0.2344	0.00230217
SVM	0.247	0.26	0.259	0.248	0.263	0.2554	0.00736885
ADA	0.208	0.211	0.213	0.214	0.21	0.2112	0.00238747
LoRAS (Em=t,p=30)	0.222	0.222	0.223	0.225	0.223	0.223	0.00122474
F1-Score average						0.19725714	

Table 42: F1-Scores for the knn model for 5 runs of 10-fold cross validation for scene dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Base	0.502	0.5	0.502	0.5	0.502	0.5012	0.00109545
SMOTE	0.698	0.68	0.701	0.7	0.7	0.6958	0.00889944
bl1	0.71	0.715	0.714	0.719	0.716	0.7148	0.00327109
bl2	0.711	0.717	0.722	0.714	0.711	0.715	0.00463681
SVM	0.704	0.724	0.722	0.702	0.725	0.7154	0.01139298
ADA	0.684	0.69	0.697	0.695	0.69	0.6912	0.00506952
LoRAS (Em=t,p=30)	0.7	0.701	0.705	0.71	0.706	0.7044	0.00403733

Table 43: Balanced accuracies for the knn model for 5 runs of 10-fold cross validation for scene dataset

Dataset: ozone_level

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Base	0.091	0.063	0.069	0.041	0.05	0.0628	0.01918854
SMOTE	0.199	0.191	0.19	0.191	0.18	0.1902	0.00676018
bl1	0.218	0.202	0.219	0.213	0.211	0.2126	0.00680441
bl2	0.18	0.172	0.194	0.186	0.186	0.1836	0.00817313
SVM	0.217	0.216	0.211	0.219	0.212	0.215	0.00339116
ADA	0.2	0.19	0.191	0.197	0.186	0.1928	0.00563028
LoRAS (Em=t,p=10)	0.216	0.204	0.209	0.205	0.205	0.2078	0.00496991
F1-Score average						0.18068571	

Table 44: F1-Scores for the lr model for 5 runs of 10-fold cross validation for ozone_level dataset

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Base	0.525	0.52	0.52	0.511	0.513	0.5178	0.00571839
SMOTE	0.812	0.795	0.805	0.804	0.785	0.8002	0.01042593
bl1	0.785	0.771	0.778	0.775	0.776	0.777	0.00514782
bl2	0.767	0.768	0.795	0.795	0.781	0.7812	0.013755
SVM	0.735	0.737	0.733	0.747	0.739	0.7382	0.0054037
ADA	0.816	0.8	0.8	0.808	0.793	0.8034	0.00882043
LoRAS (Em=t,p=10)	0.813	0.808	0.807	0.809	0.808	0.809	0.00234521

Table 45: Balanced accuracies for the lr model for 5 runs of 10-fold cross validation for ozone_level dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Base	0	0.02	0.022	0.018	0.02	0.016	0.00905539
SMOTE	0.121	0.122	0.123	0.122	0.121	0.1218	0.00083666
bl1	0.131	0.135	0.142	0.13	0.14	0.1356	0.00531977
bl2	0.169	0.135	0.142	0.13	0.14	0.1432	0.01515586
SVM	0.122	0.169	0.174	0.175	0.177	0.1634	0.02333024
ADA	0.133	0.121	0.124	0.122	0.122	0.1244	0.0049295
LoRAS (Em=t,p=30)	0.132	0.136	0.136	0.135	0.136	0.135	0.00173205
F1-Score average						0.11991429	

Table 46: F1-Scores for the svm model for 5 runs of 10-fold cross validation for ozone_level dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Base	0.498	0.505	0.506	0.503	0.504	0.5032	0.00311448
SMOTE	0.753	0.756	0.758	0.748	0.754	0.7538	0.00376829
bl1	0.756	0.775	0.785	0.746	0.787	0.7698	0.01810249
bl2	0.756	0.775	0.785	0.746	0.787	0.7698	0.01810249
SVM	0.787	0.791	0.79	0.792	0.803	0.7926	0.00610737
ADA	0.755	0.751	0.76	0.749	0.759	0.7548	0.00481664
LoRAS (Em=t,p=30)	0.778	0.782	0.782	0.774	0.788	0.7808	0.00521536

Table 47: Balanced accuracies for the svm model for 5 runs of 10-fold cross validation for ozone_level dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Base	0	0	0	0	0	0	0
SMOTE	0.095	0.098	0.117	0.112	0.129	0.1102	0.01398928
bl1	0.099	0.081	0.118	0.126	0.123	0.1094	0.01903418
bl2	0.108	0.089	0.11	0.107	0.105	0.1038	0.00846759
SVM	0.102	0.09	0.11	0.101	0.127	0.106	0.01372953
ADA	0.094	0.101	0.113	0.11	0.11	0.1056	0.00789303
LoRAS (Em=t,p=30)	0.136	0.124	0.113	0.114	0.142	0.1258	0.01296919
F1-Score average						0.0944	

Table 48: F1-Scores for the knn model for 5 runs of 10-fold cross validation for ozone_level dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Base	0.5	0.5	0.5	0.5	0.5	0.5	0
SMOTE	0.598	0.603	0.64	0.633	0.664	0.6276	0.02733679
bl1	0.574	0.552	0.602	0.617	0.606	0.5902	0.02659323
bl2	0.616	0.584	0.621	0.621	0.614	0.6112	0.01551451
SVM	0.57	0.557	0.578	0.572	0.603	0.576	0.01692631
ADA	0.595	0.61	0.635	0.627	0.624	0.6182	0.0158019
LoRAS (Em=t,p=30)	0.67	0.659	0.63	0.641	0.676	0.6552	0.01938298

Table 49: Balanced accuracies for the knn model for 5 runs of 10-fold cross validation for ozone_level dataset

Dataset: webpage

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Base	0.747	0.744	0.757	0.751	0.74	0.7478	0.00653452
SMOTE	0.913	0.093	0.093	0.093	0.092	0.2568	0.36682721
bl1	0.112	0.11	0.11	0.107	0.11	0.1098	0.00178885
bl2	0.079	0.081	0.082	0.082	0.079	0.0806	0.00151658
SVM	0.118	0.116	0.118	0.117	0.117	0.1172	0.00083666
ADA	0.093	0.096	0.095	0.094	0.093	0.0942	0.00130384
LoRAS (Em=r,p=NA)	0.098	0.101	0.098	0.102	0.095	0.0988	0.00277489
F1-Score average						0.21502857	

Table 50: F1-Scores for the lr model for 5 runs of 10-fold cross validation for webpage dataset

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Base	0.83	0.832	0.836	0.839	0.828	0.833	0.00447214
SMOTE	0.709	0.714	0.715	0.717	0.713	0.7136	0.00296648
bl1	0.768	0.763	0.763	0.756	0.762	0.7624	0.00427785
bl2	0.663	0.672	0.675	0.676	0.66	0.6692	0.00725948
SVM	0.78	0.776	0.781	0.778	0.778	0.7786	0.00194936
ADA	0.717	0.724	0.721	0.718	0.716	0.7192	0.00327109
LoRAS (Em=r,p=NA)	0.729	0.738	0.729	0.738	0.719	0.7306	0.00789303

Table 51: Balanced accuracies for the lr model for 5 runs of 10-fold cross validation for webpage dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Base	0.729	0.732	0.749	0.747	0.737	0.7388	0.00889944
SMOTE	0.087	0.088	0.088	0.088	0.089	0.088	0.00070711
bl1	0.106	0.107	0.106	0.106	0.107	0.1064	0.00054772
bl2	0.106	0.107	0.106	0.106	0.107	0.1064	0.00054772
SVM	0.118	0.118	0.119	0.117	0.118	0.118	0.00070711
ADA	0.091	0.083	0.092	0.091	0.091	0.0896	0.00371484
LoRAS (Em=r,p=NA)	0.09	0.091	0.093	0.095	0.09	0.0918	0.00216795
F1-Score average						0.19128571	

Table 52: F1-Scores for the svm model for 5 runs of 10-fold cross validation for webpage dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Base	0.817	0.814	0.832	0.823	0.825	0.8222	0.00704982
SMOTE	0.693	0.699	0.697	0.697	0.702	0.6976	0.00328634
bl1	0.752	0.754	0.752	0.752	0.757	0.7534	0.00219089
bl2	0.752	0.754	0.752	0.752	0.757	0.7534	0.00219089
SVM	0.779	0.78	0.782	0.778	0.78	0.7798	0.00148324
ADA	0.708	0.715	0.714	0.708	0.71	0.711	0.00331662
LoRAS (Em=r,p=NA)	0.7	0.708	0.712	0.85	0.702	0.7344	0.06479815

Table 53: Balanced accuracies for the svm model for 5 runs of 10-fold cross validation for webpage dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Base	0.71	0.709	0.715	0.707	0.714	0.711	0.00339116
SMOTE	0.268	0.27	0.264	0.268	0.269	0.2678	0.00228035
bl1	0.274	0.275	0.272	0.278	0.274	0.2746	0.00219089
bl2	0.291	0.287	0.285	0.287	0.287	0.2874	0.00219089
SVM	0.269	0.268	0.266	0.267	0.268	0.2676	0.00114018
ADA	0.266	0.267	0.261	0.265	0.265	0.2648	0.00228035
LoRAS (Em=r,p=NA)	0.62	0.614	0.609	0.61	0.616	0.6138	0.00449444
F1-Score average						0.38385714	

Table 54: F1-Scores for the knn model for 5 runs of 10-fold cross validation for webpage dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Base	0.804	0.804	0.808	0.806	0.806	0.8056	0.00167332
SMOTE	0.906	0.908	0.904	0.907	0.907	0.9064	0.00151658
bl1	0.9	0.901	0.9	0.903	0.903	0.9014	0.00151658
bl2	0.905	0.903	0.902	0.901	0.905	0.9032	0.00178885
SVM	0.904	0.905	0.904	0.905	0.906	0.9048	0.00083666
ADA	0.903	0.905	0.901	0.904	0.906	0.9038	0.00192354
LoRAS (Em=r,p=NA)	0.924	0.919	0.921	0.924	0.928	0.9232	0.00342053

Table 55: Balanced accuracies for the knn model for 5 runs of 10-fold cross validation for webpage dataset

Dataset: wine_quality

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Base	0.069	0.069	0.064	0.069	0.068	0.0678	0.00216795
SMOTE	0.181	0.174	0.187	0.182	0.175	0.1798	0.00535724
bl1	0.183	0.18	0.181	0.188	0.178	0.182	0.00380789
bl2	0.169	0.17	0.173	0.175	0.168	0.171	0.00291548
SVM	0.214	0.215	0.207	0.217	0.228	0.2162	0.00759605
ADA	0.181	0.18	0.181	0.182	0.18	0.1808	0.00083666
LoRAS (Em=r,p=NA)	0.2	0.198	0.199	0.196	0.194	0.1974	0.00240832
F1-Score average						0.17071429	

Table 56: F1-Scores for the lr model for 5 runs of 10-fold cross validation for wine_quality dataset

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Base	0.518	0.518	0.517	0.518	0.517	0.5176	0.00054772
SMOTE	0.723	0.709	0.731	0.724	0.707	0.7188	0.01035374
bl1	0.72	0.712	0.715	0.721	0.709	0.7154	0.00512835
bl2	0.709	0.708	0.715	0.715	0.709	0.7112	0.00349285
SVM	0.72	0.711	0.704	0.71	0.718	0.7126	0.00646529
ADA	0.723	0.722	0.718	0.726	0.718	0.7214	0.00343511
LoRAS (Em=r,p=NA)	0.739	0.732	0.736	0.733	0.731	0.7342	0.00327109

Table 57: Balanced accuracies for the lr model for 5 runs of 10-fold cross validation for wine_quality dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Base	0	0	0	0.009	0	0.0018	0.00402492
SMOTE	0.123	0.121	0.123	0.123	0.126	0.1232	0.00178885
bl1	0.125	0.119	0.12	0.122	0.118	0.1208	0.00277489
bl2	0.125	0.119	0.12	0.122	0.118	0.1208	0.00277489
SVM	0.125	0.12	0.135	0.139	0.128	0.1294	0.00763544
ADA	0.125	0.119	0.123	0.123	0.125	0.123	0.00244949
LoRAS (Em=t,p=30)	0.128	0.126	0.13	0.129	0.126	0.1278	0.00178885
F1-Score average						0.10668571	

Table 58: F1-Scores for the svm model for 5 runs of 10-fold cross validation for wine_quality dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Base	0.5	0.499	0.499	0.502	0.499	0.4998	0.00130384
SMOTE	0.689	0.68	0.687	0.687	0.696	0.6878	0.00571839
bl1	0.695	0.675	0.68	0.687	0.668	0.681	0.01046422
bl2	0.695	0.675	0.68	0.683	0.668	0.6802	0.01003494
SVM	0.692	0.671	0.687	0.691	0.67	0.6822	0.01084896
ADA	0.695	0.673	0.688	0.687	0.694	0.6874	0.00879204
LoRAS (Em=t,p=30)	0.703	0.697	0.706	0.707	0.696	0.7018	0.00506952

Table 59: Balanced accuracies for the svm model for 5 runs of 10-fold cross validation for wine_quality dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Base	0	0	0	0	0	0	0
SMOTE	0.155	0.147	0.158	0.159	0.153	0.1544	0.00477493
bl1	0.186	0.182	0.172	0.18	0.183	0.1806	0.00527257
bl2	0.165	0.171	0.167	0.167	0.166	0.1672	0.00228035
SVM	0.216	0.23	0.217	0.222	0.218	0.2206	0.00572713
ADA	0.152	0.147	0.158	0.157	0.156	0.154	0.00452769
LoRAS (Em=t,p=30)	0.156	0.156	0.157	0.163	0.154	0.1572	0.00342053
F1-Score average				.		0.14771429	

Table 60: F1-Scores for the knn model for 5 runs of 10-fold cross validation for wine_quality dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Base	0.5	0.5	0.5	0.5	0.5	0.5	0
SMOTE	0.694	0.676	0.702	0.708	0.691	0.6942	0.01217374
bl1	0.704	0.702	0.685	0.7	0.701	0.6984	0.00763544
bl2	0.698	0.714	0.704	0.71	0.705	0.7062	0.00609918
SVM	0.696	0.711	0.698	0.7	0.696	0.7002	0.00626099
ADA	0.693	0.684	0.708	0.709	0.701	0.699	0.01055936
LoRAS (Em=t,p=30)	0.693	0.693	0.701	0.711	0.693	0.6982	0.00794984

Table 61: Balanced accuracies for the knn model for 5 runs of 10-fold cross validation for wine_quality dataset

Dataset: yeast_ml8

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Base	0.023	0.031	0.02	0.032	0.011	0.0234	0.00861974
SMOTE	0.155	0.154	0.152	0.15	0.153	0.1528	0.00192354
bl1	0.142	0.147	0.15	0.175	0.155	0.1538	0.01275539
bl2	0.146	0.147	0.151	0.157	0.159	0.152	0.00583095
SVM	0.131	0.144	0.139	0.155	0.156	0.145	0.01065364
ADA	0.14	0.156	0.148	0.154	0.139	0.1474	0.00779744
LoRAS (Em=r,p=NA)	0.138	0.14	0.158	0.154	0.141	0.1462	0.0091214
F1-Score average						0.13151429	

Table 62: F1-Scores for the lr model for 5 runs of 10-fold cross validation for yeast_ml8 dataset

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Base	0.5	0.5	0.505	0.507	0.501	0.5026	0.00320936
SMOTE	0.554	0.551	0.549	0.545	0.547	0.5492	0.00349285
bl1	0.533	0.541	0.541	0.576	0.551	0.5484	0.01669731
bl2	0.541	0.54	0.543	0.552	0.558	0.5468	0.00785493
SVM	0.525	0.537	0.531	0.548	0.548	0.5378	0.0102323
ADA	0.532	0.553	0.541	0.55	0.529	0.541	0.0106066
LoRAS (Em=r,p=NA)	0.528	0.531	0.553	0.548	0.531	0.5382	0.01143241

Table 63: Balanced accuracies for the lr model for 5 runs of 10-fold cross validation for yeast_ml8 dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Base	0	0	0	0	0	0	0
SMOTE	0.149	0.14	0.15	0.143	0.137	0.1438	0.00563028
bl1	0.137	0.15	0.157	0.155	0.141	0.148	0.0087178
bl2	0.137	0.15	0.157	0.155	0.141	0.148	0.0087178
SVM	0.135	0.154	0.147	0.156	0.156	0.1496	0.00896103
ADA	0.144	0.143	0.146	0.138	0.147	0.1436	0.00350714
LoRAS (Em=r,p=NA)	0.141	0.152	0.15	0.151	0.148	0.1484	0.00439318
F1-Score average						0.12591429	

Table 64: F1-Scores for the svm model for 5 runs of 10-fold cross validation for yeast_ml8 dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Base	0.5	0.5	0.5	0.5	0.5	0.5	0
SMOTE	0.544	0.525	0.549	0.531	0.52	0.5338	0.01235718
bl1	0.52	0.545	0.561	0.559	0.529	0.5428	0.01808867
bl2	0.52	0.545	0.561	0.559	0.529	0.5428	0.01808867
SVM	0.527	0.55	0.539	0.55	0.551	0.5434	0.01040673
ADA	0.533	0.53	0.539	0.521	0.541	0.5328	0.00794984
LoRAS (Em=r,p=NA)	0.528	0.549	0.546	0.547	0.543	0.5426	0.00844393

Table 65: Balanced accuracies for the svm model for 5 runs of 10-fold cross validation for yeast_ml8 dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Base	0	0	0	0	0	0	0
SMOTE	0.153	0.153	0.15	0.154	0.15	0.152	0.00187083
bl1	0.155	0.149	0.153	0.153	0.157	0.1534	0.00296648
bl2	0.156	0.154	0.15	0.15	0.157	0.1534	0.00328634
SVM	0.158	0.155	0.162	0.156	0.162	0.1586	0.00328634
ADA	0.152	0.15	0.153	0.151	0.153	0.1518	0.00130384
LoRAS (Em=r,p=NA)	0.152	0.151	0.152	0.153	0.154	0.1524	0.00114018
F1-Score average						0.13165714	

Table 66: F1-Scores for the knn model for 5 runs of 10-fold cross validation for yeast_ml8 dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Base	0.5	0.5	0.5	0.5	0.5	0.5	0
SMOTE	0.56	0.56	0.552	0.564	0.558	0.5588	0.00438178
bl1	0.566	0.548	0.562	0.558	0.571	0.561	0.0087178
bl2	0.57	0.562	0.56	0.549	0.574	0.563	0.00969536
SVM	0.573	0.563	0.581	0.563	0.581	0.5722	0.0090111
ADA	0.56	0.553	0.563	0.553	0.563	0.5584	0.00507937
LoRAS (Em=r,p=NA)	0.558	0.555	0.558	0.561	0.565	0.5594	0.00378153

Table 67: Balanced accuracies for the knn model for 5 runs of 10-fold cross validation for yeast_ml8 dataset

Dataset: yeast_me2

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Base	0.206	0.171	0.214	0.205	0.254	0.21	0.0296395
SMOTE	0.261	0.267	0.267	0.255	0.259	0.2618	0.00521536
bl1	0.324	0.337	0.322	0.328	0.32	0.3262	0.00672309
bl2	0.276	0.279	0.28	0.284	0.274	0.2786	0.00384708
SVM	0.366	0.373	0.361	0.358	0.36	0.3636	0.00602495
ADA	0.25	0.245	0.243	0.241	0.241	0.244	0.00374166
LoRAS (Em=t,p=100)	0.287	0.285	0.29	0.286	0.286	0.2868	0.00192354
F1-Score average						0.28157143	

Table 68: F1-Scores for the lr model for 5 runs of 10-fold cross validation for yeast_me2 dataset

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Base	0.572	0.562	0.576	0.567	0.585	0.5724	0.00879204
SMOTE	0.793	0.803	0.801	0.791	0.799	0.7974	0.00517687
bl1	0.811	0.823	0.81	0.813	0.819	0.8152	0.0055857
bl2	0.805	0.807	0.814	0.817	0.82	0.8126	0.00642651
SVM	0.812	0.814	0.819	0.804	0.811	0.812	0.00543139
ADA	0.802	0.802	0.8	0.793	0.792	0.7978	0.00491935
LoRAS (Em=t,p=100)	0.809	0.809	0.808	0.81	0.808	0.8088	0.00083666

Table 69: Balanced accuracies for the lr model for 5 runs of 10-fold cross validation for yeast_me2 dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Base	0	0	0	0	0	0	0
SMOTE	0.295	0.296	0.285	0.282	0.279	0.2874	0.00770065
bl1	0.329	0.332	0.32	0.329	0.324	0.3268	0.00476445
bl2	0.329	0.332	0.32	0.329	0.324	0.3268	0.00476445
SVM	0.346	0.345	0.362	0.358	0.348	0.3518	0.00769415
ADA	0.27	0.258	0.268	0.277	0.257	0.266	0.00845577
LoRAS (Em=r,p=NA)	0.301	0.299	0.284	0.296	0.291	0.2942	0.00683374
F1-Score average						0.26471429	

Table 70: F1-Scores for the svm model for 5 runs of 10-fold cross validation for yeast_me2 dataset

Oversampling models	svm1	svm2	svm3	svm4	svm5	mean	sd
Base	0.5	0.5	0.5	0.5	0.5	0.5	0
SMOTE	0.819	0.821	0.815	0.806	0.907	0.8336	0.04143429
bl1	0.82	0.822	0.81	0.821	0.819	0.8184	0.00482701
bl2	0.82	0.822	0.81	0.821	0.819	0.8184	0.00482701
SVM	0.816	0.809	0.81	0.82	0.816	0.8142	0.00460435
ADA	0.81	0.8	0.809	0.812	0.799	0.806	0.00604152
LoRAS (Em=r,p=NA)	0.812	0.837	0.799	0.817	0.811	0.8152	0.01386362

Table 71: Balanced accuracies for the svm model for 5 runs of 10-fold cross validation for yeast_me2 dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Base	0.061	0.066	0.061	0.061	0.123	0.0744	0.02725436
SMOTE	0.32	0.342	0.319	0.329	0.345	0.331	0.01210372
bl1	0.379	0.391	0.372	0.379	0.348	0.3738	0.01595932
bl2	0.296	0.306	0.343	0.295	0.282	0.3044	0.02320129
SVM	0.393	0.385	0.388	0.398	0.379	0.3886	0.00730068
ADA	0.299	0.318	0.316	0.318	0.328	0.3158	0.01049762
LoRAS (Em=r,p=NA)	0.355	0.347	0.355	0.36	0.357	0.3548	0.00481664
F1-Score average						0.30611429	

Table 72: F1-Scores for the knn model for 5 runs of 10-fold cross validation for yeast_me2 dataset

Oversampling models	knn1	knn2	knn3	knn4	knn5	mean	sd
Base	0.517	0.524	0.518	0.519	0.537	0.523	0.00827647
SMOTE	0.809	0.855	0.819	0.839	0.849	0.8342	0.01962651
bl1	0.797	0.809	0.799	0.791	0.793	0.7978	0.00701427
bl2	0.781	0.791	0.815	0.783	0.784	0.7908	0.01404279
SVM	0.782	0.783	0.785	0.786	0.789	0.785	0.00273861
ADA	0.804	0.841	0.817	0.818	0.845	0.825	0.01739253
LoRAS (Em=r,p=NA)	0.833	0.84	0.836	0.853	0.852	0.8428	0.00920326

Table 73: Balanced accuracies for the knn model for 5 runs of 10-fold cross validation for yeast_me2 dataset

Dataset: credit fraud

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Base	0.674	0.693	0.682	0.687	0.683	0.6838	0.00499166
SMOTE	0.113	0.13	0.133	0.143	0.15	0.1338	0.00920145
bl1	0.229	0.254	0.241	0.219	0.228	0.2342	0.01528616
bl2	0.173	0.161	0.174	0.19	0.187	0.177	0.0132916
SVM	0.282	0.305	0.276	0.262	0.273	0.2796	0.01834848
ADA	0.109	0.132	0.125	0.127	0.123	0.1232	0.00386221
LoRAS (Em=t,p=30)	0.56	0.544	0.558	0.595	0.539	0.5592	0.02531139
F1-Score average						0.31297143	

Table 74: F1-Scores for the lr model for 5 runs of 10-fold cross validation for credit fraud dataset

Oversampling models	lr1	lr2	lr3	lr4	lr5	mean	sd
Base	0.83	0.846	0.833	0.84	0.838	0.8374	0.00622896
SMOTE	0.923	0.93	0.928	0.934	0.934	0.9298	0.00460435
bl1	0.927	0.93	0.928	0.93	0.928	0.9286	0.00134164
bl2	0.926	0.932	0.93	0.932	0.931	0.9302	0.00248998
SVM	0.927	0.924	0.927	0.925	0.924	0.9254	0.00151658
ADA	0.922	0.932	0.932	0.93	0.927	0.9286	0.004219
LoRAS (Em=t,p=30)	0.904	0.905	0.904	0.906	0.904	0.9046	0.00089443

Table 75: Balanced accuracies for the lr model for 5 runs of 10-fold cross validation for credit fraud dataset

Oversampling models	rf1	rf2	rf3	rf4	rf5	mean	
Base	0.67	0.669	0.664	0.667	0.675	0.669	0.00464579
SMOTE	0.36	0.366	0.355	0.359	0.357	0.3594	0.00478714
bl1	0.644	0.639	0.662	0.644	0.64	0.6458	0.01071992
bl2	0.552	0.545	0.571	0.55	0.562	0.556	0.01174734
SVM	0.743	0.741	0.745	0.741	0.739	0.7418	0.00251661
ADA	0.35	0.354	0.348	0.348	0.351	0.3502	0.00287228
LoRAS (Em=t,p=30)	0.821	0.823	0.82	0.818	0.82	0.8204	0.00206155
F1-Score average						0.5918	

Table 76: F1-Scores for the rf model for 5 runs of 10-fold cross validation for credit fraud dataset

Oversampling models	rf1	rf2	rf3	rf4	rf5	mean	sd
Base	0.775	0.775	0.772	0.774	0.779	0.775	0.00254951
SMOTE	0.922	0.923	0.922	0.922	0.925	0.9228	0.00130384
bl1	0.92	0.92	0.919	0.918	0.918	0.919	0.001
bl2	0.919	0.919	0.919	0.92	0.92	0.9194	0.00054772
SVM	0.914	0.914	0.913	0.914	0.911	0.9132	0.00130384
ADA	0.922	0.925	0.922	0.924	0.925	0.9236	0.00151658
LoRAS (Em=t,p=30)	0.905	0.906	0.904	0.904	0.904	0.9046	0.00089443

Table 77: Balanced accuracies for the rf model for 5 runs of 10-fold cross validation for credit fraud dataset